The 2022 SACNAS National Diversity in STEM Conference

October 27-29
in
San Juan, Puerto Rico

Abstract Book

Table of Contents

Student Poster Presentations

Influence of Biomolecules on ZIF-67 Metal-Organic Framework Nucleation and Growth

Discipline: Chemistry

Subdiscipline: Inorganic Chemistry

Saira Cazarez*[1], Joe Patterson[2], Rakia Dhaoui[3]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: The grand challenge in immobilization strategies for enzymes is the development of methods that result in high loading of the active form of the enzyme, as enzyme immobilization often results in loss of enzymatic activity. An emerging technology in this area is the use of metal-organic frameworks (MOFs) as support material. MOFs are porous crystalline materials assembled using inorganic metal nodes and organic linkers to form extended multidimensional structures. The overall MOF structure acts as a protective structure, where the enzymes enter the nanoscale pores of the MOF crystals (E-MOFs), allowing for dramatically increased enzyme stability. However, controlling E-MOF formation is yet to be fully realized due to insufficient understanding of the governing nucleation and growth mechanisms in E-MOF systems. The objective of this project is to obtain an in-depth analysis on nucleation and growth processes, with particular focus on how the amorphous precursors control nucleation of the hybrid E-MOF systems. To achieve this the structural evolution of E-MOFs using ZIF-67 and model protein BSA have been probed by cryo-transmission electron microscopy, revealing non classical pathways of crystal growth. The intermediate and final p-MOFs were additionally characterized by powder X-ray diffraction to assess purity, scanning electron microscopy to gain morphological-level understanding, and by UV-visible and nuclear magnetic resonance spectroscopies for molecular-level assessment. We hope to provide key information regarding the connection between synthesis conditions (i.e., ligand: metal ratio, enzyme concentration, solution pH) and E-MOF properties resulting in a synthetic biological hybrid system that can be used to develop next-generation materials.

Effect of red irradiance on the light-harvesting of coastal and oceanic strains of the diatom Phaeodactylum tricornutum

Discipline: Chemistry

Subdiscipline: Physical Chemistry

Muhammed Buhari*[1], Meghana Nittala[2], Dr. Sara Massey[3]
[1]Southwestern University, Georgetown University, [2]Southwestern University, [3]Southwestern University

Abstract: Photosynthetic Diatoms inhabit various aquatic systems. The fucoxanthin chlorophyll a/c binding protein (FCP) is a unique light-harvesting antenna complex in diatoms that is highly capable of absorbing blue-green light. These antennas move excitations via consecutive downhill energy transfers to photosystem cores, where charge separation leads to photosynthetic reactions. Preliminary results show subtle differences in energy transfer between the coastal and oceanic variants of the diatom Phaeodactylum tricornutum grown in neutral conditions. Due to varying irradiance qualities in coastal and oceanic habitats, we hypothesized that diatoms from such locations would present differences in their light-harvesting machinery and energy transfer pathways when grown under more stressful qualities of light. In the current study, we have grown our diatoms in three different light conditions— Daylight (HL) at 40 μmol/m2s, Low white-Light (LL) at 20 μmol/m2s, and red-light (RL) 630 nm at 20 μmol/m2s. We measured pigment absorption and characterized the growth rate of each strain under different light conditions using UV-Vis spectroscopy. When grown under these stressors, coastal and oceanic diatom light-harvesting shows more pronounced spectral differences. Under white-light, both coastal and oceanic diatoms have similar growth rates. However, the coastal strain exhibited a faster growth rate under red light incubation compared to the oceanic diatom. We are currently using fluorescence lifetime spectroscopy to study energy transfer dynamics of coastal and oceanic species under white and red light. The effects of our analysis reveal how photosynthetic organisms can fine-tune their light-harvesting systems to better acclimate to environmental stressors.

Heavy Metal Detection and Quantification on Blow Fly (Diptera: Calliphoridae) Larvae and Potential Forensic Entomotoxicology Applications

Discipline: Chemistry

Subdiscipline: Chemistry (general)

Daniela Bermeo G*[1], Cathleen Doherty[2], Denise Gemmellaro[3]

[1]Kean University, [2]Rutgers University, [3]Kean University

Abstract: Insects are quite cosmopolitan and are exposed to a wide range of biotic and abiotic conditions. These conditions may result in insects accumulating xenobiotics present in their food and environment. Blow flies (Diptera: Calliphoridae) will colonize and start feeding on corpses shortly after death; because of this, they are often used to estimate the minimum post-mortem interval (mPMI). Forensic entomotoxicology focuses on the use of insects to identify xenobiotics which may have been present in the corpse; these substances can also have an influence on the developmental time of the insects and consequently, this can have an impact on the estimation of mPMI. Heavy metals are toxic and non-biodegradable elements and their presence in the environment can be used to indicate health risk for all exposed living organisms. The objective of this study was to develop a protocol for the detection and quantification of heavy metals in Calliphoridae larvae. Metal accumulation and distribution were analyzed in the gut content and cuticle of the larvae; these were compared to the heavy metals detected in tissue samples of the carcass and in the soil. The results represent a first step towards a more structured protocol for the analysis of heavy metals from insects and towards a better understanding of how calliphorids accumulate metals. Future work will assess the influence of heavy metal levels and larval growth and will refine the way that Calliphoridae can be used in forensic entomotoxicology investigations.

Aroma volatiles of basil (Ocimum spp) as Impacted by variety and time of day.

Discipline: Chemistry

Subdiscipline: Analytical Chemistry

Victoria Casimir*[1], Alex Barrett[2], Utsav Kumar[3], Ariane Vasilatis[4], James E. Simon[5]

[1]University of Puerto Rico, Rio Piedras Campus, [2]New Use Agriculture and Natural Plant Products Program, Rutgers University, Department of Plant Biology-Foran Hall, 59 Dudley Road New Brunswick1, New Jersey 08901, [3]New Use Agriculture and Natural Plant Products Program, Rutgers University, Department of Plant Biology-Foran Hall, 59 Dudley Road New Brunswick, New Jersey 08901 and Soli Organics, 3156 N Valley Pike, Harrisonburg, VA 22802, [4]New Use Agriculture and Natural Plant Products Program, Rutgers University, Department of Plant Biology-Foran Hall, 59 Dudley Road New Brunswick1, New Jersey 08901, [5]New Use Agriculture

and Natural Plant Products Program, Rutgers University, Department of Plant Biology-Foran Hall, 59 Dudley Road New Brunswick1, New Jersey 08901

Abstract: The aromatic profile of plants can vary in response to environmental changes and cultural practices. Harvest time, the genetics of the plant and the stage of maturity can also have significant effects on the essential oil profile and thus the aromatic bouquet of culinary herbs. Understanding the accumulation pattern of aroma compounds over the day is a fundamental step in product standardization and the establishment of protocols that fosters consistent and reliable results when addressing biological question. For commercially important crops such as sweet basil, elucidating the effect of these conditions can provide a way to optimize future harvest timelines. Specific aromatic profiles can then be targeted through harvest at defined time points, to maximize the ratio and accumulation of targeted aromas. In this study we examine the aroma profile of three varieties of sweet basil (Ocimum basilicum L.): Rutgers' Devotion DMR, Burpee's Sweet Genovese, and a Thai basil, Queenette Thai (QT) basil, over the course of a single day. The time points studied were 5:30 am, 9:00 am, 12:00 pm, 3:00 pm and 6:30 pm. Basil aroma compounds will be analyzed using gas chromatography mass spectrometry (GC-MS) and a solid phase microextraction (SPME) methodology.

Nest Building Behavior in Mice after Withdrawal from Voluntary Binge-Like Ethanol Consumption

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Cecilia Pareja*[1]and Dr. Amanda Barkley-Levenson [2]
[1]The University of New Mexico, [2]The University of New Mexico

Abstract: Alcohol use disorder (AUD) is a neuropsychiatric and neurological diagnosis characterized by uncontrollable alcohol use due to physical or emotional dependance or a combination of both, which affects 14.1 million American adults and 414,000 American adolescents. Alcohol withdrawal in humans can produce serious physical and mental side-effects. In some individuals, desire to avoid withdrawal symptoms may also increase risk of relapse. My study will evaluate the nesting behavior of laboratory mice and how this behavior is affected by voluntary binge-like drinking episodes and withdrawal after these episodes. Nest building is very important for the survival of wild mice and is also a highly conserved behavior in laboratory animals. Analyzing the nest building behavior of mice can provide insight on how alcohol withdrawal impacts instinctual survival behaviors in mice. Previous research has shown deficits in nest building behavior in mice after alcohol withdrawal from chronic ethanol vapor inhalation, but it is unknown whether voluntary binge-like drinking produces similar changes. We hypothesize that inbred C57BL/6J mice will demonstrate decreased nest building activity and worsened nest quality after bouts of voluntary binge-like drinking of a 20% ethanol solution during a four-day drinking in the dark (DID) test compared to mice drinking water in the DID test. We will use a five-point rating scale developed by Deacon to classify nest building prior to drinking, 24 hours into withdrawal, and 7 days into withdrawal to assess the association between binge-like alcohol consumption and nest building during early and protracted abstinence.

Biodegradable polymer nanocomposites for controlled release of phosphorus during the plant growth

Discipline: Chemistry

Subdiscipline: Analytical Chemistry

Sumayo Mahad*[1]and Shital Vaidya [2]

[1]University of Minnesota, Twin Cities, [2]Connecticut Agriculture Experiement Station (CAES)

Abstract: Phosphorus is an essential element required for plant growth, especially root development. With the application of conventional phosphorus fertilizers long-term phosphorus unavailability occurs, due to the depletion of plant-usable phosphorus from runoff, leaching and the formation of complex insoluble phosphates. We are using recent advancements in nanotechnology to address the problem of unavailability of phosphorous in soil for plant use. Our collaborators at John Hopkins University have developed fertilizer composites using biodegradable polymers, including polyhydroxyalkanoate (PHA) and cellulose, to incorporate phosphorus fertilizers such as superphosphate, calcium pyrophosphate and hydroxyapatite nanoparticles. At CAES, we assessed polymer fertilizer nanocomposite performance in greenhouse studies using tomato plants by measuring microbial biodegradation of the polymers, the release of phosphorus, and the leaching of phosphorous in soil microcosms. Our studies suggest that the developed polymer-fertilizer composites can effectively deliver phosphorus during plant growth while dramatically reducing run-off and may also confer resistance to drought stress.

Comparison of groundwater and surface water dissolved organic matter in Kansas intermittent streams

Discipline: Chemistry

Subdiscipline: Analytical Chemistry

Jayde Schlesener*[1], Amy Burgin [2], Kaci Zarek[3], Connor Brown[4]

[1]University of Kansas, [2]University of Kansas, [3]University of Kansas, [4]University of Kansas

Abstract: Due to climate change and the increased frequency of droughts, once perennially flowing streams are becoming more intermittent, meaning they go dry and rewet. These periods of intermittency have potential to disrupt normal biogeochemical processes such as carbon cycling. However, even with the increased intermittency, intermittent streams and their biogeochemical processes remain understudied. Therefore, we will investigate the differences in the quality and quantity of dissolved organic carbon (DOC) between two intermittent watersheds in Kansas to address this research gap. Previous analyses indicate our two study sites have dramatically different DOC concentrations in the outflow streams. We asked: why do these environmentally similar watersheds vary in DOC concentrations and what are the different sources in DOC? To answer this question, we collected surface and groundwater samples from seven stream sites draining the Konza Prairie and Youngmeyer Ranch. We used two methods to examine the bioavailability and complexity of DOC. Our first method quantified the DOC bioavailability via a month-long incubation wherein loss of DOC due to microbial breakdown was quantified. The second method measured the complexity of the DOC over time in both watersheds. This second method used fluorescence spectroscopy to get the fluorescence and freshness indices and a total organic carbon analyzer to measure DOC concentrations at our 14 sites. Quantifying the complexity and bioavailability of the DOC will help us to better understand how stream drying affects biogeochemical processes like sources of organic carbon. We can also infer potential implications of drying events on downstream water quality.

Investigating Liquid-Liquid Phase Separation/Transition and pH Effects on Virus Transmission

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Kayla McCreary*[1], Qishen Huang [2], Miriam Freedman[3]
[1]Pennsylvania State University, [2]Pennsylvania State University, [3]Pennsylvania State University

Abstract: Viruses can be transmitted via respiratory aerosols. The survivability of viruses in aerosols was found to be sensitive to pH and relative humidity (RH) among other factors. It is suggested that aerosols undergo significant pH changes when expelled from the respiratory system. Additionally, RH changes can cause an aerosol particle to undergo a phase transition. This alters the composition of the droplet, consequently affecting virus survivability. There is a need for the development of a better model to describe these aerosol particle behaviors. More specifically, I am investigating the effects of phase transition and pH in inorganic-protein aerosols on respiratory virus transmission. Phase transitions are observed via an optical microscope. pH measurements are observed via a fluorescence microscope. The RH during measurements were controlled using an environmental chamber. I used, as a model system for respiratory aerosols for investigation of phase transition and pH, respectively, were Bovine Serum Albumin (BSA) with phosphate buffer, and phosphate buffer with fluorescein dye. As a result, I showed how composition affects phase transition behavior. With increasing phosphate buffer content, the deliquescence RH (DRH) was not affected, while the efflorescence RH (ERH) was slightly increased. In summary, I am establishing a ratiometric method, using fluorescein to achieve pH measurement. This highlights the importance for better predictors of virus survivability in virus transmission. In the future, we will characterize aerosol droplet pH under different conditions (e.g. changing RH and changing CO 2 concentration) to study how aerosol pH changes in the ambient environment.

Developing soluble de novo CD20 antigen for advanced therapeutic antibodies

Discipline: Chemistry
Subdiscipline: Other

Kiara Thompson*[1]and Zhiyuan (Zoey) Yao [2]
[1]University of North Carolina at Chapel Hill, [2]University of North Carolina at Chapel Hill

Abstract: Since 1997, Rituximab and other CD20-antibodies have been developed as monoclonal antibodies for treating illnesses like leukemia and non-Hodgkin lymphoma. CD20 is a transmembrane cellular protein expressed during B lymphocyte development and has remained an efficient target for B-cell-generated malignancies. However, due to the insolubility of this protein, studying the native CD20 binding structure with therapeutic antibodies is challenging. The lack of knowledge about CD20 binding and solubility properties makes antibody development methods, such as cell-surface display, inapplicable. In order to utilize CD20 to facilitate antibody drug development for leukemia, we used Rosetta, a computational protein design tool, to engineer a de novo antigen. This antigen maintains the native antigen binding features of CD20 with alterations that increase the stability and solubility, making it compatible for use in antibody development. To validate the binding and stability of the de novo antigen, we expressed the de novo protein along with an anti-CD20 fragment antigen-binding (Fab) antibody— Rituximab, Obinutuzumab, or Ofatumumab. We used Biolayer Interferometry (BLI) to prove the affinity between the de novo antigen with each of the Fabs and Nano Differential Scanning Fluorimetry (nanoDSF) to demonstrate the stability of the de novo antigen. We are currently trying to crystallize the binding complex of de novo antigen with the Fab antibodies and to gain a further understanding of the CD20 binding mechanism to validate the experimental viability of the engineered de novo antigen. These studies will inform design principles for future monoclonal antibody immunotherapies.

Purification and Characterization of a Bacterial Siderophore for Use as a Potential Antimicrobial Agent

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Jeffrey Ocampo*[1], Mark H. Schoenfisch[2], Chris A. Broberg[3]
[1]University of California, Dominguez Hills, [2]University of North Carolina, Chapel Hill, [3]University of North Carolina, Chapel Hill

Abstract: The problem of pathogenic bacteria becoming resistant to conventional antibiotics is an emerging healthcare crisis that has been steadily increasing. A challenge with antimicrobial drug development is finding an effective delivery of drugs to the bacterial cytoplasm. A potential method to bypass this issue may be through the use of modified small molecules which are already being produced and accepted by the pathogen. Siderophores are secondary metabolites common to many bacterial species that serve to chelate metal ions from the environment. In this project, cultures of E.coli NC101 were optimized to maximize expression of yersiniabactin (YBT) by testing media and additives known to increase expression. Subsequent purification was carried out using a combination of solid phase and ethyl acetate extractions. The resulting YBT was characterized and quantified using high performance liquid chromatography (HPLC), mass spectrometry (MS), and nuclear magnetic resonance (NMR) spectroscopy. Once sufficient yields of YBT are obtained, experiments will focus on YBT modifications that alter metal binding affinities and potentially deliver greater concentrations of toxic metal ions to within the bacteria. The ability of chemically modified YBT molecules to target Gram-negative pathogens via YBT receptors remains a future objective in developing a novel anti-bacterial agent based on a virulence factor.

Characterization and Investigation of Meta-Vivianite as a Nanofertilizer

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Emma Khorunzhy*[1], Astrid Jacobson[2], Lauren Bomer[3], Li-Ting Yen[4]
[1]The Colorado School of Mines, [2]Utah State University, [3]University of the Incarnate Word, [4]Utah State University and National Taiwan University

Abstract: The need for increased quality crop yields for the world’s increasing population is compounded by the poor efficiency of traditional bulk fertilization practices. Nanofertilizers show promise as sustainable effective nutritional amendments; however, current research often lacks appropriate controls and environmental checks. This research explores whether chitosan-coated meta-vivianite (CT-mVT) nanoparticles (NPs) supply iron (Fe) and phosphate (P) to plants, how these NPs weather in calcareous soil, and if fluorescence can track NP fate. We hypothesize: 1) slow release of Fe and P from the coated NPs may have higher bioavailability to roots than bulk products, 2) CT-mVT morphology will change more quickly than mVT morphology, and 3) fluorescent coating will provide insight on NP fate in the rhizosphere. Meta-vivianite (mVT) NPs were synthesized and characterized with SEM-EDS to examine nano-size, morphology, and elemental composition. Both fluorescent (fCT-mVT) and normal chitosan have been prepared and used as coatings for mVT. Seedling tissues from pots containing calcareous soil amended with mVT, CT-mVT or FeEDDHA are being assayed for Fe and P content using ICP-MS. Weathering of the mVT and CT-mVT NPs is being studied by adhering the NPs to aluminum stubs, incubating the stubs in calcareous soil planted with wheat or radish, and then collecting the stubs weekly for SEM-EDS analyses. Additionally, radish and wheat will also grow in pots amended with fCT-mVT to observe NP migration with fluorescence microscopy. These studies will aid in understanding the rhizosphere fate of the NPs and their efficacies as fertilizers.

Passive Air Sampling for Outdoor and Indoor Volatile and Ionic PFAS

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Loreto Paulino*[1], Jitka Becanova [2], Rainer Lohmann[3]
[1]University of Guam, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Per- and polyfluorinated alkyl substances (PFAS) have attracted global attention due to their extreme resistance to environmental degradation in aquatic environments, which leads to high toxic levels of PFAS exposure to humans. Currently, there is a growing recognition that air emissions of PFAS, significantly contribute to elevated PFAS exposure to humans. Volatile and neutral precursor PFAS can volatilize from their site of origin into the atmosphere, where they will eventually degrade into stable compounds such as ionic PFAS. Source points of these PFAS air emissions have yet to be fully understood; therefore, novel detection tools are needed to detect these volatile PFAS precursors and ionic PFAS within an air medium. Passive sampling has been proven to be an effective detection tool for the quantification of gas-phase trace organic contaminants such as volatile PFAS. Here we test the first application of an incinerated modified algae and compare it to two other promising PFAS air sampler sorbent materials: polystyrene copolymer resin (XAD) and cyclodextrin. Using two different environments with expected high PFAS concentrations: a carpet store and a wastewater treatment plant, the performance of each sampler will be evaluated based on their PFAS uptake. Volatile PFAS will be analyzed through gas chromatography-mass spectrometry (GC-MS), while Ionic PFAS will be anlayzed through liquid chromatography coupled to mass spectrometry (LC-MS/MS). Furthering research on suitable quality detection tools for PFAS will help pinpoint areas that require immediate attention and emphasize the hazards of PFAS as a whole class rather than only long-chain PFAS.

Optimizing a Cu-catalyzed cross-coupling of terminal alkynes: Insights on mechanism

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Crystal Mendoza*[1]and Blakely Tresca [2]
[1]Kalamazoo College, [2]Kalamazoo College

Abstract: Self-assembled materials are of great interest to chemists as chemical building blocks to produce diverse functional materials. Amphiphilic polymers self-assemble into stable nanosheets. Stabilization of these sheets relies on unique folding of the polymers and aggregation of hydrophilic sidechains. However, challenges faced with these materials is long-term instability due to the weak non-covalent interactions holding them together. One solution to overcome this challenge is topochemical polymerization to covalently cross-link polymers after self-assembly by reacting monomers in the crystalline state with heat or light. We set out to optimize the synthesis of 1,3-diyne amines as topochemical reactive monomers and better understand the mechanism of this asymmetric alkyne coupling reaction. Prior research introduced Cu(0) as a great catalyst for the asymmetric Glaser-Hay reaction by dissolving Cu(0) in TMEDA when reacting two terminal alkynes. When recreating this reaction for our target monomer, the desired unsymmetric product is produced in a very low and irreproducible yield with Cu(0). We report optimized conditions for the general Glaser-Hay reaction to significantly improve the yield of the asymmetric diyne product and, most importantly, the reproducibility of this reaction. A mixture of Cu(0) and Cu(I)Cl with a mixture of CHCl3:Dioxane (1:1) yielded the desired asymmetric product, up to 40%. These results are surprising due to previous reports with Cu(I)Cl alone. Our products were analyzed via GC/MS and NMR spectroscopy. Presented in this study is the mechanism of the optimized conditions . We hope to scale up the optimized reaction for new diyne monomers to incorporate into self-assembled polymers.

Synthesis and Biochemical Evaluation of Potential Inhibiting Features of Fmoc-Amino Amide Analogues on Butyrylcholinesterase for the Treatment of Alzheimer’s Disease

Discipline: Chemistry
Subdiscipline: Other

Serli Khanbabaei*[1]and Dr. Jason Schwans [2]
[1]California State University, Long Beach, [2]California State University, Long Beach

Abstract: Alzheimer’s Disease (AD) continues to affect millions of people worldwide. While there’s no cure for AD, multiple approaches are being developed. One of these approaches involves cholinesterases, enzymes involved in neuronal signaling, which have been a target due to the changes in activity observed in individual with AD. The enzymes hydrolyze the substrate, acetylcholine, a cationic neurotransmitter. Butyrylcholinestrase (BChE) is one of the two major classes of cholinesterases found in the parasympathetic nervous system. Previous studies have reported that BChE activity has been upregulated in patients with Alzheimer’s disease. Amino acid analogs bearing a 9-fluorenylmethyloxycarbonyl (Fmoc) group serve as selective inhibitors of BChE. Although Fmoc amino acids inhibit BChE, their negatively charged carboxylate group could be unfavorable in binding the enzyme. To test this hypothesis, a series of neutral Fmoc-bearing amino amides are being synthesized and biochemically evaluated. The amino amides are synthesized one step from the corresponding amino acid, purified, and characterized by NMR. The IC50 and KI values obtained from the enzyme inhibition assays were used to compare the inhibitory efficiency of the amidated Fmoc-amino acid (Leucine in this case) analog to anionic Fmoc-Leu-O - . Initial results suggest that Fmoc-Leucine-NH 2 is a more potent inhibitor compared to Fmoc-Leucine-O - , supporting the model that the negative charge is unfavorable in binding the enzyme. A series of amino amides are currently being further investigated for their selectivity, reversibility, and type of inhibition. Fmoc-amino acid scaffolds study parameters important for cholinergic inhibition, serving as potential treatment of AD.

A Fluorogenic Sensor for Detection of the Pre-Exposure Prophylaxis (PrEP)-HIV Drug Emtricitabine (FTC)

Discipline: Chemistry
Subdiscipline: Other

Rolando Albarracín Rivera*[1], Jonathan T. Sczepanski [2], Chen-Hsu Yu[3]
[1]University of Puerto Rico at Cayey, [2]Texas A&M University, [3]Texas A&M University

Abstract: The development and approval of Pre-exposure prophylaxis (PrEP) drugs for the prevention of HIV has been one of the most important breakthroughs in the history of the disease. Although HIV infection percentages have gone down over the years, there is still a significant number of people diagnosed with the disease due to inefficient adherence to the PrEP drug treatment. Current strategies for monitoring adherence to PrEP drugs have several disadvantages. For example, the current gold standard for monitoring PrEP drug levels in the body – liquid-chromatography -tandem-MS (LC-MS/MS) - relies on expensive equipment and scientifically-trained personnel to operate, and thus, is not compatible with monitoring therapy adherence at the point-of-care, especially in low-resource settings. In this work, we report an aptamer-based sensor for the PrEP drug Emtricitabine (FTC) that enables rapid determination of FTC concentrations in solution via a simple optical readout. This analysis has been achieved by a succession of binding experiments to a modified fluorogenic aptamer complex that is based on a novel FTC-binding aptamer. Overall, we conclude that the aptamer-based FTC sensor provides a simple, biocompatible, and cost-effective strategy for monitoring FTC in solution. This work lays the foundation for a novel objective adherence method that could serve as a tool for decreasing the risk patients have for contracting HIV.

Assessing Stability of Iron-Based Porphyrin Frameworks as Antidotes to Carbon Monoxide Poisoning

Discipline: Chemistry
Subdiscipline: Other

Matteo Anicetti*[1]and Leila Parker [2]
[1]Monterey Peninsula College, [2]University of California, Santa Cruz

Abstract: With 50,000 annual instances of hospital admittance and hundreds of thousands of deaths on record, carbon monoxide (CO) poisoning has been a consistent and deadly threat since the very beginnings of broad scale industrialization. The Johnstone Lab has recently developed iron(II)-porphyrin compounds featuring bulky, phenyl based substituents as viable candidates for an antidote to CO poisoning. These porphyrins are highly effective in their ability to strongly bond CO, and abstract CO from carboxyhemoglobin. Consequently, these iron(II)-porphyrin based compounds have proved both expedient and efficient in their ability to rescue CO-poisoned red blood cells. However, questions remain concerning the stability of both the iron(II)-porphyrin complexes, as well as their iron(II)-carbonyl adducts. Using IR and UV-vis spectroscopy, we will measure the elapsed time of the iron(II)-porphyrin and iron(II)-carbonyl adduct complexes to oxidize from iron(II) to iron(III). I will discuss the variation in the rate of oxidation as it pertains to the steric and electronic properties of the individual compounds. With the resulting data from this study going on to be essential for the design of further, more effective candidates for CO poisoning antidotes.

Synthetic approaches to prenylated coumaric derived natural products against type 2 diabetes

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jason Huang*[1], Taotao Ling [2], Jacqueline M Stephens[3], Fatima Rivas[4]

[1]Louisiana State University and Agricultural and Mechanical College, Baton Rouge, [2]Professor, [3]Professor, [4]Professor

Abstract: The natural product capillartemisin A is found in the plant Artemisia Scoparia, and it features a unique structural combination of a p-coumaric acid and prenylated substituents. Capillartemisin A has been reported to ameliorate the effects of type 2 Diabetes Mellitus (T2DM) through in vitro studies. T2DM occurs when the human body's cells resist the normal effects of insulin, which is to drive glucose in the blood into the cells. The incidence of T2DM has significantly increased in the United States, therefore new therapeutic strategies are needed. Herein, we present a synthetic strategy using a series of chemical reactions including oxidation, keto enol tautomerization, wittig and electrophilic aromatic substitution reactions to develop an efficient synthetic approach to access capillartemisin A. The chemical reactions will be conducted under anhydrous conditions in suitable organic solvents and monitored by thin-layer chromatography (TLC). The reaction mixtures will be worked-up with aqueous solutions, after organic layer separation, the solvent will be concentrated via evaporation. Then, the residue will be purified by normal phase silica gel column chromatography and characterized via NMR spectroscopy. The desired natural product will be compared to authentic samples available. Capillartemisin A and its derivatives will be tested via a broad range of in vitro and in vivo biological assays to investigate their mode of action. It is anticipated that an efficient synthesis to capillartemisin A and its derivatives will provide new potential therapeutic strategies to treat the rising costs and high mortality of T2DM.

Investigating the photoelectrochemical activity of Zirconium-doped hematite

Discipline: Chemistry

Subdiscipline: Physical Chemistry

Chloe Cornejo*[1], Yat Li[2], Sam Eisenberg[3]

[1]Cabrillo College, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: There is a current global energy crisis and alternate means of harvesting & storing energy such as the use of photoelectrochemical (PEC) cells have been a topic of high interest. These devices harness solar energy and convert it to chemical energy via water splitting in the form of hydrogen gas. A cheap and efficient semiconductor light absorber is necessary to accomplish a potential wide-scale implementation of these environmentally sustainable PEC cells. Hematite (Fe 2 O 3) is a promising candidate due to its non-toxicity, favorable band gap, abundance, and photochemical stability. Hematite as a material has been held back however by its relatively poor electrical conductivity. A common strategy that has been used to increase the conductivity of hematite is through the doping method, selectively inserting dopant ions into the Fe 3+ crystal lattice, with a tetravalent ion such as tin or titanium. The ion Zirconium (Ⅳ) presents itself as a good candidate due to its relative abundance and similar ionic radius to Fe 3+ . Zirconium (Ⅳ) has also not been as thoroughly investigated as other dopants. Zirconium (Ⅳ) will be doped into hematite using a high-temperature annealing process at varying concentrations. The photoelectrochemical performance of doped hematite will be analyzed with linear sweep voltammetry & chronoamperometry and compared to the pristine hematite.

In Situ Polymerization of Acrylic Acid Using DBD Plasma For Non-Contact Polymerization in Mesoporous Materials

Discipline: Chemistry

Subdiscipline: Chemistry (general)

Sky Harper*[1]and Haifeng Ji [2]
[1]Drexel University, [2]Drexel University

Abstract: Polymers can be found everywhere—both naturally occurring or artificially synthesized such as starch and toothpaste. New methods for polymer synthesis are at the forefront of materials research due to their ideal mechanical and chemical properties, such as strength, hardness, and durability. Properties can be influenced by polymer length and polymerization conditions. This research investigated a novel dielectric-barrier discharge (DBD), non-thermal plasma-based approach to preparing poly (acrylic acid) (PAA) in situ. The goal was to achieve a reduction in the energy and preparation time required to prepare PAA on specific surfaces such as porous materials, which has proven a challenge for different methods of polymerization such as UV, thermal, and traditional hot plasma polymerization. This work generated data that will provide guidance for the overall efficiency, such as the cost and polymerization time of the DBD plasma approach for the treatment of polymer coatings. This research will study the plasma-initiated polymerization of PAA and display the concept of remote polymerization. This efficient method could be applied in the industrial setting. The DBD plasma-initiated polymerization of AA will be explored with a focus on the kinetics and mechanism of polymerization and we will compare our PAA data to other studies using different polymerization methods.

Studying Lactate Metabolism in Cardiomyocytes During Hypertrophy and Heart Failure

Discipline: Chemistry
Subdiscipline: Other

Kaila Toledo*[1], Dr. Jared Rutter [2], Dr. Ahmad A. Cluntun[3]
[1]Weber State University, [2]University of Utah, [3]University of Utah

Abstract: Heart disease is the second leading cause of death in the American Indian and Alaska Native population, with about 14% relating to heart failure. Heart failure is a cardiovascular disease, resulting from the heart’s limited ability to fill and/or pump blood throughout the body. It is known that cardiomyocytes do not contain fuel reserves and thus their metabolism is flexible and dynamic to maintain sufficient ATP production to support the heart’s continuous pumping of blood. We have previously identified the pyruvate-lactate metabolic axis as a critical node in heart biology. The mitochondrial pyruvate carrier (MPC) and the lactate exporter, monocarboxylate transporter 4 (MCT4), are essential control points for this axis. However, how lactate consumption and metabolism affects the pyruvate-lactate axis in the heart remains poorly understood. We will perform 13 C heavy carbon lactate stable isotope tracing experiments in H9c2 cardiomyoblast cells in combination with various hypertrophic inducing drugs to begin to understand lactate metabolism under these conditions. We will also utilize VB124, an MCT4 inhibitor, to mitigate hypertrophy and determine its effects on lactate utilization and flux. These experiments will expand our current knowledge of heart metabolism and potentially identify novel therapeutic targets to treat this condition.

Analyzing Catecholamine Concentrations in Different Models of High Grade Serous Ovarian Cancer

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Lana Ibrahem*[1], Hannah Lusk [2], Laura Sanchez[3]
[1]Monterey Peninsula College, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: High-grade serous ovarian cancer (HGSOC) is a highly aggressive gynecologic malignancy, and the fifth leading cause of cancer-related deaths among women. HGSOC originates in the fallopian tube via the transformation of fallopian tube epithelial cells, which metastasize to the ovary (primary metastasis), and spread into the peritoneal cavity (secondary metastasis). We hypothesize this spread is governed by the exchange of small-molecules between ovarian cancer cells and the ovary and omentum. Loss of tumor suppressor, PTEN , is the only single-gene alteration capable of inducing spontaneous tumor formation in murine models of HGSOC; thus, a murine oviductal epithelial (MOE) cell line with stably expressed shRNA directed at PTEN (MOE PTEN shRNA) represents our disease model. Norepinephrine is a chemoattractant secreted from murine ovaries co-cultured with MOE PTEN shRNA cells, but not healthy cell controls – suggesting involvement of catecholamine signaling in primary metastasis. My research project is to assess the role of catecholamine signaling in HGSOC metastasis by developing a method for the extraction, isolation, and absolute quantification of norepinephrine, epinephrine, and dopamine from ovarian co-cultures using ultra-high performance liquid chromatography coupled to mass spectrometry. We plan to quantify catecholamine production in ovarian co-cultures with different ovarian cancer cell lines that have different mutations representing varying stages of disease progression. Our goal is to relate catecholamine production to both cancer pathway modifications and survival times in murine models. This will reveal how catecholamine production relates to disease aggressiveness, which is critical to understanding the significance of this pathway in HGSOC.

Antimicrobial Properties of Silver Nanoparticles Conjoined with Self-assembling Peptides

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Amaya Pablo*[1]and Dr. Naomi Lee [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: Silver is used to combat antimicrobial resistance due to its antimicrobial properties. However, the nanoparticles' antimicrobial efficiency is dependent on size, shape, chemical composition, and spatial distribution. Hybrid structures composed of self-assembling peptides that form amyloid-like fibrils were reported to increase the bioactivity and biocompatibility of displayed silver ions and nanoparticles. Thus, we hypothesize self-assembling peptides displaying silver nanoparticles will increase bioactivity against antimicrobial resistant bacteria by controlling silver ion concentrations on peptide-based scaffolds. To test the hypothesis the self-assembling peptides Ac-FKFEFKFE-NH_2 (KFE8) will be utilized due to its amphiphilic properties. Synthetic derivatives will also be synthesized, Ac-FKFEFKFC-NH_2 and Ac-C(FKFE)$_2$-NH_2 , to bond seamlessly with silver nanoparticles. The peptides will be synthesized using standard Fmoc-based chemistry and rink amide resin. The purity (%) of the peptide will be determined by reverse-phase HPLC. MALDI-TOF mass spectra will be utilized to characterize the molecular weight of the KFE8 peptides. Finally, the lyophilized peptide will be tested for fibrillization. The secondary structure of fibrils will be determined using TEM, FT-IR, and CD spectroscopy. The silver nanoparticles will be synthesized and characterized by the collaborators. Eventually, the silver nanoparticles will be conjugated to the fibril surface using a bifunctional linker. Future studies aim to assess the biocompatibility and bioactivity of the silver particle-fibril complexes.

Biocatalytic deuterium incorporation into amino acid substrates by PLP-dependent enzyme GntC

Discipline: Chemistry
Subdiscipline: Other

Alondra Maranon Rodriguez*[1], Jennifer Cordoza [2], Shaun McKinnie[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: The substitution of hydrogen atoms with their slightly heavier isotope deuterium (D) is a conservative chemical change that can have a dramatic impact on a compound’s bioactivity. Select addition of D atoms can improve the pharmacokinetics of existing drugs by reducing their oxidative metabolism, leading to an increase in their in vivo circulation and physiological effects. This strategy has been previously employed to enhance the lifespan of pharmaceutical agents like deutetrabenazine (Huntington’s disease treatment), RT001 (neurodegenerative diseases), and notably, the modified amino acid d 3 -L-DOPA (Parkinson’s disease). While chemical strategies exist to incorporate D atoms into drug-like molecules, biocatalytic approaches using pyridoxal-5’-phosphate (PLP)-dependent enzymes have become increasingly popular due to their environmentally-friendly conditions and use of deuterium oxide (D 2 O) as a D source. Recently, our lab collaboratively elucidated the biosynthetic pathway of guanitoxin, a potent cyanobacterial neurotoxin. The second biosynthetic step uses the PLP-dependent enzyme GntC to catalyze an intramolecular cyclization on a modified arginine substrate. In vitro D 2 O protein assays and liquid chromatography-mass spectrometry analyses have identified that GntC incorporates up to three D atoms in both its product and substrate. Subsequent investigation into GntC has identified that it efficiently deuterates polar and positively charged amino acids, deviating from the substrate scope of previously established PLP-dependent biocatalysts. We are continuing to investigate the applicability of GntC to produce scalable quantities of deuterated amino acid-like molecules. We intend to use this biocatalytic tool to produce deuterated substrates for use as late-stage intermediates in biomedical research.

Designed Multiple Ligands as Potential Agents Against Alzheimer's Disease and Chronic Pain

Discipline: Chemistry
Subdiscipline: Other

Ryan West*[1]and Dr. Stevan Pecic [2]
[1]California State University, Fullerton, [2]Assistant Professor Medicinal and Bioorganic Chemistry

Abstract: Alzheimer’s Disease (AD) is a major health crisis in the human population. While AD is a multifactorial disease, current therapeutics focus on inhibiting acetylcholinesterase (AChE). This enzyme is responsible for the hydrolysis of the neurotransmitter acetylcholine (Ach), which is primarily responsible for learning and memory. According to the Cholinergic hypothesis, decreased concentrations of Ach can be counteracted by inhibiting AChE. Increased levels of Ach show improved cognition and global function. AD is often co-morbid with chronic neuropathic pain. Based on a recent study, the reported prevalence of chronic pain in AD patients was 45%. Endogenous pathways utilizing endocannabinoids appear to be safer alternatives to currently

available chronic pain medication. Endocannabinoids are both produced and broken down by the body. The enzyme fatty acid amide hydrolase (FAAH) is responsible for the breakdown of specific endocannabinoids that provide analgesic effects and anti-neuroinflammation. The long-term goal of our lab is to develop dual inhibitors, a small molecule that can act simultaneously on both aforementioned biological targets involved in the pathogenesis of AD. We have synthesized several libraries of donepezil-based AChE inhibitors and 4-phenylthiazole FAAH inhibitors and were able to identify potent inhibitors of both enzymes, with IC 50 values of 51nM for AChE and 8 nM for FAAH. Using a polypharmacological design approach, we designed and synthesized new dual AChE/FAAH inhibitors libraries. We expect that these small molecules could be more effective for treating AD and related chronic pain and have the potential to prevail over limitations in the current treatments for AD.

Magnetic properties of polar quaternary sulfides

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Nethmi Hewage*[1], Kirill Kovnir[2], Georgiy Akopov[3]
[1]Iowa State University, [2]Iowa State University, [3]Iowa State University and Ames Laboratory

Abstract: The reactivity difference between the elements which are used as reactants in solid-state synthesis has been a main challenge in synthesizing phase pure compounds. Arc melting is a technique that can be used to address this challenge. An innovative synthesis method is done using arc melted precursors and sulfur to form Tb 6 (TM)Si 2 S 14 (TM=transition metals; Fe, Co, Mn) compounds, which crystalize in the noncentrosymmetric, chiral, and polar P63 space group. The precursors made from arc melting react with sulfur at high temperatures providing bulk powders and single crystals of the target quaternary sulfides. Powder X-ray diffraction was used to determine the phase purity of the compounds. Single crystal X-ray diffraction (SCXRD) was used to determine the crystal structure of the compounds. Neutron powder diffraction and Superconducting Quantum Interference Device (SQUID) were done to determine the magnetic properties of Tb 6 FeSi 2 S 14 , Tb 6 CoSi 2 S 14 , and Tb 6 MnSi 2 S 14 . 57 Fe Mössbauer spectroscopy was used to determine the magnetic properties of Tb 6 FeSi 2 S 14 . Mössbauer spectroscopy data showed that most of the spins are in a high spin state at low temperature. This may be due to Fe2+/ Fe3+ oxidation change or due to spin crossover. Further analysis using X-ray magnetic circular dichroism will be done to determine the spin ordering to observe whether it's a spin crossover or a Fe2+/ Fe3+ oxidation change.

Optimizing the fluorescent labeling reaction of amino acids in deep eutectic solvents for use in CE-LIF

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Karen Campos*[1], Jessica Torres[2], Christopher Harrison[3]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University

Abstract: The search for life on other planets is focused on finding biochemical evidence of past life. Amino acids (AA) are a biosignature target for evidence of extra-terrestrial life as they are the building blocks of life on Earth. However, they are expected to be in low abundance (low nanomolar) on planets that once housed life, so sensitive chemical analysis techniques are needed. Capillary electrophoresis with laser-induced fluorescence (CE-LIF) is capable of

nanomolar detection limits for fluorescently labeled AAs. On Earth, organic solvents are used for the fluorescent labeling reactions of AAs, but such solvents are unsuitable on other planets. We are investigating the use of deep eutectic solvents (DES) for the labeling reactions, as they are more suitable for cold, low pressure, environments. Initial results of our new reaction with DES yielded detection limits down to 2 μM using DES as the solvent for the labeling reaction. Adjusting the initial dye to AA ratio from 1:1 to 3:1 has increased reaction efficiency for AA detection four-fold. We aim to further investigate the impact of changing the pH of this reaction. It is expected that by optimizing the labeling reaction, lower concentrations of AA will be quantified, striving for nanomolar detection for future space missions. This poster will present the optimization of the labeling reaction by evaluating the efficiency of the reaction under various parameters. This novel labeling option may be useful for future space exploration, impacting fields of astrobiology and all NASA enterprises.

Using MS2 Virus-Like Particles (VLPs) as Viable Platforms for Human Papillomavirus (HPV) Vaccine Development

Discipline: Chemistry
Subdiscipline: Other

Macie Proctor-Roser*[1]and Naomi Lee [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: The human papillomavirus (HPV) is responsible for over 12,000 cases of cervical cancer in the United States each year. Currently, there are less than five vaccines available to the public and they all utilize the type-specific L1 protein from the HPV capsid. This causes vaccines to have minimal coverage for the wide variety of viral genotypes, especially types that disproportionately burden Indigenous communities. Due to a lack of protection from current vaccines, Indigenous communities have a higher prevalence of HPV infection and cancer rates than the general population. This disparity can be mitigated by expanding vaccine antigenicity to include the L2 peptide consensus sequence (GTGGRTGYVPLGTRPPTVVDV) from the HPV capsid to create a more broadly protecting HPV vaccine. The purpose of this research is to genetically engineer the AB loop of the MS2 VLP to display an additional tyrosine residue for a bio-linker attachment point. This project has two components, the bio-linker formation and the L2 conjugation. MS2 VLPs are the most appropriate choice for this modification due to their ability to spontaneously self-assemble, and high tolerance of heterologous peptide insertions. Methods used include synthesis of MS2 VLPs, polymerase chain reaction cloning into the MS2 AB loop, digestion of products and vectors, ligation and transformation, as well as assays to identify successful insertion and modification. Currently, this research is in the modification and insertion stages of development, with hopes of constructing a vaccine with a multivalent display of HPV L2 peptide antigen in the near future.

Fabrication of Low-cost, Paper-based Electrodes for Detection of Bisphenol Compounds

Discipline: Chemistry
Subdiscipline: Other

Michael Nelwood*[1], Dr. Thiagarajan Soundappan [2], Justin Platero[3], Robinson L. Tom[4], Katelyn Wilson [5], Jasmine Charley[6], Makeiyla Begay[7], Khaled Abdelazim[8], Arul Mozhy Varman[9]

[1]Navajo Technical University, Crownpoint., [2]Navajo Technical University, Crownpoint, [3]Navajo Technical University, Crownpoint, [4]Harvard University, Cambridge, [5]Navajo Technical University, Crownpoint, [6]Navajo Technical University, Crownpoint, [7]Navajo Technical University, Crownpoint, [8]Harvard University, Cambridge, [9]Arizona State University, Tempe

Abstract: Bisphenol (BP) is a chemical additive that strengthens polycarbonate plastics and epoxy resins. Bisphenol, however, is a known toxicant often categorized as an endocrine-disrupting chemical (EDC). Bisphenol absorption in the body has been implicated in contributing to metabolic disorders such as type-2 diabetes, obesity, immune toxicity, and other serious diseases. Approximately 90% of humans accumulate BP levels through exposure to food containers, plastic bottles, thermal printing papers, and other everyday plastic products. This accumulation is of special concern on the Navajo Reservation, which has a high rate of diabetes and obesity. We report the development of low-cost, flexible paper-based electrodes for the electrochemical detection of BP compounds. We fabricated paper-based electrodes using conductive carbon paste in a three-electrode system. We demonstrate that our paper-based electrodes can detect BP at 0.1mM, 0.3mM, 0.5mM, and 1mM concentrations in the laboratory at physiological pH conditions. These results demonstrate that the sensitivity of these electrodes and their linear electrochemical response make them well suited for real-time applications and point detections.

Removal of Organic Pollutants in Aqueous Matrixes using ZnO Photocatalysis

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Kerianys Torres*[1]and Dr. Sonia Bailon Ruiz, PhD [2]
[1]University of Puerto Rico in Ponce, [2]University of Puerto Rico in Ponce

Abstract: Residual dyes from various sources, such as textile and pharmaceutical industries, as well as a wide variety of persistent organic pollutants, have been introduced into our natural water resources or wastewater treatment systems, and are now a major source of water pollution. It is highly toxic and hazardous to living organisms; hence, it is critical to destroy these organic impurities. Conventional treatments have evidenced to be no adequate in the removal of these pollutants in our water resources. However, one effective way to remove them is by a photocatalytic degradation process using semiconductor nanoparticles. Zinc Oxide (ZnO) is a semiconductor material with intrinsic optical and electronic properties and is one of the most used photocatalysts for the degradation of these organic contaminants. In this research, we report the photocatalytic capacity of ZnO NPs in the degradation of Amaranth and Tropaeolin O dyes. Photo-degradation assays were evaluated in the presence of the dyes at different concentrations of ZnO NPs (250 ppm and 500 ppm). Following UV irradiation, the dyes at a certain time, it was found that 500 ppm of ZnO NPs were able to degrade ~74 % and ~80% of Amaranth and Tropaeolin O dye respectively. As in future research, we include on determining the optimum dosage of ZnO NPs and pH value to improve the catalytic activity of the particle.

The Effects of Prune Extract on Cellular Models of Bone Cancer

Discipline: Chemistry
Subdiscipline: Other

Chelsie Miller*[1], Dr. Mowaffaq Adam [2], Dr. Shirin Hooshmand[3], Dr. Changqi Liu[4], Dr. Christal Sohl [5], Grace Chao[6]

[1]San Diego State University, [2]San Diego State University, [3]San Diego State University, [4]San Diego State University, [5]San Diego State University, [6]University of California San Diego

Abstract: There is strong evidence for prunes as a health food for improvement in digestion due to their high fiber content. More recent work has shown that prunes also have a positive impact on bone health, attributed in part to the antioxidant compounds and polyphenols they possess. Despite their important antioxidant role, the anticancer properties of prunes has yet to be determined. We hypothesize that treatment of osteosarcoma cell lines with prune extracts will lead to a decrease in cell proliferation and migration, driven at least in part due to the antioxidant compounds. We will treat chondrocyte and osteosarcoma cell lines with varying concentrations of prune extract, and use a CellTiterGlo assay and in vitro scratch assays to measure the effects on cell proliferation and migration, respectively. A key component of our work is establishing the optimum cell culturing conditions and developing robust protocols for important cancer phenotype assays. This includes making the prune extract of which the cells will be treated. Upon completion of these experiments, we hope to better understand the effects of prunes on bone health and disease.

Targeting enhanced fluorescence with azetidine groups in nucleobase analogues

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Christina Rivera*[1]and Byron Purse [2]
[1]San Diego State University, [2]San Diego State University

Abstract: Fluorescent nucleobase analogues are used to study the structure and dynamics of DNA/RNA folded motifs, lesions, modifications, and binding complexes with proteins. Brightness, photostability, and relatively long absorption and emission wavelengths greater than 400 nm are key enablers of these studies, especially with current interest in single-molecule fluorescence. Prior studies in our lab have led to a new tricyclic pyrimidine nucleoside analogue that exhibits brightness greater than any other FBA when incorporated in oligonucleotides, either single-stranded and duplex. This C -linked 8-(diethylamino)benzo[b][1,8]naphthyridin-2(1 H)-one nucleoside, which we named ABN, is also among the most red-shifted fluorescent nucleobase analogue in duplex DNA, Φ em,540 = 0.50-0.53 when base paired with adenine. As seen in Janelia Fluor dyes, replacing a N , N -dimethylamino in a fluorophore with azetidine greatly improves quantum yield and photostability. This slight modification increased fluorescent lifetime while preserving extinction and emission profiles. I hypothesize that substituting an azetidine ring for the diethylamino group of ABN will result in improvements in quantum yield and photostability. This new fluorescent nucleobase analogue would be beneficial in its utility for labeling, imaging, and detection of DNA/RNA modifications. Details on the design of this new FBA and progress towards its synthesis, characterization, and applications will be presented.

Isolating Prostate Cancer-Selective Naphthoquinone Derivatives from Streptomyces sp. CP59-55

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Devin Simbol*[1], Mark Swanson [2], Frederick A. Valeriote[3], Taro Amagata[4]

[1]San Francisco State University, [2]San Francisco State University, [3]Josephine Ford Cancer Center, Henry Ford Health Systems, [4]San Francisco State University

Abstract: The Amagata research group of San Francisco State University strives to identify cytotoxic secondary metabolites produced by marine-derived bacteria of class Actinomycetia that exhibit strong human solid tumor selectivity. During the testing of more than 500 strains using a cancer cell-based disk diffusion assay, Streptomyces sp. CP59-55 exhibited significant prostate cancer (LNCaP) selectivity and was selected for further study. A reversed-phase high-performance liquid chromatography (HPLC) profile of organic extract from a 1 L medium-scale culture indicated it contained more than 15 nonpolar compounds; UV spectrum analysis indicated these secondary metabolites contained naphthoquinone moiety. Reversed-phase HPLC is being used to purify these compounds prior to structural elucidation through 1 H and 13 C nuclear magnetic resonance (NMR) spectroscopic experiments. Napyradiomycin B4, a known cytotoxic compound, has been identified. New cytotoxic compounds with high LNCaP-selectivity are expected to be discovered as the remaining compounds in Streptomyces sp. CP59-55’s organic extract are characterized.

ANNEXIN A2 EXPRESSION IN PROSTATE CANCER CELLS.

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Charles Gates*[1]and Chaudhary, Pankaj [2]
[1]Langston University, [2]University of North Texas Health Science Center

Abstract: Metastasis is a major cause of morbidity in prostate cancer patients; the primary mortality is metastasis of bone tissue. Despite substantial efforts to understand prostate cancer metastasis, the mechanisms involved in preparing the metastatic niche for colonizing the prostate cancer cells are still unknown. Therefore, there is an urgent need to identify essential regulators of bone metastasis in prostate cancer for therapeutic targets. Annexin A2 is a calcium-dependent phospholipid-binding protein overexpressed in prostate cancer's poorly differentiated high-grade adenocarcinomas. Phosphorylation of AnxA2 at tyrosine-23 creates an important event for the localization of AnxA2 to the cell surface. It provides a binding site for tissue plasminogen activators at the cell surface and converts plasminogen into plasmin, which plays an essential role in the invasion and metastasis of cancer. However, the cell surface expression of AnxA2 in prostate cancer is unknown. Therefore, in the present study, we demonstrated the cell surface expression of AnxA2 in prostate cancer cells to delineate the mechanism of bone metastasis. Prostate cancer cell lines, PC3, and DU145 were grown. Immunoblotting was used to detect the expression of pAnxA2-Y23 and AnxA2 proteins in cells. Our results demonstrated that the expression of pAnxA2-Y23 is very high in prostate cancer cells (PC3 and DU145 cells) compared to normal prostate epithelial cells. However, the expression of total AnxA2 in both prostate normal and cancer cell lines is comparable. Results suggest that the cell surface expression of AnxA2 is high in prostate cancer cells due to increased phosphorylation of AnxA2 at tyrosine 23.

Prepared to Phyte: The Bio-Desalination of Water with Haliphilic Algae

Discipline: Chemistry
Subdiscipline: Other

Ana Barrera*[1]and Hudson DeYoe [2]
[1]University of Texas- Rio Grande Valley, [2]University of Texas- Rio Grande Valley

Abstract: The purpose of this project is to develop a method to reduce water salinity by utilizing macroalgae. Every algae species has a range of salinity tolerance. If placed in higher salinity water, these algae may have the capacity to modestly lower water salinity as they acclimate. Agricultural irrigation water in south Texas has excessive salt content; if treated with macroalgae, the water salinity might be lowered enough to make water more appropriate for irrigation. We assessed the salinity tolerance by culturing the algae in a range of salinities and measure net primary production (NPPR) and respiration rates (RR) at a range of salinities by the light/dark bottle method. By identifying the salt tolerance of an alga, we can explore its capacity to reduce salinity by manipulating salinity levels in a controlled environment. Experimenting with these specific variables, and ensuring they stay viable, we can investigate the limits of each sample. One of the seaweeds seemed to tolerate the salinity changes better than the others so this species was used for the trials to see if it could reduce the salinity of ocean water. In one of the trials, it was found that a red seaweed (Palisada) could reduce seawater salinity by 3 parts per thousand (PPT) and not expire. We concurred that, by allowing the sample to acclimate for a longer time, it would extract significant amounts of salt.

Synthesis and Testing of Natural Products as Treatments for Leishmaniasis

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jasmine Keyes*[1], Kenneth Miller [2], Tristan Huskie[3], Kian Kelly[4]
[1]Fort Lewis College, [2]Fort Lewis College, [3]Fort Lewis College, [4]Fort Lewis College

Abstract: sandfly. There are two common types of leishmaniasis: cutaneous and visceral. The visceral type of the disease causes the enlargement of the spleen/liver and most commonly leads to death. Miltefosine, a common treatment for leishmaniasis, disrupts the synthesis of phosphatidylcholine and inhibits cytochrome c oxidase. However, the drug has shown impaired fertility and toxicity in the liver, renal, and gastrointestinal tracts of the body. The drug is relatively expensive especially in poverty-stricken regions. Thus, the synthesis of a drug from natural products is being considered to lower the costs and decrease the toxicity of anti-leishmanial treatments. This presentation will report the synthesis of deoxyalpinoid B and deoxyalpinoid A through a Myer-Schuster rearrangement. These products are members of a class of compounds called alpinoids, which were isolated from Alpinia officinarum , a medicinal herb native to East Asia. These compounds increase reactive oxygen species (ROS) concentrations in the body. Prior work indicates that species that increase ROS also posses potent anti-leishmanial activity. Given that upregulation of ROS is correlated with anti-leishmanial activity, we queried whether the chosen compounds could function as new treatments for leishmaniasis infections.

Design and Fabrication of Flexible Paper-based, Electrochemical Sensors to Detect the Presence of Heavy Metals in Ground Water

Discipline: Chemistry
Subdiscipline: Other

Justin Platero*[1], Thiagarajan Soundappan [2], Michael Nelwood[3], Samantha Francis[4]
[1]Navajo Technical University, [2]Navajo Technical University, [3]Navajo Technical University, [4]Navajo Technical University

Abstract: The history of mining and mineral extraction across the Navajo Nation has resulted in considerable contamination of the land and the groundwater resources, which is a significant environmental concern. Through a partnership between Navajo Technical University and Harvard University, we have designed and fabricated flexible, paper-based sensors in tandem with electrochemical techniques such as cyclic voltammetry, differential pulse voltammetry, and anodic stripping voltammetry to determine heavy metal concentrations in test samples. We have selected to fabricate paper-based electrochemical sensors because; they are low-cost, easy to make, environmentally friendly, and can be deployed for field testing across the Navajo Nation. We have demonstrated that our electrodes have successfully oxidized lead and arsenic oxide using the techniques stated above. The performance of our electrode is comparable to commercially available electrochemical sensors. Furthermore, the linear electrochemical response and sensitivity of our electrodes, for detecting heavy metals, makes them well suited for real-time sensors in field-testing applications.

Exploring the mechanisms of IDH1 pH sensitivity

Discipline: Chemistry
Subdiscipline: Other

Nicole Sierra*[1], Christal Sohl [2], Elene Albekioni[3], Isaac Marquez[4], An Hoang [5], Mowaffaq Adam[6], Brittany Bermoy[7]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University, [4]San Diego State University, [5]San Diego State University, [6]San Diego State University, [7]San Diego State University

Abstract: Globally, cancer patients are significantly impacted by the proto-oncogene isocitrate dehydrogenase 1 (IDH1). While many cancers are driven by mutations in IDH1, resulting in catalysis of a new reaction that has been shown to drive tumor formation, wild-type (WT) IDH1 has also been shown to drive many cancer types. WT IDH1 drives the oxidative decarboxylation reaction of isocitrate to alpha-ketoglutarate, with concomitant conversion of NADP+ to NADPH. This reaction can support tumor growth by synthesizing alpha keto-glutarate. We know from previous structural informatics and pKa calculations that the residue D273 in IDH1 is sensitive to changes in pH, allowing IDH1 to serve as a pH sensor. By affecting the activity of pH sensors, cellular pH can regulate protein-protein and protein-ligand interactions, including the stability and activity of a protein. D273 is located in the first third of the α10 helix, an important regulatory domain. To determine the role of D273 in pH sensitivity, experimental mutants were designed to have minimal disruption in the overall structure but still destroy the ability of the residue to ionize. The mutants produced very drastic decreases in catalytic efficiency for the forward reaction as compared with WT IDH1. Here we describe the pH sensitivity of a new ionizable mutant, D273E IDH1. Using site-directed mutagenesis, the formation of the D273E mutant was made and the enzyme was heterogeneously expressed and purified. We predict this mutant will retain pH sensitivity when measuring the rates of αKG production since it can change its ionization state.

Computationally Generated Reaction Networks: A Template-Based Tool for Predicting Reaction Outcomes

Discipline: Chemistry
Subdiscipline: Other

Samuel Pavelites*[1], Cody Aldaz[2], Todd J. Martinez[3]
[1]Cornell University, [2]Stanford University, [3]Stanford University

Abstract: To synthesize new products efficiently, chemists plan their syntheses. However, this process is difficult as there are many reactants and reactions to consider. To make this process easier, we have developed a computational tool that identifies how a given molecule could react. This tool uses templates made of essential reaction substructures; when a substructure is detected the reaction proceeds to the creation of a product. Over many applications, this process creates a reaction network containing possible intermediates and products from the initial reactants. My research goal was to build a template library using credible and diverse resources that would effectively cover the scope of organic chemistry. When compiling reactions from the literature, we regularly encountered the issue of ambiguous labels for functional groups such as “nucleophile” or “leaving group.” These were handled by substituting each ambiguously labeled functional group in the reaction to generate all combinations of possible templates. The template library was tested against known chemical reactions and produced the expected product more than 50% of the time. These results show that the proposed strategy and template library can produce useful molecules. However, more than half of the templates never produced the expected products, and often too many unnecessary reaction paths were produced. Future work can further refine the template library to improve upon coverage and reduce incorrect template applications.

A Biological Mechanism for the Reduction and Emission of Mercury from Soil

Discipline: Chemistry
Subdiscipline: Other

Kimberly Nuñez*[1], Anthony Carpi[2], Darrien Maynard[3]
[1]City University of New York John Jay College of Criminal Justice, [2]City University of New York John Jay College of Criminal Justice, [3]City University John Jay College of Criminal Justice

Abstract: Mercury is a toxic heavy metal that can easily transition between oxidation states and move through the environment. Divalent mercury can be deposited into the soil and is then reduced to elemental mercury that gets released into the environment, leading to the formation of more toxic mercury compounds. The current mechanisms by which soil mercury reduction occurs is proposed to be both a physical and geochemical process, however this work aims to observe how biological processes contribute to the reduction and emission of divalent mercury. This was done by measuring mercury emissions from soil samples after stimulating or suppressing microorganisms. We stimulated microorganisms with water and LB Broth to provide the required nutrients for microbial activity; and suppressed microorganisms by autoclaving the soil and adding the broad-spectrum antibiotic, Levofloxacin. We expected the stimulation of microorganisms to increase mercury emissions while suppression of microorganisms would decrease mercury emissions. The results indicate that the addition of LB Broth caused mercury emissions to increase compared to a water-only control, while autoclaving the soil resulted in decreased mercury emissions. The antibiotic was observed to not have a significant effect. Based on these results, biological processes contribute to soil mercury emissions.

NOx source apportionment in a coastal urban air shed using stable isotope techniques

Discipline: Chemistry
Subdiscipline: Other

kaiya shealy*[1]and Dr. Joseph Felix[2]
[1]Texas A&M University Corpus Christi, [2]Texas A&M University Corpus Christi

Abstract: NO_x ($NO + NO_2$) emission decreases urban air quality, and its subsequent deposition can be a significant source of excess nitrogen loading to coastal waters. Photochemical reactions between volatile organic compounds, and NO_x in the atmosphere creates ozone (O_3). Previous studies suggest that the City of Corpus Christi is in a NO_x limited zone, so an increase in NO_x would lead to an increase in O_3. The first step to NO_x emission mitigation is to quantify the contributions of NO_x sources. This study uses stable isotope techniques to measure point and nonpoint NO_x sources in order to quantify three main NO_x sources in the Corpus Christi air shed: vehicular, biogenic, and industrial sources. Each of these sources have unique isotopic compositions, specifically $\delta^{15}N\text{-}NO_x$ values, which are different for each source and allow the use of isotope mixing models to determine source contribution. NO_x and NO_2 passive air samplers will be deployed at three City of Corpus Christi NO_x and ozone monitoring stations each month for one year and the nitrogen and oxygen isotopic composition ($\delta^{15}N$, $\delta^{18}O$) of each sample will be measured. The $\delta^{15}N\text{-}NO_x$ value in ambient air, and the $\delta^{15}N\text{-}NO_x$ values of the NO_x sources, will be applied to a Bayesian isotope mixing model to quantify source contributions. Prelimary data suggest that vehicular emissions is the main contributor.

Binding Mechanism of Antibodies to Sea-Urchin-Argin (SEA) Domains in MUC16 for the Study of Pancreatic Cancer Immunotherapy

Discipline: Chemistry
Subdiscipline: Other

Guadalupe Romero-Viramontez*[1]and Cory Brooks[2]
[1]California State University, Fresno, [2]California State University, Fresno

Abstract: In pancreatic cancer there is an overexpression of MUC16, a Mucin family glycoprotein that creates a protective mucous barrier for epithelia surfaces. MUC16 is composed of a cytoplasmic tail, transmembrane helix, antigenic tandem-repeat region and a large unstructured O-glycosylated N-terminal domain composed of Pro/Ser/Thr residues. Each of the tandem repeats contains a sea urchin, enterokinase, and agrin (SEA Domain). These SEA domains have epitopes for the binding of antibodies AR9.6, OC125, M11 and OV197. The experimental purpose is to solve the structural and mechanical components of these domains. By solving the structure we will further explore the binding ability and structure of antibodies to the MUC16 protein. The methods planned are antibody binding experiments using the cloned SEA Domains and AR9.6 antibody. The first phase of this experiment was to insert a TRX-TEV-HIS gene into pET28a plasmid. By performing DNA cloning, transformation into E. coli Stellar cells and DNA purification we have successfully completed phase 1. The second phase focuses on cloning the SEA domains into pET28a+TRX-TEV-HIS plasmid using DH5a cells. Purified SEA domain in pET28a plasmid with a TRX-TEV-HIS insert will be introduced in E. coli strain BL21 cells to make our protein. The protein will be purified using a nickel column and protein purification protocol. A binding experiment with AR9.6 will be conducted using ELISA. The binding experiment results will be used in X-ray crystallography to correlate the SEA domain structure with the AR9.6 binding. Our results will further help us understand how antibodies block tumor growth.

Sulfur-sensitized photooxidation of conjugated terminal olefins

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Bryce Gaskins*[1]and Zarko Boskovic [2]
[1]University of Kansas, [2]University of Kansas

Abstract: Oxidative cleavage of a carbon-carbon double bond is often achieved through ozonolysis or dihydroxylation with osmium followed by periodate treatment. While exquisitely reliable, ozonolysis requires specialized equipment, and osmium is a notoriously toxic metal. Photooxidation is an attractive photochemical alternative to achieve this, without the use of special reagents or ozone and with the utilization of singlet oxygen. This reaction is also known to proceed via a dioxetane intermediate, which collapses, yielding two oxidized products. Photooxidation of conjugated olefins has also been achieved with organic sensitizers such as methylene blue. In this study, the photooxidation of conjugated terminal olefins is mediated by a readily available octasulfur, which can sensitize oxygen from air by wavelengths above 305 nm. The sensitization of singlet oxygen with octasulfur is observed to proceed at a faster rate than with a methylene blue sensitizer. Octasulfur's photochemical properties are relatively unexplored, though octasulfur is a common industrial chemical and finds use as a topical antimicrobial agent, We initiated this study by exploring photooxidation of conjugated enamines and heteroaromatic vinyl compounds. We observed that sulfur S 8 is a competent sensitizer for the formation of singlet oxygen. Upon further investigation, sulfur was found to be an efficient sensitizer for the formation of singlet oxygen with conjugated terminal olefins. We compared sulfur with other sensitizers to benchmark it for its effectiveness for this photooxidation. Future investigations into the photochemical properties of octasulfur, its ability to affect other photochemical transformations, and the expansion of these photooxidation conditions will be undertaken.

Synthesis and Reaction Optimization of Tripeptide Building Blocks Toward the Rapid and Efficient Construction of Macrocyclic Peptides in a DNA Encoded Library

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Sarah Beth Avila*[1], Grant Koch [2], Scott Lokey[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]UCSC

Abstract: DNA is the source for genetic material and has taken on many roles with the advancement of high throughput sequencing. The four chemical base pairs can be used in various arrangements as a means to store large amounts of data in our genetic code. This concept is now being utilized in a powerful, modern drug discovery technique called DNA-Encoded Libraries (DELs). The DNA is covalently linked to the drug molecule in question and is used as a barcode to encode for the chemical structure of the pendant molecule. This technology is widely employed by labs in academia and industry to efficiently and rapidly discover new lead compounds against challenging protein targets. The focus of this project is to synthesize and assess the reaction efficiency of tripeptide building blocks for use in a DEL of peptide macrocycles. Employing tripeptide building blocks instead of single amino acids allows DEL chemists to synthesize larger macrocycles in fewer steps and incorporate challenging residues such as N-methyl amino acids. The aim of this project was to create 40 unique tripeptides with highly varying n-methylation and stereochemistry at each residue to ensure greater backbone diversity. LCMS and H1-NMR were used to characterize each tripeptide

building block and assess their purity. Ultimately the library will be utilized for lipophilicity studies and bioactivity screenings against challenging drug targets.

Potential signaling regulations of stereisomeric DNA interstrand crosslinks produced by mitomycins in MCF7 cells

Discipline: Chemistry
Subdiscipline: Other

Melissa Rosas*
CUNY John Jay College of Criminal Justice

Abstract: Mitomycin C (MC) is a DNA alkylating agent broadly used in chemotherapy. MC and Decarbamoyl mitomycin C (DMC), a synthetic MC derivative lacking the carbamoyl at the C10 position, can form interstrand crosslinks (ICLs) .These ICLs are responsible for the cytotoxicity of mitomycins towards cancer cells since they prevent replication of highly proliferating cells. MC and DMC can crosslink DNA in both 5'-CpG and 5'-GpC sequence contexts, and the crosslinking is diastereospecific: At 5'-CpG, mitomycins produce trans- ICLs whereas cis -ICLs are found at 5'-GpC steps. The major ICL formed by MC in culture cells is the trans -ICL whereas DMC yields the stereoisomeric cis -ICL preferentially. Our overarching goal is to synthesize oligonucleotides bearing the cis and tran s isomeric ICLs to investigate the relationship between the ICL structure and the cellular response. There is evidence that the ICL produced by DMC triggers a p53 independent cell death and research uncovering mechanisms through which p53 independent cell death occurs is crucial to identify molecular targets to treat tumors with a mutant p53. In this study, we present different synthetic routes to access cis and trans isomeric ICLs formed by Mytomycins in their reaction with DNA. Proteomic study from MCF-7 cells transfected with the purified ICLs for 24 hours showed several interesting proteins were differently regulated by the trans - and cis -ICLs: (1) TBC1 domain family member 9 which regulates cell proliferation;(2) Core histone macro-H2A.2, involved in DNA repair ; Further validations are needed to confirm the changes.

Comparison of Hydrolysis Efficacy and Performance of Two Rapid Enzymes for the Detection of Benzodiazepines in Urine Samples

Discipline: Chemistry
Subdiscipline: Other

Daniel Aguilar*[1], Marta Concheiro-Guisan [2], Garry Milman[3], Isaiah Jewel[4]
[1]John Jay College of Criminal Justice CUNY, [2]John Jay College of Criminal Justice CUNY, [3]National Spine & Pain Centers, [4]John Jay College of Criminal Justice

Abstract: Benzodiazepines are a class of drugs that act as anxiolytics and produce amnesia. Fast and easy-to-use analytical methods that extend the window of detection in urine are critical to improve the investigation of overdose and drug facilitated sexual assault cases. The objective of the present study was to compare the efficacy and performance of two rapid enzymes, B-One and BG-Turbo (KuraBiotec), for the hydrolysis of benzodiazepines phase II metabolites in fortified and in authentic samples. For the non-hydrolyzed urine samples, urine was diluted with water, fortified with the internal standard mixture and transferred into a nanoFilter TM vial. For the hydrolysis with B-One b-glucuronidase, the same procedure was followed but with the addition of B-One enzyme and a 5-minute incubation at room temperature. For the hydrolysis with BG-Turbo b-glucuronidase, the same procedure was followed but with the addition of BG-

Turbo enzyme and a buffer mixture. The filtered samples were directly injected into the LC-MS/MS. The developed methods were applied to fortified and to 31 authentic urine samples. Limits of detection in both enzymes were between 1 and 5 ng/mL. Both performed a complete hydrolysis of lorazepam-glucuronide, oxazepam-glucuronide and temazepam-glucuronide in fortified samples at 10 and 100 ng/mL. The hydrolysis with both enzymes allowed the detection of glucuronides of midazolam, OH-midazolam, temazepam, oxazepam, lorazepam, alprazolam, OH-alprazolam, and nordiazepam, in authentic samples, yielding similar concentrations. B-One and BG-Turbo rapid enzymes performed a fast and complete hydrolysis of benzodiazepines phase II metabolites in fortified samples, and extended the benzodiazepine detectability in authentic samples.

A New Method for Compound-specific Radiocarbon Analysis of Amino Acids

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Jesus Baca*[1], Lin Zhang [2], Xiaomei Xu[3], Wing Man (Charlotte) Lee[4]
[1]Texas A&M University - Corpus Christi, [2]Texas A&M University - Corpus Christi, [3]University of California - Irvine, [4]Texas A&M University - Corpus Christi

Abstract: Radiocarbon (14C) measurements are used to provide reliable age estimates extensively in the fields of climatology, atmospheric science, and biogeochemistry. However, most radiocarbon data is generated by measuring a bulk sample (e.g., bulk sediments), averaging 14C content of all carbon (C)-containing organic compounds (after inorganic C removal) rather than the specific organic compound produced by the organisms during their life. Compound-specific radiocarbon analysis (CSRA) of amino acids (AA) can thus be a useful tool to precisely determine the age when the AAs were produced by said organisms. Robust methods for CSRA-AA are not yet widely available, partly due to the relatively small amount of C in AAs. We present a new approach of CSRA-AA combining semi-preparative ion-exchange chromatography (IC) and Accelerator Mass Spectrometry (AMS). Phenylalanine (Phe), glutamic acid (Glu), and their corresponding blanks were separated using IC and collected as individual fractions from a commercial AA mixture. Samples were graphitized and analyzed on AMS for 14C. Current blank contribution was 5.2 and 16.6 µg C with corresponding yields of 132 and 71.1 µg C for Phe and Glu respectively. The obtained fraction modern (FM) with blank subtraction and error propagation was 0.9937±0.0065 for Phe and 1.1362±0.0271 for Glu, which is in line with the modern origins of the AA standards (Phe: 1.0276±0.0017; Glu: 1.0293±0.0005). Our ultimate goal is to conduct multiple-isotope measurements (13C, 14C, and 15N) of AAs preserved in sediments and separate the N cycling signals produced by surface plankton community from influences induced by diagenesis and horizontal transfer.

High confidence computational analysis of single nucleotide variation consequences in homology models

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jill Hoffman*[1]and Scott Reed [2]
[1]University of Colorado Denver, [2]University of Colorado Denver

Abstract: Homology modeling is an efficient way to produce many protein structures without the time-consuming methods experimentally determined structures require. Recent advancements in homology modeling by using artificial intelligence programs such as AlphaFold2 developed by the DeepMind company have allowed for efficient prediction of protein structures and the consequences due to single nucleotide variations (SNVs). By using both homology and experimental structures, significant consequences to 3D structure that could result in disease can be analyzed. Using high confidence predicted native protein structures from AlphaFold2, all possible mutated structure can be accurately produced using the FASPR software, which predicts protein side chain conformations. Python code can then be used to analyze different aspects of the native proteins and their mutants using either the experimentally determined or the predicted AlphaFold2 structure. The analysis focuses on factors that would cause a significant alteration to the proteins 3D structure that due to the SNVs. This includes identifying if a cis proline is added or replaced and the effects of buried residues, such as proline, glycine, and charged residues, in relation to the surface of the protein. Future steps will be in adding deeper analysis of the buried residues to identify different bond breakages and additions. The analysis can also be customized to fit the users need by excluding low confident structures and allowing a choice between the model used. The information obtained from this software will allow for quick high confident analysis for 23,000 native and mutant homology models or experimentally obtained models.

Prioritization of novel or bioactive secondary metabolites derived from marine Gram-negative bacteria

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Samuel Mussetter*[1], Carlos Cienfuegos [2], Itzel Lizama-Chamu[3], Gabriella Amberchan[4], Erin McCauley [5], Phillip Crews[6]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]University of California, Santa Cruz, [5]California State University Dominguez Hills, [6]University of California, Santa Cruz

Abstract: Gram-negative secondary metabolites have emerged as a promising area for the discovery of novel chemistry due to being overshadowed by the metabolites produced by Gram-positive bacteria and their medicinal applications. However, the rise of antimicrobial resistance requires us to turn our attention towards Gram-negative bacteria in search of novel bioactive compounds that might by applicable to combat antibiotic resistance. Marine sediment bacteria, such as proteobacteria , produce metabolites with bioactive capabilities and are the subject of the Crews lab’s research focus. The proteobacteria were isolated from coastal sediments along the California coast. From these collections, 37 bacterial strains were isolated. The bacterial strains were grown in small scale liquid cultures, and their crude metabolites were extracted via liquid-liquid extractions. These crude extractions were semi-purified using flash chromatography. These fractionated samples served as a basis for initial bioactive screenings and high-resolution mass spectrometry (HRMS) analysis. The HRMS spectra were characterized using various molecular databases. Usage of molecular databases allows us to filter out masses associated with media components, known metabolites, and their derivatives. Therefore, instead of working with 296 fractions, they have been condensed to 4 prioritized fractions. These 4 fractions of interest were then sent through the secondary round of purification, via high performance-liquid chromatography (HPLC), to isolate a pure compound. Current work includes identifying the structure of a compound found in one of the four prioritized fractions using 1D and 2D NMR data. Future directions include screening pure compounds for antimicrobial properties and inhibition against antibiotic resistant bacteria systems.

Insight Into Ganoderma multiplicatum Phytochemistry and Its Mode of Action Against Cancer Models

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Emily Seighman*[1], Fatima Rivas [2], Lucinda Boyd[3], TaoTao Ling[4], Michelle M. Martinez [5]
[1]Louisiana State University, [2]Louisiana State Univerity, [3]Louisiana State University, [4]Louisiana State University, [5]Universidad Central del Caribe

Abstract: Ganoderma is a diverse genus of fungi with species distributed in temperate and tropical regions. Species of Ganoderma in Puerto Rico were recently recorded to be G. multiplicatum and is the focus of this study. Many species of the polypore fungus Ganoderma produce bioactive compounds with anti-cancer, antioxidant, cytotoxic, antiviral, and antibacterial activities. For instance, Ganoderma lucidum, an oriental fungus has a long history of use for promoting health and longevity in China, Japan, and other Asian countries. Particularly focusing on its anti-cancer effects, Ganoderma lucidum metabolites display cell cycle arrest, and induce apoptosis. Consequently, we hypothesized the species multiplicatum will also contain bioactive compounds that exhibit similar biological effects. Our objectives are to identify and assess the secondary metabolites of G. multiplicatum to further test their biological properties. Our methodology consists of pulverizing G. multiplicatum , Soxhlet extraction, mixture purification via silica gel column chromatography, structure elucidation, and testing the cytotoxicity against cancer cell line models. For silica gel column chromatography purification, thin-layer chromatography is used to monitor the mixture purification process. 1-Dimensional nuclear magnetic resonance (NMR) will be conducted for compound characterization (proton and carbon spectra). Our preliminary results indicate several fractions of G. multiplicatum display antioxidant activity, and cytotoxic properties against cancer cell models. Current and future studies include full structure characterization of these G. multiplicatum compounds and evaluation of their mode of action against cancer models.

Structural analysis of the catalytic mechanism of human IDH1

Discipline: Chemistry
Subdiscipline: Other

Marissa Balagtas*[1], Tom Huxford [2], Christal Sohl[3], Matthew Mealka[4], Elene Albekioni [5]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University, [4]San Diego State University, [5]San Diego State University

Abstract: Isocitrate dehydrogenase I (IDH1) is a cytosolic enzyme that employs the NADP+ co-factor to oxidize the metabolic intermediate isocitrate to alpha-ketoglutarate and carbon dioxide. The purpose of IDH1 and IDH2 is to regulate of a cellular redox status, glutamine metabolism, and lipogenesis. Several mutated versions of the enzyme are then able to employ the NADPH co-product to reduce alpha-ketoglutarate (αKG) back to 2-D-hydroxyglutarate, a verified oncometabolite. Some of these mutant forms of the enzyme are associated with cancers, including leukemias and glioblastomas. The enzyme functions as a homodimer with an active site that involves divalent metal co-factors. Lysine-212 (K212) has been proposed to function as a general base to initiate the reaction and Tyrosine-139 (Y139) behaves as a general acid to complete the reaction. A divalent Mg2+ cation stabilizes formation of intermediates on the pathway of alpha-ketoglutarate formation. In this study, we used three-dimensional molecular models derived from x-ray crystallography to analyze the human IDH1 active site and provide insight into how the reaction is carried out in the absence of mutations.

Tagging Endogenous Mitochondrial Protiens using CRISPR/ Cas9 Technology

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Laura Mejia*[1]and Dr. Tommy Lewis [2]
[1]Langston Univeristy, [2]Oklahoma Medical Research Foundation

Abstract: Mitochondria are often described as the powerhouse of the cell because they are generating most of our adenosine triphosphate (ATP), which is the energy currency of a cell. In past studies, researchers found that mitochondria can regulate their shape, hypothesizing that different shapes lead to different functions, but no one understands exactly why. Mitochondria are microscopic and often cannot be detected under a microscope unless stained. One challenge to answering the question above has been that there are no antibodies towards many mitochondrial proteins and thus researchers have not been able to assess the localization or abundance of most mitochondrial proteins in the cell. To overcome this problem, we used CRISPR/Cas9 technology to label mitochondrial proteins of interest. In developing this technology, we used molecular biology to clone guide RNA and donor DNA for MIEF1, a mitochondrial fusion promoting protein, to tag the endogenous protein with a fluorescent reporter, GFP. We then validated this reporter in NIH3T3 cells to show that our construct labels the expected mitochondrial protein. In future projects, we plan to use this construct to be able to label MIEF1 in neurons in vivo.

Electrochemical Detection of Bio Mass Derived Sugar Molecules using Flexible Paper-Based Electrodes

Discipline: Chemistry
Subdiscipline: Other

Jasmine Charley*[1]and Thiagarajan Soundappan [2]
[1]Navajo Technical University, [2]Navajo Technical University

Abstract: Glucose is one of the four C6 sugars derived from biomass such as lignocellulosic materials using microorganisms. Breaking the sugar molecules from the biomass materials is site-specific and sensitive. We have successfully utilized microorganisms and broke the sugar molecules from the biomass through this project. Further, the detection and determination of sugar molecules have to be measured to confirm the presence of sugar molecules. To ensure the sugar molecule, we have used the electrochemical analysis technique. In particular, we have targeted using paper-based electrodes to detect the sugar molecules. Paper-based electrodes are low-cost and easy to construct. The electrodes made in the Electrochemistry lab at Navajo Technical University were printed by a wax printer and then coated with carbon paste. With these flexible electrodes, we could add nanoparticles to them, such as gold nanoparticles. Gold nanoparticles were added to the electrode to improve results from carbon-paste paper electrodes. With these results recorded, we have found that glucose oxidation can be detected by using carbon-paste paper electrodes with gold nanoparticles in a phosphate buffer solution.

We are also continuing the work to detect the glucose molecules using high throughput electrochemical analysis.

Selection of Suitable Electrode and Nanomaterials to detect the Biomass Derived Sugars

Discipline: Chemistry
Subdiscipline: Other

Katelyn Wilson*[1], Makeiyla Begay [2], Jasmine Charley[3], Justin Platero[4], Michael Nelwood [5], Samantha Francis[6], Apurv Mhatre[7], Arul Mozhy Varman[8], Thiagarajan Soundappan[9]
[1]Navajo Technical University/ Crownpoint, [2]Navajo Technical University, [3]Navajo Technical University, [4]Navajo Technical University, [5]Navajo Technical University, [6]Samantha.francis@students.navajotech.edu, [7]Arizona State University, [8]Arizona State University, [9]Navajo Technical University

Abstract: Sugar molecules consist of carbon (C), oxygen (O), and hydrogen (H) atoms. At Navajo Technical University, we have started research to find and optimize the suitable electrode and nanomaterials to sense glucose, fructose, sucrose, and other BP compounds. Initially, we utilized a commercially screen-printed carbon electrode (three-electrode setup) to feel glucose using a differential pulse voltammetry technique. Therefore, the selection of suitable nanomaterials and electrodes modification studies will help us select the right composite materials for screening studies of the biomass-derived sugars. The voltammetric and aerometric techniques will be utilized to screen the sugar molecules. We expect that we will have developed a suitable electrode surface for the high throughput screening of sugar molecules upon success with this objective. Interference signals may appear, but this can be avoided by using the proper nanomaterials for the sugar screening.

Possible Anti-fungal secretion from the Isolation of Ruegeria Scottomollicae

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Carlos Cienfuegos*[1], Samuel Mussetter [2], Itzel Lizama Chamu[3], Gabriella Amberchan[4], Erin McCauley [5], Phillip Crews[6]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]University of California, Santa Cruz, [5]California State University, Dominguez Hills, [6]University of California, Santa Cruz

Abstract: Historically, Gram-positive bacteria are known for producing bioactive and diverse natural products. Less research has been focused on Gram-negative bacteria and as such, they are the main focus of the Crews lab. Specifically, the focal point of this research is on the natural products isolated from halotolerant Gram-negative bacteria collected from sand along coastal parts of California. The goal of this project is to discover unique or pharmacologica-relevant chemical compounds produced by Gram-negative bacteria. Previous expeditions have isolated and identified Gram-negative bacteria from Proteobacteria and Bacteroidetes phyla. Due to the fact that Gram-negative strains are so understudied, the focus of this research is on the unique metabolites that are produced by t hese strains. Collected from the California coast, Ruegeria scottomollicae strain 1522SB3B8b, was prioritized for extraction due to observed antifungal activity. A zone of inhibition was observed in a co-culture of the R. scottomollicae and a fungus, leading to the hypothesis that the bacteria may contain antifungal properties. This strain was

grown on a larger scale in order to extract the secondary metabolites that it produced. Further work will be taken to analyze chemistry through mass spectrometry fragmentation and NMR analysis. The novelty of these secondary metabolites will be compared against known compounds.

Machine Learning Models for Tuberculosis Drug Discovery

Discipline: Chemistry
Subdiscipline: Other

Alexandra Bozan*[1]and Dr. Joel Freundlich [2]
[1]Rutgers University, New Brunswick NJ, [2]Rutgers University, Newark NJ

Abstract: Tuberculosis (TB) is caused by the airborne bacteria Mycobacterium tuberculosis . It causes a chronic contagious infection that commonly affects the lungs. In 2020, TB was reported as the 13th leading cause of death and was the second leading infectious disease killer after SARS-CoV-2. Treatment of drug-sensitive TB consists of a cocktail of four drugs. A search for novel antitubercular drugs continues in the hopes of addressing drug resistance and shortening the duration of treatment from 6-9 months at minimum. Various machine learning (ML) techniques can be harnessed to discover new starting points for antitubercular agents. These methods employ modeling and analyses of large, publicly available data sets. The presented work will focus on recent efforts to construct, validate, and deploy innovative ML models of properties critical to the discovery of new small molecules with significant promise to seed antitubercular drug discovery efforts.

Secondary Structure and Selectivity of RNA Aptamers containing 8-oxoG: Targeting Aminoglycosides

Discipline: Chemistry
Subdiscipline: Other

Haydee Ramirez*[1]and Marino Resendiz [2]
[1]University of Colorado Denver, [2]University of Colorado Denver

Abstract: Aptamers are single stranded RNA oligonucleotides with high affinity and specificity to various targets such as small molecules, nucleotides, and proteins, making their use an attractive strategy in clinical treatments and diagnostics. This work aimed to use 7,8-dihydro-8-oxoguanine (8-oxoG) in the construction of aptamers for distinct specificity toward their cognate targets. The unique hydrogen bonding ability of 8-oxoG, due to its inherited conformational changes may alter their range of possible targets, making a promising strategy. The use of a 26-nucleotide long RNA aptamer as model [5’-GGA CUX GGC XAG AAX UUU AGU CC-3’; X= G or 8-OxoG] was employed, where the oligonucleotides were modified at one position. This RNA sequence was chosen for the ability of the canonical analog to recognize neomycin, a common antibiotic. Native PAGE was used to explore potential binding to 5 small molecules - gentamycin, geneticin, tobramycin, neomycin, and streptomycin- all possessing antibacterial properties; subtle changes, consistent with binding, were observed. K d values in the nM-uM ranges, were obtained via Isothermal Titration Calorimetry(ITC), with clear differences arising from the modified aptamers. To better understand the impact that 8-OxoG has on RNA structure, structural probing techniques were employed. While RNase A and RNase T1 experiments did not display differences, RNA SHAPE was useful in identifying structural changes. Circular dichroism was then used to assess thermal stabilities of all RNA constructs. Overall, we report that 8-oxoG

has an impact on the structure and function of the studied aptamer and can change its selectivity towards their original targets.

Understanding the Reaction Mechanisms of Vanadium-Catalyzed Olefin Metathesis

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Emma Saucerman*[1], Bess Vlaisavljevich [2], Samuel Fosu[3], Wesley Farrell[4]
[1]University of South Dakota, [2]University of South Dakota, [3]University of South Dakota, [4]United States Naval Academy

Abstract: Olefin metathesis is used in the synthesis of polymers and for drug discovery. Commonly, molybdenum and ruthenium catalysts are used in this reaction. However, presently, there has been a rise in the use of vanadium catalysts in olefin metathesis because it is cheaper and more abundant. Vanadium catalysts tend to take a decomposition pathway via beta-hydride elimination, though an alternative productive metathesis route is generally preferred. The Burkhryakov group has developed a pathway for productive olefin metathesis using a vanadium catalyst with chloride, triethyl phosphine, and pentafluoro-phenyl imido ligands (Organometallics . 2021, 40, 2939-2944). Using the Gaussian 16 package and density functional theory, I will compare my pathway to the Burkhryakov pathway for the vanadium catalyst in olefin metathesis. By tuning the ligands of the catalyst, I want to understand how the productive metathesis and beta-hydride elimination pathways will be affected. Preliminary results show that when fluorinated aryloxide, trimethyl phosphine, and 2,6-dimethylphenyl imido ligands are used transition state orientation may change. My preliminary results show different orientation of the beta-hydride elimination transition state than the previous Burkhryakov studies. Ultimately, insights from this study could contribute to the design of superior catalysts which are more favorable towards productive olefin metathesis. Understanding the decomposition pathway will help direct future attempts to make polymer synthesis and drug discovery more effective by allowing us to reuse the vanadium catalyst.

Synthesis of Bidentate N-Heterocyclic Carbene Cobalt Dinitrogen complexes with Xylyl Linkers

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Mei Matsumoto*[1]and S. Chantal E. Stieber [2]
[1]California State Polytechnic University, Pomona, [2]California State Polytechnic University, Pomona

Abstract: N -Heterocyclic carbenes (NHC) have been used to advance catalysis due to their strongly sigma donating abilities for coordinating to a variety of metals. Cobalt NHC complexes are used as catalysts for a variety of reactions such as the hydrogenation of hindered alkenes. However, bidentate NHC 2 ligands containing first row transitions metals remain less widely studied and are generally limited to nickel and iron. A ligand precursor with a o -xylyl linker was synthesized by reacting mesityl imidazole (Mes Im) with 1,2-bis(bromomethyl)benzene, producing [Mes NHC 2 Xy][Br] 2 (Mes = 2,4,6-trimethylphenyl; Xy = xylyl). The addition of the o -xylyl creates more space between the carbenes, allowing for an aryl group to be added which generates the possibility for better crystallization. The ligand precursor was deprotonated with potassium bis(trimethylsilyl)amide (KHMDS) in THF to create a bidentate carbene ligand that was reacted with $CoCl_2$ to form a new cobalt complex, (Mes NHC 2 Xy)Co II Cl 2 . The reduced cobalt dinitrogen complex, (Mes NHC 2 Xy)Co 0 (N 2), was synthesized by reacting (Mes NHC 2 Xy)Co II Cl 2 with 2 equivalents of sodium metal, catalytic naphthalene, and THF. This product was characterized by IR spectroscopy to confirm the presence of the Co-N 2 bond. These are new cobalt complexes with NHC 2 ligands and they are currently being investigated for NO reduction and catalysis.

Photocatalytic upcycling of polyethylene terephthalate to H 2 and valuable chemicals

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Audrey Washington*[1], Hongxing Kang [2], Dr. Jing Gu[3]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University

Abstract: Title: Photocatalytic upcycling of polyethylene terephthalate to H 2 and valuable chemicals Plastic pollution is a widespread problem affecting the environment. At the same time, plastics are a largely untapped resource for manufacturing and fuels. Approximately 30 million tons of poly (ethylene terephthalate) (PET) is produced annually for applications in textiles and packaging (bottles, fibers). However, only 9% of PET is recycled mainly via mechanical methods. Typically, PET is decomposed under harsh conditions (low pH, high temperature, 500-800°C) to yield value-added products. Herein, we center upon a sustainable photocatalytic technique that is capable of upcycling polyethylene terephthalate (PET) to H 2 fuel and value-added chemicals (e.g., formate). Specifically, a cheap non-toxic carbon nitride/molybdenum disulfide (C 3 N 4 /MoS 2) photocatalyst is exploited to reform PET under ambient conditions. Firstly, PET was hydrolyzed to its sub-monomers under 2M KOH in an initial pretreatment process. Followed by irradiation where H 2 and several PET upcycled products (e.g., formate and glyoxal) were evolved from the photocatalytic system. Several products were detected by proton nuclear magnetic resonance spectroscopy (1 H NMR) and gas chromatography (GC). This work demonstrates a sustainable alternative where PET waste is upcycled to value-added products and H 2 fuel addressing prominent environmental issues.

The Optimization of Immobilized Molecular Re CO2 Reduction Catalyst

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Jeremiah Choate*
The University of Southern California

Abstract: The rising global population and energy demand, together with limited fossil fuel resources drives the development of sustainable energy resources. With potential availability, solar energy can fulfill the world's energy demand. However, there is a mismatch between solar-energy use and demand due to its intermittent nature. A solution, using solar-derived electricity to drive the electrocatalytic conversion of CO 2 to CO to store solar-energy in the form of chemical bonds. Conversions with homogenous or heterogeneous catalysts have respective advantages and disadvantages. Heterogenization of molecular catalysts by tethering to substrate combines the advantages of both systems. Rhenium(I) 2,2'-bipyridine tricarbonyl chloride (Re(bpy)(CO) 3 Cl) catalyst has exhibited high selectivity and activity for CO 2 to CO conversion. I will present my efforts to vary the anchoring position in Re(bpy)(CO) 3 Cl catalyst by tethering at the 4,4'-position of the bipyridine to introduce spacing to such films for increased substrate diffusion. Films are characterized by X-ray photoelectron and inductive coupled plasma optical emission spectroscopy, along with scanning electron and atomic force microscopy. The electrochemical response and activity of the films were examined through cyclic voltammetry, electronic impedance spectroscopy, and controlled potential electrolysis. This work will advance the sustainable energy field by: (1) Optimizing the anchoring position of the catalyst to impact the growth morphology and subsequent development of materials with improved substrate diffusion for increased catalytic activity for CO 2 to CO catalysis. (2) CO products can be utilized in the Fisher-Tropsch process to produce liquid-hydrocarbon fuels for implementation in a circular-carbon economy.

Dynamic DNA Origami Nanoclock

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Tiffany Olivera*[1]and Dr. Fei Zhang [2]
[1]Rutgers University - Newark, [2]Rutgers University - Newark

Abstract: DNA is an exceptional molecular building block for nano-construction due to its base-pairing interactions that can control biological regulation, cellular behaviors, and functional pathways. Engineering bioinspired molecular systems has gained interest due to the possibility of creating complex molecular machineries that can be formed and operated through self-assembly in living cells. A novel technique called DNA Origami enables us to synthesize molecular nanostructures of almost any arbitrary shape by exploiting the double helical nature of DNA, utilizing one strand as the scaffold, and the second strand acting as individual staple strands that force the scaffold strand to conform into the desired structure. Applying strand displacement reactions (SDRs) upon a DNA Origami can cause dynamic movement and programmable direction to the structure. A DNA Origami Nanoclock was then designed using three 6-double helical DNA bundles for the 3D structure, where there are three subsections: an arm, a strut, and a ring. A second design was created to impose a DNA motor onto the arm, and fuel strands onto the ring to cause the arm of the Nanoclock to move about the ring through SDR. Preliminary data has been collected using various methods, like Gel Electrophoresis and Atomic Force Microscopy, where the results are reported in this presentation. Pursuing the construction and observation of this Nanoclock will aid in gaining insights into manipulating matter at the nanoscale level. Developing this self-assembled system will offer the ability to program smart dynamic nanorobots and promise potential applications in structural biology, nanorobotics, and drug delivery.

A polypharmacology approach: Development of dual FAAH/AChE inhibitors for the treatment of chronic pain in patients with Alzheimer’s disease

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Michael Gonzalez*[1]and Stevan Pecic [2]
[1]California State University, Fullerton, [2]Research Professor

Abstract: Alzheimer’s disease (AD) is a degenerative brain disease with no cure and limited treatments. Most existing therapies are drug therapeutics that only treat AD symptoms, lose potency, and contain side effects. These limitations have pushed pharmaceutical sciences to advance the efficacy of AD therapeutics. The cholinergic pathway, where acetylcholinesterase (AChE) breaks down the neurotransmitter acetylcholine (ACh), is a viable target of interest for improving cognition. Inhibition of AChE increases ACh concentrations, improving neuronal communication and overall brain cognition. Previous literature has shown a link between AD and pain. Fatty Acid Amide Hydrolase (FAAH) is a membrane enzyme that hydrolyzes endocannabinoid neurotransmitters. The inactivation of FAAH produces analgesic and anti-neuroinflammatory effects, improving neuronal transmission. Therefore, inhibition of FAAH presents a promising therapeutic strategy for treating pain in AD patients. In our lab, we identified potent donepezil-derived AChE inhibitors. Our detailed kinetic evaluations of the most potent inhibitor (IC 50 = 51 nM) showed a mixed inhibition mode, like donepezil. A separate study from our lab investigated a series of viable 4-phenylthiazole FAAH inhibitors, which showed competitive IC 50 values of 8.4 nM. We aim to utilize the concept of polypharmacology to combine the 4-phenylthiazole moiety from FAAH inhibitors and piperidine-pyridyl moiety from AChE inhibitors identified in our lab into a single multi-target directed ligand (MTDL), enhancing its AD therapeutic potential. All dual AChE/FAAH inhibitors were synthesized via environmentally friendly microwave-assisted synthetic routes, evaluated in In Vitro, and underwent molecular docking/ADMET predictions.

Thermoplastic Microfluidic Devices for Affinity Selection of Rare Biological Cells

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Taryn McNickle*[1], Dr. Steven Soper[2], Dr. Malgorzata Witek[3]
[1]University of Kansas, Lawrence, [2]University of Kansas, [3]University of Kansas

Abstract: Polymeric microfluidic devices are used for applications in biological and clinical assays. Each of the polymers has a different chemical makeup that results in different measures of surface energy. UV and ozone treatment is used to activate the surface of the polymers and prepare them for attachment of affinity agents. After activation, the stability of the polymers is determined by the contact angle. This project aims at developing a microfluidic system for the isolation of immune cells and Circulating Tumor Cells directly from the blood of animal models, providing vital data related to disease progression, treatment response, or pharmacokinetics. This is highly relevant to understanding diseases or treatments in humans. CTCs are rare (≤100/mL) and responsible for metastasis formation, which ultimately leads to a patient’s death. Evaluation of the CTC abundance and their molecular characteristics provide prognostic information and can lead to developmenting important targeted therapies. The challenge in such studies is that only a small blood volume can be secured without harm. When frequent blood samples are needed, the amount of an animal’s total blood volume can be collected daily is not adequate for efficient analysis. To address this challenge, we propose an in vivo, vein catheter-based miniaturized microfluidic system that can be attached to the animal, withdraw the blood samples, isolate targetted cells of interest and return the blood to the animal without causing harm. Keeping the animal alive allows us to study the same animal and enables monitoring of disease progression or treatment, over a profound period.

Iodoenamine: A precursor for tetracyclic bis-piperidine alkaloids as potential anticancer agents

Discipline: Chemistry

Subdiscipline: Organic Chemistry

Jasmine Hang*[1], Qiao-Hong Chen [2], Erik Sorensen[3]
[1]California State University, Fresno, [2]California State University, Fresno, [3]Princeton University

Abstract: The therapeutic properties of natural products for the treatment of various diseases, especially cancer, have been an area of interest. Though there are many current treatments of cancer, there are still demands for more effective treatments. A proposed treatment for cancer are tetracyclic bis-piperidine alkaloids which are a group of marine natural products that have the potential to suppress cancer cell proliferation in three types of cancer cell lines. However, the structure-activity and in vivo animal studies have yet to be studied due to limited availability. This study is the beginning of a long-term project that aims to build a structurally diverse library of bis-piperidine alkaloids for the study of the relationship between structure and activity. The focus of this two-month study was the creation of intermediate iodoenamine through a five step transformation. The first four steps of the synthesis have been achieved, with each intermediate compound being characterized through ^{1}H NMR and ^{13}C NMR. Different procedures were explored to improve the low yield and the volatility of one intermediate. The synthesis of iodoenamine is still in progress.

Comparing the Contrasting Ground States of Pyrethroids and Pyrethrins

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Kelly Kepler*[1], Sean Duncan [2], Kristina Closser[3]
[1]California State University, Fresno, [2]California State University, Fresno, [3]California State University, Fresno

Abstract: Pyrethroid insecticides are synthetically derived based on the structure of pyrethrin compounds found in chrysanthemum flowers. Both pyrethroids and pyrethrins function as nervous system disruptors on small insects, however pyrethroids are known to exhibit significantly increased stability in contrast to pyrethrins. Pyrethroids are commonly used in both residential and agricultural pesticide management, remaining pervasive in water and soil ecosystems after application. Degradation products for pyrethroids are not well defined and identification could enable more targeted approaches in defining the concentrations of these eco-toxins, therefore a comparison with the lower stability pyrethrins was conducted. We studied the ground state conformation of pyrethroids, Lambda-Cyhalothrin and Cypermethrin, and pyrethrins, Cinerin II and Jasmolin II, using Density Functional Theory. Low energy structures have been isolated using B3LYP with increasing basis sets and accounting for environmental effects through the polarizable continuum model for solvation. Using these structures, the electron orbitals and absorption spectra were compared to determine potential differences in reactivity. Future work will focus on the determination of possible photodegradation pathways based on the excited state electronic structure to illustrate the aforementioned compound’s contrasting stability.

Phase separation of metal ion/chelating polymer combinations using microfluidics

Discipline: Chemistry
Subdiscipline: Other

Shaneily Colon Morera*
University of Puerto Rico at Cayey

Abstract: Cells organize their interior volumes by membraneless organelles such as cytoplasmic P granules, and Cajal Bodies that are formed by intracellular liquid-liquid phase separation and behave as liquid-liquid droplets. Their structure has been incorporated into experimental model systems for artificial cells to mimic biological cells. A major phase-separated system used for artificial cells involves the use of associative separation, where oppositely charged polyelectrolytes separate due to ion-pairing interactions. A drawback for this artificial cell systems is that polycations can disrupt cellular processes such as transcription and translation, resulting in non-self-sustainable models. Here, we explore the possibility of replacing the polycations with metal ions such as Ca +2 and Mg +2 . The aims of this project are to determine the conditions for phase separation of metal ion/chelating polymer combinations. We study the conditions as a function of metal ion, and polymer concentration, ionic strength, pH, and macromolecular crowding. A PDMS microfluidic device is constructed to gain additional control over the production of the phase-separated droplets, where the ability of ion/polymer droplet phases to serve as artificial organelles is evaluated and compared with more traditional systems.

Synthesizing Cyclic Peptides in Effort to Develop Membrane-Permeable and Metabolically Stable Compounds for Drug Discovery

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Samantha Scarlett*[1], Scott Lokey[2], Alex Engstrom[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: The physicochemical challenges of creating effective therapeutics has attracted many different approaches within the field of drug discovery. The ability of a drug to be cell-permeable while also maintaining its function and chemistry is a fundamental component of designing an effective therapeutic. One way to approach this challenge is through the synthesis of cyclic peptides which exhibit high selectivity and affinity for targets, favorable intramolecular binding, and metabolic stability. These characteristics have proven to be of pharmacological success as many cyclic peptide drugs have been recently approved. The Lokey Research Lab has already established several cyclic-peptide libraries which continue to further the research of membrane-permeable systematic structures for optimal oral absorption. The research my project consists of developing libraries of cyclic peptides/peptoids with varying functionalities such as N-Methylation and non-traditional amino acids. The library will be synthesized via split-and-pool chemistry and the permeability assessed via Parallel Artificial Membrane Permeability Assay (PAMPA). The results of PAMPA will allow determination of the library members which were capable of passive diffusion. Liquid Chromatography-Mass Spectroscopy (LC-MS) and Nuclear Magnetic Resonance (NMR) will be used to determine and differentiate the compounds.

Collagen V Exposure Prior to Chronic Hypoxia and Alters Inflammation and Pulmonary Arterial Remodeling

Discipline: Chemistry
Subdiscipline: Other

Brendan Sanders*[1], Benjamin Lantz[2], David Jones[3], Laura Gonzalez Bosc[4]
[1]University of New Mexico, [2]Vascular Physiology Group, Cell Biology and Physiology, School of Medicine, UNM Health Sciences Center, [3]Vascular Physiology Group, Cell Biology and Physiology,

School of Medicine, UNM Health Sciences Cente, [4]Vascular Physiology Group, Cell Biology and Physiology, School of Medicine, UNM Health Sciences Cente

Abstract: Pulmonary hypertension (PH) is a well-known and slowly progressing disease characterized by elevated pulmonary pressure, usually due to several different mechanisms. Though the major mechanisms for PH have been identified, effective treatments for PH have yet to be found. When left untreated, progression of PH has disastrous implications, leading to right ventricular hypertrophy, right-heart failure, and death. One such category of PH arises from chronic hypoxia (CH). One major mechanism of CH-induced PH is the pro-inflammatory immune response. Our lab has shown collagen V (Col V)-specific pro-inflammatory cells exist under normal conditions, CH increases Col V within the lungs, and pro-inflammatory cells traffic to the lungs following CH exposure. We have also shown that nasal exposure to Col V prior to CH exposure attenuates the rise in right ventricular pressure (RVSP), an index of PH. Whether or not prior exposure to Col V affects the pulmonary vasculature is unknown. Based on our RVSP data, we hypothesize that Col V exposure prior to CH attenuates pulmonary arterial remodeling. To measure this, we will be quantifying pulmonary arterial wall thickness in lung sections from mice that received vehicle or Col V exposure followed by exposure to normoxia or CH, using immunofluorescence microscopy for a smooth muscle marker. Completion of this study will further elucidate how Col V-reactive cells affect the pulmonary vasculature in CH-induced PH, laying the groundwork for possible targeted therapies.

Synthesis of 2-substituted benzofurans from 2-alkynyl aryl ethers catalyzed by gold(I)–N-heterocyclic carbene complexes.

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Kirubel Mamo*[1], Hubert Muchalski [2], Jeremy Pisor[3], Isabella Garcia[4]
[1]California State University, Fresno, [2]California State University, Fresno, [3]California State University, Fresno, [4]California State University, Fresno

Abstract: Benzofurans are molecular motifs found in a wide variety of natural products and pharmaceutical compounds such as dronedarone, amiodarone, and naloxone. Due to the importance of benzofurans, multiple synthetic methods have been developed that focus on constructing the benzofuran motif. Among those, gold(I)-catalyzed cyclization of free phenols onto alkynes has emerged as one of the leading methods of forming the fused bicyclic structure. Although robust, the general method is limited to free phenols (R-OH) and does not work well for ether derivatives (R-OR'). We discovered that O-tetrahydropyran (OTHP) ethers can undergo efficient cyclization catalyzed by gold(I) complex. The goal of this study was to survey the scope and limitations of these new reactions by subjecting different substrates to the standard reaction conditions. The substrates for this study were synthesized by the Sonogashira cross-coupling. Reaction efficiency (product yield) was estimated using quantitative proton NMR spectroscopy (qHNMR).

Enhancing Project Based Learning with Collective Intelligence

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

David Eisenberg*[1]and Jerry Fjermestad [2]
[1]New Jersey Institute of Technology, [2]New Jersey Institute of Technology

Abstract: In STEM education, it has been debated whether PBL (Project-Based Learning) groups can best help advanced and struggling students simultaneously. By instilling real-life competencies and positive social skills, PBL's emphasis on teamwork bolsters in-demand soft-skills that STEM employers require. Student groups encourage diversity, but also rely on members to work well together. Information systems researchers have demonstrated specific characteristics of group member selection that lead to improved project outcomes, called collective intelligence. Our research identifies the best configuration of group members for PBL teams, such that every single PBL group member optimally benefits from their learning group. When PBL groups are optimized into our improved Ci-PBL (Collective Intelligence Project Based Learning) groups, they enhance every member's individual capacity to learn, be creative, and problem solve. This presentation builds on my team's previous research, which examined 42 undergraduate student groups, showing project improvements in creativity, outcome quality and individual group member satisfaction. Moreover, among 40 groups (214 subjects), optimized member configuration increased viewpoint diversity, decreased conformity, and increased cognitive effort. Current results from 5 pilot studies conducted at NJIT on 40 student groups (4 students per group) designing e-commerce projects have already identified social sensitivity, collaboration mode, and leadership capacity among group member factors that collectively enhance outcomes. My presentation will introduce these results, and further propose interventions including specific mindfulness activities, and applications of deep learning sensor technologies. PBL is used by K-12 schools, universities, and companies alike, and stands to benefit from improved group selection to enhance STEM outcomes.

Graph-Based Tractography Algorithms Applied to Diffusion Tensor Images to Establish White Matter Tracts Between Brain Regions Using a Micron Resolution Dataset

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Tiffanie Crumbie*[1], Daniel Tward [2], Bryson Gray[3]
[1]University of Central Florida, [2]University of California, Los Angeles, [3]University of California, Los Angeles

Abstract: In the past decade, neuroscientists have been attempting to develop more efficient methods for identifying irregularities in the neural pathway system. Identifying irregularities in the neural pathway system has the potential to allow better understanding and diagnosis for psychiatric and neurological disorders. Current research concludes that white matter fiber tracts can be identified reproducibly. However, connections within gray matter have not been, due to lack of high resolution data. Diffusion Tensor Imaging (DTI) tractography is an MRI technique used to estimate white matter fibers connecting different parts of the brain, based on the direction and magnitude of water diffusion. Our research proposes that by studying a unique high resolution dataset consisting of both submillimeter resolution DTI and micron resolution microscopy images stained for neurons in the human brain, we can identify these complex pathways. Using three standard graph-based algorithms (minimum spanning trees, Dijkstra's algorithm, and Viterbi's algorithm), we developed computational tools for estimating pathways between pairs of brian regions. We test the hypothesis that while minimum spanning trees will compute fastest, there will be a gap in accuracy when compared to microscopy data. We hypothesize that other algorithms are slower, but will match better with microscopy. Our

platform will serve as a starting point for developing and validating novel tractography algorithms in the future.

Strange Lupe: Competing Computationally Generated Models for Generating Song Lyrics

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Esat Boucaud*[1]and Erica Castilho-Grao [2]
[1]University of Central Florida, [2]University of Central Florida

Abstract: Researchers in Cognitive Science and Artificial Intelligence have consistently questioned what it means to symbolically represent an idea and whether conscious intentionality is required. Specifically, the concept of the Uncanny Valley was first outlined by Masashiro Mori, and more recently, Nick Montfort has done work in this field through artificially generated poetry. While current machine learning advancements in lyric creation allow for computational generation, they typically cater to experienced musicians. These models are not inclusive of novice writers who are inexperienced with the syntax of lyric writing and poems. This project aims to create a more accessible model by computationally generating song lyrics based on the results of two competing models, GPT3 and LyricStudio. These models have opposing styles of creating text based on the structure of their inputs. My model “StrangeLupe” is a less labor-intensive approach. GPT3 granularity of information is dependent on the initial material; I’ve chosen the genre of rap music due to the length of material for input. We compared these models by allowing participants to utilize each model while they created songs. We used a questionnaire commonly found in Cognitive Science and UI/UX papers that allows us to gather data on participant ease of use. The results of this project could be utilized as an educational tool to introduce students to poetry in a familiar and approachable way. Additionally, this model will allow students to interact with computational models in an artistic context, further exposing and encouraging participation in STEM earlier on in their education.

Developing a chatbot that can be used for researching information consumption and messaging interventions for political participation and behavior.

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Edona Saliu*[1]and Molly Offer-Westort [2]
[1]Minerva University, [2]The University of Chicago

Abstract: Chatbots offer a promising new research tool for engaging with users within the context of their regular social media engagement. This project will develop a Facebook Messenger chatbot that can be used for various research uses: canvassing on a broad range of topics, measuring information consumption, or studying the effect of messaging interventions on political participation and behavior. The researchers will use adaptive, data-driven algorithms that learn from user exchanges and determine optimally persuasive messaging around political events. In our studies, respondents are recruited through Facebook advertisements connected to our research page. Once we are connected with respondents, we can follow up with them over time, facilitating panel data collection of social media behavior, news, and information consumption. The panel structure allows us to understand at the individual level how respondents’ online behavior and media consumption change in response to political events

and shifts in Facebook policy. This project will require cross-disciplinary expertise: subject matter from Political Science, technical expertise, and a deep understanding of the online information ecosystem from Computer Science. This project sits firmly within the interdisciplinary field of Data Science, using methods and insights from multiple disciplines. This study can demonstrate the potential of chatbots for canvassing on a broad range of topics, with potential applications by governments, public health agencies, and political organizations. Initial studies will be launched in the summer of 2022. If we successfully develop a stable subject pool, longitudinal data collection will continue into the fall of 2022 through the midterm US elections.

WoMin African Development Alliance

Discipline: Computer & Information Science

Subdiscipline: Other Computer & Information Science

Salvador Tranquilino-Ramos*[1], Launa Greer[2], Pavan Prathuru[3], Gagandeep Kaur[4], Halli Lacanlale[5]

[1]University of Illinois at Chicago, [2]University of Illinois Chicago, [3]University of Chicago, [4]California State University, Fresno, [5]University of Illinois Chicago

Abstract: WoMin African Alliance currently records the harmful impacts of extractive projects on the local communities it serves through manual data entry. To help WoMin make a stronger case for reform and understand which geographic areas have the greatest need for its services, we propose augmenting its existing data with project records scraped from the African Development Bank (AfDB). Today, the AfDB hosts nearly 5,000 projects on its website spanning 11 economic sectors and dated from 1967 through the present. We propose programmatically collecting public AfDB project records related to WoMin’s areas of interest—i.e., mining, quarrying, sanitation, and power—and then mapping those projects alongside the sites of WoMin’s outreach efforts to conduct a detailed spatial analysis. Our research aims are two-fold: (1) clustering the projects to identify statistically significant hot spots, cold spots, and spatial outliers over time using Local Moran I's statistic and then (2) overlaying the projects with satellite pollution imagery and running linear and Random Forest regressions to understand how the projects might affect the surrounding environment. Our results will help WoMin and its alliance to more effectively concentrate their time and resources.

SoyFACE data compilation and Analysis

Discipline: Computer & Information Science

Subdiscipline: Other Computer & Information Science

Jelena Herriott*[1], Lisa Ainsworth[2], Elise Aspray[3]

[1]Langston University, [2]University of Illinois Urbana-Champaign, [3]University of Illinois Urbana-Champaign

Abstract: Soybean is sensitive to atmospheric changes including rising carbon dioxide and ozone concentrations resulting from climate change. In 2004, [CO2] had risen 30% since the Industrial Revolution, and it was estimated that levels would rise by another 30% come mid-century. Increased human activity since the Industrial Revolution has elevated CO2 levels by 50% as of 2021 (Morgan, 2004). Soybean is an Ozone sensitive crop that shows evidence of damage at higher ozone levels (Morgan, 2004), which is why testing the effects of elevated ozone on this dicotyledonous plant is imperative to interpreting future crop data related to climate change. For the past 20 years, field experiments at the University of Illinois Urbana-Champaign (UIUC) have examined the response of soybean crops to rising carbon dioxide and ozone levels using

Free-Air Concentration Enrichment (FACE). Free-Air Concentration Enrichment is a technology that releases carbon dioxide or ozone gases across crops to test how atmospheric changes will impact crop development, growth, physiology, productivity, and quality in the future. The FACE treatment is delivered by wind, and the SoyFACE team at UIUC has over 20 years of data describing wind speed, wind direction, fumigation efficiency, and additional weather metrics. The goal of my REU project this summer is to analyze the SoyFACE data to identify trends, and to determine the effects of wind speed and direction on the accuracy of the elevated carbon dioxide and ozone SoyFACE treatments.

Strategies that analyze networks in brain organoids to promote the growth of healthier and more complex neural tissue

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Edwin Ruiz*[1], Dr. Alysson R. Muotri [2], Dr. Alex Savtchenko[3]
[1]University of California, San Diego, [2]Head of the Muotri Lab and Professor in the Departments of Pediatrics and Cellular & Molecular Medicine at the University of California, San Diego, [3]Chief Executive Officer at Nanotools Bioscience at the University of California, San Diego and the Muotri Lab

Abstract: At the forefront of Neuroscience, Dr. Alysson R. Muotri and the Muotri Lab have shifted 2D Brain Models into 3D structures by mastering lab-grown neural tissues named Brain Organoids. In turn, this has transitioned clinical trials to human biology, which can better demonstrate the effects of new drugs on the brain. Current challenges involve analyzing this new type of data and vascularizing the organoids to promote a healthier and more complex neural tissue. Overcoming this question can lead to insights about the early developing brain for hints in the brain mechanism that later develops into the ability to have mental states of awareness, as well as susceptibility to mental disorders. Our experiment attempts to simulate the naturally occurring environment of developing stem cells by stimulating a brain organoid with an electrophysiological input and retaining its self-organizing properties as an output, via a closed-loop system. The aim is to statistically analyze the molecular and cellular processes, and high-frequency oscillations to develop a model of information exchange dynamics that are important to global organoid growth and function. We predict that the data comparison between natural and stimulated developing neural signals of brain organoids can reveal the mechanisms and range of affects that are needed for fostering synaptogenesis throughout a developing brain organoid. This will result in a new brain model for growing more complex neural tissue by way of a new Neural Data Analysis Tool. A program (tool) that will be designed to understand and apply this new type of neural data.

Constant Memory Video Encoder for Language Grounding

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Anthony Reyna*[1], Rodolfo Corona Rodriguez [2], Trevor Darrell[3], Dan Klein[4]
[1]Ohlone College, [2]University of California, Berkeley, [3]University of California, Berkeley, [4]University of California, Berkeley

Abstract: Given a video and sentence describing an event, a system capable of returning a small segment of video where the answer to the sentence can be found would be of immense utility to assistive technologies and beyond. Current video deep learning systems used in this domain search the entire video for every sentence to find the segments being described, making GPU memory costs untenable when dealing with videos of significant length. Furthermore, it’s computationally expensive and redundant to query the same video with multiple sentences as the entire video must be reprocessed for each sentence. In this work, we explore an implementation of a memory-augmented multiscale vision transformer, a video encoding system, in order to process videos of arbitrary length while keeping memory costs constant. By using this method, the system would only process the video once and be capable of localizing segments for multiple sentences. For our ongoing experiments, we train our model on 240 hours of the Ego4D dataset—consisting of first-person-perspective video with accompanying descriptive-captions. We compare the accuracy of our system’s returned video segments, with the correct descriptive-caption, against established baselines. We expect to show that the static memory footprint method proposed can perform comparably or better to prior work in this domain, while simultaneously relaxing assumptions that the entire video must be reprocessed for each given sentence. If our method is successful, it would improve on the current state-of-the-art by significantly improving scalability to arbitrarily long videos by keeping both memory costs and computation costs down.

Generating Custom Curriculums with Virtual Reality Scenarios

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Isaac Gonzalez*[1], Edward Kim[2], Boxi Fu[3], Daniel He[4], James Hu[5], Alton Sturgis[6], Shawn Xiao[7]
[1]Cerritos College, [2]UC Berkeley, [3]UC Berkeley, [4]UC Berkeley, [5]UC Berkeley, [6]UC Berkeley, [7]UC Berkeley

Abstract: Virtual environments are a useful tool when it comes to running simulations for any sort of test, with the Unity game engine being one of them. The goal of this study is to generate custom curriculums, or sets of scenarios that will depend on the skill mastery of a trainee, in order to effectively train them to be prepared for every situation they will come across in their field. This is approached by creating an algorithm using Scenic, a scenario modeling programming language, that allows us to create and run different scenarios on Unity for testing. These will put the trainee through different types of situations to alter their curriculum specifically for each of them. This is done by using a Virtual Reality headset that will be used to test their skills and mark if they have mastered a skill or still need more practice. To gather results, a number of participants will partake in an hour-long test using the algorithm. Through these tests, we hope to prove that a Scenic algorithm can train individuals at their own pace.

Automatic Management of Cloud Resources for Distributed Systems Experiments

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Chunrui Huang*[1]and David Chu[2]
[1]City College of San Francisco, [2]University of California, Berkeley

Abstract: Distributed systems provide high throughput, fault tolerance and availability using sets of computers in cooperation to process distributed tasks that monolithic systems cannot. But existing distributed protocols cannot effectively make use of additional machines and are hard to redesign due to hidden complexities. Our goal is to create an optimizer for distributed protocols and prove that the protocol’s behavior is preserved post-optimization. But testing distributed protocols is a mechanical yet difficult process with often unreplicable errors. We will create a pipeline of Python scripts to automatically interact with Amazon Web Services, allowing for simple changes in deployment parameters, automating common tasks such as data retrieval for analysis and log generation for debugging. It will simplify the process of testing, and allow for rapid prototyping for research projects which aim to automatically increase the scalability and efficiency of distributed protocols, reducing the need for human interventions.

Curriculum Changes Necessary for Auto-grading and A's for All

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Jorge Nunez*[1], Dan Garcia [2], Jesus Villalobos[3], Destiny Luong[4], Jordan Schwartz [5], Jose Ochoa[6], Harjot Multani[7], Sebastian Estrada[8], Kamoni Fletcher[9]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]University of California, Berkeley, [4]University of California, Berkeley, [5]University of California, Berkeley, [6]University of California, Berkeley, [7]University of California, Berkeley, [8]University of California, Berkeley, [9]University of California, Berkeley

Abstract: A’s for All through mastery learning is the pedagogy we are pursuing in the classroom. “Fixed learning, and variable time” is our mantra. Our approach for achieving such methodology is through a computer-based testing (CBT) software called PrairieLearn: a free and open-source learning tool. This gives the instructor the ability to provide students with an ample supply of practice questions for a particular concept by authoring auto-graded question generators. The Beauty and Joy of Computing (CS10) is an introductory computer science course at UC Berkeley. Within this course, the first half is taught in a block-based computing language known as Snap! A huge development we are currently working on is creating an autograder that is compatible with Snap! in PrairieLearn. It will be a tool that will be of great help for our teaching model. Yet to fully implement this within our course, we have to reconsider how we structure our curriculum. A key component when creating a question generator has to pre-encode the answers to our questions. Meaning how we decide to ask certain questions will be changed because we can no longer have rubrics where an individual is involved. Snap! provides us with the ability to have human interactions within the code, although, now we are scraping those interactions. We are still providing students with fully-functional, rich, auto-graded questions, where the curriculum is automated centered. Still, according to our research, none of the important concepts are lost, and it will foster a curriculum that enables mastery learning.

Graphical Language Models to Classify Drug Toxicity

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Lucy Zheng*[1]and Mary Silva [2]
[1]Lawrence Livermore National Laboratory; University of California, Santa Cruz, [2]Lawrence Livermore National Laboratory

Abstract: Machine learning predictive models have become increasingly popular in biologic research as a means for classifying drug toxicity in the process of drug development. The accuracy of these predictive models is based on the quality of the data collected, as well as the patterns and features identified in the data. As part of the ongoing research at Lawrence Livermore National Laboratory, we will be designing a featurization method that represents a biologic knowledge graph in order to identify compounds that possibly contribute to liver toxicity. Knowledge graphs have a visual framework with interconnected nodes and edges that capture spatial relationships and provide additional meaningful context to data observations. This knowledge graph, known as the Scalable Precision Medicine Open Knowledge Engine (SPOKE) was originally developed by UC San Francisco from a collection of multiple scientific databases. The SPOKE knowledge graph contains compound, protein, disease, pathway information and more, along with observed or experimental evidence to support relationships between them. From this graph, we have designed new graphical features which combine random traversals over the graph, link prediction between nodes, and enhanced graph embeddings using BioBERT. Bidirectional Encoder Representations from Transformers for Biomedical Text Mining (BioBERT) is a biomedical language model that is traditionally used on its own as a natural language processing method for encoding sentences or words. We adapt it for encoding linked relationships in a graph in order to predict compounds that cause liver toxicity, offering a slight advantage over simply utilizing the molecular information alone.

A BCI model to predict visual reaction time

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Kyra Weiss*[1]and Dr. Kiran George [2]
[1]Cypress College, [2]California State University Fullerton

Abstract: Brain computer interface (BCI) an emerging technology that aims to provide support for those with disabilities and enhance experiences for all. Electroencephalogram (EEG) is one of the ways data can be collected and observed in a BCI system. This project will utilize data from EEGs to create a machine learning system that can predict reaction time to a visual cue before a stimulus occurs. An EEG headset was placed on each subject and they were instructed to watch a short video on the computer screen. When the green visual cue flashed across the screen, subjects paused the video. The time from the visual cues appearance to the pausing of the video was recorded. In MATLAB, the EEG data was analyzed to recognize patterns in the subjects reaction time and the brain activity directly before the visual cue. Also in MATLAB, machine learning was used to create an algorithm to autonomously predict reaction time from brain activity. Considering reaction time can be influenced by a number of factors including age and hours of sleep, EEG alone can not be used to predict reaction time with great accuracy. This project however can be built upon, and used in conjunction with other tests to build a model with greater accuracy. In the future, BCI systems that predict reaction time can be used for drivers and surgeons, as well as in situations where quick decision making is vital.

Smartphone as an Edge for Context-Aware Real-Time Processing for Personal E-Health

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Muhammad Bangash*[1]and Dr. Ahmed Ezzeldin Khaled [2]
[1]Northeastern Illinois University, [2]Northeastern Illinois University

Abstract: The medical domain is facing an ongoing challenge of how patients can share their health-related information and timeline with healthcare providers. This involves secure sharing, diverse data types, and formats reported by healthcare-related devices. We proposed a multilayer framework to address these challenges in the context of the Internet of Medical

Things (IoMT). In our framework, we utilized sensors, external services, and medical devices that measure vital signs and communicate such data with smartphones. The smartphone is used as an “edge device” to visualize, analyze, and report context-aware data to the cloud-layer, providing a secure database for users’ medical information and a set of services for processing. Our focus is on medical device connectivity, data collection, and interoperability for friction-less data processing to build context-aware personal medical records (PMRs). These PMRs are securely stored through a communication protocol, Message Queuing Telemetry Transport (MQTT), and utilized by other authorized medical staff and institutions. MQTT is a lightweight, intuitive, and easy to use messaging protocol suitable for IoMT applications and devices. Consequently, these PMRs are further processed in a cloud computing platform, Amazon Web Services (AWS). Through AWS and its services, our framework boasts a customized data pipeline from the mobile user to the cloud which then displays useful analytics, a dashboard for medical professionals, and sms-notifications. Our results demonstrate that this framework preserves the patient’s health-related timeline and shares this information with medical professionals. Our simulation aims to give researchers the foundational architectures for further expandability and improvement.

Reasoning with Compositional Concepts in the Probabilistic Language of Thought

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Laila Johnston*[1], Max Siegel[2], Tobias Gerstenberg[3], Josh Tenenbaum[4]
[1]University of Central Florida, [2]Massachusetts Institute of Technology, [3]Stanford University, [4]Massachusetts Institute of Technology

Abstract: Humans organize the world with concepts: we say that people run, and we can imagine nonexistent ideas like unicorns . We also easily assign meaning to new concepts which we may have never thought of before, like a running unicorn . How do we understand the meaning of new concepts? Past theories have usually approached the study of concepts in one of two ways: 1) Symbolic approaches explicitly define the meaning of concepts. For example, running is an action with a certain set of properties. This allows concepts to be combined with other concepts to form new ones with derived meanings, but doesn’t allow for uncertainty in learning, representation, and reasoning. 2) Statistical approaches learn concepts from data and represent concepts probabilistically. These allow for uncertainty but lack the formal compositionality key to symbolic approaches; new concepts must be learned from scratch. Here we investigate the probabilistic language of thought hypothesis (PLoT), which naturally expresses the compositional and probabilistic nature of concepts in a unified computational framework. We evaluate PLoT in an intuitive “tug-of-war” tournament scenario in which uncertainty and compositionality play key roles. For example, the concept of winner is defined as the team that most strongly pulls the rope, where team, pulling, and strength are also concepts in the model. Predictions from the PLoT model closely track human judgements and compare favorably with alternative models, including current large language models, demonstrating the viability of PLoT as a model for how humans learn, represent, and reason with concepts.

Exploring Multi-wavelength Computational Imaging

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Thi Lan Nhi Pham*[1]and Charles Dove[2]

[1]Chabot College, [2]University of California, Berkeley

Abstract: In conventional microscopy, an image is collected by bending light using a simple lens. A significant problem with this method, however, is that it is hard to get 3D images, especially with translucent, thick materials. To solve this, computational imaging combines the physics of light with computational modeling to reconstruct high-quality 3D images. Optical Diffraction Tomography (ODT) is a crucial computational imaging method which uses a reconstructive algorithm to make a 3D image from pictures being taken by tilting a light at different angles under a sample. In this research, we expand conventional ODT by using multiple light wavelengths. This approach focuses on analyzing the relationship between wavelengths, angles, and image quality.

Small Molecules Targeting RNA A-bulge sites using Computer-Aided Drug Design

Discipline: Computer & Information Science

Subdiscipline: Other Computer & Information Science

Maureen Tanner*[1]and Ilyas Yildirim [2]

[1]Harriet L. Wilkes Honors college of Florida Atlantic University, [2]Harriet L. Wilkes Honors college of Florida Atlantic University

Abstract: Alzheimer's Disease (AD) is a neurodegenerative disease that affects memory. Currently, AD has no cure even though multiple studies have tried to solve this painful disease. In addition, researchers have been looking for specific mechanisms that trigger AD and novel therapeutics for AD. One of the mechanisms behind AD is due to overproduction of 4R isoform of tau protein caused by a single mutation at exon 10-intron junction hairpin in the microtubule-associated protein tau (MAPT) mRNA, which has an RNA adenosine bulge (A-bulge). Targeting the RNA A-bulge motif in MAPT mRNA has the potential to stabilize the junction site and balance the tau isoforms. The Disney Laboratory at Scripps discovered compounds (6va2, 6va3, and 6va4) targeting and stabilizing the RNA A-bulge site, where they determined the bound states using NMR spectroscopy. Next would be to optimize these lead compounds with functional groups, using quick computer-aided simulations. We investigated the binding properties of these compounds and their stabilities using molecular dynamics (MD) calculations. Results showed that the bound states discovered by the Disney laboratory matches partially well with the MD predictions. We found that 6va3/RNA A-bulge complex is stable throughout one microsecond MD simulation. Our results are important because predicting the correct binding properties of small molecules targeting RNA loop motifs opens doors to utilize computer-aided MD simulations in silico drug design, which can accelerate optimization of lead compounds. Future studies will involve optimization of 6va2-4 using dynamic binding methodology to discover novel drugs having potent binding affinities and specificities.

Automating Data Collection of Pollinator Studies using Deep Learning and Computer Tracking

Discipline: Computer & Information Science

Subdiscipline: Computer & Information Sciences

Luke Meyers*[1]and Remi Mégret [2]

[1]Seattle University, [2]University of Puerto Rico Río Piedras

Abstract: Honeybees play an important role in our modern agriculture systems as pollinators of many critical crops. Research to understand the behavior and ecology of bees is therefore important for assuring continued food production and stability. A partnership at the University of Puerto Rico Río Piedras has previously used customizable artificial flowers for studying honeybee foraging behavior and decision making. However, these studies are currently limited by the capacity of visual identification by researchers and cannot study a large number of individuals. To automate the data collection of studies of managed pollinator behavior, we are developing a video and analysis pipeline to measure honeybee visits to an artificial flower patch. We recorded videos of foraging honeybees on an edge computing system with the power to host real time data collection and analysis. We use pose detection models based on deep convolutional networks to detect individuals within each frame and use them to generate identity-based tracks. A custom script is used to count the total number of visits using the proximity of the predicted tracks to known flower locations. An evaluation on 3 validation videos showed that the pipeline could detect all 98 human recorded visits, with total counts higher by around 9% due to double detections. In summary, our system demonstrates the potential to increase the throughput of critical studies of pollinator behavior by automating data collection using machine learning tools.

Heuristic Evaluation of an mHealth Prototype for Cancer Survivors with Disabilities

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Jocelyn Sotelo*[1], Dr. Rachel Adler [2], Paulina H. Morales[3], Kevin Baez[4], Melissa Delgado [5], Beija Teoli[6], Susan Magasi[7]

[1]Northeastern Illinois University, [2]Northeastern Illinois University, [3]Northeastern Illinois University, [4]Northeastern Illinois Universtiy, [5]Northeastern Illinois University, [6]University of Illinois at Chicago, [7]University of Illinois at Chicago

Abstract: New physical, cognitive, psychological, and social challenges arise for cancer survivors in managing life after cancer treatments. Coping with these consequences can be difficult to navigate and many survivors are left to manage them on their own. Mobile health (mHealth) interventions can be an effective way to support survivors. We are designing a high-fidelity prototype of an mHealth application using Marvel to empower the community of survivors to self-manage the lifelong effects of cancer and its treatment. To identify usability issues and improve on the design, we conducted a heuristic evaluation of the prototype with 22 students taking a Human-Computer Interaction course. The heuristic evaluation was based on Neilson's 10 principles and conducted using Maze. Students were grouped together into 6 groups consisting of 3-5 people and given different scenarios and tasks to complete. Afterwards, students were asked to identify and describe at least 3 issues, name the heuristic that was violated, and then rate the severity of the issue from 0 to 4, with 4 being a usability catastrophe. Results of the heuristic evaluation were positive. The highest rated issues found by students were rated a 3.These issues included missing navigation buttons, lack of help guides, and some students could not find the accessibility features. Modifications are being made to the prototype based on these results. Future work will include usability testing on cancer survivors with disabilities. The results of this research will lead to the development of an mHealth application for cancer survivors suffering from long-term cancer effects.

Characterization of resistomes in gastrointestinal and respiratory tracts.

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Derrick McNealy*[1]and David Garrett Brown PhD [2]
[1]Mississippi Gulf Coast Community College, [2]University of Utah

Abstract: Antimicrobial resistance (AMR) complicating respiratory tract (RT) infections is associated with the deaths of millions annually. The community of microorganisms that colonize the human body, termed the microbiome, has widespread effects on the human health, and notably contains a reservoir of AMR genes, collectively referred to as the resistome. Understanding the characteristics of this system will improve our understanding of AMR in colonizing pathogens. Though horizontal gene transfer occurs between genomes isolated from different body sites, the relationship between the gastrointestinal (GI) tract and respiratory tract (RT) resistomes have not been deeply investigated. To better characterize this relationship, we analyzed a publicly available dataset from the Human Microbiome Project (HMP) to test for similarities and differences between resistomes of samples from the throat and GI tract of healthy humans. Based on this characterization, we then perform further analysis to understand differences in AMR diversity between samples in the same subjects as well as between subjects over time. Analysis is currently ongoing. Our work has the potential to inform how resistance profiles of bacteria in the gut may impact the respiratory tract.

Determining the Splicing Pattern of TCGA database

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Rakshya Sharma*[1], Dennis Mulligan [2], Alexis Thornton[3], Angela N. Brooks[4]
[1]University of California, Santa Cruz, [2]Department of Biomolecular Engineering, University of California, Santa Cruz, [3]Department of Biomolecular Engineering, University of California, Santa Cruz, [4]Department of Biomolecular Engineering, University of California, Santa Cruz

Abstract: The goal of this project is to find the complete RNA splicing profile for a large, diverse set of cancer samples, study the performance of splicing analysis tool Mutually Exclusive Splicing Analysis (MESA) with different datasets including The Cancer Genome Atlas (TCGA) and analyze the results generated. Errors in RNA splicing can cause a number of human disorders. Identifying all instances of incorrect RNA splicing can provide an opportunity to treat numerous cancer related diseases. RNA-seq is used to look at gene expression levels in general and gene isoform abundance. MESA is a new method created by the Brooks lab for quantifying alternative splicing events. It detects many forms of alternative splicing with a single metric, and provides an easily understood percent-spliced (PS) value for each junction from each sample in the input data. It has several filtering to help remove false junctions and improves the output accuracy. MESA is a set of Python programs and its quantification analysis focuses on mutually exclusive junctions, which are splicing events where the intronic intervals overlap and cannot coexist on the same transcript. The main aim of this project is to apply MESA to the entire TCGA dataset of 20,000 tumor samples and create a publicly available database of splicing patterns used for a variety of analyses. The database is significant because MESA makes it easier to look at the entire splicing profile, unlike other splicing quantification tools, and MESA can be run with large numbers of samples.

Scrubbing of the Amino Acid Header (SAAH) for T-Coffee - An Algorithm for Cleaning Protein FASTA Headers

Discipline: Computer & Information Science

Subdiscipline: Other Computer & Information Science

Charles Lett Jr.*[1], Sharon Lewis [2], Yonathan Tilahun[3]

[1]Langston University, [2]Langston University, [3]Langston University

Abstract: Sequence alignment plays a key role in identifying relationships between DNA, RNA or in this case, protein sequences. An accessible tool for sequence alignment is T-Coffee, an online-based, multiple sequence aligner. One of the caveats with T-Coffee, however, is that it cannot align sequences that contain irrelevant data within their headers. For example, FASTA formatted sequences from UniprotKB, a database for protein sequence and functional information, can have this issue, preventing T-Coffee from aligning the affected sequence(s) without header modification. Previously, sequence headers were modified manually, leading to a large amount of time dedicated to curating headers before sequences could be aligned with T-Coffee. SAAH, an algorithm developed using Python, was created to streamline this process. To test the efficacy of SAAH, several sequences and their respective headers were isolated from the KAT2B gene, where tests were conducted to compare the times taken manually and algorithmically to modify sequence headers. Results showed that SAAH completes header cleaning in a fraction of the time it would take manually, therefore, reducing the time needed to curate a file of protein sequences before it can be aligned using T-Coffee.

An analysis of electric vehicle home charging station energy consumption in Austin, Texas

Discipline: Computer & Information Science

Subdiscipline: Computer & Information Sciences

Jerry Adams*[1]and Eleftheria Kontou [2]

[1]Chaminade University of Honolulu, [2]University of Illinois at Urbana-Champaign

Abstract: The widespread adoption of Electric Vehicles (EV) by consumers has likewise resulted in consumer home electric charging stations to support EVs. Despite this, there is limited understanding of the magnitude and variability of the cost of electricity for this application. This information gap may hinder optimal investing and planning for electric grid infrastructure support. In this project, the data was analyzed from electricity consumption of home-based EV charging stations based on 500 households utilizing commercial electricity grid rates for 2018 in Austin, Texas. The energy consumption from EV chargers was cross-referenced with the commercial electricity grid rates. Results show that electricity use varies dramatically per kilowatt-hour, depending on station design and high uncertainty in use. The main driver of cost is low utilization, which results from a combination of few charging events and limited energy recharged during each event. Low utilization leads to significantly higher electricity costs, particularly for rates with demand charges; however, cost decreases rapidly as utilization increases. For high-utilization stations, selecting rates with demand charges can actually reduce electricity costs compared to non-demand-charge rates. Moreover, significant opportunities for cost savings based on existing rates include preferential charging during off-peak hours and limiting station power to prevent maximum power consumption.

Case closed: Developing Computations Models to Reconstruct Low Coverage DNA Samples for the Purpose of Solving Cold Cases

Discipline: Computer & Information Science

Subdiscipline: Other Computer & Information Science

Eduardo Garcia*[1]and Remy Nguyen [2]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz
Abstract: When attempting to use old DNA samples to solve decades-old forensic cases, the samples in question are minute, contaminated, or heavily degraded. Efforts to sequence these low-coverage samples for identity and kinship analysis are unsuccessful. Our goal is to use computational approaches to genetically identify these samples. We have created and implemented an algorithm that calculates likelihood ratios to find identity-by-descent (IBD) ratios at several single-nucleotide polymorphic (SNP) sites between a sample and variant information from a reference population. Then we develop methods to complete the reconstruction of mitochondrial haplotypes from forensic sample mixtures. This work will assist in cold cases with limited genetic evidence and allow for the analysis of kin relations in low-quality forensic specimens.

Analysis on Skin Pigmentation Variation in Indigenous American Populations

Discipline: Computer & Information Science
Subdiscipline: Other Computer & Information Science

Maria Flores*[1]and Abigail Bigham [2]
[1]University of California, Los Angeles, [2]University of California, Los Angeles
Abstract: Pigmentation is known to be a phenotype with considerably high variation in human populations. While there has been extensive research on pigmentation in mouse models, as well as an understanding of the genes involved in the pigmentation pathway, their role in human pigmentation is not well characterized. Past studies in African, Asian, and European populations have identified and analyzed genes that could be contributing to skin pigmentation differences among these groups. However, these studies have neglected to include Indigenous populations, particularly in the Americas, contributing to a lack of understanding of the genetic architecture surrounding pigmentation variation in these populations. This presentation will investigate variants that could potentially be contributing to skin pigmentation differences between Europeans and 101 Maya individuals from Chiapas, Mexico via the implementation of GWAS analysis and admixture analysis. Data collection involved a quantitative measure of Melanin (M) using a dermaspectometer (DSM-II) from the Left Arm (LA), Right Arm (RA), Forehead (F), and Hair (H). Our goal is to identify new genes that contribute to European/non-European skin pigmentation differences providing insight into the genetic structure of human skin pigmentation variation aiding in the effort to improve our understanding of these admixed populations.

The influence of grouping features on explainable artificial intelligence for a complex fog prediction deep learning model

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Evan Krell*[1], Scott A. King [2], Hamid Kamangir[3], Josh Friesand[4], Waylon Collins [5], Philippe Tissot[6], Julianna Judge[7]
[1]Texas A&M University - Corpus Christi, [2]Texas A&M University - Corpus Christi, [3]Department of Agricultural and Environmental Engineering, University of California Davis, [4]Robotics Institute, College of Engineering, University of Michigan - Ann Arbor, [5]National Weather Service, [6]Conrad

Blucher Institute for Surveying and Science, Texas A&M University - Corpus Christi, [7]Texas A&M University - Corpus Christi

Abstract: Advances in machine learning enable modeling complex relationships, but are increasingly reliant on "black boxes" like deep learning where it is impractical to determine why predictions are made. This limits trust in the model, motivating eXplainable Artificial Intelligence (XAI) to provide tools to understand how models make decisions. XAI techniques are used to explain FogNet: a model for predicting coastal fog whose input is a raster of 384 atmospheric variable channels. XAI techniques struggle with feature correlations, making it challenging to explain FogNet. For example, a group of 108 channels represents the lower atmosphere thermodynamic profile. This gradient is used by forecasters to predict fog but has strong spatial-wise and channel-wise autocorrelation. Grouping related features may improve XAI accuracy. Here, XAI techniques are applied with features grouped at multiple levels of granularity. The coarsest divide s the channels into five groups based on physical similarity. The second is to treat each channel as a feature, and finally superpixels within each channel. To analyze explanation sensitivity from the feature grouping used, the more granular outputs are aggregated into coarser groups. This allows direct comparison of, for example, channel-wise explanations when using channels as feature groups, and when using superpixels within those channels as groups. The results show that the feature grouping scheme influences the explanations, complicating interpretation of XAI. However, consistencies also emerge that provide confidence in certain aspects of the explanations. Combined with forecaster domain knowledge, we demonstrate using the XAI outputs to generate hypotheses that drive future model development.

Using Machine Learning on Mobility Data to Inform Consumer Trends from 2018-2021

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Mariana Duarte*[1], Dr. Kelly Gaither[2], Dr. Justin Drake[3]
[1]University of Illinois at Urbana-Champaign, [2]University of Texas at Austin, [3]University of Texas at Austin

Abstract: The COVID-19 pandemic changed consumer behavior. Non-pharmaceutical interventions were implemented to reduce COVID-19 spread. These included mask mandates, social distancing, regulations on outdoor gatherings of over 100 people, and restrictions placed on businesses and services. While fast food service thrived during the pandemic from a gross population perspective, little is known about sub-populations disaggregated by ethnicity. Whataburger is an American regional fast food restaurant chain that began in Corpus Christi, Texas in 1950 and later moved headquarters to San Antonio, Texas. Additionally, Texas has the second largest percentage of Hispanic/LatinX people (39.34%) in the US. The hypothesis for this research was that the non-pharmaceutical interventions that were put in place to prevent the spread of COVID-19 altered consumer behavior. To investigate this hypothesis, this research examined Hispanic and non-Hispanic consumer behavior by looking at visits to Whataburger locations in Texas using Safegraph Mobility data (SM). Machine learning algorithms: Linear Regression, K-means, and Support Vector Regression, used pre-pandemic and pandemic visitor behavior disaggregated by ethnicity to predict trends. Python was used to integrate SM data and Census data to estimate this disaggregated consumer behavior. By using census data collected in census block groups, we were able to estimate the ethnicity of visitors to Whataburger locations. The results, during the year of 2019 there was a significant increase of Latinx consumers at Whataburger locations; this increase might be influenced by the regulations implemented. The findings of this research inform consumer behavior when populations experience significant disruptive events such as the COVID-19 pandemic.

Automating the imaging and identification of foraminifera with the ForaBot

Discipline: Engineering
Subdiscipline: Electrical Engineering

Gabriella Dangler*[1], Dr. Edgar Lobaton [2], Turner Richmond[3], Erik Modesto Reyes[4]
[1]North Carolina State University, [2]Professor / researcher (principal investigator), [3]Graduate researcher, [4]Undergraduate researcher

Abstract: The manual imaging and identification of foraminifera (forams), tiny fossils around the size of a grain of sand, is very time-consuming and tedious. The purpose of the ForaBot is to alleviate this burden and allow for an enhanced understanding of aquatic microorganisms, giving scientists an insight into environments throughout Earth's history. The hypothesis of this study is that the ForaBot can effectively and efficiently automate the process of identifying forams. The ForaBot is a robotic platform capable of manipulating and imaging forams. It is composed of an aluminum chassis, appendages that hold a camera and microscope, and robotic arms and containers that are controlled by servos and stepper motors. The bot begins with a supply of forams in a funnel and isolates a single foram. This foram is then imaged, and the images are run through machine-learning algorithms to properly identify it. The foram is finally sorted into a container according to its classification. Each new iteration of the ForaBot requires the construction of the chassis, modeling and printing various 3D-designed components, soldering and wiring the electrical components, and various rounds of testing to ensure proper functionality. The results have shown that the ForaBot has 80% accuracy, as compared to the 63% accuracy of a human expert. The bot is being continually refined to reduce errors in both transporting and imaging the forams. This project has found that the ForaBot will assist biologists in their discovery and understanding of Earth's various time periods and microorganisms.

Simplifying the Design of a Tendon Actuated Soft Gripper into an Easy-To-Follow, Low-Cost Toolkit for High School Level Students

Discipline: Engineering
Subdiscipline: Electrical Engineering

Jonathan Chinana*[1], Lucas F. Gerez [2], Harrison Young[3], Abby Lockhart Calpito[4]
[1]Navajo Technical University, [2]Harvard University, [3]Harvard University, [4]Harvard University

Abstract: Soft Robotics Toolkit open-source platform was created at the Harvard Biodesign Lab to educate students, teachers, and hobbyists on the fundamentals of electronics, soft robotics, and engineering. After a successful pilot of a new tendon-actuated soft gripper (TASG) kit in the high school setting, several improvements to the design of this tendon-actuated gripper kit were identified such as high production cost and the use of complex electronics. The soft gripper toolkit currently has a plug and play aspect which does make it easy to assemble, but also hinders students overall learning objectives and doesn't fully immerse them in the engineering design process. The aim of this research is to update the current design of the TASG toolkit by using accessible materials to reduce production cost and by simplifying the electronic circuit design by moving from custom built electronics to off-the-shelf reconfigurable electronics. To do this, we switched out the custom electronics from the previous soft gripper design and inserted a breadboard with an Arduino microcontroller: this change will allow students the ability to program, implement, and test off-the-shelf electronic components on their own circuit. We expect that these design changes will give students more creative control of how they want to structure their soft grippers and electronics, while giving educators the confidence to understand and implement the toolkit in their engineering focused curriculum.

Electronic Mode Stirring Improves Wireless Communications in an Animal Cage Environment

Discipline: Engineering
Subdiscipline: Electrical Engineering

Sara Reyes*[1], Matt Reynolds [2], James Rosenthal[3]
[1]University of Washington, [2]University of Washington, [3]Swiss Federal Institute of Technology Lausanne

Abstract: In vivo recordings of neural ensemble activity in non-human primates (NHPs) have contributed to the understanding of how neural activity relates to motor function and intent. Traditionally, neural recording has been conducted in constrained environments, such as head-fixed experiments using bulky wired equipment to achieve high data throughput and reduce measurement noise. To collect more natural data from free-moving NHPs requires a high speed, low power wireless uplink of the neural data. However, wireless communication inside a metal NHP cage suffers from dense multipath interference, due to multiple signal bounces from the cage walls, which decreases communication reliability. We explored an approach called "Electronic Mode Stirring" to obtain better communication reliability. We found that by adding 4 switchable reflecting antennas to the roof of the cage to perform mode-stirring we were able to improve the mean one-way path loss and improved the worst-case signal loss across 126 measured positions in the primate cage. We expect that the reduced signal loss with the mode stirring system will lead to improved wireless communication reliability inside the cage.

Simulation of a Water-cooling Block for Thermal Management in a Nanoparticle Synthesis Process

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Chase Duncan*[1]and Joaquin Camacho [2]
[1]San Diego State University, [2]San Diego State University Professor

Abstract: Nanoparticle technology has a wide range of applications that can be used to improve current technology and benefit society. Applications such as creating a better delivery system for cancer drugs, remediation of environmental pollutants, and can potentially be used to create low-cost long range batteries to power electric cars that will eventually replace cars powered by the combustion engine. This project focuses on the thermal management of a nanoparticle synthesis process that is driven by a flame. An aluminum cooling block currently being used to collect flame-synthesized manganese oxide nanoparticles. By creating a three-dimensional model of the cooling block and manipulating various parameters through simulations, this model was able to study how the magnitude of the water velocity through the block, the intensity of the heat flux, and the temperature of the water affect the body temperature of the

cooling block. These computer simulations have helped map out the flame's radial temperature distribution over the volume to give a clear understanding of how we can manipulate the cooling block. In this study, it is important to understand how temperature will change over the body of the cooling block because it explains the properties of the nanoparticle film that collects on the cooling block during the flame-synthesis process.

Characterizing Properties of Thiol-ene Crosslinked Hyaluronic Acid Hydrogels for Meniscus Tissue Engineering

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Kayla Castillo*[1], Jenny Robinson [2], Phil Elrod[3]
[1]University of Kansas, [2]University of Kansas, [3]University of Kansas

Abstract: Maladaptive repair of meniscal injuries results in loss of motion, pain, and onset of knee osteoarthritis. Hyaluronic acid (HA) hydrogels provide a potential tissue regeneration method as their viscoelastic properties can be modulated via polymer chemistry. In this study, reactive -ene groups were functionalized on the backbone of HA by varying molar ratios of HA to pentenoic anhydride to generate a library of degrees of substitution (DOS) to further characterize network formation and physical properties. A thiol-ene click chemistry mechanism was used for hydrogel synthesis. Gels were swelled in ultra-pure water, phosphate buffered saline, or cell growth media. Dynamic mechanical analysis (DMA) was used to assess compressive properties at a single strain (.005mm/s) and viscoelastic properties at 1 Hz. Enzymatic degradation was assessed by mass loss studies in hyaluronidase (250 active units/mL). The hypothesis was that increasing DOS would result in increased crosslinking density (CLD) therefore decreasing swelling and rate of enzymatic degradation and increasing the compressive modulus and storage modulus at 1 Hz. For gels swelled in water, increasing DOS resulted in a decrease in swelling, increase in compressive modulus, increase in storage modulus, and decreased enzymatic degradation. Gels swelled in PBS and growth media followed the same trends with overall reduced values compared to water due to osmotic deswelling. Results indicated that controlling CLD by modulating the DOS of HA results in mechanical and viscoelastic properties that recapitulate those of native meniscus tissue. Current work is focused on determining the impact of these properties on meniscal fibrochondrocyte behavior.

Purification of Brewery Wastewater Using the Formation of Propane Hydrates

Discipline: Engineering
Subdiscipline: Chemical Engineering

Geuris German*[1], Devinder Mahajan [2], Sihan Li[3], Hugo Ramos[4]
[1]Stony Brook University, [2]Stony Brook University, [3]Stony Brook University, [4]Stony Brook University

Abstract: Water treatment facilities are becoming increasingly needed as the climate change crisis continues to alter ecosystems around the globe. Take the water issues currently persisting in the western coastal region of the United States. California has been experiencing its worst drought in over 1000 years. While many potential solutions have been proposed, we are exploring the possibility of utilizing brewery wastewater for water purification. ** California has almost double the number of breweries of any state in the country (931). According to a publication by The Equipped Brewer, craft brewers on average use three gallons of wastewater

per gallon of beer produced, and large brewery facilities on average use seven gallons of wastewater per gallon of beer. * Brewery effluent typically contains high levels of suspended solids, primarily yeasts, hops, other grains, and sugars. These solids are difficult for water treatment plants to break down and can consume too much oxygen in the process, disrupting the delicate balance of bacteria and microorganisms that sewage plants rely on. Our approach utilizes the formation of clathrate propane hydrates by mixing propane at 60 psi with wastewater in a windowed reactor and using a cooling bath to lower the temperature to +1-3℃. The collected clean water is achieved by separating the hydrates and then decomposing these hydrates by warming them to room temperature. The water purity is then tested using Total Suspended Solids (TSS). The formation of propane hydrates reduces the number of suspended solids in brewery wastewater and therefore increases water purity.

DNA Circuit Strand Cascades: Leak Reduction in the Seesaw Gate Motif

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Spencer Winter*[1]and Dr. Lulu Qian [2]
[1]California State University, Monterey Bay, [2]California Institute of Technology (Caltech)

Abstract: DNA-based molecular programming has reached new levels of complexity in recent years. Seesaw gates, a powerful design for DNA computation, use a fuel strand to amplify the signal of an input strand, allowing for thresholds and, as a result, the creation of totally chemical logic circuits. However, the more complex the systems become, the greater the issue of leak, or unintended chemical reactions. In the seesaw gate, fraying on the output toehold can lead to the fuel displacing the output without the addition of an input, creating noise in the system that scales as the computations become more intricate. As a solution, a novel design of the seesaw gate complex is proposed that changes the conformation of the gate between the attachment of the input and displacement of the output, preventing the fuel strand from unintended interaction. This new gate design will be simulated before being synthesized and tested. A strand displacement cascade reaction will be conducted with a fluorescent output, which will be recorded and analyzed against a control reaction. The reaction trajectories will then be modeled and compared to the simulation. It is anticipated that leak, indicated by premature fluorescence, will be significantly reduced compared to standard seesaw cascades. As a major barrier to the field of molecular programming, reduction of leak is necessary to continue scaling DNA computations to the level of their electronic counterparts. As a result, the proposed new design for gate complexes is a breakthrough and paves the way for increasingly sophisticated biomolecule-based computers.

Energy Analysis for Hurricane Resilience in Culebra, PR

Discipline: Engineering
Subdiscipline: Electrical Engineering

Michael Vazquez Nieves*[1]and PhD. Eduardo Ortiz [2]
[1]University of Puerto Rico at Mayaguez, [2]University of Puerto Rico at Mayaguez

Abstract: The island municipality Culebra located at the east of Puerto Rico is energized by a 38 kV submarine cable coming from Vieques, which in turn comes from Naguabo, PR. In September 2017, Puerto Rico including Culebra was impacted by Hurricane Maria. This category 5 hurricane with sustained winds of 175 mph caused catastrophic damage to the flora, fauna, communications, access to drinking water, but mainly, to the electric power distribution.

According to reports, the electric service in Culebra was repaired after 6 months, and hundreds of deaths. So, what options can be explored to avoid the interruption of basic services, and therefore safeguard the lives of the inhabitants of Culebra? We proposed to design, and simulate two hybrid PV systems of 372.6 kW, and 414.0 kW to generate enough electricity to cover the demand of the island's critical buildings using Aurora Solar software. Once the PV systems were simulated, the required technologies along with their specifications were selected, and evaluated through a power analysis, and shadow reports were analyzed to quantify the solar energy production efficiency resulting in a TSRF of 98%, and a TSRF of 95%, respectively. which are acceptable. In addition, the resilience of a rechargeable battery system to withstand 6 months of power outage recommended by the ReOPT software was evaluated. Finally, a financial analysis was performed which breaks down an initial investment of approximately $2,000,000. Incentives and rebates can be used to recover the initial investment in approximately 6 years which is feasible.

Convex Optimization for Electric Vehicle Charging

Discipline: Engineering
Subdiscipline: Electrical Engineering

Gil Marc Sia*[1]and Nathaniel Tucker [2]
[1]University of California, Santa Barbara, [2]University of California, Santa Barbara

Abstract: Electric vehicles (EVs) have been rising in popularity since the past decade in hopes to minimize carbon emissions made by gas-fueled cars. Parking lots have acquired charging stations to offer EV owners the option to charge outside their homes. Although a growing number of EVs is seen as a positive trend, the overall demand for electricity is rising exponentially. This introduces a new problem involving our current sources of energy—renewable sources. When demand exceeds supply, power grids may have to switch to carbon-based power plants to meet such energy needs, destroying the purpose of electric vehicle production and renewable energy infrastructures which is to reduce carbon footprint. Our goal is to design an algorithm that outputs an optimized charging schedule for individual EV units. To achieve this, first, we analyze historical data of each vehicle to learn charging patterns, electricity pricing, and output from power grids. Second, we take advantage of convex optimization techniques to determine an optimal charging schedule which: 1) predicts a departure time, 2) adjusts charging power outputs as influenced by current electricity pricing, and 3) accounts for the energy consumption state of the parking lot. Designing this optimized charging algorithm provides increased efficiency in renewable energy usage, ensures a net decrease in carbon emissions, and in addition, reduces charging cost.

Effectiveness of UVC Treatment in Minimizing Biofouling on Polymer Adsorbents for Seawater Critical Mineral Extraction Systems

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Mirelys Carcana-Barbosa*[1], Maha N. Haji [2], Olivia Murphy[3]
[1]University of California, Berkeley, [2]Cornell University, [3]Cornell University

Abstract: Meeting the world's clean energy goals and keeping pace with the rise in demand for electric vehicles will require increased energy storage via batteries. However, terrestrial sources of minerals key to batteries, such as lithium and cobalt, are limited. Luckily, seawater is a potential source of dissolved forms of these critical minerals.The Symbiotic Engineering and Analysis (SEA) Lab at Cornell University specializes in building systems for harvesting these minerals in a sustainable and cost-effective manner. A primary obstacle to overcome in deploying polymer adsorbents in the ocean is biofouling, the accumulation of microorganisms inhabiting the material surface and creating an organic film. Biofouling has been shown to reduce the maximum mineral uptake of polymer adsorbents and to reduce adsorbent reusability. Previous studies have found that treatments exposing adsorbents to UV-C light in increments of 6 hours significantly reduced biofouling over a 20-day period. This study investigates the effect of varying UV-C light exposure (6 hour, 12 hour, and 24 hour) on polymer adsorbents to reduce biofouling while minimizing polymer degradation. Four systems of polymer adsorbents with varying UV-C light exposure were deployed in a local water source for a 20-day period and the growth of microorganisms was monitored through mass changes over time and scanning electron microscopy. Results of this study will be used to inform biofouling mitigation strategies to optimize the extraction of critical minerals in an environmentally-friendly and autonomous way.

Development of GM-CSF encapsulated Cell-Membrane Coated Nanoparticles for Cancer Immunotherapy

Discipline: Engineering
Subdiscipline: Chemical Engineering

Dana Allababidi*[1], Jyothi U. Menon [2], Andrea Gonsalves[3]
[1]University of Rhode Island, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Granulocyte-macrophage colony-stimulating factor (GM-CSF) is a potent cytokine used in cancer immunotherapy as it promotes dendritic cell differentiation and has also been shown to directly inhibit cancer cell proliferation. However, GM-CSF has a very short half-life (~60 minutes), reducing its therapeutic efficacy. As a result, GM-CSF is currently used only in the treatment of palpable tumors (e.g. melanoma). We hypothesized that the blood half-life and therapeutic efficacy of GM-CSF can be enhanced by encapsulating it within nanoparticles for sustained drug delivery. We successfully synthesized poly lactic-co-glycolic acid polymer nanoparticles (PLGA NPs) encapsulating GM-CSF with a diameter and polydispersity index (PDI) of 130 d.nm and 0.232 respectively. A 'burst' release of GM-CSF was observed from the NPs within 24 hours followed by sustained release over the remaining 21 days. The NPs were coated with cancer cell membrane (CCNPs) to enhance the delivery of GM-CSF to the tumor site, as the homotypic properties of cell membranes can interact with the tumor. CCNPs were synthesized using an extruder, with an average diameter and PDI of 165.8 d.nm and 0.282 respectively. EVOS imaging following fluorescent dye loading in the cell membrane and the PLGA layers confirmed the core-shell nature of the formulation. Ongoing studies are focused on optimizing the ratio of cell membrane to nanoparticles, following which GM-CSF will be encapsulated. We will then carry out physicochemical characterization of the final formulation, and assess its therapeutic efficacy in vitro using three-dimensional (3D) tumor cell cultures.

Fabrication of Novel Aluminum Welding Fillers Reinforced with Nanoparticles for Aerospace Applications

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Norman Burgos*[1]and Oscar Marcelo Suarez [2]
[1]University of Puerto Rico at Mayaguez, [2]University of Puerto Rico at Mayaguez

Abstract: Aerospace components bearing innovative and reliable weld fillers are critical in manufacturing lightweight and cost-effective structures for space exploration missions. Aluminum alloys are the filler of choice for such exacting applications, AA5356 being the most used alloy. These fillers, however, have a high fabrication cost due to the many alloying elements needed and the post-welding treatments the component must undergo to render optimum mechanical properties. Hence, to address these shortfalls, the use of nanoparticles, such as diborides, has been proposed. These diboride particles have shown to enhance the fillers' mechanical strength, providing higher service temperature, and hardness, when compared to unreinforced fillers. Furthermore, we suggest that an addition of 4% magnesium, along with nanoparticles, will guarantee better-welded, AA6xxx-based alloys able to withstand extreme conditions typically encountered during space exploration. This study focuses on developing and optimizing the proposed aluminum/magnesium-based filler reinforced with diboride nanoparticles for the development of multifunctional aerospace structures. We manufactured XbB 2 nanoparticles by fragmenting XbB 2 pieces in a high energy ball mill to produce nanocomposite pellets (Al/XbB 2) via cold welding. The pellets were then inoculated into molten Al-Mg alloys through stir casting, leading to a simple, inexpensive, and reproducible means of fabrication. Preliminary mechanical test results (tensile tests and Vickers hardness) on aluminum welds with nanoparticle-reinforced fillers showed an improvement of up to 40% when compared to unreinforced welds. These findings evinced that the reinforcing nanoparticles enhance the mechanical properties of the welds, to ultimately render more reliable components, at an affordable cost.

Multi-Robot Collaborative Planning for Package Transportation

Discipline: Engineering
Subdiscipline: Electrical Engineering

Elias Morley*[1], Ellis Ratner [2], Jason Choi[3]
[1]Diablo Valley College, [2]University of California, Berkeley, [3]University of California, Berkeley

Abstract: Robots have rapidly improved warehouse automation where distribution centers now rely on a variety of different robots for specific purposes. Traditionally this has been accomplished through the utilization of manipulators, whose purpose is to pick up and distribute packages, and wheeled robots, whose purpose is to transport the packages throughout the warehouse. Wheeled robots have several limitations, some of which include the inability to respond to dynamic and unstructured environments. It is common for warehouses to have stairs, ledges, sharp corners, and low friction terrain from dust and liquid. These types of obstacles highlight some of the limitations wheeled robots have in warehouses and illustrate the need to implement more versatile delivery robots. One of the main challenges when utilizing more advanced robots and sensor systems is managing uncertainties. Sensor noise, actuation noise, human interaction, and modeling and mapping of a dynamic environment are just some of the many challenges when attempting to implement adaptive and versatile robots. Our work entails implementing a cutting-edge robot known as a quadruped, which mimics the structure and movement of a four-legged animal with the aim to develop robust strategies to resolve uncertainties in both navigation and integration between robots. Specifically, this work concentrates on dynamic pathfinding of the quadruped robot, coordination between the manipulator and the quadruped when distributing complex and diverse packages; and

pathfinding under an unstable load. Our results demonstrate successful strategies and solutions for integrating multi-robot systems for package delivery in unstructured and dynamic environments.

Integration of Additive Manufacturing with MEMS motors to Extend their Range of Application using Robust Mechanisms at the Millimeter Scale

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Oliver Aceves*[1], Alexander Alvara[2], Kristofer Pister[3]
[1]University of Notre Dame, [2]University of California, Berkeley, [3]University of California, Berkeley

Abstract: This research seeks to apply additive manufacturing, or 3D Printing (3DP), to micro electro-mechanical systems (MEMS) motors and extend their range of application to robust out of plane motion of up to 3 degrees of freedom (DOF) through the use of mechanisms at the millimeter scale. Application of the MEMS linear actuators has been limited because of the planar nature of their fabrication, thus we seek to negate their shortcomings through the incorporation of 3D linkages. The 3DP will be accomplished on a Objet260 3D printer using VeroPlus ($\varepsilon = 0.45$, $E = 1191$ MPa) for rigid links and TangoPlus ($\varepsilon = 0.57$, $E = 0.34$ MPa) for compliant joints; both materials are variations of photopolymer acrylic based resin. Preliminary designs include a 1DOF “Walker”, a 2DOF “Runner”, and a 3DOF “Reacher''. The Walker is two conjoined four bar mechanisms and converts linear motion in one direction to linear motion in the opposing direction and improves force output by a factor of 1.5. The Runner will utilize a serial chain of four bar mechanisms on a rotating base and prioritize the power production with an input-to-output displacement ratio of 1:10. The Reacher will prioritize controlled range of motion (ROM) with a slider mechanism on a ball and socket base, which will produce a hemispherical ROM with stationary motors. The results of the project will allow for a larger application of MEMS motors and will lead to a greater ability to scale down in the field of robotics.

Anionic Nanogels for Use in the Development of Oral Cancer Screening Assays

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Kenndal Williams*[1]and Marissa Elizabeth Wechsler[2]
[1]University of Texas at San Antonio, [2]University of Texas at San Antonio

Abstract: Oral cancer is often preceded by a clinical premalignant phase accessible to visual inspection by physical examination of the intraoral mucosa under bright light for signs of oral potentially malignant disorders. However, early-stage cancers are often asymptomatic and mimic benign conditions prompting the need for more precise and accurate detection methods. Non-invasive liquid samples, such as saliva, represent a source of tumor derived biomarkers for the identification of disease indicators for early screening/diagnostic applications. For this reason, there is a need to develop biosensors capable of detecting changes in oral cancer specific biomarker expression in saliva using stable and selective receptors. This project aims to utilize synthetic, polymeric, nanomaterials as the receptor towards the development of an oral cancer screening assay. Nanogels were synthesized via free-radical precipitation polymerization. N-isopropylacrylamide (NIPAM) was co-polymerized with methacrylic acid (MAA) using N,N’-methylenebisacrylamide as the crosslinker. Synthesis of poly(NIPAM-co-MAA) nanogels was confirmed by Fourier transform infrared spectroscopy. Nanogel size, polydispersity, and zeta potential in phosphate buffered saline (PBS, pH 7.4) was determined using dynamic light scattering. Adsorption capacity of IgG (high pI protein) and albumin (low pI protein) to the synthesized nanogels was performed via equilibrium partitioning in PBS. The free-radical precipitation polymerization utilized resulted in the synthesis of monodisperse, anionic nanogels. Increases in adsorption capacity for IgG to P(NIPAM-co-MAA) nanogels was observed due to electrostatic interactions compared to that of albumin. Further optimization of the nanogel receptors has the potential to increase early detection of oral cancer towards the development of disease screening assays.

Applications of Machine Learning and Gas Chromatography for Rapid COVID Detection

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Luis Tafoya*[1], Justin T Baca [2], Robert M Taylor[3], Jameel K Remtullah[4], Xander Augustson [5], Virginia Severns[6], Andrea Howard[7], Sarah Lavelle[8], Silas Bussmann[9]

[1]The University of New Mexico, Albuquerque, [2]Department of Emergency Medicine, University of New Mexico, [3]Department of Emergency Medicine, University of New Mexico, [4]Department of Emergency Medicine, University of New Mexico, [5]Department of Emergency Medicine, University of New Mexico, [6]Clinical Translational Sciences Center, University of New Mexico, [7]Department of Emergency Medicine, University of New Mexico, [8]Department of Emergency Medicine, University of New Mexico, [9]Department of Emergency Medicine, University of New Mexico

Abstract: Gas chromatography (GC) has been applied to industries with the purpose of identifying different substances and compounds within a mixture by measuring travel speed. After the unforeseen pandemic of COVID-19, the world was forced to stop almost entirely, crashing the economy, drastically changing the way we socialize, and creating a need for rapid testing and diagnosis. Current COVID-19 diagnostics can be intrusive and have lag times prior to receiving results. This study focuses on analysis of patient breath samples, using GC and machine learning (ML), to create a diagnostic tool. One hundred and fifty volunteers were recruited for feasibility studies. Of these, 50 were symptomatic and PCR positive, 50 were asymptomatic and PCR positive, and 50 were PCR negative for SARS-CoV-2. After written consent, subjects provided up to 2.0 L of breath into a Tedlar collection bag secured via a mouthpiece connected to a high-efficiency particulate air (HEPA) filter, ensuring no virus traces. Clinical characteristics including PCR results and demographics were also collected. Metabolic signature differences in breath were then measured over a run time of <800 seconds. ML was performed using Scikit-learn libraries in python to predict positive, negative, and positive-asymptomatic individuals using the GC intensity and time data. Models with metrics are currently being generated and compared with the use of different algorithms (logistic regression, decision tree, etcetera) Based on preliminary data, we expect the breath analysis with GC, in combination with ML approaches, will allow the prediction of COVID-19 cases with an accuracy higher than a 70%.

Computational paper-based sensors for high sensitivity C- Reactive Protein Quantification

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

jovan morales hurtado*[1]and Artem Goncharov [2]

[1]University of California, Santa Cruz, [2]University of California, Los Angeles

Abstract: Cardiovascular diseases (CVDs) are common ailments that plague all populations worldwide and disproportionally affect people living in underserved communities. Proper treatment of CVDs relies on timely and accurate diagnostics after the onset of symptoms. Conventional diagnostics procedures are based on the detection of cardiac markers from the bloodstream and employ centralized lab facilities that are not accessible to people living in underserved regions. To provide more affordable diagnostic equipment for these demographics we present a paper-based computational vertical flow assay (VFA) for quantitative detection of cardiac markers. As a use case, we demonstrate the performance of our sensor for quantification of C-Reactive Protein which is a common inflammation marker and can act as an indicator of CVDs when present in lower concentrations. Our VFA represents a stack of paper layers that guide injected solutions towards the multiplexed sensing membrane that represents a grid of 9x9=81 immunoreaction spots. These spots contain seven different immunoreaction conditions that react with the sample in unique ways. Signals from all 81 spots are further processed by an automated machine learning-based quantification algorithm that outputs CRP concentration. Multiplexed sensing and machine learning-based analysis account for common limitations of point-of-care sensors such as high batch-to-batch variations and the hook effect. We tested our computational VFA on 85 human serum samples and achieved high linearity (R 2 = 95) and competitive coefficient of variation (CV = 11.2 %). In summary, computational VFA is a promising candidate to expand access to CVD diagnostics in remote and low-resource settings.

Clonal Tracking of CD39+ CD8 T Cells Between Peripheral Blood and Tumor in Merkel Cell Carcinoma Patients

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Tran Luu*[1], Heeju Ryu [2], Evan Newell[3]

[1]University of Washington, Seattle, WA, [2]Fred Hutchinson Cancer Research Center, Seattle, WA, [3]Fred Hutchinson Cancer Research Center, Seattle, WA

Abstract: Merkel cell carcinoma (MCC) is an aggressive skin cancer with 80% of cases caused by Merkel cell polyomavirus (MCPyV). Anti-PD-1 therapy showed a promising survival for MCC in clinical trials, yet the efficiency needs to be improved for patients with partial response. Previous studies showed that tumor-infiltrating lymphocytes (TILs), specifically CD8 T cells, express CD39 biomarkers, and co-expression of CD39 and CD103 markers indicates cancer-reactive CD8 T cells in solid tumors. Our recent analysis of blood suggests that these markers can also be used to identify peripheral recirculating tumor-reactive T cells. Here, we track clonotypic profiles of T cells expressing CD39 and CD103 biomarkers in peripheral blood mononuclear cells (PBMC) to compare with clonotypes of CD8 TILs in MCC patients. We hypothesize that these phenotypes could share TCRs, demonstrating that CD39/CD103-expressing T cells in blood are enriched for tumor-derived and tumor-reactive cells. I sorted T cell populations that express CD39 and CD103 from PBMC of MCC patients using flow cytometer. Subsequently, I isolated RNA from the sorted T cells and performed bulk T cell receptor (TCR) sequencing to obtain the TCR repertoires. The collected sequence was submitted to the library for validation and sequencing. The anticipated result should show similarity between TCR sequences from sorted PBMC populations and the previously performed TCR sequences of TILs. Findings in this project provide a better understanding of biomarkers that can be used to track anti-PD-1 therapy response in MCC and motivate deeper studies into the potential of utilizing blood lymphocytes in immunotherapy.

Optimizing a Microtrack Platform to Investigate Mechanical Memory in Cancer Cell Migration

Discipline: Engineering
Subdiscipline: Chemical Engineering

Andrea Valero*[1], Jenna A. Mosier [2], Cynthia A. Reinhart-King[3]
[1]The University of Texas at San Antonio, [2]Vanderbilt University, [3]Vanderbilt University

Abstract: Around 170,000 people in the United States are living with metastatic breast cancer. Metastatic cancer, which occurs when cancer cells leave the initial tumor and spread to other tissues and organs, is responsible for a large portion of cancer-related fatalities. In our lab, we employ a microtrack device to examine cell migration, a key process in metastasis, in a 3D collagen system that closely resembles the size, topography, and confinement of the tracks left behind by migrating cells in vivo. Previously, we showed that cells in this confinement increase speed. We now aim to understand the long-term changes that result from confinement, called mechanical memory. Preliminary results indicate that cells have memory dependent on the duration of confinement experienced and can maintain increased speed even upon exiting confinement. However, due to the inability to collect cells after confined migration, we are unable to determine this mechanism. To overcome this, we designed a PDMS-based, 2-layer pattern containing inlet feeder channels to control starting positions of cells and outlet channels to collect cells post-migration. The PDMS microchannel device can be coated in collagen and seeded with cells. We will compare the behavior of cells undergoing various levels of confinement, including their speed, cytoskeleton organization, and mitochondrial localization once they have left the confined space. This will allow us to understand how the cells behave in a tumor microenvironment, and this could potentially open the doors to a targeted drug therapy.

Designing a Bio-Inspired Robotic Prey Fish for Predator-Prey Experiments

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Moyoninuoluwa Oyedeji-Olaniyan*[1]and Alberto Soto [2]
[1]Harvey Mudd College, [2]Harvey Mudd College

Abstract: Predatory fish contend with dynamic fluid conditions and evasive maneuvers as they track and pursue prey. To investigate how the pursuit strategy of predatory fish is influenced by the motion of prey, it is necessary to conduct controlled and repeatable experiments. However, this is not feasible with live prey. Here, we present a bio-inspired robotic prey that can be programmed to mimic fish swimming behaviors and respond to a live predator. The central objective of the robotic prey is to elicit robust pursuit behavior from live predatory fish. The robotic prey consists of a flexible fish model with a magnetic base attachment. A mobile wheeled robot situated under the aquarium is magnetically coupled to the fish model and controls its motion. Our robotic prey is highly maneuverable, capable of achieving linear velocities of (~8.33 body lengths/s) and angular velocities up to (~ 2.8 rad/s). We have also implemented feedback control that allows our robotic prey to respond to a predatory attack in real-time. In future research, we will use this system to evaluate whether or not predators use a fixed pursuit strategy across different prey motion and behavior. Our bio-inspired robotic prey system

presents an exciting opportunity to conduct animal-robot experiments and can serve as a model for research into complex animal behavior and biomechanics.

Using total internal reflection fluorescence microscopy (TIRFM) to elucidate the signaling dynamics of PD-1, CD28, and the TCR complex.

Discipline: Engineering
Subdiscipline: Chemical Engineering

Julian Rojo*[1], Diane S. Lidke [2], Elizabeth M. Bailey[3]
[1]University of New Mexico, [2]Thee University of New Mexico, [3]University of New Mexico

Abstract: T-cell receptor (TCR) signaling is an essential part of the adaptive immune response. The strength of TCR signaling is modulated by signals sent by coreceptors, preventing both hypersensitivity and immunodeficiency. Programmed cell death protein 1 (PD-1) is a coinhibitory receptor that dampens T-cell activation and is a prevalent target for cancer immunotherapies. These therapies prevent interactions between PD-1 and its ligand, enabling the T-cell to remain active and detect malignant cells. However, the signaling mechanisms of PD-1 and how they integrate with those of stimulatory receptors like the TCR and CD28 are incompletely understood. PD-1 is thought to inhibit signaling by forming a complex with the phosphatases SHP-1 and SHP-2, leading to the dephosphorylation of nearby positive signaling proteins. However, these phosphatases are also found to serve as transient positive modulators in other pathways. We hypothesize that PD-1 can mediate both positive and negative signaling depending on its proximity to inhibitory tyrosine residues and stimulatory receptors, respectively. To test this, we are using various activating substrates functionalized to a mobile or immobile surface. These samples were interrogated using various microscopy techniques such as total internal reflection fluorescence microscopy and the single-molecule pull-down assay, which allows for the quantification of protein phosphorylation at specific tyrosine residues. Ultimately, this project aims to better understand how PD-1/TCR/CD28 interact and how these interactions impact T-cell activation. Understanding these signaling mechanisms will give us better insight into immunotherapies and why they may not work, allowing researchers to improve the prognosis of patients.

Dose-Dependence of EdU for Localization and Tracking of Proliferating Chondrocytes

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Kaitlyn Strandberg*[1], Nasim Eshragh Nia [2], Arya A. Suprana[3], Alborz Jelvani[4], Erica Gacasan [5], Albert C. Chen[6], Van W. Wong[7], Robert L. Sah[8]
[1]University of California, San Diego, [2]University of California, San Diego, [3]University of California, San Diego, [4]University of California, San Diego, [5]University of California, San Diego, [6]University of California, San Diego, [7]University of California, San Diego, [8]University of California, San Diego

Abstract: In tissue engineering and regenerative medicine, localizing and tracking proliferating cells are critical to understanding cell fate. One possible approach is to incubate cultures with 5-ethynyl-2'-deoxyuridine (EdU), a thymidine analog, that is incorporated into newly synthesized DNA. The incorporated EdU can then be reacted with azide-modified fluorophores to allow detection. If cells can be labeled with EdU at concentrations sufficiently low to be non-toxic, EdU could also be used as a cell tracer. However, previous studies indicated 5-10μM EdU for >24hrs is cytotoxic. We hypothesized that incubation of chondrocytes at sufficiently low

concentrations of EdU will allow normal growth as well as identification of proliferating cells. The effect of EdU concentration on cell growth and tracing was assessed by daily phase contrast and endpoint fluorescence microscopy. Bovine calf chondrocytes were seeded at 10,000 cells/cm 2 , and incubated for 3 days in DMEM+20%FBS, supplemented with 0, 0.002, 0.02, 0.2, or 2μM of EdU (N=4 cultures/group), and analyzed by 2-way ANOVA. Cell growth was affected by EdU in a dose-dependent manner (p<0.0001). At day 3, cultures at low concentrations (0, 0.002, 0.02μM EdU) increased to 23,600-30,500 cells/cm 2 , whereas those at higher concentrations grew less (15,900 and 9,300 cells/cm 2 at 0.2μM and 2μM, respectively, each p<0.05). These results suggest that low doses of EdU might be useful for cell tracing. Ongoing analysis is assessing whether the incorporated EdU is detectable.

Sex Related Gene Expression Differences for Heart Failure: Initial Focus on Non-Failing Hearts

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Maydha Kumar*[1], Dr. Brisa Peña [2], Matthew R.G. Taylor[3], Luisa Mestroni[4], Anis Karimpour-Fard [5]
[1]University of Colorado Denver, [2]1.Department of Bioengineering, University of Colorado School of Medicine, Aurora, Colorado, USA. 2.Division of Cardiology, University of Colorado School of Medicine, Aurora, Colorado, USA., [3]Division of Cardiology, University of Colorado School of Medicine, Aurora, Colorado, USA., [4]Division of Cardiology, University of Colorado School of Medicine, Aurora, Colorado, USA., [5]Pharmacology Department, University of Colorado, Aurora, Colorado, USA.

Abstract: Heart failure (HF) contributes significantly to the global burden of cardiovascular disease. Although, the data suggests that HF pathogenesis differs between sexes, therapies for HF continue to be applied similarly to both men and women, despite most data were derived from predominantly male-population studies. The goal of our project is to develop the first understanding of the normal and diseased female heart transcriptomes, with an initial focus on non-failing (NF) hearts. It is hypothesized that there are important sex-specific pathways associated with biomechanical signaling that differ between sexes in NF hearts. Our team has a unique transcriptome human heart NHLBI TOPMed dataset (~750 paired DNA/RNA sequenced human heart samples), with both sexes. For this project, we will identify cardiac genes that differ in NF hearts between sexes, using Ingenuity Pathways Analysis (IPA) software. We found that the top two upregulated genes for NF hearts are eif4 and p70s6k signaling and SNARE Signaling. Regulation of eif4 and p70s6k implies use of the autophagic mTOR pathway commonly associated with heart failure when under or over expressed. The SNARE signaling pathway is associated with insulin resistance - a risk factor for heart failure. The top two downregulated genes are XIST and PTX3. Overexpression of XIST increases cardiac proliferation and fibrotic proteins. PTX3 plasma rises acutely after heart failure. These data validate the use of gene expression analysis to identify NF signaling pathways differing between sexes in NF hearts. Our next study will investigate sex-related biomechanical pathways differences in HF patients.

Ultrahigh Drug Loading of Micelles for Drug Delivery Applications

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jean Jerome*[1], Richard D’Arcy [2], Kristopher Castillo[3]

[1]University of Central Florida, [2]Vanderbilt University, [3]Vanderbilt University

Abstract: Site-specific targeting and delivering chemotherapeutics can be difficult to overcome for several types of cancers. Nonspecific distribution, solubility, and inadequate drug loading remain as obstacles in accomplishing this goal. Targeted delivery of therapeutics can overcome many toxicities associated with conventional small-molecule drugs with improved therapeutic outcomes. The major drawbacks of current drug delivery platforms, such as liposomes, PLGA and Pluronics are their poor drug loading which severely limits the drug doses that can be administered to the patient. We hypothesize that tailoring the nanocarrier chemistry to appropriately interact with the drug will lead to improved drug loading and better therapeutic outcomes. Herein we have designed a nanocarrier (polymer) library with tailored degrees of hydrogen bond donor (OH) and π-π interacting moieties. We have screened the loading of these nanocarriers with a plethora of drugs, including EGFR tyrosine kinase inhibitors, paclitaxel and cyclosporin. Drugs are loaded via a thin-film rehydration protocol and loading efficiency is quantified by High-Performance Liquid Chromatography (HPLC). When tailored to an optimal OH/π-π interacting, many drugs loaded with extremely high efficiency (>80%) and with loading capacities in the 'ultrahigh' range (>35%). These levels of loading are likely to overcome many of the shortcomings of current nanomedicine not currently addressed. Overall, this work can be used to better deliver effective therapeutics for patients, decrease cancer-related mortalities, and increase quality of life for cancer patients.

Lung volume and posture are determinants of complex interaction of kinematics of diaphragm and lower rib cage during forceful efforts following airway occlusion

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Noralis Rodriguez*[1], Aubri Ford [2], Aladin Boriek[3], Jarrett Wallerson[4], Zeeyad Boriek [5], Nichelle Solomon[6]

[1]Texas Southern University, [2]Texas Southern University, [3]Baylor College of Medicine, [4]Fordham University, [5]Baylor College of Medicine, [6]Baylor College of Medicine

Abstract: We hypothesized that lung volume and posture are determinants of kinematics of diaphragm and lower rib cage (LRC) during forceful efforts following airway occlusion. To test this hypothesis, radiopaque markers were attached along three adjacent costal muscle fibers and lower three ribs in six dogs (8.2-9.5 kg). Three-dimensional locations of markers were tracked by a biplane video fluoroscopy during quiet spontaneous breathing (QSB), and during forceful efforts at functional residual capacity (FRC) and at total lung capacity (TLC) in supine and prone postures. Diaphragm muscle shortening (DMS), and volume displacement (VD) of diaphragm and LRC were computed using MATLAB and Rhino 6 during QSB and during forceful efforts at active states at FRC (FRCactive) and at TLC (TLCactive). In supine posture, for the FRCactive, DMS was nearly 14.87±3%, while corresponding VD of the LRC increased relative to QSB by nearly 96.9%. In the prone posture, DMS at FRCactive was nearly 13.7%± 2%, while the corresponding VD of LRC increased relative to QSB by nearly 45%. In the supine posture, DMS at TLCactive was nearly 31.2±7%, while the VD of the LRC increased relative to QSB by nearly 134%. In the prone posture, DMS at TLCactive was nearly 29.5%±12%, while VD of the LRC increased relative to QSB by nearly 103%. Our data support the hypothesis that lung volume and posture play a combined role in modulating a complex kinematics of diaphragm and its effect on LRC during forceful efforts against occluded airway.

Investigating Molybdenum Hybrid Nanoparticles over Graphene for Electrocatalysis

Discipline: Engineering

Subdiscipline: Chemical Engineering

Dylan Pollard*[1], Andrew J. Adamczyk[2], Ashraf Ali[3], Xinyu Zhang[4], Shatilia Sarwar[5], Zhen Wei[6], Ruigang Wang[7]

[1]Auburn University, [2]Auburn University, [3]Auburn University, [4]Auburn University, [5]University of California at San Diego, [6]University of Alabama, [7]University of Alabama

Abstract: Each year 500 billion cubic meters of hydrogen gas are produced with only 4% created through renewable methods, primarily using water electrolysis via the hydrogen evolution reaction (HER). Due to nanotechnological advancements, new catalytic systems show promise to reduce electrolysis costs. The most widely used catalysts for electrolysis are noble transition metals, which are both scarce and costly. Transition metal dichalcogenide (TMD) nanoparticles over a graphene support are a promising alternative due to their competitive electrocatalytic properties and lower costs. The chosen TMDs under study are Mo9Se9Te9 and Mo9S6Se6Te6, and the binding free energies of these nanoparticles were compared to those of noble transition metals. The bare nanoparticles with graphene support were atomistically simulated and geometrically optimized with modeling software with various properties determined using density functional theory. Their binding energies with and without adsorbed hydrogen atoms were then compared for 11 different active sites for the HER. Because of its low ionization energy, molybdenum with adjacent chalcogen active sites tended to adsorb H + too strongly, whereas chalcogen-chalcogen active sites adsorbed more weakly. The most salient binding energy value obtained was -0.14 eV, which corresponds to the Mo-Te edge on Mo9S6Se6Te6. The computationally measured binding free energies were not comparable to historical values of noble metal catalysts but still provide insight on the effects that molybdenum and chalcogens have on the HER and each other. Possible future solutions, such as new molybdenum-to-chalcogen stoichiometric ratios or other TMD nanocatalysts could result in HER binding free energies closer to zero.

Rapid infection diagnostics using 16S droplet digital PCR and LNA probes

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Saamiya Syed*[1]and Pavan Kota[2]

[1]University of Houston, [2]Rice University

Abstract: Rapid pathogen characterization is critical in delivering timely patient care for patients susceptible to septic shock to improve patient survival and antibiotic stewardship. Conventional clinical tests culture samples for days before testing and are unrepresentative of the bacterial load in real time. Rapid diagnostic alternatives use target-specific sensing mechanisms which limit multiplexing capacity. To improve clinical utility, molecular diagnostics must have broad coverage of bacterial pathogens. Since the 16S rRNA gene is present in nearly all bacteria, it’s an efficient target for bacterial quantification and identification. Internal sequence differences are typically analyzed with sequencing after PCR. For faster, cost-effective analysis, we obviate followup sequencing by assigning unique barcodes to bacterial taxa with nonspecific hydrolysis probes based on the probe binding profile to each 16S gene. The primary objective of this study was to design and validate 14 probes for use in the development of barcodes with ddPCR. Individual probes must be nonspecific and bind to multiple bacteria to efficiently generate distinct barcodes. Shorter probes are inherently less specific but require locked nucleic acid

(LNA) substitutions to increase their melting temperature to compatible levels for PCR. We validated the ability of 10 different LNA-spiked probes to match our computationally predicted barcodes. We also assessed performance differences of probes of the same sequence with different LNA positions. Finally, we highlight the importance of developing new melting temperature prediction models for LNA-spiked probes to improve the concordance between predictions and experiments.

Analysis of Potential Wind and Solar Sources for Meeting Hourly Energy demand in India

Discipline: Engineering
Subdiscipline: Engineering (general)

David Lopez*[1]and Guillermo Terren Serrano [2]
[1]University of California, Santa Barbara, [2]postdoc

Abstract: This project aims to assess the power capacity of solar and wind energy in India. A numerical weather prediction dataset is used to analyze the variability of local wind and solar resources over multiple years. Our objective is to develop a model of the power capacity of solar and wind technologies using weather variables to estimate the potential energy that can be generated from wind and solar power plants in India. This contributes to the main research goal of proposing an energy generation plan for reducing greenhouse gas emissions in emerging and developing countries. The proposed energy generation plan is important to execute an economically feasible schedule for the decommissioning of carbon emitting power plants and commissioning of zero-emission generation systems based on renewable energy and storage systems (i.e., batteries). All this is done to help countries achieve the Paris's Agreement of limiting global warming to well below 2℃.

Fabrication of Thin Film Transistors for Microrobotics

Discipline: Engineering
Subdiscipline: Electrical Engineering

Jorge Gutierrez*[1], Camilo Velez Cuervo [2], Guoduan Liu[3]
[1]University of California, Santa Barbara, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Advancing the fabrication of transistors and electronics specifically designed for microrobotic applications that could have the size of cells and be utilized to solve medical conditions inside the body. However, current microrobotic technology is not autonomous due to the lack of electronics such as transistors, resistors, and capacitors. Transistors are the most pivotal component of microrobotic electronics as they act as switches, controlling the current and ultimately, the power consumed by the microrobot. To this end, we proposed a thin film transistor (TFT) that does not require a bulk substrate and uses a ~50 nm layer of amorphous-Indium-Gallium-Zinc-Oxide (a-IGZO) as semiconductor. Currently, a-IGZO TFTs are being used heavily in liquid screen displays (LCDs) but have not yet penetrated the market in microrobot applications. The proposed device fabricated inside the Clean Room at the Integrated NanoSystems Facility at UCI uses a ~50 nm thick gold bottom gate, top contact architecture and ~50 nm Al_2O_3 as insulation, making it extremely flexible. A key parameter to monitor during the fabrication of these TFTs is the oxygen concentration inside the semiconductor. We conducted experiments varying this concentration and characterized the electrical and material properties of the semiconductor (Hall mobility and carrier concentration using magnetometer, and resistivity using Van der Pauw method) and evaluated the performance of the transistor. Ultimately, we are trying to optimize the TFTs to operate at a low voltage, mitigating power consumption and prolonging lifetime. Once completed, these microrobotics will be able to perform simple decisions based on their surrounding environments.

Characterization of Dissolved Organic Carbon throughout the Arcata Marsh Wastewater Treatment Plant

Discipline: Engineering
Subdiscipline: Other Engineering

Angel Cortez Ramirez*[1]and Tesfayohanes Yacob [2]
[1]California State Polytechnic University, Humboldt, [2]Assistant Professor

Abstract: There are no federal mandatory regulations for the removal of pharmaceuticals and personal care products (PCP) in wastewater. This is a problem because pharmaceuticals and PCPs are prevalent in wastewater and are known to cause adverse effects to the environment. Natural treatment systems such as wetlands provide a low-energy sustainable treatment system. Wetlands allow for the interaction between sunlight and dissolved organic carbons (DOC), potentially causing photochemical reactions to occur within the wastewater resulting in the removal of pharmaceuticals and PCPs. The characterization of DOC is important to determine if the right conditions are present for these photochemical reactions. This report will be presenting the first step into the identification of photochemical pathways that lead to the removal of pharmaceuticals and PCPS within the Arcata Wastewater Treatment Plant (AWWTP) by the characterization of DOC. Wastewater samples were collected from points within AWWTP treatment train for data analysis. Data parameters collected include DOC, biological oxygen demand (BOD), pH, ultraviolet-visible spectroscopy (UV/VIS), and fluorescence excitation matrix (EEM). Parallel factor analysis (PARAFAC) models will be constructed from the data. The data collected will allow for the characterization of DOCs within the influent and effluent of the post oxidation ponds, treatment wetlands, and enhancement wetlands. We expect to identify the potential to remove pharmaceuticals using the characterized DOCs. We further anticipate the data will show the transformations of DOCs within the treatment train that potentially remove pharmaceuticals and PCPs. We can now hypothesize about the indirect treatment of pharmaceuticals and PCPs within the AWWTP.

ALPHA GENERATION QUADFLAPPER IMPLEMENTING FLAPPING-WING MICRO AIR VEHICLES

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Antonio Loaiza*[1], Kevin Huang [2], Haithem Taha[3]
[1]University of California, San Diego, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Through evolution, animals and insects proficiently acquired a flight flapping wing mechanism enhancing aerial control. Flapping-wing micro air vehicles (FWMAV) research can potentially implement the efficient laws of nature that rule on animals and insects into the field of unmanned aerial vehicles (UAV), allowing drones to acquire sensations with unimaginably stable in-flight performances. FWMAVs research deconstructs the physical attributes behind the

flapping wing mechanism by studying a variety of fluid computations and force analysis of the flapping motions of the wings. The purpose of this research on flapping-wing micro air vehicles is to investigate the effects of the wing's "Clap Gap" throughout the assembly of the "Alpha Generation'' Quadflapper. FWMAVs rely on unsteady aerodynamics and nonlinear flight mechanisms for their flight performances. Three main components must undergo an aerial evaluation to replicate the aerial capabilities of the flapping wing mechanism; the nonlinear flight mechanism, the aerodynamic flow field, and the force generated. The data collected is obtained via measuring the "Alpha Generation" Quadflapper under a wind tunnel. Combining the operations of the flight controller with load cells on the vehicle will illustrate the amount of thrust produced by the FWMAV, the power required to lift the vehicle, and efficiency upon which the "Alpha Quadflapper '' operates. The objective is to combine the data from each flight element and conclude quantifiable results that illustrate the high performance of flapping-wing micro air vehicles (FWMAVs). Under the observation of nature, humanity may obtain remote flight tools that efficiently promote hovering and flight functions.

Optimization of a bimetallic catalyst for the hydrodeoxygenation of tetrahydrofuran 2,5-di carboxylic acid to obtain adipic acid

Discipline: Engineering
Subdiscipline: Chemical Engineering

Titus Szobody*[1], Samir F. Castilla-Acevedo[2], Alan M. Allegeir[3], Cameron M. Boydston[4], Jacob St. John[5]
[1]North Carolina State University, [2]University of Kansas, [3]University of Kansas, [4]University of Kansas, [5]University of Kansas

Abstract: Bimetallic catalysts comprised of a metal and a metal oxide have been proved to be efficient to perform hydrodeoxygenation (HDO) of biomass-derived chemicals. However, further investigations are needed to overcome selectivity challenges for a more sustainable process. We investigated the optimization of a bimetallic catalyst and operational parameters to successfully perform tetrahydrofuran 2,5-di carboxylic acid (THFDCA) ring-opening HDO using different catalysts to obtain adipic acid (AA) as the main product. Three different types of Pt-MOx/TiO2 catalysts (MOx: WOx, MoOx, ZrOx) were prepared while varying the metal oxide-metal molar ratio (MOx:M - 0.5:1, 1:1, 1.5:1, and 2:1). The reaction vials of 1.5 mL are loaded with the substrate solution, the PTFE stirring bar, and the catalyst to be tested to a stainless-steel rectangular base reactor. After reaction, the samples are filtered and measured in a HP 1100 series HPLC chromatograph. The highest conversion was obtained by the Pt-MoOx/TiO2 but Pt-WOx/TiO2 achieved the highest selectivity and yield towards AA. It was observed that increasing the amount of metal oxide increases the conversion, AA selectivity, and yield. However, the THFDCA conversion increased where the metal oxide is increased at higher temperatures than 140°C but the selectivity and yield decreased significantly, indicating that decarboxylation reactions become predominant at high temperature. We demonstrated that the efficient ring-opening hydrogenolysis of THFDCA to target AA is possible using a bimetallic catalyst where the proximity between WOx and Pt plays an important role. However, this WOx-Pt interaction also increases decarboxylation.

Separation of R-410A using amorphous fluoropolymers

Discipline: Engineering

Subdiscipline: Chemical Engineering

Yuniva Mendoza-Apodaca*[1], Abby N. Harders [2], Mark B. Shiflett[3]

[1]North Carolina State University, [2]University of Kansas, [3]University of Kansas

Abstract: Hydrofluorocarbons (HFCs) are commonly used refrigerants that are facing regulations due to environmental legislation. HFCs and HFC mixtures can exhibit high global warming potentials (GWP), meaning they can trap heat in our atmosphere. There are currently millions of kilograms of HFCs in global circulation with no means for efficient separation. Membrane technology provides the opportunity to achieve a selective separation of HFC refrigerants within a mixture with lower energy consumption and capital requirements in comparison to other commonly used separation methods. This study explores the use of amorphous perfluoropolymers for the separation of R-410A, an azeotropic mixture composed of 50 wt% difluoromethane (HFC-32, CH 2 F 2) and 50 wt% pentafluoroethane (HFC-125, CHF 2 CF 3). The permeability, solubility, and diffusivity of HFC-32 and HFC-125 was measured in copolymers of perfluoro(butenyl vinyl ether) (PBVE) and perfluoro(2,2-dimethyl-1,3-dioxole) (PDD). Pure gas permeability of HFC-32 and HFC-125 were measured using a static membrane apparatus and the pressure-rise method. Solubility measurements were obtained using a gravimetric microbalance and diffusivity was modeled using a Fickian model. Results indicate that a high selectivity of HFC-32/HFC-125 can be obtained at intermediate compositions of PBVE/PDD copolymers and that the separation is diffusion-driven throughout the entire range of compositions tested.

Towards evaluating astronaut's performance via proprioception-perception analysis through stimulation of the nervous system.

Discipline: Engineering

Subdiscipline: Other Engineering

Kimberly Lopez*[1]and Jose Baca [2]

[1]Texas A&M University-Corpus Christi, [2]Texas A&M University-Corpus Christi

Abstract: Recent studies have found that many basic mental abilities, like motivation, attention, problem-solving, and sensorimotor skills like body coordination seem to deteriorate in space, particularly during long-duration space missions. The main objective of this work is to develop a methodology that will assist in evaluating astronauts' performance and identify parameters or critical indicators that can be used to monitor user performance decrements. The goal is that through the implementation of this methodology, we should be able to detect early-stage of sensorimotor or mental problems. For this work, we are combining a body-tracking system, VICON, with K-Invent Forces sensor technologies. For this study, male and female subjects (hispanic and white) between the ages of 20 and 25 will be supervised through a series of activities, for instance, specific supination and pronation motion of their arms while pressing the force sensor to a specific value. We will look at the body's proprioception performance, which is the sense of self-movement, force, and body's position in space. If critical indicators can be identified during subject interaction, a set of aspects can be identified and used to improve crew members' immersion, motivation, attention, and body coordination. We expect to create a methodology that will assist in identifying and detecting key indicators of decrements in user performance, which can also be used as a platform to mitigate the problem by generating detection, prevention, and treatment programs that target sensorimotor skills and mental abilities.

IGFBP-6 overexpression is associated with increases in rates of glycolysis and oxidative phosphorylation

Discipline: Engineering

Subdiscipline: Chemical Engineering

Sarena Gneiting*[1], Francisco Lariz[2], Samantha Valentino[3], Kevin D. Houston[4]

[1]University of New Mexico, [2]New Mexico State University, [3]New Mexico State University, [4]New Mexico State University

Abstract: The Insulin-like growth factor (IGF) system is essential to cell growth, proliferation, and survival in several cancers. The two IGF signaling molecules, IGF-I and IGF-II, are modulated by a family of six IGF-binding proteins (IGFBPs). IGFBPs bind IGFs and prevent binding to its receptor, IGF1R. IGFBP-6 is distinct in that it binds IGF-II with a 50-fold affinity over IGF-I. IGFBP-6 also has actions independent of IGF-II including inhibition of angiogenesis, promotion of apoptosis, and promotion of cell migration. IGFBP-6 is shown to be down-regulated in many cancer cell lines and proposed to be a tumor suppressor. Cancer cells characteristically prefer glycolysis to oxidative phosphorylation for energy production to increase cellular proliferation. IGFBP-6 has been shown to bind prohibitin-2, a mitochondrial protein which stabilizes mitochondrial respiratory enzymes and regulates mitochondrial respiration. Thus, it is hypothesized that IGFBP-6 overexpression would increase the rate of oxidative phosphorylation. To investigate metabolism in cells overexpressing IGFBP-6, MCF-7 cells were stably transfected to overexpress IGFBP-6 and analyzed using the Agilent Seahorse HS Mini. An ATP flux rate assay was used to assess the metabolism of the overexpressing cells. Results from the ATP flux rate assay showed both an increased oxygen consumption rate (OCR) and extracellular acidification rate (ECAR) in IGFBP-6 cells. Both oxidative phosphorylation and glycolysis rates are increased in IGFBP-6 overexpressing cells. Although IGFBP-6 is believed to be a tumor suppressor, these results demonstrate a shift in metabolism that promotes cell survival despite IGFBP-6 overexpression.

Contribution of Protein Glycosylation in the Extracellular Matrix to in vivo Cancer Dependencies

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Nathan Rojas Ocampo*[1]and Dean Procter[2]

[1]Columbia University, [2]Broad Institute of MIT and Harvard

Abstract: Utilizing in vitro 2D cancer screens, researchers have uncovered many cancer dependencies, however, there are many shortcomings with these models. To provide more physiologically relevant screenings, we attempt to create a pipeline for the discovery of novel cancer dependencies using engineered organoid models and in vivo intracardiac injection xenograft murine models of metastasis. Further, we characterized in vivo cancer dependencies that arose from our screens that were not seen in parallel 2D screens. Specifically, we investigated integrin beta 1 (ITGB1), a transmembrane protein that connects to the extracellular matrix (ECM), and Zip9 (SLC39A9), a zinc transporter protein. To study both proteins, we are developing organoid models that can be perturbed with CRISPR/enCas12a through gene knockout, gene overexpression, and endogenous tagging of proteins with a split mNeonGreen construct. ITGB1 was characterized in different organ ECMs to see the effect on cell state and viability, and SLC39A9 was characterized in zinc deprived environments. Because of the lack of characterization of SLC39A9, we also investigated the mechanism via which glycosylation processes are disrupted and confirmed its localization in multiple cell models. We plan to analyze differential gene expression to determine the transcriptional profile of cancer cell lines with these dependencies and identify associated genes. These novel organoid platforms will help provide a more relevant picture of both dependencies than traditional 2D studies. The understanding of both targets has led us to highlight possible explanations of what cancer cells require in the tumor microenvironment.

Preparation and characterization a DMOG releasing skin-derived hydrogel for the treatment of diabetic wounds.

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Sushma Chappidi*[1], Abby Jiang [2], Yaqing Huang[3], Themis Kyriakides[4]
[1]Virginia Commonwealth University, [2]Portledge School, [3]Yale University, [4]Yale University

Abstract: Wound healing in diabetic patients has been shown to be slower compared to that in healthy patients and represents a critical unmet clinical need. Hydrogels have been developed for the treatment of wounds due to their hydrophilic nature and overall biocompatibility. However, their overall efficacy remains limited. Previous studies have shown that certain native ECM-derived hydrogels can increase tissue remodeling, vascularization, and epithelization without requiring the addition of growth factors. Specifically, hydrogels derived from the skin of thrombospondin-2 knockout (TSP-2 KO) mice were shown to promote enhanced wound healing in diabetic animals. Despite such improvement, TSP2 KO hydrogels did not achieve full healing. To further improve their efficacy, we plan to prepare hydrogels containing dimethyloxalylglycine (DMOG), to address an identified deficiency in diabetic wounds involving persistent destabilization of hypoxia-inducible factor (HIF-1α). We will incorporate DMOG into hydrogels and control the rate of release in order to improve wound healing. Here, describe the use of Polydopamine nanoparticles (PDA) cross-linked with Hyaluronic Acid-Cysteamine (HA-Cys) conjugate to control the drug release of DMOG through Michael-type addition. These nanoparticles will be added to the pre-gel phase of the hydrogel and analyzed with transmission electron microscopy. The overarching goals of this project include controlling DMOG release from TSP2 KO hydrogels in a time scale consistent with the need for HIF-1α stabilization and evaluation of its efficacy in a diabetic wound healing model.

Isolation and Characterization of Diverse Microorganisms Involved in Carbon Recycling

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jasmine Amaya*[1], Brandon Enalls [2], Romy Chakraborty[3]
[1]Diablo Valley College, [2]Lawrence Berkeley National Laboratory, [3]Lawrence Berkeley National Laboratory

Abstract: The metabolic diversity among microbes and their ubiquity in nature emphasize the vital roles they play in the global carbon cycle. Our group has previously enriched microbes from terrestrial subsurface environments using a wide variety of carbon sources, including organic matter extracted from sediments and microbial necromass (dead or decaying material). In this previous work, we were able to culture a wider variety of microbes using these naturally occurring carbon sources. We expand upon this work by continuing to isolate and characterize microbes that can use microbial necromass as a carbon and energy source. To accomplish this we are enriching the microbes in liquid and solid media using bacterial cell lysates that will simulate necromass found in nature. We can then extract and sequence the DNA from these isolates, allowing us to give them taxonomic assignments. The collection of microbes we isolate is likely involved in recycling biological material in their native environments, highlighting their contribution to the carbon cycle.

Smart Solar Planter (SSP)

Discipline: Engineering
Subdiscipline: Other Engineering

Nahal Ranjbar*[1], Ravi Novan [2], Javier Andres Velez Carmona[3], Jesse James Martinez[4]
[1]Northwest Vista College, [2]Southwest Research Institute, [3]Northwest Vista College, [4]St. Phillip's College

Abstract: In many homes growing plants, especially fruits and vegetables could be very challenging due to different circumstances such as unpredicted weather, animals, and insects. The Smart Solar Planter (SSP) was constructed in Solidworks and incorporates an Arduino Nano, which we programmed to function as an autonomous planter that provides synthetic sunlight, an automated water system, temperature and humidity sensors, and a timer that alerts you when it is time to replace the soil. One great feature about this planter is that it is solely powered by a solar panel that was calculated to provide enough voltage to the Arduino functions which will not only save energy in the future but requires no outside input other than a change of water. The SSP will assist in growing plants indoors more efficiently since it waters the plant by the root and concentrates on providing the plant with the optimal quantity of synthetic sunshine for growth. This will benefit those who live in apartments and do not have the luxury of a rear or front yard. In this study, two plants were administered, one outdoors in an uncontrolled setting and the other indoors with the SSP in a controlled environment. Our results have proven that a plant grown in a controlled environment grows both more efficiently and at a faster rate than one in an uncontrolled environment.

Controlling Unmanned Aerial Vehicles Through Hand Gesture Recognition

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Roxana Nevarez*[1]and Junfei Xie [2]
[1]Southwestern College, [2]San Diego State University

Abstract: Transmitters used to control Unmanned Aerial Vehicles (UAVs) have become more complicated as technology advances. Consequently, the transmitters’ complexity has significantly minimized the number of people who can utilize drones. Yet by implementing deep learning into their research, scientists have successfully proven that drones can be controlled through hand gesture recognition. In this project, the goal is to replace UAV transmitters with hand gestures to make drones user-friendly, enabling a vast population to utilize drones without requiring them to learn a transmitter’s complex components. Currently, the materials used for this project are a DJI Tello drone, a computer with a camera, Wi-Fi, PyCharm, Python programming, GitHub, and a finger-tracking solution. Initially, Python source codes provided by GitHub were run on PyCharm to evaluate the drone’s ability to perform basic commands. After completing the assessment, additional code was written and run to have the drone execute advanced motion, picture, and recording commands. Lastly, GitHub files and Python packages were installed to examine the accuracy of the finger-tracking solution. Though results have yet

to be achieved, the next steps for this project will be to capture and record multiple hand images, use the captured images to train the convolutional neural network (CNN), and eventually have the CNN categorize diverse hand images into the unique hand gestures that will control the drone in real-time. Completing this project will not only support previous research conducted, but it will also allow a larger population to receive benefits and assistance from UAVs without difficulty.

Molecular coating of Au/p-GaN for photoelectrochemical CO2 conversion

Discipline: Engineering
Subdiscipline: Chemical Engineering

César Lasalde-Ramírez*[1], Dr. Harry Atwater[2], Dr. Aisulu AIbekova[3]
[1]University of Puerto Rico at Mayagüez, [2]California Institute of Technology, [3]California Institute of Technology

Abstract: Carbon dioxide (CO2) is the main driver of climate change because it is the primary greenhouse gas. One approach to decrease the concentration of this pollutant in the atmosphere is to capture and convert it into useful products. This project focuses on performing this process using metal/semiconductor materials and solar energy. To execute this process, we use photoelectrochemistry: a process where light is illuminated on a semiconductor to trigger an electrochemical reaction. This route was chosen because it allows harnessing the abundant solar energy to convert the harmful pollutant gas into fuels and chemicals. This process, however, suffers from poor selectivity because it leads to undesirable side products that decrease the acceptable amount of valuable product. To solve this challenge, the effect of how the properties of gold (Au) nanoparticles supported on p-type gallium nitride (p-GaN) semiconductors affect the performance in solar-driven CO2 conversion was studied. While illuminated by visible light, Au nanoparticles get excited and provide electrons for CO2 conversion while the p-GaN semiconductor provides a material to harvest holes from the photoexcited nanoparticles. In this talk, (1) the fabrication process of Au/p-GaN will be described; (2) characterization of these structures will be shown; and (3) testing results will be explained. Results will show that the initial structure of these devices has a significant effect on the performance of these materials. Understanding the interactions between light, semiconductors, and nanoparticles is essential to creating a device that can solve our current and concerning CO2 problem.

Nonlinear Dynamics of Optoelectronic Oscillators

Discipline: Engineering
Subdiscipline: Electrical Engineering

Marco Marrufo*[1], Yanne Chembo[2], Thomas Murphy[3], Rajarshi Roy[4]
[1]California State University, Long Beach, [2]University of Maryland, College Park, [3]University of Maryland, College Park, [4]University of Maryland, College Park

Abstract: Optoelectronic oscillators (OEOs) are nonlinear dynamic systems that consist of an optical and electrical path connected in a closed feedback loop with non-negligible delay T. These self-sustained laser-driven oscillators can output electromagnetic signals in both the microwave (0 - 100 GHz) and optical (50 - 100THz) spectral domains. They can also display a wide variety of dynamical behaviors, such as periodic or chaotic oscillations. Owing to these properties, they have found a wide variety of applications such as reservoir computing, ultra-pure microwave generation, optical communications, and cryptography. In this work, we

perform a theoretical analysis of OEOs with an emphasis on finding the critical gain value that triggers an oscillatory behavior via a Hopf bifurcation. Numerical integration methods such as the fourth-order Runge-Kutta algorithm are employed to solve the system of differential equations that govern the dynamics in our OEO. We also investigate in detail the effect of the delay in the OEO dynamics. We find that our theoretical results are in excellent agreement with numerical simulations.

Preparation of Carbon Dioxide Foams at Elevated Temperatures and Pressures for Underground Carbon Dioxide Sequestration and Tertiary Oil Recovery Mechanisms

Discipline: Engineering
Subdiscipline: Chemical Engineering

Benjamin Jacobs*[1], Esteban Urena-Benavides[2], Mohammad Jahid Hasan[3], Alicia Ruvalcaba-Miyasaki[4]
[1]Northwest Vista College, [2]University of Texas at San Antonio, [3]University of Texas at San Antonio, [4]University of Texas at San Antonio

Abstract: Globally, CO2 emissions account for the largest contributor towards climate change. To mitigate the impact of CO2 in our atmosphere, scientists are placing an increasing emphasis on carbon capture and storage. This project is concerned with the sequestration of CO2 in deep saline reservoirs and depleted oil fields. Supercritical CO2 can be dispersed as bubbles in American Petroleum Institute (API) brine at high temperatures and pressures in order to mimic the harsh conditions encountered in underground environments. A reduced interfacial tension (IFT) of the CO2/brine interface can effectively reduce the probability of the greenhouse gas escaping back to the atmosphere or seeping to groundwater streams by increasing the stability of the CO2 bubbles trapped in the reservoirs. In this work, a drop shape analyzer DSA100HP1750 (Krüss, Hamburg, Germany) is used to measure the IFT of pendant drops of API brine with added cocoalkylamine (CAA) surfactant and/or cellulose nanocrystals (CNC) inside of a CO2 pressurized view cell. The IFTs of API brine solutions with added stabilizers will be measured at 60ºC and pressures ranging between 500 and 3000 psi. Our hypothesis assumes that the combination of both CAA and CNC with API brine will lower the IFT and increase the stability of the CO2 in brine emulsions and foams formed in subsurface reservoirs.

Reduction of Drag in a Closed Pipe Using a 3D Printed Riblet Structure

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Jacob Lopez*[1], Daniel Lim[2], Grace Gu[3]
[1]Fullerton College, [2]UC Berkeley, [3]UC Berkeley

Abstract: The unique microstructured geometry of mako shark skin is a key example of an evolutionary design that motivated new implementations of drag-reducing, and antifouling technologies. Their toothlike scales known as denticles decrease drag as the shark moves underwater through effectively controlling the turbulent vortices occurring near the shark skin. As such, biologists and engineers put forth extensive effort in mimicking the motion and complex structure of shark denticles to recreate the hydrodynamic and aerodynamic reaction created by sharks in nature. Our research group achieved unit denticle size down to 500 micrometers, one-fourth the size of previous proposed designs, using digital light processing 3D printing. We were able to fabricate pipe models with synthetic structure built in the inner

diameter necessary for our closed wind tunnel experiment, which was impossible to be manufactured with the conventional manufacturing method. In addition to the simple microsurface geometry such as triangular riblets validated from the previous literature, we present complex three-dimensional denticle geometries that could fully capture drag reducing capability with the optimized denticle structure fabricated using additive manufacturing.

De Novo Design of a Novel pH Sensitive Protein Switch

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jiya Fowler*[1], Aubrie Weyhmiller[2], Brian Kuhlman[3]
[1]Spelman College, [2]University of North Carolina, Chapel Hill, [3]University of North Carolina, Chapel Hill

Abstract: Current protein design studies are effective in developing proteins that can adopt a single stable conformation. However, many natural proteins have the ability to adopt more than one stable conformation in order to perform complex tasks such as signaling and functional regulation. Developing protein design methods for conformational switching will open the field of protein engineering to a wider range of functional ability. This research studies the switching ability of a novel, pH sensitive interaction that is stable at low pH and unstable at neutral pH. A bidentate hydrogen bond interaction is tested in a hairpin homodimer system, where it is placed between one set of parallel helices from each hairpin. We hypothesize that at low pH the dimer will be stable within the bidentate interaction, but at neutral pH, the homodimer system will dissociate to become a monomer. Rosetta software was used to computationally generate primary parallel helical backbones to sample the positions of the bidentate interaction. The models indicating the best bidentate interaction position based on computational scoring terms were chosen for further development. Future research on this project includes loop remodeling on the designed models to complete the hairpin homodimer system, and experimental tests to determine the characteristics of the interaction. Possible future implications of this research include growth of protein design methods and within subjects such as cell signaling use (i.e. the dimerization of a cell surface receptor), and stability of a protein in low pH environments such as the endosome or the lysosome.

The "Sociality Game": a new method to teach biology students data science skills

Discipline: Engineering
Subdiscipline: Other Engineering

Kalem Schrock*[1], Joshua Garland[2], Gerald Carter[3], Elizabeth Hobson[4]
[1]Iowa State University, [2]Arizona State University, [3]Ohio State University, [4]University of Cincinnati

Abstract: Data science skills are important for undergrads to learn but integrating them into biology courses can be difficult. We developed the “Sociality Game” - an engaging multiplayer game that combines animal behavior topics with data science training. Using game logic inspired by slither.io, we created a flexible Node.js-based platform which runs on the browser window. Players are assigned an avatar with a unique id and spawn point at the start of a game. We use the WebSocket package to dynamically update player locations as they move around the virtual environment. To guide their movements, players are given “missions” inspired by animal behavior topics. For example, each player might portray a vampire bat that forages for cow blood, where students play two iterations of the game: 1) their only goal is to find food, and 2) they need to socially forage by moving around with a buddy. We added food sources (cows) to the game landscape for players, where they earn points from finding and eating the blood of a cow. On the server, we record all the locations and scores of all players as they play the game, then compile the data so students can download the data. Students then use our tutorials to analyze their data and build data science skills. This allows students to connect with the data and build hypotheses on their interactions. As of now, we have a working prototype in beta testing, and we plan to make it widely available for educational purposes.

Miniature Liver Inserts: A High-Throughput Screening Method to Evaluate Prodrugs on Tumor Organoids

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Miranda Diaz-Infante*[1], Peyton Tebon [2], Jazmine Chism[3], Alice Soragni[4]
[1]University of California, Los Angeles, [2]University of California, Los Angeles, [3]University of California, Los Angeles, [4]University of California, Los Angeles

Abstract: Functional precision medicine aims to match drugs to patients through direct testing of compounds on a patient’s own tissue. Our lab has developed a platform to screen hundreds of drugs on patient-derived tumor organoids to identify individualized responses. One limitation in this type of pipeline is the study of prodrugs, compounds that require to be metabolized to convert to the active drug and exert their therapeutic effect. To address this limitation, we created a high-throughput screening method using miniature liver inserts (MLIs) which allow for the growth of liver organoids that can metabolize prodrugs of interest. First, we discuss the design of the MLI which positions liver organoids millimeters from the bottom of the well where patient-derived tumor organoids are grown as mini-rings. The MLI can be inserted and removed from any well of a 96-well plate with no contact or disruption to the tumor organoid culture component. The biocompatible transparent resin we use allows for non-invasive imaging throughout drug screening experiments along with quantitative analysis of the growth of each cell type. We then discuss optimization parameters and validation of the presence of enzymes that activate prodrugs using metabolic assays and immunohistochemistry. Finally, we will present our findings on the impact of prodrug treatments on our co-culture of liver and tumor cell lines. Drug screening with the MLI allows us to studyclinically used prodrugs in a high-throughput culture system enabling the rapid selection of effective therapies for individual patients.

Reconstruction of microelectrode trajectories in the Centromedian & Pedunculopontine Nuclei using 3D models

Discipline: Engineering
Subdiscipline: Other Engineering

Manuela Lizarazu*[1], Alex Doyle [2], Joan Dao[3], Matthew D. Johnson[4]
[1]University of Iowa, [2]University of Minnesota, [3]University of Minnesota, [4]University of Minnesota

Abstract: Parkinson’s disease (PD) is the second most prevalent neurodegenerative disorder, affecting more than 10 million people worldwide. One of the symptoms of PD that is difficult to treat with medication or deep brain stimulation (DBS) is gait dysfunction, including freezing of gait, which is characterized by the inability to behaviorally shift out of shuffling gait patterns. The centromedian nucleus (CM) and pedunculopontine nucleus (PPN) are two non-dopaminergic nuclei in the brain that are thought to be involved in processing unexpected environmental events that lead to attentional or behavioral shifts, but the relationship is unclear. This study supported the investigation of signaling changes in CM and PPN from a naïve to a parkinsonian state in a preclinical PD animal model. Computer models of the CM, PPN, caudate nucleus, globus pallidus, subthalamic nucleus, periaqueductal gray region, medial dorsal nucleus, were segmented and electrode pathways were reconstructed from histology to analyze what areas of the brain were targeted by the electrodes. Forty-two percent of the intended electrodes reached the target of CM while thirty-three percent of the intended electrodes reached the PPN target region. These data will be critical to assess neuronal spike activity changes in PPN and CM in the parkinsonian condition.

Design analysis of an aerial drone-based imaging payload system for deep-sea exploration.

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Adriana Munoz-Soto*[1], Brennan Phillips [2], Catalina Martinez[3]
[1]University of Puerto Rico, Mayaguez Campus, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Setting sight on exploring deep-sea ecosystems in a low-cost manner, a reel-based payload system is being considered in order to visually explore and sense the water column and seafloor. Because of its compact size, the reel system can be deployed from a small ship, eliminating the need of large exploration vessels and industrial scale remotely operated vehicles (ROVs) currently used. This approach reduces preparation time, environmental pollution, and financial investment needed for current deep-sea robotic exploration. The research in this project was conducted in the Undersea Robotics and Imaging Laboratory at the University of Rhode Island (URI), with field testing at the Bermuda Institute of Ocean Science (BIOS). The system provides high definition imagery of the sea floor and water column with little sound and movement produced, retrieving real time data such as visual, temperature and depth recordings that help understand underwater behavior. Components of the system were designed using computer-aided design (CAD) software, 3D-printed prototyped using stereolithography (SLA) printers and tested on different ocean floors such as coastal Rhode Island waters and deep ocean waters adjacent to Bermuda. Efforts were centered on design, 3D printing and treatment of water and pressure resistant components, including sensor mounts and multiple versions of a slide for the fiber optic fishing line to smoothly reach the water surface and mechanical terminations that can hold various sensors and payloads.

The Angler, a Low-Cost, Novel 810nm LED Transcranial Photobiomodulation Headcap Device

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Claire Sissons*[1], Caroline Carter [2], Sally Miller[3], Han Liu[4]
[1]University of Texas at Arlington, [2]University of Texas at Arlington, [3]University of Texas at Arlington, [4]University of Texas at Arlington

Abstract: Recently, the need for Transcranial Photobiomodulation (tPBM) devices have increased due to its treatment for neurocognitive disorders. It is highly desirable to develop a device that is lightweight, low cost, and able to deliver tunable light intensity without overheating the tissue.

We created the Angler device by implementing one high-powered infrared (IR) 810-nm LED unit, heat sink and miniature fan into a 3-D printed polyurethane (PUR) housing box. This design can comfortably hang from a head cap. All components were wired in parallel on a PCB board, which resides inside the housing box. The housing box was wired to an adjustable power supply to achieve an optical power density of ~135mW/cm^2. Both the heat sink and fan were found to considerably lower the heat of LED from 160 °F to ~ 90 °F. in vivo testing showed that the 8-min LED delivery of tPBM on the human forehead by our Angler enabled us to significantly increase the prefrontal oxygenated and total blood concentration as compared to those without any tPBM stimulation or at the pre-tPBM period. Our goal was achieved in creating a working, low-cost, versatile, and lightweight device that can effectively simulate the same changes as shown by the hemodynamic and metabolic changes. A functional LED device used for tPBM was fabricated for further in-vivo clinical trials to safely and potentially treat a variety of diseases relating to memory loss.

Intestinal Organoids as a Tool to Understand Gut Repair Following Radiation

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Briana Martin-Villa*[1], Katarina Christina Klett[2], Sarah Christine Heilshorn[3], Victoria Villareal[4], Stavros Melemenidis[5], Vignesh Viswanathan[6], Rakesh Manjappa[7], Billy Loo[8], Erinn Rankin[9]
[1]Stanford University, [2]Stem Cell Biology and Regenerative Medicine, [3]Materials Science and Engineering, [4]Materials Science and Engineering, [5]Radiation Oncology, [6]Radiation Oncology, [7]Radiation Oncology, [8]Radiation Oncology, [9]Radiation Oncology, Obstetrics and Gynecology

Abstract: Conventional radiation, which delivers doses over long time intervals (i.e., minutes), is known to destroy both cancerous and healthy cells, reducing a patient's quality of life. Alternatively, a novel method of radiation known as FLASH radiation delivers doses of radiation over ultra-short time intervals (i.e., a fraction of a second). FLASH radiation has been shown to be equally as effective as conventional radiation at targeting cancerous cells while preserving healthy gut tissue in mouse models. However, this phenomenon has not yet been studied in humans. Intestinal organoids, three-dimensional (3D) cultures that recapitulate the native tissue structure and cell function, provide an exceptional tool to study human tissue. In this work, we leveraged intestinal organoids to study the effects of conventional and FLASH radiation on organoid growth and morphology. Specifically, mouse and human intestinal organoids were radiated with doses ranging from 2 Gy to 8 Gy and were subsequently analyzed for organoid growth post-radiation. Our results demonstrate that intestinal organoids radiated with FLASH radiation grew significantly larger than organoids radiated with conventional radiation. Additionally, we observed drastic morphological differences across groups that received no radiation, conventional radiation, or FLASH radiation. Our results suggest that intestinal organoids can serve as powerful tools to understand gut repair following radiation. In the future, I plan to analyze gene expression changes post-radiation to explore the cellular mechanisms driving intestinal tissue regeneration.

Class Attendance Blockchain Algorithm

Discipline: Engineering
Subdiscipline: Electrical Engineering

Jeremis Morales*[1]and Carmen Caiseda[2]
[1]InterAmerican University of Puerto Rico Bayamon Campus, [2]Professor

Abstract: Title: Class Attendance Blockchain Algorithm Web 3.0 is a data-oriented and semantic internet that uses decentralized and distributed storage such as blockchain to record transactions. This third-generation internet tool seeks to give users greater control of their data, security, and privacy in the management of information, which contrasts with controversial practices that exploit the user's data for a profit. Using fictitious student information and the R software to distribute the generated parameters (i.e., Veteran Status, Course/Section, QR scans for class dates), we designed and simulated a blockchain-structured class attendance platform that facilitates the process of generating attendance reports from in-person and virtual class records. We then used the panda library in Python to construct an interface that automatically cleans the data and facilitates the process of generating a report that includes the following federal compliance attendance requirements: 1) administrative withdrawal (AW), 2) attendance, 3) unauthorized withdrawal with last day of attendance (UW), and 4) withdrawal requested by the student (W). Outcomes show that blockchain technology is a promising tool that provides privacy, security and complies with federal regulations regarding college students' attendance.

Photobiomodulation Enhances Blood Oxygenation and Tissue Metabolism By Near Infrared Laser and Light Emitting Diode

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Caroline Carter*[1], Dr. Hanli Liu[2], Dr. Tyrell Pruitt[3]
[1]University of Texas Arlington, [2]University of Texas Arlington, [3]UT Southwestern

Abstract: NASA will launch a mission to Mars in 2024; during the trip Astronauts will experience muscle atrophy from microgravity. To solve this problem, we hypothesize that photobiomodulation (PBM) using laser and light-emitting diodes (LED) at near-infrared (NIR) wavelength can improve the muscle conditions of astronauts. PBM was used on the human forearm to stimulate its blood oxygenation and tissue metabolism which were measured by optical NIR spectroscopy. Subjects were measured before, during, and after 8-min PBM and sham conditions with 808-nm and 852 nm-nm lasers as well as an 808-nm LED unit. PBM results were compared between the two lasers and between the laser and LED-based on two-sample t-tests. Statistical analysis showed that PBM by the lasers enabled the creation of equivalent and significant enhancement of blood oxygenation and tissue metabolism on the human forearm. Also, LED at 808 nm resulted in significant PBM effects on the forearm compared with sham conditions. 8-min PBM induced significant increases in blood oxygenation and tissue metabolism of the human forearm by NIR laser or LED units, indicating that LED-based PBM may have vast potential for mitigation of muscle atrophy caused by long-term spaceflight microgravity exposure.

Effects of Electronic Cigarettes Liquid Components on Airway Mucus Swelling Kinetics

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Scott Garcia*[1], Dr. Wei-Chun Chin[2], Carlos Vazquez[3]
[1]University of California, Merced, [2]University of California, Merced, [3]University of California, Merced

Abstract: Electronic cigarettes or e-cigarettes have gained major traction in several domestic markets across the globe in recent years, with a significant increase in use among underage individuals. E-cigarettes have been repeatedly marketed as a safer alternative in comparison to tobacco products, with lures such as flavored e-cigarettes becoming incredibly successful in targeting younger audiences. With the emergence of these new electronic cigarettes, current research has focused on the direct toxicity of these devices, however, our study focuses on addressing the gap regarding the rheological effects on airway mucin secretion associated with e-cigarette use. Furthermore, our study investigates the health impacts correlated to these devices, specifically common lung diseases, such as chronic obstructive pulmonary disease and asthma. We utilized A549 human epithelial carcinoma cell lines alongside video microscopy to monitor the swelling kinetics of mucus when exposed to liquid e-cigarette components: propylene glycol or vegetable glycerin at varying concentrations. Propylene glycol and vegetable glycerin are organic solvents often found in food, cosmetics, and medications. Vegetable glycerin and propylene glycol are both deemed safe for human consumption by the FDA, however, when inhalation occurs the health implications of PG and VG remain largely undetermined. Our results indicated that e-cigarettes with varying concentrations of propylene glycol (PG) or vegetable glycerin (VG), lead to abnormally viscous mucus placing an individual at a higher risk for developing respiratory diseases. More importantly, these results may be used to refine or improve protocols involved in electronic cigarette production and more so the regulation of e-cigarettes.

Sustainable Sorbent Technology for Mercury Remediation in Freshwater Aquatic Systems

Discipline: Engineering
Subdiscipline: Other Engineering

Caridad Estrada*[1]and Johnbull Dickson [2]
[1]Florida International University, [2]Florida International University - Applied Research Center

Abstract: Remediation of mercury under prevailing geochemical conditions found across the growing number of mercury-contaminated sites globally is a challenging and costly endeavor due to the persistent geochemistry of mercury. Here, eight sustainable, low-cost sorbent media were evaluated for removal of mercury from contaminated freshwater streams. Batch studies were performed in simulated creek water and deionized water and analyzed with a direct mercury analyzer. Model-calculated kinetic parameters indicate the applicability of the nonlinear pseudo-second-order model as the best predictor of kinetic parameters for mercury sorption onto the evaluated sorbents. Moreover, kinetic data suggest that liquid film diffusion was the rate-limiting steps governing mercury sorption. Higher sorbent dosages resulted in faster kinetics of mercury sorption. Overall, the rate of mercury sorption onto sorbent media decreased in the following order: PAC > Sorbster > FeS+PAC > Si-thiol ≅ RemBind > Biochar > Filtrasorb 300 > Organoclay PM 199. These evaluated sorbents could provide sustainable solutions for cost-effective remediation of mercury in contaminated environments. Understanding the fate of mercury in the presence of a suite of sorbent media is an important first step in the management of mercury species in contaminated ecosystems.

CRISPR/Cas9-Based Genome Editing in the Filamentous Fungus Neocallimastix Californiae

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jessy Gonzalez*[1], Tejas Navaratna[2], Michelle O'Malley[3]
[1]University of California, Santa Barbara, [2]University of California, Santa Barbara, [3]University of California, Santa Barbara

Abstract: Obligate anaerobic fungi, found in the rumen of herbivores, secrete a diverse suite of enzymes that can decompose rigid cell wall components, such as cellulose, hemicellulose, and lignin which, without these enzymes, are insoluble. Likewise, these fungi are ubiquitous in multi-kingdom communities, demonstrating the production of biotechnologically valuable products, including small bioactive molecules and short- and medium-chain fatty acids. However, due to a lack of robust genetic engineering strategies and the low efficiency of traditional genetic tools, it is a challenge to industrialize anaerobic fungal activity. Towards this goal, we are establishing an efficient CRISPR/Cas9-based genome editing tool for N. Californiae . In conjunction with fluorescence-activated cell sorting (FACS) and electroporation, we have delineated transformation conditions for high levels of Cas9 protein entry and cellular viability in zoospores. We are actively (i) comparing the SV40 (SV40 NLS) and endogenous histone 2B (H2B NLS) nuclear localization signals to enable the import of Cas9 into the fungal nucleus; and (ii) generating a series of ribonucleoproteins (RNP) to target the URA3 homolog via non-homologous end joining (NHEJ) with 5-fluoroorotic acid (5-FOA) selection. If successful, this strategy may be generalizable to other non-model organisms and improve anaerobic fungal enzymatic activity to prioritize biomass degradation in an affordable and efficient manner.

Encapsulation of Native American Plant Extracts for Therapeutics

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Layla James*[1], Jesslyn Chief[2], Yan Liu[3], Dr. David A. Weitz[4], Dr. Abraham Meles[5], Dr. Irene Ane-Anyangwe[6], Dr. Thiagarajan Soundappan[7]
[1]Navajo Technical University, [2]Navajo Technical University, [3]Harvard University, [4]Harvard University, [5]Navajo Technical University, [6]Navajo Technical University, [7]Navajo Technical University

Abstract: Escherichia coli (E.coli) are bacteria that are present in the intestines of humans. Most types of E. coli are harmless, but some strains can cause mild to severe illness. Juniper berries and Navajo tea are traditional Native American plants with a history of treatment of intestinal distress. The goal of this project is to encapsulate these plant extracts into micron-sized pectin-based microgels to protect the extracts in the acidic environment of the stomach and then be released in the intestines. This study used polydimethylsiloxane (PDMS) microfluidic devices to controllably encapsulate these plant extracts into the pectin-based microgels. The microgels were then co-cultured with E. coli at 37℃, and the growth of E. coli was monitored by the turbidity of the culture media each hour for 17 hours. The encapsulated extracts of Navajo tea and Juniper berries both demonstrated lower turbidity values compared to a control bacteria culture, indicating promising antibacterial properties. In future work, we plan to investigate the mechanism for inhibition of E. coli growth by these extracts, to quantify the protection offered by the microgels in the gut, and to study the kinetics of the sustained release of the plant extracts in the slightly alkaline conditions of the intestine.

Development of Platelet-Coated Nanoparticles for the Treatment of Pulmonary Fibrosis

Discipline: Engineering
Subdiscipline: Chemical Engineering

Camila Cersosimo*[1], Dr. Samantha A. Meenach [2], Matthew Freeman[3]
[1]University of Rhode Island, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Respiratory diseases represent a significant public health challenge owing to their frequency and difficulties in treatment. Pulmonary fibrosis (PF) is a lung disease that occurs when lung tissue becomes damaged where thickened, stiff tissue decreases lung function, and afflicted patients become progressively short of breath. Treatment options for PF are currently limited to two FDA-approved drugs, which are in turn limited by a repetitive treatment regimen requiring multiple daily doses to ensure efficacy. Thus, there is an urgent need for both more effective therapeutics and more effective methods to deliver PF-related drugs to the lungs. We have developed platelet-coated nanoparticles (PCNP) that are capable of homing to and/or binding with activated fibroblasts, diseased endothelium, and/or collagen present in PF-related tissue to provide tissue-specific delivery of anti-fibrotic therapeutics with enhanced retention in the lungs to better attenuate PF. Biodegradable NP loaded with the PF drug, pirfenidone (PIR), were coated with NP and evaluated for their size, presence of membrane-associated proteins, toxicity, and binding in PF-related cells and collagen. Preliminary results indicated that the NP are appropriate in size (~200 nm) and are successfully coated with platelet membranes. Future work will involve the evaluation of the NP impacts on tissue toxicity and their ability to interact with PF cells and bind to collagen. We hypothesize that PCNP will bind with cells typically activated in PF to deliver PIR to lung tissue in a more targeted approach, in comparison to unencapsulated PIR, thereby increasing the efficacy in the treatment of PF.

Investigation of the Antimicrobial Properties of Cerium Oxide Nanoparticles

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Rebeca Ramirez*[1], Jaqueline Rojas Robles [2], Dr. Jeremiah Abiade[3]
[1]University of Illinois at Chicago, [2]University of Illinois at UIC, [3]University of Illinois at Chicago

Abstract: Currently, the spread of drug-resistant pathogens is making it more difficult to treat common infections with available antibiotics. One strategy to minimize the spread of drug-resistant pathogens is to use alternative antimicrobials like metal oxide nanoparticles. In this project, cerium oxide nanoparticles were made via hydrothermal synthesis and tested for their antimicrobial activity using agar well diffusion assays. It was shown that the cerium oxide nanoparticles at a concentration of 260 mg/mL showed signs of inhibiting escherichia coli (E.coli), as indicated by the presence of zones of inhibition. This work suggests that cerium dioxide may be used as an antimicrobial agent that can be incorporated into nanomaterial coatings to combat the spread of drug-resistant pathogens.

Influence of obesity on biomechanics models and simulations

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Iris Borunda*[1], Aurelie Azoug [2], Jerome[3], Kara Marchetta[4]

[1]Oklahoma State University, [2]Oklahoma State University, [3]Oklahoma State University, [4]Oklahoma State University

Abstract: Biomechanics simulations of a subject's body are commonly developed using a generic model scaled to the weight and height of the subject. This method implies that the relative contribution of each body segment to the total weight remains constant for all subjects. As the Body Mass Index (BMI) of the subjects increases, this assumption is not valid and introduces an error on mass and inertia. A precise segmental weight distribution has not been developed for overweight and obese subjects and is necessary for accurate modeling. The overall objective is to quantify the BMI above which a subject-specific musculoskeletal model is necessary for the accurate evaluation of body dynamics. In this first step, male and female subjects of various BMIs between 18 and 40 years old have been recruited. Subjects wearing tight fitting clothes are scanned with a 3D scanning Structure sensor controlled with an iPad. Each scan is decomposed into body segments in Matlab. The weight of each segment is determined from its volume through density values found in the literature. This weight distribution can be compared to the one predicted by the generic model. This study will ultimately allow researchers to correctly predict the body dynamics of overweight and obese subjects.

Population Genomic Analysis on the North American Black Bear

Discipline: Engineering
Subdiscipline: Other Engineering

Andrea Galvez*[1], Megan Supple[2], Beth Shapiro[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California Santa Cruz

Abstract: The American Black Bear is recognized as an important species to the North American ecosystem. Black bears provide natural dispersal of seeds and nutrients, maintain deer and other prey populations, and are used for recreational hunting. Although black bears face no immediate threats, scientists must monitor their numbers to ensure a healthy population size. With help from the California Department of Fish and Wildlife, University of Santa Cruz researchers were able to obtain 96 individual black bear samples from which DNA has been sequenced. Using these data, we will analyze current population health, genetic structure, and environmental conditions to determine if there has been any significant change in their habitat. We will begin by ensuring that the black bear sequencing data are of sufficient quality for analysis by using the FASTQC program. From this project, we hope to ensure the stability of the black bear population and use the data to maintain or increase their well-being over the coming years. By understanding how black bears continue to thrive while many sympatric species are declining, we hope to determine which genomic characteristics indicate healthy populations. In the future, researchers may apply these characteristics to improve the viability of threatened populations.

Self-Organizing Maps for Soil Temperature Profiles Clustering from NASA's Earth Data Science

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Jamie Vazquez*[1]and Dr. Carmen Caiseda[2]

[1]Interamerican University of Puerto Rico Bayamon Campus, [2]Interamerican University of Puerto Rico Bayamon Campus

Abstract: Self-Organizing Map (SOM) is an unsupervised neural network algorithm that classifies multidimensional data into groups of similar characteristics shown in a lower dimensional map. The use of this algorithm has been proposed in literature to locate anomalies in space weather events among other applications. Thus, the aim of our work is to showcase the functionality of Self-Organizing Maps and evaluate its performance in the analysis of historical data by taking into consideration global warming motivation. By using “MiniSom”, a Python tool that facilitates the algorithm methodology, we have implemented the basic usage features from the module to a dataset of Soil Temperature Profiles, which include more than 2,000 observations, retrieved from NASA’s Earth Data Science resource. The data was preprocessed, and the module’s initial parameters were set according to provide visualization at different iteration steps and evaluate the precision of the algorithm. We will report on the number of steps that produces the best maps as well as discussing the resulting soil temperature clusters, with special attention to the singularities of soil temperatures, and different visualizations such as: distance map and seeds map. The significance of this work is to provide insights of whether there are singularities of interest that will give us new weather knowledge spotted via unsupervised neural network applications while evaluating the Self-Organizing Map performance for this dataset.

Exoskeleton Assistance on the hip, knee, ankle: A Multi-joint Assistance Study

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Ricardo Reyes*[1], Patrick W. Franks[2], Gwendolyn M. Bryan[3], Russell M. Martin[4], Steven H. Collins[5]
[1]Stanford University, [2]Stanford University, [3]Stanford University, [4]Stanford University, [5]Stanford University

Abstract: Exoskeleton devices that provide assistance at the hip, knee, and ankle have reduced the metabolic cost of walking. However, comparisons of assistance of a combination of these joints, have not been seen. Assisting multiple joints may be more beneficial than the sum of the individual energy reduction benefit, because muscles often span multiple joints, or less effective, because single-joint assistance can indirectly aid other joints. In this study, we used a bilateral hip-knee-ankle exoskeleton emulator coupled with human-in-the-loop optimization to determine single-joint and whole-leg assistance profiles that optimized for the largest reduction in the metabolic cost of walking. Knee-only assistance reduced the metabolic cost of walking by 13% relative to no assistance with the device on, demonstrating that effective knee assistance is possible (N = 3). Assisting all three joints reduced the metabolic cost of walking by 50%, showing that half of the metabolic energy expended during walking can be saved through exoskeleton assistance (N = 4). Changes in kinematics and muscle activity indicate that single-joint assistance indirectly assisted muscles at other joints, such that the improvement from whole-leg assistance was smaller than the sum of its single-joint parts. A single well-chosen joint can be more efficient when considering weight and cost but for largest gain whole leg assistance is best.

From Brown Tides to Bio-Based Materials

Discipline: Engineering
Subdiscipline: Chemical Engineering

Alexandra Diaz Collazo*[1], Omar Movil-Cabrera[2], Kristie M. Rivera[3], Eduardo Vega[4]

[1]Polytechnic University of Puerto Rico, [2]Polytechnic University of Puerto Rico, [3]Polytechnic University of Puerto Rico, [4]Polytechnic University of Puerto Rico

Abstract: Bacterial Cellulose (BC) has received attention due to its many advantages such as high mechanical strength, purity, crystallinity, liquid-absorbing capabilities, and biodegradability. Unfortunately, the main drawbacks associated with BC production are (1) its high cost which is higher than plant-based cellulose, and (2) the used of food products like sugar and green/black tea for its production. Therefore, the main goal of the present research work is to overcome the limitations associated with BC production by using seaweed as a cheaper source of both carbon and nitrogen. To achive this goal, BC will be synthesized via fermentation using Kombucha "symbiotic culture of bacteria and yeast" (SCOBY) as the seed, which will be immersed in a solution of acetic acid containing the algae extracts. After 3 weeks of fermentation, the obtained BC films will be rinsed (with water), dried in an oven, and weighed in a balance to determine the process yield. Morphology of the BC will be evaluated via optical microscopy, SEM and AFM. Chemical characterization will be performed via FTIR, while crystallinity and crystal size will be determined via XRD diffraction. Mechanical properties of the obtained BC films will be evaluated via tensile test. For comparative purposes BC will also be produced via fermentation using food-grade sugar and green tea as the sources of carbon and nitrogen, respectively.

Functionality of the Gracilis Collateral is Impaired Following Arteriogenesis and Cell Transplantation

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ada Tadeo*[1]and Trevor Cardinal [2]
[1]California Polytechnic State University, San Luis Obispo, [2]California Polytechnic State University, San Luis Obispo

Abstract: Peripheral Arterial Disease involves narrowed arteries, reducing blood flow to limbs. Increasing blood flow to those extremities is possible by redirecting the blood to flow through natural bypasses (i.e. collateral arteries), which can enlarge via arteriogenesis to maintain blood supply once the prominent arteries have become occluded. This study aims to investigate how arteriogenesis affects collateral function, if cell transplantation can stimulate collateral growth, and how that in turn may affect collateral function. Femoral artery ligation was performed to mimic the blockage that occurs in patients with ischemic diseases on lean mice and mice with diet induced obesity (DIO). A bioprinted polymer containing cells, or no cells, was then placed deep to the primary collateral artery. Seven days post-surgery, the collateral bypass artery was exposed and prepared for imaging. To quantify the functionality of the collaterals, photomicrographs of the collaterals were captured from both the operated and control hindlimb. Images were collected of the collateral at rest and following muscle contraction via electrical stimulation. Results showed that arteriogenesis occurred in lean and DIO mice. Phenotype combined with cell treatment had a significant influence on collateral diameter - DIO with cells had smaller diameters vs DIO control, meanwhile lean with cells had larger diameters vs lean control. Thus, cells did not make more arteriogenesis, but appeared to accelerate vessel maturation. This line of research can ultimately lead to the development of an alternative, minimally invasive, therapy to treat patients with ischemic diseases that would benefit from natural bypass enlargement and function.

Recycled Concrete Aggregate for Eco-Friendly Construction in Idaho

Discipline: Engineering

Subdiscipline: Civil Engineering

Berenice Sosa Aispuro*[1]and Mustafa Mashal[2]
[1]Idaho State University, [2]Idaho State University

Abstract: Idaho uses tens of thousands of cubic yards of concrete for construction of buildings, sidewalks, bridges, and roads. It is the second most used material after water. The aggregates in concrete add to the CO2 emissions. Idaho is restricted on the aggregates it sources. Most of the aggregates in Idaho undergo Alkali-Silica Reaction. This is when the aggregates react with silica. At present, Idaho does not use demolished concrete projects as Recycled Concrete Aggregate (RCA) in fresh mixes for civil infrastructure. Majority of the demolished concrete ends up in landfills; therefore, increasing the carbon footprint along with having a negative impact on the environment. RCA can replace some or all coarse aggregates. Advantages that come with using RCA concrete mixes include: 1) Reducing the carbon footprint of concrete; 2) Reducing environmental impacts of demolished projects (RCA has 3-5% less emissions compared to fresh coarse aggregate); 3) Providing durability. The source of RCA and climate of the region where the RCA was supplied were factors that were considered. Future work involves experimental testing for structural properties and durability of concrete mixes incorporating RCA with different designs and mix portions. Results will then be compared against a benchmark mix from local ready-mix plants that use fresh aggregates.

Bacterial cellulose as a sustainable and green biomaterial for drug delivery to the brain

Discipline: Engineering

Subdiscipline: Chemical Engineering

Gabrielle Balistreri*[1], Elizabeth Nance[2], Eleftheria Roumeli[3], Andrew Jimenez[4], Tessa De Souza Machado[5]
[1]University of Washington, [2]University of Washington, Chemical Engineering, [3]University of Washington, Materials Science & Engineering, [4]University of Washington, Materials Science & Engineering, [5]University of Washington, Materials Science & Engineering

Abstract: Bacterial cellulose (BC) is a biodegradable, biocompatible, and mechanically strengthened material overlooked and underutilized as a drug delivery system. BC-based drug delivery systems are of growing interest with the need for sustainable materials in nanomedicine. Currently, poly(lactic- co -glycolic acid) (PLGA), with or without polyethylene glycol (PEG) copolymerized, is an FDA approved material clinically used in drug delivery, where fabrication of PLGA is not sustainable nor a green process. Therefore, our goal is to evaluate the potential of bacterial cellulose nanofibers (BCN), compared to PLGA and PLGA-PEG nanoparticles as drug delivery systems, with application in the brain. Natural BC fibers are ultrasonicated and homogenized to generate BCN, and characterized using dynamic light scattering, Fourier Transform Infrared Spectroscopy, electron microscopy, and confocal microscopy. The BCN length is ~200-700 nm and ~10 nm in cross-sectional diameter, a desirable size range to achieve penetration within the brain based on our prior work. BCN have high surface area, hydrophilic layering from hydrogen bonding, and a polydispersity index of ~0.250. Next, BCN are evaluated for penetrability and toxicity in organotypic whole hemisphere brain slices from rats, a model routinely used in our lab to screen nanotherapeutic platforms. Cell viability and cell localization of BCN are compared to that of PLGA-PEG nanoparticles made in surfactant. Our long-term goal is to lay the foundation of the next generation of sustainable nanomedicine platforms in terms of preparation, functionalization, and overall optimization of the chemical and physical properties, with capability to deliver therapies to the brain.

Assessment of Emerging Contaminants in Surface Waters, Sediment, and Biosolids Following Wastewater Treatment Plant Processes

Discipline: Engineering
Subdiscipline: Other Engineering

Kyra Sigler*[1], Tiffany Messer[2], Eduardo Santillan-Jimenez[3]
[1]University of Kentucky, [2]University of Kentucky, [3]University of Kentucky

Abstract: Per- and polyfluoroalkyl substances (PFAS) and neonicotinoid insecticides are two classes of emerging contaminants that have been recently detected in many environmental compartments including soil, surface water, groundwater, and finished drinking water. Exposure to these contaminants has been associated with human health impacts including high cholesterol and cancers, as well as stressors to ecological food webs and agroecosystems. The objective of this project was to investigate wastewater treatment plant (WWTP) end products (biosolids and effluent) as point sources of PFAS and neonicotinoids into the environment (surface waters and sediment). PFAS and neonicotinoids were monitored at two WWTPs in central Kentucky during April and July 2022. Sampling occurred in surface waters and sediment upstream and downstream of the WWTP, as well as at influent, effluent, and finished biosolids. Data was collected using a polar organic chemical integrative sampler and analyzed using a Waters Xevo TQS UPLS tandem mass spectrometer to determine concentration and mass loadings of the emerging contaminants. Supplemental surface water conditions at the stream sites were monitored using a YSI Professional Pro multiparameter instrument. Dissolved oxygen ranged from 9.73 to 14.5 mg/L; conductivity ranged from 558 to 744 μs/cm; and pH ranged from 7.23-8.19. These parameters can influence PFAS and neonicotinoid partitioning to sediment, water, and air, as well as impact their transformation processes and end products. Thus, the implications of these parameters will be considered when analyzing contaminant data. Findings from this work will provide guidance regarding implications of WWTP processes to transformation of PFAS and neonicotinoid insecticides.

Environmental Disparity Analysis on Los Angeles Neighborhoods Air Quality Levels Before and During the COVID-19 Pandemic

Discipline: Geoscience
Subdiscipline: Environmental Science

Dulce Garcia*[1]and Tianjun Lu[2]
[1]California State University, Dominguez Hills, [2]California State University Dominguez Hills

Abstract: Adverse air quality is an environmental justice issue as it disproportionately affects marginalized and disadvantaged populations worldwide, such as black, indigenous, and people-of-color (BIPOC) communities. The COVID-19 pandemic revealed global structural inequalities and deepened environmental justice issues, including environmental health. The preliminary lockdown measures enforced early in the pandemic intended to control the spread of the Coronavirus-19 and limit travel, social, and industrial activities. The restrictions may have alleviated air pollution emissions; however, whether this is true for disadvantaged communities where neighborhoods are in proximity to potential emission sources (e.g., highways, industrial facilities) is uncertain. This study focuses on the COVID-19 effects on air quality levels in disadvantaged communities of Los Angeles County -a highly compacted urban city whose residents fit in a range of socioeconomic statuses. Using openly available socioeconomic data from CalEnviroScreen 4.0 and crowdsourced air quality data from the PurpleAir website (one of the most widely used low-cost sensor networks), this study will investigate air pollution concentrations (i.e., Particulate Matter), focusing on a comparison before and during the COVID-19 pandemic. Through statistical analysis in R Studio and geospatial analysis in ArcGIS Pro, this research aims to determine whether existing environmental disparities in air quality levels persisted through the COVID-19 pandemic, especially among disadvantaged communities. While some studies have explored pandemic restrictions' effects on air quality, the impact associated with the disparity in urbanized areas is understudied. In summary, this project will help provide valuable insights into environmental justice, community resilience, and health intervention policies for disadvantaged communities.

Connection of Clear and Turbid Cenotes to Regional Flow

Discipline: Geoscience
Subdiscipline: Geology

Bianca Mendez*[1], Megan Brown, Ph. D. [2], Melissa Lenczewski[3], Lorena Vargas[4]
[1]University of Puerto Rico, Mayagüez, [2]Northern Illinois University, [3]Northern Illinois University, [4]New Mexico State University

Abstract: Sinkholes, locally called cenotes, are surface features connected to the aquifer that supplies drinking water to the Yucatán Peninsula. Despite being close to each other, many cenotes have different characteristics; while water is clear in some, it may seem turbid in others. Some of these differences may be closely related to the direction and amount of water flow. This study will examine regional flow patterns of various cenotes with different turbidity levels to determine if connectivity or lack thereof is correlated with turbid conditions. In this study, we are testing new methods to characterize the flow within individual cenotes and use that data to improve our understanding of regional flow and its connection to water quality within cenotes. For example, CHIRP (Compressed High-Intensity Radiated Pulsed) is used as a fish finder, and Aquadopp has been implemented in oceanic environments as a current meter. In this research, CHIRP is employed for bathymetry and Aquadopp to see if we can measure flow into and out of the cenote. If these methods can effectively be used to characterize smaller scale flow within a cenote, the data generated can be used to connect to the regional scale flow. Additionally, surveying to find water level and using GPS technology has been helpful when conducting research. At last, it is essential to consider that the data collected in this research will be beneficial for the economy and environment of the Yucatán Peninsula and the water quality control in communities surrounding these sinkholes.

Quantified effect of taconite and precious metal mining on wild rice watersheds of eastern Minnesota

Discipline: Geoscience
Subdiscipline: Earth Science

Nick Salgado-Stanley*[1], Dr. Nathan Johnson [2], Diana Dalbotten[3], Dr. Nievita Bueno Watts[4]
[1]California State Polytechnic Institute, Humboldt, [2]University of Minnesota, Duluth, [3]University of Minnesota, Twin Cities, [4]California State Polytechnic Institute, Humboldt

Abstract: Industrial activities in northern Minnesota, particularly the taconite and proposed precious metals mining in the 'Iron Range,' release chemicals that can harm native plant growth. Specifically, pollutants from the extraction of iron ore have released water that can harm wild rice (Zizania palustris) due to high amounts of sulfate entering lakes and streams where wild rice has historically grown. For centuries, wild rice, or manoomin in the local Ojibwe language, has been a staple diet for Minnesota's Indigenous people. Domestic cultivation and combined harvesting of wild rice are relatively new technologies; wild rice is grown commercially as a field crop on around 20,000 acres in Minnesota. This poster aims to quantify sulfate pollution entering Minnesota watersheds from the most impactful point dischargers. To develop a process for evaluating the magnitude of contamination from different sources, two ~7500 km2 watersheds are compared. One watershed is impacted by the Iron Range mining operations and the other has mostly municipal wastewater discharges. The St. Louis River basin is directly downstream from the largest mines in the state, including the Hull-Rust Mahoning Mine which adds water containing at least 800 mg/L of sulfate to tributaries of the St Louis River. In contrast, the Upper Mississippi headwaters has fewer large industrial polluters. This poster evaluates the potential effects to wild rice waters produced by the Iron Range industry sulfate releases and considers the implications of enforcement of the Clean Water Act and State of Minnesota's sulfate standard.

A legacy of pollution leading to increased trace metals in Mystic River, MA

Discipline: Geoscience

Subdiscipline: Environmental Science

Sarah Purvis*[1], Karen Johannesson [2], Jaxon Dii Horne[3], Larissa P Costa[4]
[1]Mount Holyoke College, [2]Umass Boston, [3]Umass Boston, [4]Umass Boston

Abstract: Woburn, Massachusetts has a history of unregulated industry leading to the accumulation of trace metals. In the 1800s chemical manufacturers supplied chemicals like benzyne, insecticides made with lead and arsenic, sulfuric acid, chromium, and even explosives. These materials supported Woburn's industrial boom from local leather tanning companies to piggeries. The waste from these products was dumped into the Aberjona Watershed which flows into the Mystic River. Today, Woburn residents have many concerns, for example, cancer rates are above the national average and the Mystic River often has a foul smell of unknown origin. This project aims to record the concentrations of chromium in the Aberjona watershed, upstream and downstream of industrial sites in the Upper and Lower parts of Mystic River. I hypothesize that the samples from upstream of the industrial sites will have the lowest concentrations of chromium and the samples below the industrial sites will have concentrations above the EPA's water quality standards. We will collect water and sediment samples from along the Aberjona watershed and the Mystic River. Then pulverize, digest, and leach the sediment and put the solution in the inductively coupled plasma mass spectrometry (ICP-MS). The ICP-MS will help us calculate the concentrations of chromium within the sediments. To calculate the concentration for the water samples, we will filter the water in the field with a .45 filter, and place it into the ICP. This study can therefore be used to determine if the old industry is still affecting the rivers today.

Does Theory Support Measurement? Determining the Freshwater/Saltwater Interface At A Cenote in the Yucatán Peninsula

Discipline: Geoscience
Subdiscipline: Other Geoscience

Kiara Burgos*[1], Phil J. Carpenter[2], Jorge Perera[3]
[1]New Mexico Institute of Mining and Technology, [2]Northern Illinois University, [3]Centro de Investigación Científica de Yucatán

Abstract: The economy in the Yucatán Peninsula is driven by tourism. The excessive pumping of groundwater from the karst aquifer for tourist activities and to support the local population is decreasing overall water supplies. The freshwater aquifer lies above a saltwater aquifer throughout the region and minor fluctuations in the location of the freshwater and saltwater interface occur naturally but can drastically vary due to coastal groundwater pumping. Cenotes provide access to the aquifer, where direct measurements of the interface can be made through conductivity measurements. This project focuses on one cenote that allows for indirect measurement of the interface using geophysical techniques. The Ghyben-Herzburg principle allows for the theoretical calculation of the location of the interface using the amount of groundwater above sea level. The objective of this project will be to test the Ghyben-Herzberg principle and measure the freshwater/saltwater interface at the cenote using electrical resistivity methods and direct conductivity measurements on water samples. The Schlumberger resistivity method uses electrodes to create a circuit between rock, soil, and water to measure the apparent resistivity. The resistivity will change between freshwater and saltwater, thus locating the depth of the interface. The interface measurement and the conductivity measurements will then be used to determine the application of the Ghyben-Herzberg principle. This research project gives insight into how much freshwater is available in the region, and also will provide confirmation if the Ghyben-Herzburg principle can be used to determine the amount of freshwater available for use within other similar aquifers.

Quantifying symbiont communities in Galápagos Pocillopora coral

Discipline: Geoscience
Subdiscipline: Other Geoscience

Matt Biermann*[1], Dr. Cheryl Logan[2], Katrina Giambertone[3], Chris Shenoy[4]
[1]San Diego Mesa College, [2]California State University Monterey Bay, [3]California State University Monterey Bay, [4]California State University Monterey Bay

Abstract: Climate change has had relentless negative impacts on tropical coral reef ecosystems. Mass coral bleaching is occurring more frequently and becoming more intense, particularly during severe El Niño-Southern Oscillation (ENSO) events. Corals in the Galápagos archipelago have experienced severe bleaching during ENSO events and are exposed to a wide range of temperatures throughout the year due to the convergence of multiple oceanographic currents. Previous work determined that Pocillopora corals from warmer northern sites had greater heat and cold tolerances in comparison to corals from the southern islands that experience cooler and more variable temperatures on average. The mechanisms underlying these thermal tolerance patterns are currently unknown. We hypothesize that thermally tolerant corals may have a greater relative abundance of heat-tolerant algal symbionts (genus Durusdinium) over heat-sensitive symbionts (genus Cladocopium). Utilizing quantitative PCR, we quantified symbiont communities in coral colonies from two islands containing comparatively stress-tolerant (Darwin) and stress-sensitive (Isabela) corals to investigate the role of symbiont community in setting thermal tolerance. We expect to find higher proportions of Durusdinium over Cladocopium in the northern site of Darwin relative to the southern site of Isabela. Our

results will contribute to the success of future restoration projects by determining if symbiont communities could increase survival of Galápagos pocillporid corals under future climate change.

VS30 Site Characterization Near the Strong-Motion Recording Site at Fremont Central Park, California, Using S-wave Refraction Tomography and Multichannel Analysis of Surface Waves Methods

Discipline: Geoscience
Subdiscipline: Geology

Ahkayla Gomez*[1], Rufus D. Catchings [2], Mark R. Goldman[3], Joanne H. Chan[4], Coyn J. Criley [5], Delton A. Samuel[6], Ashley R. Piña[7]
[1]University of California, East Bay, [2]USGS, [3]USGS, [4]USGS, [5]USGS, [6]USGS, [7]USGS

Abstract: To better understand earthquake-generated ground shaking at Central Park in Fremont, California, we evaluated Vs30, the time-averaged shear-wave velocity in the upper 30 m of the subsurface, near a network strong-motion seismometer (CE.57213) located inside the Fremont Police Department, ~100 m from the mapped trace of the Hayward Fault. We acquired 2D active-source seismic data at the site and recorded both body and surface waves along a 118-m-long linear array of three-component nodal seismometers. We generated P- and S-waves using a sledgehammer to strike an aluminum block both vertically and horizontally, respectively, every 2 m along the array, coincident with each nodal seismometer. We used refraction tomography to develop 2D tomographic models of Vp, Vs, Vp/Vs ratios and Poisson's ratios along the seismic profile, and we use the Multichannel Analysis of Surface Waves (MASW) method to evaluate Rayleigh and Love waves to develop additional 2D Vs models. From the tomographic Vs model, we calculated Vs30 at the site nearest the strong-motion seismometer. Our tomography model shows that Vs30 ranges from approximately 236 m/s to 360 m/s along the profile, with a Vs30 value of 338 m/s nearest the strong-motion seismometer. These Vs30 values suggest the site is a NEHRP Class D (stiff soil) site. The MASW models of Vs will also be compared to Vs30 values calculated from each method.

El Nino Southern Oscillation-like Climate Variability Without East-West Asymmetries

Discipline: Geoscience
Subdiscipline: Earth Science

Oscar Gandara*[1], Pedro DiNezio [2], Jeremy Klavans[3]
[1]Metropolitan State University of Denver, [2]University of Colorado Boulder, [3]University of Colorado Boulder

Abstract: El Nino Southern Oscillation (ENSO) - the leading mode of global climate variability - arises from the east-west asymmetries that characterize the climate of the tropical Pacific Ocean. Are these east-west asymmetries essential to produce ENSO-like climate variability? We explored this question using a simulation of global climate in which continents are removed resulting in a global ocean. This "AquaPlanet" has east-west symmetry but it still exhibits strong interannual variability at the equator. North-south asymmetries - including a strong temperature gradient about an anomalous belt of cold water at the equator - drive a 7-year equatorial sea surface temperature oscillation. North-south winds and the oceanic response to these winds help to both amplify ocean temperature anomalies and transition to the opposite phase of the oscillation. Our results show that north-south asymmetries can produce tropical variability

resembling ENSO. This opens the possibility that north-south asymmetries could be important to understand and predict ENSO.

Radiogenic Sr isotope analysis of subducted sediments and basalts from trench to volcanic arc in Southwest Japan

Discipline: Geoscience
Subdiscipline: Geology

Sarah Perez*[1]and Dr. Maureen Feineman [2]
[1]Pennsylvania State University, [2]Pennsylvania State University

Abstract: This project is intended to utilize 87 Sr/ 86 Sr isotope ratios to understand the behavior of sediment- and basalt-derived fluids during the subduction process. Sixteen samples have been collected from cores drilled in the Nankai Trough, where the Philippine Sea Plate is subducting beneath the Eurasian Plate, and the Shimanto Shale and Sanbagawa Schist, both exhumed portions of the subducted plate now exposed on Shikoku Island. The marine clays represent a lower set of 20-150°C temperatures, relative to the intermediate range of shales (100-258°C), while the schists present a range of 300-500°C, approaching the region of arc magmatism. This research presents these samples as a continuous set, reflective of increasing temperatures and pressures, by establishing their initial compositions to remove outliers. It allows us to assess the extent to which sediment-derived Sr infiltrates and overprints the original mantle-derived 87 Sr/ 86 Sr isotope ratios in subducted altered oceanic crust. The 87 Sr/ 86 Sr for the subducting sediments is approximately 0.710-0.721, while unaltered basalts are about 0.703. From our results, the altered basalts have shown 87 Sr/ 86 Sr values that are intermediate between sediments and unaltered mid-ocean ridge basalt, with a range between 0.706-0.709. Volcanic rocks from the Southwest Japan arc, interpreted to have a strong subducted sediment component, have 87 Sr/ 86 Sr of ~0.705. A deeper look at exchange processes between basalt and sediment will provide a better understanding of slab dehydration and melting processes, and the resultant arc magmatism observed in the Southwest Japan Arc.

Ecohdrology of the coastal wetland-forest ecotone.

Discipline: Geoscience
Subdiscipline: Environmental Science

Christopher Freyland*[1], Elizabeth Watson [2], Daouda Njie[3], Andrew Payne[4]
[1]Drexel University, [2]The Academy of Natural Sciences of Drexel University, [3]The Academy of Natural Sciences of Drexel University, [4]The Academy of Natural Sciences of Drexel University

Abstract: Coastal wetlands are ecologically significant ecosystems that provide habitat for both aquatic and terrestrial organisms, including many rare and protected species. In addition, they mitigate greenhouse gas emissions, protect shorelines from erosion, improve local water quality and offer flood protection to surrounding areas. As climate change accelerates, sea levels will continue to rise, threatening the future of coastal marshlands and their ability to continue functioning. One way that coastal wetlands are adapting to these changes is inland migration, where the wetlands expand upslope as suitable habitats migrate inland. This migration results in the formation of new marshes as upland vegetation is replaced by marsh plants. Here, we employ electromagnetic induction surveys to map salinity changes across the marsh-forest border and use machine learning classification of drone imagery to identify habitat zones and their salinity with the purpose of identifying the role of salinity in causing habitat transitions.This is important data for predicting which areas will become marshland in the future allowing us to take more steps to enact conservatory regulations in advance of changes resulting from climate change.

Quantifying Inequitable Exposure to Air Pollution in Bexar County, Texas

Discipline: Geoscience
Subdiscipline: Environmental Science

Alyssa Arcos*[1], Kristen E. Brown, PhD [2], Christina Kastely[3], Klaus Bartels[4]
[1]The Alamo Colleges District - San Antonio College, [2]The University of Texas at San Antonio, [3]The University of Texas at San Antonio, [4]The Alamo Colleges District - San Antonio College

Abstract: High concentrations of airborne particulate matter small enough to enter the human bloodstream (<2.5 micrometers in diameter, PM 2.5) can cause serious health complications. As such, it is important to understand the characteristics of the urban atmosphere to justify adaptation and mitigation efforts where necessary to promote public health. Bexar County is home to the seventh-largest city in the US, San Antonio, Texas. Sizeable military, industrial, and agricultural operations, racial/ethnic diversity, and several economically segregated neighborhoods provide an interesting dynamic for urban air research. We predict that many of the highest PM 2.5 concentrations will be co-located with the highest ambient temperatures, large industrial facilities, and neighborhoods earning the lowest wages. Using the ArcGIS mapping application, we created map layers of historical census data, meteorological (temperature and wind) conditions, and busy roadways. With this visualization of data, PurpleAir optical sensors were methodically placed to capture PM 2.5 concentration variations across the county. Six existing PurpleAir sensor sites were observed for preliminary findings, and the results support our hypothesis. Three sensors consistently measured higher PM 2.5 concentrations. All three were in densely populated areas with the highest ambient temperatures, and two were within statistically disadvantaged neighborhoods along large industrial routes. Our added sensors and larger monitoring network should indicate the primary locations where changes in public health policies and allocation of resources are necessary to ensure equitable health outcomes for all Bexar County residents.

Preserving Seawater Samples for Dimethylmercury

Discipline: Geoscience
Subdiscipline: Environmental Science

Abril Hernandez*[1], Amina Schartup [2], Hannah Adams[3], Carl Lamborg[4]
[1]Southwestern College, [2]Scripps Institution of Oceanography, University of California San Diego, [3]Scripps Institution of Oceanography, University of California San Diego, [4]University of California Santa Cruz

Abstract: Dimethylmercury (DMHg) is a naturally occurring species of organomercurials, a class of compounds that also includes the better-known bioaccumulative neurotoxicant monomethylmercury (MMHg). DMHg is very toxic and a potential source of MMHg to marine biota, but we know very little about why and how it is produced in the oceans. The lack of knowledge is partially due to a lack of consistent analytical techniques and intercomparison between research groups. DMHg is volatile and degrades rapidly making it hard to analyze, preserve and share samples for inter-calibration. Here we test different approaches to preserve samples for DMHg analysis. Seawater was collected weekly off the Scripps Pier for 5 months. 160 mL samples were purged onto a Tekran 2710 containing a 50/50% Carbo-Tenax trap, then thermally desorbed into a Tekran 2700 for detection. Instruments were calibrated daily using a DMHg standard prepared in-house. Concentrations during the study period ranged from non-detect to 150 fM, covering the range of DMHg concentrations measured in the open ocean. We tested changes in DMHg under a range of temperature and light conditions. Our results show that DMHg is better preserved if the sample is frozen when compared to other methods. We conclude that freezing a seawater sample causes no degradation of DMHg and thus frozen samples can be shipped for inter-calibration exercises.

Detection of Human Impacts in the Groundwater Microbiome

Discipline: Geoscience
Subdiscipline: Environmental Science

Elizabeth Abila*[1]and Matthew Schrenk [2]
[1]Michigan State University, [2]Michigan State University

Abstract: Most of the groundwater we use for drinking, industry, and agriculture is “young” and susceptible to contamination. Microbes found in this groundwater likely respond to human impact, such as the introduction of contaminants, antibiotic resistance genes, and pharmaceutical compounds. The genetic information found in microbial populations is a resource of information, as they show how microbes respond to environmental conditions. In this study, we evaluated whether the genetic information in microorganisms in Michigan groundwater shows human impact. The study employed a dataset of environmental DNA sequences obtained from agriculturally impacted and pristine groundwater near Traverse City, MI. Genes for the metabolic pathways of denitrification and dissimilatory nitrate reduction were identified within metagenome assembled genomes (MAGs) using the online software GhostKOALA which compares predicted proteins to the KEGG database. Using this approach, we found that the agriculturally impacted sites (Wells G7 and B2) harbored MAGs with more genes for nitrogen cycling, with the process of denitrification being prevalent. whereas the more isolated site (Well B1) had relatively few. These differences are important as excess nitrate can contribute to the nutrient load of water resources and impact aquatic species. Denitrification in particular, can convert nitrate to nitrous oxide, a potent greenhouse gas, that contributes to global warming. Additionally, understanding how the nitrogen cycle works in groundwater microbial ecosystems can serve as a proxy for processes related to environmental health including the proliferation of organic chemicals and antibiotic resistance genes. In the future, the effect of contaminants will be evaluated using similar methods.

Explorations in GEOCARBSulf Earth Model

Discipline: Geoscience
Subdiscipline: Earth Science

Edwin Lotero*[1]and Ying Cui, PhD [2]
[1]Rutgers University-Newark, [2]Montclair State University

Abstract: The long-term relationship between changes in atmospheric CO 2 concentration and global average temperature is known as Earth-system sensitivity (ESS), and is a key parameter in Earth System Models (ESM). Beyond merely simulating the Earth’s climate, ESMs include parameters relevant to biological, physical, and chemical processes throughout the planetary system. One such model is GEOCARBSULFvolc (GEOCARB). Like all ESMs, GEOCARB is subject to sources of uncertainty in its parameters which then propagate into simulation output data. To account for uncertainty in our study, ensembles of model configurations are generated via random sampling methods for model parameters: latin hypercube sampling for the constant parameters and inverse Wishart sampling for the time-dependent parameters. Our goal is twofold: 1. To find the best parameter set that matches a new set of observed pCO 2 records the best, and 2. Interpret the mechanism(s) of the changes in pCO 2 in the Paleozoic (and quantify climate sensitivity). The new records collected are in the form of >1,000 carbon isotope data from C3 land plant remains preserved in the sedimentary records dated from 423.0 to 251.9 million years ago. Ensembles of acceptable parameters are constructed by running simulations coupled with the previously randomly sampled parameters and discarding those simulations that do not agree well with temperature reconstructions and CO 2 proxy data within a given precalibration window. The results of this research will serve to improve the trade-off between Earth System Model data fitting and bias by adjusting for the way parameters are selected for simulations.

Relationship between Soil Microbial Diversity and Carbon Cycling in Mediterranean Vineyards in Napa Valley

Discipline: Geoscience
Subdiscipline: Environmental Science

Luisa Robles*[1], Cristina Lazcano [2], Noelymar Gonzalez-Maldonado[3], Erika Yao[4]
[1]University of California, Davis, [2]University of California, Davis, [3]University of California, Davis, [4]University of California, Davis

Abstract: Soil biodiversity plays a significant role in ecosystem functions that include: nutrient cycling, waste decomposition, and long-term climate regulation through carbon (C) sequestration. Microbes and their diversity are key to understanding carbon cycling since they are involved in litter decomposition, carbon biomass, and respiration. Soil microbial diversity has shown to be important for stabilizing organic matter which helps regulate and store carbon; however, there is little known of its direct relationship with carbon in vineyard soils. We conducted a field survey of 30 commercial vineyards in Napa Valley during the spring of 2021. At each vineyard we collected soil samples from the interrow (n=3) and under the vine (n=3) at two depths (0-10 and 10-20 cm). Our methods encompass testing for soil respiration, microbial biomass carbon (MBC), concentration of active C or permanganate oxidizable carbon (POXC), concentration of total C, microbial community structure using phospholipid fatty acids (PLFAs), and analysis of microbial diversity using high throughput sequencing of bacterial and fungal markers . Our hypothesis was that sites with higher microbial diversity will contain a higher total C, MBC, and POXC. We also hypothesized that sites with higher microbial diversity will have a higher carbon use efficiency (CUE) compared to sites with lower microbial diversity. This research will inform grower’s decision whether increasing microbial diversity through soil management practices can contribute to carbon storage. Addressing this question will have further implications on the relationships between microbial diversity and carbon sequestration, soil health, and ecosystem functioning.

Nitrate and Arsenic Concentrations in the Ogallala Aquifer of Texas, 2010-2020

Discipline: Geoscience
Subdiscipline: Environmental Science

Dayani Davilla*[1]and Paul Hudak [2]
[1]University of North Texas, [2]University of North Texas

Abstract: Concentrations of arsenic and nitrate exceed regulatory standards for drinking water in several wells in the Ogallala aquifer of west Texas. This unconfined aquifer, consisting of sand, gravel, and clay, is the major source of water consumed in west Texas. Geological processes and agricultural practices potentially influence concentrations of arsenic and nitrate in the groundwater of the Ogallala aquifer. Permeable soils above the aquifer enhance the threat of contamination from sources near the land surface, especially in the southern part of the study area. Previous studies have identified spatial and temporal trends in arsenic and nitrate concentrations in subareas of the aquifer over older time periods. This research applies geostatistical models with ArcMap Pro to estimate and portray arsenic and nitrate concentrations annually, from 2010 to 2020. Associations between arsenic nitrate, arsenic, and well depth were also computed, and overlying land uses were studied to provide additional insight into potential sources of contamination. Results of this research can guide public health intervention, including more intensive, localized monitoring efforts, to reduce the risk of diseases associated with long-term consumption of water contaminated by arsenic and nitrate.

Comparison of the Accuracy of Satellite Precipitation Measurements to Ground Precipitation Gages in South Africa

Discipline: Geoscience
Subdiscipline: Environmental Science

Marie Sullivan*[1], Phillip Palmer[2], David Kahler[3]
[1]Duquesne University, [2]Duquesne University, [3]Duquesne University

Abstract: Precipitation data are needed for water resources management in agriculture and for drought and flood models. The Limpopo River Basin of southern Africa has a sparsely distributed precipitation gage network. Global Precipitation Measurement (GPM) mission uses satellites to take temporally (daily) and spatially distributed measurements. To validate the GPM data, they were compared to standard precipitation gage data in R. The data were compared at a range of temporal and spatially averaged resolutions. The results showed that precipitation measurements from satellites are reliable when the area covered is fairly large. This accuracy wanes as the areas become more precise. The GPM daily measurements were less accurate compared to the GPM monthly measurements.

Behavior and distribution of water-soluble and carbonate-bound chemical elements in shallow drylands

Discipline: Geoscience
Subdiscipline: Geology

Carmel Murillo*[1], Mark A. Engle[2], Lin Ma[3], Mark Engle[4], Lin Ma[5]
[1]University of Texas at El Paso, [2]University of Texas at El Paso, [3]University of Texas at El Paso, [4]University of Texas at El Paso, [5]University of Texas at El Paso

Abstract: A common feature of dryland environments is a generally low abundance of water and a great potential for the development of carbonate minerals (Caliche in southwest US) which form from high evaporation rates. As part of a larger series of investigations focused on water, carbon, and nutrient cycling in dryland environments (Dryland Critical Zone project), we collected 43 soil samples at depths of 10 cm to 100 cm from two geographic areas in The Jornada Experimental Range in south-central New Mexico: an upland piedmont fan site (a site of running active erosion) and a lowland playa (a site of sediment and water accumulation). Samples were subjected to a two-step sequential extraction process. We applied 10 mL of deionized water to ~10 g of soil in an ultrasonic cleaner for five minutes, centrifuged the samples for three minutes at 3000 rpm, and extracted liquid from the sample. In the second extraction step, 10 mL of acetic acid was added to each sample, followed by shaking for 24 hours, centrifuged and removed the liquid. Major and trace elements in each fraction were quantified using Inductively Coupled Plasma-Optical Emission Spectrometry. Patterns identified are as follows Highly soluble elements (e.g., B, Cl, S) exhibit strong enrichment in water leachable fractions from the playa with increasing concentration at depth. Results suggest influx of water at playas allows accumulation of these elements during drier periods. Exceptionally high concentrations of Ca and Mg in acetic acid leachable samples suggest these elements are largely held in carbonate minerals

Monitoring lunar regolith leachate and plant matter composition for nutrients and toxins

Discipline: Geoscience
Subdiscipline: Environmental Science

Kaitlin Marry*[1], April Ulery [2], Nicole Pietrasiak[3], Mikaela Hoellrich[4], Maya Gabitzsch [5], Karina Tovar[6], Jonathan Consford[7], McKenzie Stock[8], Ashley Riggs[9]
[1]New Mexico State University, [2]New Mexico State University, [3]New Mexico State University, [4]New Mexico State University, [5]New Mexico State University, [6]New Mexico State University, [7]New Mexico State University, [8]New Mexico State University, [9]New Mexico State University

Abstract: Long-term exploration of space is limited by the availability of a renewable food supply for astronauts. We measured the leachate composition of the simulated regolith over a ten-week growing period as a part of NASA's Plant the Moon Challenge. Four treatments (100% regolith "R", 50/50 regolith/compost "RC", 50/50 regolith/vermiculite "RV", and 50/25/25 regolith/compost/vermiculite "RCV" all by volume) were planted with Anasazi beans (Phaseolus vulgaris) and irrigated daily with tap water. Leachate was collected every two/to three weeks and was evaluated for various elemental and nutrient concentrations, pH, and electrical conductivity. At the end of the ten-week growth period, the stem, roots, and pods of the plants were collected and analyzed for numerous elements. We hypothesized that nutrient levels in the soil leachate would decrease with successive watering and the plants would have a decrease in the composition of macronutrients. Preliminary results showed the composition of the leachates of all treatment types changed over the course of this experiment with the largest change occurring in pots containing compost. We observed decreases in most nutrient concentrations, particularly in nitrate and phosphorus, which are vital macronutrients, and an increase in aluminum, which may be toxic at higher concentrations. Additionally, pots containing vermiculite had a higher rate of plant emergence than those without. This suggests that both the composition and density of the material may play a key role in plant growth. Further experiments should include additional nitrate and phosphorus nutrient sources, and an increase in overall fertilization to supplement nutrient losses.

Karst Conduit Identification Using Geophysical Surveys in Northeast Yucatán, Mexico

Discipline: Geoscience
Subdiscipline: Other Geoscience

Rosario Cecilio-Flores-Elie*[1], Phillip Carpenter[2], Bryan Olivieri[3], Jorge Adrián Perera-Burgos[4], Rosa Maria Leal-Bautista[5]
[1]Lehman College CUNY, [2]Northern Illinois University, [3]Polytechnic University of Puerto Rico, [4]Centro de Investigación Científica de Yucatán A.C., [5]Centro de Investigación Científica de Yucatán A.C.

Abstract: The Yucatán Peninsula features one of the world's largest karstic aquifer systems, and freshwater is the region's only supply of drinking water. Cenotes, or sinkholes, are common in the area, resulting from limestone bedrock collapse, exposing groundwater. In recent years, tourism demand has risen in the Riviera Maya, particularly along the Ruta de Los Cenotes, a famous road between Puerto Morelos and Leona Vicario famed for its numerous cenotes. Because of the inflow of tourists and migration to the area, anthropogenic contamination of the aquifers and nearby areas may have grown. The SuperSting Geophysical Resistivity Meter was used to collect data in order to better understand how water travels in the area, both in the vadose and saturated zones, and whether new conduits or sinkholes are emerging. Because there is limited data on how water moves in these regions, three sites near the Holbox fracture zone were chosen (Soccer Field in Agua Azul, Cenote Verde Lucero, and the Cancun South Aeropuerto Wellfield site). Based on our results, fractures were found going north-south were discovered on two of the sites (Verde Lucero, Agua Azul). A conduit, most likely an air-filled hollow, was discovered in the soccer field's center, posing the possibility of future collapse. We also found a new sinkhole near the end of Wellfield Road, which we suspect is part of a larger network of sinkholes in the region. Sinkholes discovered towards the wellfield's end indicate possible water seepage, and we anticipate a network of other sinkholes in the region.

Understanding Water-System Concepts through a Diné Lens

Discipline: Geoscience
Subdiscipline: Geology

Hozhoo Emerson*[1]and Steven Semken[2]
[1]Arizona State University, [2]Arizona State University

Abstract: English speakers have a plethora of Earth science teaching materials and resources for study. This is not necessarily true for other cultural communities, such as Indigenous nations, who are also disproportionately affected by Earth-science-related issues such as water quality and availability. The Navajo Nation, one of the largest Indigenous communities in the US, struggles with drought and lack of good water infrastructure. Our objective is to create tools that foster better education while preserving the Diné (Navajo) language, for teaching future generations to better protect water resources for their communities. In this place-based approach it is important to have people with cultural knowledge of their environment involved in decision-making. We are using ethnographic and literature-search research methods in ethnogeology and ethnohydrology to create cross-cultural, bilingual teaching materials and resources that will serve needs in Navajo country.

Using StoryMaps to Communicate the Success of a Tribal Stream Restoration Project

Discipline: Geoscience
Subdiscipline: Geology

Lori Huck*[1]and Chauncey Means[2]
[1]Oklahoma State University, [2]Confederated Salish and Kootenai Tribes

Abstract: Stream restoration projects can mitigate water quality issues and restore riparian ecosystem functions. The Confederated Salish and Kootenai Tribes recently implemented such a restoration project on the Mission Creek in Western Montana. Several benefits are visible from the project such as bank stabilization, improved water quality, and habitat restoration. The Mission Creek Project's (MCP) main goal was to restore fish habitat to Mission Creek that once held a population of the endangered bull trout. Communicating the science and outcomes of this type of project to the public can be challenging. The MCP attempted to assist the Tribe by developing an interactive virtual Story Map of the completed project for Tribal education and outreach. This poster serves as a summary of the MCP and the Communicating Science (CS) outcomes for the project. It is intended to illustrate an alternative way to present science to communities and deliver outreach that is less fleeting, more capable of evolving, and capable of reaching a broader audience.

Tiny crystals and big secrets: remapping Yellowstone's most recent supereruption

Discipline: Geoscience
Subdiscipline: Geology

Raymond Salazar*[1], Madison L. Myers [2], Colin J.N. Wilson[3]
[1]Montana State University, [2]Montana State University, [3]Victoria University of Wellington

Abstract: The Lava Creek Tuff (LCT) supereruption from Yellowstone volcano generated two massive ignimbrite units, referred to as Members A and B, which are deposits of ground-hugging, molten rock, crystals, and gas. The two members are currently distinguished by the presence of the mineral amphibole in Member A, and a textural change driven by cooling. However, recent dating of multiple ignimbrites in the Sour Creek Dome (SCD) of Yellowstone National Park has revealed that units mapped as the older Huckleberry Ridge Tuff supereruption are actually visually distinct, new units of the LCT. Due to their nature and stratigraphy, these ignimbrites are thought to represent precursory outbursts of the supereruption. This project aims to 1) document the spatial distribution and source areas, 2) estimate volumes and 3) determine how these ignimbrites geochemically relate to the overall LCT eruption. In the newly recognized deposits, one unit presents as welded ignimbrite chunks found in a lag deposit, implying the LCT eruption lasted longer than previously thought. The second new unit is a cliff-forming, densely-welded ignimbrite which conformably lays atop the first and is found throughout the SCD. This second unit is easily distinguished by the presence of dark scoria, potentially representing the source magma feeding the eruption. Preliminary geochemical analyses of sanidine from Unit 1 are found to closely align with those from a sample taken from Member A, but differ significantly from other LCT outcrops. Future work will continue to physically and chemically define these new units.

Diversity of aquatic macroinvertebrates between rural and urban ponds of North Texas, USA

Discipline: Geoscience
Subdiscipline: Environmental Science

Rahiza De Thomas*
Oregon State University, OR

Abstract: Aquatic macroinvertebrates are an important part of pond ecosystems. Yet, there's little information about macroinvertebrate community composition, especially in semitropical climates. In addition, the influence of rural and urban systems on these communities has been overlooked. The objective of this study was to identify whether there were differences in the community diversity of macroinvertebrates between urban and rural ponds in the North Texas region. I hypothesized that urban systems would contain less diverse communities than rural ponds due to the impact of human activities (i.e., impervious surfaces, contamination, and habitat modification). I collected three replicated samples from six ponds (three in urban areas and three in rural areas), from September to December 2020. I found seven families including Caenidae, Chironomidae, Corixidae, Gerridae, Haliplidae, Lestidae, and Libellulidae. In both types of ponds, Caenidae was the most common and Haliplidae the least abundant. Diversity indices showed differences between rural and urban ponds with the last slightly more diverse. Hickory Creek (rural pond) was the only pond in which I was able to identify members of all seven families. In addition, rural ponds showed more similarity among them with no one specific family dominating the observed abundances. In the three urban ponds, macroinvertebrate diversity was dominated by Caenidae. Interestingly, in November and December, there was an observable reduction in the amount and diversity of macroinvertebrates found, due to decreasing water temperatures. The information collected in this project can help us evaluate the human impact on pond ecosystems in subtropical regions.

Identifying entrainment cues underlying the circatidal clock in fiddler crab embryos

Discipline: Geoscience
Subdiscipline: Other Geoscience

Caitlin BrabbleRose*[1]and Paola Lopez-Duarte[2]
[1]University of North Carolina at Charlotte, [2]University of North Carolina at Charlotte

Abstract: Living clocks are expressed in all studied eukaryotes and can be attributed to geophysical cycles, such as the ebb and flow of the tide (12.4-hr). The circatidal clock is associated with this cycle and is thought to provide adaptive advantages to intertidal organisms, allowing them to synchronize their activity to changing tides. In the Atlantic fiddler crab (Uca pugilator), fertilized eggs are attached to abdominal appendages on the female where embryos develop throughout the incubation period. Attachment to the female is necessary for survival, synchronous development, and successful larval hatching. The overall objective of this study is to determine when and how the circatidal clock is entrained in embryonic fiddler crabs, specifically focusing on physiochemical influences from ovigerous (egg-carrying) crabs, such as stereotypic pumping behavior and pheromone release. While characterization of the circatidal clock is well-documented in many species, there is little understanding of how these rhythms are entrained in embryos throughout development. To identify behaviors associated with entrainment, ovigerous crabs will be monitored throughout development to measure pumping activity – the flexing of the abdomen to aerate embryos. Additionally, seawater conditioned by ovigerous crabs will be collected and examined using liquid-chromatography mass spectrometry (LC/MS) to identify pheromones released during development. This study will hold implications for understanding the key role that the ovigerous crab plays in developmental and larval release synchrony, as synchronization of larval release is a critical dispersal mechanism for larval survival and success.

Quantifying Aquatic Habitat Provided from Various Streambank Treatments on the Restored Phases of the Upper Clark Fork River, Montana

Discipline: Geoscience
Subdiscipline: Other Geoscience

Morgan Schultz*[1], Alex Leone[2], Robert Pal[3], Joe Griffin[4]
[1]Montana Techonological University, [2]Montana Technological University, [3]Montana Technological University, [4]Montana Technological University

Abstract: The upper Clark Fork River floodplain ecosystem was severely damaged when the cataclysmic 1908 flood washed down millions of cubic yards of contaminated mining tailings from the “Richest Hill on Earth”. Cleanup efforts over the last decade have effectively removed toxic contaminants from the floodplain and streambanks. These actions also result in the replacement of clean material, a multitude of different streambank treatments, and riparian plantings leading to a total reset on floodplain habitat. However, the recovery of aquatic and riparian habitats can take decades. Records and observations from local anglers show that trout communities are depleted in the remediated areas of cleanup that has occurred. Literature reviews indicate that monitoring restoration sites is commonly overlooked, which raises the question of effectiveness for the implemented practices. Therefore, a modified fish habitat assessment was developed to gather qualitative and quantitative data on essential fish habitat components such as undercut banks, overhanging cover, and bank material composition. ArcGIS was utilized to analyze spatially explicit data related to streambank treatment types and infield measurements. The upcoming steps are to utilize MANOVA and ordination to better understand relationships between the environmental data. Results are preliminary yet suggests drastic differences in available refuge between the various streambank treatment types, implying that the adaptive management plans still have room for improvement for the remaining cleanup work on the upper Clark Fork River.

Detailed Numerical Modeling of Glacial Isostacy in Iceland, Implications for Mantle Stress Change and Future Volcanic Hazard

Discipline: Geoscience
Subdiscipline: Other Geoscience

Thomas Givens*[1], Peter LaFemina[2], Richard Alley[3], Byron Parizek[4], Halldor Geirsson[5], Peter Schmidt[6]
[1]The Pennsylvania State University, University Park, [2]The Pennsylvania State University, University Park, [3]The Pennsylvania State University, University Park, [4]The Pennsylvania State University, University Park, [5]University of Iceland, Iceland, [6]Uppsala University, Sweden

Abstract: Glacial Isostatic Adjustment (GIA) is a geodynamic phenomenon in which the solid earth deforms to maintain isostatic equilibrium when under the influence of a large ice load. Previous studies suggest that GIA can alter stress conditions in the mantle enough to increase mantle melt generation, underplating, and magma supply to volcanic zones. This is especially relevant to Iceland, which has large melting ice caps centered on active volcanic zones. A finite-element GIA model is typically generated to evaluate the extent of such a stress change by simulating the geodynamic response to lithospheric unloading. Such a model consists of a finite element earth model, an ice load model, and a calibration geodetic dataset to converge upon. My modeling seeks to forecast a predicted increase in future melt supply in Iceland due to major ice mass loss since 1890 by incorporating greater rheological detail than previous efforts in the form of lateral variation and power-law flow. This study is important to draw connections between the loss of ice caps and the resulting impact on the solid earth. Due to Iceland’s location and the explosive character of many of its volcanoes, an increase in the supply of magma to Iceland’s volcanic zones increases the volcanic hazard they pose to trans-Atlantic and European air travel, as well as citizens and tourists. Our study seeks to assist in understanding the level of change to these hazards face due to feedback from the anthropogenic loss of ice from Iceland’s surface through ongoing numerical modeling efforts.

Constraining the controls on bar preservation in braided rivers

Discipline: Geoscience
Subdiscipline: Geology

Safiya Alpheus*[1]and Elizabeth Hajek [2]
[1]Pennsylvania State University, [2]Pennsylvania State University

Abstract: The fluvial stratigraphic record is an important resource for understanding and reconstructing the history of Earth’s surface environments. Feedbacks between flow and sediment transport control the shape, scale, form, and movement of channels and their bar deposits. Fingerprints of these dynamic movements are recorded in sedimentary deposits, providing a lens through which we can reconstruct formative flow conditions from ancient river systems. In active systems, bar deposits grow and decay in response to channel thread kinematics at zones of thread- confluence and thread-splitting. Similarly, the architecture of ancient channel fills has been interpreted to infer channel morphodynamics in ancient fluvial systems. Here we aim to connect plan-view channel-thread movements to trends in stratigraphic preservation of braided river bars. We use a numerical model to explore how channel-thread movements are recorded in braided river stratigraphy. We investigate the degree to which the preserved internal architecture and sedimentary character of bar packages record bar kinematics and channel morphodynamic processes observed in active braided rivers. We document characteristic preservation dynamics that connect channel-thread kinematics to specific stratigraphic products. Our results describe the range of variability persistent in braided channel fills. They help geologists to contextualize the degree to which the architecture of these deposits reflects changing flow and sediment supply conditions, and the stratigraphic measurements most useful for interpreting signals of past landscape change. Finally, this work contributes to our understanding of the sensitivity of river systems to changes in discharge and sediment supply, proving useful for assessing flooding risks in floodplain areas.

Beyond Science into Pō: Reevaluating the Vulnerability of Lalo (French Frigate Shoals)

Discipline: Geoscience
Subdiscipline: Environmental Science

Kainalu Steward*[1]and Dr. Haunani Kāne [2]
[1]University of Hawaiʻi at Hilo, [2]Arizona State University, School of Geographical Sciences and Urban Planning

Abstract: As climate change accelerates globally, improved understanding of exposure and vulnerability to climate induced impacts becomes increasingly vital in navigating the future of atoll island communities. Sea-level rise (SLR) is identified as the biggest threat to atoll island communities due to their low lying elevation. Future SLR estimates exceed the elevation of many atoll islands within the next 100-200 years. Lalo, also known as French Frigate Shoals is an open atoll consisting of a large, crescent-shaped reef located within the Papahānaumokuākea Marine National Monument (PMNM). On October 4, 2018, a category 3 hurricane named Walaka swept through Lalo, devastating the terrestrial and marine habitats and nearly wiping out entire sandy islets. Following this event, there was an urgent need to understand the future stability of Lalo. This study aimed to quantify the monthly shoreline recovery of multiple sandy islets between October 2018 and October 2021. Using satellite derived imagery and ArcGIS programs, this study identified the monthly rate of erosion and accretion among Lalo as well as areas that show consistent stability. These results, using a near instantaneous hurricane event, will help us better understand the long term impacts of SLR to Lalo. The overarching goal of this project is to better understand these environmental pressures at short and long term timescales that will contribute to developing an action plan to include best management practices and strategies for the future of Lalo. Additionally, this project aimed to incorporate Native Hawaiian values and knowledge within the overall research process.

Effects of soil properties and dairy manure management on greenhouse gas and ammonia emissions from California agricultural soils.

Discipline: Geoscience
Subdiscipline: Environmental Science

Michael Rodriguez*[1]and Francesca Hopkins [2]
[1]University of California, Riverside, [2]University of California, Riverside

Abstract: Agriculture accounts for about 8% of California's total greenhouse gas (GHG) emissions and about 72% of total ammonia (NH3) emissions due to livestock manure management and fertilizer applications. However, very few studies have measured emissions from land application of manure or capture variability in soil properties and manure managements that can exist at dairy farms. The goal of this research is to compare GHG and NH3 emissions from soils after application of dairy manure and determine the control of specific soil properties (pH, texture, and moisture), manure nitrogen (N) dynamics, and their interactions on emissions. In laboratory experiments, five soils representing the major California dairy regions were fertilized with liquid dairy manure with an ammonium (NH4+) to total N ratio of 0.6, 0.7, and 0.8 and incubated at about 50, 65, and 80% of the soil's water holding capacity (WHC). Carbon dioxide (CO2), methane (CH4), nitrous oxide (N2O), and NH3 fluxes were measured using cavity ringdown spectroscopy in either a closed loop or dynamic chamber system. Soils incubated at higher %WHC had greater CO2, CH4, and N2O emissions and N2O and NH3 emissions increased with the NH4+: total N ratio of applied liquid manure. Relative emissions and the impact of treatments between locations were controlled by soil properties where soil texture significantly impacted CO2 and N2O emissions and soil pH significantly impacted N2O and NH3 emissions. This work will help model spatial variability in GHG and NH3 emission inventories as a response to specific on farm characteristics and management.

Modeling Nitrogen Plumes in the Bay of Bengal

Discipline: Geoscience
Subdiscipline: Earth Science

Nicolas Maxfield*[1], Maximillian Brown [2], Charles Vorosmarty[3]
[1]City University of New York, [2]City University of New York, [3]City University of New York

Abstract: Unprecedented anthropogenic manipulation of the magnitude and distribution of reactive nitrogen has had consequences on riverine and coastal water quality. As part of a NASA Interdisciplinary Research in Earth Science project titled Coastal Hypoxia Analysis and Risk

Tracking, we developed a Geographic Information Science-based spatial and temporal model of the transport of reactive nitrogen to river mouths in Southern Asia spanning from the southern tip of India to the southern tip of Viet Nam. The model is based on a previously published global nitrogen transport model, with suggested new parameters for wetlands and recalibration to reflect contemporary observations. The study region is made up of over 10,000 subbasins, which are analyzed for the period of 2001-2019. Preliminary findings show the greatest nitrogen flux at the mouths of the Padma, Godavari, Krishna, Kolkata, and Irrawaddy rivers. Results also suggest highest growth in nitrogen flux in the Padma, Godavari, Krishna, Soái Rap, and Irrawaddy rivers. Model applications include estimating the flux (mass) of reactive nitrogen as well as the in-stream concentrations (mass/volume) which have important implications for human and ecosystem health. This can be used for assessing the policy/technology/management strategies and scenarios implemented at local and regional scales.

Did persistently low oxygen conditions slow diversification during the Cambrian?

Discipline: Geoscience
Subdiscipline: Geology

Kayla Irizarry*[1], Mark Patzkowsky [2], Kimberly Lau[3]
[1]The Pennsylvania State University, [2]The Pennsylvania State University, [3]The Pennsylvania State University

Abstract: The Middle-Upper Cambrian (509 to 485 Ma) is defined by repeated mass extinction events and a diversity plateau. Elevated extinction levels may have been triggered or amplified by persistently low oxygen conditions, which is supported by large carbon isotope excursions that occur throughout the Cambrian. The Drumian Carbon Isotope Excursion (DICE) records a negative 2 to 4‰ shift in δ 13 C globally during the lower Drumian and has been interpreted as recording upwelling of anoxic 12 C-rich water onto the shelf during a transgression. The relationship between the DICE and palaeoecological change is not well defined. If the DICE records an interval of expanding anoxic conditions that influenced extinction patterns, then the record of marine invertebrates with high O 2 requirements should show lower abundances and diversity through this interval. To test this hypothesis, I will identify the DICE in two SW Montana stratigraphic successions. Fossils points counts will be used to measure faunal changes through the DICE. I will identify selective extinction using hypoxia thresholds determined using experimental data on modern analogues and palaeoecological data. To determine local redox conditions, I will use sulfur isotopes (δ 34 S cas and δ 34 S pyrite) and rare earth element distributions as proxies for the oceanic redox state. Preliminary lithological results show a disappearance of burrowing organisms and an increase in flat pebble conglomerate (indicative of a lack of bioturbation) through the lower Drumian. The disappearance of burrowing organisms may reflect an expanding low O 2 water mass.

Measuring the Thermal Conductivity of Iron at Extreme Conditions Using Laser-Driven Ramp Compression

Discipline: Geoscience
Subdiscipline: Other Geoscience

Tyler Perez*[1]and June Wicks [2]
[1]Johns Hopkins University, [2]Johns Hopkins University

Abstract: Within the Earth's interior, the thermal conductivity of Fe and Fe-rich alloys at core pressure-temperature conditions (135-360 GPa, 2500-5000 K) is a key parameter for heat transport models and plays an important role in determining the temperature profile and energy balance of our planet. An accurate measurement of this value has direct relevance to our understanding of mantle and core temperatures, generation of the geodynamo, and the age of the inner core. However, both theoretical and experimental studies on the thermal conductivity of iron at core conditions are limited and not in agreement. Our study provides a new experimental technique to measure thermal conductivity at extreme conditions using dynamic compression at the OMEGA laser at the Laboratory for Laser Energetics (LLE). We use a recently developed stagnating plasma-piston setup to quasi-isentropically compress an iron sample to outer core conditions while simultaneously sending a thermal pulse through the iron. The sample consists of three planar targets of different thicknesses arranged in a stair-step shape. By using a streaked optical pyrometer (SOP), we obtain time-resolved thermal emission curves from each step on the side opposite to the heat source. These emission curves can be compared to the outputs of a finite element heat diffusion code in order to constrain thermal conductivity. The experiments presented here were conducted at ~200 GPa (pressure of outer core) and temperatures exceeding 10,000 K with the possibility of achieving even higher pressures in the future. Initial results suggest moderate agreement with most recent theoretical and experimental values.

How are Dust and Drought related over the past 3,000 years at Columbine Lake, Colorado?

Discipline: Geoscience
Subdiscipline: Earth Science

Franklyn Telles*[1], Nicholas McKay [2], Stephanie Arcusa[3]
[1]Northern Arizona University, [2]Northern Arizona University, [3]Arizona State University

Abstract: Title: How are Dust and Drought related over the past 3,000 years at Columbine Lake, Colorado? The Southwest United States is experiencing an emerging megadrought, a phenomenon reflected by severely depleted water resources in the environment for at least two consecutive decades. Past megadroughts are recorded by tree rings, and are relatively common in the region. Dust deposition is typically expected to increase during periods of drought; However, recent studies from lake cores from the San Juan Mountains do not reflect this, however those studies are limited to century and longer timescales. Here, I use an annually-layered (or varved) sediment core to create a higher resolution, multi-decadal reconstruction of dust deposition for the region. I combine varve thicknesses, combined with geochemistry, grain size and density to create dust flux reconstructions, while propagating the uncertainties. The resulting dust flux reconstructions are resolved at decadal or finer timescales, allowing me to assess dust and drought relationships during megadroughts over the last 3000 years. Furthermore, I investigate whether human impacts of land use development during the past 150 years modified the dust-drought relationship, by comparing intervals of megadroughts to dust flux reconstruction, concentration estimates, and accumulation rates. This study is relevant to policymakers, as it gives insight about natural and anthropogenic causes of dust in an area limited by water availability and land cover changes in a region experiencing aridification amplified by climate change.

Lithospheric foundering beneath Harrat Ash Shaam, Saudi Arabia: evidence from olivine compositions

Discipline: Geoscience
Subdiscipline: Geology

Angelina Santamaria*[1], Tanya Furman[2], Shelby Bowden[3]
[1]The University of Pennsylvania, University Park, [2]The Pennsylvania State University, [3]The Pennsylvania State University

Abstract: Continental basalt lavas are abundant on the surface of our planet, yet the processes by which they form are not well understood. We use the geochemistry of olivine crystals in lavas and mantle xenoliths from Harrat Ash Shaam volcanic field in northwestern Saudi Arabia to address this question. Olivine crystals hold significant potential for understanding the melting histories of mantle-derived rocks. Their minor and trace element compositions provide insight into mantle melting conditions and processes, e.g., temperature, pressure, source mineralogy, metasomatic history. We use petrographic observations on individual rock samples, electron probe micro-analysis (EPMA), and in-situ single crystal mass spectrometry (LA-ICP-MS) to explore the chemical systematics of olivines and gain insight into the geodynamic evolution of this region. Olivine phenocrysts (Fo 80-86) define three compositional groups that correspond to lavas with distinctive pressures and temperatures of melt equilibration. Group 1 lavas (olivines with moderate CaO and MnO) include all Miocene samples (5.3-23 Ma) and yield calculated formation conditions of 15.5-18 kb (50-60 km) and ~1274-1409 o C. Group 2 lavas (olivines with highest CaO and MnO) are primarily Pliocene in age (2.6-5.3 Ma) and formed at ~1271-1421 o C and 14-16 kbar (45-55 km). Group 3 lavas (olivines with lowest CaO and MnO) are Quaternary in age (<2.6 Ma) and are calculated to have formed at the greatest depths: 19-23 kb (62-75 km) and 1420-1424 o C. The data support generation of deeper melts in the Quaternary, likely through heating of foundered metasomatized lithosphere at the craton margin.

Modeling the pathways and relative contributions of microplastics from oceanic and riverine sources in the Arctic Ocean

Discipline: Geoscience
Subdiscipline: Other Geoscience

Hailey Greenleaf*[1], Dr. Wieslaw Maslowski[2], Dr. Jaclyn Clement Kinney[3], Dr. Younjoo Lee[4], Dr. Robert Osinski[5]
[1]Maine Maritime Academy, [2]Naval Postgraduate School, [3]Naval Postgraduate School, [4]Naval Postgraduate School, [5]Institute of Oceanology Polish Academy of Sciences

Abstract: This study will focus on the pathways and relative contributions of microplastics from several oceanic and riverine sources into the Arctic Ocean. Microplastics have become a major marine pollutant, even reaching remote locations such as the Arctic. The majority of microplastics are buoyant, hence they are transported in the ocean by surface currents, which are strongly influenced by near-surface winds. We will use the Regional Arctic System Model (RASM) to introduce multiple sources of microplastics and complete a 40-year hindcast (1979 to 2021) to investigate the pathways and spatial distribution of microplastics originating from four different sources, the Barents Sea, North Pacific, Eurasian rivers and North American rivers. We hypothesize that the anticyclonic Beaufort Gyre in the western Arctic acts as the northernmost convergence zone for the accumulation of microplastics. We also hypothesize that the majority of microplastics in the Arctic Ocean originate from the lower latitude oceans, and are advected

northward with surface currents. Finally, we hypothesize that the relative contribution of microplastics from the Eurasian rivers is larger than that from the North American rivers draining into the Arctic. To date, the relative contributions of microplastics originating from riverine and oceanic sources in the Arctic Ocean are relatively unknown. This study will provide a baseline for pinpointing locations in need of observational studies of Arctic microplastic pollution, which in turn, will help to constrain models to better understand and interpret the origins and extent of plastics in the Arctic Ocean.

Spatial modeling of Chagas vector infestation patterns in novel human settlements

Discipline: Health
Subdiscipline: Public Health

Gustavo Nativio*[1]and Michael Z. Levy[2]
[1]University of North Carolina Chapel Hill, [2]University of Pennsylvania

Abstract: Chagas disease is a neglected tropical disease present primarily in rural regions of Central and South America. It is transmitted by the Trypanosoma cruzi parasite, its main vector being the triatomine insect, Triatoma infestans . There are an estimated 6.5 million infected individuals today, with common Chagas symptoms of heart disease, digestive complications, and nerve damage causing upwards of 9,000 deaths annually. Due to immigration from Latin America to the U.S., over 300,000 individuals in the U.S. today live with T. cruzi infection, with a potential for other animals, such as bed bugs, to become vectors for the disease. With 800,000 disability-adjusted life years lost annually, Chagas is a major global public health concern. In southern Peru, triatomine infestation, along with Chagas disease, is particularly rampant. One agricultural community in Arequipa department, El Pedregal, has developed rapidly in the past few decades, making it an ideal study site for novel triatomine infestation patterns. In our project, we chose to investigate periods of development and urbanization of city lots as covariates of triatomine bug infestation. We used Google Earth historic satellite images to classify levels of development for a sample of lots in El Pedregal, and R for data wrangling and analysis. After correcting for clustering biases, we expect to see lower odds of triatomine infestation in more recently developed lots. This research allows us greater understanding of how T. cruzi- carrying triatomine bugs colonize new human settlements and is relevant to constructing effective interventions against triatomine infestations and Chagas disease.

Predictors of Engagement of Condomless Sex In a National Sample of Adults Requesting HIV Home Self-Testing Kits

Discipline: Health
Subdiscipline: Public Health

Justise Wattree*[1], Adedotun Ogunbajo MPH, PhD[2], Mitchell Brooks MPH[3], DeMarc Hickson MPH, PhD[4]
[1]San Jose State University, [2]Us Helping Us, People Into Living Inc., [3]Us Helping Us, People Into Living Inc., [4]Us Helping Us, People Into Living Inc.

Abstract: The HIV epidemic in the United States (U.S.) continues to persist, with over 1.2 million people currently living with HIV and 13% being unaware of their HIV status. Engaging in HIV testing provides pertinent information that can facilitate linkage to HIV care or engagement in HIV prevention services. HIV self-testing (HIVST) is an innovative approach to HIV testing that provides instant results. It can circumvent structural barriers like transportation and stigma, and

increase HIV testing behavior. However, there is a dearth in the literature on the demographic characteristics and sexual health patterns of individuals utilizing HIVST services. The current study investigated the correlates of condomless sex and PrEP knowledge in a national sample of adults who ordered HIVST kits. Between 07/2021 and 06/2022, clients ordered free HIVST kits advertised on geosocial network applications (i.e Jackd, and Grindr) and were asked to complete a quantitative survey. Bivariable and multivariable binomial logistic regression models with a 95% confidence interval using SPSS were made to fit to determine predictors of condomless sex and PrEP knowledge. Individuals who had a history of sex work had lower odds of knowing about PrEP. Individuals who had recently been tested for HIV had higher odds of condomless sex compared to those who were never tested for HIV. It is important that HIVSTs are packaged within the HIV prevention tool kit and prioritized for at-risk populations such as those who engage in sex work.

Advancement of 3D printed microneedle arrays for interstitial fluid (ISF) extraction

Discipline: Health
Subdiscipline: Medicine

Carina Anastasio*[1], Robert M. Taylor[2], Justin T. Baca[3]
[1]New Mexico State University, [2]University of New Mexico, [3]University of New Mexico

Abstract: Interstitial fluid (ISF) is a novel source of biomarkers that has the potential to challenge the diagnostic capabilities of conventional extracted fluids such as blood, plasma, or urine. ISF constitutes approximately 15% of total body weight but has yet to be fully characterized for diagnostic applications. The demand for minimally invasive diagnostic technology is rapidly amassing scientific attention. We previously reported in vivo extraction of ISF using 3D-printed microneedle arrays and BD ultra-fine nano pen needles at a penetrating depth of 1500 μm. Here, we describe improvements to the previously reported 3D-printed microneedle arrays. We varied the number and spatial arrangement of the microneedles to improve extraction volume and decrease the size of the device. We explored various extraction methods to eliminate the need for glass components and increase the efficiency of extraction. We conjectured that the local hydrodynamic forces generated by the device interface were sufficient to extract ISF without the need of glass capillaries. We also added a hinged lid to provide a compartment for ISF extraction and storage before analysis. The arrays were modeled using SolidWorks software and printed using an MJP 2500 printer. The anticipated result is the array shape, improved extraction, and reduced profile of the microneedle device will have improved the existing designs for clinical applications. The future direction of this research path is to complete a manufacturable microneedle device design that maximizes the performance and efficiency of ISF extraction.

Hyper-local geospatial analyses of violent crime risk and its association to later-life cognitive outcomes in African Americans

Discipline: Health
Subdiscipline: Public Health

Genesis Tan*
Rutgers University Newark

Abstract: Research on Area Deprivation Index (ADI) suggests that neighborhood stressors (e.g., violent crime risk) play a role in later-life cognitive function. While ADI is useful in facilitating efficient integration of social determinants of health into models of cognitive aging, it does not

consider micro-level measures of neighborhood stressors which may also affect cognitive function. Therefore, the purpose of this study was to determine whether violent crime risk contributes to later-life cognitive function above and beyond ADI in older African Americans. Analyses included 149 older African Americans aged 60 and above (M age = 68.68, SD = 7.25; M edu = 13.99, SD = 2.43) who are part of an ongoing university-community collaboration at Rutgers University-Newark focused on community engagement and health education. Cognitive function was assessed via the acquired equivalence task, a measure of one’s ability to generalize past learning to novel task demands. Violent crime risk was calculated using a geospatial risk assessment that evaluates the influence of the built environment on the distribution of crime. The results showed that individuals living in areas with higher violent crime risk had poorer ability to generalize past learning to novel task demands. These findings suggest that for African Americans in an urban setting, hyper-local violent crime risk appears to be supplemental with ADI at capturing the impact of neighborhood disadvantage on cognitive function and Alzheimer’s disease risk. Thus, for African American individuals’ later-life cognitive health, it is important to consider micro-level measures of neighborhood stressors such as violent crime risk.

Post-Translational Modification of the Glucocorticoid Receptor Induction in Castration-Resistant Prostate Cancer

Discipline: Health
Subdiscipline: Medicine

Leslie McClinton*[1], Remi Adelaiye-Ogala [2], Surendra Gulla[3]
[1]Tougaloo College, [2]University at Buffalo, [3]University at Buffalo

Abstract: Title: Post-Translational Modification of the Glucocorticoid Receptor Induction in Castration-Resistant Prostate Cancer Castration-resistant prostate cancer (CRPC) is the second leading cause of cancer among men in the United States. Hormone therapy, known as androgen receptor (AR) suppression therapy, is the main treatment for advanced prostate cancer. However, sustained response is limited and acquired resistance develops within 6-12 months. An emerging mechanism of resistance to AR targeted therapy/AR blockade is induction of the glucocorticoid receptor (GR).Inhibition of PI3K/AKT signaling pathway and Enhancer of Zeste Homolog 2 (EZH2) leads over expression of GR.However, the role of PI3K/AKT and EZH2 on GR induced in advanced prostate cancer is unclear. Based on our previous knowledge, we hypothesized that the induction of GR following AR blockade, is modulated by PTMs determinants such as EZH2 and PI3K/AKT signaling. Targeting these modifications, will re-sensitize these resistant PC to standard therapy and improve overall clinical outcome for men with resistant prostate cancer. Model selection with GR expression in sensitve and resistant prostate cancer cell lines were determined. Following model selection, GR expression in determinants following exposure to enzalutamide treatment was performed by conducting a cell vitability assay and protein and gene expression. Laslty, functional studies were concluded by conducting a rapid immunoprecipitation mass spectrometry of endogenous protein (RIME) and ChIP-sequencing. Our results concluded that GR expression is induced when exposed to enzalutamide. This an emerging mechanism of resistance to enzalutamide and possibly a therapeutic target for advanced prostate cancer, when AR targeted therapy becomes resistant.

Genetic Adaptation in Malaria from blood group systems in the Great Apes

Discipline: Health
Subdiscipline: Public Health

Lennae Nockideneh*[1], Ellen Leffler[2], Paige Eberle[3]
[1]Utah Tech University, [2]University of Utah, [3]University of Utah

Abstract: In humans, blood group variations have been associated with pathogenic infections and diseases. Examples include Rh blood group with hemolytic disease of the newborns, the ABO blood group with COVID19 and Duffy or ABO blood groups with malaria. Intriguingly, some variants in the ABO blood group are present in other primates species ,including the great apes, who are also affected by malaria. In humans, blood type O is thought to be protective against severe cases of malaria caused by Plasmodium falciparum , a parasite that invades the Red blood cells (RBCs). However, some of the Great Apes are thought to lack blood type O. Another blood group involved in malaria susceptibility and resistance in humans is Duffy, which involves a glycoprotein on RBCs that acts as a receptor for P. vivax Like P. falciparum, P.vivax invades the RBCs causing malaria. Yet, a connection between Duffy variations and malaria resistance in the great apes is unclear. More generally, the extent of genetic variation affecting blood groups in the great apes has not been explored. In this study we will analyze genetic variation in genes underlying blood groups, ABO and Duffy, in sequencing data from the Great Ape Genome Project. We will identify functional variants that are predicted to generate blood group variation and compare them to patterns of human polymorphism. This comparative approach may reveal similar or alternate genetic adaptations to malaria that have evolved in these blood group systems in the great apes.

Neighborhood Safety Perceptions are Associated with Amygdala Activity and Functional Connectivity

Discipline: Health
Subdiscipline: Public Health

Lola Ortiz-Whittingham*[1], Liang Zhan[2], Erika Ortiz-Chaparro[3], Melissa Lamar[4], Tiffany Powell-Wiley[5]
[1]National Heart, Lung, and Blood Institute, [2]University of Pittsburgh, [3]National Heart, Lung, and Blood Institute, [4]Rush Alzheimer’s Disease Center, [5]National Heart, Lung, and Blood Institute & National Institute on Minority Health and Health Disparities

Abstract: Unsafe neighborhood perceptions are associated with poor physical and mental health outcomes. While the amygdala is considered a neural marker of chronic stress, the relationship between neighborhood safety perceptions and amygdala activity and functional connectivity remains unclear. Forty-eight adults (mean age 68±7, 52% female, 47% non-Hispanic Black, 2% Hispanic) from a larger community-based cohort study of non-demented older adults in Chicago were included in our sample. Resting state functional magnetic resonance imaging was acquired with a GE MR750 Discovery 3T scanner using a fast echo-planar imaging (EPI) sequence. The standard preprocessing pipeline in the CONN toolbox was applied to denoise and extract the mean blood oxygenation level dependent (BOLD) amygdalar signals. Functional connectivity between the amygdala and regions of interest was derived using pairwise BOLD signal correlations, which were converted to z-scores using Fisher's r-to-z transformation. Participants completed the Perceptions of Neighborhood Environment Scale, with higher scores of safety indicating more favorable perceptions. Regression modeling was used in our analyses, and age, sex, race, depression, and education were included as covariates. Regression modeling revealed more favorable safety perceptions associated with lower left amygdala activity ($\beta=-0.33$, $p=0.02$)

but not right amygdala activity. After correction for false discovery rate, more favorable safety perceptions also associated with reduced left amygdala functional connectivity with the bilateral insular cortices and the left anterior insula. Our findings indicate neighborhood safety perceptions play an important role in altered amygdala activity and functional connectivity and support the importance of targeted community-level safety interventions to promote positive health outcomes.

CBD Use to Prevent COVID-19 Infection Early in the Pandemic: Findings from a Web-based Survey of Adults in the U.S.

Discipline: Health

Subdiscipline: Public Health

Giselle Burns*[1], Ziva Cooper [2], Stephanie Lake[3], Ryan Assaf[4]

[1]University of California, Los Angeles, [2]University of California, Los Angeles, [3]University of California, Los Angeles, [4]University of California, Los Angeles

Abstract: Preclinical studies show promise for cannabidiol (CBD), a non-intoxicating component of the cannabis plant, as a prophylaxis for coronavirus disease 2019 (COVID-19) infection. Despite limited human clinical research on CBD, public interest in therapeutic applications of CBD has grown substantially. We sought to assess COVID-19-motivated CBD use early in the pandemic, specifically examining the prevalence and modes of administration of CBD use to prevent COVID-19 infection. In August 2020, we conducted a web-based survey of adults (≥18 years) in the United States (U.S.) with past-year cannabis/CBD use. We used descriptive statistics to examine the prevalence and modes of CBD use to prevent COVID-19 infection. We also explored socio-demographics associated with CBD use to prevent COVID-19 using Chi-square tests and t-tests. In total, 752 respondents (39.9% of the survey sample) reported past-year use of CBD-only products, of whom 518 (68.9%) reported CBD use to prevent COVID-19 infection in the three months prior to survey completion. Inhalation was the most common mode of CBD use to prevent COVID-19 infection (78.0%). Those who used CBD to prevent COVID-19 were often male and living in a state where only CBD is legal. They were also younger and less likely to report concurrent use of THC-containing cannabis for medical and non-medical purposes (all p<0.001). Despite a lack of clinical human evidence, we observed a high prevalence of CBD use to prevent COVID-19 infection. Our findings provide new insight into CBD use patterns in the U.S. in the context of COVID-19.

Barriers and Effective Interventions to Engage Latina’s Participation in Breast Cancer Clinical Studies

Discipline: Health

Subdiscipline: Public Health

Monica Padilla*[1]and Gregory S. Karczmar [2]

[1]University of Chicago, [2]University of Chicago Cancer Comprehensive Center

Abstract: Breast cancer is the most commonly diagnosed cancer and is the leading cause of cancer-related death among Latinas. Latinos make up 17% of the population but only 1% of clinical trial participants. Latino culture dictates a significant role in whether Latinas participate in clinical trials. 77% of Latinos practice Catholicism and 21% of Latinos only speak Spanish. The goal of this study is to examine the prevalence of breast cancer-related barriers among Latinas and to determine the extent to which these barriers might influence Latinas enrolling in breast cancer clinical trials. If language and religion are the reason Latinas enroll less in breast cancer clinical trials then increasing the availability of translated materials and a priest of a Catholic Church advertising the studies will increase the enrollment rate of Latinas. Interviews were conducted with Latino organizations to understand current barriers Latinas face within the medical field. Based on these findings, an intervention was conducted at a Latino serving Church consisting of an information booth, delivered an announcement regarding Research Study 9127(breast cancer clinical study) in Spanish, and had bilingual Latinas available to help women enroll in Research Study 9127. At the end of the church intervention, 33 Latinas were enrolled in Research Study 9127, seeing a 550% increase in Latinas participating in Research Study 9127. This study can inform efforts to increase clinical trial participation in Latinas by highlighting important motivators and informing future interventions aimed at encouraging participation in clinical trials in a culturally sensitive and effective way.

Detection of ant-MSSA compound laurenobiolide from different parts of the tulip tree (Liriodendron tulipifera)

Discipline: Health
Subdiscipline: Public Health

Nana Oblie*[1]and Dr. Matthew Bertin [2]
[1]University Of Rhode Island, [2]University Of Rhode Island

Abstract: The tulip tree (Liriodendron tulipifera) has a long history in Native American medicine, and was also used during the Civil War to treat sick or wounded soldiers. Scientists later investigated these medicinal claims with modern chemical and biological tools and found that a tulip tree extract showed antimicrobial activities against methicillin-susceptible Staphylococcus aureus (MSSA). MSSA is a bacterium that causes infections in different parts of the body, and can be lethal if left untreated. Because of its resistance to commonly used antibiotics, these infections are becoming increasingly difficult to treat, and new small molecule agents are necessary to overcome resistant strains. The tulip tree organic extract from the Principle Rhode Island Secondary Metabolite (PRISM) Library showed an inhibitory effect in MSSA growth, and subsequent bioassay-guided isolation workflows using high-performance liquid chromatography (HPLC) and mass spectrometry (MS) highlighted the known compound laurenobiolide, a sesquiterpene lactone, as the active antibacterial agent. My project aimed to determine the abundance of laurenobiolide in different parts of the tulip tree. All the plant parts collected showed the presence of the active compound except for the bark, and the branches showed the highest quantity of the metabolite. Further examination of the branches showed that the molecule was sequestered to the outer layers of the branches, which provokes intriguing questions with respect to the ecological role of the molecule for the plant. Additionally, this information will create more efficient extraction and isolation workflows for the continued accumulation of this compound for future biological evaluation.

Evaluating the capacity of human lung cancer cell lines to process and present specific tumor antigens

Discipline: Health
Subdiscipline: Medicine

Erinda Aidoo*[1], Katerina Politi, PhD [2], Jordan Cardenas[3]
[1]Illinois State University, [2]Yale, [3]Yale

Abstract: Lung cancer is the leading cause of cancer-related death in the world. Immunotherapies, such as immune checkpoint inhibitors, have greatly benefitted lung cancer patients by allowing for sustained tumor responses by activating the patient's own immune system. However, several clinical trials of immune checkpoint inhibitors have reported a high incidence of acquired resistance, by which the tumor initially regresses upon therapy but eventually stops responding. A commonly noted mechanism of resistance is the lack of HLA Class I (HLA-I) antigen presentation by tumor cells. Antigen presentation is an essential process that allows adaptive immune cells to recognize tumor cells. The mechanisms that lead to altered HLA I antigen presentation in cancer cells are yet to be fully understood. My project aims to develop methods to analyze alterations in HLA-I antigen presentation on cancer cells which can be then useful for understanding these mechanisms. To do this, we are testing specialized antibodies that recognize HLA-antigen complexes in human lung cancer cell lines using flow cytometry. We will then use this assay as a read-out of HLA-I antigen presentation in cells in which we introduce changes that may alter antigen presentation. The overall goal of the project is to optimize in-vitro methods for the analysis of antigen presentation in lung cancers.

Comparison of resuscitation products in canine hemorrhagic shock.

Discipline: Health
Subdiscipline: Other Health

Ranger Gunville*
University of Nebraska Lincoln

Abstract: Hemorrhagic shock is a significant cause of morbidity and mortality in severely traumatized patients, with an estimated 1.5 million cases occurring each year. Current resuscitation paradigms rely on blood products that require refrigeration or freezing. While this is easily implemented in urban areas, this proves more challenging in underserved areas or combat zones. We are testing novel resuscitation strategies that use shelf stable products:, freeze-dried plasma (FDP) + hemoglobin based oxygen carrier (HBOC) + lyophilized platelets (LP). We will compare those strategies to the use of lactated ringer solution (LRS) + hetastarch (HEs), fresh frozen plasma (FFP) + packed red blood cells (pRBC), and chilled whole blood (CWB), freeze-dried plasma (FDP) + hemoglobin based oxygen carrier (HBOC). We hypothesize that a combination of shelf-stable HBOC, FDP and LP will be non-inferior to canine CWB to resuscitate in hemorrhagic shock. Seven dogs underwent general anesthesia and 40% of the blood volume was removed (T0) over 1 hour to induce hemorrhagic shock, then left untreated for 45 minutes. Animals were randomized to receive LRS+HEs or FFP+pRBC or CWB or FDP+HBOC or FDP+HBOC+LP. Citrated blood was collected at T0, T105, T135, T180 as well as 24 hours and 2 weeks after each experiment. Coagulation parameters were assessed using thromboelastography. Overall, TEG data (R, k, alpha, maximal amplitude) showed no significant differences between the shelf-stable and non shelf-stable strategies. Our data showed that FDP + HBOC + LP is resonable alternative to conventional resuscitation strategies. Our findings are vital and relevant to combat zones.

Development and Validation of a Novel Patient-Reported Outcome Measure for Bleeding Quality of Life in Older Adults

Discipline: Health
Subdiscipline: Medicine

Alyssa Lopez*[1]and Anna Parks [2]
[1]University of Kentucky, [2]University of Utah

Abstract: Anticoagulants prevent thromboembolic stroke in atrial fibrillation (AF) and treat venous thromboembolism (VTE) but at the expense of increased bleeding risk. Current definitions of bleeding events underrepresent older adults' experience of bleeding and do not capture many minor bleeding events. In hematology, there is a lack of patient-centered measures on the effect of anticoagulant-related bleeding on quality of life (QoL) in older adults. Since few studies incorporate patient-centered goals, providers and patients face challenges in applying evidence and recommendations for treatment. Creating a patient reported outcome measure (PROM) related to minor bleeding events can help clinicians and other researchers create a better understanding of the QoL in older adults taking anticoagulants with AF and/or VTE. This presentation will summarize the efforts already made towards creating a questionnaire about measuring the QoL in elderly patients taking anticoagulants for AF and/or VTE. This includes part one of the project where focus groups were conducted to refine a conceptual model that forms the basis for developing the PROM. Using this information, a pilot questionnaire has been created that will be given to 20-30 participants through cognitive interviews. After receiving this feedback, the questionnaire will then be revised, where items may be eliminated to then go through a multi-step process including expert review to create the final questionnaire. We hypothesize that this novel measure will better characterize older adults' experience of bleeding than existing measures. This is the first step toward incorporating the voice of older adults into our understanding of bleeding on anticoagulants.

Neighborhood built environment, psychosocial stressors, and telomere length of birth parents and infants from San Francisco, California

Discipline: Health
Subdiscipline: Public Health

Hasibe Caballero-Gomez*[1], Lara Cushing [2], Nicholas Depsky[3], Stephanie Eick[4], Erin DeMicco [5], Jue Lin[6], Tracey Woodruff[7], Rachel Morello-Frosch[8], Ana C. Pelegrini Guimaraes[9]
[1]University of California, Los Angeles, [2]University of California, Los Angeles, [3]University of California, Berkeley, [4]Emory University, [5]University of California, San Francisco, [6]University of California, San Francisco, [7]University of California, San Francisco, [8]University of California, Berkeley, [9]San Francisco State University

Abstract: Shorter telomere length is a biomarker of cellular aging previously associated with chronic stress and exposure to air pollution. Aspects of the neighborhood built environment can contribute to stress and air pollution exposures. For this reason, we examined the joint associations between residential greenspace, traffic, noise, and individual-level measures of psychosocial stressors on telomere length in birth parents and their newborns. Telomere length (T/S ratio) was measured in delivery cord blood of 490 newborns and 288 second trimester parental whole blood samples from the Chemicals in Our Bodies cohort from San Francisco, California. Three measures of neighborhood built environment were constructed from secondary data based on residential address: greenspace (normalized difference vegetation index [NDVI]), traffic volume, and noise. Perceptions of neighborhood quality, stress, and depression were collected via a second trimester questionnaire. We used quantile g-computation to assess joint associations between these exposures and newborn and parental T/S in separate models that controlled for age, race/ethnicity, education, parity, pre-pregnancy BMI, and gestational age(cord T/S only). A simultaneous one quartile increase in all exposures

was associated with a mean change of- 0.02, 95% confidence interval[-0.08, 0.04] in newborn T/S and -0.04 [-0.10, 0.01] in parental T/S. Effect estimates were stronger but less precise in paired samples (-0.06, [-0.16, 0.04] for newborn and -0.05 [-0.12, 0.03] for parental T/S), with depression assigned the largest negative weight. Results from this cross-sectional study suggest prenatal exposure to adverse built environments and psychosocial stressors are associated with small reductions in telomere length ofnewbornsandtheir birth parents

CADM2 is Implicated in Impulsive Personality and Numerous Other Traits by Genome- And Phenome-Wide Association Studies in a Multi-ancestral Cohort Comprising up to 3 million Individuals

Discipline: Health
Subdiscipline: Medicine

Sevim Bianchi*[1], Sandra Sanchez-Roige [2], Mariela V Jennings[3], Hayley H A Thorpe[4], Jazlene E Mallari [5], Lieke C van der Werf[6], Calvin Lee[7], Travis T Mallard[8], Samuel A Barnes[9], Jin Yi Wu[10], Abraham A Palmer [11]

[1]University of California, San Diego, [2]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [3]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [4]Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph, Ontario, Canada, [5]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [6]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [7]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [8]Psychiatric and Neurodevelopmental Genetics Unit, Center for Genomic Medicine, Massachusetts General Hospital, Boston, MA, 02114, USA, [9]Department of Psychiatry, University of California San Diego, San Diego, CA, USA, [10]Department of Psychiatry, University of California San Diego, San Diego, CA, USA,[11]Department of Psychiatry, University of California San Diego, San Diego, CA, USA

Abstract: Impulsivity is a multidimensional, heritable phenotype that refers to the tendency to act prematurely and is associated with forms of psychopathology. We performed genome-wide association studies (GWAS) of impulsive personality traits from the Barratt Impulsiveness Scale and the short UPPS-P Impulsive Personality Scale (N=123,509-133,517 23andMe research participants), and a measure of Drug Experimentation (N=130,684). Variants in the gene cell adhesion molecule 2 (CADM2) were robustly implicated with impulsivity and identified in independent GWAS of other risky and substance use behaviors, and multiple other traits. To further explore the role of CADM2 across social and health-related outcomes, we performed a phenome-wide study (PheWAS) of five variants in and around CADM2 that have been most strongly implicated by the prior GWAS in a multi-ancestral 23andMe cohort (N=3,229,317, European; N=579,623, Latin American; N=199,663, African American). We examined close to 1,300 traits, most without published GWAS. PheWAS for CADM2 variants identified associations with 378 traits in European participants, and 47 traits in Latin American participants, replicating associations with risky behaviors, cognition, and BMI, and revealing novel associations including allergies, anxiety, and migraine. We identified no significant associations in the African American cohort, which may reflect a lack of sufficient power in this relatively smaller sample or potential differences in ascertainment and environmental and cultural factors. Our findings provide evidence of the overarching role of CADM2 on impulsivity and its impact on human health. Future studies are urged to further examine the role of CADM2 on behavior at the molecular and circuit levels.

"I don't love the word clean"...Sexual Scripts and STI Status Among College Students

Discipline: Health

Subdiscipline: Public Health

Gabriella Snow*[1]and Joni Roberts[2]

[1]California Polytechnic State University, San Luis Obispo, [2]California Polytechnic State University, San Luis Obispo

Abstract: Sexual scripts influence the interpretation of behavior and guide interactions within romantic and sexual contexts, including conversations about STI status and condom usage (Hill & Andrews, 2017). Exposure to sexual scripts begins in school, with messages about sex and sexual behavior (Hauck, 2015). These scripts may include terminology such as “clean” or “clean status” when describing negative STI status (Hill & Andrews, 2017). With a desire to identify predominating student sexual scripts, including the use of the word “clean” on a college campus, this study was developed to ascertain whether college students adhere to the clean status sexual script when deciding to engage in sexual activity. One-on-one interviews (n=30) were conducted with college students, which were subsequently analyzed using NVIVO coding software. Students had different responses about their perceptions of and adherence to sexual scripts. While 86.7% of participants understood the concept of “cleanliness” within a sexual context, many recognized this verbiage’s flawed and stigmatized nature throughout their interview. 14 of the 30 participants stated that they did not prefer using the word ‘clean’ in a sexual health context, given its perpetuation of a negative stigma surrounding sexual activity and STIs. These preliminary findings reveal that college students understand the negative implications of some sexual scripts. Subsequent interventions should therefore explore the formation of such sexual scripts and potential alternatives which can be employed to foster more open communication while addressing STI status stigma.

Increasing Rates of Firearm-involved Suicide and Homicide for Non-Hispanic Black males in the United States

Discipline: Health

Subdiscipline: Public Health

Kamiah Brown*[1]and Sally Curtin[2]

[1]The George Washington University, [2]Centers for Disease Control and Prevention/ National Center for Health Statistics

Abstract: Objectives— This presentation will feature the rates of firearm-involved suicide and homicide for non-Hispanic Black males in the United States. Trends also present three leading methods of suicide, (firearms, suffocation, and poisoning) and homicide (firearms, cut/pierce, and unspecified injuries). This assessment will inform prevention efforts on firearms and other leading methods of suicide and homicides among Non-Hispanic Black men. Methods— Data from the 2000-2020 Detailed Mortality were tabulated using the CDC WONDER underlying cause of death query tool. Suicide and homicide rates among Non-Hispanic Black men were computed for each year between 2000 and 2020, with sufficient cases to produce reliable rates (at least 20 deaths in the numerator). The Joinpoint Regression Program was used to estimate proportions on the logarithmic scale. Rates for Non-Hispanic Black men are based on multiple-race mortality data that were bridged to single-race categories based on the 1977 Office of Management and Budget standard for the classification of race and ethnicity. Firearm homicide and firearm suicides were examined by age and ethnicity. Results— Nationally, suicide rates are higher for Non-Hispanic White than Non-Hispanic Black, however, the rates for Non-Hispanic Black males are increasing while Non-Hispanic White males are declining. Conclusions and Implications for Public Health Practice— Firearms are the most common method of homicide and suicide for non-Hispanic Black males and rates for both have increased. The public health approach should be used to address firearms and the underlying social determinants that contribute to the risk of violence and suicide to reduce disparities.

Loss of macrophage derived Dnase1L3 causes increased autoantibodies in autoimmune disease, Lupus

Discipline: Health
Subdiscipline: Public Health

Angelica Infante*[1], Minal Engavale [2], Peter A. Keyel[3]
[1]Texas Tech University, Lubbock, Texas, [2]Department of Biological Sciences, Texas Tech University, Lubbock, Texas., [3]Department of Biological Sciences, Texas Tech University, Lubbock, Texas.

Abstract: One leading cause of death in women is autoimmunity. One prominent autoimmune disease is Systemic Lupus Erythematosus (lupus). During lupus, inflammation is driven by autoantibodies that target cell-free DNA. Cell-free DNA is degraded by two serum endonucleases, Dnase1 and Dnase1L3. Dnase1L3 is secreted by macrophages and dendritic cells. The loss of Dnase1L3 causes lupus in humans and mice, but the amount of Dnase1L3 necessary to prevent lupus onset is unknown. We hypothesized that loss of macrophage-derived Dnase1L3 is sufficient to cause lupus-like phenotypes in mice. We generated conditional knockout (cKO) mice lacking Dnase1L3 expression in macrophages. Sera was collected weekly from these mice until 50 weeks of age. To measure autoantibody induction, total IgG, total IgM and anti-dsDNA antibody levels were analyzed at 4, 20, 30 and 50 weeks respectively. Sandwich ELISA was used to quantitate antibody levels in control and cKO mice. We found that total IgG and anti-ds DNA antibody (Ab) levels increased starting 20 weeks in cKO mice. We conclude that SLE-like phenotypes arise in mice due to the loss of macrophage Dnase1L3. This suggests that Dnase1L3 levels are critical to controlling lupus.

The parabrachial to central amygdala pathway mediates injury-induced behavioral hypersensitivity

Discipline: Health
Subdiscipline: Medicine

Jeitzel M Torres Rodriguez*[1], Yarimar Carrasquillo [2], Torri Wilson[3], Sarah Chaudhry[4]
[1]National Institutes of Health, [2]NIH, [3]NIH, [4]NIH

Abstract: The parabrachial nucleus (PbN) receives and relays nociceptive information from the spinal cord to the brain through the spino-ponto-amygdaloid pathway. Multiple studies further suggested that maladaptive plasticity of the PbN to Central Amygdala (CeA) pathway contributes to injury-induced hypersensitivity. However, recent studies suggested that this pathway does not mediate nociceptive behavior. To elucidate these conflicting results, we addressed the functionality of these neurons in a context of injury-induced sensitization. We first tested whether these neurons were activated after noxious stimulation. To do this, we used a chemo genetic intersectional approach in which C57BL/6J mice were co-injected with a Cre-expressing

retrograde Adeno-associated virus (AAV) into the CeA and a Cre-dependent designer receptor exclusively activated by designer drugs (DREADD) into the PbN. Following pinching of the hind paw, c-fos a surrogate for neuronal activation, was measured. Our results showed that ~20% of the activation was localized to Cea-projecting PbN neurons. We then addressed the causality between this activation and injury-induced hypersensitivity using the cuff model of neuropathic pain coupled with the Acetone, Hargreaves, Vonfrey and Randall-Selitto to assess cold, heat, tactile and pinch hypersensitivity. Our results revealed that chemogenetic inhibition of CeA-projecting PbN neurons reverses cuff-induced hypersensitivity in all modalities. Further experiments showed that chemogenetic activation of these neurons in the absence of injury results in bilateral hypersensitivity to cold, tactile, and pinch, but not heat stimulation. Altogether, our results demonstrate that CeA-projecting PbN neurons are necessary and sufficient for pain modulation during pathological states, but not for baseline nociception.

Hearing the Voices of Native Mothers

Discipline: Health
Subdiscipline: Public Health

Reham Perry*[1]and Michelle Debbink [2]
[1]New York University, [2]Physician at the University of Utah Hospital

Abstract: Nationally, American Indian and Alaskan Native women are 54% more likely to develop Severe Maternal Morbidity (SMM) than their Non-Hispanic White counterparts. We hypothesize that factors such as historical traumas (child-mother forced separation, rushed c-sections, forced sterilizations) and systemic barriers (access to birthing centers and doulas, generational poverty, culturally insensitive care) impact patient-physician communication, produce mistrust, and impact health outcomes and quality of care. Qualitative data is collected from a series of 8-10 listening groups across Utah that include 8-10 women from each tribe, who have given birth in the last five years. Participants are compensated for their contributions to a semi-structured conversation about pregnancy complications and experiences. The first Talking Circle was conducted in English virtually on March 20, 2022, via Zoom and was recorded (audio and video) and transcribed. Preliminary results from focus groups suggest that cultural practices and community are important to the pregnancy experience of urban Native women, the first pregnancy and delivery are more difficult due to a lack of information provided to the mother prior to labor, and there is mistrust toward providers that stems from the physician's insensitivity in delivering care. There is a lack of research tracking the outcomes of culturally-sensitive community interventions regarding prenatal disparities for Native Americans. Community-based interventions should consider ways to implement cultural sensitivity and advocacy into prenatal care and labor, most realistically through the form of a culturally trained doula or midwife. Women should also have community spaces to learn about pregnancy early in the experience.

Avoidance Coping and Marijuana Use Among Pregnant Black Women

Discipline: Health
Subdiscipline: Public Health

Christabelle Toso*[1]and Dawn Misra [2]
[1]Georgia State University/Emory University, [2]Michigan State University

Abstract: Abstract (200 Words) Objectives The objective of this project is to compare avoidance coping scores for pregnant Black women who do and do not report using marijuana during

pregnancy. This study hypothesizes that pregnant Black women who report using marijuana are more likely to score in the highest quartile for the avoidance coping subscale. Methods Frequencies and distributions of variables were examined. T-tests were used to compare means for continuous variables. Chi square was used for categorical variables. Regression was conducted as indicated to control for confounding variables. Sample Quantitative date from the 609 women enrolled in the Biosocial Impact on Black Births, a NIH-funded research study at prenatal care clinics in Michigan and Ohio was analyzed. Results 26.5% of the participants self-reported to using marijuana or hash anytime during pregnancy. Among the women who reported yes , 38.9% used marijuana or hash daily. The mean score of avoidance coping remained higher among participants who reported using marijuana or hash during pregnancy in comparison to nonusers. Conclusion Participants who reported marijuana or hash use were more likely to score higher on avoidance coping subscale. We recommend enhancing healthy coping strategies among vulnerable populations and increasing population awareness through education on marijuana or hash use and its intended users.

Examining the Association Between the ‘Southern Diet’, Socio-demographics, and Obesity Status Among Women in Alabama

Discipline: Health

Subdiscipline: Public Health

Lourdes Romañach Álvarez*[1], Valerie Lobato [2], Clementine Sikpe[3], Emma Risner[4], Yenni Cedillo [5], Anarina Murillo[6], Tiffany Carson[7]

[1]University of Puerto Rico, Mayagüez Campus, [2]University of California, Berkeley, [3]Ohio State University, [4]New York University, [5]University of Alabama at Birmingham, [6]New York University, [7]Moffitt Cancer Center

Abstract: According to the CDC, Alabama ranks third in adult obesity prevalence with 39% of the population having obesity. Social determinants of health such as economic instability, racism, and less access to healthy foods are associated with increased risk of obesity. This study examined the association between diet, socio-demographic factors, and obesity in a sample of Alabama residents. Secondary data analysis was conducted for a study of 71 women residing in Birmingham, Alabama. Data were collected on BMI (weight (kg)/height (m2) <30 kg/m2 for non-obese and ≥30 kg/m2 for obese) and diet using an Automated Self-Administered 24-Hour (ASA24) recall and Healthy Eating Index-2010 (HEI-2010) score (HEI score < median for low quality and HEI score ≥ median for high quality). Socio-demographic variables included race, income, and education. T-tests were used to examine mean differences in dietary intake based on obesity status. Chi-square tests were used to assess associations among socio-demographic factors and obesity status. Participants were predominantly Black (60.5%), had an income over $50,000 (47.1%), and some had postgraduate education (15.5%). Also, 43.7% of participants had obesity, of which 77.4% were Black. Household income (p=0.27), race (p=0.21), age (p=0.64), and education (p=0.57) were not significantly associated with obesity status. Our preliminary results suggest that obesity status among our sample are not associated with socio-demographic factors. Our ongoing analysis focuses on diet which may be better explained by socio-demographic factors. These findings may inform future interventions that address the driving influence of socio-demographic factors to promote health across Southern communities.

17beta-Estradiol may suppress HIV induced Neurotoxicity in Human Macrophages

Discipline: Health
Subdiscipline: Medicine

Kersten Pierre*[1]and Dr. Kimberly Williams [2]
[1]Spelman College, [2]Spelman College

Abstract: Approximately 1.2 million people are affected by Human Immunodeficiency Virus (HIV) in the U.S. Combined anti-retroviral treatments have increased the longevity of HIV patients, with the median age of persons living with HIV being 50 years old. Despite this success, 40-50% of HIV patients still suffer from HIV-associated neurocognitive disorders, and this number is expected to increase as patients age. Immune cells, macrophages and microglia, play a pivotal role in the protected reservoir of HIV in the brain. The ensuing inflammatory macrophage/microglia activation and secretion of neurotoxins cause damage to neurons, which are not infected. Studies utilizing broad anti-inflammatory and antioxidant therapeutics to mitigate disease progression have been unsuccessful. Targeting signaling pathways that decreases inflammation and oxidative stress may be more advantageous. 17β-estradiol, the most active form of estrogen, has been reported to reduce oxidative stress and neuroinflammation. Therefore, we hypothesize that increasing concentrations of 17b-estradiol will reduce HIV-induced neurotoxicity. To test this hypothesis, we treated human monocyte-derived macrophages with increasing concentrations of 17b-estradiol prior to inactivated HIV exposure. Whole cell lysate was collected to measure expression levels of antioxidant proteins. Conditioned media was also collected and placed onto rat neurons to assess neurotoxicity. Macrophages treated with increasing doses of 17b-estradiol increased antioxidant protein expression. HIV-infected macrophage media killed 50% of cultured rat neurons. 17b-estradiol blocked the neurotoxic effects of HIV in an estrogen receptor-dependent manner. This data suggest that 17b-estradiol may be a potential therapeutic for suppression of HIV-induced neuroinflammation.

Alkylation Damage of RNase H1 and RNase H201 Genes

Discipline: Health
Subdiscipline: Medicine

Deanna Garcia*[1], Peng Mao [2], Mingrui Duan[3]
[1]New Mexico Institute of Mining and Technology, [2]University of New Mexico School of Medicine, [3]University of New Mexico School of Medicine

Abstract: Alkylation damage is a standing effect of damaging cells during chemotherapy and radiation. In many cases cells are developing mutations in order to repair the damage that alkylation drugs cause during the replication process of single stranded DNA. In this experiment the focus is to see the repair process of yeast cells that have been treated with alkylation drugs at different stages and different genetic mutations. The standing hypothesis is that single stranded DNA and R-loops will have more gene damage than that of double stranded DNA due to the instability of the genes and replication process. Three mutants were made from a yeast wildtype strain by extracting genomic DNA using PCR to cut out RNase H1 and RNase H201 genes in the yeast genomes. These genes were then replaced with Trp-1 and hygromycin to define the mutations. These mutants were verified and treated with different amounts of alkylation drugs in order to see the reaction in the single strand of the genome, affecting the replication and repair process on damaged genes. Further repetition will occur in single and double strands in order to see the increased susceptibility of both strands and the R-loop reaction. The project thus far has cut out all the necessary genes using yeast transformation,

identified all three mutants with successful PCR in identifying the Trp-1 and hygromycin gene markers. The next steps will be to treat the according strains with alkylation drugs and see the difference between single and double strands as well as R-loops.

Using Surface Enhanced Raman Spectroscopy (SERS) to Determine Diseases

Discipline: Health
Subdiscipline: Medicine

Marian Jimenez*[1]and Gabriel Montano [2]
[1]University of Arizona, [2]Northern Arizona University

Abstract: Cancer has been a public health focus for many years and continues to be on the rise. Records from 2020 show that Breast Cancer (BC) was the highest cause of cancer deaths in the world amongst the female population. The gold standard technique used to detect BC is called Mammography, sensitivity ranges from 72%-88%. A mammography compresses the breast with two plates exerting radiation and it is only available to patients over the age of forty, meaning that early detection is difficult for those under forty. After undergoing mammography screening, women frequently develop fibrous tissue in their breasts making it difficult to distinguish between the dense tissue and a possible cancerous tumor. Sialic Acid (SA), also known as N-Acetylneuraminic Acid in the human body, is highly expressed when cancerous cells are present. SA is abundantly distributed throughout the human body fluids, however its highest concentration is in saliva. Salivary sialic acid could thus be used as a biomarker and has advantages as obtaining saliva is simple, efficient, non-invasive, and cost-effective. In this work, we are exploring the use of Surface-Enhanced Raman Spectroscopy (SERS) to detect SA. Specifically, I am synthesizing silver nanowires that help to intensify the traditional Raman Spectroscopy signals and looking for signal enhancement as they bind the SA. This new tool proposes an alternative test to increase the sensitivity of detecting BC using nanotechnology.

Understanding Patient and Caregiver Knowledge of Condition in Differences of Sex Development

Discipline: Health
Subdiscipline: Other Health

Mariah Lee*[1], Kristina Suorsa-Johnson [2], Melissa Gardner[3], Alexandra Britt[4], Zoe Lapham [5], David E. Sandberg[6]
[1]Diné College, [2]University of Utah, [3]University of Michigan, [4]University of Utah, [5]University of Michigan, [6]University of Michigan

Abstract: Disorders/Differences of Sex Development (DSD) is an umbrella term describing congenital conditions where chromosomal, gonadal, or anatomic sex development is atypical. Now considered a foundation of patient-centered care, patient autonomy has not always been the norm, particularly in pediatric populations. Healthcare providers need to provide patients (and families in pediatric settings) with clear and relevant information about their condition and its management. Patient comprehension of their DSD is important for patients understanding how their body works and for decision-making regarding their care. Project aims are: (1) assess patient and caregiver understanding of the condition and (2) evaluate response consistency within families. As part of the DSD-Translational Research Network, a national biopsychosocial DSD registry, patients (n=81) and their caregivers (n=376) completed the Knowledge of Condition Self Report (KoC-SR) and Caregiver Report (KoC-CR) forms. These forms evaluate understanding of the DSD diagnosis. The majority of caregivers reported knowing the name of their child’s medical condition (83%), but not knowing what caused the DSD (65%). Caregivers also indicated that 29% of patients were aware of their DSD. Forty-nine percent of patients reported knowing the name of their DSD diagnosis. The average age of patients finding out about their DSD was 13 years. Early and ongoing education is a central element of patient centered care. Clinically, the KoC-SR and KoC-CR allow providers to understand patient and caregiver knowledge and offer additional education and support.

Targeted Drug Therapy Extends the Life of Cancer Patients

Discipline: Health
Subdiscipline: Medicine

Gianna Perez*[1], Hope Lancero[2], Hope Lancero[3]
[1]College of San Mateo, [2]Stanford University, [3]Stanford University

Abstract: Combinations of the Polo-Like Kinase Inhibitor (PLK), and BRAF inhibitor dabrafenib show rapid and sustained responses in patients with BRAF V600E-mutated low-grade glioma, but tumor rebound after treatment discontinuation is frequent. Moreover, a lack of response is common in patients with high-grade glioma raising the need for further research into Dabrafenib and PLK inhibitors on tumors. We showed previously that BRAF V600E-mutated glioma cells positive for CD133 (Prominin-1), a marker of brain tumor stem cells, show decreased sensitivity to BRAFi, indicative of their role in promoting therapy resistance. We hypothesize that a combination of Dabrafenib and PLK inhibitor will have greater efficacy compared to a single drug therapy. BRAF V600E-mutated murine and human cells obtained from ATCC (BRAF V600E-mutated cell lines) DBTRG (cells from patient with glioblastomas) and 2341 (mouse cells) were analyzed for changes in gene expression in response to 48 hrs treatment and 72 hrs treatment with BRAFi dabrafenib and PLK inhibitor. RNA from these cells were analyzed by real-time RTqPCR while cell culture supernatant was analyzed for cytokine production. In vivo studies are currently being conducted in the lab where syngeneic, orthotopic BRAF V600E-mutated tumor allograft-bearing mice were treated with BRAFi+PLK Inhibitor.

Glutamate Release Stimulated by Norepinephrine in the Ventromedial Hypothalamus in Response to Hypoglycemia

Discipline: Health
Subdiscipline: Medicine

Abigail McDonald*[1], Owen Chan[2], Daniel Appadurai[3]
[1]Montana State University, [2]University of Utah, [3]University of Utah

Abstract: Recognition of decreasing glucose levels during hypoglycemia is dependent, in part, on glucose-sensing neurons located in the ventromedial hypothalamus (VMH) in the brain. The neurotransmitters norepinephrine and glutamate are supportive in restoring plasma glucose levels by initiating a counterregulatory hormone response. Studies have shown that when norepinephrine and glutamate are released into the VMH in response to hypoglycemia, they bind to B2-adrenergic and kainic acid receptors, activating counterregulatory hormone responses to hypoglycemia. However, the organization of the neural circuitry leading to the release of glutamate is unclear. This study's objective was to clarify the neural circuit(s) involved in hypoglycemia detection and to determine if norepinephrine is required to stimulate glutamate release. Immunohistochemistry was used to examine if B2-adrenergic receptors co-localize with VGlut2, a marker for glutamatergic neurons. Our data shows that B2-adrenergic receptors are expressed on VMH glutamatergic neurons. We then conducted microdialysis studies by infusing norepinephrine into the VMH to evaluate its effects on glutamate and counterregulatory hormone release. Subsequently, we co-delivered norepinephrine and a kainic acid receptor blocker to determine whether norepinephrine-stimulated glutamate release is necessary to trigger counterregulatory hormone secretion. Our data shows that NE stimulates glutamate release in the VMH, which was associated with a rise in both glucagon and epinephrine. Notably, the elevation of glucagon and epinephrine was ablated in the presence of the kainic acid receptor blocker. We, therefore, conclude that glutamatergic neurons are positioned downstream of noradrenergic neurons in the VMH, and norepinephrine-stimulated glutamate release is required to trigger glucagon and epinephrine secretion.

Immediate Lymphatic reconstruction for preventing cancer-related lymphedema: preliminary experience of a single center.

Discipline: Health
Subdiscipline: Medicine

Timina Powaukee*
University of utah

Abstract: Immediate lymphatic reconstruction for preventing cancer-related lymphedema: preliminary experience of a single center. Cancer-related lymphedema affects 20-45% of patients with breast cancer and up to 50% of patients with melanoma and develops after lymphatics are disrupted during lymph node dissection or radiation. It results in pain, swelling, and decreased quality of life. A lymphovenous bypass procedure is done to re-establish lymphatic flow by rerouting cut lymphatics into nearby veins and may be performed at the time of lymph node dissection in a procedure known as immediate lymphatic reconstruction (ILR). ILR is supported by a growing body of evidence, though data regarding long-term efficacy is lacking. In this study, we aim to describe the experience of ILR at our institution through a retrospective chart review using a REDCap database. Thirty-seven patients underwent ILR at the time of lymphadenectomy. Nine patients were excluded from analysis due to pre-existing lymphedema. Breast cancer affected 70.4% of patients, while 25.9% had melanoma and 3.7% had squamous cell carcinoma. The majority of our patients underwent adjuvant radiation therapy (73.1%). Patients underwent LVA in the axilla (74.1%), inguinal region (22.2%), and antecubital fossa (3.7%). The average follow-up duration was 7 months. 85.2% of patients did not have lymphedema based on the physical exam at their last follow-up appointment. Our findings indicate that ILR may be a safe and effective strategy for reducing post-operative lymphedema in the cancer population.

Evaluation of Race/Ethnicity on HPV Vaccination Initiation and Completion Among Adolescents Aged 11-17 Years

Discipline: Health
Subdiscipline: Public Health

Sydney Fisher*[1]and Courtney McCracken [2]
[1]Brown University, [2]Kaiser Permanente Center for Research and Evaluation

Abstract: The human papillomavirus (HPV) is the most common sexually transmitted infection in the United States and has been linked to several forms of cancer. Fortunately, most HPV-related

cancers are preventable through vaccination. However, HPV vaccination rates are low, and studies disagree on whether there are racial and ethnic disparities in HPV vaccination initiation and series completion. The goal of this study was to identify factors associated with HPV initiation and completion and to determine whether there are racial and ethnic differences in vaccine initiation and completion among commercially insured Kaiser Permanente Georgia (KPGA) adolescents aged 11-17 years. We performed a retrospective cohort study of adolescents insured by Kaiser Permanente Georgia (KPGA) between 1/1/2012 and 12/31/2019. The outcome measures of interest were HPV vaccination initiation and completion. Multivariable logistic regression models were used to assess the association between patient demographics and HPV vaccination outcomes. Factors associated with both initiation and completion included cohort year, age, sex, and history of a sexually transmitted infection. In adjusted analysis, non-Hispanic Black (AOR=1.41, p<.0001), Asian (AOR=1.80, p<.0001), and Hispanic (AOR=1.96, p<.0001) adolescents were all more likely to initiate the HPV vaccine series compared to non-Hispanic White adolescents. Asian (AOR=1.34, p<.0001) and Hispanic (AOR=1.18, p=.002) adolescents were also more likely to complete the HPV vaccine series but non-Hispanic Black adolescents (AOR=0.95, p<.0001) were less likely to complete the series compared to non-Hispanic White adolescents. These findings suggest that the likelihood of initiation and completion of the HPV vaccine series does vary by race and ethnicity.

Assessing Oxytocin levels, a biomarker of resiliency, among Latina Breast Cancer Survivors: The Nuevo Amanecer- II Study

Discipline: Health
Subdiscipline: Other Health

Adriana Mejía López*[1], Health & Equity Research Lab, Leticia Márquez-Magaña PhD[2], Cathy Samayoa, PhD[3], Odessa Garay BS[4], Rebecca Mendez, MPH[5], Anna Maria Napoles, PhD, MPH[6], Jasmine Santoyo-Olsson, MS[7], Anita L. Stewart, PhD[8]
[1]San Francisco State University, [2]San Francisco State University, [3]University of California, San Francisco, [4]San Francisco State University, [5]San Francisco State University, [6]National Institutes of Health, [7]University of California, San Francisco, [8]University of California, San Francisco

Abstract: Breast cancer is the leading cause of death for Latina in the United States. These disparities in cancer outcomes are impacted by social factors, and emerging evidence indicates that chronic stress may also be driving these inequities. Oxytocin is a neuropeptide that modulates the stress response by acting on the HPA axis, buffering cortisol, mitigating pain, and promoting resiliency. Social support has been shown to increase salivary oxytocin and diminish cortisol levels, suggesting that stress management interventions may have the potential to impact cancer outcomes among vulnerable populations through the release of oxytocin. The objective of this study is to 1) examine endogenous salivary oxytocin levels and 2) determine the relationship between oxytocin, somatization, and measures of stress among Latina breast cancer survivors participating in the community-based Nuevo Amanecer-II stress management intervention. Saliva was collected from Spanish-speaking rural Latina breast cancer survivors (n=103) using saliva collection kits. Salivary oxytocin will be extracted and quantified using an Enzyme Immunoassay. We will estimate the association between oxytocin and self-reported measures of somatization and stress collected through surveys and between cortisol, a stress biomarker. We expect that the community-based behavioral stress management intervention will increase salivary oxytocin levels. This increase in oxytocin levels will be inversely correlated to cortisol levels, perceived stress, and somatization. This study will examine oxytocin levels, a

biomarker of resiliency, among Latina breast cancer survivors and evaluate the impact of a stress-management intervention on relevant biomarkers. These findings will uncover the biological mechanisms involved in breast cancer disparities.

Interrelationships between total body adiposity, visceral adiposity, and adipokines among Black and Latinx adolescents with overweight or obesity

Discipline: Health
Subdiscipline: Public Health

Renee Medina*[1], Claudia Toledo-Corral, PhD[2], Marc Weigensberg, MD[3]
[1]California State University, Northridge, [2]California State University, Northridge, [3]University of Southern California

Abstract: The activation of the human inflammatory response has been largely associated to contribute to the development of chronic disease. Past studies have revealed adipose tissue (also known as body fat), particularly visceral or abdominal adipose tissue, can produce numerous inflammatory cytokines (adipokines) in adults, but the literature is sparse in pediatric populations with higher risk for chronic disease. Similar to adults , our hypothesis was higher body fat and higher visceral fat will be associated with higher levels of adipokines in Black and Latinx adolescents with overweight or obesity. To study this question, a sample of 190 adolescents (ages 14-17 years) who had a body mass index (BMI) of 25 kg/m2 or greater and who identified as Black race or Latinx ethnicity were assessed using fasting blood samples, including inflammatory markers Interleukin (IL)-1B, IL-6, IL-8, and monocyte chemoattractant protein-1 (MCP-1). Total body adiposity (as total body fat percentage) was measured with a dual x-ray absorptiometry (DeXA) scan and visceral adipose tissue (VAT) was measured with 3-Tesla magnetic resonance imaging. Spearman correlations were used to assess the relationships between total body fat percentage and VAT with four adipokines. Preliminary analyses show that VAT was positively associated with MCP-1 (r=0.320, p<0.001) but were not associated with IL-1, IL-6, IL-8 or TNF-alpha. There were no associations with total body fat and adipokines (all p>0.05). Abdominal fat associated with inflammation suggests the need for more studies to further investigate these inflammatory markers and mechanisms in youth to prevent chronic disease.

The Effects of TAML and Ethinyl estradiol (EE2) exposure on African clawed frogs, "Xenopus laevis", Gonadal Development and Metamorphosis.

Discipline: Health
Subdiscipline: Medicine

Estephannie Alvarez*[1]and Tyrone B. Hayes[2]
[1]University of California, Berkeley, [2]University of California, Berkeley

Abstract: Ethinyl estradiol (EE2) is a synthetic estrogen commonly found in oral contraceptives. The human body has limited ability to degrade EE2, resulting in it being released in urine. EE2 contamination in waterways may result in the feminization of male wildlife or otherwise interfere with reproduction. For example, EE2 induces ovarian development in genetically male African clawed frogs, Xenopus laevis . TAML, a compound that can degrade EE2 in pure lab water, municipal effluents, and EE2-spiked synthetic urine, can potentially be used to rid the aquatic environment of this compound. However, before introducing TAML as a wastewater treatment strategy, we must identify any effects of TAML itself. We examined ZZ (genetic male)

Xenopus laevis from two lines that differ in their sensitivity to estrogen. Animals were exposed to either TAML (1.3 mg/L, 13 μg/L, .13 μg/L), estradiol (E2), EE2 (positive control), or ethanol solvent control. Gonads were examined using gross morphology and histology of the gonads to determine the sex ratio after exposure throughout larval development. The frog lines differed in their response/sensitivity to E2, however, EE2 was nearly 100% effective at inducing ovaries in both frog lines. TAML did not affect the sex differentiation of the gonads in either population. These data suggest that TAML may be safely used without effects on gonadal development. Future studies will examine if TAML protects against the effects of EE2.

AKT-Dependent Glucose Metabolism of an Adenoviral Protein E4orf1

Discipline: Health

Subdiscipline: Other Health

Daniela Ramos*[1], Marleigh Hefner [2], Nikhil V. Dhurandhar[3], Vijay Hegde[4]

[1]Obesity and Metabolic Health Laboratory, Department of Nutritional Sciences, Texas Tech University, Lubbock, Texas 70409, [2]Obesity and Metabolic Health Laboratory, Department of Nutritional Sciences, Texas Tech University, Lubbock, Texas 70409, [3]Obesity and Metabolic Health Laboratory, Department of Nutritional Sciences, Texas Tech University, Lubbock, Texas 70409, [4]Obesity and Metabolic Health Laboratory, Department of Nutritional Sciences, Texas Tech University, Lubbock, Texas 70409

Abstract: Type 2 Diabetes (T2D) prevalence has risen to epidemic levels in recent decades. T2D is characterized by altered proximal insulin signaling with impaired binding of insulin to its receptor and reduced insulin receptor kinase activity. As a result, hyperglycemia and dyslipidemia tend to occur. Our lab has shown that adenoviral protein, E4orf1 (E4) can bypass the proximal insulin pathway, directly phosphorylating downstream AKT for cellular glucose uptake. However, it is unclear if E4 mediated glucose metabolism uses AKT1 isoform, which mainly focuses on lipid metabolism or AKT2, which mainly focuses on glucose uptake. An immortalized mouse embryonic cell line with reduced expression of AKT1 (AKT1 knock-down) or without expression of AKT 2 (AKT2 knock-out) were cultured to determine downstream effects of AKT isoforms. Cells were transfected with E4 protein for 5hrs using PULSin liposome-mediated delivery system. Control cells with normal AKT1 and AKT2 expression were treated with 100 nM of insulin for 30min serving as positive control. In AKT2 knock-out cells, E4 is unable to increase glucose uptake and expression of downstream genes of AKT such as GLUT4, pGSK3α/β, and FOXO1 compared with AKT1 knock-down cells. Data collected indicate that E4 selectively uses the AKT2 isoform for its role in AKT mediated glucose homeostasis. Findings from this study will lead to enhanced understanding of E4 mechanism for its anti-diabetes therapeutic benefits and unveil its potential in the treatment of other chronic diseases affected by alterations in AKT1 or AKT2 expression, such as cardiovascular diseases, neurodegenerative diseases, or certain cancers.

Identifying Individual and Interpersonal Level Predictors of Access to Cancer Clinical Trials Among Cancer Survivors

Discipline: Health

Subdiscipline: Public Health

Yaideliz M Romero Ramos*[1], Margaret S. Pichardo, MPH [2], Catherine Aluoch Ochieng, Bsc[3], Ana I. Velazquez, MD, MSc[4]

[1]University of Puerto Rico, Humacao, PR, [2]1. Howard University College of Medicine, Washington, DC 2. Yale School of Public Health, Department of Chronic Disease Epidemiology, New Haven, CT, [3]FACES, Lumumba Clinic, Kisumu, Kenya, [4]1. Division of Hematology/Oncology, Department of Medicine, University of California, San Francisco, CA 2. UCSF Helen Diller Family Comprehensive Cancer Center, San Francisco, CA

Abstract: Cancer clinical trials (CCT) can be potentially lifesaving treatments, yet racial/ethnic minoritized groups continue to be underrepresented among CCT participants. Potential barriers to participation include lack of health literacy, limited CCT knowledge, and limited access to healthcare. We examined predictors of access to CCT among diverse cancer survivors. We used data from the Health Information National Trend Surveys (HINTS) 4 cycles 2 and 4, and HINTS 5 cycles 1 and 4. In unweighted and weighted bivariate tests, we examined associations between individual (i.e., gender, age, education, race/ethnicity, income, nativity, and English proficiency) and interpersonal level (i.e., trust, sources of information, and information seeking behaviors) predictors of patient-provider discussion of CCT as a treatment option and reported prior participation in a CCT. Among a sample of 14,457 respondents, 14.77% (n=2,136) reported ever having a cancer diagnosis. In this subgroup, 58.38% were female, 30.01% were ages 50-64, 66.39% identified as non-Hispanic White (NHW) and 89.07% were US born. Only 10.81% (n=231) of cancer survivors reported having discussed CCT as a treatment option, while just 4.40% (n=94) reported prior participation in a CCT. In weighted bivariate tests, cancer survivors who were U.S. vs. foreign born (p=0.021) and NHW vs. other racial/ethnic group (p=0.05) were significantly more likely to discuss CCT as a treatment option. In subsequent analysis, we will conduct multivariate regression models to examine the association between predictors of interest and access to CCT. Our results will enable targeted interventions to increase representation of racial/ethnic minoritized groups in CCT.

Determining the effect of lactation support resources on the comprehensiveness of lactation accommodation policies in 4-year public universities in California

Discipline: Health
Subdiscipline: Public Health

Zakariah Robinson*[1], Kacie Blackman[2], Kalila Houston[3], Wyconda Cotton-Curtis[4]
[1]California State University, Northridge, [2]California State University, Northridge, [3]California State University, Northridge, [4]California State University

Abstract: Lactating students in academia confront a number of difficulties as they attempt to breastfeed continuously during their studies. California Assembly Bill 2785 requires an educational institution to provide lactation accommodations to express, store milk and address other needs related to breastfeeding. This study aims to determine the effects of lactation support resources on the comprehensiveness of lactation accommodation policies in 4-year public universities in California. We created a lactation accommodation coding tool and key data system evaluating all CSUs and UCs in California State University Systems. Lactation policies were reviewed via a policy audit tool. Having a lactation policy was assessed (yes/no). Lactation support resources were measured across 4-items (breastfeeding support; lactation consultant available; on-campus resources; off-campus-related resources). The inclusion criterion was the institution had to have a policy that was publicly accessible or provided upon request from the Title IX or Human Resources coordinator. Descriptive statistics and unpaired T-Test were used to analyze the data. The majority of universities had available policies (87.8%). When comparing schools with comprehensive policies and lactation support to schools without comprehensive policies and lactation support, the findings revealed that there were non-statistically significant differences. (t= -1.980 ; df=27 ; p=.058) Policies are necessary, but lactating students (current and future) will continue to be unprotected and unsupported without adequate resources. To ensure that students achieve their breastfeeding goals and enhance their own and their child's health, it is vital to equip them with suitable support resources.

Short Telomeres Among Latina Breast Cancer Survivors: The Nuevo Amanecer-II Study.

Discipline: Health

Subdiscipline: Medicine

Alexander Orellana*[1], Rebecca Mendez [2], Leticia Márquez-Magaña[3], Cathy Samayoa[4], Cathy Samayoa [5], Anna María Nápoles[6], Anita L. Stewart[7], Jasmine Santoyo-Olsson[8], Jessica Magaña[9]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University, [4]University of California, San Francisco, [5]University of California, San Francisco, [6]National Institute of Health, [7]University of California, San Francisco, [8]University of California, San Francisco, [9]San Francisco State University

Abstract: Latinas experience breast cancer health disparities which may be due in part to experiences of chronic stress. Stress has been shown to impact biological aging. Short telomeres are associated with negative health outcomes and predict poorer cancer survival. However, studies of telomere length among Latina breast cancer survivors (LBCS) are lacking. The purpose of this study is to: a) characterize relative telomere length (rTL) among LBCS; and b) determine the impact of a stress-management intervention on rTL between the control and intervention groups.Rural LBCS (N=103) who participated in the Nuevo Amanecer-II RCT study were asked to provide saliva samples for DNA analysis. rTL was used to assess cellular aging. DNA was extracted from buccal cells and quantitative polymerase real-time chain reaction (qPCR) was used to examine the relative telomere to single-copy gene (T/S) ratio. The mean age was 56 years, 78% had a high school education or less, and 37% reported financial hardship. Preliminary analysis (n=51) shows a mean T/S ratio of 1.24 at baseline and a mean T/S ratio of 1.26 at follow-up. This is the first study to measure rTL among rural LBCS. We demonstrate that LBCS present with short telomere lengths, which are indicative of premature biological aging. Findings from this study will uncover the impact of a peer-delivered stress management intervention on telomere length among a vulnerable population. Interventions that can mitigate stress-induced telomere length attrition have the potential to decrease breast cancer health disparities.

Understanding gender inequities regarding water security in the Choco Region of Ecuador

Discipline: Health

Subdiscipline: Public Health

Natalia Patritti Cram*[1]and Barbara Piperata [2]
[1]The Ohio State University, [2]Faculty

Abstract: Water insecurity is defined as “insufficient and uncertain access to adequate water for an active and healthy lifestyle”. Access to water is essential for a healthy lifestyle. It is ideal for households to have stable access, to clean water always. However, around 4 billion people experience severe water scarcity at least one month per year. It is known that water scarcity in a household affects its members differently. El Choco, Ecuador has communities that lack constant access to water. This presentation will discuss how gender influences the experience of water insecurity in a household. To do this, we will use quantitative, qualitative, and ethnographic tools to measure the extent of water insecurity in households in El Choco. Using surveys, we will assess the water access in the household. The water quality of the access points will be evaluated through quantitative measures. To understand how the members of the household perceive water scarcity, we will do a rapid ethnographic assessment. We predict that water scarcity affects the members of the household differently on the role of the individual in the household, these roles are often, gender assigned.

Multiple Myeloma Tumor Gene Expression to Predict Clinical Outcomes

Discipline: Health
Subdiscipline: Medicine

Camila Nieto*[1], Nicola J. Camp [2], Brandt Jones[3], Michael Madsen[4], Brian Avery [5]
[1]University of Utah, [2]Professor, Internal Medicine, [3]Lab Manager, [4]Biostatistician, [5]Biostatistician

Abstract: Multiple myeloma (MM) is a malignancy of plasma cells in the bone marrow. Incidence continues to increase, and although treatments have improved, most patients do not survive beyond 5 years. Identifying high-risk groups is a critical need. SPECTRA is a promising new statistical technique that characterizes global gene expression (the transcriptome) of a tumor into various tumor dimensions. Dimensions can then be used in prediction modeling to identify high and low-risk groups. Publicly available transcriptome data from 768 patients in the international CoMMpass study, 39 MM spectra, were derived. Each patient received a unique spectra profile (barcode). Spectra-identified risk groups are used in prediction modeling for survival and time to treatment failure. In this way, a patient's tumor transcriptome can be used to predict their risk for mortality and their response to treatment. To replicate CoMMpass data findings, we are collecting and processing local biological samples from MM patients at Huntsman Cancer Hospital. We collect bone marrow, whole blood, and saliva. Bone marrow is cell-sorted to identify tumor (CD138+) cells. DNA and RNA are extracted and sequenced to generate transcriptome data. A SPECTRA barcode is then calculated. This technique provides an improved understanding of MM by characterizing the tumor. Our future research will include an investigation of whether inherited variations (in normal DNA) are linked to the risk of particular characteristics of MM. We are pursuing the SPECTRA technique in several other cancers.

Uncoupling Protein 1-Independent Browning Effects of Eicosapentaenoic Acid in Subcutaneous Adipose Tissue of Diet-induced Obese Female Mice

Discipline: Health
Subdiscipline: Medicine

Jose Andrade*[1], Yujiao Zu [2], Naima Moustaid-Moussa[3], Mandana Pahlavani[4], Latha Ramalingam [5], Shane Scoggin[6]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech, [4]Texas Tech University, [5]Texas Tech University, [6]Texas Tech University

Abstract: Obesity is a major health issue in the US which can be combatted by browining, activation and recruitment of thermogenic cells in white subcutaneous adipose tissue (SAT) mediated by uncoupling protein 1 (UCP1). We previously reported that the omega 3 fatty acid eicosapentaenoic acid (EPA) protects against obesity independently of UCP1. In this study, we focused on investigating the role of EPA and UCP1 in SAT browning in female mice and whether these effects are temperature-dependent. We hypothesized that EPA promotes SAT browning at both ambient and thermoneutral environments, independently of UCP1. Female Wild-type (WT) and UCP1 Knock-out (KO) littermates were housed at ambient temperatures (22 °C) or thermoneutrality (28-30 °C) and fed a high fat (HF) diet (45% kcal fat) supplemented with or without EPA (36g/kg) for 14 weeks. Body weight and food intake were measured weekly, and thermogenic gene and protein expression levels were assessed in SAT. Data were statistically analyzed via three-way ANOVA using GraphPad Prism software. Mice at thermoneutrality had significantly higher weight gain(p<0.05), without differences in food intake. The mRNA levels of brown fat markers (Dio2 and Cidea), brown-fat adipokines (batokines Bmp8b and Fgf21), and lipid-metabolizing markers (Cpt1b and Gpd1) were all significantly upregulated in KO mice at ambient temperature. There were no significant differences between HF and EPA groups. Female mice lacking UCP1 were protected from diet-induced obesity and had higher SAT browning at ambient temperature More genes will be measured to understand the mechanisms mediating effects of EPA and UCP1 in SAT browning.

The Dual Delivery of Y15 and Metformin in a PLGA Scaffold for the Treatment of Platinum Resistant Ovarian Cancer

Discipline: Health
Subdiscipline: Medicine

Viviana Villalobos*[1], Hannah Obregon[2], Emily Jordan[3], Marco Arriaga[4], Dr. Sue Anne Chew[5]
[1]The University of Texas at Rio Grande Valley, [2]The University of Texas at Rio Grande Valley, [3]The University of Texas at Rio Grande Valley, [4]The University of Texas at Rio Grande Valley, [5]The University of Texas at Rio Grande Valley

Abstract: Ovarian cancer is the fifth leading cause of cancer mortality among women in the US. High mortality is linked to resistance to platinum compounds. Currently there is no treatment for platinum resistant ovarian cancer (OCpt). Platinum resistance shows increased activity of focal adhesion kinase (FAK). Y15 is a FAK inhibitor and increases OCpt sensitivity to chemotherapy. Metformin induces apoptosis, has no increased cytotoxicity, and works synergistically with Y15 in OCpt cells. Biomaterial scaffolds deliver drugs locally, maximizing drug concentration and bioavailability while minimizing systemic toxicity. PLGA polymer has excellent biocompatibility, versatility, and a tailorable degradation rate. The objective of this study is to utilize biomaterials as a dual drug delivery system and investigate if the combined delivery of Y15 and Metformin would result in synergistic effects on cell viability. A mold-less technique combining PLGA and the drugs in tetraglycol were injected into PBS to form a globular scaffold. An MTT assay was used to analyze cell viability in OCpt OVCAR3 cells at an absorbance of 570nm with a microplate reader. Metformin and Y15 resulted in cell viabilities of 66% and 54%, respectively. When combined, the viability decreased to 23%. In studies with the fabricated PLGA scaffolds, cell viabilities were 74% and 89% for Metformin and Y15. When combined, cell viability decreased significantly to 5%. The delivery of Y15 and Metformin in a biomaterial scaffold can result in a synergistic effect on cell viability and thus, can be a promising approach for the treatment of OCpt.

Including International Perspectives in the Development of the Nurture Neurodiversity App

Discipline: Health

Subdiscipline: Other Health

Lois Adrianne Umali*[1], Maria Resendiz[2], Micaela Vargas[3]
[1]Texas State University, [2]Texas State University, [3]Texas State University

Abstract: 1 in 100 children are diagnosed with autism spectrum disorder (ASD). Participating in social situations is a challenge for people with ASD. Identifying emotions is difficult for most people with ASD. A collaboration between Communication Disorders and Engineering aims to develop an app that identifies emotions for people with ASD. The Nurture Neurodiversity app uses machine learning to teach the Nurture Neurodiversity app to identify the seven universal emotions (happy, sad, angry, surprise, disgust, neutral, fear) using visual, auditory, and gestural information. Considering the end user is key to creating an app that will meet the real-world needs of people with ASD. Interviews were conducted with people with ASD, family members of people with ASD, and therapists who work with people with ASD in the United States and the Philippines. The long-term goal for the Nurture Neurodiversity app is to provide global access to people with ASD, their family members, and therapists with whom they work. Preliminary findings show that in both the United States and the Philippines, early access to services is key to better long-term outcomes. In the Philippines, people wanted more access to resources and individualized services. In the United states, cost of resources and lack of advocacy were mentioned as key barriers. Considering the perspectives of people from the United States and the Philippines, the Nurture Neurodiversity app will reduce financial and geographic barriers by being available at no-cost for download on smart devices without compromising the technological development of the Nurture Neurodiversity app.

Examining Potential Inequities in the USDA Nutrition Programs Serving Indigenous Communities through Regression Analysis

Discipline: Health
Subdiscipline: Other Health

Kelly Beym*[1]and Cindy Farley[2]
[1]New Mexico State University, [2]Native American Agriculture Fund

Abstract: The Food Distribution Program on Indian Reservations (FDPIR) offers nutritional assistance to households living on or near reservations that meet income eligibility requirements. FDPIR distributes monthly food boxes with federal commodities and other food items as available whereas the Supplemental Nutrition Assistance Program (SNAP) disperses a monetary monthly benefit on an Electronic Benefit Transfer (EBT) card. SNAP and FDPIR are only two of 15 USDA Food and Nutrition Services Programs providing nutrition assistance for food insecure (FI) households in the United States. Currently, the CFR regarding FDPIR outlines a “Prohibition on Dual Participation” stating clients may participate in either FDPIR or SNAP, but not both simultaneously. However, one in four American Indian and Alaskan Natives (AIAN) endure the impacts of food insecurity, double that of the national rate while research also shows that SNAP can reduce food insecurity by up to 30%. The objective of this research is to determine regressors that explain the variation in monetary food benefits for FDPIR and SNAP, independently, to find similar explanatory variables by utilizing regression analysis. We seek to investigate each program's monetary food benefits as a function of variables assumed to influence federal nutrition assistance, such as FI rates, unemployment, participation and recessions. Considering FDPIR’s prohibition on dual participation with SNAP, it is vital to ensure that if these restrictions are in place, equity must also hold a solid ground. The goal is to utilize

these preliminary findings to advocate policy change in the upcoming renewal of the Farm Bill in 2023.

The Assessment of Lower Extremity Range of Motion in Division III Collegiate Rodeo Athletes: Comparison of Goniometry, Manual Muscle Testing, and Overhead Squat.

Discipline: Health
Subdiscipline: Other Health

Brandon Mayers*[1]and Dr Shanna Moody[2]
[1]SUL ROSS State University, [2]Kinesiology and Human Performance

Abstract: Collegiate rodeo athletes are a unique group of competitors. While they compete for and represent their college in competition, due to the financial nature of the sport, rodeo it is not considered an NCAA sport. Therefore, these athletes do not receive training, medical attention, or other institutional support provided to traditional sports' athletes. Additionally, there is little research or data collected on these athletes. Evidence suggests that injury pathologies to the shoulder, hip, knee, and ankle have a correlation with limited muscular flexibility and range of motion deficits based on goniometry results. The purpose of this study is to identify the relationship between lower extremity range of motion and posture dysfunction by obtaining baseline joint goniometric measurements, muscular imbalance, and strength in division three collegiate rodeo athletes by performing goniometry, manual muscle testing, and an overhead squat assessment.This research will provide baseline data to identify limitations, compare rodeo athletes to other sports, and to create corrective exercise programming. It is hypothesized that collegiate rodeo athletes will score below the normal range on goniometry measurements on dorsiflexion and knee extension and that the most common postural dysfunction to be knee valgus with heel rising. The relationship of lower extremity range of motion with injuries in collegiate rodeo athletes will help bring awareness that these athletes' bodies are potentially movement compromised and warrant support services from their university to decrease injury risk.

Hepatic Effects of Fish Oil in Male UCP1-Deficient Mice at Thermoneutrality

Discipline: Health
Subdiscipline: Public Health

Kirk Balderas*[1]and Naima Moustaid-Moussa[2]
[1]Texas Tech University, [2]Texas Tech University

Abstract: Nonalcoholic fatty liver disease(NAFLD) is a common comorbidity of obesity characterized by an accumulation of triglycerides(TG) in the liver. Previous studies in our lab have shown fish oil(FO) attenuates adiposity and fatty liver in mice fed a high fat diet(HF; 45% kcal fat). These improvements may be mediated through Uncoupling Protein 1(UCP1), which was upregulated by FO in brown adipose tissue(BAT). Therefore, we sought to determine the metabolic effects of FO in livers of UCP1 knockout mice fed a HF diet without fish oil(KO-HF) or with fish oil(KO-FO) for 14 weeks in a thermoneutral environment(28º-30ºC). We measured body weight(BW), TG content and conducted gene expression analyses in liver tissues from these mice. FO significantly reduced hepatic TG despite no significant differences in BW. Hepatic RNA sequencing was conducted to determine differentially expressed genes(DEG) between KO-HF and KO-FO. Ingenuity Pathway Analysis®(IPA) was used for functional analyses and interpretation of significantly altered pathways relevant to NAFLD and obesity. We identified pathways that may be related to the reduced TG. One pathway, fatty acid β-oxidation, a pathway that breaks down fatty acids to create energy, was significantly upregulated in the KO-FO group. IPA identified multiple genes such as Ehhadh, Acox1, Pex5, Pparα, and Cpt1 and Cpt2, all of which are involved in fatty acid oxidation. Using western blotting and gene expression we are currently validating these findings. In summary, FO is effective at improving hepatic steatosis in the absence of UCP1, independently of changes in BW, in part by upregulating hepatic lipid oxidation.

Characterization of the distribution and roles of B cells in soft-tissue sarcoma

Discipline: Health
Subdiscipline: Medicine

Thien Nguyen*[1], Joseph Kendal [2], Michael Shehata[3], Serena Lofftus[4], Nicholas Bernthal [5], Fritz Eilber[6], Anusha Kalbasi[7], Joseph Crompton[8]
[1]University of California, Los Angeles, [2]University of California, Los Angeles, [3]University of California, Los Angeles, [4]University of California, Los Angeles, [5]University of California, Los Angeles, [6]University of California, Los Angeles, [7]University of California, Los Angeles, [8]University of California, Los Angeles

Abstract: Tumor-infiltrating lymphocytes are an important component of the tumor microenvironment and have shown to play a critical role in regulating tumor progression. B lymphocytes are a subset of tumor-infiltrating lymphocytes, but whether B lymphocyte populations play a role in anti-sarcoma immunity is not well understood. It has recently been discovered that the circulating B cell compartment is altered in chronic inflammatory conditions in pathologic contexts such as infection and autoimmunity. A link between chronic antigen stimulation and expansion of B-cells has been shown to play a central role in the induction of anti-humoral immunity, but this population has not been explored in the chronic inflammatory sarcoma microenvironment. For this reason, characterizing the difference of B-lymphocyte compartments between sarcoma patients and healthy individuals, and a deeper analysis of the role of B-lymphocyte subsets in cancer progression, needs to be conducted. We hypothesize the number of B cells is increased in soft-tissue sarcoma patients compared to healthy individuals and B cells play a critical role in the pathophysiology of soft-tissue sarcoma. To examine the alteration in the number of B-lymphocytes, we isolated peripheral blood mononuclear cells and tumor-infiltrating lymphocytes and performed flow cytometry to compare the percentage of B cells in soft-tissue sarcoma patients and healthy individuals. The flow cytometry data shows an expansion of B cells in soft-tissue sarcoma patient samples. Using B-cell receptor-triggered Ca2+ mobilization and cytokine production assays, we will evaluate functional properties of B cells in the sarcoma microenvironment. Our findings might have implications for anti-sarcoma humoral immunity.

Effects of pre-workout supplementation on muscular strength, muscular endurance and self-rated performance in college age women during menstruation

Discipline: Health
Subdiscipline: Public Health

Emily Jillson*[1]and Christopher Herrera [2]
[1]Sul Ross State University, [2]Sul Ross State University

Abstract: Almost all female athletes report menstrual cycle-related symptoms, and 67% of them consider these symptoms as significant performance impairments (Findlay et al. 2020). Recent studies have demonstrated the use of multi-ingredient pre-workout supplementation (MIPS) prior to exercise improves energy, focus and performance in both upper and lower body resistance exercises. Although some benefits have been found, there appears to be a placebo effect, and the effect in women, especially during menstruation is greatly unknown. Therefore, the purpose of this study is to determine the effects of MIPS, if any, on resistance training exercises in women during menstruation. The study will test the effects of caffeinated-MIPS vs placebo on a resistance training protocol consisting of max bench press and back squat (1RM), followed by a repetition to failure (RTF) at 50% max in thirty college female athletes. Self-rated energy, focus and performance will be compared between conditions using a 10cm visual analogue scale. The study will follow a randomized control-group, pretest-posttest design. It is hypothesized that the caffeinated pre-workout supplement taken 30min prior to resistance training exercise will elicit a greater improvement in 1RM and RTF as well improve self-rated energy, focus and performance. The potential findings of this study would benefit women that regularly exercise or train for sports during menstruation.

The Effects of Cannabidiol (CBD) on Inflammatory Responses in Epithelial Cells

Discipline: Health
Subdiscipline: Medicine

Nicole Shock*
Fort Lewis College

Abstract: With the increase of knowledge about the detrimental effects of opioids and the use of herbal medication becoming more relevant, the use of cannabidiol (CBD) compounds need proper scientific evaluation. Previously cannabis sativa plant extracts have been shown to decrease inflammatory responses and are currently used to ‘treat’ different conditions such as arthritis. Proper dosing with cannabis and what type of CBD extract is effective need evaluation. There are pure cannabidiol extracts and different grades of extracts with multiple plant components. The purpose of these studies was to learn more about what dosage of CBD is effective and safe for human cells culture and to determine which type of cannabidiol extract is most effective at reducing pro-inflammatory cytokine production in vitro . As demonstrated in this paper, the effects of CBD on inflammatory responses in human normal and carcinoma epithelial cells can be partially evaluated through cytokine analysis and viability assays. This study demonstrates that in both types of epithelial cells with the addition of cannabidiol products in vitro the production of inflammatory cytokines was inhibited or promoted by varying the cannabinoid and cell model. For example, the human intestinal epithelial carcinoma cell line (T84) demonstrated essentially no response to the varied CBD products regarding production of Interleukin-6 (IL-6) in stark comparison to normal human intestinal epithelial cell line (HIEC-6). Whereas HIEC-6 cells demonstrated an increase in MIP-1a with the CBD products and T84 cells a marked drop in MIP-1a expression across the CBD products.

Influences of Benzophenone-3 on the Reproductive Physiology of Yellowfin Tuna in Oʻahu Seawaters

Discipline: Health
Subdiscipline: Medicine

Pashyn Morimoto*
University of Hawaii West Oahu

Abstract: Each year, Hawaiʻi sees an average of more than 10 million tourists; due to beaches and other outdoor activities attracting visitors, sunscreen use in Hawaiʻi is high. Active ingredients in sunscreens are examples of chemicals detected in seawater; sunscreen's active ingredients are found to have negative effects on aquatic biota including changes in morphologies, reduced population growth, and changes in biochemical markers. The research aims to investigate the influence of benzophenone-3 (BP-3) on the reproductive physiology of yellowfin tuna in Oʻahu seawaters. BP-3, an effective UV filter commonly used in sunscreens, washes off easily in water and infiltrates aquatic ecosystems. Due to human's continuous interactions with coastlines, non-natural chemicals have a constant pathway into the environment. Sunscreens containing BP-3 are proven to have negative effects on the morphologies, population growth, and reproductive physiologies of various aquatic species, but local effects have yet to be identified. To investigate effects on Oʻahu, Hawaiʻi, local fishermen will be employed to catch yellowfin tuna, the researcher will collect blood from the fish and collect seawater samples where fish are caught. Reproductive effects will be assessed using a vitellogenin assay with blood plasma samples from male yellowfin tuna. Based on results from previous studies, data from the research will likely show above-average levels of vitellogenin protein present in the blood plasma of males. If true, results could indicate significant external exposure to BP-3; thus raising concerns for changes in reproductive physiologies of Oʻahu yellowfin tuna as well as food and economic security in Hawaiʻi.

Evaluating the immunogenicity and efficacy of a novel Zika vaccine

Discipline: Health
Subdiscipline: Other Health

Manette Tanelus*[1], Krisangel López [2], Shaan Smith[3], John A. Muller[4], Danielle L. Porier [5], Dawn I. Auguste[6], William B. Stone[7], Albert Jonathan Auguste[8]
[1]Virginia Polytechnic Institute and State University, [2]Virginia Polytechnic Institute and State University, [3]Virginia Polytechnic Institute and State University, [4]Virginia Polytechnic Institute and State University, [5]Virginia Polytechnic Institute and State University, [6]Virginia Polytechnic Institute and State University, [7]Virginia Polytechnic Institute and State University, [8]Virginia Polytechnic Institute and State University

Abstract: Flaviviruses are a genus of mosquito-borne viruses that are nearly globally distributed, and infection can result in life-threatening diseases. Zika virus (ZIKV) is an RNA virus belonging to this genus that has been linked to Guillain Barré Syndrome (a debilitating autoimmune disorder that affects the nerves) in adults and congenital birth defects including microcephaly (a neurodevelopmental disorder) in infants. Insect-specific flaviviruses (ISFVs) are viruses that infect mosquitoes but do not impact human health. Aripo virus (ARPV) is a recently discovered ISFV isolated in Trinidad in 2008. We developed a chimeric vaccine for Zika (i.e., Aripo-Zika) by substituting genes of ZIKV into the ARPV genome. Thus, removing the virus' ability to replicate while also providing immunogenicity. Here, we explore and optimize the safety and efficacy of Aripo-Zika (AZ) vaccination by determining the optimal dosage regimen, exploring the effects of boosters, and evaluating the likelihood of maternal antibody transfer during gestation in murine models. Our results indicate a near-linear relationship between increased dose and immunogenicity, with 10 10 GC/mL being the most effective dosage. The inclusion of boosters increased the immunogenicity of Aripo-Zika. Passive transfer of maternal antibodies to pups resulted in complete protection from a lethal ZIKV challenge (P=0.001). In vitro co-infection of ZIKV with ARPV, and ZIKV with AZ in African green monkey kidney cells (i.e., Vero76) indicated ARPV and AZ remain incapable of replication in vertebrate cells. Altogether, our data suggest that the insect-specific platform is a safe and effective strategy for the development of flavivirus vaccines.

The effect of different sanitation treatments on the frequency of Listeria monocytogenes detected on non-food contact surfaces in apple packinghouses

Discipline: Health
Subdiscipline: Public Health

Marysabel Mendez Acevedo*[1], Jasna Kovac[2], M. Laura Rolon[3], Priscilla Sinclair[4], Dumitru Macarisin[5], Luke F Laborde[6]
[1]Penn State University, [2]The Pennsylvania State University, [3]The Pennsylvania State University, [4]The Pennsylvania State University, [5]U.S. Food and Drug Administration-Center for Food Safety and Applied Nutrition, [6]The Pennsylvania State University

Abstract: Listeria monocytogenes is a pathogenic microorganism that can contaminate fruits and vegetables. To control this pathogen in fresh fruit, effective cleaning and sanitizing procedures must be applied in fruit packinghouses. The aim of this research was to evaluate the effect of four cleaning and sanitizing treatments on the microbiota and L. monocytogenes in three apple packinghouses. Over two packing seasons, we sampled five sites underneath a packing line using sterile 3M sponges. Sampling was carried out before and after application of four sanitation treatments. Treatment 1 (T1) was a baseline treatment already practiced by facilities. Treatments T2, T3, and T4 included an application of a dewaxer, alkaline chlorinated cleaner, and peracetic acid. T3 had an additional application of an acid cleaner and T4 included the application of a biofilm remover. Collected samples were analyzed to determine the aerobic plate count (APC) and detect L. monocytogenes using the FDA BAM protocols. APCs before and after each treatment were statistically compared using a t-test. Statistical differences in the frequency of L. monocytogenes detection before and after each treatment were assessed using chi-square. The mean APC values were significantly (p<0.05) reduced by an average of 0.53, 1.28, 1.82, and 2.12 log 10 CFU/sponge after applying T1, T2, T3, and T4, respectively. However, T4 was the only treatment that reduced (p<0.05) the frequency of L. monocytogenes. This data demonstrates that even though all sanitation treatments administered reduced aerobic bacteria, the application of the biofilm remover achieved substantial reduction of L. monocytogenes on non-food-contact surfaces.

Greater Exposure to Ambient Particulate Matter (PM 2.5) is Associated with Higher Insulin Secretion in Ethnic Minority Children in Los Angeles

Discipline: Health
Subdiscipline: Public Health

Karina Barragan*[1], Claudia Toledo-Corral[2], Marc Weigensberg[3]
[1]California State University, Northridge, [2]California State University, Northridge, [3]University of Southern California

Abstract: Recent epidemiological studies suggest that long-term exposures to air pollution such as particulate matter with aerodynamic diameter <2.5microns (PM2.5) has adverse effects on glucose homeostasis. The objective of this study was to determine if PM2.5 was associated with type 2 diabetes (T2D) risk factors which include acute insulin response (AIR), insulin sensitivity (SI), and disposition index (DI) in minority overweight children. Participants (N=135, M age = 14.6 ± 2.8 years; 62.3% male; 62.3% Latinx) from the Diabetes Risk due to Ectopic Adiposity (DREAM) study were assessed for glucose and insulin values during an intravenous glucose challenge were then used in minimal modelling (MinMod Millennium) for determination of SI, AIR, and DI. Self-reported mailing addresses were geocoded to identify census tract number and associated PM2.5 exposure derived by CalEnviroScreen 3.0. Multivariable linear regression was used to test relationships while controlling for age, ethnicity, sex, and total body fat percentage (by DEXA). Higher PM2.5 exposure was associated with higher AIR (β=0.181, 95%CI= 0.001, 0.361, p=0.049) after adjusting for covariates. There was an inverse, but not significant association between PM2.5 and SI (β= -0.178, 95%CI= -0.374, 0.018, p=0.075) and DI (β= 0.001, 95%CI= -0.167, 0.176, p=0.959). Our results suggest that higher exposure to ambient air pollutant PM2.5 may have adverse effects on metabolic health in the form of lower insulin sensitivity and higher insulin secretion. More importantly, using a readily accessible pollution exposure database could be used to assess possible metabolic risk in urban populations that may be at high-risk for T2D.

Targeting the RXR Pathway to Inhibit HER2+ Breast Cancer Cell Growth

Discipline: Health
Subdiscipline: Medicine

Autumn Sunderland*[1], Powel H. Brown [2], Cassandra Moyer[3], Abhijit Mazumdar[4]
[1]University of Toledo, [2]MD Anderson Cancer Center, [3]MD Anderson Cancer Center, [4]MD Anderson Cancer Center

Abstract: Human epidermal growth factor receptor 2 (HER2) is a tyrosine kinase receptor. HER2+ breast cancer causes epithelial cell growth and differentiation and has a higher predisposition to metastasize to the brain. The RXR agonists (or “rexinoids”) Bexarotene and LG10068, have been shown to prevent HER2+ breast cancer in mice. The drug IRX-4204 is a second generation rexinoid. We are investigating whether IRX-4204 will suppress the growth of established breast cancer using HER2+ vs. HER2- breast cancer cell lines. For this study, we hypothesized that the growth of HER2+ breast cancer cell lines will be suppressed by the rexinoid IRX-4204 . To test this hypothesis, we ran a series of experiments to determine the effect of IRX-4204 on the growth of a panel of breast cancer cell lines. We tested the effect that IRX-4204 (at 1 uM dose) has on the cell growth of HER2+ and HER2-negative breast cancer cell lines. Cell lines used were MCF7 (ER+, HER2-), MDA361 (ER+, HER2+), SkBr3 (ER-, HER2+), and AU565 (ER-, HER2+). IRX-4202 suppressed the growth of the MDA361 HER2+ cell line, but did not suppress the growth of a MCF7 HER2-negative cell line. Experiments testing the sensitivity of AU565 and SkBr3 cell line are ongoing. The growth of the HER2-positive breast cancer cell line, but not the HER2-negative cell line was suppressed by IRX-4204. Based on our results, IRX-4204 may be an effective drug to inhibit the growth of HER2+ breast cancer cell lines.

Determining Implementation Barriers to Project Take CHARGE: A Campus-based Intervention to Reduce the HIV/AIDS Burden Among African American Students

Discipline: Health
Subdiscipline: Public Health

Alyssa Bernadette Cahoy*[1], Rhonda Holliday [2], Samantha Martin[3]
[1]Rice University, [2]Morehouse School of Medicine, [3]Morehouse School of Medicine

Abstract: Black and African Americans face the most severe human immunodeficiency virus (HIV)/acquired immune deficiency syndrome (AIDS) burden among racial and ethnic groups in the United States (US). There have been increased HIV rates among students attending historically Black colleges and universities (HBCUs), which are often located in underserved areas with high poverty levels. Limited information is available regarding the development and evaluation of HIV testing and education strategies at HBCUs. This study describes institutional barriers (administrative capacity, stigma, etc.) to the implementation of a HIV testing strategy and educational intervention for Black and African American college students. Administrative personnel, faculty, and staff at four participating institutions in rural and urban Georgia were recruited to participate in semi-structured interviews through purposive sampling. In accordance with Braun and Clarke's six-phase thematic analysis approach, patterns in transcript content were organized into codes with working definitions. Data from the qualitative interviews revealed four emergent themes that indicated barriers to the implementation of the HIV campus intervention: (1) stigmatizing views surrounding sexual health, (2) administrative processes and priorities, (3) difficulty with logistical operations in resource-constrained settings, and (4) inconsistent marketing and outreach strategies. While there are several institutional, cultural, and logistlcal factors to consider in program implementation, partnering with HBCUs and other minority-serving institutions (MSIs) could prove an effective strategy for facilitating HIV risk reduction. Further research is needed to assess how barriers may be systematically addressed and to develop a translational toolkit to disseminate the evidence-based HIV intervention to other MSIs across the nation.

A bacterial operon is necessary for immune cell activation via the inactivation of anti-inflammatory compounds

Discipline: Health
Subdiscipline: Medicine

Lorenzo Ramirez*[1], Margaret Alexander[2], Peter J. Turnbaugh[3]
[1]Department of Microbiology & Immunology, University of California San Francisco, San Francisco, CA 94143, USA / San Francisco State University, [2]Department of Microbiology & Immunology, University of California San Francisco, San Francisco, CA 94143, USA, [3]Department of Microbiology & Immunology, University of California San Francisco, San Francisco, CA 94143, USA. and Chan Zuckerberg Biohub, San Francisco, CA 94158, USA

Abstract: Human gut microbiota have been linked to immune function, and researching these bacterial-host interactions are essential for understanding and improving treatment of various diseases. Eggerthella lenta , a prevalent member of the human gut microbiota, is enriched in human inflammatory diseases. The cardiac glycoside reductase (cgr) operon of E. lenta strain 2243 activates inflammatory T helper subset, Th17 cells, by lifting inhibition of transcription factor Rort and has been shown to inactivate IL-17a inhibitors in bacterial brain heart infusion (BHI) media. Colonization of mice with E. lenta strains that naturally vary in the presence of the cgr operon led to the expected differences in Th17 cell activation; however, due to the inability to make targeted deletions in E. lenta and the differences in strain gene content, the necessity of the cgr operon is not established. Here, we show that the cgr operon of E. lenta 2243 is necessary to deactivate IL-17a inhibiting compounds in BHI. We found that cgr knockout E. lenta 2243 (Δ cgr) resulted in less Th17 activation compared to wild-type E. lenta 2243 (WT). Furthermore, IL-17a levels of Th17 cells were enriched in the presence of BHI cultured WT supernatant. Our results show that the cgr operon present in E. lenta is essential in deactivating

IL-17a inhibitors. We anticipate this work will be integral in identifying IL-17a inhibitory compounds present in BHI. Identifying these compounds may provide insight into endogenous immunomodulatory IL-17a inhibitors metabolized by members of the microbiota that may be present in humans.

Bottlenose Dolphins in the Texas Coastal Bend: Population abundance using photo-identification

Discipline: Life Sciences

Subdiscipline: Marine Sciences

Ally Wilkins*[1]and Dara N. Orbach[2]

[1]Texas A&M University - Corpus Christi, [2]Texas A&M University - Corpus Christi

Abstract: Bottlenose dolphins (Tursiops truncatus) are the only marine mammal species residing in the Texas Coastal Bend. This population of dolphins has been identified as imperiled by the National Oceanic and Atmospheric Administration, yet no research has been published on the population since 1983. As the Texas Coastal Bend has subsequently expanded dramatically in industrial growth with associated anthropogenic disturbances to marine life, it is important to monitor the local dolphin population to inform policymakers of conservation mitigation needs. The population abundance of dolphins inhabiting the Texas Coastal Bend was determined by counting the number of animals based on unique markings on their dorsal fins captured in photographs. Since 2018, boat-based photo-identification surveys (n = 63) were conducted quarterly to sample and resample dolphins following Polluck's Robust Design model. Photographs were quality control checked, cropped, and matched by a minimum of two researchers. The population of bottlenose dolphins is estimated to consist of 858 individuals, indicating a substantial population growth from the 281 dolphins reported in 1977. Of the 858 individuals, 415 individuals were photographed in Corpus Christi Bay, 409 near Port Aransas/Redfish Bay, and 34 in both bay systems. Findings from this study and additional photo-identification surveys will provide insights on the stability of the population that can be used as baseline data for conservation, including if dolphins are year-round residents and frequently inhabit areas of high vessel traffic.

Should state land in Southern California be allocated to warehousing goods or housing people? Analyzing transportation, climate, and unintended consequences of supply chain solutions

Discipline: Life Sciences

Subdiscipline: Environmental Science

Kenneth Perez*[1], Tianjun Lu[2], Jian-yu Ke (Fisher)[3], Fynnwin Prager[4], Mahmoud Salari[5], Patricia Valladolid[6], Azure Fisher[7]

[1]California State University, Dominguez Hills, [2]California State University, Dominguez Hills, [3]California State University, Dominguez Hills, [4]California State University, Dominguez Hills, [5]California State University, Dominguez Hills, [6]California State University, Dominguez Hills, [7]California State University, Dominguez Hills

Abstract: California supply chain constraints have prompted investigation for short-term warehousing as a temporary solution for supply chain disruptions. During the COVID-19 pandemic, the manufacturing industry faced operational constraints from lockdowns, which were followed by rapid import demands from U.S consumers in 2021. These constraints alongside unprecedented cargo surges resulted in supply chain disruptions. California's current warehousing availability has not been sufficient to alleviate backlogged ships sitting at anchor, thereby resulting in longer waiting periods for materials and products; subsequently leading Southern California to become a significant bottleneck to the U.S. supply chain. Our goal is to investigate the land-use paradox in warehousing construction for economic (alleviating supply chain constraints), and environmental goals (traffic-related air pollution, and greenhouse gas emissions). This study will utilize literature reviews, regression models, and Geo-Spatial Information Systems to analyze available state-owned properties near congested ports. Community LINE Source Model (C-Line) system will quantify the environmental impacts of increasing warehousing operations to investigate four principal ideas (1) How would increasing warehousing affect emissions and local air quality in Port-surrounding neighborhoods, warehousing-adjacent neighborhoods, and routes in between? (2) How would increasing warehousing interplay with South Coast Air Quality Management's indirect source rules? (3) How do the reviews and potential prioritization of state-owned property for warehousing development intersect with prioritization for housing and homelessness? (4) What other potential unintended consequences may be overlooked? This study explores how to prioritize the use of state lands while considering warehousing, public and private housing, and associated climate and environmental impacts.

Understanding the mechanism by which Lis 1 activates dynein

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jennifer Rodriguez*[1], Eva Karasmanis [2], Samara Reck-Peterson[3]
[1]University of California, San Diego School of Medicine, [2]University of California, San Diego School of Medicine, [3]University of California, San Diego School of Medicine

Abstract: The microtubule motors dynein and kinesins drive intracellular transport of protein cargoes and organelles. Localization of these cargoes at the right place and time is necessary for cellular function and defects in dynein lead to diseases such as cancer and neurodegeneration. Lissencephaly 1 (Lis1) is a key regulator required for dynein's function. Lis1 gene is mutated in patients with the neurodevelopmental disease lissencephaly. Dynein motors are autoinhibited in a "Phi" conformation and undergo a series of conformational changes to form active complexes, which consist of two dynein dimers, the dynactin complex and activating adaptor(s). We and others have recently shown that Lis1 is required to form these active dynein complexes but how Lis1 activates dynein and promotes dynein motility, is poorly understood. Here, using cryo-electron microscopy, we solve a high-resolution structure of two Lis1 dimers 'wedged' on each side of an autoinhibited dynein motor dimer. Our structure reveals two new contact sites between dynein and Lis1 and is suggestive of the mechanism by which Lis1 promotes the relief of dynein autoinhibition. Using structure informed mutagenesis, we disrupted each of these sites and show that they are required for Lis1's regulation of dynein in vivo in S. cerevisiae. The in vivo significance of the mutations for Lis1's regulation of dynein were evaluated by nuclear segregation and dynein localization imaging assays. We propose that our structure represents an intermediate in dynein's activation pathway and the study of these sites sheds light into how Lis1 regulates dynein and promotes intracellular transport.

Catecholamine Signaling in CA1 Correlates with Novelty, Movement, and Sleep State

Discipline: Life Sciences

Subdiscipline: Biology (general)

Meenakshi Kakani*[1], Infania E Pimentel[2], Tia Donaldson[3], Samuel A. McKenzie[4]
[1]Virginia Commonwealth University, [2]University of New Mexico, [3]University of New Mexico, [4]University of New Mexico

Abstract: Norepinephrine (NE) and dopamine (DA) signaling in the hippocampus are important for normal learning and memory. Recently invented genetically-encoded fluorescent indicators of catecholamine binding allow for imaging real-time neurotransmitter dynamics. Previous microdialysis studies have found an increase in hippocampal catecholamines in response to novel environmental exposure or exercise. Since animals move in response to contextual novelty, it is unknown whether the changes in transmitter release are due to novelty per se or other changes in behavior or arousal. Outside of the hippocampus, arousal, novelty detection, reward, and sleep state are all related to catecholamine signaling. In this study, we investigated how catecholamine signaling in the hippocampus relates to novelty and movement. These variables were de-confounded by presenting novel stimuli when mice are normally at rest, thus triggering the onset of movement to explore. Mice were also presented with novel stimuli while moving across a track, thus causing mice to stop and inspect. When mice initiated exploratory movement, we found a strong increase in DA/NE with initial object presentation that decreased over time. If the response is related to novelty and not movement, we expect to see a similar catecholamine increase in our experiments in which mice stop to explore. We further predict that these novelty responses will decrease as objects become familiar. Finally, we observed increases in DA/NE binding during the transition from sleep to waking, highlighting the need for these behavioral controls. We conclude that novelty, movement, and arousal from sleep all contribute to hippocampal catecholamine signaling.

Diesel exhaust particles effects on lung vascular permeability of juvenile mice

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Gimarie Batista*[1], Héctor J. Rosa López[2], Nicole A. Pagán[3], Loyda B. Méndez[4]
[1]Universidad Ana G. Mendez, Carolina Campus, [2]Universidad Ana G. Mendez, Carolina Campus, [3]Universidad Ana G. Mendez, Carolina Campus, [4]Universidad Ana G. Mendez

Abstract: Asthma is a chronic inflammatory disease that affects the lungs. Among the environmental factors associated with the exacerbation of asthma is Particulate Matter (PM). Studies have shown that PM can affect the airways through diverse mechanisms including oxidative stress, inflammation, and lung injury. Increased vascular permeability is observed in asthmatic individuals, usually preceding inflammation. Therefore, the main goal of this research is to evaluate if diesel exhaust particles (DEP), a type of PM, affect vascular permeability in the lungs. We hypothesized that exposure to DEP will increase vascular permeability in juvenile mice. To test this, both male and female naïve C57BL/6J mice (n=10/group) were exposed intranasally to saline or increasing concentrations of DEP during postnatal days (PND) 25 to 33. On PND39, mice were euthanized and the bronchoalveolar lavage fluid was collected and centrifuged. The cell pellets were further processed for differential staining to assess cellular inflammation. Meanwhile, the supernatants were used to measure albumin levels as marker of vascular permeability by means of an enzyme-linked immunosorbent assay. Our results showed that DEP exposure did not increase albumin levels when compared to controls, even though it caused an influx of proinflammatory cells into the airways. Therefore, our results suggest that DEP induced inflammation could be mediated by other mechanisms.

The effects of Particulate Matter exposure on HPA-axis activation in pre-pubertal mice

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Angelimar Ortiz*[1], Héctor J. Rosa [2], Loyda B. Méndez[3]
[1]Universidad Ana G. Mendez, Carolina Campus, [2]Universidad Ana G. Mendez, Carolina Campus, [3]Universidad Ana G. Mendez, Carolina Campus

Abstract: Ambient particle pollution is the leading environmental health risk factor worldwide. Among the adverse health effects associated with particulate matter (PM) exposure are the exacerbation and progression of respiratory, cardiovascular, and neurobehavioral conditions. Oxidative stress and inflammation are the main mechanisms by which PM induces adverse health effects. In-vivo studies have also shown that PM can activate the hypothalamic-pituitary-adrenal (HPA-axis) as part of a neuroendocrine stress response. In addition, a recent epidemiological study found an association between PM exposure and greater HPA-axis responsivity to stress in anxious adolescent girls. Therefore, the main goal of this research is to examine if exposure to diesel exhaust particles (DEP) activates the HPA-axis in juvenile female mice. We hypothesized that exposure to DEP will dysregulate the function of the HPA-axis and provoking changes in the release of corticosterone. To test this hypothesis male and female C57BL/6 mice (n=9/group) exposed intranasally to saline or increasing concentration of DEP during postnatal days (PND) 25-33. On PND 39, mice were euthanized, and serum was collected by cardiac puncture. Corticosterone levels in the serum were measured using a competitive ELISA assay. Results showed that mice exposed to DEP had significantly lower level of corticosterone when compared to controls. When assessing for sex differences, female mice had higher corticosterone levels than male at the highest DEP dose. Reductions in corticosterone levels in juvenile mice suggests that DEP exposure can dysregulate the HPA-axis, which can have implication in mental and neurological disorders.

Does diesel exhaust particle exposure cause oxidative stress in juvenile mice?

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Celiane Tapia*[1], Hector Rosa [2], Loyda B. Mendez[3]
[1]Universidad Ana G. Mendez Carolina Campus, [2]Universidad Ana G. Mendez Carolina Campus, [3]Universidad Ana G. Mendez Carolina Campus

Abstract: Ambient particle pollution is the leading environmental health risk factor associated with the exacerbation of respiratory, cardiovascular and neurological conditions among others. In urban areas, diesel exhaust particles (DEP) are main contributors to particle pollution. The main mechanisms by which DEP exerts adverse health effects are through oxidative stress, inflammation and cell injury. The objective of this study is to assess if exposure to DEP at physiologically relevant doses induces oxidative stress in the lungs of juvenile mice. To this extent, we measured nitrite, a non-volatile product of nitric oxide, as a biomarker of oxidative stress. Briefly, both female and male C57BL/6J mice (n=9/group) were treated with different doses of DEP or saline through intranasal administration during postnatal days (PND) 25-33. On PND 39 animals were euthanized and bronchoalveolar lavage fluid (BALF) was collected. The Griess Reagent Assay was used to detect nitrite in BALF samples. Results showed no significant changes in nitrite levels in groups exposed to DEP were compared to the control group In addition, no significant differences between sexes were observed. Overall, we conclude that the tested doses of DEP did not induce oxidative stress in the lungs.

CIRTS Constructs are Effective in Targeting Microsatellite Repeat Expansion Disorders

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Allison Li*[1], Gene Yeo [2], Maya Gosztyla[3]
[1]University of California, San Diego, [2]University of California, San Diego, [3]University of California, San Diego

Abstract: Microsatellite repeat expansion (MRE) disorders are caused by sequence repetitions within the human genome. These repetitions cause aberrant repeat-expanded RNA, leading to disorders such as Huntington’s disease (CAG repeat), frontotemporal dementia (GGGGCC repeat), and myotonic dystrophy (CUG repeat). One viable way to treat these diseases is to knock down the repeat expanded RNAs. A tool previously utilized for this purpose is CRISPR-Cas13d, which can target and degrade RNA transcripts. However, Cas13d is a bacterial protein and thus can cause an immune response, limiting its therapeutic utility. In contrast, CRISPR-Cas-inspired RNA targeting system (CIRTS) overcomes this limitation by engineering programmable RNA effectors from human proteins. By eliminating bacterial proteins, this strategy avoids triggering an immune response. CIRTS has previously been validated only for non-repetitive target transcripts. Thus the objective of this project is to determine the effectiveness of CIRTS in eliminating RNAs that cause MREs. To test this, we transfected HEK293T cells with three plasmids: 1) a repeat plasmid encoding 105 CAG or CUG RNA repeats, 2), corresponding guide RNAs (gRNAs) targeting these repeats, and 3) the CIRTS construct. Then we extracted RNA and performed RNA dot blots to quantify the repeat-containing transcripts. We observed a strong knockdown of CAG and CUG repeats using their appropriate gRNAs when compared to non-targeting gRNAs. In contrast, there was no significant knockdown of CAG repeats by the CUG-targeting gRNA, or vice versa, suggesting strong sequence specificity. These results demonstrate that CIRTS could be an effective RNA targeting technology in MRE disorders.

Improving Cancer Screening Accessibility, Compliance, and Equity for American Indian and Alaska Native Adults: A Scoping Review

Discipline: Life Sciences
Subdiscipline: Biology (general)

Dana Baca*[1], Dr. Kate Cartwright [2], Dr. Shiraz Mishra[3], Judith Sheche[4]
[1]Duke University, [2]University of New Mexico, [3]University of New Mexico, [4]University of New Mexico

Abstract: American Indians and Alaska Natives (AIAN) are disproportionately diagnosed with more advanced stages of screen-detectable (i.e., breast, colon-rectum, cervix) cancers because of their lower rate of screening. This late-stage disease diagnosis contributes to higher mortality rates for these screen-preventable cancers. Many interventions have been implemented to improve rates and timeliness of cancer screening in concordance with recommended guidelines. We are conducting a scoping review of the current AIAN cancer screening research to analyze the current AIAN cancer screening practices. We will analyze patterns, attitudes, and outcomes

to identify where improvements have been made and to assess factors which could still be addressed. We are using Covidence, an online software program, to facilitate this scoping review, following the PRISMA guidelines. We searched PubMed, CINAHL, and Web of Science for the following terms: “American Indian/Native American/Indigenous American'' in combination with “cancer screening/cancer prevention.” After sorting out duplicates, 979 abstracts remained that will be sorted in two stages. In stage one, team members will screen titles and abstracts for eligibility. In stage two, the eligible full-text articles will be screened again and selected for the final set of articles for the review. Finally, these articles will be analyzed for themes, patterns, and gaps. This scoping review will synthesize the current literature and help inform future aims for AIAN cancer screening research.

Investigating Non-Coding Circular RNA, Circvopp1: A Potential Regulator of Aberrant Peripheral and Central Nervous System (CNS) Immune Interactions due to Prenatal Alcohol Exposure

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ariana Pritha*[1], Michela Dell’Orco [2], Andrea Pasmay[3], Joshua J. Sanchez[4], Jacob E. Sanchez [5], Suzy Davies[6], Daniel D. Savage[7], Nikolaos Mellios[8], Erin. D. Milligan[9], Shahani Noor[10]
[1]University of New Mexico - Main Campus, [2]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [3]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA, [4]Department of Neurosciences, School of Medicine, University of California, San Diego, CA, USA, [5]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [6]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [7]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [8]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [9]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA., [10]Department of Neurosciences, School of Medicine, University of New Mexico, Albuquerque, NM, 87131,USA

Abstract: Previous studies suggest that prenatal alcohol exposure (PAE) is a risk factor for developing pathological touch sensitivity (e.g., allodynia) following minor peripheral nerve injury that is thought to be due to heightened proinflammatory peripheral and spinal glial immune activation. However, mechanisms and gene expression profiles underlying neuroimmune dysregulation and proinflammatory immune function due to PAE are poorly understood. Non-coding circular RNAs (circRNAs) are novel modulators of mRNA expression. Here, we hypothesized that dysregulation of circRNAs caused by PAE may play regulatory roles in gene expression. Our microarray data identified 15 circRNAs that were differentially expressed in blood leukocytes from adult PAE rats compared to control (Sac) rats (p <0.05) with a fold change of >1.5. Utilizing the bioinformatics software, Ingenuity Pathway Analysis (IPA), we analyzed “top networks” of the genes associated with these differentially expressed circRNAs. The bioinformatics analysis identified distinct canonical pathways including NF-κB pathway, which is activated by innate immune receptor TLR4 signaling. Interestingly, our microarray data identified the circRNA, circ-Vopp1, which originates from the Vopp1 gene and is involved in regulating the transcriptional activity of NF-κB. Therefore, using real-time PCR and melting curve analysis, our ongoing work is focused on designing primers for detecting circ-Vopp1 to validate our findings and to assess whether these primers specifically amplify the circular, but not the linear Vopp1. Together, our results suggest that circRNA dysregulation could be a potential underlying mechanism of PAE-induced neuroimmune dysregulation and circ-Vopp1 may be a novel circRNA involved in TLR4 pathway sensitization due to PAE.

After-effects of Reproduction on Energy Intake in the Olympia oyster, Ostrea lurida

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Natalie Frontella*[1], Deo Scott[2], Jacob Harris[3], Kerstin Wasson[4], Luke Gardner[5], Amanda Kahn[6]
[1]California State University - Monterey Bay, [2]University of Arkansas, [3]Moss Landing Marine Laboratories, San Jose State University, [4]Elkhorn Slough National Estuarine Research Reserve, [5]California Sea Grant, University of California, San Diego, [6]Moss Landing Marine Laboratories, San Jose State University

Abstract: Olympia oysters are an important foundation species in estuary ecosystems. In addition to providing habitat for other species, they are integral to nutrient cycling through their filtration activity. Many populations are declining, and restoration efforts are focused on re-establishing populations in their native habitats. As populations grow, it is important to assess how reintroducing a healthy population of Olympia oysters will affect existing communities. Their effects on nutrient cycling may vary throughout the year depending on seasonal variations in food availability, activity levels, and life stage. The reproductive period is energetically costly for Olympia oysters and preliminary observations suggest it affects their ability to feed. Therefore we hypothesize that the reproductive period will have direct effects on oysters' ecosystem functions. We estimate that their energy balance will shift to prioritize their needs at different times, due to the change in energy intake caused by reproduction. Energy budgets before, during, and after the spawning period was measured as a balance of energy intake via feeding, and outputs of metabolism (maintenance and growth) and excretion. We measured energy intake through feeding rates of phytoplankton (as clearance rates). Energy used for metabolism was measured as respiration using closed chamber respirometry. Energy excreted was quantified by measuring total feces and pseudofeces production. This information will present new information for understanding their energy requirements and how they allocate their energy. The differences we determine in physiology indicate effects on their surrounding community and will provide insight into their energy requirements throughout their lifetime.

Examining the synergistic effect of GCN2 inhibition and depleting asparagine in Acute Lymphoblastic Leukemia

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Rodney Claude*[1], Ji Zhang[2], Sankalp Srivastava[3]
[1]Indiana University Purdue University at Indianapolis, [2]Indiana University Purdue University at Indianapolis, [3]Indiana University Purdue University at Indianapolis

Abstract: Acute lymphoblastic Leukemia (ALL) accounts for a quarter of the cancer diagnoses in people under the age of 15. Despite the progress of ALL treatment with the use of L-asparaginase (L-ASNase) as a first-line therapy, some ALLs develop resistance to L-ASNase. L-ASNase kills ALL cells by depleting extracellular asparagine (Asn) which they require for proliferation. Asparagine synthetase (ASNS) is an enzyme that produces Asn which can lead to resistance if ASNS is highly expressed. During Asn depletion, general control nonderepressible 2

(GCN2) is activated to cause a downstream effect to increase ASNS expression. To investigate the role of GCN2 in ALL cells, we utilized GCN2ib to inhibit GCN2. Then we selected four T-ALL cell lines with different basal expressions of ASNS and exposed each cell line to four conditions (+Asn, +Asn + GCN2ib, -Asn, and -Asn + GCN2ib). Cell growth was monitored and counted over the span of 3 days. We found that GCN2 inhibitor synergistically suppressed cell growth and survival when exogenous asparagine was removed. In addition, after 24 hours of incubation in these four conditions, we extracted RNA and protein to determine the expression of GCN2 downstream effector molecules, including ASNS and ATF4. The western blot showed that ASNS expression increased in -Asn condition, but the increase was blocked when GCN2 was inhibited. These findings suggest that ASNS can be used as an indication of response to L-ASNase and that the inhibition of GCN2 can cause synergistic effects when combined with the depletion of exogenous Asn.

Lateralization of Memory Impairment in a Mouse Model of Temporal Lobe Epilepsy

Discipline: Life Sciences
Subdiscipline: Neurosciences

Cathy Dang*[1], Laura A. Ewell[2], Brittney L. Boublil[3], Gergely Tarcsay[4], Usean J. Redic[5]
[1]University of California, Irvine, [2]Assistant Professor, [3]Post-doctoral Scholar, [4]Graduate Student, [5]Undergraduate Student

Abstract: In humans with temporal lobe epilepsy (TLE), the severity of their seizures and comorbidities, such as impairments in memory, have been shown to be lateralized. Lateralization is the tendency for neural functions to be specialized to one hemisphere. To better understand the relationship between memory impairment and lateralization, we utilized a mouse model of TLE in which the epileptic focus is targeted to either the left or right hippocampus. Mice received supra-hippocampal injections of kainic acid on the left or right side ($n = 14$; 7 left-injected, 7 right-injected) and were perfused 6 weeks later. We examined histological changes in the hippocampus of epileptic mice. In right-injected mice, the CA3 area tended to be smaller than the non-injected side (paired t-test, $p \leq 0.05$), whereas in left-injected mice no difference in size was observed. These data suggest that mice with the epileptic focus on the right may show more pronounced loss of hippocampal function. Thus, we hypothesize that right-injected mice would have a greater memory impairment than left-injected mice on a spatial delayed alternation task (DAT). To test this, mice are being run on a continuous and delayed version of the task, where they must alternate between left and right turns to receive a reward. Understanding the relationship between lateralization and memory impairment in temporal lope epilepsy may help develop tailored treatments targeted at comorbidities for patients with left or right epilepsy.

Identification and characterization of the root accumulating sesquiterpenoid glycosides in the bioenergy crop switchgrass (Panicum virgatum) using metabolomics and bioassay

Discipline: Life Sciences
Subdiscipline: Biochemistry

Lina Blanco*[1], Xingxing Li[2], Robert Last[3]
[1]University of Puerto Rico, Mayaguez, [2]Michigan State University Post-Doc, [3]Michigan State University

Abstract: Switchgrass (Panicum virgatum) is a perennial grass native to North America being developed as a dedicated bioenergy crop. It has become a leading candidate to be used as feedstock for biofuel production given its high yield and capacity to be cultivated with low agronomic input in lands not suited for traditional agriculture. Previously conducted studies utilizing untargeted liquid chromatography-mass spectrometry (LC-MS)-based small molecule analysis revealed a distinctive metabolite profile in the subterrain tissues of switchgrass, with abundant steroidal saponins, sesquiterpenoids and diterpenoids. We hypothesize that these compounds play an essential part in the rhizosphere by promoting or inhibiting growth of beneficial and pathogenic microorganisms, respectively. In this study, we focused on identifying and determining the function of glycosylated compounds based on C15 sesquiterpene cores. Screening 13 switchgrass cultivars using LC-MS revealed that these sesquiterpenoids exclusively occurred in the underground tissues of upland switchgrass ecotypes. Untargeted and targeted LC-MS will be used to determine in which developmental stage these sesquiterpenes are accumulated by dividing the root into parts such as the rhizome and upper root, setting a standard for future extraction for metabolomics analyses. We will also perform fungal bioassays using six fungal species isolated directly from the switchgrass rhizosphere with purified compounds to characterize their bioactivities. The acquired knowledge demonstrates beneficial metabolites that can aid in breeding efforts aimed at developing optimized crops that show high yields without the use of chemical pesticides and fertilizers.

How seasonal thermal variation within the intertidal zone and body condition affects the thermal escape behavior of Petrolisthes cinctipes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cesar Estrada Aguila*[1]and Jonathon Stillman [2]
[1]San Francisco State University, [2]San Francisco State University

Abstract: Temperature influences population distribution, body size, metabolism, making it a driving ecological and evolutionary factor. Due to climate change, sea surface temperatures are expected to increase by 1.8-3.5 °C by the end of the century and extreme climate events are predicted to become more intense and frequent. My research seeks to understand how thermal seasonal changes and physiology can influence the thermal behavior of Porcelain crabs living in the thermally dynamic intertidal zone. I assessed temperature avoidance behaviors (escape temperatures) by using a behavioral assay and video analysis. I investigated relationships between regional weather data and under-rock microhabitat temperature to generate the ability to make predictive inferences of crab thermal avoidance and temperature fluctuations in the intertidal zone. I hypothesized that thermal avoidance varies across long-term seasonal thermal variation and during extreme heat events and that thermal avoidance is impacted by body condition. Results show that escape temperature did not vary significantly across different seasons ($P = 0.549$). Escape temperature was shown to increase as maximum habitat temperatures increases 4 days prior to conducting behavioral trials ($P = 0.01786$). This supports my hypothesis that escape temperatures increase during heating events. Body condition was shown to have no significant influence on escape temperature ($P = 1.00$). However, when observing the impact physical injuries have on escape temperature, we see that individuals' missing legs have significantly higher escape temperatures. Overall, my research will contribute to the knowledge and understanding of how marine invertebrates are affected by climate change.

Spatial Variation of Sea Star Recovery in Response to Sea Star Wasting Disease

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jonah Gier*[1]and Alison Haupt [2]
[1]The University of the South - Sewanee, Tennessee, [2]California State University, Monterey Bay

Abstract: Diseases act as ecological disturbances that can change relative species abundances and have a wide range of impacts on ecosystems. Since 2013, sea star wasting disease has caused large-scale mortality of sea stars in the eastern Pacific ocean. Along the central coast of California, one of of the sea stars most impacted by sea star wasting disease is the ochre sea star (Pisaster ochraceus), a keystone species and important shaper of intertidal communities through predation on the California mussel (Mytilus californianus). Loss of P. ochraceus in intertidal communities could lead to increases in mussel populations which might outcompete other species, such as the endangered black abalone, for crevice space. We are interested in the spatial variation of P. ochraceus recovery along central California and what factors might be driving said variation. We used swath surveys, quadrat surveys, and timed searches at low tide to obtain count and size data of all sea stars at 10 sites along the Monterey Bay area. Additionally, we used data from the Multi-Agency Rocky Intertidal Network (MARINe) to see how sea star populations and sizes have been changing over time. We found that P. ochraceus recovery is highly variable across sites and that bat stars outnumbered P. ochraceus at every site except one. Our data show that P. ochraceus densities are still low at the majority of our sites, which is concerning, given that they are keystone species and thus have a disproportionately large impact on their ecosystem.

Diving In: Annual differences in sea-ice foraging associations of breeding Adélie penguins in the Ross Sea.

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Sofia Franco Cruz*[1], Rachael Orben [2], Suzanne Winquist[3]
[1]University of Rochester, [2]Faculty at Oregon State University Hatfield Marine Science Center, [3]Graduate Student at Oregon State University Hatfield Marine Science Center

Abstract: Title: Diving In: Annual differences in sea-ice foraging associations of breeding Adélie penguins in the Ross Sea. Climate change threatens ecosystems by altering energy flow and interrupting critical biochemical and physical processes. With climate change increasing its ecological impact, it is important to describe its effect on upper trophic level predators. In Antartica, climate models suggest that increases in temperature will cause substantial changes in the timing, duration, and extent of sea-ice coverage. Describing the foraging behavioral patterns associated with the presence of sea-ice could provide insight into how Adélies interact with this habitat feature and its impact on foraging strategy. For this project, I am focusing on the importance of ice presence on the foraging behavior of Adélie penguins (Pygoscelis adeliae). Video loggers were deployed on Adélie penguins (n=51) from Cape Crozier, Antarctica during the breeding seasons of 2018/2019 and 2021/2022. The video footage was manually annotated to identify prey capture events and ice associated dives. I will assess the influence of sea-ice on behavioral patterns including the type of prey captured and average dive depth. I will also compare two years of video data and satellite images to determine annual differences between sea-ice concentration and the frequency of ice associated foraging dives. Preliminary results suggest that Adélie penguins are foraging at shallower depths when there is sea-ice present. The results of this study will help to understand the role of sea-ice in the foraging ecology of breeding Adélie penguins and the potential role climate change plays in it.

Revealing how wildfires can affect river sediments and chemistry during droughts and after precipitation

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexandra Yokomizo*[1]and Dr. John Olson [2]
[1]California State University, Monterey Bay, [2]California State University, Monterey Bay

Abstract: With climate change increasing the frequency of wildfires and droughts in California and around the world, it is vital we learn how these events interact. The River, Carmel, and Dolan Fires burned during the summer of 2020 and were followed by an abnormally dry winter. We measured nutrient concentrations and sediment sizes at three sites on the Carmel River downstream of the fires in the summer of 2021 and summer of 2022 to see how droughts change the effects of wildfires on rivers. In addition to our data, we also used the California Environmental Data Exchange Network (CEDEN) which provides us with water quality data from the Carmel River prior to the fires. We examined the impacts of wildfires on the size of sediment and nutrients concentrations using general linear models, and comparing pre- and post-fire data. At the three sites during the 2021 sampling period, the levels of nitrate were not significantly different after the fire whereas phosphate concentrations increased post-fire at both sites where phosphate was measured . We also observed that sediment sizes shifted from being dominated by cobbles before the fires to a bimodal distribution split between fines and cobbles after the fires. Despite there being little rainfall to transport nutrients and sediment, increased nutrients and fine sediment occurred downstream of the fires. By looking at pre-fire data and post-fire data, one and two years after the fire, we can see a fuller picture of the impacts wildfires can have on river sediment and water chemistry.

Revealing Novel Factors in Somatic Hypermutation

Discipline: Life Sciences
Subdiscipline: Biochemistry

Miriam Kopyto*
Yale University

Abstract: The immune system is a dynamic process involved in preventing disease and responding to foreign invaders. The adaptive branch of the immune response recognizes a broad range of pathogens and produces antibodies that bind and neutralize an antigen. Somatic Hypermutation (SHM) is a critical mechanism of adaptive immunity. SHM is responsible for introducing point mutations, insertions, and deletions into the immunoglobulin variable (IgV) regions in early B-cells. The mechanism of SHM targeting and regulation are poorly understood. The factors involved in SHM levels and targeting to the IgV locus remain elusive. We identified novel SHM regulatory factors using CRISPR-Cas9 knockout in Ramos derived Rapid Assay for Somatic Hypermutation (RASH) cell lines containing a GFP (Green Fluorescent Protein) assay for SHM activity. A CRISPR screen identified 10 statistically significant genes using the SHM-GFP assay. These 10 genes were individually knocked out in RASH cells, and results demonstrated that knockout of Retinol Dehydrogenase 13 (RDH13) and Leukocyte Receptor Cluster Member 1 (LENG1) caused a statistically significant decrease in SHM activity compared to non-targeting control CRISPR-Cas9 cells. These results indicate that RDH13 and LENG1 are involved in increasing SHM at target sequences. Little literature describes the function of RDH13 and LENG1; however, further validation and analysis of these factors can reveal potential importance in SHM regulation and mechanistic control.

Utilizing CRISPR/Cas9 to integrate N-sulfoglucosamine sulfohydrolase (SGSH) gene into Mucopolysaccharidosis type IIIA (MPS-IIIA) derived induced pluripotent stem cells (iPSC)

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jacqueline Hernandez*[1]and Dr. Michelina Iacovino [2]
[1]The Lundquist Institute, [2]The Lundquist Institute

Abstract: Mucopolysaccharidosis type IIIA (MPS-IIIA) is a fatal, inherited lysosomal storage disease that causes neurodegeneration, loss of brain volume, and neuro-inflammation defects soon after birth. MPS-IIIA patients exhibit dementia, hyperactivity, seizures, and aggressive behavior. This disorder is caused by a loss of function mutation in the gene encoding N-sulfoglucosamine sulfohydrolase (SGSH), the enzyme needed to degrade complex sugars, glycosaminoglycan (GAGs), in lysosomes. Currently, no effective treatments exist. In our current research, we utilized CRISPR/Cas9 to insert a functional copy of the SGSH gene into the safe locus, AAVS1, by nucleofection into in induced pluripotent stem cells (iPSC) derived from MPS-IIIA patients. We hypothesize that by adding a functional copy of the SGSH gene into MPS-IIIA derived iPSC this will increase the production of the SGSH enzyme to restore normal lysosomal and ultimately cell function. To test our hypothesis, corrected MPS-IIIA iPSCs were evaluated for proper SGSH integration by SGSH enzymatic assay, PCR, and Western blot. Validated corrected MPS-IIIA iPSC were then differentiated into neural progenitor cells (NPCs) and then SGSH enzyme levels were then measured. Furthermore, the NPCs were differentiated into forebrain mature neurons and astrocytes and analyzed for known markers via immunohistochemistry. Preliminary results suggested that MPS-IIIA iPSC corrected cell lines restore SGSH enzyme levels in comparison to both the wildtype and MPS-IIIA disease lines. Further investigation to analyze the implantation of NPCs in immunodeficient mice is needed to confirm the use of corrected MPS-IIIA iPSC as a potential therapy.

Characterization of a novel role of citrate mediated root development in Arabidopsis thaliana.

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Jesus Peng Zhao*[1], Alexandra Jazz Dickinson [2], Tao Zhang[3]
[1]University of California, San Diego, [2]University of California, San Diego, [3]University of California, San Diego

Abstract: Root development is an adaptative process that plants modulate to survive in a variety of different environments and conditions. Anchor roots and root hairs are important root structures that plants rely on to withstand natural adversities such as drought, nutrient deficiency, and soil disruption. Anchor roots emerge from the junction between the root and the shoot, often as a response to nutrient deficiency and environmental stress. Root hairs are elongated cells that increase the root-soil surface and facilitate plants to absorb nutrients and water. However, the molecular mechanisms underpinning the development of these structures remain unclear. Here, I report a role for citrate in the pathways controlling the formation of these two important root structures in the model organism Arabidopsis thaliana that differ from its conventional role in ATP generation. Using buffered exogenous treatments, it was found that increasing citrate concentrations induce anchor root formation and suppress root hair growths. By characterizing genetic report lines for major plant hormones such as auxin, cytokinin and abscisic acid, the changes in hormonal levels uncovered indicate a crosstalk of signaling pathways with citrate. Furthermore, histochemical staining for reactive oxygen species (ROS) revealed that citrate causes significant changes in ROS concentration in developing roots. Finally, citrate treatments improve vigor in plants grown in phosphate deficient soils without relying on unsustainable chemical fertilizers. Therefore, understanding these uncharacterized mechanisms that enable plant survival is not only important for improving agricultural practices today but might even prove vital in a near future threatened by climate change.

Assessing Cognitive Impulsivity in 3 Isogenic Mouse Populations using an Automated Maze-based Delay Discounting Task

Discipline: Life Sciences

Subdiscipline: Neurosciences

Brittney Mazen*[1]and David Linsenbardt[2]

[1]Coastal Carolina University, [2]University of New Mexico

Abstract: Impulsivity is thought to be a risk factor for the development of Substance Use and Alcohol Use Disorders (SUDs/AUDs). Furthermore, it has been shown that genetics plays a role in determining both impulsivity levels and SUD/AUD risk. Thus, identifying the ways in which genes control impulsivity may aid in determining key mechanisms of susceptibility to addiction that might be used as treatment targets. In the current study, impulsivity was assessed in three genetically unique lab mouse strains, including C57BL/6J (B6), B6SJLF1/J (F1), and DBA/2J (D2) mice, using an automated maze-based delay discounting task. Following acclimation/habituation sessions, mice were provided the opportunity to choose between a large/delayed reward (4 food pellets; 0s, 2s, 4s, 8s, or 16s) or a small/immediate reward (1 pellet; 0s). High impulsivity subjects place less value on rewards that are delayed in time and choose immediate rewards with high frequency. We hypothesized that impulsivity would vary by genotype, with F1 displaying the greatest impulsivity, B6 displaying low impulsivity, and D2 displaying impulsivity values somewhere between these two strains. Strain-specific behavioral differences were observed, including perseverative goal tracking in B6, wall jumping in F1 and D2 mice, and differences in magnitude discrimination learning rate. Given these early findings, we anticipate robust genotype difference in large vs small choices once incrementally larger and larger reward delays are imposed. Should these differences occur, follow up studies will be warranted to rule out potential difference in motivation, as well as to further test the relationship between impulsivity and drug-seeking behavior.

Plastic particulate inhalation during pregnancy linked to postpartum cardiomyopathy.

Discipline: Life Sciences

Subdiscipline: Physiology/Pathology

Jarett Reyes George*[1]and Phoebe Stapleton [2]
[1]Rutgers, The State University of New Jersey, [2]Rutgers, The State University of New Jersey

Abstract: Pregnancy is a delicate state in which the mother’s body undergoes massive physiological changes to support fetal development. Changes to the cardiovascular system include an increase in heart size, or cardiac hypertrophy. Normally the mother’s heart returns to its pre-pregnancy size after birth; however, in some cases the heart stays enlarged, resulting in post-partum cardiomyopathy (PPCM), a pregnancy-specific cardiac failure. Our lab focuses on the impacts of particulate inhalation during pregnancy. We recently began exploring the outcomes of micro-nano-plastic particles (MNPs) exposure. We hypothesized that maternal inhalation of MNPs would lead to the development of PPCM. Sprague Dawley rats were exposed to MNPs in repeated whole-body inhalation exposures from gestational day (GD) 4-19. We removed the hearts from exposed rats on GD 20 and 3 wks postpartum. Hearts were fixed, trimmed, sectioned, stained, and anatomically measured. We identified a significant increase in overall heart width (9.71±0.15 mm vs. 8.85±0.35 mm) and left ventricular area (5.84±1.77 mm vs 3.00±0.55 mm) in compared to control at GD 20. We also identified a significant increase in right ventricular area (3.53±0.69 mm vs 2.12±0.72 mm) and decrease in wall thickness (0.78±0.07mm and 1.01±0.13 mm) as compared to control. We found no significant changes at 3wks postpartum. These results may identify the development of a dilated cardiomyopathy after maternal inhalation of MNPs during gestation, with recovery taking place within 3wks. PPCM presents similarly to a dilated cardiomyopathy, making it difficult for the heart to push blood to the rest of the body.   Supported by: NIH-R01-ES031285

Substrate and Tidal Elevation Impact on Condition Index of Mytilus galloprovincialis

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Leanne De Leon*[1]and Danielle Zacherl [2]
[1]California State University, Fullerton, [2]California State University, Fullerton

Abstract: Over the past decades, estuarine ecosystems have suffered significant habitat loss. Implementation of multi-habitat living shorelines (MHLS) can restore lost habitat function. Researchers constructed a MHLS in 2016 in Newport Bay, California by restoring eelgrass and oyster beds together and in isolation. Five years later, we sought to compare the health of bivalves recruiting to the restored oyster beds vs bivalves recruiting to human-introduced substrates while also exploring the effects of tidal elevation on bivalve health. Urbanized estuaries such as Newport Bay with various natural and anthropogenic habitats set the foundation to study how per capita condition index changes among a native and two non-native bivalves. The non-native Mediterranean Mussel, Mytilus galloprovincialis provide ecosystem services including shoreline stabilization and filtration function. I hypothesize the condition index will change across substrates and amongst tidal elevations. M. galloprovincialis were collected from seawalls, restored oyster beds, and cobbles and their condition indices were quantified. M. galloprovincialis were collected on seawalls and cobbles at one site, and tidal elevation was recorded for each individual collected. M. galloprovincialis experienced a substrate interaction effect, with a significantly higher condition index on cobble and restored oyster beds. Understanding the relationship filter feeders share with substrates and tidal elevation will inform future management decisions about how comparable MHLS are to anthropogenic habitats.

Vegetative Shade Coverage and Mosquito Abundance Across Neighborhoods of Different Socioeconomic Status.

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Oscar Elier Hernandez Reyes*[1], Megan Wise de Valdez [2], Daniel Guerra[3]

[1]Northwest Vista College, [2]Texas A&M University San Antonio, [3]Texas State University

Abstract: In the U.S., socioeconomic status (SES) of neighborhoods has been associated with mosquito abundance. However, determining which aspects make a neighborhood most suitable for mosquito breeding is difficult. Some studies have reported high mosquito numbers in low-income neighborhoods due to excessive discarded water-filled containers, ideal for mosquito larval development. Other studies suggest that high-income neighborhoods have more mosquitoes due to more shade and regular yard watering. Our study focuses on whether vegetative shade coverage is indeed greater in high-income neighborhoods than in low-income neighborhoods and whether mosquito abundance is correlated with shade coverage. We conducted our study in San Antonio, TX, the 7 th largest city in the U.S. and one of the most economically segregated. It is also home to mosquito species known to vector West Nile, Zika, and Dengue viruses. Each week, from June-August, 2022, we randomly selected six neighborhoods and set two mosquito traps at a randomly selected home (84 sites by end of summer). The neighborhoods were classified by income and shade coverage using the U.S. Census data and LIDAR data/ARCGIS, respectively. Preliminary data show that that shade coverage does not significantly differ among high-, moderate-, and low-income neighborhoods. When combined across species, mosquito abundance was not correlated with shade coverage. However, when analyzed separately, Aedes aegypti, was positively correlated with shade. These preliminary findings indicate that, unlike other large cities, shade coverage does not across neighborhoods SES in San Antonio, TX and that only some species of mosquitoes are influenced by the amount of shade.

Establishing a Framework for Stewardship-based Coral Reef Conservation

Discipline: Life Sciences

Subdiscipline: Environmental Science

Julia Rakowsky*[1]and Katrina Armstrong [2]

[1]Ursinus College, [2]Hopkins Marine Station, Stanford University

Abstract: Coastal communities of developing countries rely heavily on coral reef ecosystems for sustenance, livelihood, and protection against coastal erosion. Stressed by global climate change and anthropogenic impacts many corals have been unable to regenerate fast enough to overcome bleaching events. To combat these changes, management and restoration of these systems is essential. Historically, passive restoration efforts, such as Marine Protected Areas (MPAs), were utilized to counteract reef degradation. However, these methods have not been effective in alleviating long term damage. To avoid pitfalls associated with passive restoration and management, active rehabilitation strategies have been employed. Unfortunately, many of these efforts are performed by scientists who fail to acknowledge or engage with the local community, a practice coined “parachute science”. Restoration methods involving communities have both ecological, cultural, and socioeconomic benefits. Therefore, it is imperative to establish a restoration framework that effectively incorporates stewardship. To establish this

framework, I performed a literature review and comparative analysis to determine which restoration strategies resulted in successful restoration. I also analyzed the success of active restoration practices to determine their compatibility with various stakeholder involvement. To supplement the literature review, I conducted semi-structured interviews with reef restoration researchers and practitioners. Based on previous studies, low-cost and simple restoration methods may be most effective both socioeconomically and ecologically when implemented using a bottom-up approach, led by local communities and nongovernmental organizations (NGOs). Using the knowledge gained from this study, I establish a framework for stewardship-based coral reef restoration, prioritizing local knowledge and low-tech restoration practices.

Osiris family genes regulate Drosophila tracheal tube maturation through endosome mediated protein trafficking

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Niraj Dhakal*[1], Lan Jiang [2], Istri Ndoja[3], Aaron Scholl[4]
[1]Oakland University, Oakland County, Michigan, [2]Oakland University, [3]Oakland University, [4]Food and Drug Administration

Abstract: Despite several efforts, the fundamental process of biological tube formation remains unclear. The Drosophila trachea is an ideal model to study conserved and fundamental mechanisms of tubulogenesis. In Drosophila , we have identified the Osiris genes that are expressed only in the trachea. It is speculated that Osi proteins coordinate endosome-mediated protein trafficking during tracheal formation. Therefore, we investigated how these Osi proteins are involved in the protein trafficking system of wildtype and mutant flies. We used immunohistochemistry followed by confocal microscopy to study the co-localization of these Osi proteins with various markers of trafficking pathway. CRISPER-Cas9 was used to generate Osiris loss of function mutant flies. We also studied the genetic interaction between the Osiris genes and components of the protein trafficking system. Wild type flies were used as the control group. Three Osiris genes, Osiris9, Osiris15 and Osiris19 were analyzed. Only triple mutant flies showed severe defects. Osi proteins were significantly colocalized with Rab7, Rab11 and Lamp which are components of the late endosome, recycling endosome and lysosome respectively. The expression of Rab7, Lamp and Rab11 were reduced in mutants. DE-cadherin, which is a Rab11 cargo and a core component of the adherens junction was defective in Osi mutants. Osi proteins also regulated the clearance of luminal proteins through Rab7 mediated endocytosis. Osiris genes regulate tracheal tube maturation by coordinating the intracellular protein trafficking process. They mediate luminal clearance through endocytosis and lysosomal degradation. Meanwhile, they maintain the stability of tracheal epithelial cells through recycling endosomes.

Snap25Δ3 differentially contributes to Gαi receptor function in the nucleus accumbens

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jose Zepeda*[1], Brad Grueter [2], Kevin Manz[3], Zack Zurawski[4], Heidi E. Hamm [5]
[1]Vanderbilt University, [2]Vanderbilt University, [3]Vanderbilt University, [4]Vanderbilt University, [5]Vanderbilt University

Abstract: The nucleus accumbens (NAc) guides vital motivated-behaviors such as food-seeking and reproduction. NAc medium spiny projection neurons (MSNs) require glutamatergic drive from other brain regions to generate action potentials, in turn MSNs project long-range GABAergic axons to other brains regions. Neuromodulatory systems within the NAc can dampen glutamatergic neurotransmission through activation of Gi/o G-protein-coupled receptors (GPCRs). Previous work has shown that Gβγ subunits bind directly to the t-SNARE protein SNAP-25, but it remains unknown what contribution SNAP-25 may have on Gi/o GPCR signaling within the NAc. We hypothesized that SNAP-25 may differentially couple to the Gβγ complexes of different Gi/o GPCRs located in the NAc. We used a mouse line (Snap25Δ3) which contains a C-terminal three amino acid deletion of Snap25 that impairs its ability to associate with the Gβγ complex to survey how SNAP-25 may be contributing to Gi/o GPCR signaling at excitatory synapses within the NAc. Using a combination of whole-cell voltage-clamp electrophysiology and pharmacology we demonstrate that the Snap25Δ3 mice have altered basal excitatory neurotransmission properties, and that SNAP-25 contributes to the depression of glutamatergic signaling cause by activation of GABAB, 5HT1 B/D, and Mu-opioid receptors, but not Kappa-opioid, CB1, group II mGluRs, and H3 receptors in the NAc core. The NAc is conserved from mice to humans and has been strongly implicated within various human brain disorders such as generalized anxiety disorder, eating disorders, major depressive disorder, and substance use disorders. These studies advance our understanding of key molecular mechanisms that guide neuromodulation within the NAc.

Influence of Precipitation on the Spatial Development of Algae in a Large Eutrophic Lake

Discipline: Life Sciences
Subdiscipline: Environmental Science

David Ortiz*[1]and Emily Stanley [2]
[1]University of Wisconsin - Madison, [2]University of Wisconsin - Madison

Abstract: Precipitation driven non-point pollution is one of the largest issues that freshwater ecosystems have faced. Increased precipitation paired with a changing climate have decreased water quality and increased algal concentrations in most lakes. Increased algal concentrations can produce fish-killing swings in oxygen and harmful toxins. Most monitoring programs only sample for algae at the center of lakes. We hypothesized that the two major inlets of Lake Mendota will have a distantly different algal concentrations and communities when compared to the center of the lake because of proximity to the source of nutrients entering the lake. We are especially interested in the spatial and temporal influence of each of Lake Mendota's inlets on the development of algae blooms across the lake after precipitation events. We sampled the lake's surface water, using high frequency sensors twice a week. Collecting approximately 15,000 sample locations for algal concentrations, dissolved oxygen, and pH. We were able to identify statistically different (p<0.05) clusters of algae and water chemistry composition at each inlet and the center of the lake. We were also able to identify periods of extreme algal growth and decomposition, corresponding to when blooms started and ended. Our results suggest that incorporating multiple sampling locations for a monitoring program is important to better capture the true extent of algae cross the lake. Therefore, allowing a better prediction of when blooms will occur, where they will occur, and their magnitude can inform lake management when to issue lake warnings and closures.

Relic Beaver Meadow Carbon Storage on the Kenai Peninsula: Diamond Creek as an Initial Survey

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Rohith Moolakatt*[1], Coowe Walker[2], Jacob Argueta[3]
[1]University of California, Berkeley, [2]Reserve Manager, Program Watershed Ecologist - Kachemak Bay National Estuarine Research Reserve, [3]Research Technician - Kachemak Bay National Estuarine Research Reserve

Abstract: This project investigates the historic role of beavers in carbon storage on the Kenai Peninsula in Alaska. Decades prior, significant beaver populations lived on the Kenai Peninsula, but the beavers are now almost entirely absent from the region due to ecological and trapping pressures. Our goal is to determine the carbon content of beaver meadows relative to riparian soil from the same location. Our hypothesis is that beaver meadow carbon storage will yield much greater carbon stored due to higher biomass and biodiversity from previous beaver activity. The survey was conducted in the Homer Demonstration Forest, along Diamond Creek, where beavers were last documented in 2002. Soil core samples were taken from six transects spanning Diamond Creek and two beaver meadows. Soil bulk density and carbon content of samples were determined through dehydration and loss-on-ignition protocols respectively. Preliminary findings indicate that relic beaver meadows stored more carbon compared to riparian banks. Recognizing the limits of this initial survey, we call for further research to be conducted across the extent of previous beaver habitats in the Anchor River watershed on the Kenai Peninsula. Additional scientific engagement with regional beaver meadows is necessary as literature suggests that relic beaver meadows likely leak stores of previously carbon richer meadows under active beaver management. Further investigation into the historical role of beavers in the Kenai Peninsula may enlighten local beaver protection movements to restrict trapping while opening a new potential tool for climate mitigation in Alaska through beaver reintroduction.

Determining how host genetic difference influence infection with tumorigenic gamma-herpesviruses

Discipline: Life Sciences
Subdiscipline: Microbiology

Claudia Mañán Mejías*
Tufts Graduate School of Biomedical Sciences

Abstract: The same viral infection can cause severe disease in some individuals, while others remain asymptomatic. This is true for gamma-herpesviruses; large DNA viruses that establish latency in their hosts, causing tumors in immunocompromised individuals and contributing to autoimmune diseases. Epidemiological data suggest that these infections and the corresponding diseases vary depending on host genetics, but it is unclear which host determinants are important. This is in part due to difficulties in studying the human gamma-herpesviruses, Kaposi’s sarcoma-associated herpesvirus (KSHV), and Epstein-Barr Virus (EBV), in animal models. To use animal models to study genetic determinants of gamma-herpesvirus infection, I am combining mouse genetic analysis with infection with the murine gamma-herpesvirus MHV-68, which is commonly used as a small animal model of gamma-herpesvirus infection. Because classic laboratory mice strains are genetically homogeneous, I am modeling the genetic diversity found in natural populations by using wild-derived mouse strains. Wild-derived mouse strains have enough genetic diversity from each other to impact infectious and immune phenotypes. I have identified differences in viral mRNA expression between MHV68-infected wild-derived and classical laboratory strains of mice and am now investigating whether this reflects differences in viral replication. Establishing MHV-68 as a model for gamma-herpesvirus infection in genetically divergent individuals of the same species will allow us to determine how the genetic makeup of the host impacts the course of gamma-herpes viral infection. Moreover, it will lead to the unbiased identification of genes responsible for infection and disease differences.

The triterpenoid CDDO-Methyl ester polarizes human lung tumor-educated macrophages

Discipline: Life Sciences
Subdiscipline: Pharmacology

Jannaldo Nieves-Salvá*[1], Karen Liby[2], Jessica Moerland[3]
[1]University of Puerto Rico at Arecibo, [2]Michigan State University, [3]Michigan State University

Abstract: Lung cancer is the leading cause of cancer deaths in the United States. Most cancer treatments have limited efficacy and adverse side effects, so there is a need for the development of new treatments for lung cancer. Macrophages are the most common immune cell in lung cancer and are potential therapeutic targets because they can change to either an anti-tumor or tumor-promoting phenotype. Anti-tumor macrophages are pro-inflammatory and rely on cytoprotective mechanisms to maintain their phenotype. The Nrf2 pathway is a master regulator of oxidative stress and activators of this pathway have anti-cancer effects in preclinical cancer models. The triterpenoid CDDO-Methyl ester (CDDO-Me) is a potent, well-tolerated Nrf2 activator that has advanced to human clinical trials. Previous studies have shown that CDDO-Me polarizes mouse tumor-educated macrophages from a pro-tumor phenotype to an anti-tumor phenotype in vitro , which may explain the reduced tumor burden in mouse cancer models. To test the effects of CDDO-Me in human macrophages, THP-1 differentiated macrophages were cultured in conditioned media from human lung cancer cancers to induce a pro-tumor phenotype, then treated with CDDO-Me. This model, CDDO-Me increased mRNA expression of the pro-inflammatory cytokines TNFα and IL-6 and decreased mRNA expression of the angiogenic factor VEGF and the chemokine CCL2, indicating a switch from a pro-tumor phenotype to an anti-tumor phenotype. Importantly, these data are consistent with observations from previous studies in mouse-macrophages and show that CDDO-Me can polarize human lung tumor-educated macrophages to an anti-tumor phenotype and thus may reduce human lung tumor burden.

Impacts of Giant Reed Removal on Aerial Invertebrates in Non-Perennial Rivers

Discipline: Life Sciences
Subdiscipline: Environmental Science

Natalie Hunter*[1], John R. Olson[2], Savannah Saldana[3]
[1]California State University, Monterey Bay, [2]Professor, [3]Graduate student

Abstract: Monitoring freshwater ecosystems is required for their conservation to ensure they provide ecological services like climatic stability, rich biodiversity, nutrient distribution, and recreational opportunities. However, most existing monitoring processes focus on perennial or long-term running streams. Processes for intermittent rivers and streams that do not have a

continuous yearly water flow is not as widely understood, but are needed for a complete assessment of ecosystem health. Riparian zones within these habitats are especially susceptible to environmental stressors, like invasive giant reed (Arundo donax). This robust, bamboo-like plant negatively influences macroinvertebrate body size and life cycle patterns, natural fire patterns, and native species distribution. We used aerial macroinvertebrates as bioindicators to provide a thorough, short-term assessment that measured any impacts giant reed has on the health of the arid Salinas River. We sampled two sites; one site that was previously treated with the removal of arundo and one site left untreated. We placed five adhesive traps evenly along a 250m transect of the river channel. The traps remained for eight days and upon collection each sample was identified down to order for comparison with past collections sampled using the same methodologies. This research helps to determine whether the removal of arundo will benefit, worsen, or have no impact on the ecological health of the Salinas River.

Efficacy of Olaparib and p53 Reactivators Separately and Combined to Overcome PARP Inhibitor Resistance in COV362 Ovarian Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Angelina Licor*[1], Lanie Smith[2], Jamie Padilla[3], Kimberly Leslie[4]
[1]St. John's University, [2]University of New Mexico Cancer Research Facility, [3]University of New Mexico Cancer Research Facility, [4]University of New Mexico Cancer Research Facility

Abstract: Ovarian cancer is the most lethal gynecologic malignancy, resulting in only 16-21 months median progression free survival. Ovarian cancer patients are typically prescribed PARP inhibitors for maintenance therapy following initial surgery and chemotherapy. PARP (poly ADP-ribose polymerase) is a protein that participates in base excision repair (BER), a DNA repair pathway. Inhibition of PARP leads to inhibition of BER and the subsequent buildup of single-stranded breaks in DNA. Single-stranded breaks lead to double-stranded breaks in DNA, which leaves the cancer cell dependent upon pathways such as homologous recombination (HR). The protein BRCA is one of many that takes part in HR; hence, in cancer cells with mutated BRCA, PARP inhibitors prevent DNA repair and result in cell killing. However, patients commonly develop resistance to PARP inhibitors over time, and alternative treatments are urgently needed. In addition to BRCA mutations, about 90% of ovarian cancers exhibit mutations in the tumor suppressor p53. Reactivating the normal p53 functions inhibits cancer proliferation, and we hypothesize that using p53 reactivators alone or in combination with PARP inhibitors can reverse or prevent PARP inhibitor therapeutic resistance. Ovarian cancer COV362 cells, harboring both a BRCA1 and a p53 mutation, were analyzed to determine the effectiveness of p53 reactivator drugs (APR-246 and HO-3867) and a PARP inhibitor, olaparib, both separately and combined. Initial results indicate that COV362 cells are resistant to olaparib but highly sensitive to HO-3867 (IC50 = 1μM), thus supporting our hypothesis.

Asymmetric nuclear positioning during female meiosis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jordan Duong*[1]and Francis J. McNally[2]
[1]California State University, Los Angeles, [2]University of California, Davis

Abstract: In oocyte meiosis, chromosomes are segregated by a microtubule-based structure called the spindle which is asymmetrically positioned near the plasma membrane. During prophase of female meiosis in C. elegans , the nucleus of the oocyte translocates close to the cortex such that when the nuclear envelope breaks down, the meiotic spindle forms near the cortex and then moves the rest of the way there. The motor protein, kinesin-1, which transports cargo toward the plus ends of microtubules, is required in moving both the oocyte nucleus and meiotic spindle to the cortex. However, given that plus ends of microtubules are oriented toward the interior of the oocyte rather than outward toward the cortex, the mechanism of kinesin-1 on nuclear positioning is unknown. Different C-terminal domains of Kinesin-1 bind to different cargo molecules, and the extreme C-terminus binds to a second microtubule allowing kinesin to slide two microtubules relative to each other. We hypothesize that Kinesin-1 either moves the nucleus, the spindle, or both by binding either a second microtubule or a different non-nucleus, non-spindle cargo. To test this, differential interference contrast (DIC) microscopy of anesthetized C. elegans and quantitative image analysis will be used to measure the position of nuclei in kinesin mutant oocytes missing their C-terminal microtubule-binding domain. Elucidating the mechanisms of kinesin-1 dependent nuclear positioning in C. elegans oocytes will allow a better understanding of the mechanisms that take place in positioning meiotic spindles in human oocytes.

Assessment of Antibiotic Resistances in Escherichia coli Isolates from Freshwater and Comparison to Machine Learning Predictions

Discipline: Life Sciences
Subdiscipline: Microbiology

Karina Rodriguez Escobar*[1], Aaron Best[2], Michael Pikaart[3], Clay Ihle[4], Caleb Brezezinski[5], Zach Elmore[6], Nicole Prihoda[7], Benjamin Turner[8], Adam Slater[9]
[1]Hope College, [2]Hope College, [3]Hope College, [4]Hope College, [5]Hope College, [6]Hope College, [7]Hope College, [8]Hope College, [9]Hope College

Abstract: Antimicrobial resistance (AMR) is a problem worldwide. In response, we have applied machine learning to predict antibiotic resistance profiles of bacterial pathogens from genome sequencing data. As part of ongoing monitoring of the Macatawa watershed (Holland, MI), we have isolated over 7000 strains of Escherichia coli from freshwater sources and have sequenced over 400. We see differences in the number of predicted AMR genes between subpopulations of watershed strains and known E. coli reference genomes. We are applying a recently published machine learning approach (Nguyen et al., 2019; doi:10.1128/JCM.01260-18) trained on a database of clinical E. coli genome sequences with antibiotic resistance data to predict resistance for 194 sequenced watershed strains. Approximately 15% of strains were predicted to be resistant to 2 or more antibiotics per strain, 60% to be resistant to 1 antibiotic, and 25% to be resistant to none. Ten antibiotics were among the predicted resistances, with an accuracy of 92%. Those with highest accuracies (100%) were piperacillin-tazobactam, tobramycin and cefotaxime; all strains were predicted to be susceptible. Ampicillin had the lowest accuracy of 30%; the majority of incorrect predictions were predictions of resistance where experimental data showed susceptibility. An overall accuracy of 62% was observed. This work has produced a data set of linked freshwater Escherichia genomes and experimentally determined antibiotic resistance profiles that can be used to improve training sets for machine learning approaches to predicting resistance profiles and provide insight into the genomic context of resistance profiles.

Serotonin Type 2 Receptors Modulate Decision Making in Zebrafish

Discipline: Life Sciences
Subdiscipline: Neurosciences

Kevin Villafane*[1]and Roshan Jain [2]
[1]Haverford College, [2]Haverford College

Abstract: Many neurological disorders result from an imbalance of neurotransmitters in the brain. Learning how these neurotransmitters function through their diverse sets of receptors and what roles they play in affecting behavior can bring us closer to understanding neurological disorders like Schizophrenia and ADHD. Serotonin (5-HT) signaling alters the response selection of zebrafish exposed to acoustic stimuli. However, 5-HT affects many neuroreceptors and it's unknown what receptors are causing this change in behavior. We are investigating the effects of the 5-HT 2 receptor subtype using a quantitative behavioral assay following pharmacological treatment or genetic manipulation by CRISPR/Cas9. To test these effects, we recorded the responses of zebrafish when exposed to acoustic stimuli. Startled zebrafish choose between short-latency startles (SLC) or long latency startles (LLC) based on stimulus intensity and context. We quantify the relative selection bias between SLC and LLC responses to determine if a drug or genetic mutation changed the way zebrafish respond to stimuli. To test the 5-HT 2 receptor, we used several agonists and antagonists selective for 5-HT 2 receptor subtypes. Treatment with a 5-HT 2B/2C agonist (VER 3323) shifts larval bias towards SLC responses. Treatment with a 5-HT 2B/2C antagonist (SB 206553) shifts larval bias towards LLC responses. Treatment with a 5-HT 2A antagonist (EMD 281014) shifts larval bias toward SLC responses. We will also test the behavioral selection biases of zebrafish where we used CRISPR/Cas9 to mutate individual 5-HT 2A/2B/2C receptors to directly test their function. These highlight the importance of 5-HT2 receptors in regulating decision-making.

Antimicrobial resistance of Enterobacteriaceae isolated from an urban tropical estuary in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Environmental Science

Olvin Moreno*[1], Karla M. Casillas [2], Loyda B. Mendez[3]
[1]Instituto Tecnologico de Puerto Rico, Recinto de Manati, [2]Universidad Ana G. Mendez, Recinto de Carolina, [3]Universidad Ana G. Mendez, Recinto de Carolina

Abstract: Estuaries are transitional environments where freshwater mixes with saltwater from the ocean creating a diverse ecosystem for wildlife, seagrass beds and mangrove forests. The largest estuary in Puerto Rico is the "Estuario de la Bahía de San Juan", composed of more than 14 water bodies. This estuary is part of the USEPA National Estuary Program and the only one located in a tropical zone. In addition, this estuary is surrounded by urban areas which constantly endangers its ecosystem. Therefore, the purpose of this study is to evaluate the microbial water pollution of the Suarez Channel, which is a 3.9 km channel within the estuary that is heavily impacted by anthropogenic activities and is frequently used for non-commercial shore fishing and other recreational activities. Specifically, we evaluated antimicrobial resistance patterns in Escherichia coli (n=4) and Klebsiella pneumoniae (n=2) strains isolated from the Suarez Channel. To this extent, we determined the minimum inhibitory concentrations of 3 metals (Fe, Ni, V) and 24 antibiotics. Antimicrobial resistance patterns were evaluated using the microbroth dilution technique. For metals, the tested concentrations ranged from 0.31 to 16 mg/mL. For antibiotics, we used the Sensititre GN4F antimicrobial susceptibility panel.

Preliminary results showed that most strains were resistant to Fe (n=4) and Ni (n=3). Antibiotic resistance was observed for Amikacin (n=1), Ertapenem (n=2), Ceftazidimine (n=1), Aztreonam (n=4), Ceftriaxone (n=1), Tetracycline (n=1) and Ampicillin (n=1). Our results highlight the need to have monitoring programs for estuaries in order to protect its ecosystem and human health.

Sonoran Desert Mammal Species Diversity and Usage of Tinajas as a Water Source

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Conor Handley*
University of Arizona

Abstract: Water is a limited resource for many wildlife species in arid desert regions. Biodiversity in arid regions tends to be highest in areas with water, even if it is ephemeral. In the Sonoran Desert, permanent sources of water are rare, and ephemeral and isolated waters are often the primary sources for many wildlife species. One type of water source in these environments are tinajas. Often occuring below waterfalls, tinajas are depressions carved in rock formed through either water flow or sediment scouring intermittent streasm, which collect water following rain events. Tinajas are vital for mammals, reptiles, birds and invertabrate wildlife species in some of the driest areas of the Sonoran Desert. As water sources, they often stay filled for months after a rain event and contribute to a limited network of water resources for desert wildlife. We monitored 12 tinajas for 2 years using motion sensor cameras and catagorized the mammals that utilized them as a water source. We found that the tinajas water duration did not have a significant effect on the species richness observed at each site but that there was significant difference according to the size of the tinaja and its location in either the Pinacate Biosphere Reserve in Sonora or Organ Pipe Cactus National Monument, Arizona. This research can be used to inform reserve managers about the diversity of mammals present in their park and how changes in rainfall and the hydroperiod of the tinajas will affect them.

Function and Quality of Life over one Year for Individuals Post-Stroke

Discipline: Life Sciences
Subdiscipline: Biology (general)

Tatiana Willis*[1]and Heather Hayes [2]
[1]Mississippi State University, [2]University of Utah

Abstract: Every year, more than 795,000 people have a stroke, which is the leading cause of disability in the United States. Stroke can negatively impact quality of life. Quality of life (QoL) in individuals is worse after stroke with increasing disability. The purpose of this study is to describe the functional ability using the Activity Measure for Post-Acute care, Computer Adapted Test (AM-PAC) and quality of life using the EuroQol 5 Dimension 5L (EQ-5D-5L) in individuals post-stroke at four time points over one year. A prospective study, on 123 individuals with acute ischemic stroke were assessed at four time points, at discharge from the acute hospital, at discharge from an inpatient rehabilitation facility, at 6-months and 12-months. The primary outcome measures assessed function and QoL. The AM-PAC measures the degree of difficulty or assistance in performing 3 domains: Basic Mobility, Daily Activity, and Applied Cognition. The EQ-5D-5L has questions in 5 dimensions; mobility, self-care, usual activities, pain/discomfort, and anxiety/depression. Characteristics of individuals in the study: 55 females; average age 65.3 years (range 26.5 – 96.5); 39 employed, 16 unemployed, 67 are retired; 73 left hemiparesis, 3 bilateral hemiparesis; 82 did not receive tPA; average length of acute care stay is 7.1 days (range

1 – 21). The average BMI is 29.1. 82 of the patients did not receive tPA. This study is still in progress and currently does not have results. This study will help clinicians understand the long-term impact of stroke disability and function over 1 – year.

In vivo CRISPR screens reveal the landscape of immune evasion across cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Andrea Rosario*[1], Juan Dubrot[2], Peter P. Du[3], Sarah Kate Lane-Reticker[4], Emily A. Kessler[5], Audrey J. Muscato[6], Arnav Mehta[7], Samuel S. Freeman[8], Peter M. Allen[9], Kathleen B. Yates[10], Robert T. Manguso[11]
[1]Broad Institute of MIT and Harvard, [2]Broad Institute of MIT and Harvard, Center for Cancer Research at Massachusetts General Hospital, [3]Broad Institute of MIT and Harvard, [4]Broad Institute of MIT and Harvard, [5]Broad Institute of MIT and Harvard, [6]Broad Institute of MIT and Harvard, [7]Broad Institute of MIT and Harvard, Center for Cancer Research at Massachusetts General Hospital, [8]Broad Institute of MIT and Harvard, Center for Cancer Research at Massachusetts General Hospital, [9]Broad Institute of MIT and Harvard, [10]Broad Institute of MIT and Harvard, Center for Cancer Research at Massachusetts General Hospital,[11]Broad Institute of MIT and Harvard, Center for Cancer Research at Massachusetts General Hospital

Abstract: Immune checkpoint blockade (ICB) is a form of immunotherapy designed to interfere with the mechanisms cancers use to evade the immune system. These medications are successful in enhancing anti-tumor immunity within several disease contexts. However, many patients still do not respond to treatment. There remains a limited understanding of the exact pathways tumor cells use to avoid the immune response. We adopted an in vivo CRISPR screening approach to systematically explore the immune evasion mechanisms employed by different cancer types. Using eight (8) murine cancer cell models, we screened for genes that enhance sensitivity or resistance to the antitumor immune response. Our analyses highlighted the interferon signaling and major histocompatibility complex class I (MHC-I) pathways as depleted–or sensitizing–hits. Antigen presentation by MHC-I is upregulated by interferon signaling. This process drives the adaptive immune response by inducing the activation of cytotoxic CD8+ T-cells. However, our findings in animal models suggest that interferon sensing–generally regarded as an enhancer of ICB response–can have an inhibitory role in the tumor microenvironment. This context-dependent effect is directly tied to the expression of classical MHC-I–which inhibits natural killer (NK) cells– and the non-classical MHC-I Qa1-b (HLA-E in humans)–which inhibits CD8+ T-cells. Further analyses of patient data suggest that interferon sensing can mediate resistance to ICB in humans. Thus, we conclude that in vivo CRISPR screens are a valuable tool in revealing new immune inhibitory pathways that can inform future therapeutic developments.

Prediction of photogrammetry-based habitat complexity using a trait-based approach on coral reefs in Guam

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Sofia Ferreira*
University of Hawaii at Hilo

Abstract: Scleractinian or stony corals are the primary contributors of the structural complexity in coral reefs, underpinning the biodiversity and ecosystem services they support. Despite substantial research, the exact mechanism by which Scleractinia contribute to habitat complexity is still debatable. This study investigated the use of a trait-based approach to provide new insights into the relationships between habitat complexity and coral assemblages and tested the predictability of such relationships. Novel 3D photogrammetry techniques were used to survey 28 sites on the island of Guam (West Pacific) from which structural complexity metrics were derived and traits were quantified. Three traits at the individual coral level (morphology, size, genera) and two site level traits (wave exposure, substrate-habitat type) were examined. Common taxonomy-based metrics were also included at the study-plot level (coral abundance, richness, diversity) for comparison. Different traits were found to disproportionately contribute to different photogrammetry-based complexity metrics. Large Porites colonies with laminar columnar morphology showed the highest contribution to surface complexity and vector ruggedness. Whereas, branching Pocillopora showed the highest contribution to planform and profile curvature. These results highlight the importance of considering coral traits for the understanding of structural complexity and provide a framework to enable worldwide comparisons to predict the trajectory of reefs under changing environmental conditions.

Characterization of the role of the Bacteroides fragilis in amyloid plaque and neurofibrillary tangle development in mice modeling Alzheimer’s Disease pathologies

Discipline: Life Sciences

Subdiscipline: Microbiology

Antonio Ivie*[1], Dr. Emily Cope [2], Kathryn Conn[3], George Testo[4], Emily Borsom [5]
[1]Northern Arizona University, [2]Professor/Researcher, [3]PhD student, [4]Undergraduate student researcher, [5]PhD student

Abstract: Alzheimer’s Disease (AD) is a neurodegenerative disease that can cause cognitive function decline due to formation of amyloid-beta plaques in the brain and neurofibrillary tangles. The gut microbiome communicates bidirectionally with the brain, and may play a role in progression of AD pathologies. Our prior studies have demonstrated enrichment of Bacteroides fragilis in the gut microbiome of 3xTg-AD mice, which model plaques and tangles, compared to wild type controls. To assess the effect of Bacteroides fragilis on AD pathologies, we inoculated mice with 1010 CFU/ml B. fragilis in an applesauce mixture. Mice were dosed for 5 days after weaning and received monthly maintenance doses. After giving both strains of mice the B. fragilis, we collected fecal samples biweekly. DNA and RNA was extracted, and the V4 region of the 16S rRNA gene was sequenced. At weeks 8 (baseline, no pathologies), 24 (when amyloid plaques develop), and 52 (when neurofibrillary tangles develop) we sacrificed the mice and harvested the ileum, cecum, and colon for microbiome analysis. We collected the hippocampus and frontal cortex to quantify AD pathologies. We expect that B. fragilis will increase the progression rate and burden of the amyloid-beta plaques and neurofibrillary tangles. In the future, understanding the mechanism by which Bacteroides influences AD pathologies could lead to novel therapies to reduce amyloid-beta plaques and tangles. Based on the increased rate Alzheimer’s Disease is being diagnosed in the eledry population, this research could prove crucial to future treatment developments to lessen the severity of Alzheimer’s Disease.

Characterizing the relationship of Lgl1 and Akt in the Murine Neural Stem Cell Niche

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Loowyza Colegrove*[1], Natalie Pedicino [2], Yoko Hirata[3], Claudia Petritsch[4], Amy Sprowles [5]
[1]Cal Poly Humboldt, [2]Cal Poly Humboldt, [3]Stanford University, [4]Stanford, [5]Cal Poly Humboldt

Abstract: Asymmetric cell division is critical for neural stem cell differentiation and brain development. When these processes are dysregulated in neural progenitor cells (NPCs), developmental defects and disease can result. Lgl1 is a tumor suppressor gene whose loss of function leads to abnormal brain development and cancers, including glioblastoma multiforme (GBM). Findings in our laboratory suggest LGL1 regulates AKT signaling in neural progenitor cells (NPCs) isolated from genetically matched Lgl1 -/- and Lgl1 +/+ mice, but we have not evaluated AKT phosphorylation in situ. Our working hypothesis is that LGL1 regulates AKTsignaling in the NPCs residing in the neural stem cell niche. To test this hypothesis, we are characterizing AKT phosphorylation patterns in the subventricular zone (SVZ) of the lateral ventricles of GFAP-CRE and NG2-CRE Lgl -/- and Lgl +/+ mice. Initial results suggest AKT signaling is active in the murine neural stem cell niche and loss of Lgl1 affects AKT phosphorylation. This study will contribute to understanding how LGL1 affects neural cell differentiation, cancer stem cells, and GBM progression.

Investigating the growth response of lettuce and petunia transplants to the full and partial substitution of chemical fertilizer with food-waste fertilizer

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Jasmine Goode*[1], Zhihao Chen [2], Yujin Park[3]
[1]Arizona State University, [2]Arizona State University, [3]Arizona State University

Abstract: Current crop production depends on the use of chemical fertilizers, which offer a consistent and fast-acting nutrient source for crops. However, global fertilizer shortage and adverse impacts of the overuse of chemical fertilizer on soil and water sources create opportunities for sustainable fertilizers. This study investigated if food waste fertilizer can replace or at least reduce the use of chemical fertilizer for growing lettuce (Lactuca Sativa) and petunia (Petunia × hybrida) transplants. The seedlings of lettuce 'Nancy' and petunia 'Easy Wave Velour Berry' were grown for four weeks inside an indoor vertical farm at 22℃ under sole-source lighting at a photosynthetic photon flux density of 180 μmol·m -2· s -1 with a 20-h photoperiod. The seedlings were sub-irrigated with tap water mixed with food-waste fertilizer (0.06N-0.026P-0.1191K), chemical fertilizer (15N-2.2P-16.6K), and a 50/50 chemical and food-waste fertilizer mix at the electrical conductivity of 0.7 mS·cm -1 . In both lettuce and petunia, seedlings treated with chemical or 50/50 chemical and food-waste fertilizer mix similarly had 93-152% larger leaf area and 82-141% greater shoot fresh weight than those treated with food waste fertilizer. However, the leaf number, SPAD value, and root fresh weight were similar between all treatments. This result suggests that food waste fertilizer can at least partially replace chemical fertilizer to grow young plants with similar growth attributes.

Comparative analysis of the chloroplast genomes of Quercus x morehus and the presumptive parents Q. wislizeni and Q. kelloggii (Fagaceae) confirms its hybrid status

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Juan Chavez*[1]and Jeffery R. Hughey[2]
[1]Hartnell College, [2]Hartnell College

Abstract: The Abram's oak, Quercus morehus , was originally proposed in 1863 from a single specimen from northern California, USA. It was described as a small tree (9.14 meters in height) with black bark, oblong-lanceolate leaves, and oblong nuts. Subsequent workers based on field observations and morphological examination concluded that Q. morehus was not a distinct species, but rather a hybrid between the interior live oak Q. wislizeni and the black oak Q. kelloggii . To date however, no genetic studies have been performed on Quercus x morehus to confirm this hybrid designation. Here, we present the complete chloroplast genomes of Quercus x morehus , Q. wislizeni , and Q. kelloggii from California to test the hybrid origin hypothesis. The three genomes are 161,119 – 161,130 base pairs in length and encode 132 genes. Quercus x morehus and Q. wislizeni are identical in sequence, but differ from Q. kelloggii by three insertion/deletion events and eight single nucleotide polymorphisms. Phylogenetic analysis of the chloroplast genomes with representative oaks from around the world fully resolved all three in the Lobatae clade. These results support the conclusion that Quercus x morehus is a natural hybrid between Q. wislizeni and Q. kelloggii , as well as show that genomics is a powerful tool for deciphering the genetic history of plants.

The influence of global warming on melanized fungi

Discipline: Life Sciences
Subdiscipline: Microbiology

Marcos Marmolejo*[1]and Adriana L. Romero-Olivares[2]
[1]New Mexico State University, [2]New Mexico State University

Abstract: Melanins are pigments found in all kingdoms of life including fungi. They are considered an important stress-tolerance factor because it allows fungi to tolerate environmental stress, such as those brought by global climate change like high temperature and nitrogen pollution (i.e., global change drivers). Moreover, melanin is an important virulence factor because it allows fungi to withstand environmental stress inside hosts (e.g., high temperature, low carbon). However, the production of melanin is energetically expensive and might be produced at the expense of other fungal traits, such as growth rate (i.e., tradeoff). As global climate change makes our environment more stressful, will we see an increase in the prevalence of melanin in the soil microbial community? Our objective was to determine if the production of melanin elicited a tradeoff on fungal growth under environmental stress. We hypothesized that melanized fungi will grow less than unmelanized fungi under global change drivers because fungi require more energy to produce melanin compared to unmelanized fungi, consequently eliciting a tradeoff with growth. To test our hypothesis, we inoculated fungal strains with a spectrum of melanin content and compared their growth and heterotrophic respiration at different temperatures and different nitrogen concentrations. We found evidence of a tradeoff between melanin content and growth under global change drivers. Studying fungal traits tradeoff and how it relates to fungal pathogenicity under global change drivers is important because it will allow us to better understand the threats that global climate change poses to public health.

Effects of Tart Cherry on Lifespan of a Caenorhabditis elegans, Amyloidogenic Strains for Alzheimer’s-Disease

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Rama Supraja Balaga*[1], Yujiao Zu [2], Dr Naima Moustaid-Moussa[3], Hannah Petry[4], Caitlin Tayag [5], Tasnim galalla[6], Mahsa Yavari[7], Dr Siva A. Vanapalli[8], Mizanur Rahman[9], Shasika Jayarathne[10]
[1]Texas Tech University, Lubbock, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University, [5]Texas Tech University, [6]Texas Tech University, [7]Texas Tech University, [8]Texas Tech University, [9]Nemalife, [10]Texas Tech University

Abstract: Alzheimer’s disease(AD) is a neurogenerative age-related disorder, characterized by amyloid plaqus (Aβ), Tau tangles in the brain, C.elegans has emerged as a premier model system for aging and AD research, due to their simple body plan and short lifespan of 3 weeks. We previously reported the beneficial effect on longevity of tart cherry extract (TCE), rich in anthocyanins, in wildtype C.elegans . The objective of this study is to investigate the effect by which TCE extends lifespan in transgenic amyloidogenic C.elegans strains. For this experiment, age synchronized C.elegans, GRU102 and GMC101, which express human Aβ, were loaded into microfluidic chips, and used the Nemalife infinity machine to perform lifespan experiments for 18-26 days at ambient temperature. Worms received 20 mg/ml of E. coli, OP50, along with one of the following treatments: control (no-supplementation), 6, or 12µg anthocyanin/ml, of TCE. We found that TCE supplementation at 6µg/mL, increased (p < 0.05) the medium lifespan of GRU102 strain (23 days), when compared to control worms (16-17 days). For GMC101 strain, TCE at 6, and 12 µg/mL, increased the medium lifespan of worms by 15 and 15.5 days, respectively, compared to control worms (13 days). Our results indicate that anthocyanin-rich TCE exhibit beneficial effects in Aβ expressing C.elegans strains via increasing their lifespan. Thus, tart cherry consumption may provide an efficient approach for combating AD and other aging-related diseases in human, warranting future studies to determine underlying mechanisms.

Isolation of pAD123 for SIGEX Screening of Chemical and Physical-Environmental Factors by Generation of a Promoter-Trapping Metagenomic Library

Discipline: Life Sciences
Subdiscipline: Microbiology

Ricardo Roman*[1], Carlos Ríos Velázquez [2], Luis A. Montalvo Rivera[3], Luis G. Montalvo González[4], Victor O. López Ramírez [5]
[1]University of Puerto Rico, Mayaguez Campus, [2]University of Puerto Rico, Mayaguez Campus, [3]University of Puerto Rico at Mayaguez, [4]University of Puerto Rico at Mayaguez, [5]University of Puerto Rico at Mayaguez

Abstract: Substrate- Induced Gene Expression (SIGEX) is an effective method for screening of environmental metagenomes since it can detect gene induction in response to certain stimuli. In addition, glyphosate- based herbicides (GBHs) are commonly used in plants that have potential applications in agriculture, industrial spaces, homes, among others. Recently, it has raised public and health concerns due to the high levels reported on the environment. The main objective of this study is the generation of a promoter-trapping metagenomic library from samples that were obtained from agricultural coffee soils near the Güayo Reservoir in Adjuntas, Puerto Rico which we believe that it could potentially contain glyphosate remnants. DNA extraction was done using FastDNA Spin Kit for Soil by MP Biomedicals, following isolation and purification and ligation of pAD123, and transformation of electrocompetent E. coli DH5α cells. Then, SIGEX screening will be performed and consists of GFP induction, following positive clone isolation, and DNA purification with DNA GELase. We expect to optimize the experimental design by increasing the size of the metagenomic library, use PCR screening to amplify glyphosate-responsive genes, perform transformant screening to confirm insertion, and validate the pAD123 operon trap with an inducible promoter. Positive-induced clones are currently being analyzed by functional assays of chemical and physical-environmental conditions including heavy metals, chemical effectors, temperature, pH, and salinity. These results will bring insights into the use of promoters and gene regulation capable of acting as biosensors in addition to understanding the biological pathways involved.

Monitoring habitat preferences of local amphibians in the Monterey Bay area of California

Discipline: Life Sciences
Subdiscipline: Environmental Science

Monica Urias*[1], Jennifer Duggan[2], Joshua Beasley[3]
[1]California State University, Monterey Bay, [2]California State University, Monterey Bay, [3]California State University, Monterey Bay

Abstract: In order to understand habitat preferences for amphibians in the Monterey Bay area, we conducted observational night surveys of these nocturnal animals in the Fort Ord National Monument (FONM) during March and April of 2022. Sites were evenly distributed across habitat types (Oak Woodland, Coastal Scrub, and Annual Grassland) and varied in distance from ponds (i.e., amphibian breeding habitat). During surveys, we documented each amphibian sighting with a GPS point and photo. The FONM points were combined with data obtained from iNaturalist (iNat). Additionally, we collected data on amphibian sightings at the UCSC Fort Ord Natural Reserve (UC FONR) using iNat and previous students' identifications of amphibians in the reserve. We used GIS software to create a map illustrating the locations of all amphibian sightings, as well as the habitat type in which each occurred. Last, we tested if the frequency of amphibian sightings varied significantly across habitat types. An improved understanding of habitat preferences for local amphibians will be useful for determining areas where habitat connectivity is critical for both least-concern and special-status species in the Monterey Bay area of California.

A Forward Genetics Approach for Identification of Novel Genetic Interactors Of The Mitochondrial Fusion Proteins Mfn1 and Mfn2

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jennifer Bocanegra*[1], Irini Topalidou[2], Stephanie Sloat[3], Briar Jochim[4], Dana Miller[5], Suzanne Hoppins[6]
[1]University of Washington, Seattle, [2]University of Washington, [3]University of Washington, [4]Fred Hutchinson Cancer Research Center, [5]University of Washington, [6]University of Washington

Abstract: Mitochondria rely on the dynamic properties of fusion, division, and movement to maintain mitochondrial and cellular health. These processes are tightly regulated to coordinate mitochondrial functions with cellular demands. Mitochondrial outer membrane fusion is mediated by the mitofusins, Mfn1 and Mfn2. Several disease-associated variants of the mitofusins exhibit perinuclear clustering of mitochondria, in contrast to the cytoplasmic distribution observed in wild-type cells. The mechanistic basis of this drastic change in mitochondrial distribution remains unknown. We hypothesized that the disease-associated mitochondrial perinuclear clusters are caused by factors that regulate mitofusin activity. We set out to identify these regulatory components in a forward genetic screen. Using the nematode C. elegans, we expressed a variant of mitofusin which caused perinuclear clustering of mitochondria . We observed fewer mitochondria in the axons and an uncoordinated locomotion phenotype indicative of neuronal dysfunction. We screened for suppressors of the locomotion and mitochondrial phenotype. In one strain, the suppressor mutation was mapped, and candidate genes were identified by whole-genome sequencing. Genes likely involved in maintaining mitochondrial structure or function have been prioritized for further analysis. Genetic interactions will first be confirmed in C. elegans and then tested in mammalian cells where we will fully characterize the role of the interactor(s). This work leverages the power of forward genetics for identifying novel genetic regulators of mitochondrial dynamics.

Geometric morphometrics reveal shape differences in the toes of urban lizards

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Bailey Howell*[1], Josef Uyeda [2], Kristin Winchell[3], Travis Hagey[4]
[1]Virginia Polytechnic Institute and State University, [2]Virginia Polytechnic Institute and State University, [3]Princeton University, [4]Mississippi University for Women

Abstract: Urbanization offers species unique opportunities to exploit novel niches, and it is unclear how organisms must adapt to survive in urban environments. Previous studies suggest that adhesive pad-bearing lizards with larger toepads cling more successfully, which is imperative when climbing smoother, man-made substrates where the claw is less effective. While we have some understanding of how toepad size changes due to urban selection pressures, previous studies have neglected how toepad shape changes. We investigate how Puerto Rican crested anoles have adapted to living in urban areas using geometric morphometrics to determine how toepad shape shifts between urban and forest lizards. Our results indicate that urban Anolis cristatellus lizards do not simply display isometric increase in toe size. Toes of urban populations have a larger proportion of the toe length covered in adhesive toepad. In addition, the toepads of urban lizards increase more in length than width. Lastly, lizards in urban populations exhibit both increased number of lamellae (specialized adhesive scales) as well as increased spacing between individual lamellae. We also observed regional variation, with urban specimens having significantly more disparity, suggesting similar processes of urban adaptation are likely happening in parallel across the island, yet with region-specific idiosyncrasies. In conclusion, our results highlight the value of considering toepad morphology in more detail beyond adhesive pad area or number of lamellae, as it reveals interesting variation which could be connected to functional demands. Geometric morphometrics can elucidate subtle differences in shape to better connect changes in morphology to ecology and performance.

Investigating the Interaction of Mva1 Restriction Endonuclease DNA Cleavage

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Julissa Cruz Bautista*[1], Candice Etson [2], Nirmala Shrestha[3], Sophia Morgan[4], David Jusino [5], Yun Huynh[6]

[1]Wesleyan University, [2]Department of Physics and MB&B, Wesleyan University, Middletown, CT, USA, [3]Department of Physics, Wesleyan University, Middletown, CT, USA, [4]Department of MB&B, Wesleyan University, Middletown, CT, USA, [5]Department of MB&B, Wesleyan University, Middletown, CT, USA, [6]Department of MB&B, Wesleyan University, Middletown, CT, USA

Abstract: Restriction endonucleases are enzymes that are able to cleave duplex DNA at or near a specific nucleotide sequence. MvaI is a Type IIP restriction endonuclease found in Kocuria varians. Most Type IIP restriction endonucleases are homodimers that cleave a palindromic DNA sequence. However, MvaI has been shown to bind and cleave the pseudopalindromic sequence CC/WGG (where W can be A or T) as a monomer. Previous studies of the related monomeric restriction endonuclease BcnI revealed that this enzyme cleaves both strands of its pseudopalidromic sequence during a single binding event by flipping on the DNA. This kind of reorientation may require the protein to enter a pseudobound state, which can be disrupted by high salt concentration. Alternatively, the protein may maintain nonspecific contacts with the DNA backbone, rendering the transition insensitive to ionic strength. Preliminary work with BcnI suggests that it does not pass through a pseudobound state. We are now investigating whether the same is true for MvaI. We use a total internal reflection fluorescence microscopy (TIRF) based single molecule assay to observe DNA cleavage and determine how salt impacts the reaction mechanism. We also use DNA substrates that are designed to report on either duplex cleavage or nicking of a specific strand of the pseudopalindromic sequence to determine whether there is a bias in initial binding orientation. Our overall goal is to establish a model for how monomeric Type IIP restriction endonucleases bind and cleave duplex DNA.

Engaging Tribal Nations of the Great Lakes Region on Chronic Wasting Disease through a community-based participatory research approach

Discipline: Life Sciences

Subdiscipline: Other Life Sciences

Roger Faust*[1], David Fulton[2], Tiffany Wolf[3]

[1]University of Minnesota, Twin Cities, [2]USGS, [3]University of Minnesota, Twin Cities

Abstract: Chronic wasting disease (CWD) is a contagious neurological disease found in the family Cervidae in roughly half of the US, including Minnesota and other upper Midwest states, in addition to several countries abroad. The continuing spread of CWD poses a threat to wildlife health and related human activities. To keep CWD prevalence low, and to prevent spread to novel regions, government agencies, researchers, policymakers, and stakeholders, including hunters and landowners, must work together. While CWD management requires robust communication and cooperation between managers and stakeholders, research has suggested the traditional methods of communications used by wildlife agencies have failed to reach culturally diverse hunting communities. Beginning in 2019, our team at the University of Minnesota has worked to develop and deliver CWD outreach to diverse hunting communities, including Native American, Hmong, and Amish groups, as well as learn how the MN Department of Natural Resources can further extend their own outreach efforts. Through community-partner-led interviews, we hope to identify information sources, knowledge gaps, and perspectives on CWD. Surveys will help us characterize hunting activities, perceptions, and responses to CWD management for each group. Our ultimate goals are to help develop educational materials on CWD that reflect the communities' cultural values and perspectives on risk related to wildlife disease, in addition to better including these communities in CWD management and control.

Accelerated GABAergic Neuron Maturation in a Human Induced Pluripotent Stem Cell-Derived Neuronal Model of SLC6A1-Related Developmental and Epileptic Encephalopathy

Discipline: Life Sciences
Subdiscipline: Neurosciences

Maria Varela*[1], Tyler Thenstedt[2], Michael Uhler[3], Jack Parent[4]
[1]University of Michigan, Ann Arbor, [2]University of Michigan, Ann Arbor, [3]University of Michigan, Ann Arbor, [4]University of Michigan, Ann Arbor

Abstract: Myoclonic atonic epilepsy (MAE) is a severe developmental and epileptic encephalopathy (DEE) that has been linked to mutations in the SLC6A1 gene. SLC6A1 encodes for the most abundant brain GABA transporter, GAT-1, which regulates the reuptake of GABA at the synapse and is expressed primarily in interneurons. While loss of function (LOF) of GAT-1 leads to epilepsy and cognitive delays, how GAT-1 knockout and haploinsufficiency affects early neuronal development remains elusive. Here, we use a human induced pluripotent stem cell (iPSC)-derived neuronal model to test the hypothesis that GAT-1 LOF alters interneuron development. We reprogrammed human foreskin fibroblasts into iPSCs with concurrent CRISPR/Cas9 gene editing to generate out-of-frame insertions/deletions in the SLC6A1 gene. Compound heterozygous (KO), heterozygous (Het), and isogenic control (WT) iPSC lines were generated and differentiated into induced GABAergic neurons (iGNs) using inducible expression of ASCL1 and DLX2. We performed immunolabeling and RT-qPCR on iGNs from 1-4 weeks to investigate interneuron development and specification. GAT-1 mRNA expression was decreased 80-95% in KO and 10-70% in HET iGNs compared to WT (n=3 lines each). WT iGNs displayed the expected GABAergic and mature neuronal marker expression and morphology while KO iGNs displayed accelerated maturation with earlier increases in potassium-chloride cotransporter 2 (KCC2) and somatostatin expression compared to WT. Our findings suggest that LOF mutations in the SLC6A1 gene that are predicted to increase ambient GABA levels in early brain development would have deleterious effects on interneuron maturation. Further investigation into this phenotype could provide treatment targets for SLC6A1 -related DEEs.

Postmortem Interval Identification through Microbial Composition

Discipline: Life Sciences
Subdiscipline: Microbiology

Zethus Avery*[1], James Crill II[2], Jonathan Jacobs[3], Katherine Smith[4]
[1]Syracuse University, [2]Syracuse University, [3]American Type Culture Collection, [4]Syracuse University

Abstract: A death investigation must answer four major questions: what is the cause of death, mechanism of death, manner of death, and time of death. The key to answering the last question, time of death, is discovering how long the body has been dead - otherwise known as the postmortem interval (PMI). Currently, death investigations utilize visual sightings or last communications, which can be unreliable being based on the limitations of human memory; insect activity, which can be inconsistent depending on the availability of insects associated with decomposition; and biochemical changes in the body, which are subjective with limited standardization. Microorganisms live within the body but the community that they exist in is disrupted after death, causing predictable changes during the stages of decomposition.

Preliminary findings have shown that these changes in microbial composition are regular enough to create a ‘clock’ to increase the accuracy and precision of estimation. This project is the first step in creating a new method for PMI identification using an amplicon panel of identified microorganisms. In constructing a list of microorganisms associated with the stages of decomposition, lapses in genomic information necessary for accurate and specific amplicon primer generation were identified. To address this disparity, two fungi of interest, Yarrowia lipolytica and Stachybotrys cylindrospora , were sequenced at the strain level, thus allowing the generation of more specific primers for the final amplicon panel. This project has produced the beginnings of a new method using microbial composition - the basis for revolutionizing postmortem interval identification.

Temperature Variation, diversity, and disease

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jenavier Tejada*[1], Katie Schroeder[2], Alex Strauss[3], Daniel Suh[4]
[1]Denison University, [2]University of Georgia, [3]University of Georgia, [4]University of Georgia

Abstract: Title: Effects of temperature fluctuation on disease transmission in multi-host communities The dilution effect seeks to explain disease transmission in environments with multiple species. Essentially, the dilution effect predicts an increase in diversity will lead to a decrease in disease transmission. In zooplankton communities, the resistant diluter, Ceriodaphnia dubia can lessen disease in the host Daphnia dentifera caused by the parasite Metschnikowia bicuspidata . However, dilution is only effective when diluters and hosts co-exist; because when they compete, competitive exclusion can occur. Fitness of both D. dentifera , and C. dubia depend on temperature. Specifically, C.dubia benefits in warmer temperatures and D. denifera in cooler temperatures. Therefore, in environments where temperatures fluctuate, this may lead to co-existence, greater abundances of the diluter, and less disease transmission. We are testing whether the dilution effect reduces infection prevalence when a diluter is present, and how dilution effects differ at a constant 20˚C versus a fluctuating temperature around the same mean. We designed a multi-generational mesocosm experiment with communities that contained the host and parasite, and communities that contained the hosts, parasites, and diluters at both constant and fluctuating temperatures. We hypothesize that the changing environmental conditions caused by fluctuating temperature will lead to more diluters, causing a greater dilution effect via co-existence of the host and diluter. This project will help us learn more about the possible effects of climate change – especially variable temperature – on disease dynamics in communities with multiple species.

Evolution of antibiotic resistance in the pathogenic bacterium Pseudomonas aeruginosa

Discipline: Life Sciences
Subdiscipline: Microbiology

Kade Townsend*[1], Josephine Chandler[2], Rhea Abisado[3], Brielle McKee[4], Kate Woods[5]
[1]University of Kansas, [2]University of Kansas, [3]Atenea de Manila University, [4]University of Kansas, [5]University of Kansas

Abstract: The often-fatal infectious pathogen Pseudomonas aeruginosa is particularly difficult to treat due to its propensity to mutate to become highly antibiotic resistant. P. aeruginosa is a model for understanding a type of bacterial communication called quorum sensing, which controls and coordinates certain group behaviors when the population reaches a critical density or “quorum.” A type of quorum sensing in P. aeruginosa involves a secreted signal, acyl-homoserine lactone, which at a sufficient concentration binds to the transcription factor LasR to cause it to activate specific genes. Paradoxically, lasR- null mutations are commonly isolated from chronic infections of antibiotic-treated patients, suggesting lasR- null mutants somehow persist under antibiotic selection despite having enhanced susceptibility. Here, we use a laboratory evolution model to explore the hypothesis that lasR- null mutants persist in the presence of antibiotics because they acquire adaptive mutations that alter the role of LasR in antibiotic resistance. We find one mutation in the translation elongation factor FusA1 that increases resistance of lasR mutants more substantially than the wild type parent. Thus, fusA1 mutations can confer a selective advantage to lasR mutants in the presence of antibiotics. Our results show that the mechanism might be through changes in regulation of an antibiotic efflux pump called MexXY. Mutations in fusA1 are common in clinical P. aeruginosa isolates and may provide a possible avenue for the emergence of lasR mutants during chronic infections of antibiotic-treated patients.

Investigating the Relationship Between Aggression and Longevity

Discipline: Life Sciences
Subdiscipline: Biochemistry

Abigail McInnes*[1], Dr. Johannes Bauer[2], Arwa Al-Rakabi[3]
[1]California State University, Sacramento, [2]California State University, Sacramento, [3]California State University, Sacramento

Abstract: Aging is a complex process that is still incompletely understood. It has been suggested that an organism’s genetics has a relatively smaller impact on the rate of aging than previously thought, and that behavioral and environmental factors play a much more important role. Social environment, for example, has been strongly linked with longevity. Drosophila melanogaster fruit flies are a common model organism for social and behavioral studies due to the well-documented and sophisticated nature of their social behaviors. It is thus possible to use fruit flies to study the impact of altered behavior or social environment on lifespan and aging. On a molecular level, insect behavior is governed by pheromones, small hydrophobic molecules that are presented on the fly cuticle. We have previously shown that modulation of pheromone levels changes not only fly behavior, but also longevity. In this study, we further investigate the impact of social behavior on pheromone expression, behavior, and aging. Previous studies have identified a gene associated with aggression in fruit flies, Cyp6a20 . Using a combination of behavioral tests, longevity evaluation, and GC/MS analysis, our data shows that male Cyp6a20 knockdown flies are hyper-active, hyper-aggressive, and tend to socially isolate. Importantly, these flies have a decreased lifespan and an altered pheromone profile, suggesting that pheromones modulate longevity. However, the molecular mechanisms remain unclear. Our study offers insight into the interplay between behavior, social environment, and longevity. It also lays the foundation for future studies investigating the molecular mechanism by which Cyp6a20 and pheromones modulate longevity.

Mitochondrial Cytochrome Oxidase I variation in freshwater crayfish in the Coastal Plain of Georgia

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Valeria Ensenat Rivera*[1], J. Checo Colón-Gaud [2], J. Scott Harrison[3]
[1]Georgia Southern University, [2]Georgia Southern University, [3]Georgia Southern University

Abstract: Crayfish are freshwater decapods related to shrimps, crabs, and lobsters. The state of Georgia has a substantial diversity of crayfish, containing over 30 species in the genus Procambarus . As highly endemic organisms, many of the species found in these river basins occur nowhere else in the world; however, little is known about their ecology and distribution. This project aims to bridge the gap in knowledge by using a combination of morphological and genetic techniques to identify species sampled in the Coastal Plain of Georgia and by assessing the variation of the mitochondrial Cytochrome Oxidase I (COI) genes present in select species along various river basins within Georgia’s Coastal Plain. Crayfish were obtained from the Savannah, Canoochee, Ogeechee, Altamaha, and Satilla River basins as well as from Sapelo Island using passive (e.g., baited minnow traps) and active sampling techniques (e.g., dip nets and kick nets). Tissue sample was extracted from tail muscle and the presence of genetic material was quantified using the NanoDrop spectrophotometer. Polymerase chain reaction (PCR) was used to isolate and amplify a 600bp fragment of the COI gene which was subsequently sequenced. After obtaining the information, the sequences were matched with those on the NCBI database and used in phylogenetic analysis with sequences of known species. At the end of this project, we will be able to contribute new information regarding the variation of COI genes, distribution, and phylogeny of the crayfish species that inhabit Georgia's Southeastern Coastal Plain.

Exploring the Functions of C1ORF109, SPATA5, & SPATA5L1, Three Understudied Universal Essential Human Genes, in Cell Viability and the Cell Cycle

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Emiliano Soto-Romero*[1]and Laura Diaz-Martinez [2]
[1]Gonzaga University, [2]Gonzaga University

Abstract: The human genome contains ~25,000 genes but only 486 genes are required for cell viability. These genes are termed Universal Essential (UE). Many UE genes are very understudied and thus their functions at the molecular and cellular level are not well understood. Studying the roles of UE genes is key to understanding essential cellular functions. We investigated the functions of three understudied UE genes: C1ORF109, SPATA5, and SPATA5L1 (collectively termed CSS). Recently, these proteins were shown to physically interact and perform roles in ribosome biogenesis. Overexpression of C1ORF109 was previously shown to result in increased DNA damage and cell proliferation. Given their reported function as UE genes, their physical interaction, and C1ORF109’s effects on DNA damage, we hypothesized that the CSS genes have a joint role in genome maintenance and the cell cycle. To test this, we first sought to determine whether CSS genes were universally expressed and universally essential in cancer and non-cancer cells via qPCR and cell viability assays. Then, roles of CSS genes on genome maintenance and the cell cycle were tested by quantitative microscopy and flow cytometry. Consistent with a role as UE genes, CSS expression was detected in all cell lines tested and transfection of siRNAs against CSS genes decreased cell viability. Depletion of C1ORF109 but not SPATA5/SPATA5L1 resulted in increased DNA damage and cell cycle defects. Our results confirm that CSS genes are

UE and point to C1ORF109 having roles in genome maintenance and the cell cycle independently of its interaction with SPATA5/SPATA5L1.

Examining Relationships between Gut Microbiome Diversity and Hippocampal Volume in Cognitively Unimpaired Adults

Discipline: Life Sciences
Subdiscipline: Neurosciences

Muhaison Ibrahim*[1], Dr. Barbara Bendlin[2], Gilda Ennis[3], Margo Heston[4], Federico E. Rey[5], Sterling C. Johnson[6], Sanjay Asthana[7], Rob Knight[8], Antonio González Peña[9], Rima Kaddurah-Daouk[10]
[1]University of Wisconsin - Eau Claire, [2]University of Wisconsin-Madison, [3]University of Wisconsin-Madison, [4]University of Wisconsin-Madison, [5]University of Wisconsin-Madison – Madison, [6]University of Wisconsin - Madison, [7]University of Wisconsin - Madison, [8]University of California, San Diego – La Jolla, [9]University of California, San Diego – La Jolla, [10]Duke University Medical Center – Durham

Abstract: Gut microbiome composition is hypothesized to play a role in Alzheimer's disease (AD) development. Individuals diagnosed with AD dementia were found to have lower microbiome diversity. In another study, lower microbiome diversity was linked to lower scores on working memory tests. However, relationships between microbiome diversity and early AD-associated brain changes pre-clinically have been understudied. Utilizing a sample of cognitively unimpaired adults, we hypothesized that lower microbiome diversity would be associated with lower volume of the hippocampus—a brain structure that undergoes atrophy prior to cognitive decline. 157 cognitively unimpaired study participants provided fecal samples and T1-weighted neuroimaging through the Microbiome in Alzheimer's Risk Study, Wisconsin Alzheimer's Disease Research Center, and Wisconsin Registry for Alzheimer's Prevention. The sample likely contained participants in the preclinical stage of AD since it had an increased proportion of participants with the AD risk allele APOE e4. 16S rRNA V4 sequencing was performed on fecal sample to obtain microbiome composition and diversity measures. CAT12 and SPM12 were used to preprocess images and quantify hippocampal volumes with the Automatic Anatomically Labeled Atlas 3. Multiple regression was performed to test relationships between hippocampal volume and Chao1 and Faith's phylogenetic alpha diversity measures, controlling for intracranial volume, age, and sex. We found no significant associations between gut microbiome diversity and hippocampal volume (ps=0.886,0.927) within this sample. Our future directions include further investigation into specific microbial species and their metabolites in order to examine the relationship between microbial factors and brain amyloid deposits, a key pathologic hallmark of AD.

Understanding adipocyte enhancer binding protein 1 (AEBP1) inhibition in reducing fibrosis

Discipline: Life Sciences
Subdiscipline: Biology (general)

Nishoni Huber*[1], Thirupura Sundari Shankar[2], Stavros Drakos[3], Georgiy Polishchuk[4], Ty Lunde[5]
[1]Northern Arizona University, [2]University of Utah, [3]University of Utah, [4]University of Utah, [5]University of Utah

Abstract: Heart failure patients are often diagnosed with multi-organ failure and multi-organ fibrosis. There is a notable role of adipocyte enhancer binding protein 1 (AEBP1) in fibroblast differentiation and extracellular matrix deposition. Previous research has shown an increase of AEBP1 in liver, lungs, and white adipose tissue fibrosis and AEBP1 knockdown (KD) resulted in a reduction in active fibrosis in these organs. The role of AEBP1 in cardiac and skeletal muscle fibrosis needs further understanding. Our current research will establish the role of AEBP1 in these organs, thereby making AEBP1 a potential therapeutic target for multi-organ fibrosis. Our preliminary data shows that AEBP1 overexpression independently drives cardiac fibroblast activation, evident from an increase in SM22, early fibroblast differentiation marker (n=6, p=0.06) and AEBP1-KD resulted in a significant reduction in SM22 (n=6, p=0.03). Angiotensin (1.5µg/g/day) and phenylephrine (50µg/g/day) were injected in mice for 4-weeks to induce multi-organ fibrosis (established fibrosis model). A subset of mice received adeno-associated virus 9 (AAV9) containing shRNA that results in AEBP1-KD, remaining mice received control virus. In vitro studies on mice heart showed a reduction in SM22 (n=6, p=0.07) upon AEBP1-KD. A significant reduction in SMA, marker of activated fibroblasts, was also observed in skeletal muscle (n=6, p=0.001) upon AEBP1-KD. Overall, our results suggest a unique role of AEBP1 in cardiac and skeletal muscle fibrosis. A greater understanding of AEBP1-mediated fibrotic pathways can lead to using AEBP1 as a potential target for multi-organ fibrosis.

Examining the Protective Role of p62 in Ischemic Heart Disease

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Eric Norman*[1], Sihem Boudina [2], Rajeshwary Ghosh[3]
[1]Lewis & Clark College, [2]University of Utah, [3]University of Utah

Abstract: Ischemic Heart Disease (IHD) is a leading cause of heart failure. IHD induces tissue hypoxia, which can induce myocardial cell death. Under hypoxic conditions, Hypoxia-Inducable Factor 1 Alpha (HIF1a), a transcription factor, is stabilized and promotes the expression of cardioprotective genes. Hence, HIF1a stabilization presents a potential pathway for developing IHD therapeutics. Previous studies show that Sequestosome 1 (p62), a ubiquitin-binding protein, stabilizes HIF1a in cancer cells by inhibiting prolyl hydroxylase isoform 3 (PHD3), an enzyme essential for HIF1a degradation. In cardiac cells, p62 accumulates under hypoxic conditions, and deletion of p62 reduces HIF1a stabilization. Therefore, we hypothesize that p62 stabilizes HIF1a in response to ischemic distress in cardiac cells to an extent that is functionally relevant. In order to test our hypothesis, H9c2 cardiomyoblasts will be transfected with control and p62 siRNA to knock down the p62 gene. Afterward, cells will be exposed to hypoxia and normoxia. Next, gel electrophoresis and immunoblotting will be used to determine HIF1a and p62 levels. Thereafter, we'll characterize HIF1a activity by quantifying the expression of HIF1a target genes using qPCR. We anticipate heart cells with p62 knockout to decrease HIF1a levels and activity. We will then track the hydroxylation of HIF1a to access the p62 knockout effects on PHD3 activity to characterize the hypoxia pathway. We anticipate PHD3 activity to increase in the absence of p62. As there are no viable HIF1a stabilizers for IHD treatment, p62 presents a novel approach to HIF1a stabilization that can serve as a target in IHD therapeutics.

Grainyhead regulates myosin and the endocycle during wound healing in Drosophila

Discipline: Life Sciences
Subdiscipline: Genetics

Abbey Avila*[1], Vicki Losick [2], Levi Duhaime[3]
[1]Boston College, [2]Boston College, Professor, [3]Boston College

Abstract: Tissue repair is a complex process occurring routinely throughout a human's lifetime. The mechanics behind this process involve efficient cell replacement during wound healing, which can be modeled in Drosophila melanogaster . Previous studies have implicated the importance of polyploid cells - cells with greater than 2C DNA content - during epithelial tissue repair in this organism. Additionally, the transcription factor Grainyhead (Grh) has been shown to regulate cell-cycle and cytoskeletal proteins, both of which are critical to wound-induced polyploidization in Drosophila abdominal epithelium. We hypothesized that downregulating Grh expression would affect these proteins necessary for the wound repair process, resulting in altered epithelial mechanics and disruption of polyploid cell growth. We used RNA interference to produce fly progeny with epithelial specific Grh knockdown, then analyzed the tissue and abdominal mechanics of transgenic flies 3 days post injury. Here, we first observed that Grh is required for polyploid cell growth as it regulates entry into the endocycle and cell fusion. Next, we found that Grh regulates cytoskeletal organization in wound-induced polyploid cells by visualizing localization of non-muscle myosin II expression. Lastly, we observed the impact of Grh knockdown on epithelial mechanics and measured a decrease in male fly bending efficiency. Taken together, we find that Grh has a plethoric effect on wound-induced polyploidization as it affects both the generation of polyploid cells and abdominal mechanics by altering myosin organization. Further analysis of the cellular processes regulated by Grh will be vital to understanding the role of polyploidy in tissue repair.

Tau-Induced Alterations in Clock-Driven Activity in a Drosophila Model of Alzheimer's Disease

Discipline: Life Sciences
Subdiscipline: Neurosciences

Victor Sanchez-Franco*[1], Masashi Tabuchi [2], Masashi Tabuchi[3]
[1]Case Western Reserve University, [2]Case Western Reserve University School of Medicine Department of Neurosciences, [3]Case Western Reserve University School of Medicine Department of Neurosciences

Abstract: Recent studies have reinforced the role of tau, a microtubule-associated protein, in the prevalence of sleep disturbances in Alzheimer's disease (AD). While emerging data from our group suggests that tau can modulate circadian rhythmicity in AD, the mechanisms underlying this relationship are poorly understood. In this study, we were specifically interested in characterizing the mechanistic underpinnings underlying tau's impact on circadian clock-driven activity. We used a Drosophila melanogaster model of AD due to the variety of genetic tools available and the fly's functional similarities to mammalian sleep and AD pathology. To manipulate the expression of tau in a tissue-specific manner, the Gal4/UAS binary expression system was used. Specifically, we crossed a DN1 circadian clock neuron-specific driver line with a tau reporter line—which led to the expression of tau in the DN1 circadian clock neurons of Drosophila . Behavioral alterations of clock-driven activity due to tau expression were characterized by measuring daytime and nighttime sleep duration, sleep bout number, and sleep bout length. Tau-induced morphological alterations of clock neurons were characterized by dissection and immunostaining of DN1 neurons in Drosophila . We hypothesized that tau modulates clock-driven activity via alterations in sleep architecture and DN1 morphology. We found that tau expression in DN1 neurons significantly altered sleep architecture and circadian rhythmicity. Strikingly, we observed significant increases in the length, volume, and area of DN1 clock neurons of tau-expressing flies. Establishing the quantitative relationship between AD pathology, altered tau activity, and sleep can open up the possibility of developing novel AD-modifying therapeutics.

Different neural subtypes produce distinct amyloid structures in mouse models of Alzheimer's disease

Discipline: Life Sciences
Subdiscipline: Neurosciences

Gabriella Perez*[1], Joanna L. Jankowsky[2], Rong Zhao[3], Danish M. Uddin[4], Jonathan C. Bean[5]
[1]Baylor College of Medicine, [2]Baylor College of Medicine, [3]Baylor College of Medicine, [4]Baylor College of Medicine, [5]Baylor College of Medicine

Abstract: Alzheimer's disease (AD) is the most common form of dementia and characterized by the formation of extracellular amyloid plaques in the brain. Although plaques are diagnostic of AD, they can look qualitatively different between subjects and it is not known how these differences arise. Clinical symptoms also vary among patients, leading to the hypothesis that distinct plaque conformations contribute to clinical heterogeneity. To study this issue in the laboratory, plaque formation has been modeled in mice by overexpressing the amyloid precursor protein (APP). All neurons express APP in the human cortex, however, many of the existing AD mouse models overexpress APP largely from excitatory neurons. Inhibitory neurons serve a different function in the brain and often do not express APP in many AD mouse models. We hypothesized that the neuronal source of APP may contribute to plaque and clinical diversity found in patients. To test this, we generated two mouse models expressing APP in either excitatory or inhibitory neurons. We used immunofluorescence and histological staining to examine plaque structure in the brains of our mice. Although both models produced amyloid plaques, their structures were completely different. Excitatory plaques stained for both amyloid peptide and thioflavin dye, which is a diagnostic standard for human AD. In contrast, the inhibitory model stained for amyloid peptide but lacked thioflavin staining. Our findings suggest that inhibitory and excitatory neurons produce distinct amyloid structures that may contribute to variation in AD pathology, presentation, and progression.

Connecting Refractive Power to Quaternary Structure of Lens Beta-crystallins

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sophia Hernandez*[1], Michael Bergman[2], Leila Deravi[3]
[1]Northeastern University, [2]Northeastern University, [3]Northeastern University

Abstract: Crystallins (alpha, beta, and gamma) are the primary constituents of the eye lens and play a role in maintaining its structure and refractive power. These proteins have published refractive index increments (dn/dc) of .190, .187, and .203 mL/g for alpha, beta, and gamma-crystallin respectively. Previous work has shown that the concentration of each crystallin type varies across the lens, creating a refractive index gradient. The center of the lens is heavily populated with gamma-crystallin proteins, which are the most refractive. 25% of the cortex of the lens is made of beta-crystallins. They are the least refractive and the dn/dc value has only been established for the heterogenous mixture. We asked if the refractive increment of beta-crystallins was dependent upon their quaternary structure. We focused on isolating beta-

crystallin oligomers b H and b L2 by size from calf lens lysates utilizing size exclusion chromatography (SEC). After purification, we quantified each sample collected to determine their refractive power as dn/dc at 589 nm. We found that the larger oligomers exhibited slightly lower average dn/dc value compared to the dimers (p < 0.05). The experimental values obtained were lower than those previously reported, potentially suggesting a role for additional protein-protein interactions among beta-crystallins in elevating refractive power. We have been investigating these interactions using surface tensiometry to identify conditions with cohesive interactions. Our results indicate that the quaternary structure of beta-crystallins affects molecular behavior at the air-liquid interface and these interactions may be important for molecular packing necessary for producing light refraction.

Investigating the effects of GIRK1 channels on sleep-dependent memory consolidation in Fragile X Syndrome

Discipline: Life Sciences
Subdiscipline: Neurosciences

Roxanne Perez Tremble*
Temple University

Abstract: Fragile X Syndrome (FXS) is a genetic disorder - caused by the silencing of the Fragile X messenger ribonucleoprotein 1 (FMR1) gene - that leads to one of the most common forms of neurobiological intellectual disability. The FMR1 protein product FMRP is responsible for developing neuronal synapses and promoting neuronal communication. These mechanisms are disrupted in FXS-affected individuals and can lead to difficulties in both cognition and sleep. Sleep loss itself disrupts learning and memory processing. However, the contribution of sleep loss to disrupted cognitive function in FXS is unclear. We hypothesize that restoring sleep in a mouse model of FXS (Fmr1 KO) will allow for proper consolidation of memories. We used a novel hypnotic compound called ML297 that directly activates G-protein inward rectifying potassium (GIRK) channels. Activation of these GIRK channels prompts inhibitory neurotransmission and selectively promotes non-rapid eye movement (NREM) sleep. Using ML297, we tested if restoring sleep can also rescue cognitive deficits in Fmr1 KO mice. Our paradigm had mice undergo contextual fear conditioning followed by injection of vehicle or ML297. Mice were tested 24-h later for the effects of GIRK activation on memory consolidation. Hippocampal sections were collected for immunohistochemistry to visualize the expression of activity-dependent neuronal markers such as cFos tied to memory consolidation. We predict that GIRK activation rescues fear memory and increases hippocampal c-Fos formation in Fmr1 KO mice compared to vehicle controls. These results could offer insight on how sleep promoting hypnotics could improve cognition in individuals who suffer from FXS.

Cellular Rearrangements and their Interactions with the Extracellular Matrix Display Similar Somite Formation Trends in the Xenopus genus

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sophia Huang*[1], Carmen Domingo [2], Julio Ramirez[3]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University

Abstract: In vertebrates, the paraxial mesoderm gives rise to segmented structures known as somites, which differentiate into the dermis, cartilage, skeletal muscles, and tendons in the

adult. Analysis of somite formation in the tetraploid species, Xenopus laevis , is well documented but not in a closely related diploid species, Xenopus tropicalis . To understand muscle formation in X. tropicalis , embryos were injected with a membrane-targeted GFP and immunostained to visualize individual cell shapes at different time points during somite formation. Using two and three-dimensional imaging analysis, we characterized muscle formation in X. tropicalis to capture changes in cell shape and their relationship to the surrounding extracellular matrix (ECM). Our measurements in cell length, surface area, and other shape descriptors at various points indicate that muscle progenitors first elongate and form filopodia before undergoing somite segmentation and rotation. Furthermore, three-dimensional analysis indicates that ECM deposition and cell rotation are well synchronized during somitogenesis. Our quantitative analysis also demonstrates that the sequence of morphological changes in muscle progenitors in X. tropicalis and X. laevis are very similar as they undergo similar cell shape changes and a 90-degree rotation. One distinction is that the timing of these morphological events is accelerated in the smaller X. tropicalis embryo. Since X. tropicalis has retained the ancestral diploid number of chromosomes, it will be more straightforward to determine the molecular underpinnings that control muscle formation in this species and its evolutionary significance to other vertebrate species.

“Flat and Fearsome: a Newly Discovered Carnivorous “Palm Frond Sponge” from the Deep Northeast Pacific Ocean”

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kaylee McKay*[1], Dr. Amanda S Kahn[2], Lonny Lundsten[3], Craig McClain[4]
[1]California State University Monterey Bay, [2]Moss Landing Marine Labs, [3]Monterey Bay Aquarium Research Institute, [4]Louisiana University Marine Consortium

Abstract: The deep ocean is a vast frontier, largely unexplored, with new species yet to be identified and described by science, including many sponges (Porifera). Describing and classifying sponges can be challenging because their morphology is often quite variable. Sponges are typically classified into taxonomic groups using morphology, careful analysis of spicules (hard skeletal elements made of silica or calcium carbonate), and, more recently, molecular techniques. This research aims to taxonomically classify the recently discovered “Palm Frond Sponge”, a leaf-shaped carnivorous sponge. We collected and preserved 18 specimens from deep waters ranging from central California to northern Canada. We identified and measured 5 spicule types including (n=50 for each type): small and large oxeas (length: 71-288-1136 µm; width: 0.91-11-29 µm; min-mean-max), strongyles (length: 645-655-664 µm; width: 10-10-10 µm), forceps (32-53-62 µm), and palmate anisochelae (18-20-24 µm). Amphipods and other small crustaceans were observed within the sponge tissue, suggesting active carnivory at the time of collection. The suite of spicules identified confirm that this species is a Cladorhizidae (the family of carnivorous sponges). Our goal for this project is taxonomic identification and formal description with assignment of a scientific name if it is confirmed to be a new species, which we believe it is. Ultimately, this unknown species will contribute to a clearer picture of evolutionary relationships within the Cladorhizidae and will be the foundation of further investigations of taxonomic, evolutionary, and ecological relationships within both its family and genus.

Role of Pyruvate Kinases M1 and M2 in the Regulation of the mSWI/SNF Chromatin Remodeling Enzymes

Discipline: Life Sciences
Subdiscipline: Biochemistry

Imaru Di Bartolomeo*[1], Teresita Padilla-Benavides [2], Monserrat Olea-Flores[3], Anthony N Imbalzano[4]
[1]Wesleyan University, [2]Wesleyan University, [3]University of Massachusetts Chan Medical School, [4]University of Massachusetts Chan Medical School

Abstract: Pyruvate kinase muscle (PKM) isozyme has different isoforms, PKM1 and PKM2, that differ due to alternative splicing. These proteins have key roles in glycolysis, and they can act as protein kinases that phosphorylate other substrates, which affect other biological events. PKM1 and 2 are known to have roles in myoblast proliferation and differentiation. Other proteins involved in our study are the mSWI/SNF complexes, which are chromatin remodeling enzymes that consist of three subfamilies called BAF, ncBAF, and PBAF. Each of these subfamilies has unique subunits including BAF250-A, BRD9, and BAF180 respectively. These subfamilies have distinct functions, in addition to different subunit compositions. Our group recently determined that BAF and ncBAF contribute to myoblast proliferation and/or differentiation. Our goal in this project is to determine the roles of PKM1/2 in myoblast proliferation and/or differentiation as well as to see if there is any connection between these proteins and the expression of subunits of the mSWI/SNF complexes. Multiple experiments were conducted including western blots, cell cultures, immunohistochemistry, ChIPs, and qPCR with knockdowns of PKM1/2 to determine the specific roles and connections, if any, between PKM and mSWI/SNF enzymes. So far, our efforts have confirmed that PKM regulates the proliferation and differentiation of myoblasts. Preliminary results have shown that there is a connection between PKM1/2 and the expression of specific subunits of the mSWI/SNF complex in myoblast proliferation and differentiation, but further investigation is needed to determine the mechanism.

Evaluating the efficiency of a germline structural variant classifier

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ipsa Mittra*[1], Simona Dalin [2], Sean Misek[3], Rameen Beroukhim[4]
[1]University of Maryland, College Park, [2]Broad Institute of MIT and Harvard, [3]Broad Institute of MIT and Harvard, [4]Broad Institute of MIT and Harvard

Abstract: Most commonly used cancer cell lines were derived from patient samples collected many years ago, but these cell lines rarely have paired normal samples. Without a matched normal, we cannot know which structural variants, or genetic rearrangements, in these samples are germline (inherited) or somatic (cancer-related). Our team has developed a computational approach, a linear support vector machine (SVM), to distinguish whether a structural variant is germline or somatic using training and testing data from a single structural variant caller. However, different structural variant callers rely on different assumptions and methods, and it is unknown how well our SVM performs using these alternate structural variant callers. To determine the performance of our SVM across structural variant callers, we will evaluate our SVM on data from multiple callers, including Snowman, SvABA, and Manta. Understanding the efficacy of our SVM for each combination of caller input for training and testing will inform us which callers we can use for our tool. Future applications include distinguishing germline and somatic structural variants in commonly used cancer cell lines and in panel sequencing data (a

common method to clinically assess patients) which often don't include matched normal data. These results will help better understand the role of structural variants in cancer and therapeutic response.

Interactions between C. glabrata and E. faecalis impact polymicrobial biofilm architecture

Discipline: Life Sciences
Subdiscipline: Microbiology

Sabrina Hernandez*[1]and Jesus Antonio Romo [2]
[1]University of Massachusetts Boston, [2]Tufts University School of Medicine

Abstract: Candida glabrata is an opportunistic pathogenic fungus and common colonizer of the gastrointestinal tract (GI). Our group has shown that C. glabrata can interact with bacterial pathogens found in the human gut, impacting disease outcomes. We used a biofilm assay to grow C. glabrata with a variety of bacteria found in the GI to identify polymicrobial interactions. A combination of biofilm biomass (Crystal violet), metabolic activity (PrestoBlue and XTT), and colony-forming unit (CFU) measurements were used to characterize overall biofilm formation and composition. Moreover, confocal scanning laser microscopy (CSLM) was used to analyze biofilm architecture. Here, we show that C. glabrata and Enterococcus faecalis form polymicrobial biofilms with a distinct matrix composition. The C. glabrata quorum sensing molecule, tyrosol, did not significantly impact E. faecalis biofilm formation. However, media spent by C. glabrata impacted E. faecalis growth in a dose-dependent manner suggesting that the interaction could be partly due to a C. glabrata secreted molecule, metabolic competition, or a metabolic byproduct. Interestingly, previous studies have shown that E. faecalis can impact the biology of the fungus Candida albicans . Additional studies have characterized the chitinolytic machinery of E. faecalis , highlighting the ability to utilize chitin, a significant component of fungal cell walls. Both findings suggest that E. faecalis interacts with a variety of fungi. While further characterization of these interactions is required, the preliminary data presented here suggest that interaction between C. glabrata and E. faecalis impacts biofilm architecture, which could impact therapeutic interventions and host responses.

Forest Carbon Cycling Belowground: Changes in Root-Based Carbon Flux Under Warming Temperatures

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cristina Winters*[1], Nikhil Chari [2], Thomas Muratore[3], Gabriela Martinez[4], Serita Frey [5], Benton Taylor[6]
[1]California State Polytechnic University, Humboldt, [2]Harvard University, [3]University of New Hampshire, [4]Xavier University, [5]University of New Hampshire, [6]Harvard University

Abstract: Terrestrial soils are Earth's largest organic carbon sink; however, the effect that warming temperatures have on soil carbon cycling as it relates to roots and their mycorrhizal (fungal) associates is not well understood. Shifts in plant species composition under climate change, specifically in northeastern temperate forests (a critical U.S. carbon sink) may have significant consequences for soil carbon storage. Plant roots and their fungal associates regulate carbon flux belowground via root exudation (release of organic compounds into soil) and root respiration (release of carbon dioxide), and warming may affect both metabolisms uniquely. We investigate (1) how long-term soil warming alters the relationships between root exudation and respiration; and (2) if roots associated with different mycorrhizal types experience the change in the relationship between exudation and respiration differently. This is important as species composition in New England forests shifts toward a greater proportion of arbuscular-associated trees, especially maples. In forested plots that are warmed using buried heating cables, we took paired root exudation and respiration measurements from arbuscular- and ectomycorrhizal-associated tree species in response to long term soil warming at the Harvard Forest Long Term Ecological Research (LTER) site in Petersham, MA. Additionally, we measured the respiration levels of these fine root systems once exudate collection was complete. We expected the slope of the relationship between root exudation and respiration to increase under warming, indicating a greater proportion of root exudates immediately respired and potentially decreasing the total belowground exudate-based carbon storage. This could have ecosystem-scale consequences for total carbon storage.

The Effects of C1q in Endothelial Wound Healing

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Enidh Padron*[1], Deborah Fraser[2], Mehernaz Haque[3]
[1]California State University Long Beach, [2]California State University Long Beach, [3]California State University Long Beach

Abstract: Atherosclerosis is a chronic inflammatory disease that is very common and is a major cause of death in the USA. This disease causes damage to the endothelium that lines blood vessels and leads to infiltration of monocytes/macrophages and low density lipoproteins (LDL) into the arterial wall. LDL can then become oxidized also known as oxLDL, which is pro-inflammatory. Innate immune protein C1q is known to be produced by macrophages in atherosclerotic lesions, and binds oxLDL. C1q has beneficial effects on macrophage functions but the effect of C1q on endothelial functions in atherosclerosis is not well known. The aim of our study was to test C1q modulation of endothelial migration. We tested the hypothesis that C1q bound to oxLDL will increase endothelial wound healing compared to oxLDL alone. To test this, a wound healing assay was performed. A wound was generated in a confluent culture of human aortic endothelial cells (HAEC) using 3-well culture inserts and a sterile pipette. Cells were treated with oxLDL with and without C1q in 1% serum media and monitored for 24-48 hours using live cell imaging. 10% serum was used as a positive control. The average width of the gap was calculated at different time points for each treatment. Data showed that the presence of C1q substantially increased wound healing, even above levels seen in our positive control. This data suggest C1q may have a beneficial effect on the damaged endothelium in atherosclerosis.

Visualization of Alpha Synuclein Fibrils in Neurons to Better Understand Function Relative to Antiviral Immune Response

Discipline: Life Sciences
Subdiscipline: Microbiology

Giovanni Tovar*[1], J. David Beckham[2], Kelsey Lesteberg[3]
[1]Pomona College, [2]University of Colorado Anschutz Medical Campus, [3]University of Colorado Anschutz Medical Campus

Abstract: Alpha synuclein aggregates (fibrils) in the substantia nigra pars compacta have been linked with Parkinson's Disease pathogenesis. Lewy Bodies form in key sectors of the central nervous system, leading to neuroinflammation and subsequent deficits in dopaminergic neurons. While traditionally thought to be immune privileged, recent data suggests that the central nervous system, through alpha synuclein, may assist with innate and adaptive immune responses. Understanding why alpha synuclein is primarily found in neuronal cells and how the protein interacts with type 1 interferon (T1IFN) can help identify its function beyond PD-pathogenesis. The activation of JAK-STAT in T cells relies on a dimerization moment which leads to downstream signaling that depends on phosphorylation of type 1 interferon. Little is known about the role of alpha synuclein and how it interacts with the JAK-STAT pathway to modulate antiviral adaptive immune responses. Our lab has shown that survival rates decrease in mice that have been genetically modified to lack the SNCA gene (asyn) after infection with West Nile Virus and Venezuelan Equine Encephalitis Virus. Creating a method to visualize and identify the cellular localization of alpha synuclein fibrils, using confocal microscopy and nuclear flow cytometry, and determining if T1IFN stimulation induces formation of alpha synuclein aggregates in primary (prenatal cortical tissue) and secondary (Ren Cells) neurons will help us better understand the potential role of this protein in innate and adaptive immune signaling. We hypothesize that type 1 interferon stimulation induces post-translational modifications in alpha-synuclein that are associated with PD pathogenesis.

How Consumer Familiarity with Seafood Ecolabels Effects the Success of Sustainable Seafood

Discipline: Life Sciences
Subdiscipline: Environmental Science

Ashlee Wells*[1], Rosemary Kosaka [2], Rosemary Kosaka[3], Kristy Wallmo[4]
[1]Sonoma State University, [2]National Oceanic and Atmospheric Administration Fisheries, [3]National Oceanic and Atmospheric Administration Fisheries, [4]National Oceanic and Atmospheric Administration Fisheries

Abstract: Seafood ecolabels provide consumers with information about the ecological impact of their product choice. Ecolabels can tell consumers if a seafood product depletes fish populations through overfishing or involves by-catch which are marine animals unintentionally caught while fishing. These labels have the ability to influence consumer purchasing choices towards more sustainably-caught seafood. Understanding consumer familiarity with seafood ecolabels is crucial in supporting the efforts of sustainable fisheries to ensure the health and survival of fish populations. My research aims to understand the familiarity West Coast consumers have with ecolabels and the environmental impacts of fishing. I investigated whether low levels of familiarity with seafood ecolabels are a barrier to the success of sustainable fisheries and if an increase in awareness can promote sustainable seafood. My research team conducted a web-based stated preference economic survey, collecting data from over 3,000 participants in California, Oregon, and Washington. The questionnaire gathered data from consumers about the seafood they purchase, their purchasing habits, familiarity with seafood ecolabels and sustainable seafood practices. Results show that 72-89% of respondents were unfamiliar with seafood ecolabels. Results also indicated that respondents are unaware of the environmental impacts of fishing such as by-catch. This research found that informing consumers about seafood practices has the potential to influence their purchasing decisions. Seafood ecolabel familiarity must increase in order to successfully support sustainable fisheries.

Genetic tools and morphology clarify the identity of mystery puddle frogs in natural history collections

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Chloe Allen*[1]and Rayna Bell [2]
[1]University of North Georgia, Dahlonega, [2]California Academy of Sciences

Abstract: The African puddle frogs (Family Phrynobatrachidae) are a diverse radiation of nearly 100 species that occur throughout sub-Saharan Africa. Due to their small size and extensive within-species color and pattern variation, species in this group have been notoriously challenging to identify in the field. The advent of DNA-sequencing for species identification has enabled a number of recent studies to clarify species diversity and relationships in some groups; however, many specimens in natural history collections remain unidentified or misidentified. This uncertainty impacts how the specimens and their associated data can be used for research and conservation planning. In this study we use a combination of DNA-barcoding and morphological traits to update the identifications of dozens of “ Phrynobatrachus sp. ” in the Herpetology Collection of the California Academy of Sciences. This set of specimens includes individuals collected from Burundi, Cameroon, Eritrea, Gabon, Sierra Leone, and Uganda over the last several decades. By comparing the genetic and morphological data from these unidentified frogs with the Academy’s extensive reference collection of African frogs we were able to provide updated identifications in the Academy’s database. These updated records and data are also archived in the GenBank database of DNA sequences and in data aggregators that collate species distribution data from natural history museum specimen records where they are freely available to the research and conservation community.

Defining Age-dependent Fibroblast Responses to Influenza Virus Infection

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Abram Rodriguez*[1], David Boyd [2], Summer Jordan[3]
[1]: University of California, Santa Cruz., [2]Primary Investigator, [3]Graduate student

Abstract: Influenza viruses are leading causes of respiratory infections in humans which can result in severe distress to the lungs with long-lasting effects. In many cases, tissue damage caused by the host immune response is the main cause of mortality. Therefore, the host must keep a balance of fighting the infection and maintaining the lungs function to promote recovery. Mesenchymal cells such as fibroblasts, play a key role in the inflammatory response in the lung. Fibroblasts vary depending on their location in the lung, but little is known about whether their functional responses change with age. Our preliminary data show that fibroblasts isolated from four key stages of lung development -(Saccular,Early Alveolar,Late Alveolar,Mature) - have distinct responses to influenza virus infection in vitro. Fibroblasts from early in lung development are tolerant of infection, while those from mature lungs are resistant. We hypothesize that fibroblasts isolated from these stages of lung development represent cells in distinct differentiation states that determine how they respond to infection.To address this hypothesis, we are assessing fibroblast differentiation and activation states during lung development using flow cytometry. Our strategy includes markers that define fibroblasts in distinct locations in the respiratory tract and their activation in response to viral infection. We

are also investigating age-dependent fibroblast responses in vivo in mouse models of severe influenza disease. Categorizing these fibroblast responses may identify novel therapeutic targets to develop age-dependent anti-inflammatory drugs.

Effect of Serum Platinum on Cisplatin-Induced Toxicities

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Freddy Rodriguez*[1], Eileen Dolan [2], Xindi Zhang[3]
[1]Georgetown University, [2]University of Chicago, [3]University of Chicago

Abstract: Cisplatin is a curative treatment for testicular cancer; however, survivors typically experience tinnitus, hearing loss, peripheral sensory neuropathy, and/or Raynaud phenomenon which can be lifelong and detrimental for young men. Serum platinum levels are measurable for years after completion of cisplatin-based chemotherapy. In this study, we explored whether serum platinum levels were associated with these toxicities. We hypothesized that circulating platinum contributes to the severity and persistence of cisplatin-induced toxicities. Using a data set of 832 testicular cancer survivors, linear regression was used to analyze the time since treatment, creatinine clearance, peripheral sensory neuropathy, Raynaud phenomenon, hearing loss, and tinnitus. Cumulative burden of morbidity (CBM) score for cisplatin-induced toxicities was discerned by combining scores for adverse health outcomes (i.e., peripheral sensory neuropathy, hearing damage, tinnitus, and kidney disease). We found a significant negative association between normalized platinum levels and time since treatment (P=5.8e-06). When adjusting for time since treatment, we found a negative association between normalized platinum levels and creatinine clearance (P=.0004) and a significant positive association between normalized platinum levels for the following three: cumulative burden of morbidity score (P=6.87E-05), peripheral sensory neuropathy (P=4E-06) and hearing loss (P=.02). From this data, we were able to conclude that as survivors grew older they experienced more health-related problems and were more likely to experience peripheral sensory neuropathy and hearing loss with residual levels of cisplatin.

Thermoregulatory behavior after diving in the semi-aquatic anole, Anolis aquaticus

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Alva Mihalik*[1], Lindsey Swierk [2], Alexandra Martin[3], Diane Cordero[4]
[1]University of Florida, [2]Binghamton University, [3]Binghamton University, [4]California State Univeristy, San Marcos

Abstract: Ectotherms are highly dependent on environmental temperatures for physiological function. Reptiles often perform thermoregulatory behaviors to succeed in thermally challenging conditions at the cost of other important behaviors, such as mating and defending territory. Anolis aquaticus (Taylor), the water anole, is an under-studied semi-aquatic lizard native to southwestern Costa Rica. The species is a thermoconforming ectotherm and has not yet been observed to engage in any thermoregulatory behaviors. A. aquaticus is able to dive underwater for several minutes to escape predators. This behavior has been demonstrated to significantly reduce their body temperature, but it is unclear how the water anole compensates for such a thermally costly behavior. In order to address this question, we captured a representative sample of adult water anoles from the Java River population at the Las Cruces Biological Station in San Vito de Coto Brus, Costa Rica and observed their behaviors after a

thermal challenge in a climate-controlled lab. Half of the sample was cooled to simulate the effect of a dive while the other half received no thermal challenge. Individuals from both the treatment and control group were then placed in a thermal gradient and allowed to select their preferred microhabitat. We expect that the cooled anoles will select a warmer microhabitat and move towards higher temperatures within the gradient than anoles that had not been cooled. With this research, our goal is to better understand the physiology and behavior of A. aquaticus and how ectotherms compensate in challenging and changing environments.

Urban Growing Practices of Immigrant Agriculturalists in Greater Providence, Rhode Island

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Yuvi Cambero*[1]and Dr. John Taylor [2]
[1]University of Rhode Island, [2]University of Rhode Island

Abstract: The metropolitan Greater Providence area in Rhode Island has an impressive network of food-producing community gardens, urban farms, and home gardens- a large proportion of which are tended by immigrants from diverse countries. This results in agriculturalists in Providence with completely different agricultural experiences regarding the climate, growing spaces, crops, growing practices, cultures, and bodies of traditional ecological knowledge. However, those experiences adapting to a new social and biophysical environment are understudied in academia and underappreciated in policy circles. In this project, approximately ten immigrant agriculturalists in Providence, Rhode Island, are interviewed to learn more about the ways in which they adapt their growing practices to the conditions of their new environment. The data collected includes background information on the growers and how they came to be active in agriculture in Providence; data about the crops they currently produce and production techniques; and the specific ways in which they have adapted traditional ecological knowledge from their place of origin to production in a new environment. I hope to learn more about what, why, and how immigrants are growing, the role they play in the local food system, the challenges they experience during their adaptation, and explore ways in which these challenges can be addressed during policy change. Conducting research on the production dynamics of underrepresented and understudied immigrant populations can allow them to express their distinct experience of urban agriculture and increase public knowledge of the contributions they make to the social, economic, and environmental sustainability of local food systems.

Characterization of Leptin and Aromatase in the Xenopus laevis brain and body

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Malik Alhadi*[1], Tyrone Hayes [2], Alina Nguyen[3]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]University of California, Berkeley

Abstract: Although the physiology of growth and reproduction is well studied in anuran amphibians, not much is known about the interactions between leptin and aromatase (the enzyme that produces estrogens) or their distribution in the brain and body in amphibians. Leptin is a hormone that is released from fat tissue to regulate satiety. It impacts the allocation of energy, which is vital for growth and reproduction. Leptin regulates reproductive hormones by stimulating the enzyme aromatase. Xenopus laevis is a tractable model amphibian to study the relationship between leptin and aromatase because its physiology has been well studied. Leptin and aromatase are known to be located in the liver, gonads, brain, and heart of other animals, but they may be found elsewhere in frogs. I will use immunohistochemistry to examine leptin and aromatase distribution in X. laevis . Leptin and aromatase are likely produced in the fat body, skin, lungs, kidney, and bone. Examining the relationship between leptin and aromatase (and estrogen production) is important for understanding how amphibians allocate resources to growth and reproduction. Further, these studies will lead to other investigations to help understand the impact of external stressors on growth and reproduction in amphibians.

Targeting an Active Chromatin Domain to the X-chromosome

Discipline: Life Sciences
Subdiscipline: Genetics

Claire Gray*[1], Dr. Erica Larschan [2], Joseph Aguilera[3]
[1]Brown University, [2]Brown University, [3]Brown University

Abstract: Transcription must be tightly regulated to drive normal organismal development and to prevent the formation of disease states from cancer to neurodegeneration. To coordinate the regulation of genes, chromatin domains are formed to concentrate key factors at discrete genomic loci that activate or repress sets of genes. Pioneer transcription factors–which have the ability to bind to closed chromatin, recruit chromatin remodelers to open chromatin, and target additional transcription complexes–play a significant role in generating active and repressive chromatin domains. Using the male Drosophila dosage-compensated X-chromosome as a model, I am investigating how protein-binding domains of the genome-wide pioneer transcription factor, Chromatin Linked Adaptor for MSL Proteins (CLAMP), functions to specifically target an active chromatin domain to the X-chromosome. I hypothesize that mutations in CLAMP protein-binding domains will alter proper chromatin domain formation, resulting in the misregulation of dosage compensation. First investigating CLAMP genome-wide targeting, I performed Cleavage Under Targets and Release Using Nuclease (CUT&RUN) on wildtype and clamp mutant larvae to reveal the role of CLAMP protein-binding domains in its global binding. Concurrently, I checked the functionality of dosage compensation in all larvae by performing mRNA-seq, specifically monitoring for significant changes in the X-chromosome transcript output. This study will reveal the importance of specific CLAMP protein-binding domains in chromatin domain formation, which is critical in robust dosage compensation. Subsequently, I will perform Hi-ChIP to define the three-dimensional chromatin interactions mediated by CLAMP, shedding a complete light on the basic mechanisms of chromatin domain formation.

Acute behavioral deficits following a single and repeated mild traumatic brain injuries in mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

Devon Hatcher*[1], Russell Morton [2], Natalie Pinkowski[3]
[1]Western New Mexico University, [2]Assistant Professor, [3]Graduate Student / Research Assistant

Abstract: Mild traumatic brain injury (mTBI) affects millions of people every year, with many experiencing more than one mTBI. These injuries are diagnosed by the symptoms and signs of neurological disfunction including unconsciousness, inability to concentrate, disorientation, imbalance, and/or confusion. However, these symptoms are not required for an mTBI to have occurred. Repeated mTBIs (RmTBIs) are associated with exacerbated clinical symptoms and longer recovery. The purpose of this study is to investigate the relationship between multiple mTBIs and the associated behavioral deficits. Using a closed-skull two-hit mTBI model in mice, the acute behavioral deficits following a single mTBI or RmTBI at 24 hours were investigated. Mice were tested on motor function using several walking tasks – Rotarod, LadderWalk, and CatWalk. Preliminary data suggest that the mTBI animals exhibited significant behavioral deficits following a single mTBI and exacerbated deficits following a RmTBI. These data agree with clinical findings that suggest the more mTBIs experienced, the more severe the behavioral deficits. Future studies are investigating the functional mechanisms underlying these observed deficits.

Growth and chemotaxis response of marine gammaproteobacteria Cobetia and Vibrio to the nitrogenous metabolite homarine

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Tykeedrien Burris*[1], Oscar Sosa [2], Anitra Ingalls[3], Katherine Heal[4]
[1]Barry University, [2]University of Puget Sound, [3]University of Washington, [4]Integral Corp.

Abstract: Homarine is a nitrogenous metabolite produced by a variety of marine phytoplankton and is a significant component of particulate organic nitrogen in the ocean. Because of its widespread production, homarine is expected to be an essential source of nitrogen and carbon to marine heterotrophic bacterial communities. Gene expression analysis of a marine gammaproteobacterium capable of grwoing on homarine indicated that homarine induces upregulation of flagellar biosynthesis genes for swimming motility. We hypothesized that homarine functions as a chemical attractant of heterotrophic bacteria. Chemotaxis towards homarine would enable bacteria to find phytoplankton sources of organic nutrients to support its growth and to promote remineralization of organic compounds. In this experiment, we used two gammaproteobacteria isolates, from the genus Cobetia and Vibrio , to test if homarine promotes swimming motility towards homarine. Both isolates can use homarine as their primary source of carbon and nitrogen. The chemotaxis assays were performed with soft agar seawater media plates containing glucose and several concentrations of homarine. The motility rate was determined by measuring the change in bacterial growth area on soft agar over time with time-lapse imaging. Plate images were analyzed with the ImageJ software. We predicted that the bacteria would display increased motility when higher concentrations of homarine were provided. Preliminary measurements indicate that marine bacteria exhibit a positive motility response to homarine.

Influence of Early Life Adversity on Levels of CaMKIIb and GABAa in the lateral habenula (LHb)

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jessica Kissi*[1]and Maya Opendak [2]
[1]Bates College, [2]Johns Hopkins University

Abstract: The lateral habenula (LHb) is a small midbrain structure that regulates the dopaminergic and serotonergic systems. Cross-species research in adults has demonstrated evidence of LHb hyperactivity in psychiatric disorders, particularly major depressive disorder (MDD). Although these disorders often have their roots in early life, little is known about LHb function in either typical or perturbed development. To assess the impact of early experience on LHb function, rats were either control or adversity-reared from postnatal (PN) days 8 to 12. Adversity-rearing involves providing the rat mother with limited bedding, which increases rough handling of pups. Habenulae were then collected at PN14 and PN27, a pre-weaning and post-weaning age, respectively.To study early LHb activity, we measured levels of calcium/calmodulin-dependent protein kinase II beta (CaMKIIβ) and GABAb receptor in the lateral habenula using Western blot, both of which have been shown to be dysregulated in MDD. An upregulation of CaMKIIβ was observed in control and adversity-reared pups at PN27 in comparison to PN14. In contrast, we detected a downregulation of GABAb receptor in rats across conditions. This upregulation of CAMKIIB and downregulation of GABAb receptor at the post-weaning age was significant in adversity-reared animals only. These findings suggest that LHb activity emerges with age and is sensitive to early life experience, which is important for identifying targets of early intervention and improving clinical treatments.

Assessing arthropod diversity along the vertical organic matter profile (OM) in red mangrove forests surrounding the bioluminescent Laguna Grande, Fajardo, Puerto Rico

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alondra S. Ortiz Sotomayor*[1], Katherine Delgado Durán [2], Maria F. Barberena Arias[3]
[1]Interamerican University, San Juan, [2]Interamerican University, San Juan, [3]Interamerican University, San Juan

Abstract: Arthropods play key roles in ecosystem processes such as decomposition of mangrove leaves, i.e. the breakdown of organic matter resulting in nutrient mineralization that later become available in waters of bioluminescent ecosystems. Laguna Grande in Fajardo, Puerto Rico is one of three bioluminescent ecosystems that exist in Puerto Rico, serving as nursery and habitat for many organisms and as source of employment for local communities. In recent years, bioluminescence has decreased rising concerns about biodiversity loss. This study aims at exploring decomposer arthropod diversity along the vertical OM profile, information to be used to decide better methodologies for later monitoring surveys. We expect arthropods to be more diverse in shallower parts of the OM profile because they need slightly higher temperatures and humidity for survival and reproduction. For this, two 100-m transects were established in the red mangrove forest surrounding Laguna Grande. In each transect, two sampling locations were selected to collect samples. Using a soil corer, OM samples were collected and subdivided into three fractions: whole decomposing leaves, fragmented leaves, and humus. Each fraction was placed in Berlesse funnels for two weeks, collected arthropods were counted and identified to the lowest taxonomic category possible. Abundance was standardized to ind/g dry matter. Preliminary results suggest that there is a greater abundance in whole decomposing leaves samples and a variation of Collembola, Mites, Psocoptera , Isopoda, Diptera, and Larvae. Results will be used for methodology standardization for future projects aiming at understanding the relationship between the mangrove decomposing OM and bioluminescence.

CSRP2 a novel copper binding protein that regulates myoblast proliferation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jaime Carrazco Carrillo*[1], Teresita Padilla-Benavides [2], Dave Klein[3], Michael Quinteros[4], Meili Stanten [5], Sarah J. Hainer[6]
[1]Wesleyan University, [2]Wesleyan University, [3]University of Pittsburgh, [4]Wesleyan University, [5]Wesleyan University, [6]University of Pittsburgh

Abstract: Title: CSRP2 a novel copper-binding protein that regulates myoblast proliferation Copper (Cu) is an essential trace element for the development of mammalian cells and tissues, but it can also be toxic in greater quantities. Cu homeostasis is maintained by a complex network of transporters, chaperones, and transcriptional regulators. Loss of Cu homeostasis leads to the development of pathologies such as Wilson's and Menkes diseases. The Metal Regulatory Transcription Factor 1 (MTF1) is an essential transcription factor that regulates metal homeostasis. Our lab showed that MTF1 possesses a key role in the differentiation of primary myoblasts derived from mouse skeletal muscle, in a Cu-dependent manner. However, MTF1 does not act alone; immunoprecipitation analyses coupled with mass spectrometry showed a potential interaction of MTF1 with chromatin remodelers and a novel set of Cu-binding proteins in proliferating and differentiating myoblasts. Among these, we identified CSRP2 as a novel Cu-binding protein as a potential contributor to myoblast growth. Deletion of CSRP2 using CRISPR/Cas9 suggested a role in proliferation and regulation of cell cycle. Confocal microscopy analyses showed that CSRP2 is in the cytosolic and nuclear fractions, suggesting different regulatory roles in myoblasts. We are investigating the changes in gene expression of cells lacking CSRP2 control myoblasts by RNA-seq. Our work has the potential to identify a novel network of Cu-dependent transcriptional regulators that may be essential for the development of skeletal muscle and may represent potential targets for treatment in Cu-dependent myopathies and muscular phenotypes observed in Menkes and Wilson's disease patients.

Analysis of a novel bispecific antibody and its neutralizing potential against SARS-CoV-2

Discipline: Life Sciences
Subdiscipline: Microbiology

AbuBakr Sangare*[1], Christopher Barnes [2], Adonis Rubio[3]
[1]Williams College, [2]Stanford University, [3]Stanford University

Abstract: Understanding the structure-function details for many of the proteins encoded by SARS-CoV-2, the virus that causes COVID-19, has proven crucial towards the development of preventative care (e.g., mRNA vaccines) and novel monoclonal antibody (mAb) therapeutics that recognize the SARS-CoV-2 Spike protein. Synthetic mAbs delivered as monoclonal therapies (singular), antibody cocktails (two or more mAbs delivered together), or as a singular bispecific (bsAb) reagent (an antibody format that recognizes two distinct epitopes on each respective arm) have all entered clinical trial and proven effective in the treatment of COVID-19. However, the persistent emergence of new variants of concern (Delta, Omicron, etc.) harboring mutations in the SARS-CoV-2 spike protein have lowered the efficacy of vaccines and abrogated the neutralizing activity of many first-generation antibody therapies. In this study, we characterize binding, kinetics, and neutralizing activity of a novel anti-SARS-CoV-2 bsAb. Our bsAb was engineered to be resistant to variants of concern by targeting conserved, neutralizing epitopes within the N-terminal Domain of the S1 region and the stem helix preceding the heptad repeat 2 region in the S2 region of the SARS-CoV-2 spike protein. The bsAb was expressed and purified using Expi293F cells and characterized for neutralizing activity using a SARS-CoV-2 pseudovirus neutralization assay across several variants of concern, including Omicron BA.4/BA.5 lineages. Overall, engineering bsAbs with different specificities and mechanisms of neutralization may prove useful in the fight against COVID-19 and continued SARS-CoV-2 antigenic drift.

Ticks and Tickborne Diseases Across a Gradient

Discipline: Life Sciences
Subdiscipline: Biology (general)

Gabriela Reynoso Tale*[1], Brianna Beechler[2], Rhena Hanselmann[3], Michelle Steinauer[4], Justin Sanders[5], Anna Jolles[6], Daniel Capasso[7], Kathleen Shea Woodley[8], Alexis Ybarra[9], Michelle Mccorkell[10]
[1]Oregon State University, [2]Oregon State University, [3]Western University, [4]Western University, [5]Oregon State University, [6]Oregon State University, [7]Oregon State University - Vet Student, [8]Oregon State university, [9]Wester University - vet student, [10]Western University - vet student

Abstract: Tick vectors are responsible for zoonotic transmission of bacterial infections such as Lyme disease, Rocky Mountain spotted fever, and Ehrlichiosis. Urgency for research remains high due to global increase of vector borne zoonoses of human and animal arthropod-borne diseases; yet, there is sparse research on disease distribution. This presentation will report the distribution and abundance of ticks and the bacterial organisms they harbor across a land use gradient. We will be sampling for ticks in agricultural and urban areas along Mary’s River in the Willamette Valley (Western Oregon) and White River in Tygh Valley (Eastern Oregon) using a drag cloth method over low vegetation. Climate, increasing vector-host interactions, and land use play a major role in the growth of tick-borne diseases. Knowing this, our first step focuses on determining the quantity and presence of ticks and their life stages across land gradients. The two locations both provide natural undisturbed and disturbed urban areas making tick sampling within each environment along transects paralleling both rivers ideal. Once ticks are collected, they will be identified using tick species confirmed in the area (Ixodes pacificus, Dermacentor variabilis, Dermacentor occidentalis and Rhipicephalus sanguineus) and grouped based on sex and developmental stage (larval, nymphal, and adult). We expect there to be a difference in tick abundance across land use types. In a future step, we will extract and amplify tick DNA in order to screen for pathogenic presence and determine risk of disease transmission.

Understanding the role of acute stress on developing sensory circuits in Xenopus laevis tadpoles

Discipline: Life Sciences
Subdiscipline: Neurosciences

Talia Fernandez*[1], Carlos Aizenman[2], Adrian Thompson[3], Hannah Park[4]
[1]Brown University, [2]Brown University, [3]Brown University, [4]Brown University

Abstract: Acute stress changes how we perceive the world, informing how we perform context-specific behaviors. However, we do not fully understand the cellular mechanisms by which stress affects the brain to alter sensory perception and change behavior. Corticotropin-releasing factor (CRF) is best known for its role in the HPA axis. However, previous work has shown that CRF can directly affect the Xenopus optic tectum, a midbrain structure involved in sensory processing, to modulate feeding behavior. Here, we investigated whether acute exposure to stress or CRF affects behaviors that rely on sensory processing. We used the collision avoidance assay to compare the processing of visual information in CRF-exposed and control tadpoles and assess their ability to implement avoidance maneuvers to prevent collisions with approaching objects. We found that CRF-exposed tadpoles had an increased change in swim velocity in response to collisions compared to controls, suggesting that CRF affects visual perception. Next, we used the schooling assay to measure differences in the integration of sensory and social cues between stressed, CRF-exposed, and control tadpoles. We found that stressed tadpoles showed increased schooling, which was rescued by exposing stressed tadpoles to the CRF receptor antagonist, NBI-34041. In contrast, we found that CRF-treated tadpoles showed decreased schooling, which may indicate that stress and CRF exposure affect behavior via alternate mechanisms. By characterizing the effects of stress and CRF exposure on sensory perception and behavior, we will be able to gain important insights into the mechanisms by which stress alters sensory circuits to influence behavior.

Emissions from Flaming and Smoldering Plastic Disrupt Mitochondrial Function in Upper Respiratory Cells

Discipline: Life Sciences
Subdiscipline: Environmental Science

Elisa WaMaina*[1], Keith Rogers[2], Yong Ho Kim[3], Ian Gilmour[4], Ilona Jaspers[5]
[1]Oakwood University, [2]Curriculum in Toxicology & Environmental Medicine, UNC-Chapel Hill, [3]Center for Environmental Medicine, Asthma, and Lung Biology, UNC-Chapel Hill, [4]Curriculum in Toxicology & Environmental Medicine, UNC-Chapel Hill ; U.S. Environmental Protection Agency, [5]Curriculum in Toxicology & Environmental Medicine, UNC-Chapel Hill ; Center for Environmental Medicine, Asthma, and Lung Biology, UNC-Chapel Hill ; Department of Pediatrics, UNC-Chapel Hill

Abstract: Respiratory exposure to emissions from burning plastic is an urgent and increasing health concern as there is currently an estimated 6.3 billion tons of plastic trash in the world, with over 90% of trash being stored in landfills or disposed of by incineration. Annually, 70 million tons of plastic waste is incinerated globally, introducing over 500,000 tons of respiratory toxins into the air. Whether and how inhalation of emissions from burning plastics present a health hazard by interfering with essential cellular processes, such as mitochondrial function, is currently not well understood. We hypothesized that emissions from burning plastic would disrupt mitochondrial function in human nasal epithelial (HNEC) cells in vitro and that these effects are dependent on incineration temperature. Plastic materials were burned at flaming (640°C) or smoldering (500°C) temperatures in a quartz tube furnace system, and emissions were collected as condensates in a series of cryotraps. HNECs from male and female donors were cultured to confluence for analyses of mitochondrial function and cellular bioenergetics using the Seahorse XFe24 Extracellular Flux Analyzer. Cells were then exposed to either 25 or 50 ug/cm 2 of smoldering or flaming plastic emission condensates (PEC) and analyzed for changes in mitochondrial respiration and glycolysis. Our data suggest that exposure to smoldering and flaming PECs disrupt critical mitochondrial functions including basal respiration, ATP production, and coupling efficiency. These results reveal that inhalation of PECs adversely affect human respiratory cells by impairing mitochondria activity, likely resulting in adverse upper respiratory health effects and disease.

Variation in grazing rates of coral reef fish in the Chagos Archipelago

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ann Gobei-Bacaylan*[1], Fiorenza Micheli[2], Jamie McDevitt-Irwin[3], Gwendolyn Zoob Donahue[4]
[1]University of California, Santa Cruz, [2]Hopkins Marine Station of Stanford University, [3]Hopkins Marine Station of Stanford University, [4]Hopkins Marine Station of Stanford University

Abstract: Herbivorous fishes play integral roles in managing harmful overgrowth of macroalgae and inhibiting coral-algal phase shifts on coral reefs. However, overfishing on coral reefs typically leads to disproportionate decreases in large-bodied, macroalgae-consuming herbivores (e.g. Scaridae, Acanthuridae). Remote and unfished reefs provide unique opportunities to assess herbivorous reef fish assemblages and behavioral patterns. Our study explored fish grazing rates on coral reefs across one of the largest marine protected areas, the Chagos Archipelago. We compared grazing rates of benthic feeding fishes across six islands up to ~160 km apart, between and within fish functional groups, and determined how these grazing rates varied with shark abundance. We hypothesized that grazing rates would vary both within and between functional groups with stronger variation in the latter, and that shark abundance would have a strong negative effect on grazing rates. To test these predictions, we evaluated two-hour stationary videos of 1 m2 plots to observe fish identity and grazing rates across six sites with varying shark abundance. Preliminary results are pending and will include any significant variation in grazing rates across the testing sites and compared to shark abundance. This study provides deeper insight into the feeding patterns of benthic feeding coral reef fish, especially in remote and unfished ecosystems. As coral reef fishes play an integral function in coral reef health and recovery but are declining worldwide, the results from this study will help us better understand the ecological consequences of this decline.

Targeting the Calcineurin Pathway to Develop Antifungal Drugs in Mucor lusitanicus

Discipline: Life Sciences
Subdiscipline: Microbiology

Gabriela Maldonado*[1]and Soo Chan Lee[2]
[1]The University of Texas at San Antonio, [2]The University of Texas at San Antonio

Abstract: Mucormycosis is a recently emerging fungal infection found mainly in immunocompromised individuals. Fungi from the order Mucorales are the causative agent of mucormycosis. Mucorales fungi are highly resistant to antifungal drugs thus, treatment options remain limited. I will be investigating a serine/threonine phosphatase calcineurin in Mucor lusitanicus (formally called Mucor circinelloides) that plays a large role in the virulence factor of this pathogenic fungus. Without calcineurin, Mucor can only grow as yeast and the virulence pathway is blocked. Calcineurin would be an ideal target antifungal drug, however human calcineurin and fungal calcineurin are structurally similar. Inhibiting fungal calcineurin would also inhibit the human calcineurin and would leave an individual immunocompromised, since human calcineurin controls T cell response. The goal of this project is to investigate an intermediate downstream gene of calcineurin called bycA . This gene may be the key to understanding an alternative mechanism of calcineurin inhibition. Calcineurin and bycA are inversely related. When calcineurin is inhibited, bycA is overexpressed, and virulent hyphal growth is inhibited as well. We hypothesize that via genetic transformation of Mucor , we will be able to create a bycA -overexpressing strain of Mucor that can be used for antifungal drug discovery targeting the calcineurin pathway. Understanding how elevation of bycA inhibits

calcineurin will help further the development of an antifungal drug that will allow a less toxic treatment plan for individuals with a mucormycosis infection.

Illuminating the localization and functions of SPD-1 during sperm meiosis in Caenorhabditis elegansmales

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cuc Huynh*[1]and Diana Chu [2]
[1]San Francisco State University, [2]San Francisco State University

Abstract: While male infertility brings significant challenges to human reproduction, little is known about the molecular mechanisms that drive male meiotic chromosome segregation required for efficiently generating healthy sperm. During mitosis and oocyte meiosis, chromosomes segregate by the pushing forces from the central spindle structure. The central spindle forms in the midzone area during anaphase after SPD-1 protein bundles microtubules while recruiting other midzone proteins. In Caenorhabditis elegans nematode, there is a unique unpaired lagging X chromosome present in males and interestingly, the central spindle formation is minimized during sperm meiosis. This led to the question of whether sperm meiosis relies on the central spindle for proper chromosome segregation due to the presence of the lagging unpaired X chromosome. Utilizing immunostaining and live confocal microscopy, I aim to determine the spatial-temporal localization of SPD-1 during anaphase of sperm meiosis. Results show that SPD-1 localizes and remains at the midzone region as the unpaired lagging X chromosome travels to one polar end during sperm meiosis. This suggests that SPD-1 functions to stabilize microtubule organization which is essential for accurate chromosome segregation during sperm meiosis. In addition, its interaction with other midzone proteins could help with promoting the completion of cell cleavage and regulating the final cell division process, cytokinesis. Taken together, this research will elucidate SPD-1 functions during sperm meiosis, especially whether it’s involved in forming the central spindle which can further reveal the factors that cause male infertility.

Photoperiod alters ovarian mRNA expression of genes in the retinoic acid pathway

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Amber Simonpietri*[1], Alex B. Yuan [2], Kelly A. Young[3]
[1]California State University, Long Beach, [2]California State University, Long Beach, [3]California State University, Long Beach

Abstract: Cyclic ovarian function requires the orchestration of multiple signaling pathways; however, most vertebrate ovaries do not cycle continuously due to seasonal pauses in reproduction. While the endocrine regulation of seasonal ovarian change is well understood, how changes in ovarian function impact other signaling pathways remain unknown. Because the retinoic acid (RA) pathway is involved in ovarian cell proliferation, differentiation, apoptosis, and oocyte maturation, we hypothesized that the genes in the RA pathway would be differentially expressed in ovaries that are cycling, non-functional, and returning to function. To address our hypothesis, we used ovaries from seasonally-breeding Siberian hamsters who were exposed to 16-weeks of long-days (16h light:8h dark; LD; cycling ovaries), or short-days (8L:16D; SD; regressed ovaries), or 16-weeks of SD followed by 2, 4, or 8-weeks post-transfer to LD (PTw2-8;

recrudescing ovaries). Real time PCR expression showed that retinoic acid receptor-γ and retinoid X receptor-β, both of which bind the RA ligand, were present in LD ovaries and decreased significantly with SD exposure. Expression of these receptors was restored to LD levels in the PTw2, 4, and 8 groups. In contrast, mRNA expression of RA-degrading enzyme Cyp26b1 increased significantly in SD as compared to the LD group, with expression returning to lower LD levels in the recrudescing groups. Our results suggest that the RA signaling pathway is active in cycling Siberian hamster ovaries, with decreases in RA binding concomitant with increases in RA degradation in regressed ovaries, and restoration of RA binding occurring as photo-stimulated ovaries return to function.

How Life-Like are Finite Element Models?: validating computer simulations with real-world examples

Discipline: Life Sciences
Subdiscipline: Biology (general)

Gabriella Cale*[1], Dr. Z Jack Tseng [2], Emily L. Bogner[3]
[1]Utah State University, [2]University of California, Berkeley, [3]University of California, Berkeley

Abstract: Finite element analysis (FEA) is a computer simulation method that analyzes how objects react to forces. This method is utilized in a variety of biological fields to analyze the mechanical behavior of bone without destructive/ invasive sampling. Although FEA is a common method in morphological research, few validation studies have been conducted comparing FE models to their real world counterpart. This study aims to compare a FE model to mechanical experimental data to validate the accuracy of this method. Because FE models do not account for variation of mechanical properties throughout an object, the data is relatively simple. It is hypothesized that FE models will not accurately portray strain experienced by biological structures under the same conditions. To test FE accuracy, the humerus of a domestic cat (Felis catus) was 3-D scanned and modeled using FEA to replicate a three-point bending experiment. A force of 300N was directed downward anteriorly on the mid-shaft of the humerus with constraints placed at the humerural ends. The real-life humerus was then subjected to a three-point bending test using the same constraints stated above with an electromechanical testing frame. Principal strains were collected from both models, and compared. FEA produced compression principal strain values that were two orders of magnitude lower than the values of the electromechanical testing; however, the tensile strain values fell within the same magnitude. Future use of FEA based on mechanical properties published in the literature should be performed with caution, if compressive strain are the values of interest.

Weed Management in Organic Agriculture Systems: Assessing Complex Interactions of Crop Rotation, Cover Cropping, and Fertilizer Application

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Abigail Lazier*[1], Jennifer Reeve [2], Maya Schaefer-Fiello[3]
[1]Delaware Valley University, [2]Utah State University, [3]Utah State University

Abstract: Managing populations of competing weeds is critical to the success of organic farmers who face increasing demands despite worsening climatic stressors and economic hardships. The goal of this study is to determine synergistic effects of organic weed management strategies represented by differences in cover crop and weed biomass measurements and plant nitrogen acquisition. Using a complete randomized block designed with split-split plots and three replicates, the effects of cover crops, crop rotation, and fertilizer on the success of weed competition were investigated at a long-term research site in Greenville, UT. The whole plot factor was winter cover crop: alfalfa [Medicago sativa], hairy vetch [Vicia villosa], wheat [Triticum aestivum], or a biculture of wheat and vetch. The split plot factor were three crop rotations of varying intensity: R1 - potato-buckwheat-beans-corn; R2 - buckwheat-alfalfa-alfalfa-corn; and R3 - buckwheat-beans-buckwheat-corn. The split-split-plot factor was fertilizer treatment including plots receiving no amendment, fresh cattle manure, or composted cattle manure applied at 200 lb N per acre. We have identified four major weeds in the plots through visual assessment and are using biomass measurements to compare their growth with that of the cover crop. Preliminary findings show the greatest biomass in fertilized and crop rotation R3 plots, and significant differences between cover crop and weed biomass ratios across plots. We anticipate that the supply of soil N influences weed growth dependent on fertilization and cover crops dependent on their competition. This research contributes to understanding weed management for organic systems to optimize sustainable crop production.

Investigation of evolutionary relationships in cave adapted moths and crickets from Hawaiian lava tubes

Discipline: Life Sciences

Subdiscipline: Biology (general)

Rachael Dargan*[1], Rebecca Chong [2], Megan Porter[3], Mirelle Steck[4], Emma Christensen [5]
[1]University of Saint Mary's, [2]University of Hawaii at Manoa, [3]University of Hawaii at Manoa, [4]University of Hawaii at Manoa, [5]University of California at Merced

Abstract: Other moths across the island, with the exception of one sample that was divergent from all other samples. Further research can help identify the degrees of divergence across the island.

Investigating Off Target Toxicity of The Cancer Drug Ralimetinib and its Role as an EGFR Inhibitor

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Jaweria Bakar*[1], Erin Sausville, BS [2], Jason Sheltzer, PhD[3]
[1]Yale University, [2]Yale University, [3]Yale University

Abstract: MAPK (mitogen-activated protein kinase) p38 functions as a tumor promoter, and dysregulation of p38 MAPK levels is associated with short survival in several cancer types. The small-molecule drug Ralimetinib was developed as an inhibitor of p38 MAPK. Recent research from the Sheltzer Lab indicates that Ralimetinib is effective at killing cancer cells even when its putative target, p38 MAPK, was knocked out. Preliminary data on Ralimetinib suggests it may act as an Epidermal Growth Factor Receptor (EGFR) inhibitor rather than a p38 inhibitor. Gain of function mutations in the EGFR gene cause hyperactivation of EGFR signaling and can drive the development of multiple cancer types, including non-small cell lung cancer. In vitro kinase assays showed that Ralimetinib was potent against wild-type EGFR (IC50: 180 nM) and a common cancer-causing mutation EGFR-L858R (IC50: 179 nM). This research aims to study the effects of Ralimetinib as a potential EGFR inhibitor. Ralimetinib's IC50 was determined in various cancer cell lines with or without EGFR mutations. Ralimetinib's inhibitory effect on the

phosphorylation of EGFR at Tyr1068 and downstream EGFR target ERK Thr202 was determined by western blotting. Results indicate cancers driven by EGFR are more sensitive to Ralimetinib than cancers driven by other mutations, which is similar to what was observed with other known EGFR inhibitors, Erlotinib and Gefitinib. Identification of Ralimetinib's target is highly important in order to ensure that the patients who will exhibit the most robust response are being treated with Ralimetinib.

Effects of optogenetic stimulation of orexinergic projections from the lateral hypothalamus to the paraventricular thalamic nucleus on the expression of sign-tracking behavior

Discipline: Life Sciences
Subdiscipline: Neurosciences

Daniela Pereira*[1], Amanda G. Iglesias[2], Justin Chung[3], Stephen E. Chang[4], Sara R. Westbrook[5], Shelly B. Flagel[6]
[1]Virginia Polytechnic Institute and State University, [2]University of Michigan-Rackham Graduate School, [3]University of Michigan Undergraduate Program, [4]Michigan Neuroscience Institute, [5]Michigan Neuroscience Institute, [6]Michigan Neuroscience Institute and the Department of Psychology

Abstract: Animals learn to associate cues in their environment with rewards via Pavlovian conditioning and such cues come to elicit motivated behavior. Using rats, we can classify cue-motivated behavior according to the value attributed to the reward-associated cue. Both goal-trackers (GTs) and sign-trackers (STs) place predictive value on the cue; but STs also attribute incentive value to the cue. Upon reward-cue presentation, STs approach the cue itself, rather than the food cup (location of reward). Sign-tracking behavior is often maladaptive and resembles key features of impulse-control disorders. We hypothesize that sign-tracking behavior is driven by subcortical input to the paraventricular thalamic nucleus (PVT), a critical node that integrates multiple subcortical inputs and sends output to the nucleus accumbens. Here, we assess the role of orexinergic outputs from the lateral hypothalamus (LH) to the PVT in sign-tracking behavior. Male and female Long Evans rats expressing Cre-recombinase in OX neurons were used to selectively express channelrhodopsin in OX neurons projecting to the anterior PVT (aPVT). These neurons were optogenetically excited during reward-cue presentation over the course of Pavlovian training. Preliminary results indicate that excitation of OXergic inputs from the LH-aPVT increase both sign-tracking and goal-tracking behaviors in a sex-dependent manner. Specifically, male rats show an increase in these behaviors at the end of training while laser stimulation did not appear to affect the behavior of females. Although preliminary, these findings will lay the foundation for understanding the role of subcortical circuits in cue-motivated behaviors associated with psychopathology.

Southern Rockhopper Penguins: Are you trying to Krill me?

Discipline: Life Sciences
Subdiscipline: Environmental Science

Emily Svetlik*[1], Dr. Amanda Laubmeier[2], Nina Pyron[3], Bridgette Epps[4]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University

Abstract: Global warming is causing extinction starting at the bottom of ecological hierarchies. In the Falkland Islands, Southern Rockhopper Penguins are vulnerable due to issues at the foundation of the food chain, which is highly sensitive to temperature change. Increasing temperatures are causing algae blooms in the South Atlantic Ocean, suffocating the krill populations. Organisms such as krill are highly important to feed secondary predators, such as penguins, within the ecosystem. We hypothesize that the Southern Rockhopper Penguins are at high risk of extinction due to lack of krill. To study this, we developed a penguin population model which represented reproduction cycles in discrete functions, and natural feeding and death cycles in continuous functions. Then, we implemented a temperature change function, increasing temperatures according to current rates of climate change. We modeled how increased temperature causes a decline in krill reproduction and penguin chick survival rates. Population modeling allows us to study isolated climate change effects on krill alone, compared to the ecosystem as a whole. Our model demonstrates that within the next 250 years, if global warming continues at current rates, then krill populations drop to dangerous levels, which guarantees the demise of Rockhopper Penguin populations. If climate change were reversed, our model suggests the ecosystem would recover to full capacity over time, instead of leading to extinction. We find that bottom-up collapse of the foundation of the Falkland Island ecosystem endangers Southern Rockhopper penguins.

Using predicted protein structures to study host genes captured by viruses

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Carlos Sepulveda*[1], Ian Boys [2], Nels Elde[3]
[1]University of Puerto Rico - Rio Piedras Campus, [2]University of Utah School of Medicine, [3]University of Utah School of Medicine

Abstract: Poxviruses, a family of DNA viruses that include important human pathogens such as monkeypox, are known to “capture” genes from their hosts via horizontal gene transfer. Over evolutionary time, some captured host genes are modified to benefit the virus by altering host processes and interfering with immune responses, often by acting as molecular mimics of host proteins. The study of viral mimics of host proteins provides insight into virology and host biology, but sequence divergence can obscure relationships between virus and host proteins, limiting their study. We use AlphaFold, a breakthrough algorithm capable of accurately predicting protein structures, to model the proteome of vaccinia virus, a model poxvirus. Through structural homology searches we identified several possible mimics of host proteins, including vaccinia protein B6, which has structural similarity to proteins in the BCL2 family proteins. BCL2 family proteins are known to regulate apoptosis, and B6 shares most structural similarity with anti-apoptotic members. We hypothesize that B6 has a role in preventing cell death. For this study, B6 will be expressed alongside various BCL2 family proteins in cell culture and perform apoptosis assays to determine if and how they interact. Additionally, we have used immunofluorescence microscopy to assess the subcellular localization of B6, and preliminary results suggest that B6 is localized to the endoplasmic reticulum. Within the context of our homology screen, understanding the role of B6 will provide valuable information on the relationships between protein structure and protein function, illuminating new ways that viruses use mimicry to promote their survival.

Relating blue marlin vertical behavior patterns to light availability in the Eastern Tropical Pacific

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Michelle Moczulski*[1], Danielle Haulsee [2], Hannah Blondin[3], Larry Crowder[4]
[1]Villanova University, [2]Stanford University, Hopkins Marine Station, [3]Stanford University, Hopkins Marine Station, [4]Stanford University, Hopkins Marine Station

Abstract: Understanding blue marlin behavior and distribution in the Eastern Pacific Ocean (EPO) is crucial to implementing conservation efforts, especially since there is a lack of understanding regarding the vertical behavior of this species in this region. Blue marlin have an oscillatory dive behavior pattern, where they dive to deeper depths to attack prey or access cooler water, and then swim back to the surface. This behavior is thought to vary depending on many conditions, but fishers and researchers often suspect light availability (solar and lunar) is an important factor affecting dive behavior, because blue marlin are visual predators. In this study, three pop-off satellite archival tags (PSATs) that were attached to blue marlin off the coast of Costa Rica, were recovered and their high-resolution data were obtained. These tags measured and archived the fish’s depth, and water temperature data for 8 to 67 days at liberty. The average depth for the tags varied from 7.1 meters to 26.7 meters. The maximum depths recorded by each tag ranged from 73.5 meters to 128.0 meters. The high-resolution data allows us to investigate if variations in light (solar: time of day, and lunar: lunar phase and illumination) impact blue marlin dive behavior and the depth at which blue marlin occur. It’s expected that they will dive deeper and more frequently during the daytime and when the moon is more illuminated. This information is important to understand as resource managers design conservation practices for fisheries to help limit overexploitation and bycatch of blue marlin.

Microsatellite cross-species amplification: assessment and utilization in the captive-bred population of the Visayan spotted deer (Rusa alfredi)

Discipline: Life Sciences
Subdiscipline: Genetics

Noelle Tavares*[1], Perise Mark Q. Sienes [2], Christopher Bird[3], David Gauthier[4], Robert Guino-o II [5]
[1]Maine Maritime Academy, [2]Silliman University, [3]Texas A&M - Corpus Christi, [4]Old Dominion University, [5]Silliman University

Abstract: The Visayan spotted deer, Rusa alfredi, is endemic to the western islands of the Central Philippines. Categorized as Endangered by the International Union for Conservation of Nature (IUCN), Rusa alfredi was placed in captivity at the Center for Tropical Conservation Studies (CENTrop), in Dumaguete, Philippines, in 1990, and a breeding program was established from four breeding pairs to rebuild the population. However, incomplete paternity records in the current population of 86 have led to uncertainty in familial relationships, the potential introduction of inbreeding and further reduction of genetic diversity. The genus Rusa is closely related to Cervus , which includes the common deer, Cervus nippon for which 29 microsatellite loci have been developed. These markers were tested for cross-species amplification and variability within Rusa alfredi using PCR and gel electrophoresis. Of the 29 markers, 22 were readily amplified in at least 8 of 10 individuals, and 3 exhibited variation, suggesting they are viable for kinship, inbreeding, and genetic diversity assessment. I will further present the results of genotyping each individual at each viable locus using precise fragment lengths of the microsatellite alleles, estimate inbreeding and pairwise relatedness (r xy) coefficients, the heterozygosity and effective population size of the CENTrop population. Developing microsatellites for Rusa alfredi will allow for the determination in paternal lines within the

captive species, giving insight towards the level at which inbreeding occurs. This data is crucial for monitoring population genetics of Visayan spotted deer, and important in managing the captivity status of the population.

The Effects of mTOR inhibitors on Tuberous Sclerosis Patients

Discipline: Life Sciences
Subdiscipline: Neurosciences

Erlyn Clermont*[1]and Francis J. DiMario Jr [2]
[1]Trinity College, [2]Connecticut Children's Medical Center

Abstract: Tuberous sclerosis complex (TSC) is a genetic disorder that causes noncancerous tumors to develop in many organs throughout the body. TSC is caused by mutations in TSC1 or TSC2 genes, which results in overactivation of the mTOR signaling pathway, causing unregulated cell growth, proliferation, and hamartomatous lesions: Subependymal giant cell astrocytomas, (SEGA), renal angiomyolipomas (AML) and facial skin angiofibromas among others. The link between TSC and the mTOR pathway has led to treatment with topical and oral mTOR inhibitors. This study analyzed the effectiveness of topical sirolimus and oral everolimus in lesion reduction for TSC patients ages 0-25 years old treated in the CT Children’s TSC clinic with (SEGA/AML) and skin lesions. The lesion size pre and post treatment using MRI imaging and clinical examination through a retrospective chart review were examined. Lesion volume changes and subjective/ objective skin changes, demographic, and descriptive statistics were compiled and analyzed. There were 20 TSC patients receiving treatment. However, 6 patients did not meet inclusion/exclusion criteria, and only 14 patients comprised the study cohort. 3 patients used topical sirolimus and 11 patients used oral everolimus. Five patients had AML and the average percent volume reduction in the kidney (left > right) was -55%. Six patients had SEGA and the average percent volume reduction was -56%. Lastly, the 3 patients who had only facial angiofibromas had successful reduction of their skin lesions. Overall, sirolimus and everolimus were effective in reducing brain and kidney lesion volumes and reducing redness and size of skin lesions.

Modeling SLC6A1-related developmental and epileptic encephalopathies using a novel human induced pluripotent stem cell-derived brain organoid model

Discipline: Life Sciences
Subdiscipline: Neurosciences

Tyler Thenstedt*[1], M. Carmen Varela [2], Juan G. Valdivieso[3], Jack M. Parent[4]
[1]University of Michigan, Ann Arbor, [2]University of Michigan, Ann Arbor, [3]University of Michigan, Ann Arbor, [4]University of Michigan, Ann Arbor

Abstract: Mutations in the SLC6A1 gene are linked to developmental and epileptic encephalopathies (DEEs). The SLC6A1 gene encodes for the GABA transporter 1 (GAT-1), responsible for reuptake and regulation of GABA, and in the cortex, is primarily expressed on interneuron axon terminals. GAT-1 loss of function (LOF) results in reduced GABA uptake, disrupting the GABA homeostasis vital for brain development. Exactly how GAT-1 LOF affects early cortical development is unknown. We hypothesize that SLC6A1 null or haploinsufficient cells will display abnormal developmental and network-related marker expression compared to isogenic controls (WT). We used dual reprograming and CRISPR/Cas9 gene editing to produce human SLC6A1 null or haploinsufficient induced pluripotent stem cells (hiPSCs), generating isogenic control (WT), heterozygous (Het), and compound heterozygous (KO) iPSC lines. These were differentiated into 3D ventral brain organoids using our self-organizing single rosette spheroid (SOSRS) model. Ventral and dorsal organoid fusion protocols were used to examine interneuron migration and integration into the cortex. Immunostaining and RT-qPCR were used to evaluate relevant marker expression. We found an 81.64 ± 7.2% reduction of GAT-1 expression in the KO SOSRS compared to WT. We observed accelerated GABAergic neuron maturation in KO ventral SOSRS with earlier increases in potassium-chloride cotransporter 2 (KCC2) and somatostatin (SST) expression compared to WT. We also observed putative migratory deficits in KO and Het ventral SOSRS. Our findings suggest that SLC6A1 LOF impairs interneuron migration and maturation. Further investigation into this phenotype will inform treatment targets for SLC6A1-related neurodevelopmental disorders.

Manganese-Induced Enteric Nervous System Toxicity & Neurodevelopmental Behavioral Abnormalities

Discipline: Life Sciences
Subdiscipline: Neurosciences

Celine Campos*[1], Karin Striefel [2], Julie Moreno[3]
[1]Regis University, Colorado, [2]Regis University, [3]Colorado State University

Abstract: Metal toxicity is a major issue due to manufacturing that create metal byproducts that end up in food, water, and crop soil. When ingested, many metals are known to cause neurological issues. Manganese (Mn) is an essential trace metal, however in excess it is a potent neurotoxin. The long-term health effects of excess Mn exposure have been extensively studied in adults, however recent evidence demonstrates its impact upon the developing nervous system. Previous studies have focused on inflammatory activation of the central nervous system (CNS), as excessive Mn exposure has demonstrated to prompt cognitive and behavioral deficits in juveniles. The first site of exposure due to ingestion is the enteric nervous system (ENS) therefore we postulate that the ENS comprised of enteric glial and neuronal cells are activated prior to the inflammation observed in the CNS. Mice were administered with environmental-relevant levels of Mn, 50 mg/kg MnCl2, daily via drinking water from d21-d90 postnatal and evaluated locomotor function, glial activation, and catecholamine levels. We systematically addressed this by attaining behavioral analysis of mice treated and collecting tissues from the ENS and CNS to indicate the initial site of inflammatory activation. Preliminary results from these studies have replicated sex-dependent behavioral changes in the juvenile mice. Our analysis of the inflammatory biomarkers, GFAP and s100B, shows sign of inflammation in the ENS prior to the CNS. These data indicate that exposure to Mn during development leads to inflammatory activation of the ENS prior to CNS, with exposure potentially leading to behavioral modifications.

Analysis of sex ratios of Mytilus edulis in Massachusetts across time

Discipline: Life Sciences
Subdiscipline: Environmental Science

Zengel Chin*[1], Helen Poynton [2], Garrett Evensen[3]
[1]Boston College, [2]University of Massachusetts, Boston, [3]University of Massachusetts, Boston

Abstract: Mytilus edulis , the blue mussel, is a widely used monitoring organism for surrounding pollution. One group of pollutants, endocrine disrupting compounds (EDCs), has detrimental impacts on mussels. These compounds may lead to impaired gonadal development, reduced juvenile survival, and sex reversal. Estrogenic EDCs have been shown to cause male mussels to change sex and produce oocytes, rather than sperm. Determining sex ratios of mussels can provide insight into whether mussels are exposed to EDCs. In particular, this is most evident by feminized sex ratios. In 2019, there were significantly more females than males (7% males) at North River, MA. In addition, the sex ratio at one site in the Boston Harbor is dynamic, with strong variations annually. Here, we will analyze mantle tissue samples collected from three sites in Massachusetts (Savin Hill Cove, Folger Point, and North River) using RT-qPCR to determine sex ratios. This will be done using the difference in expression of a female-biased gene (VERL) and a male-biased gene (VCL). These results will be compared to previous samples taken in 2019 and 2021 to evaluate the stability of sex ratios at these sites. We hypothesize that sex ratios will remain constant from 2019 to 2022, with sex ratios being feminized at Savin Hill and North River. These results will provide valuable insight into whether a single time point is enough to fully evaluate the sex ratio of mussels at a site or whether multiple annual time points are required.

Preliminary quantification of in-vivo work during a frog jump at different temperatures

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Dustin Tran*[1], Eman Azizi [2], Elizabeth Mendoza[3], Rebecca Richards[4]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine, [4]University of California, Irvine

Abstract: Many physiological processes are temperature sensitive (e.g. locomotion). This poses a challenge to ectothermic organisms that rely on environmental temperatures to regulate these processes. In locomotion, some ectotherms have been shown to circumvent temperature effects through the use of elastic recoil to drive movement. This mechanism redistributes energy generated by slow muscle contractions to be released over a shorter time frame through recoil of elastic structures (e.g. tendon). Frog jumps use this mechanism (i.e., elastic recoil), yet they are more sensitive to temperature than expected. Here, we investigate how temperature affects elastic energy release in live frogs by (1) quantifying the amount of work produced by the plantaris longus muscle at different temperatures and (2) assessing the role of the nervous system in mediating temperature effects on muscle force and activity in frogs. We instrumented the plantaris longus muscle of bullfrogs (Rana catesbeiana) with sonomicrometry crystals, electromyography (EMG), and a tendon buckle and measured jump performance at 10, 20, and 30°C. As found in other studies, the fascicles experienced ~30% strain. In general, majority of work was performed during the loading phase. Loading time generally was longer in the colder trials. Characterizing the flow of energy in frog jumping will allow us to assess the relative contributions of elastic recoil and muscle to jumping.

The Effect of Green Tea on Non-Small Lung Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Paul Donato*[1], Adam McConnell [2], Idara Ibok[3], Daniel Moloney[4]
[1]Suffolk County Community College, [2]Queensborough Community College, [3]Nassau Community College, [4]Stony Brook University

Abstract: Much research indicates that green tea has chemo-preventive effects mediated by its polyphenols known as catechins which have been reported to inhibit cell proliferation and exhibit robust antiradical antioxidant activity. Epigallocatechin gallate (EGCG) is a type of catechin composed of the ester of epigallocatechin, and gallic acid found abundantly in green tea. This project aimed to investigate if EGCG could inhibit the proliferation of cancer cells and study its mechanism of action. We hypothesized that levels of EGCG in green tea would induce apoptosis in cultured treated lung cancer cells. The large cell lung cancer cell line H460 was used in this study to investigate the anti-cancer properties of EGCG. The Effect of EGCG on H460 cell proliferation was measured by an XTT assay which quantitates cellular NADH levels. Induction of apoptosis was also examined through a fluorescent Caspase assay. Our results indicate that EGCG from green tea effectively inhibits the proliferation of H460 lung cancer cells and induces apoptosis using concentrations present in everyday consumption of Green Tea. We examined H460 cells before, during, and after exposure to varying concentrations and determined that EGCG could cause H460 lung cancer cells to undergo apoptosis, which was proven using an XTT assay. Many proposed signaling pathways are possible means by which EGCG causes these cells to undergo apoptosis, but further experimentation is required to identify the exact method or methods by which this result is being attained.

The influence of MPAs and human population on changes in reef fish diversity in the centers of marine diversity and adversity

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Rebecca Ruiz*[1], Dr. Chris Bird [2], John Whalen[3], Dr. Kent Carpenter[4]
[1]Texas A&M University - Corpus Christi, [2]Texas A&M University - Corpus Christi, [3]Old Dominion University, [4]Old Dominion University

Abstract: Maintaining biodiversity in marine ecosystems benefits society by providing sustenance and other ecosystem services. The Philippines is the center of global marine diversity and yet its Central Visayas are the center of marine conservation adversity due to overfishing, habitat degradation, and recent declines in species diversity. To address these impacts, an extensive network of marine protected areas (MPAs) has been delineated to support biomass and biodiversity, and promote sustainable fisheries production in the surrounding areas via the spillover effect. The purpose of this study is to test for an effect of MPAs and human population size on changes in reef fish species diversity in the Central Visayas between surveys conducted in 1978-79 and 2016-22. The historical and contemporary datasets of species abundance were collected with similar methodologies enabling a rare opportunity to make meaningful comparisons between eras. Preliminary species accumulation curves are consistent with a reduction in reef fish species richness between historical and contemporary surveys. We constructed an index of MPA influence using a principal components analysis of factors associated with MPA influence. I will present the results of a mixed-model analysis designed to test for effects of MPA influence and population size on species richness, while controlling for covariates such as depth and habitat type. The results of this study can be used to assess the effect of MPAs on species diversity outside of their boundaries, which can better inform spatial marine management strategies, both in the Central Visayas and beyond.

Depression and anxiety are associated with distinct neural systems in neurological patients

Discipline: Life Sciences
Subdiscipline: Neurosciences

Hope Msengi*[1], Dr. Daniel Tranel [2], Jax Skye[3]
[1]The University of Texas at San Antonio, [2]University of Iowa, [3]University of Iowa

Abstract: Depression and anxiety are common following brain lesions and impact recovery of function by worsening prognosis, interfering with post-injury rehabilitation, and decreasing quality of life. Symptoms of depression and anxiety are positively correlated in the context of brain damage and their development may be influenced by lesion location. The purpose of this study is to replicate prior findings that depression and anxiety symptoms are positively correlated following chronic focal brain damage and add to the understanding of potential overlapping network correlates. Specifically, we predicted that higher depression scores and higher anxiety scores would be associated with damage to the same neural structures and networks in neurological patients with focal brain lesions. This study investigated 467 subjects from the Iowa Neurological Patient Registry who were administered the Beck Depression Inventory (BDI; n=466) and/or Beck Anxiety Inventory (BAI; n=149) and had structural neuroimaging data. We correlated performance on the BDI and BAI in patients who had scores for both inventories using linear regression. Next, we derived lesion-associated networks using normative resting-state functional connectivity MRI data. Depression and anxiety were positively correlated. We found non-overlapping functional networks (p=.0013) associated with higher BDI scores (more depression symptoms) in the ventral attention network and higher BAI scores (more anxiety symptoms) in the frontoparietal and default mode networks respectively. We interpret these findings to be novel evidence for nonoverlapping biological mechanisms for depression and anxiety. However, contrary to our hypothesis, we found remarkably distinct functional networks were implicated in lesion-associated depression and anxiety.

Is There a Meiotic Checkpoint Response to a Threshold Number of Crossovers?

Discipline: Life Sciences
Subdiscipline: Genetics

Sarah Semple*[1], Needhi Bhalla [2], Bhumil Patel[3]
[1]Monterey Peninsula Community College, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: Meiosis is necessary for producing gametes and sexual reproduction and it is imperative that the gametes have the correct number of chromosomes. When they do not have the correct number of chromosomes, it can produce birth defects, infertility, and miscarriages. In meiosis, cells deliberately form double-strand breaks to initiate homologous recombination and produce meiotic crossovers. Crossover recombination exchanges genetic alleles among homologous chromosomes and promotes correct chromosome segregation. We have shown that pachytene checkpoint protein 2 (PCH-2) localizes to meiotic chromosomes when they are competent for crossovers in C. elegans. Lack of PCH-2 accelerates the events of recombination, producing an increase in meiotic defects. To better understand how PCH-2 regulates crossover recombination and prevents defects, we have taken advantage of a mutant that makes fewer double-strand breaks and fewer crossovers, dsb-2. In dsb-2 mutants, we observe that PCH-2 persists in some nuclei, and these nuclei have a reduced number of crossovers. Similarly, others have reported that Polo-like kinase 2 (PLK-2) localization is also controlled by the number of crossovers. Our objective is to understand the localization of these two checkpoint proteins, PCH-2 and PLK-2. Using cytological tools, we will analyze the localization of antibodies specific to PCH-2 and PLK-2 and quantify changes between the wild-type background and the mutant dsb-2 C. elegans germlines. These experiments will address the following hypotheses: Does the localization of PCH-2 and PLK-2 correlate, suggesting similar regulation, or do they not correlate, indicating independent regulation?

Sampling, isolation, identification, and sequencing of freshwater microalgae on Puerto Rico for data base creation and bioremediation capabilities.

Discipline: Life Sciences
Subdiscipline: Environmental Science

William Fortun*[1], Karin Milan Diaz[2], Karlo Malave Llamas[3], Linda Rivera Rivera[4], Carlos Hernandez Rodriguez[5], Johan Ortiz Morales[6], Jayleen Diaz Mercado[7]
[1]Universidad Ana G. Mendez Recinto de Carolina, [2]Universidad Ana G. Mendez Recinto de Carolina, [3]Universidad Ana G. Mendez Recinto de Carolina, [4]Universidad Ana G. Mendez Recinto de Carolina, [5]Universidad Ana G. Mendez Recinto de Carolina, [6]Universidad Ana G. Mendez Recinto de Carolina, [7]Universidad Ana G. Mendez Recinto de Carolina

Abstract: The photosynthetic organism also known as microalgae are the main organism of this research. Microalgae's form part of cutting-edge research on many areas, from pharmacology, agriculture, bioremediation, and energy departments. Currently no freshwater microalgae database exists for Puerto Rico Island. Meaning that new research areas are still to be developed. Including the possibility of undiscovered microalgae on Puerto Rico freshwater bodies. The investigation follows a collection, purification, identification, and storage and disclosure procedure. Samples are collected using a 50μm filtration net, and direct collection the samples are storage at a portable cooler until arrival at the lab. A composite is made from the environment samples. From this composite 200ml are added to 400 ml of growing broth BG11 which been added antibiotics and antifungal components. The samples are placed on a magnetic stirrer with a pellet, the containers are seal on top with cotton to prevent contamination and still letting air in and out. A white fluorescent light source is place on top of the samples and let to grow. After 2 weeks, using a micropipette and microscopy, we start to isolate the observed microalgae, and place on fresh system to perform a fed batch culture. The purpose is to create enough isolated biomass to perform a DNA extraction using Zymo Research Quick DNA kit ®. A complete DNA sequence is performed using MinION®. All the information including GPS coordinates, sampling parameters, lab procedures, sample grown images and DNA sequence of every alga identified is uploaded into the created database.

Sex differences in ozone air pollution effects on lung inflammation and microbiome profiles in asthmatic mice

Discipline: Life Sciences
Subdiscipline: Environmental Science

Keishla Colon Montanez*[1], Patricia Silveyra[2], Nathalie Fuentes[3]
[1]The University of Chicago, [2]Indiana University Bloomington Campus, [3]Penn State College of Medicine

Abstract: Ambient ozone is known to be one of the most dangerous air pollutants. Ozone inhalation can aggravate lung diseases like asthma, which is more prevalent in females than males. Despite this, the mechanisms underlying the effects of ozone in the male and female lungs remain unknown. We hypothesized that exposure to ozone exerts differential inflammatory responses in the male and female asthmatic lung. To examine this, we triggered asthma in male and female C57BL/6J mice by a 5-week intranasal administration of house dust mite. We then exposed mice to 2 ppm of ozone or filtered air (FA, control) for 3 hours, and collected lung tissue. We extracted RNA, and measured the expression of 92 inflammatory genes with a TaqMan® qPCR Array (ThermoFisher). We also extracted DNA to determine lung microbiomes via 16S rRNA amplicon sequencing. Results were summarized and significance was estimated as implemented in QIIME2. Our data show that, after exposure to ozone, asthmatic male mice had higher lung expression of cell surface receptors and signaling genes, whereas asthmatic females had higher expression of pro-inflammatory cytokines and immune regulators. We also identified sex differences in microbiome profiles in asthmatic mice and in mice exposed to ozone, including a higher content of Firmicutes and Firmicutes/Bacteroidetes ratio in males than females. Asthmatic females also displayed higher lung bacterial diversity. We conclude that ozone exposure triggers differential inflammatory mechanisms in the male and female lungs of asthmatic mice, and that these mechanisms could be mediated by lung resident microbes.

Genetic diversity and selection in Puerto Rican horses

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Stephanie Castro Marquez*[1], Taras K. Oleksyk[2], Walter W. Wolfsberger[3], Alondra Diaz Lameiro[4], Khrystyna Shchubelka[5], Juan Carlos Martínez-Cruzado[6], Audrey Majeske[7]
[1]Oakland University, [2]Oakland University; University of Puerto Rico-Mayaguez; Uzhhorod National University, [3]Oakland University, [4]University of Puerto Rico - Mayaguez, [5]Oakland University, [6]University of Puerto Rico - Mayaguez, [7]Oakland University

Abstract: Since the introduction of modern horses by colonizers to America, several local varieties and breeds have been established. Over the years, these local horses have been selectively bred for specific traits, such as appearance, endurance, strength, and gait. The Puerto Rican Paso Fino breed (PRPF), notorious for its unique four-beat gait, which is particularly comfortable for the rider, is an example of this process. It is thought that the PRPF shares a common ancestor with the fast-growing Puerto Rican Non-Purebred (PRNPB) or “criollo”, yet the gait is not observed in the latter. We investigated the genetic ancestry and diversity of these Puerto Rican horse populations using two approaches: 1. mitochondrial DNA D-loop (668bp fragment) in 200 horses from 27 locations on the island and 2. genotyping 24 samples with the Illumina Neogen Equine Community genome-wide array (65,000 SNPs). Furthermore, we genotyped all 200 horses for the “gait-keeper” DMRT mutant allele previously associated with the paso gait. Our analysis shows a genetic connection between the two varieties in Puerto Rico, consistent with the hypothesis that PRNPB horses represent the descendants of the original genetic pool, a mix of horses imported from Europe. The PRNPB horses, and not the purebred PRPF, carry a signature of selection in the genomic region containing the DMRT3 locus. The original founders of PRNRB population must have carried the DMRT3 allele upon arrival to the island. From this admixture, the local people selected the desired traits over centuries to breed the PRPF.

shRNA Validation of mRNAs associated with T-Cell Activation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Maria Valentina Chirinos Pena*[1], Kole Roybal, Ph.D.[2], Nate Perry, M.S.[3], Raymond Liu, Ph.D.[4]
[1]City College of San Francisco, [2]University of California, San Francisco. Roybal Lab, [3]University of California, San Francisco. Roybal Lab, [4]University of California, San Francisco. Roybal Lab

Abstract: Cancer treatment using Chimeric Antigen Receptor (CAR) T-cells has emerged as a promising field in immunology. CAR T-cell immunotherapies have shown clinical efficacy for B-cell malignancies but face challenges against solid tumors; such as T-cell exhaustion. This state of cellular dysfunction can be addressed by inducing transient cessation of CAR signaling or rest, but this has only been achieved through the administration of drugs which inhibit tyrosine kinase activity. As an alternative, we are exploring the use of Short Hairpin RNAs (shRNAs) to induce periods of rest by silencing genes associated with T-cell activation. Here, we report a methodology to evaluate shRNA knockdown efficiency, an important first step in the identification of shRNAs that can complement CAR T-cell therapies. In this study, we targeted two genes that participate in T-cell activation, CBL-B and FYN. We created a stable Jurkat line expressing green fluorescent protein (GFP), tagged with CBL-B and FYN mRNA target sequences. After transducing the stable Jurkat cells with shRNAs against these target sequences, we measured GFP expression to calculate shRNA potency. We evaluated five different shRNAs for each target gene and our results show a range of shRNA knockdown efficiencies. We demonstrate that our methodology allows for effective and rapid validation of large numbers of shRNAs, accelerating identification of shRNA candidates which are complementary to CAR T-cell therapies.

The role of Follistatin on Neovascularization during muscle regeneration after freeze-injury

Discipline: Life Sciences
Subdiscipline: Biochemistry

Esther Pincate*[1]and Hyojung Choo[2]
[1]Bates College, [2]Emory University School of Medicine Department of Cell Biology

Abstract: The ability of muscles to maintain mass is of vital importance as they not only aid in the regulation of the metabolic systems of the body, but also support activities of daily living that require strength, mobility, and power. Fibro-adipogenic progenitor (FAP) cells reside in muscle tissues and play a critical role in muscle regeneration and maintenance of skeletal muscle fiber size. FAPs secrete several myokines that aid in muscle regeneration and repair, one of them being Follistatin. Follistatin (FST) is a glycoprotein that inhibits proteins associated with limiting muscle growth thus allowing regeneration to occur. Previous research has also associated Follistatin with angiogenin, a key protein implicated with the activation of endothelial cells and stimulation of new blood vessel growth, however, the specific role of follistatin in regard to endothelial cell recruitment, angiogenesis, or vascularization has yet to be confirmed. We examine the role of follistatin in neovascularization in freeze-injured muscle using follistatin-null and control wild-type mice and HUVEC cells. We hypothesize that the freeze-injured muscles without Follistatin will be impaired to form new blood vessels after injury. To determine the capability of FST to promote vasculogenesis in vivo, we will look at endothelia cells using CD31 immunostaining on follistatin-null mice muscles after freeze-injury and vasculogenesis in vitro by utilizing HUVEC cells with follistatin null cells. Determining the role of FST is integral because it could be a promising agent for improving skeletal muscle healing after injury and muscle diseases such as muscular dystrophies.

Targeting Dosage Compensation to the Drosophila Male X-chromosome

Discipline: Life Sciences
Subdiscipline: Genetics

Angelica Aragon*[1], Joseph L. Aguilera [2], Erica N. Larschan[3]
[1]Brown University, [2]Brown University, [3]Brown University

Abstract: Sex differences in res ponse to clinical therapeutics are common but little is understood about the underlying mechanisms. Therefore, a deep understanding of male versus female gene regulation is essential to reveal these mechanisms. As a model for understanding sex differences in gene regulation, we are investigating how the Drosophila single male X-chromosome achieves its essential sex-specific role of upregulating all its active genes approximately two-fold, a phenomenon known as dosage compensation. A key pioneer transcription factor, Chromatin Linked Adaptor for MSL Proteins (CLAMP), is critical in targeting dosage compensation to the male X-chromosome. However, CLAMP is also found on all chromosomes in the male and female genomes. I hypothesize that CLAMP works alongside other cofactors to form a specific chromatin environment which helps target the Dosage Compensation Complex (DCC) specifically to the male X-chromosome. By performing Cleavage Under Targets and Release Using Nuclease (CUT and RUN), I will map all CLAMP and DCC binding sites in both male and female larvae for wild-type and clamp mutant lines. Preliminary data has shown there is a loss in wild-type DCC binding but an increase in ectopic autosomal DCC binding in clamp mutants. After identifying novel loci via CUT and RUN, I will then perform bioinformatic analyses, MEME and R-cis-target, which will reveal novel motifs and cofactors involved in X-chromosome targeting of dosage compensation. My research will provide novel insight into sex differences in gene regulation, which will shed light on how future therapeutics will affect males and females differently.

Application of MALDI-TOF technology in the rapid detection of emerging infectious foodborne Cronobacter sakazakii strains associated with powdered infant formula contamination

Discipline: Life Sciences
Subdiscipline: Microbiology

Quincy Kumfert*[1]and Irshad M. Sulaiman [2]
[1]University of California, Davis, [2]Microbiological Sciences Branch, Southeast Food and Feed Laboratory, Office of Regulatory Science, Office of Regulatory Affairs, U.S. Food and Drug Administration, 60, 8th Street NE, Atlanta, GA 30309, USA

Abstract: Cronobacter is a genus of opportunistic pathogenic bacteria that is known to cause neonatal meningitis and necrotizing enterocolitis. Although Cronobacter has been isolated from a wide variety of environments, powdered infant formula has been recognized as a major vehicle of transmission of Cronobacter and poses a threat to neonatal health worldwide. Cronobacter sakazakii contamination is of particular concern due to its high virulence. Given that the mortality rate of neonatal meningitis has been found to be as high as 40-80%, it is crucial to have rapid, reliable diagnostic tools to identify and contain Cronobacter outbreaks as quickly as possible. In this paper, we perform a systematic literature review of studies regarding

Cronobacter contamination of infant formulas and their production facilities as well as clinical cases from the past ten years. We discuss the challenges of accurate Cronobacter identification and the development of various identification methods, particularly the development and utilization of DNA-sequencing-based diagnostic technology such as multi-locus sequence typing (MLST) and whole genome sequencing (WGS). We find that DNA-sequencing-based methods are the most discriminate and accurate, but MALDI-TOF mass spectrometry may serve as a robust preliminary diagnostic tool for Cronobacter identification. Additionally, we tested 16 Cronobacter sakazakii -like isolates from environmental archive samples on the VITEK MS system and received a positive identification for all isolates. These findings merit further examination of MALDI-TOF mass spectrometry as a rapid identification method.

Altered masp1 levels affect gene expression patterns during gastrulation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Aaliyah Tovar*[1], Heather Ray[2], Heather Ray[3]
[1]Idaho State University, [2]Idaho State University, [3]Idaho State University

Abstract: Mannan-binding lectin associated protease 1 (MASP1) is a component of the lectin complement pathway of the innate immune system.Previous research identified mutations in Masp1/3 , the gene that codes for MASP1, in patients with 3MC Syndrome, a developmental disorder which causes craniofacial malformations, cleft palate, and cognitive impairment. This suggests that MASP1 has an important function during early development Here, we are using embryos from the African Clawed Frog (Xenopus laevis) to better understand the role of Masp1 in development. Embryos were injected at the 4-cell stage with either masp1 RNA (overexpression) or masp1 morpholino (knockdown) and allowed to further develop. A number of phenotypes were identified including defects in gastrulation and cement gland development. RNA probes were made for a number of genes that are involved in gastrulation and cement gland development. Injected embryos were fixed at gastrulation and in situ hybridization was then used to visualize the expression patterns of these genes and to identify the impact of either overexpressing or knocking down masp1 . masp1 overexpression showed an increase in the expression of the genes bmp4, chordin, and otx2 while masp1 knockdown results in increased noggin expression.These findings demonstrate that Masp1 impacts the expression of genes during gastrulation, which can in turn have long term consequences on development. Continuing studies will determine how these gene expression changes occur over developmental time. The results of this study will shed light on how MASP1/3 mutation could lead to 3MC Syndrome.

FISHtank: A Community Database featuring DNA Specific Oligonucleotide Probes

Discipline: Life Sciences
Subdiscipline: Biochemistry

Caleb Kono*[1], Brian Beliveau[2], Robin Aguilar[3]
[1]University of Washington, [2]University of Washington, [3]University of Washington

Abstract: The 3D organization of nucleic DNA impacts key aspects of genomic functions like gene expression and DNA replication timing. However, large regions of the 3D are composed of repetitive DNA sequences (e.g. satellite DNA) and are challenging to map with sequencing-based methods, interfering with our understanding about the functions of these regions and their impacts on human disease. This study seeks to overcome obstacles in mapping and imaging by

engineering two tools to more efficiently and precisely visualize the position and distribution of repetitive DNA: 1) Tigerfish designs fluorescently labeled oligonucleotide (oligo) probes specifically against these repetitive regions; and 2) FISHtank will be a pan-genomic database containing oligo probes for emerging human and model organism genome assemblies. I use recent advances in DNA synthesis technology to construct Fluorescent In Situ Hybridization (FISH) probes entirely from synthetic oligos. I then use oligo-FISH probes derived from Tigerfish to image and catalog novel probes for specific repetitive regions of DNA so that these images can be featured as validated probe data for future FISHTank users. Tigerfish and FISHtank will be broadly applicable for validating genome assemblies, karyotyping, and for resolving how repetitive DNA shapes genomic architecture. This work could establish a highway for repetitive DNA imaging, opening the topic of repetitive DNA investigations and their relationship to human disease to the wider scientific community.

A novel artificial intelligence-assisted method of geometric analysis for abdominal aortic aneurysms

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Paola Garcia Polanco*[1], Wei Yin [2], Marina Fandaros[3], James Kaan[4], Apostolos Tassiopoulos [5]
[1]Universidad de Puerto Rico at Cayey, [2]Department of Biomedical Engineering, Stony Brook University, Stony Brook, NY, 11794, [3]Department of Biomedical Engineering, Stony Brook University, Stony Brook, NY, 11794, [4]Department of Vascular Surgery, Stony Brook University Hospital, Stony Brook, NY, 11794, [5]Department of Vascular Surgery, Stony Brook University Hospital, Stony Brook, NY, 11794

Abstract: Abdominal aortic aneurysm (AAA) is a degenerative dilatation of the aortic wall that can lead to rupture and death. Progression of disease is asymptomatic and varies between individuals in regard to aneurysm growth rate and morphologic evolution. While growth rate and aneurysm size are the primary prognostic factors for rupture risk, particular morphologic features such as aortic neck diameter and angulation determine preoperative planning and risk of postoperative complications. However, there is a lack of consensus for measuring AAAs, which is performed manually. This leads to variability in measurements and calculation of growth rate. The goal of this study is to evaluate a novel method of geometric analysis of the abdominal aorta and to provide additional metrics by which clinicians can manage AAA. ITK-Snap, Autodesk Meshmixer/Netfabb, and VMTK Lab were used to segment and characterize aorta geometries from computed tomography (CT) scans from patients. The automatically-derived maximal diameter of the aneurysm sac (3.85±0.98 cm) and aortic neck (2.54±0.504 cm) were automatically calculated and extracted (n=10). The model's accuracy was validated by comparing these values with manually-extracted measurements by vascular surgeons. All automatically-derived measurements were within 2mm of ground-truth measurements. Total aortic volume, tortuosity (vessel length / linear distance) and maximal curvature were also extracted (110.8±49.7 cm 3 , 1.11±0.067, 0.069±0.020 mm). Preliminary data demonstrates a means by which AAA dimensions can be quantified using an automated approach that avoids the problem of interobserver variability. Further investigation with robust longitudinal data may elucidate key geometric features predictive of rapid growth.

Differential Expression of Stress Survival Pathway Genes in Colorectal Cancer Cell Lines

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Frances Rangel*
University of Texas at El Paso

Abstract: Colorectal cancer (CRC) is the one of the most diagnosed and second deadliest cancer affecting almost 1.9 million people every year across the globe. Higher incidence and mortality rates of colorectal cancer can be attributed to age, ethnicity, diet, lifestyle, and genetics. Reactive oxygen species (ROS) are known to cause DNA damage or mutation. Consequently, apoptosis is interrupted, leading to uncontrolled cell division potentially causing tumor development. Here, we took up a bioinformatics approach to analyze the Oncomine and GEO cancer microarray databases to identify 26 stress-survival pathway associated genes that were differentially expressed in CRC. To validate their expression in CRC cells, we checked the expression of these genes in disease free colon cells CCD841 and colorectal adenocarcinoma cell line CaCO2 by quantitative reverse-transcriptase polymerase chain reaction (qRT-PCR) technique. Among the 26 genes tested, 14 were seen to be upregulated and 3 were downregulated in the CRC CaCO2 cell line as compared to the normal colon cells. The results indicate that oxidative stress and apoptosis regulate CRC progression. The genes identified in this study can be used as potential genomic biomarkers for CRC screening in the future.

Accessing impacts of the Huntington Beach oil spill on benthic invertebrate communities in Talbert Marsh

Discipline: Life Sciences
Subdiscipline: Environmental Science

Emily Montes*
California State University Long Beach

Abstract: In October 2021, Huntington Beach, California experienced an offshore oil spill that released ~127,000 gallons of crude oil into surrounding marine ecosystems, especially Talbert Marsh in the Huntington Beach Wetlands complex. This coastal salt marsh is directly linked to the Pacific Ocean and experienced oil inundation, which may persist for long periods of time. Talbert Marsh is a highly dynamic ecosystem that maintains ecological services such as carbon sequestration, nutrient cycling, and harbors biodiversity. Past studies have documented the effects of oil spills, such as the Deep-Water Horizon, including adverse ecological impacts like a decrease in benthic invertebrate diversity. However, there is a lack of information on how oil spills will affect these communities on California's coast. The goal of this project is to determine the short- and long-term impacts of oil exposure on the sediment decomposer communities in Talbert Marsh. We hypothesize that there will be a short-term reduction in diversity, followed by a long-term recovery. To determine impacts on the benthic invertebrate community, sediment cores are being collected from four sites within the marsh quarterly between October 2021 and October 2022. Sediment samples are being sieved, observed under a microscope, and classified using taxonomic keys. Three of the five quarterly samples have been collected and taxonomic identification is underway. Statistical testing will be used to test for shifts in the invertebrate community over time once all data are collected. These findings will allow us to determine the impacts of the oil spill on this important coastal ecosystem.

Identifying Combinatorial Therapeutic Strategies with BET Inhibition in Ewing sarcoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Rohda Yase*
University of washington

Abstract: Ewing sarcoma (ES) is a bone and soft tissue tumor that occurs in children and young adults. The tumor is driven by an oncogenic fusion gene that fuses the EWSR1 gene to FLI1 , an ETS family transcription factor. The EWS-FLI1 fusion promotes tumorigenesis through transcriptional and epigenetic dysregulation. Despite maximally intensive chemotherapy, the outcomes for metastatic ES patients remains poor, thus the need to identify new therapeutic strategies. Given ES's epigenetic dependencies, there is strong rationale to investigate epigenetic modifying drugs. Bromodomain and extra terminal domain (BET) proteins function as epigenetic readers that facilitate transcription. I have shown that BET inhibitors (BETi) slow the growth of ES cells in vitro but will not be successful as a single agent. I hypothesize that the combination of BETi with other biologically targeted agents will be synergistic. Based on our preliminary results from RNA-seq data and an in silico drug screen on BETi-treated ES cells, we prioritized testing of top predicted small molecule inhibitors. Using standard in vitro cytotoxic assays and calculating synergy using the Chou-Talalay method, my preliminary results showed strong synergy between Copanlisib and BMS-986158. Ongoing studies are testing the selected kinase inhibitors, and promising combinations will be tested in in vivo xenograft models. It is our goal to identify drug combinations that will enhance the cytotoxic effects of BETi in ES.

Gut Microbiota and Hashimoto's Thyroiditis: A Systemic Review and Meta-analysis

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jennyfer Zarate*[1]and Ashwini Kucknoor [2]
[1]Lamar University, [2]Lamar University

Abstract: Hashimoto's thyroiditis (HT) is one of many autoimmune diseases, however, the risk factors of this disease are not fully understood by the scientific community. Though the exact cause of HT is poorly understood, genes associated with susceptibility to Hashimoto's are mostly immunoregulatory genes along with environmental factors, like diet, smoking, and drugs. Since diet affects the gut microbiota, a connection between the gut flora and Hashimoto's has been implicated, though definitive conclusions have not been reached due to mixed study results. Thus, the goal of this meta-analysis is to mine data from published reports to investigate the relationship between gut microbiota, specifically dysbiosis, and HT. Data from studies that involved HT and gut microbes, published as of May 2022 were obtained from electronic databases such as PubMed, CENTRAL, Cochrane Library, and Google Scholar. All identified articles (n = 416) were exported to the web-based tool RAYYAN, and duplicates were removed; seven articles were selected for this meta-analysis. It was found that Bacteroides , Actinobacteria , and Cyanobacteria , among others, were augmented in HT patients compared to controls. It was also found that Bifidobacterium , Bacillaceae , and Firmicutes , among others, were significantly reduced in HT patients compared to controls. However, some studies had conflicting data that could be attributed to regional, diet, and ethnic-origin differences. Data suggested altered ratios in the composition of the gut microbiota when comparing HT and

healthy controls at the phyla, family, and genera levels. Further analysis on gut microbial dysbiosis is currently underway.

Probing the molecular mechanism of Receptor Tyrosine Kinase activity through the in vivo analysis of the C. elegans FGF Receptor, EGL-15

Discipline: Life Sciences
Subdiscipline: Biology (general)

Rachel Fuller*[1]and Michael Stern [2]
[1]Northeastern Illinois University, [2]Northeastern Illinois University

Abstract: Fibroblast growth factor receptors (FGFRs) are cell-surface receptor tyrosine-kinases (RTKs) that phosphorylate specific intracellular tyrosine residues to trigger downstream responses such as cell proliferation, migration, and differentiation. The study of the EGL-15 FGFR in the nematode C. elegans has long been used to understand principles of RTK signaling, since defects in the processes mediated by EGL-15 result in striking phenotypes that provide powerful genetic tools. One such process is the regulation of fluid homeostasis. Hyperactivation of EGL-15 causes the excessive accumulation of clear fluid inside the worm's body (the Clr ["clear"] phenotype). The isolation of Suppressor Of Clr (Soc) mutants has led to the identification of many of the core components of EGL-15 signaling, such as the Grb2/SEM-5 adaptor protein that links RTK signaling to the RAS/MAPK pathway. Although SEM-5 is required for EGL-15 signaling, a mutation that truncates EGL-15 and eliminates its SEM-5 binding sites does not confer a Soc phenotype. These data suggest the existence of an alternate pathway that links EGL-15 to SEM-5/Grb2. To identify components of this alternate pathway, a screen was conducted for Soc mutants in this egl-15 mutant background. Of the 28 mutants analyzed, 24 define two previously known and two novel soc genes. The characterization of the remaining 4 alleles may define additional components important for EGL-15 signaling.

Testing Executive Functioning in Panic Disorder Patients

Discipline: Life Sciences
Subdiscipline: Neurosciences

Sebastian Nunez*[1], Dr. Theresa M. Desrochers [2], Dr. Christina Boisseau[3], Dr. Steven Rasmussen[4], Dr. Sarah Garnaat [5], Hannah Doyle[6]
[1]Brown University, [2]Brown University, [3]Brown University, [4]Brown University, [5]Brown University, [6]Brown University

Abstract: Executive functioning (EF) is a set of cognitive skills involved in goal-directed behavior which include working memory, inhibitory control, task switching, etc. The prefrontal cortex (PFC) is a region involved in EF, and researchers have found that people with panic disorder (PD) have altered PFC activity (Killgore et al., 2014;Chechko et al., 2009). However, researchers have reported mixed results on EF deficits in people with PD. Sequential processing is an EF skill that has not been closely investigated in PD. Research has found that the PFC is necessary for sequential performance (Desrochers et al., 2015). Therefore, previously reported altered PFC activity in PD could underlie a sequential processing deficit specifically versus a general EF deficit. In this study we aimed to assess if there are EF deficits, specifically in sequential processing, in people with PD compared to healthy controls (HC). We hypothesized that people with PD will show greater behavioral deficits in sequential processing compared to HC. PD (N = 21) and HC (N = 40) participants were administered a sequential task that also assessed the ability to task-switch, a general measure of EF. Participants internally monitored 4-item task sequences, making simple image color or shape judgements. Preliminary results show that PD participants exhibited significantly higher reaction times at sequence initiation compared to the HC group, but task-switching performance did not differ between groups. In conclusion, PD participants convey a specific sequence processing deficit, which may be the facet of EF that arises from previously reported dysfunctional PFC activity.

Crustose calcifying red algae: an unknown flora that drives important ecological processes on coral reefs

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Anela Duenas*[1]and Tom Schils [2]
[1]University of Guam, [2]University of Guam

Abstract: Crustose calcifying red algae (CCRA) are dominant and essential reef builders in the Mariana Islands. Mesocosm experiments are often used to assess the ecology of CCRA as substrate colonizers, reef builders, and invertebrate recruitment substrates under varying environmental conditions. However, little is known about the degree of cryptic diversity and (micro)habitat specificity of CCRA in experimental and natural environments. Here, we compare the community composition of CCRA between (1) natural reef systems, (2) biofouling communities in an experimental flow-through seawater system, and (3) coral recruitment tiles conditioned in a mesocosm environment. We hypothesize that the floristic and community composition of CCRA will differ between the biofouling communities, the recruitment tiles, and coral reef assemblages. To conduct this study, CCRA species were identified using DNA barcoding. Images of the tank walls were taken to assess the benthic cover of CCRA species using ImageJ. The CCRA composition of the biofouling communities was then compared to data from previous studies, which characterized the CCRA communities of recruitment tiles and natural reefs. We conclude that environmental factors at the scale of microhabitats drive CCRA community composition even within the controlled conditions of experimental setups. The DNA barcoding effort revealed new taxonomic records for Micronesia and new species to science, further supporting previous studies that document high degrees of cryptic diversity in tropical seaweeds. Knowledge of the taxonomic and community diversity of CCRA in conjunction with their ecological function in tropical reef systems is important to guide coral reef conservation and management.

Effectiveness of Thiol compounds in improving metabolic function in model Dravet Syndrome zebrafish larvae

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alexis Meeks*[1], Manisha Patel [2], Rajeswari Banerji[3], Annagabriela Figueroa[4], Ruth Fulton [5], Ariana Crary[6]
[1]Wesleyan College, [2]University of Colorado Anschutz Medical Campus, [3]University of Colorado Anschutz Medical Campus, [4]University of Colorado, [5]University of Colorado Anschutz Medical Campus, [6]University of Colorado

Abstract: Dravet syndrome is a severe developmental and epileptic encephalopathy. The disease results from de novo mutations in the SCN1A gene in roughly 80% of all cases and is highly pharmacoresistant, driving the need for further studies. The SCN1A gene is a voltage-activated sodium channel; the mutations in this gene cause the sodium channel to be dysfunctional, which has been linked to metabolic dysregulation in children diagnosed with Dravet Syndrome through studies examining hypometabolism and the effectiveness of the ketogenic diet in patients. We are studying the possibility of decreasing seizure behavior and improving metabolic function pharmacologically in the Patel Lab using SCN1Lab zebrafish larvae. Given the nature of Dravet Syndrome, we are testing the abilities of thiol compounds with the aim of inhibiting TSPO expression and increasing cellular glutathione levels in order to decrease neuroinflammation. By targeting TSPO expression and cellular gluthathione directly, we were able to significantly decrease seizure behavior beyond threshold of -40 when measuring velocity in terms of percent change from baseline with two of the thiol drugs, Dimercaprol(DMP) and 1-3-Propanedithiol(1,3-P). Behavioral data was collected using the Noldus Locomotion tracker after a 4-hour drug incubation period. We were also able to show a trending increase in glucose levels when normalized to total protein and measured in percent change from vehicle using the Amplex Red Glucose/Glucose Oxidase Kit. This data, coupled with previous data, suggests that there should be a decrease of seizure behavior and an increase of metabolic function in patients when treated with DMP or 1,3-P.

Investigation of Protein Biomarkers for Cerebral Amyloid Angiopathy In Different Disease Stages of the rTg-DI Rat Model

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jessica Devlin*[1], Dr. William Van Nostrand [2], Dr. Joseph Schrader[3]
[1]University of Rhode Island, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Cerebral Amyloid Angiopathy (CAA) is a common cerebral small vessel disease of older adults and prevalent comorbidity of Alzheimer's disease (AD). CAA is characterized by progressive deposition of amyloid beta-peptide in the cerebral vasculature leading to cerebral microhemorrhaging, stroke, perivascular neuroinflammation, white matter damage, and severe cognitive impairment. Despite hallmark imaging characteristics of CAA, definitive diagnosis requires post-mortem confirmation, and no validated biomarkers have been established. The underlying mechanisms leading to CAA-related vasculopathies are poorly understood and currently have no effective treatment. Thus a better understanding of potential protein biomarkers of CAA, and underlying molecular mechanisms of disease progression, is vital to developing novel treatment strategies and diagnostic tools. In this study, we investigated the longitudinal expression of proteins identified as potential markers of CAA in the established rTg-DI preclinical model of CAA via protein mass spectrometry and immunoblotting. In both emergent and advanced CAA stages, the elevated expression of ANXA3, HTRA1, and APOE proteins was revealed in rTg-DI brains. Immunolabeling revealed strong colocalization between APOE and amyloid deposits in rTg-DI rat brain regions, while strong enhancement of ANXA3 and HTRA1 were associated with areas of amyloid deposition and severe vasculopathies. Hence, we explore important findings regarding these three potential markers of CAA in rTg-DI rats.

Investigation of the Role of the Coenzyme F420-Dependent Oxidoreductase Cao12 in the Generation of D-Amino Acids in Cacaoidin

Discipline: Life Sciences

Subdiscipline: Biochemistry

Isaiah Lopez*[1], Haoqian Lainey Liang [2], Wilfred van der Donk[3]
[1]University of Illinois at Urbana-Champaign, [2]University of Illinois at Urbana-Champaign, [3]University of Illinois at Urbana-Champaign

Abstract: Ribosomally synthesized and post-translationally modified peptides (RiPPs) are a growing class of natural products. One class of RiPPs is the lanthipeptides, which feature the thioether linkages lanthionine (Lan) and/or methyllanthionine (MeLan). We are studying cacaoidin, a lanthipeptide with antimicrobial activity, produced by Streptomyces cacaoi . A unique characteristic of cacaoidin is its five D-amino acids. This project focuses on the function and mechanism of the coenzyme F 420 -dependent oxidoreductase Cao12 encoded in cacaoidin's biosynthetic gene cluster. We hypothesize that Cao12 generates D-alanine and D-butyrine by catalyzing the reduction of dehydroalanines and dehydrobutyrines, respectively, while oxidizing the F 420 . This study will report efforts to reconstitute this reaction in vivo and in vitro , using E. coli as a biosynthetic host equipped with an F 420 biosynthesis plasmid. After heterologous expression, we aim to purify active Cao12 using immobilized metal affinity chromatography (IMAC) and size exclusion chromatography (SEC). Upon in vitro incubation of the active enzyme with the substrate and F 420 , modification will be examined by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) to detect mass shifts. The same reaction will be investigated in vivo by co-expressing the substrate with the tailoring enzymes and coenzymes and purification of the final reduced product. This ongoing study of cacaoidin's modifying enzymes will expand the knowledge of cacaoidin's biosynthetic pathway, RiPP biosynthetic enzymes, and modifications to be applied to other bioengineering challenges, such as introducing D-amino acids into other natural products to increase stability and combat antibiotic resistance.

Categorizing Subtypes of IDH1-mutant Skin Cutaneous Melanoma

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Brianna Francis*[1], Elena Torlai Triglia [2], Gisselle Velez-Ruiz[3]
[1]Johns Hopkins University, [2]Broad Institute of MIT and Harvard, [3]Broad Institute of MIT and Harvard

Abstract: Skin cutaneous melanoma is a form of cancer with a very high mutation burden. Varying combinations of mutated genes can affect tumor development, prognosis, and the efficacy of therapy. A common gain-of-function mutation in melanoma is in the IDH1 gene, which has been shown to impact DNA methylation. Other mutations known to impact melanoma phenotype are in the BRAF or NRAS genes. Previous studies have not explored the potential synergy between these mutations. We aim to investigate whether there are significant differences in gene expression and DNA methylation between melanomas with IDH1-NRAS and IDH1-BRAF mutations. Uncovering differences between the two groups would allow us to understand the distinctive pathways of each combination of mutations. We are analyzing skin cutaneous melanoma DNA methylation array and gene expression mRNA-seq data from The Cancer Genome Atlas. Thus far, we have found that all tumor samples with IDH1 gain-of-function mutations have relatively high DNA methylation levels and downregulated gene expression. At a subset of loci, those with IDH1-NRAS mutations display higher levels of DNA methylation than samples with IDH1-BRAF or IDH1 mutations. We have found that these regions are enriched in polycomb target genes. Polycomb complexes are known to repress genes important for early development. We are currently investigating how IDH1-NRAS and IDH1-BRAF mutations impact gene expression and DNA hypermethylation at polycomb target genes. Analyzing these epigenomic differences across tumor samples will allow scientists to develop targeted therapies so that patients with melanoma receive the most effective treatments based on their tumor subtype.

Searching for slightly deleterious alleles of eggshell calcification genes in the critically endangered Puerto Rican parrot

Discipline: Life Sciences
Subdiscipline: Genetics

Pamela Wiscovitch-Roque*[1], Juan C. Martínez-Cruzado [2], Diego S. Aviles-Perez[3], Diego Flores-Ayala[4], Leigh A. Maldonado-Santiago [5], Deyna Morales-Carrasquillo[6], Xaymaris Teruel-Padilla[7]
[1]University of Puerto Rico Mayaguez campus, [2]University of Puerto Rico Mayaguez campus, [3]University of Puerto Rico Mayaguez campus, [4]University of Puerto Rico Mayaguez campus, [5]University of Puerto Rico Mayaguez campus, [6]University of Puerto Rico Mayaguez campus, [7]University of Puerto Rico Mayaguez campus

Abstract: The Puerto Rican parrot (Amazona vittata) is a critically endangered species whose population had shrunk to only 13 individuals by 1975. Fragile eggshells are often produced in breeding sites, probably as the result of this severe bottleneck. We are manually annotating parrot genes whose orthologs have been shown to be differentially expressed in the chicken uterus, where the eggshell is laid, aiming to identify amino acid changes specific to A. vittata that may affect eggshell strength. The UniProt ID of validated isoforms is used to search for the gene in the UCSC Genome Browser. Synteny analysis is usually needed to identify the scaffold holding the gene from other scaffolds holding paralogs. Exon coordinates are determined by combining BLAST analysis with visualization in the browser, where informative tracks, such as RNA-Seq coverage, are used. Splice junctions of the resulting gene model are revised using the Genomics Education Partnership's Gene Model Checker, and the predicted protein sequence is aligned to its chicken and budgerigar orthologs. Predictions on the effect on protein function of amino acid changes occurring in the parrot in positions otherwise conserved between the chicken and the budgerigar are examined in SIFT and Polyphen-2. Amino acid changes likely to affect protein function are examined in A. ventralis, the sister species of A. vittata. Of 23 genes annotated, only one, CACNA1D, has shown an amino acid change specific to A. vittata predicted to affect protein function. Further annotation should produce additional candidates that can then be tested using CRISPR gene editing.

Examining the Accessible Chromatin Regions Between Duplicated Gene Copies in the Tetraploid Leucaena trichandra

Discipline: Life Sciences
Subdiscipline: Genetics

Kitti Banga*[1], Donovan Bailey [2], Bob Schmitz[3]
[1]New Mexico State University- summer research expereince with the University of Georgia, Athens, [2]New Mexico State University, [3]University of Georgia

Abstract: Chromosomal and genic duplications are key sources of genetic novelty in evolution. When duplication events occur, two copies of the genes are usually not necessary, which results in one being lost through mutational processes. However, duplicate copies can also be retained, going on to gain new functions or subfunctions between the daughter genes. The plant genus Leucaena , which contains 19 species with tetraploid genomes, provides exceptional opportunities to investigate the evolutionary changes brought forth by chromosomal and genic duplications. Species in the group are good models because they grow relatively quickly for trees and they have many uses as multipurpose crops in the tropics. Here we use the genome of the tetraploid L. trichandra and An Assay for Transposase-Accessible Chromatin (ATAC-seq) to determine the changes to the accessible chromatin regions between different copies of the chromosomes. The results of the ATAC-seq analysis will provide an important annotation for future research and allow us to make conclusions about the accessible regions that have experienced gene expression differences since the duplication of the chromosomes. Determining these regions will provide key information regarding how chromatin accessibility varies among the different copies and the relative fate of duplicated gene copies.

Modeling in vivo cancer dependencies on ezrin using engineered organoids

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Kamryn Graham*[1], Dean Procter[2], Gisselle Velez-Ruiz[3]
[1]The Broad Institute of MIT and Harvard, [2]Broad Institute, [3]The Broad Institute of MIT and Harvard

Abstract: Various cancer studies have highlighted two genes, ezrin (EZR) and ras homolog A (RhoA), as metastatic cancer biomarkers because of their roles in facilitating cytoskeletal arrangement, cell polarity, adhesion, and–when upregulated–cell motility. Previously, EZR and RhoA gene dependencies were found to be enhanced in vivo, with EZR displaying stronger enhancement, indicating that each gene may contribute to interactions in the tumor microenvironment that are not maintained in 2D tissue culture. Therefore, to develop an improved in vitro model of gene dependencies identified in vivo , we engineered an EZR knockout in cancer organoids selected from the Human Cancer Models Initiative (HCMI) catalog. Organoids allow us to analyze the contribution of resource and spatial competition, cell differentiation, cell state, and differential protein localization to tumor cell survival in vitro , thus allowing us to more adequately model the complexity of in vivo gene dependencies. Using wild-type and engineered organoids, we visualized the localization of EZR and RhoA to understand their facilitation of cancer cell survival within tumor burdened tissue samples from in vivo studies. We used endogenous split-fluorescent protein tagging via homology directed repair to visualize EZR and fluorescent biosensors to visualize RhoA activity. Fluorescent protein tagging allowed us to analyze protein localization dynamics across different stages of tumor development. These comparisons allow us to understand how EZR dependencies form over time and then contextualize those differences in EZR dependencies across different organs.

The N-terminus regulates protein synthesis and stability in human cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Adina Abudushalamu*[1], Dr. Olivia S. Rissland[2], Evan J. Morrison[3]
[1]University of New Mexico, [2]University of Colorado Anschutz Medical Campus, [3]University of Colorado Anschutz Medical Campus

Abstract: The primary structure of a protein dictates its secondary and tertiary structures, function, and localization. However, emerging evidence suggests that the primary structure is also critical to controlling the levels and dynamics of gene expression. In particular, the N-terminus of a protein exerts substantial control over protein synthesis and stability. In one instance, we found that the fusion of N-terminal amino acids to one reporter dramatically enhanced expression, while the fusion of the same N-terminal amino acids to another reporter completely diminished expression. Despite this knowledge, there is still minimal understanding of the mechanisms governing the connections between primary structure and gene expression. I hypothesize that the biochemical properties of the N-terminal amino acids in the primary structure control gene expression through N-terminal processing. To test this model, I will determine how reporters with different N-terminal amino acid fusions control gene expression. I will use in vitro translation systems, as well as live cells, to determine the difference in expression due to protein synthesis and stability. This project will elucidate the mechanisms underlying N-terminal-dependent gene regulation. Since misregulation of gene expression contributes to several disease phenotypes, our results will enhance our understanding of how gene expression is regulated in these contexts.

Identifying factors that reinforce lung fibroblast identity in vitro to study responses to influenza virus infection

Discipline: Life Sciences
Subdiscipline: Microbiology

Jimmy Gomez*[1], David Boyd[2], Shally Saini[3], Charles Winterbottom[4]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]University of California, Santa Cruz

Abstract: Respiratory viral infections, such as influenza, can lead to severe health complications, such as acute respiratory distress syndrome, even after the clearance of an infectious virus. Lung fibroblasts with distinct identities are imperative to help clear an infection, organize immune responses, and maintain tissue function. As a result, the inflammatory activity of lung fibroblasts can determine the severity of respiratory viral disease. Recent work has shown that lung fibroblasts represent diverse cell types with unique functions based on location in the respiratory tract. We hypothesize that location within the respiratory tract determines how fibroblasts respond to influenza infection and lung inflammation. To address this hypothesis, we are developing in vitro culture methods to reinforce fibroblast identity and to study the responses of lung fibroblasts from distinct locations in the respiratory tract to infection. Based on computational analyses of single-cell gene expression and spatial transcriptomic data from mouse lungs, we identified fibroblast growth factor (FGF) signaling through FGFR3 as differentially regulated in alveolar lung regions, which may be necessary for fibroblast identity. We are now testing the ability of individual fibroblast growth factors (FGFs) to reinforce alveolar fibroblast identity in vitro assessing cell identity by quantitative polymerase chain reaction (qPCR) and flow cytometry. Applying growth factors will reinforce the fibroblasts' phenotypes and help us understand how distinct fibroblast responses determine disease severity. Overall, these analyses will help identify therapeutic targets in fibroblasts to reduce inflammation and persistent respiratory disease.

Investigating EDC Presence in Microfibers Through Comparative Analysis of Adipogenesis-Differentiated MSCs Exposed to Microfibers, Plastics, and Obesogens

Discipline: Life Sciences

Subdiscipline: Environmental Science

Truman Natividad*[1], Raquel Chamorro-Garcia, PhD [2], Gabriella (Gaby) Amberchan, PhD[3], Francisco (Cisco) Jimenez[4]

[1]University of California, Santa Cruz, [2]Assistant Professor and Researcher; Dep. of Microbiology and Environmental Toxicology; University of California, Santa Cruz, [3]ACCESS Program Associate Director and Researcher; Department of Chemistry and Biochemistry; University of California, Santa Cruz, [4]Professor; Department of Chemistry; Cabrillo College

Abstract: Environmental toxicology is the field of science concerned with studying how different chemical, biological, and physical agents impact living organisms and the ecosystems they are a part of. As humans continue to address their needs through industrial and technological means, it is imperative that the reactants and products of our operations are researched thoroughly before they are released into the environment and cause irreversible damage to the world around us. One group of substances to be particularly wary of are those found in microfibers (MFs)–the anthropogenic, microplastic pollutant that has become increasingly ubiquitous to terrestrial, airborne, and predominantly aquatic environments in the last decade. While their health effects have remained enigmatic throughout their research, MFs and their plastic additives have become associated with obesity and other metabolic conditions, like type-2 diabetes. My project aims to determine if the compounds found in MFs have the ability to induce fat development and, therefore, contribute to the current obesity epidemic. I will differentiate mouse bone marrow mesenchymal stem cells (mBMSCs) into adipocytes in the presence and absence of water contaminated with different types of microfibers (polyester, cotton) and plastics (single-use water bottles). I will then quantify lipid accumulation and compare the result with cells that were exposed to distilled water. I hypothesize that exposure to MFs will inappropriately stimulate fat accumulation in differentiated mBMSCs; it is expected that exposure to MFs will cause the adipocytes to exhibit a higher lipid content than normal–just as if they were exposed to EDC obesogens.

Describing Four New Species of Cadlina, Bergh 1879 from South Africa and Their Phylogeny

Discipline: Life Sciences

Subdiscipline: Animal Sciences/Zoology

Cesca Ledesma*[1], Terrence M. Gosliner [2], Rebecca F. Johnson[3], Lynn Bonomo[4]

[1]Lawrence University (Appleton, Wisconsin), [2]California Academy of Sciences, [3]California Academy of Sciences, [4]California Academy of Sciences

Abstract: Species of the nudibranch mollusk genus Cadlina , Bergh 1879 have been known to exist in the South African region but have not been thoroughly studied. It has been hypothesized that four species from the region likely represent undescribed species. These species of Cadlina were found in South Africa in the late 1980s and appear to be the only representatives of the genus found in this area. Since most species within the genus Cadlina have similar external characteristics, we used different methods to differentiate each species based on morphological and genetic features. Gross dissection was undertaken to observe external morphology and reproductive systems, while scanning electron microscopy was used to examine other important features for species differentiation in nudibranchs namely the jaws, radulae, penial spines, and mantle spicules. Genetic sequencing using both COI and 16S genes was done for each species available. The genetic data was used to describe these four new species from and create molecular phylogenies using RAxML and Mr. Bayes. The new genetic sequences were also combined with GenBank sequences for other Cadlina species to create phylogenetic trees that exhibit the relationships between the new South Africa species and other Cadlina species from around the world. This presentation is the first to highlight the diversity of Cadlina species in South Africa and presents a new molecular phylogeny of Cadlina . The phylogenetic tree and morphological descriptions of these new species provide clear distinctions between the four species described here.

Light-induced changes in the behavior and photosymbiosis of the upside-down jellyfish, Cassiopea (Cnidaria: Scyphozoa: Rhizostomeae)

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Rebecca Salas*[1], Bastian Bentlage [2], Colin Anthony[3]
[1]University of Guam, [2]University of Guam, [3]University of Guam

Abstract: The benthic upside-down jellyfish, Cassiopea , lives in mangroves and coastal tropical waters. Cassiopea are mixotrophic organisms that rely heavily on both photosynthetic endosymbionts and stinging nematocysts for nutrients. This trophic plasticity allows for high environmental resiliency. Photopigments within dinoflagellate endosymbionts absorb visible light, which supplies nutrients to the cnidarian host. Bell pulsations, while necessary for locomotion, also push water through the oral arms, which should influence photosynthetic productivity and food availability. To identify behavioral plasticity during light acclimation, pulsations and photopigments of two functionally distinct Cassiopea were measured through 14-day light and dark acclimation periods. Preliminary results have shown a direct relation between pulsation rate and jellyfish diameter. Once rates were compensated for diameter, mean pulsation rates dropped significantly after dark exposure. However, some interesting escape mechanisms have begun to reveal themselves. As I expand this research, I expect that pigment abundance and pulsation rate reveal themselves as tightly correlated characteristics. Understanding the relationship between behavior and function will help us reveal the resilient upside-down jellyfishes' adaptive potential amid the Anthropocene.

Investigation of the Mechanism of Glioblastoma Initiation in the Brains of Mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jazmin Xiong*[1]and Tou Yia Vue [2]
[1]University of Northern Colorado, [2]University of New Mexico

Abstract: Cells within the body will form tumors or become cancerous when they expand relentlessly and uncontrollably. Tumor suppressor genes function to prevent this overgrowth of cells; however, mutations that occur within these tumor suppressor genes cause their function to be altered or disabled, resulting in tumor formation. TP53, NF1, and PTEN (TNP) are three of the most mutated tumor suppressor genes in glioblastoma, a highly aggressive and invasive brain tumor that remains incurable. How glioblastomas form in the brain and the genetic mechanisms that are responsible for the growth of these tumors remain unclear. Previous work in our lab shows that glioblastoma tumors can be induced in the brains of mice by electroporating CRISPR plasmids encoding Cas 9 and guide RNAs to delete the TNP genes in neural progenitor cells in the dorsal cortex. Furthermore, we also demonstrate that initiation of the glioblastoma tumors required the expression of transcription factors, ASCL1 and OLIG2. In

this study, we aim to determine if single or double deletion of the TNP genes is sufficient to induce the expression of ASCL1 and OLIG2, including tumor formation in the brain. Analysis of the transcription factors expression was examined through immunostaining. Our preliminary results showed that expression of ASCL1 and OLIG2 and formation of a tumor are present regardless of any deletion of any tumor suppressor gene; however, observations showed increased migration and growth of tumor cells when TP53 was deleted, indicating that the TP53 gene pathway may be the main driver for glioblastoma tumor development.

Characterization of human immune cell development in a next-generation humanized mouse model

Discipline: Life Sciences
Subdiscipline: Microbiology

Hannah-Marie Santos*[1], J. Victor Garcia [2], Sarah Wessel[3], Angela Wahl[4]
[1]University of North Carolina at Chapel Hill, [2]University of North Carolina at Chapel Hill, [3]University of North Carolina at Chapel Hill, [4]University of North Carolina at Chapel Hill

Abstract: Highly relevant human pathogens like HIV, SARS, MERS, etc. that cause significant mortality and morbidity have very limited tropism and can't be studied in vivo using conventional animal models, hindering the development of novel interventions. Our goal is to develop a human/mouse chimera model that supports replication of human-specific pathogens to investigate critical aspects of host/pathogen interactions and test novel pre-clinical interventions. Human/mouse chimeric animals were created by implanting human thymic and liver tissue into immunodeficient animals. These animals were then administered a bone marrow transplant with autologous human hematopoietic stem cells. Overtime, these animals developed a systemic human immune system as determined by flow cytometric analysis for the presence of human immune cells in peripheral blood. We then determined the presence of human immune cells in tissues (liver, lung, thymus, lymph nodes, spleen, kidney, and thymic organoid) using immunohistochemistry. Our results demonstrate the presence of human immune cells in all tissues analyzed, including human monocytes/macrophages, dendritic cells, NK cells, B cells, and T cells. Finally, we evaluated human antibody production in these animals which revealed substantial amounts of human IgG1 (711.19 ng/mL), IgG2 (>30,000 ng/mL), IgG3 (26.48 ng/mL), IgG4 (51.72 ng/mL), IgM (>2500 ng/mL), and IgA (1166.71 ng/mL). In summary, our results demonstrate that transplantation of human tissue and hematopoietic stem cells results in reconstitution of immunodeficient mice with a human immune system. Having completed this fundamental proof of principle, our goal is to use these human/mouse chimeras to evaluate novel pre-clinical approaches to treat highly relevant infectious diseases.

Looking for the Signal: Determining How Dormant Uropathogenic Escherichia coli Exit Dormancy

Discipline: Life Sciences
Subdiscipline: Microbiology

Andrea Miranda Duarte*[1], Dr. Jodi Camberg [2], Josiah Morrison[3]
[1]University of Rhode Island, [2]University of Rhode Island, Cell and Molecular Biology Department, [3]University of Rhode Island, Cell and Molecular Biology Department

Abstract: More than half of all women will experience at least one urinary tract infection (UTI) in their lifetime. The majority of UTIs are caused by Uropathogenic Escherichia coli (UPEC) and

many infections are recurrent within six months. UPEC may enter a dormant state termed quiescence in vivo, which allows cells to be tolerant to antibiotic treatment. In vitro, UPEC are unable to grow on minimal media containing glucose as the sole carbon source, a state that we termed quiescence. We have previously demonstrated that fragments of a bacterial cell wall component, peptidoglycan (PG), can stimulate UPEC growth. This could provide the potential benefits of preventing UPEC quiescence, and thus antibiotic tolerance, in vivo. The goal of this project is to determine which genes are involved in UPEC exit from quiescence via uptake of PG. Using the classic ST73 lineage of UPEC CFT073, we generated a library of mutant strains via a transposon screen that randomly inserted into the CFT073 genome. We identified CFT073 mutants unable to respond to PG fragments. Arbitrarily primed polymerase chain reaction (AP-PCR) distinguished which genes were inactivated and their significance was confirmed via gene deletion. Several genes have been found in this manner including ridA, an enamine/imine deaminase. Future experiments will attempt to determine the exact nature of how these genes are involved in PG uptake by CFT073. These experiments to understand UPEC pathogenicity will help guide the design of novel therapeutics.

A blast from the past: effects of environmental conditions on early life stages in an intertidal snail

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Heidi Waite*[1]and Dr. Cascade Sorte [2]
[1]University of California Irvine, [2]University of California Irvine

Abstract: As the climate changes, marine organisms are on the move. In addition to tracking shifts in these species' ranges, it is essential to understand how the demographic rates of these shifting species respond to environmental conditions (such as temperature) to better predict their population size and impacts. We studied two intertidal whelks, Acanthinucella spirata and Mexacanthina lugubris , which are expanding their northern range boundaries along the California coast. Both species are predatory with strong top-down effects and important for ecosystem functioning. This research documented the current abundance distributions and reproductive output (# of egg masses) of both species along the California coast. In addition, we conducted an intensive study at Thousand Steps Beach, Laguna Beach, CA to quantify the thermal conditions M. lugubris egg masses experienced in the field (using temperature loggers) and impact of thermal exposure on early life stages (by measured lethal thermal tolerances of developing larvae). We found that the majority of egg masses were laid in shaded areas in crevices or overhangs in the intertidal zone for both species. We will analyse the abundance of egg capsules per m 2 . At Thousand Steps Beach, while exposure (maximum and 90th percentile temperatures) to thermal extremes varied across the tidal gradient, larval thermal tolerances did not appear to vary by thermal exposure at corresponding tide heights. This implies that egg masses are potentially buffered by the microhabitat in which they are laid, which might promote persistence of these species and continued expansion under a changing climate.

Putative Egg Attendance Behavior in The Emerald Glass Frog (Centrolenidae: Espadarana prosoblepon)

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Noemi Rodriguez*[1]and Johana Goyes Vallejos [2]
[1]Cal Poly Humboldt , Wildlife Department, 1 Harpst Street, Arcata, CA 9552 USA., [2]University of Missouri, Division of Biological Sciences, Columbia MO 65211 USA.

Abstract: Parental care is any action that increases reproductive fitness. In frogs, parental care is variable and diverse, with egg attendance being the most common form of care. Parental hydration during egg attendance has been shown to increase reproductive success by aiding offspring survivability. While many members in Centrolenidae exhibit egg attendance behavior it has yet to be proven for Espadarana prosoblepon . In this study, we aim to understand if females of E. prosoblepon are providing hydration for the egg clutch immediately after oviposition. Female removal experiments were conducted in Las Cruces Biological Station's Botanical Garden in Costa Rica. We randomly assigned pairs to a control treatment (females remaining with clutch) and removal treatment (females removed from clutch). To measure if any supplemental hydration was provided to the egg clutch we used a novel method to estimate the distance/thickness of the gelatinous casings between eggs using the software FIJI to measure the nearest neighbor distance (Nnd) among eggs within a clutch and posteriorly calculating the average nearest neighbor distance (μNnd) per clutch. A greater Nnd distance among eggs (used as a proxy of gelatinous thickness) between control and treatment clutches suggests that females are providing supplemental hydration to their offspring. Conversely, no differences in the μNnd values between treatments will constitute evidence that E. prosoblepon does not exhibit parental care behavior. Detailed information about the presence or absence of parental care behavior is critical for future studies looking at the evolution of this behavior among frogs.

Glacial meltwater affecting keystone species Mytilus trossulus's shells

Discipline: Life Sciences
Subdiscipline: Biology (general)

Ricardo A Medina Medina*[1], Scott Gabara [2], Michael Navarro[3]
[1]University of Alaska Fairbanks, [2]UAF, [3]university of Alaska Southeast

Abstract: Mussels serve a foundation species role in the rocky intertidal. The spaces among mussels and their byssal threads creates habitat for other organisms. Global warming is increasing global temperatures and disproportionately affecting high latitude areas, leading to melting of glaciers and increases in glacial meltwater downstream. Glacial melt may alter water parameters like salinity, possibly affecting the Pacific blue mussel (Mytilus trossulus). Previous work in Lynn Canal and Kachemak Bay, Alaska provided evidence that blue mussels from sites with more glacial melt had weaker shell strength. We evaluated whether glacial melt affected the ability of a predatory gastropod (the filed dogwinkle Nucella lima) to drill into mussels. Mussels were collected from sites with watersheds containing a range in glacial coverages (0-60%) located in two regions that differ in oceanic input: Katchemak Bay and Lynn Canal. We hypothesized that glacial melt would weaken the shells of M. trossulus and N. lima would more easily drill into mussel shells from sites with higher glacial coverages and how oceanic input may buffer these changes. The team conducted a laboratory-based experiment using 10 replicate bins with a pair of M. trossulus and N. lima in each container sourced from 3 sites in each region. This research study will determine how glacial melt 1. Affects water parameters in intertidal zones, 2. keystone specie's shell condition and 3. Predation by N. lima.

Determining the effects of disease-associated non-coding variants on NKX2-5 DNA binding

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alejandro Rivera-Madera*[1], José A. Rodríguez-Martínez [2], Edwin G. Peña-Martínez[3], Leandro Sanabria-Alberto[4], Brittany M. Rosario-Cañuelas [5]
[1]University of Puerto Rico at Cayey, [2]University of Puerto Rico, Rio Piedras Campus, [3]University of Puerto Rico, Rio Piedras Campus, [4]University of Puerto Rico, Rio Piedras Campus, [5]University of Puerto Rico, Rio Piedras Campus

Abstract: Transcription factors (TFs) are DNA-binding proteins that control gene expression. Regulation by TFs contributes to the differentiation of cells by expressing genes in a tissue-specific manner. Mutations affecting NKX2-5 binding, a cardiac TF involved in heart development, are associated with Congenital Heart Defects (CHDs). Over 90% of disease-associated mutations occur within non-coding regions involved in TF binding like promoters and enhancers. However, there is a gap in knowledge about the molecular mechanisms of non-coding variants linked with many diseases. Targeting disease-associated variants located within NKX2-5 binding sites will provide insight into how these mutations are associated with CHDs by determining changes in TF-DNA binding affinity. We previously identified over 900 disease-associated non-coding variants predicted to affect NKX2-5 binding using a Position Weight Matrix (PWM) predictive model. Three variants with the highest predicted impact on TF-DNA binding were selected: rs7719885(PWM= -212), rs747334 (PWM= -187), and rs3892630 (PWM=146). A positive score predicts an increase in binding affinity, and a negative score a decrease. For in vitro validation, NKX2-5 was produced in a bacterial expression system and purified with Ni-NTA affinity chromatography. Changes in binding affinity were observed for all three predicted non-coding variants after using Electrophoretic Mobility Shift Assay (EMSA). These changes were confirmed by quantifying TF-DNA binding and calculating the dissociation constant (Kd). Our findings suggest that differential TF binding could be a key point in assigning causality for disease-associated non-coding variants. Elucidating the molecular mechanisms behind these variants will contribute to early diagnosis and treatment of these diseases.

Host tree and mycorrhizal diversity of epiphytic orchids native to Guam

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Michael Fernandez*[1]and Mari Marutani [2]
[1]University of Guam, [2]University of Guam

Abstract: Orchidaceae depend on orchid mycorrhizal fungi (OMF) for basic nutrition. This symbiotic relationship and other ecological interactions shape the distribution and evolution of orchids especially in tropical Pacific islands which have some of the highest number of rare endemics. We studied the host tree preferences, OMF associations, and mycorrhizal colonization rates of six native, epiphytic orchid species in the Pacific island of Guam: Coelogyne guamensis , Luisia teretifolia , and Taeniophyllum mariannense and the threatened Bulbophyllum guamense, Dendrobium guamense, and Tuberolabium guamense . Eight sites around Guam were surveyed, encompassing the island’s three distinct habitat types: limestone forest, volcanic ravine forest, and urban areas. A total of 147 orchid specimens were recorded on 22 different host tree species. The common T. mariannense was observed on a greater diversity of native trees in native limestone and volcanic ravine forests and novel invasives in urban areas. Through Sanger sequencing of isolated root OMF, it was found to associate with OMF groups Ceratobasidiaceae and Sebacinaceae and several non-OMF fungal endophytes, likening it to a generalist species. Less common, threatened orchids such as B. guamense, D. guamense, and C. guamensis were restricted to native trees in native forests with mycorrhizal diversity limited to OMF groups Ceratobasidiaceae, Tulasnellaceae, and Atractiallales, suggesting ecological specialization. Furthermore, mycorrhizal colonization rates were greater in seedlings (89%) compared to adults (57%) suggesting early dependence on OMF in Guam's native, epiphytic orchids. Our findings expand on existing ecological knowledge of Guam’s native, epiphytic orchids with potential to supplement ongoing conservation efforts.

Evaluating the impact of genetic diversity on Pfs230 – a transmission-blocking malaria vaccine candidate

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Awa Cisse*[1], Amy Bei [2], Ife Desamours[3], Khadidiatou Mangou[4], Fatoumata Diallo [5], Seynabou D. Sene[6], Mariama N. Pouye[7], Alassane Thiam[8], Bacary Djilocalisse Sadio[9], Ousmane Faye[10], Alassane Mbengue [11]

[1]Yale University - Department of Epidemiology of Microbial Diseases - Laboratory of Epidemiology in Public Health, [2]Yale University, [3]Yale University, [4]Institut Pasteur de Dakar, [5]Institut Pasteur de Dakar, [6]Institut Pasteur de Dakar, [7]Institut Pasteur de Dakar, [8]Institut Pasteur de Dakar, [9]Institut Pasteur de Dakar, [10]Institut Pasteur de Dakar,[11]Institut Pasteur de Dakar

Abstract: Pfs230 is a transmission-blocking vaccine candidate for Plasmodium falciparum , one of the five species of Plasmodium that causes malaria in humans. Despite having multiple tools to combat malaria, progress in malaria control has stagnated. A novel vaccine candidate is needed to eradicate the disease. Studies have shown the promise of Pfs230 for inclusion in a malaria transmission-blocking vaccine, which would prevent transmission to the Anopheles mosquito vector, decreasing downstream transmission. Previous findings uncovered that monoclonal antibodies that recognize Pfs230 during parasite sexual development and showed it has transmission-blocking activity. However, the genetic diversity variation in this locus may affect the transmission-blocking efficacy of Pfs230 antibodies. To determine the impact of genetic diversity on function, we combine genomic and experimental genetic approaches. Here, we employ targeted amplicon sequencing of Pfs230 obtained in a high-transmission zone: Kédougou, Senegal. Using Illumina Next-Generation sequencing on a NovaSeq6000, we are sequencing Pfs230 to identify non-synonymous mutations. By introducing prioritized mutations in domain I into an isogenic parasite background, a domain previously shown to contain the most potent inhibitory activity, we will analyze the impact of specific different SNPs on function combinations. Functional evaluation of transmission inhibition will be performed using monoclonal antibodies and the standard membrane feeding assay. This approach helps identify specific polymorphisms in Pfs230 that can decrease potential efficacy. The findings from this study will permit the rational prioritization of new alleles and combinations of alleles in future iterations of transmission-blocking vaccines for malaria.

Identification of novel biomarkers of human Pluripotent Stem Cells: TEK and TM4SF18

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Saul Ruiz*[1], Luis G. Villa-Diaz [2], Suraj Timilsina[3]
[1]Oakland University, [2]Oakland University, [3]Oakland University

Abstract: Human pluripotent stem cells (hPSC) have been a major topic of discussion within various fields of biology, from reproduction to clinical trials. They are responsible for developing, regenerating, repairing, and maintaining organs and tissues within our bodies. Their potential use in regenerative and therapeutic medicine is the major reason of interest. Stem cell research is highly dependent on the ability to properly identify and isolate individual cells from a tissue or a cell niche. For these reasons, it is highly important to have protein identifiers specific to the cells, also known as biomarkers. Previous research has identified a specific transmembrane biomarker that is commonly found in over 35 populations of stem cells, ranging from primitive embryonic stem cells to adult stem cells. This protein is Integrin α6 (also known as CD49F). Using flow cytometry, Western Blot and RNA seq analysis of hPSCs with high and low expression of CD49f we identified two potential biomarkers: TM4SF18 and TEK. We hypothesize that these two cell surface proteins play a significant role in the self-renewal mechanisms of hPSCs, and will aid in identifying truly undifferentiated stem cells over lineage-committed progenitor cells found in heterogeneous populations.

Understanding Hemozoin Crystal Movement in Malaria Parasites

Discipline: Life Sciences
Subdiscipline: Biochemistry

Raissa Kodia-Batamio*[1], Paul Sigala [2], Erica Hastings[3]
[1]Howard University, [2]University of Utah, [3]University of Utah

Abstract: Malaria is a deadly disease caused by single-celled Plasmodium parasites. Malaria still lacks a broadly effective vaccine available and caused over half a million deaths in 2020 (WHO 2021). Plasmodium falciparum is the most common and virulent species of the parasite. Due to parasite complexity and growing drug resistance, this deadly disease remains a major threat within many global communities. A fundamental component of Plasmodium falciparum anatomy and survival during its infection of human red blood cells is hemoglobin digestion and the mitigation of cytotoxic heme. Hemozoin is a crystalline structure composed of heme produced in the parasite food vacuole as a mechanism to detoxify excess heme during hemoglobin digestion. Hemozoin formation is essential for parasite health and after crystals form, they adopt a tumbling motion in the food vacuole whose origin is poorly understood. A lipocalin-like protein targeted to the parasite food vacuole has been shown to contribute to heme crystallization and motion, however, its functional roles remain undefined. To better understand hemozoin motion and cellular determinants, I am using fluorescent molecular dyes and live-cell microscopy to study the relationship between moving hemozoin and the properties of key organelles, including polarized mitochondria and an enclosed food vacuole. Also, using CRISPR-Cas9 technology to disrupt the lipocalin gene, I will study the relationship between the lipocalin protein and the movement of hemozoin. Studying this phenomenon will reveal fundamental understanding of a critical heme-detoxification mechanism of this parasite, help identify new drug targets, and eventually, lead to a decrease in Malaria-related deaths.

Foraging for answers: A citizen science approach to studying forage fish communities through diet analysis

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Clara Benadon*[1]and Chris Guo [2]
[1]Bowdoin College, [2]University of Alaska Fairbanks

Abstract: Forage fish, the prey of fishery-targeted species, are trophically crucial and globally understudied. Monitoring changes in forage fish communities can help us understand the stability of predatory fish populations, such as Pacific Halibut and Alaskan King Salmon, which are of particular economic importance in the Gulf of Alaska. I created a citizen science initiative where participants photograph game fish stomach contents, which often include forage fish. Users place a caught fish's stomach contents on a "diet card," record general spatiotemporal and size information, and then send in a picture through an online form. I tested this system by analyzing Pacific Halibut gut contents, asking fishermen what questions they have about predation, and then creating an R markdown website that answers these questions through automated data visualization. The diet card program will engage local environmental and educational agencies and foster collaboration between scientists and fishermen. Ultimately, the Kachemak Bay Research Reserve will distribute these tried-and-true diet cards to fish cleaning stations and individual fishermen, continuing to enhance the program's ease of use and ability to answer scientists' and fishermens' most pressing questions.

Population Structure of Lathys maculina Gertsch in the Southeastern United States (Araneae: Dictynidae)

Discipline: Life Sciences
Subdiscipline: Biology (general)

David Canseco*[1], Katherine O. Montana [2], Sarah Crews[3]
[1]University of California, Riverside./ California Academy of Sciences, [2]California Academy of Sciences, [3]California Academy of Sciences

Abstract: The genus Lathys comprises 54 species of small spiders that are typically found in leaf litter throughout the Holarctic. Lathys was described by Simon in 1884, but since that time the only studies of the genus have been descriptions of new species. In this study, we provide the first data of the population structure of L. maculina, a species occurring primarily in the eastern United States. We used the COI gene from 50 specimens from 16 populations to determine how populations are structured across their range in the southeastern United States. Our results indicate that there are genetic differences among and between populations. Additionally, we compared somatic and genitalic characters among adult specimens within and among populations and found variation; however, the variation is not consistent with the genetic differences, a pattern seen in other spider groups. Our study provides a basis of comparison for studies of other Lathys or litter-dwelling animals with similar distributions and represents the first molecular study of the genus.

The Relationship Between crAss-like phages and Capsular Polysaccharides within Bacterial Hosts

Discipline: Life Sciences
Subdiscipline: Microbiology

Kelsey Racacho*[1], Danica Schmidtke [2], Angela Hickey[3], Rachael Chanin[4], Ami Bhatt [5], Gavin Sherlock[6]

[1]University California Davis, [2]Stanford University, [3]Stanford University, [4]Stanford University, [5]Stanford University, [6]Stanford University

Abstract: Bacteriophages in the human gut microbiome are highly under characterized. crAssphages are a large, diverse, and highly abundant family of phages associated with the gut. The impacts of crAssphages on human health are unknown, however, they are abundant in healthy individuals and crAssphage abundance may decrease in patients with colorectal cancer and Inflammatory Bowel Disease. CrAssphages are predicted to infect Bacteroidete s which express capsular polysaccharides (CPS), that modulate human immune-response, and susceptibility to phage infection. For example, Bacteroides thetaiotaomicron encodes 8 different CPS (CPS1-8), 5 of which are under phase variable promoters allowing rapid changes in expression. It was previously shown that one phage, SJC01, robustly infects wild type B. theta . However, SJC01 does not infect the constative CPS3-only expressing B. theta mutant. In contrast, B. theta infecting, crAssphages (DAC15 and DAC17) most efficiently infect B. theta expressing CPS3. Here, I compare the susceptibility of untreated wild type B. theta to DAC15 and DAC17 compared to B. theta , pretreated with SJC01 and vice versa. I utilize qPCR and shotgun sequencing to determine changes in orientation of phase variable CPS promoters which regulate their expression. In conclusion, this project will contribute to unraveling the indirect effects of phage infection on the human immune system via selection for specific CPS, as well as the co-evolutionary dynamics of mixed populations of phages and their hosts in the gut microbiome.

Identifying key drivers of gene regulatory networks in drosophila dosage compensation

Discipline: Life Sciences
Subdiscipline: Genetics

Melissa Aldana*[1], Erica Larschan [2], Joseph Aguilera[3]
[1]Brown University, [2]Brown University, [3]Brown University

Abstract: Precise and coordinated regulation of gene expression during growth and development is essential for the viability of all organisms and to prevent diverse diseases ranging from cancer to neurodegeneration. Gene regulatory networks (GRNs) drive gene regulation during development and in response to environmental cues or therapeutics. However, the key drivers of gene regulatory networks are hard to predict. Therefore, I am disrupting an essential pioneer transcription factor in Drosophila called Chromatin-linked Adaptor for MSL complex (CLAMP) and identifying the GRNs that it regulates. CLAMP is critical in Drosophila dosage compensation, which is the two-fold upregulation of all the genes along the male X-chromosome; to achieve this upregulation, CLAMP recruits the Dosage Compensation Complex (DCC) to precise locations spread throughout the male X-chromosome. I performed Cleavage Under Targets and Release Using Nuclease (CUT & RUN) on wildtype and clamp mutant larvae to reveal the native and ectopic binding sites of CLAMP and the DCC. Concurrently, I performed mRNA-seq in all larvae to determine how dosage compensation was affected, specifically examining the male X-chromosome transcript output. My computational analysis using machine learning approaches will allow us to predict drivers of GRNs from CUT & RUN and mRNA-seq data. I will then compare the GRNs that I identify with those that have been identified for other critical transcription factors through the modENCODE project. Importantly, by understanding the fundamental mechanisms of gene regulation and regulatory networks, we can shed light on the complete effects of modern therapeutics.

Bacterial endophyte biocontrols impact wheat growth traits and yield

Discipline: Life Sciences
Subdiscipline: Biology (general)

Odalis Curzio*[1]and Briana K. Whitaker [2]
[1]Northeastern Illinois University, [2]USDA, Agricultural Research Service, National Center for Agricultural Utilization Research, Mycotoxin Prevention & Applied Microbiology Unit

Abstract: Animals and plants both play host to diverse microbial communities, collectively known as the microbiome. These microbes are everywhere and can impact their hosts in both beneficial and negative ways. Bacterial endophytes are a specific group of microbes that live inside of plant tissues and are increasingly recognized for their potential as biocontrols to improve host growth and yield, including in agricultural systems. However, we still don't understand whether bacterial endophytes promote crop growth directly via stimulation to plant growth traits, or indirectly via their interactions with the rest of the microbiome. Therefore, we inoculated seven bacterial endophyte strains, or a sterile control, onto wheat seeds ('Norm' variety) and planted them into either sterile or non-sterile soil, and then compared differences in plant growth traits and yield. These seven bacterial endophytes were selected based on previous research showing their beneficial impacts on wheat leaf physiology. We measured impacts of the bacterial endophytes on seed germination, leaf number, tiller number, plant height, and chlorophyll content, as well as final plant biomass, as metrics of crop growth and yield. Preliminary results indicated little difference among bacterial endophyte treatments on seed germination. Germination rates for bacterial treatments ranged from 80.0%-94.6%, while the sterile control was 91.4%. Overall, our work will benefit the agricultural community and sustainable agricultural practices, by showing the mechanisms by which bacterial endophyte biocontrols can promote better crop yields.

The role of hematopoietic stem cells in lung cancer response to radiation therapy

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Carolina Martinez*[1], Gerard Madlambayan [2], Morgan Markel[3], Ethan Wilborn[4], Crystal Poma [5], Tyler Parsons[6]
[1]Oakland University, [2]Oakland University, [3]Oakland University, [4]Oakland University, [5]Oakland University, [6]Oakland University

Abstract: Non-small cell lung carcinoma (NSCLC) comprises approximately 85% of all lung cancer cases in the United States. We demonstrated that after radiation therapy (RT), bone marrow-derived hematopoietic stem cells (HSCs) are recruited to the tumor microenvironment (TME). We hypothesized that tumor-associated HSCs are maintained within tumors and can participate in tumor response to RT by differentiating into specific macrophage populations. Using Lewis Lung Carcinoma, a mouse model of non-small cell lung carcinoma, we demonstrated that RT induces the TME to produce CSF-1, a factor that promotes the differentiation of HSCs into tumor supportive M2-macrophages, thus allowing tumors to regrow post-RT. The supportive effects of M2-macrophages were abrogated using a therapeutic inhibitor of the CSF-1 receptor (GW2580). We further hypothesized that maintenance of HSCs within tumors was mediated through interactions between laminin 5-1-1 (LAMA5), in the tumor extracellular matrix, and integrin alpha 6 (ITGA6), present on the surface of HSCs. Interestingly, we observed that the expression of each was diminished following RT. Analysis of a factor associated with stem cell pluripotency and maintenance, NOTCH, using RT-PCR showed a significant decrease in expression following RT.

Taken together, this data suggests that RT disrupts LAMA5/ITGA6 interactions releasing HSCs from maintenance signals. Concomitantly, RT induces the production of CSF-1 which induces these “released” HSCs to differentiate into tumor supportive M2-macrophages to promote tumor regrowth post-RT. Overall, our data identifies HSCs as mediators of tumor response to RT and identifies new cellular and molecular pathways to target in the treatment of lung cancer.

Using CRISPR-engineered Mouse Neural Cells Expressing An Optimized MANF Variant to Explore Mechanisms Of MANF Neuroprotection

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ted Daniel Llera*[1], Neel Singhal [2], Dengke Ma[3]
[1]University of California, Berkeley, [2]University of California, San Francisco, [3]University of California, San Francisco

Abstract: Heart disease and stroke are among the top five causes of death in the United States, leading to billions of dollars in healthcare expenditures. This disease is caused by cellular dysfunction and death due to metabolic stress and hypoxia, which are the hallmarks of heart disease and stroke. Unfortunately, clinical treatments for these conditions often cannot reverse cellular damage. Interestingly, Arctic ground squirrels (AGS) are extreme hibernators that can reduce their metabolic rate and temperature without suffering from ischemic injuries. Based on the lab’s prior work, we have identified that mesencephalic astrocyte-derived neurotrophic factor (MANF) is among the cytoprotective genes responsible for the AGS’s resiliency against metabolic stress and hypoxia. Hence, studying AGS neural cells may help provide insights into new treatments. This study aims to utilize CRISPR-gene editing in mouse neural cells to express AGS MANF and investigate the specific role of this protein in cellular stress during ischemic injuries. Mouse neural cells expressing AGS MANF were created using the CRISPR-Cas9 gene-editing, and the survival rate of AGS MANF variants under metabolic stress and response to unfolded protein response (UPR) markers were analyzed. We found that mouse cells expressing AGS MANF survived better than those expressing endogenous MANF under cellular stress, followed by the reduction of UPR genes after the treatment of metabolic toxins–such as rotenone and thapsigargin–to induce metabolic stress. Future studies will be required to narrow the mechanistic basis of this cytoprotection which may be a promising therapy for conditions such as strokes and heart attacks.

The role of paternal folate deficiency in epigenetic inheritance and offspring health

Discipline: Life Sciences
Subdiscipline: Genetics

Jasmine Esparza*[1]and Satoshi Namekawa [2]
[1]University of California, Davis, [2]University of California, Davis

Abstract: Worldwide, over 15% of couples have difficulty conceiving a child. Long-term fertility in males is governed by spermatogenesis, the developmental program responsible for producing mature sperm. Although sperm are thought to be mere DNA carriers, recent work has demonstrated that sperm’s epigenetic information is critical for embryonic development. Nutrition can influence the epigenome by altering the abundance of substrates required for chromatin-modifying reactions and is dependent on diet. My work aims to understand how a father’s diet and nutrition affects offspring health. Despite overwhelming evidence that maternal folate status is essential in preventing embryonic congenital diseases, the role of paternal folate status contributing to offspring health is not well studied. To address this gap in knowledge, I am studying the role of folate (vitamin B9), a substrate required for histone and DNA methylation, in establishing epigenetic state during spermatogenesis and epigenetic inheritance. Using a folate-deficient diet mouse model, I am isolating representative developmental stages of spermatogenesis; stem cell-like spermatogonia, meiotic germ cells, and postmeiotic germ cells. To assess changes in the epigenetic state due to folate deficiency, I am using ATAC-sequencing and Cleavage Under Targets and Release Using Nuclease (CUT&RUN) against histone H3 lysine 4 and lysine 27 trimethylation (H3K4me3 and H2K27me3). Given the low abundance of methyl groups due to the folate deficiency, we hypothesize that lowly DNA- and histone-methylated regions of the genome will be most affected, and embryonic development genes will be "protected". The overarching goal is to improve preconception guidelines by ensuring healthy paternal diet guidance.

The Role of Hepatic IRE1 in Protecting the Host During Sepsis

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Elizabeth Barroso*[1], Ling Yang [2], Mark Li[3]
[1]University of Iowa, [2]University of Iowa, [3]University of Iowa

Abstract: The liver maintains systemic homeostasis through immuno-metabolic responses for surviving sepsis, the frequent cause of intensive care mortality. The notion that anti-inflammatory therapies fail to improve survival in septic patients urges the need for understanding sepsis through the lens of metabolic adaptations. The liver plays a central role in providing lipids as energy substrates to support heart function during sepsis. Inositol-requiring enzyme 1 (IRE1) is a protein which regulates liver lipid metabolism and is necessary for secretion of liver lipids. However, the extent of IRE1-dependent crosstalk between the liver and the heart is unknown in sepsis. Therefore, we hypothesize that hepatic IRE1 is crucial for liver-mediated lipid secretion, which supports septic heart function. To this end, the liver and heart functions of wild-type and IRE1 liver-specific knockout mice were assessed in a septic experimental model. We measured IRE1 level in the liver and found that sepsis significantly suppressed its expression. Hepatic IRE1 deletion sensitized mice to sepsis-associated heart dysfunction. The knockout animals had reduced mitochondrial respiration and increased immune cell infiltration in the heart. In addition, we noted IRE1 deletion resulted in major alterations of circulatory lipid profile and found that IRE1 regulates secretion of liver lipids in response to sepsis. Finally, we showed that these lipids protect cardiomyocytes against sepsis-associated mitochondrial and calcium dysfunctions. Together, our study provides the first insight that disruption of hepatic IRE1-mediated lipid regulation impairs sepsis-associated cardiac adaptation. Overall, this knowledge could contribute to developing novel therapies for liver-mediated lipid homeostasis in sepsis-induced heart dysfunction.

Rate change alters the phase-dependent sensitivity to inputs in repetitively firing external globus pallidus neurons

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jacob Pena*[1], James A. Jones [2], Charles J. Wilson[3]

[1]The University of Texas at San Antonio, [2]Department of Neuroscience, Developmental, and Regenerative Biology, The University of Texas at San Antonio, [3]Department of Neuroscience, Developmental, and Regenerative Biology, The University of Texas at San Antonio

Abstract: The external globus pallidus (GPe) is a central nucleus of the basal ganglia, a collection of subcortical nuclei involved in motor and cognitive functions. GPe neurons are autonomous oscillators that fire tonically in the absence of synaptic input. GPe neurons differ widely in their firing rate, and individual neurons vary their firing rates over time. The response of an oscillating neuron to inputs depends on the oscillation phase at which the inputs arrive and is captured in a neuron's phase-resetting curve (PRC). To measure PRCs of GPe neurons, we injected contiguous sequences of brief current pulses with amplitudes drawn from a Gaussian distribution and recorded their spiking responses. The phase-resetting method is thought to be valid over a limited range of input amplitudes, and to be most accurate for small inputs. We measured the PRCs of GPe neurons using a range of input amplitudes by varying the standard deviation of the amplitude distribution. We found that increasing pulse amplitude over a wide range (s.d. = 20-120 picoamps), maintained sizes and shapes of the PRCs, suggesting the assumptions of the phase-resetting method are met for brief inputs. It’s known that rate change may alter the oscillation of a neuron, changing the PRC and the phase-dependent sensitivity to inputs. We tested this by measuring the PRCs of GPe neurons at different rates, imposed by constant current injection. Changing the rate of a GPe neuron produced moderate changes in the shape of its PRC, indicating rate changes alter spike-time responses to synaptic inputs.

Longitudinal GWAS Identifies Novel Genetic Variants and Complex Traits Associated with Resilience to Alzheimer's Disease

Discipline: Life Sciences
Subdiscipline: Genetics

Jared Phillips*[1], Timothy Hohman[2], Logan Dumitrescu[3], Derek Archer[4], Alexandra Smith[5], Shubhabrata Mukherjee[6], Seo-Eun Choi[7], Michael L. Lee[8], Phoebe Scollard[9], Emily H. Trittschuh[10], Jesse Mez[11]

[1]Vanderbilt University, [2]Vanderbilt Memory and Alzheimer's Center, Vanderbilt University Medical Center, Nashville, TN, [3]Vanderbilt Memory and Alzheimer's Center, Vanderbilt University Medical Center, Nashville, TN, [4]Vanderbilt Memory and Alzheimer's Center, Vanderbilt University Medical Center, Nashville, TN, [5]Vanderbilt Memory and Alzheimer's Center, Vanderbilt University Medical Center, Nashville, TN, [6]Department of Medicine, University of Washington, Seattle, WA, [7]Department of Medicine, University of Washington, Seattle, WA, [8]Department of Medicine, University of Washington, Seattle, WA, [9]Department of Medicine, University of Washington, Seattle, WA, [10]Department of Psychiatry and Behavior Sciences, University of Washington School of Medicine, Seattle, WA,[11]Department of Neurology, Boston University School of Medical, Boston, MA

Abstract: We completed a large genetic analysis of resilience to cognitive decline in Alzheimer's Disease (AD) and discovered novel variants, genes, and complex traits associated with better-than or worse-than-expected cognitive performance given an individual’s age, sex, and APOE genotype. Leveraging 15,933 non-Hispanic white participants across four longitudinal cohort studies of aging and AD, our group determined the effects of genetic variants on resilience metrics using mixed-effects regressions. Models adjusted for age, sex, APOE ε4 allele count, presence of the APOE ε2 allele and all covariate interactions with interval (years from baseline). The outcomes of interest were residual cognitive resilience, quantified from residuals in three cognitive domains (memory, executive function, and language), and combined resilience, summarized as the covariance of educational attainment with residual cognitive resilience. Post-GWAS analyses included gene tests using MAGMA and estimates of genetic correlation with 65 complex traits using GNOVA. We observed genome-wide significant associations at multiple established AD loci, including BIN1 and CR1 . We observed a novel association with combined resilience on chromosome 13 (top SNP: rs11838654, MAF=0.06, $P=4.7x10^{-8}$). Gene-level tests identified associations of CD2AP (P.fdr=0.027) and ZNF146 (P.fdr=0.049) with residual cognitive resilience and combined resilience, respectively. Additionally, we identified negative genetic correlations of combined resilience with ischemic stroke and coronary artery disease (all P.fdr<2.5x10 -2). Taken altogether, we uncovered novel genetic drivers of resilience through this approach. Such findings will require future replication but suggest a trajectory-based definition of resilience holds substantial promise for discovery.

DNA Barcoding of Cryptococcus neoformans to Understand Pathogen Dissemination

Discipline: Life Sciences
Subdiscipline: Genetics

Payton Compton*[1], Jessica C. S. Brown [2], Joseph Bednarek[3]
[1]The Ohio State University, [2]University of Utah, [3]University of Utah

Abstract: Cryptococcus neoformans is an opportunistic fungal pathogen that causes lethal meningoencephalitis in immunocompromised populations. There are an estimated 215,000 cryptococcal infections per year, with a mortality rate of 30-70% and a high prevalence in areas of limited medical infrastructure, such as Africa. Dissemination and organ seeding of C. neoformans are poorly understood. Since the disseminated brain infection is the primary cause of mortality, studying these aspects of pathogenesis is crucial to developing new therapeutics. The purpose of this research is to insert a 12-base pair segment of DNA into the fungal genome that acts as an identifying “barcode” to track fungal dissemination. We will use barcoded fungi to study organ seeding, the colonization of organs by fungi. We hypothesize that seeding events are rare early in infection and increase in frequency later in infection. We used cloning and Gibson assembly to create a barcode bound to an antifungal resistance cassette integrated into a plasmid. Using PCR, we amplified this segment and inserted it into a genomic safe haven (SH2 locus) of C. neoformans using CRISPR-Cas9. Through serial plating on antifungal media, we selected for barcode-containing fungi and then sequenced the barcoded strains to confirm insertion into the SH2 locus. We successfully created several barcoded C. neoformans strains with SH2 locus insertion. In summary, CRISPR-Cas9 was used to insert a DNA barcode into the fungal pathogen C. neoformans. We will use these barcoded strains in subsequent studies to define the kinetics of organ seeding and dissemination.

Genetic variation in Norwegian cervid prion protein influences risk and susceptibility to chronic wasting disease in CPCA

Discipline: Life Sciences
Subdiscipline: Microbiology

Margaret Tyer*[1], Glenn Telling [2], Julianna Sun[3], Jifeng Bian[4]
[1]Colorado State University, [2]Colorado State University, [3]Colorado State University, [4]Colorado State University

Abstract: Chronic wasting disease (CWD) is a transmissible, universally fatal neurodegenerative disease caused by the pathogenic misfolding of prion protein. CWD is endemic to North America, and most recently has been identified in Norwegian reindeer and moose . Interestingly, isolates collected from Norwegian CWD cases have shown Norwegian CWD (NoCWD) to possess unique strain characteristics from its North American counterpart. Polymorphisms in the coding residues of cervid prion protein (PrP) are associated with changes to risk and clinical progression of CWD. Previous research from our group has shown that variations in residue 226 of cervid PrP are associated with increased susceptibility to CWD infection. However, there is no research into the risk associated with the genetic variation s identified in Norwegian cervid populations. As NoCWD is an emerging threat possessing unique strain characteristics , further investigation into the risk factors of its hosts is required . In the present study, we use cervid prion cell assay (CPCA) to investigate CWD risk/resistance associated with specific structural polymorphisms identified through genetic screening of Norwegian cervids . CPCA utilizes rabbit kidney epithelial cells expressing cervid PrP with polymorphisms of interest to interrogate prion susceptibility, through the measurement of the number of infected cells post-inoculation with a CWD isolate. The results of this research will provide the first insight into how the genetic variation of Norwegian cervid PrP influences risk and susceptibility to CWD infection. These data will guide the direction of future research investigating genetic features influencing No CWD pathogenicity.

Development of a high throughput method to analyze glycans from clinical Multiple Myeloma samples

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Alina Johnson*[1], Rebecca Treger[2], Susan Fink[3]
[1]Barnard College, Columbia University, [2]University of Washington, [3]University of Washington

Abstract: Multiple Myeloma (MM) is a plasma cell cancer characterized by the overproduction of monoclonal antibodies, leading to end-organ damage. MM can be diagnosed by detecting monoclonal antibodies, but no biomarkers currently exist to predict MM treatment responses and/or disease course. All antibodies contain different glycans on different parts of the protein that enable crucial downstream immune functions. Changes in glycan patterns have been observed in MM, but it is not known whether they change over time or relate to patient prognosis. These glycans, therefore, represent a potential novel biomarker for MM. Our study involves developing a protocol to quantify antibody glycosylation to understand and potentially predict if patients might develop severe MM. To investigate this, we will capture monoclonal antibodies from 114 samples from 57 MM patients, collected at 2 time points from routine clinical testing under an IRB-approved protocol. We will sever the glycan from the antibody, fluorescently label the glycan, and identify and quantify glycan composition. This approach will allow us to analyze inter-individual glycan changes, intra-individual glycan variation over time, and the effect of light chain usage. This project, the largest survey to-date of MM glycans, will establish a methodology for glycosylation in our clinical laboratory, and will enable subsequent studies to assess glycosylation profiles as novel biomarkers for treatment and progression in MM. We don't yet fully understand the biology behind MM, but we hypothesize that understanding glycosylation may inform us about how MM develops, its underlying mechanisms, and help us improve treatment plans and outcomes.

Physiological Mechanisms Underlying Cold Stress in the Holobiont of the Northern Star Coral

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kellie Navarro*[1], Loretta Roberson[2], Mayra Sánchez-García[3]
[1]Bowdoin College, [2]Marine Biological Laboratory, [3]Marine Biological Laboratory

Abstract: The Northern Star Coral, Astrangia poculata , inhabits hard-bottom environments from the Gulf of Mexico to Massachusetts. In its northern range, it must withstand large seasonal variations in temperature (-2 to 26 °C). A previous study of stress responses in aposymbiotic colonies of A. poculata found that more genes upregulate in response to cold stress compared to heat stress. However, our understanding of the response of the holobiont (coral host and endosymbiont) to thermal stress is limited. This experiment characterizes physiological changes in both the host and symbionts under summer (17.5-21 ºC) and chemically induced cold temperatures (utilizing Camphor). Physiological characterization includes calcification rates, symbiont density, reactive oxygen species (ROS), differential gene expression, and in-situ hybridization to better understand the underlying mechanisms of this species' stress response. Calcification and symbiont density aid in understanding the impact of cold temperature stress on the growth of the coral and the role of symbionts. ROS monitoring is a proxy for increased stress responses in A. poculata . RNAseq will be used to characterize gene expression of replicate symbiotic and aposymbiotic corals (n=8) and in-situ hybridization to localize genes. A differential expression analysis will be presented for both host and algal genes to test the hypothesis that one of the symbiotic partners plays a dominant role in the cold stress response. Understanding the cellular mechanisms of the temperature stress response in complex symbioses such as corals can help predict the future of coral populations in both temperate and tropical environments under increasing climate variability.

What Makes Hummingbirds Tick: Flowers or “Friends?”

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kyaralind Vasquez Liriano*[1], Abe Borker[2], Erika Zavaleta[3], Jeffrey Hwang[4], Mikaela Salvador[5]
[1]Wellesley College, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]Duke University, [5]Stanford University

Abstract: Animals become territorial over aggregated resources when faced with competition. Hummingbirds must maximize consuming nectar and insects to meet their daily energy requirements. However, they must compete with other hummingbirds and nectarivores for resources, even within their species’ respective territories. We studied hummingbird behavior in response to intraspecific and interspecific calls in large and small resource patches along trails in Big Sur, California. We hypothesized that switches in behavior, a measure of agitation and vigilance, would increase in the presence of high-value resource patches and intraspecific competition. We conducted our study in various flower patches throughout the coastal scrub habitats of Landel-Hills Big Creek Reserve. We recorded behavioral states (foraging, chasing, perching, and flying) of the Allen’s and Anna’s hummingbirds for a total of ninety seconds (n = 32 hummingbirds) over three thirty-second intervals, before, during and after a thirty-second playback of hummingbird calls. To each bird, we played either an Anna or Allen call as a proxy for interspecific and intraspecific interactions. We found that the interaction call itself and the type of call (intraspecific or interspecific) did not influence the time allocation both hummingbirds spent on each behavioral state after the call was made, however, these intraspecific interactions increased the frequency of behavior switching. In addition, our results indicated that hummingbird territoriality increases with higher resource availability. As climate change and its devastating effects becomes increasingly prevalent, understanding territoriality can help predict animal behavioral responses to changing ecosystems.

Investigating how MCM10 affects telomere length during human immune cell differentiation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Anjali Raju*[1], Anja Katrin Bielinsky[2], Ryan Baxley[3], Megan Schmit[4]
[1]Case Western Reserve University, [2]University of Minnesota, [3]University of Minnesota, [4]University of Minnesota

Abstract: MCM10 (minichromosome maintenance protein 10) is essential for DNA replication and promotes genomic stability. It also plays a significant role in preventing telomere erosion. Despite all cells requiring MCM10 expression for proliferation, MCM10 patient mutations cause tissue-specific disease phenotypes. In one patient, natural killer (NK) cells were unable to reach their final stage of differentiation, likely due to premature senescence. We hypothesize that MCM10 deficiency exacerbates telomere erosion during differentiation of NK cells, thus stalling them in an immature stage of development. Our goal is to quantify telomere length in induced pluripotent stem cells (iPSCs) that carry an MCM10 mutation as they are undergoing in vitro differentiation into NK cells. We will apply two complementary techniques to measure telomere length. Telomere restriction fragment analysis examines average telomere length in a cell population. Telomere fluorescence in situ hybridization quantitatively measures telomere signals within individual cells and allows the comparison of signals between MCM10 deficient cells and parental wildtype cells. Previous experiments with colorectal cancer cells indicate that mutant MCM10 causes telomere erosion. We predict that we will make similar observations in our iPSC model. These studies will provide insight into MCM10's role for maintaining telomere length during NK cell development. We are investigating this problem with the hope of understanding how the deficiency of an essential gene contributes to a tissue-specific developmental phenotype.

Phylogenetic relationships of freshwater gobies on Negros Island using three mtDNA markers

Discipline: Life Sciences
Subdiscipline: Biology (general)

Karen Kohama*[1], David T. Gauthier[2], Christopher E. Bird[3], Robert S. Guino-o II[4]
[1]The City College of New York, [2]Old Dominion University, [3]Texas A&M University – Corpus Christi, [4]Silliman University

Abstract: Most freshwater fish species in the Philippines remain unnamed, misclassified, or remain undiscovered and undocumented. Freshwater environments face habitat degradation such as domestic and industrial pollution, agricultural runoff, overfishing, and introduction of invasive species. Smaller fishes such as gobies can be more sensitive to alteration of river morphology and exploitation leaving them vulnerable to these detrimental changes. Gobies are relatively small fishes (< 10 cm) inhabiting both fresh and saltwater habitats, and they are the most diverse family of fishes in the Indo-Pacific. Although they are common in rivers around the world, gobies have not been studied in the Malaunay River on Negros Island in the Philippines. DNA barcoding is a standardized tool for species identification and delineation that uses a short fragment of a single gene (COI) to identify species. The technique has yet to be applied to freshwater goby species found in the Malaunay River. We examined the phylogenetic relationship of morphologically distinct gobies in the Malaunay River to each other and previously barcoded species in GenBank using three mtDNA markers: COI, Cyt-b, and 16S. Here I will present results on the phylogenetic diversity present in the 40 gobies collected and report the amount of cryptic diversity. This effort is critical to identifying and conserving the biodiversity of freshwater fishes on tropical Indo-Pacific islands and serves as a model to explore freshwater fish diversity in other major rivers throughout Negros Island, the Philippines, and beyond.

Relating Nitrogen Speciation to Phytoplankton Taxonomy Using Remote Sensing Imagery

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Gabby Muniz*[1]and Sherry Palacios [2]
[1]California State University Monterey Bay, [2]California State University Monterey Bay

Abstract: Phytoplankton play an important role in the marine ecosystem, being the base of the food web, and are responsible for 70% of oxygen production on Earth. Light, temperature, and nutrients (often nitrogen, N), are the main factors for optimal growth for this autotrophic community. When nitrogen input exceeds output, physical and chemical norms change in coastal ecosystems and can cause harmful algal blooms (HAB). During a HAB event, some phytoplankton species can grow at a rapid rate and release toxins in the water. Several consequences include ecosystem disruption in the environment, economic hardship, and some cases can lead to severe human illness if unmitigated. Climate change and ocean warming are creating HAB suitable conditions, leaving global communities challenged by these consequences. Many states and international organizations are monitoring these events to understand and forecast future blooms. This study focuses on the nitrogen speciation through fixation to the relative occurrence of HAB events. Using remote sensing imagery as a tool to capture chlorophyll-a as a proxy will be used to validate the blooms. Derived results will determine if there is a correlation with phytoplankton taxonomic group and favorability of N forms from nitrogen fixation. Completing this project will add to the knowledge of a HAB cycle, and provide an insight into how N forms play a role, and forecasting recurring blooms.

Determining whether the host protein Annexin A2 is a novel binding partner of HIV-1 Nef

Discipline: Life Sciences
Subdiscipline: Microbiology

Thomas Carrillo*[1], Dr. Peter Ramirez [2], Francisco Acosta[3]
[1]California State University, Long Beach, [2]California State University, Long Beach, [3]California State University, Long Beach

Abstract: Human Immunodeficiency Virus type-1 (HIV-1) codes for a series of accessory proteins (Vif, Vpu, Vpr, and Nef) that aid in viral pathogenesis. Nef (negative factor) is expressed relatively early in the HIV-1 replication cycle and associates with membranes via a myristate moiety.

Moreover, expression of Nef enhances the infectiousness of viral particles (virions). Clinically, Nef is necessary for the progression to AIDS. How Nef creates a more infectious virion and whether this relies on the interaction with specific host proteins is still unclear. Using virion-associated proteomics, we identified candidate "dependency" factors, or proteins that Nef utilizes to enhance infectivity. One of these proteins was AnnexinA2 (ANXA2), a membrane associated protein that participates in several biological functions, including membrane dynamics, and that has also been implicated in several viral infections. Our preliminary studies indicate that silencing ANXA2 decreased HIV-1 virion infectivity. Therefore, we hypothesize that Nef physically interacts with ANXA2. To test this, we will use a Bi-Molecular Fluorescence Complementation (BiFC) assay. In BiFC, two proteins of interest are fused to two halves of a fluorescent protein. If the proteins interact, fluorescence is generated and can be quantified via flow cytometry or immunofluorescence. If Nef interacts with ANXA2, we will then map the region(s) of interaction. This study will enhance our understanding of HIV-1 pathogenesis and may lead to the development of novel anti-viral therapeutics.

Feeding rates of different sex and reproductive classes of humpback whales along the Western Antarctic Peninsula

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Martin Gil*[1], Logan Pallin[2], Ross Nichols[3], Ari Friedlaender[4]
[1]University of California, Santa Cruz, [2]UCSC, [3]UCSC, [4]UCSC

Abstract: Antarctic humpback whales annually migrate large distances to their feeding grounds where cold waters and sea ice support large populations of krill. The gestation period for humpbacks is about 11 months and some females are likely able to breed soon after giving birth. Feeding during the austral summer is crucial for these organisms but little is known about their feeding rates and how sexual and reproductive factors effect how they feed. Due to extra metabolic needs that come with pregnancy, we hypothesize that females and especially pregnant females would display higher feeding rates. We used high-resolution, motion-sensing biologging tags attached to non-calf humpback whales around the Western Antarctic Peninsula in order to collect foraging data. We used remotely collected skin-blubber biopsy samples to determine the sex and pregnancy status of each tagged whale. Preliminary comparisons show no significant differences between male (n=19) and female (n=19) as well as pregnant (n=8) and non-pregnant (n=10) mean feeding rates, however evidence suggests seasonal differences which we will continue to investigate. This work aims to identify differences in foraging behavior between male and female Antarctic humpback whales during the feeding season. Given the differing energy demands of males and females, quantifying differences in foraging behavior is crucial for informing policy related to population recovery, as well as assessing impacts from anthropogenic stressors such as direct vessel interactions, fishing of krill stocks, and climate change.

Morphological analysis of the compound and dentary bones of North American snakes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Autumn Magnuson*[1], John J. Jacisin III[2], David Ledesma[3], Melissa E. Kemp[4]

[1]University of Louisville, [2]The University of Texas at Austin, [3]The University of Texas at Austin, [4]The University of Texas at Austin

Abstract: Snakes are specialized vertebrates with a broad geographic distribution in the fossil record and have been an important part of North American ecosystems for millions of years. While the snake fossil record is primarily comprised of isolated vertebral and skull elements, relatively little is known about interspecific variation in North American snake skulls. As such, accurate identification of these skeletal elements is crucial for evaluating the fossil record. Problematically, few prior studies of Quaternary (2.85 mya-Present) herpetofauna have compared taxa from outside of the study site's immediate location or ecosystem. This introduces a geographic identification bias, as it neglects to account for shifting ranges of taxa through time. Here, we document interspecific variation among North American snakes in the morphology of two bones recovered as fossils: the compound and dentary bones. We assembled a morphological dataset representing over 68 North American species, photographed both elements for 76 osteological specimens, and generated 3D models of those bones in the 16 species for which CT data were available. We evaluated observations of our data and previously published characters for distinguishing taxa and determined several taxonomically informative characters for isolated elements. This information will assist our identifications of snake fossils from Hall's Cave, a Quaternary fossil site in Central Texas. Furthermore, this study will help identify taxonomically useful characters for assigning snake fossils to family or genus. In conclusion, this data will be valuable for better understanding the past of North American snakes through the lens of fossil records.

Characterization of the developing human esophagus reveals a transient multi-ciliated cell population

Discipline: Life Sciences

Subdiscipline: Developmental Biology

Helena Yllescas*[1], Jason Spence [2], Daysha Ferrer-Torres[3], Tristan Frum[4], Zhiwei Xiao [5], David E. Bayer[6]

[1]University of Puerto Rico Bayamon, [2]University of Michigan Medical School Ann Arbor, [3]University of Michigan Medical School Ann Arbor, [4]University of Michigan Medical School Ann Arbor, [5]University of Michigan Medical School Ann Arbor, [6]University of Michigan Ann Arbor

Abstract: Multiple diseases have been found to arise in the esophagus during development and adulthood. Currently, many efforts have led to the characterization of adult esophageal normal and disease tissue, such as cancer. Nonetheless, there is a significant lack of understanding of fetal esophagus development. Therefore, utilizing single-cell RNA-sequencing we have characterized cell types found in the developing human esophagus by developmental age. Even further, we have identified a transient-multiciliated cell population. We validated this key finding by immunofluorescence, showing the presence of cells with multiciliated cell cilia marked acetylated tubulin (AcTb) at the luminal surface of the fetal esophagus. Additionally, we describe a method for the successful long-term expansion and formation of a 3-dimensional (3D) esophageal fetal organoid in vitro . We validated the fetal-specific cellular organization of 3D suspension organoids derived from the fetal esophagus containing multiciliated cells positive for AcTb. Altogether, this work provides a comprehensive map of molecular markers for esophageal development and an in vitro model to study esophageal development and disease.

Identifying hypothalamic metabolism-associated regulatory regions contributing to Alzheimer’s disease pathology

Discipline: Life Sciences
Subdiscipline: Neurosciences

Deanine Dilworth*[1], Christopher Gregg [2], Adriana Cristina Rodriguez[3], Elliot Ferris[4]
[1]Amherst College, [2]University of Utah, [3]University of Utah, [4]University of Utah

Abstract: Alzheimer’s Disease (AD), the most common form of dementia, is a neurodegenerative disease affecting many regions of life, including cognitive, autonomic, and pituitary functions. Notably, the metabolic pathways controlled by the hypothalamus are dysregulated early in AD. The regulatory regions, cis -regulatory elements (CREs), involved in these pathways have yet to be identified. A 72-hour fasting regimen in wild-type mice causes large scale changes to metabolism, allowing the identification of gene regulatory systems involved. Preliminary RNA-seq data shows large-scale transcriptome changes in the hypothalami of fasted mice. Our project will define the metabolic and AD-associated hypothalamic CREs by looking at epigenetic changes in fasted wild-type mice and the AD mouse model, 5XFAD mice, respectively. We have optimized OMNI-ATAC-seq for mouse hypothalamus tissue, improving both our nuclei isolation and transposase efficiency. We use this optimized method to identify regulatory regions within the wild-type hypothalamus impacted by fasting and compare this to RNA-seq data to identify metabolically relevant CREs. We also use this approach to identify metabolic CREs and regulatory pathways involved in recovery from fasting via refeeding experiments. Repetition of this in 5XFAD mice at different ages will allow identification of CREs sharing involvement in metabolism and AD pathways. In the future, we will functionally investigate the effects of silencing identified CREs and monitor phenotypic changes in 5XFAD and fasted wild-type mice. Identification of these CREs and their associated pathways will open a gateway to understanding the relevant metabolic pathways, novel drug targets, and improved AD treatments.

The Effects of Fishing Pressure on the Reproductive Biology of a Sex Changing Wrasse (Halichoeres scapularis)

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ingrid Bartlett*[1], David T. Gauthier [2], Christopher E. Bird[3], Abner Bucol[4]
[1]Oregon State University, [2]Old Dominion University, [3]Texas A&M University– Corpus Christi, [4]Silliman University

Abstract: Sex change among tropical fish species is a common phenomenon. Wrasses within the genus Halichoeres exhibit protogynous sex changes in their life history, beginning as functional females, and changing to functional males in response to the loss of a dominant male from the population. Protogyny is favored when large males have a fitness advantage because they can monopolize smaller females and breeding territories according to the size-advantage model. Because sex is correlated with size, and humans tend to target larger fish, higher fishing pressure can cause females to reach maturity and change sex at a shorter lengths, leading to decreased maximum sustainable yield. Furthermore, smaller protogynous species have been understudied compared with larger and more charismatic taxa such as groupers. Here we test for an effect of fishing pressure on the reproductive biology of the small, protogynous wrasse Halichoeres scapularis . Collection sites were selected based upon the intensity of fishing pressure. Measurements of fish including total length, the standard length and weight of each fish, and the weight of the gonads will be used to test the primary hypothesis that fishing pressure will be associated with the age and size at sex change from female to male. Reproductive biology parameters of this species will be compared with those of larger protogynous species. The results of this research can be utilized to improve fishery management of small-bodied yet exploited reef associated fish species thereby improving sustainable extraction of marine resources.

Introduction of Y Chromosome Long-Noncoding RNAs to Mouse Lung Cancer Cells to Induce Radiation Senstivity

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Marelessis Palomino*[1], Michael T. Winters [2], Travis Rawson[3], Ivan Martinez[4], Emily S. Rice [5]
[1]University of New Mexico, [2]Department of Microbiology, Immunology & Cell Biology, West Virginia University School of Medicine, [3]West Virginia University Cancer Institute, [4]Department of Microbiology, Immunology & Cell Biology, West Virginia Cancer Institute, [5]Department of Microbiology, Immunology & Cell Biology, West Virginia Cancer Institute

Abstract: Lung cancer is the leading cause of cancer related deaths. Radiation therapy is the most common treatment for lung cancers, unfortunately radiation resistance continues to be a problem. The discovery of new molecular pathways related to radiation resistance are essential to develop better treatments. In the last decade, the field of noncoding RNAs has given us new information about radiation resistance. Recently, our lab discovered a group of long non-coding RNAs (lncRNAs) known as Linc-SPRY3 RNAs that give radiation sensitivity to human lung cancer cells. Interestingly, these lncRNAs are expressed from the human Y chromosome, and are only present in primates. To develop an animal model of these lncRNAs, we will artificially introduce linc-SPRY3 RNAs into two different mouse lung cancer cell lines. Our hypothesis is the introduction of these human lncRNAS to mouse lung cancer cells will sensitize them against radiation because of the conserved molecular pathways shared between mammals. We will artificially introduce these lncRNAs into these mouse cell lines by using retroviral vectors containing the linc-SPRY3 RNAs. After antibiotic selection, we will radiate these cells and measure radiation sensitivity using colony information assay. Our preliminary results will show the creation of radiosensitive mouse lung cancer cell lines expressing the human linc-SPRY3 RNAs, giving us an essential tool to investigate the conserved molecular pathways affected by these non-coding RNAs. Furthermore, we will be able to use these new mouse cell lines to study syngeneic in vivo mouse model systems to understand the importance of the tumor microenvironment.

Recollection, Growth, and Isolation of Freshwater Microalgae for DNA Extraction and Identification.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Carlos Hernandez-Rodriguez*[1], William Fortun Rosado [2], Karin MIllán Diaz[3], Jayleen Diaz Mercado[4], Dr. Karlo Malavé-Llamas [5], Dr. Linda Rivera Rivera[6], Johan Ortiz Morales[7]
[1]Universidad Ana G. Méndez - Carolina, Carolina Puerto Rico, [2]Undergraduate Researcher, [3]Investigation specialist, [4]curriculum specialist, [5]Dean of School of Science and Technology, [6]Assistant Professor, [7]Undergrad Research Student

Abstract: Most freshwater algae are microscopic. Many kinds are gregarious and occur in such numbers that can form water blooms or pond scums. In the past decades we have been able to see that freshwater algae have an economic importance and biological relevancy. The purpose of this study is to recollect wild freshwater microalgae and develop a method to grow these microalgae efficiently, present an isolation procedure that will ensure pure colonies and identify them for the creation of a database that can function as a reference for future bioremediation studies. The samples are recollected from the Pitahaya River located in Luquillo, Puerto Rico by using a net which filters out microalgae and stores it in a bottle. These are grown in the laboratory utilizing BG-11, a medium that focuses on microalgae growth, we have modified it by adding penicillin, a wide spectrum antibiotic to limit bacterial growth. After growing the samples, they are viewed under microscope and get sub-cultured in separate microtubes with the same media to attempt purification. After growing the microtubes we can observe them under the microscope to ensure the growth of microalgae. We have found that with this culture media the growth of microalgae is present. Our methods for growing our microalgae can be considered successful since we have not had any visual bacterial growth. Our future project plan is to work with molecular techniques to identify the microalgae utilizing a MinION, a portable device that allows rapid, real time long read sequencing of nucleic acids.

Advancements in Visual Sciences: The Role of Macrophages in Newt Lens Regeneration

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Sophia Ratvasky*[1], Dr. Katia Del Rio-Tsonis[2], Georgios Tsissios[3]
[1]Miami University, Oxford, OH, [2]Miami University, [3]Miami University

Abstract: For many decades, scientists have been trying to better understand the fascinating scar-free injury response known as regeneration. Many studies have shown that macrophages are required for successful regeneration across a wide demographic of animals. We aimed to investigate the role of macrophages during lens regeneration in the Pleurodeles waltl . To pursue this, we utilized a transgenic line that fluorescently labels macrophages with the intent to see macrophage kinetics during lens regeneration. We observed an increase in macrophage quantity at 4 days post lentectomy (dpl) and went back to baseline at 30 dpl. Additionally, to see how macrophage depletion affects lens regeneration, we depleted macrophages by the use of clodronate. Fascinatingly, all the macrophage-depleted eyes failed to form a lens. Early macrophage depletion resulted in a significant decrease in cell proliferation, induced an unresolved cellular accumulation, prolonged inflammation, caused a fibrotic-like response as well as abnormalities in extracellular matrix remodeling. Our results show that macrophages are necessary for lens regeneration and that when depleted, newts sustain a fibrotic response as seen in humans. Further investigating this phenomenon will unlock the secret to inducing regeneration in mammals.

Unraveling iron-dependent mechanisms of faster antimalarial activity by doxycycline

Discipline: Life Sciences
Subdiscipline: Neurosciences

Dylan Bia*[1], Shai-anne Nalder[2], Paul Sigala[3]

[1]University of Utah, [2]University of Utah, [3]University of Utah

Abstract: Malaria is a worldwide disease that kills over 600,000 people annually. Malaria is caused by single-celled Plasmodium parasites, which have an essential organelle named the apicoplast. Since human cells lack an apicoplast, it’s a key target for therapeutic drugs. Doxycycline is an antimalarial that kills the parasite slowly at low doses. We discovered using a clinically achievable higher dose of doxycycline kills the parasites faster. This faster activity involved novel iron-dependent mechanisms in the apicoplast remain undefined. Doxycycline has a known property of chelating metal ions, iron having the highest affinity. The focus of my project is if doxycycline binds iron and limits availability within the apicoplast. Iron-dependent processes will be treated with doxycycline impact. These processes include synthesis of LipA enzyme and its attachment to pyruvate dehydrogenase (PDH) and the synthesis of several proteins that require an iron-sulfur cluster for stability ferredoxin, LipA and IspH. I’ll treat parasites with higher-dose doxycycline and use western-blot analysis to measure lipoylated PDH levels and epitope-tagged iron-sulfur proteins relative to a loading-control protein and untreated parasites. If I observe diminished signals of these proteins in doxycycline-treated parasites, I will add exogenous iron to test if protein levels are restored. The anticipated results is that levels of lipoylated PDH and iron-sulfur proteins are reduced in doxycycline-treated compared to untreated parasites but restored in the presence of doxycycline and iron. These results will inform our understanding of the mechanisms by which doxycycline targets malaria parasites and can improve clinical use of this valuable antiparasitic drug.

Reversal of Amyloid-β-induced neuronal cofilin-actin rod pathology by antagonists of cytokine/chemokine receptors.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Omar Yanouri*[1], Laurie S. Minamide [2], Keifer P. Walsh[3], Thomas B. Kuhn[4], Lubna H. Tahtamouni [5], Michael Ruff[6], James R. Bamburg[7]

[1]Colorado State University, [2]Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO, [3]Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO, [4]Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO, [5]Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO; Department of Biology and Biotechnology, The Hashemite University, Zarqa, Jordan, [6]Creative Bio-Peptides, Inc., 10319 Glen Road, Suite 100, Potomac, MD, [7]Molecular, Cellular and Integrative Neuroscience Program, Colorado State University, Fort Collins, CO; Department of Biochemistry and Molecular Biology, Colorado State University, Fort Collins, CO

Abstract: The role of neuroinflammation in multiple neurodegenerative diseases is receiving considerable attention. Alzheimer’s disease (AD), the most common dementia, afflicts >24 million people worldwide. Bundles of cofilin-saturated actin filaments (rods) are a pathological feature of AD, accumulating within both axons and dendrites, disrupting vesicular transport and synaptic function. Components of a common pathway mediating rod formation include cellular prion protein (PrPc), NADPH oxidase (NOX), and a chemokine/cytokine receptor, CXCR4 or CCR5. Disease-associated factors, such as amyloid- β (Aβ) in AD or HIV gp120 in AIDS dementia, induce production of reactive oxygen species (ROS), leading increased active cofilin and its dimerization through sulfhydryl oxidation, stabilizing rods. Injection of the CCR5-binding domain of gp120 into brains of wildtype mice led to cognitive impairments which were reduced when performed in CCR5 null mice, making this receptor a potential pharmacological target in dementia. The CCR5 antagonist RAP-103 inhibits both gp120- and Aβ-induced rods in rodent and human neurons. We hypothesize that RAP-103 will reverse rods already formed. To test this hypothesis, we express a fluorescent protein-tagged mutant cofilin which incorporates into rods but does not induce them when overexpressed. We then induce rods with overnight Aβ-treatment and follow rods by live-cell fluorescence time-lapse imaging after adding RAP-103. Following treatments and imaging, cells are fixed and immunolabeled for rods. Identical fields are reimaged to determine if loss of rods is due to photobleaching (stained rod still present) or rod disassembly. Preliminary live cell results show full rod reversal suggesting RAP-103 might have significant therapeutic benefits.

Change to spare: understanding the developmental timing of food-induced plasticity during larval development of the Pacific sand dollar.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Isabel Villafuerte*[1], Dr. Douglas Pace [2], Ariana Lee[3]
[1]California State University, Long Beach, [2]California State University, Long Beach, [3]California State University, Long Beach

Abstract: Phenotypic plasticity is the ability of a single genome to produce different phenotypes based on environmental interactions and is a critical adaptive response mechanism for animals experiencing climate change. Benthic marine invertebrates require larval recruitment in order to sustain their adult populations. Larvae of the Pacific sand dollar, Dendraster excentricus, experience food-induced plasticity where larvae developing in low food concentrations will make longer arms in order to capture more food. Larvae in high-food conditions will make shorter arms and redirect resources to faster development. It is unknown whether this adaptive phenotypic response can occur throughout all of larval development or only during the early stages when feeding begins. We hypothesized that as low-fed larvae develop, they will gradually lose their ability to morphologically respond to increases in food availability (i.e., switch from long-armed to short-armed phenotype). Results did not support our hypothesis. Low-fed larvae exhibited a robust response when switched from low to high food conditions throughout the entirety of larval development. Upon switching low-fed larvae to a high food diet, we observed a reduction in post-oral arm growth and an increase in midline body length, a response similar to constantly high-fed larvae. These results show that the plastic responses observed by larvae early in development are maintained throughout all of larval development. These results help to link lab-based research with realistic natural conditions of changing food availability. Importantly, they advance our understanding of the range of adaptive responses available to organisms experiencing rapid environmental changes resulting from human-linked activities.

Does U2AF1S34F ameliorate KRASG12V Oncogene Induced Senescence within Human Bronchial Epithelial Cells?

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Robert Hays*[1], Dr. Angela Brooks [2], Dr. Eva Hrabeta-Robinson[3], Dr. Ali Shariati[4], Abolfazl Zargari Khuzani [5]

[1]California State University, Monterey Bay, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]University of California, Santa Cruz, [5]University of California, Santa Cruz

Abstract: The U2AF1S34F splicing factor mutation is found in a variety of cancers, yet its disease role is unclear, since neither removal of this mutation from cancer cell lines nor introduction into immortalized cell lines alters the neoplastic potential of cells. This lack of a driver mutation function for U2AF1S34F prompts a search for possible synergistic effects with other well-known oncogenes. From existing lung cancer patient data, we discovered that U2AF1S34F is co-enriched with KRAS mutations. The KRAS oncogene, found in over 30% of lung adenocarcinoma, has been implicated in oncogene induced senescence (OIS) known to have tumor suppressive functions and produce enlarged, non-dividing cells. Using live cell imaging of genetically manipulated immortalized human bronchial epithelial cell lines, we aim to investigate whether cells harboring U2AF1S34F are capable of ameliorating OIS.We hypothesize that, over time, a larger portion of the cell population harboring KRAS mutations in the U2AF1 wild type background will exhibit reduced cell division rates due to the onset of OIS in comparison to the U2AF1S34F background. To test this hypothesis, we used live cell imaging over a 72 hour period to collect images from cultures of single mutant, double mutant, and control cell lines. Image analysis will be done using a novel program called DeepSea to track and label cells. Outputs from DeepSea will enable us to distinguish senescent cells in a cell population by their division rate and size. Profiling the senescent cell population in each background will reveal whether U2AF1S34F is capable of suppressing KRAS-induced senescence.

Fungal Pathogen Modelling

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Seth Pua*
Haskell Indian Nations University

Abstract: Microstegium vimineum, an invasive grass to North America, acts as a reservoir for the fungal pathogen Bipolaris and can spread the disease to native plant species. The spread of the pathogen suppresses both the invasive and native species but could ultimately benefit the invasive species in competition. To better understand how Bipolaris spreads, we created a mathematical model that includes infection and cross-infection rates. We follow the numbers of the two different species of plant, which then can either be susceptible or infected. These four different variables are set as differential equations to show the rates of change that will affect the sizes of the populations of infected and uninfected plants over time. A set of parameters affects these rates of change, such as infection, death, and reproduction rates. From these equations we were able to calculate a basic reproduction number (0) that will allow us to see which parameters cause the disease to spread more and which cause it to decline. In the future, we plan to use numerical estimates of parameter values from the literature to consider how population sizes change over time and a sensitivity analysis to how changes to the values of parameters can affect the variables.

Biogeographical Comparisons of Concrete's Extreme Microbial Communities

Discipline: Life Sciences
Subdiscipline: Microbiology

Alena Kelleher*[1], Julia Maresca [2], Helene Ver Eecke[3], Jamie Bui[4]

[1]Metropolitan State University of Denver, [2]University of Delaware, [3]Metropolitan State University of Denver, [4]Metropolitan State University of Denver

Abstract: Concrete is an extreme environment, with high pH and salt levels, and low water and nutrient contents; however, complex microbial communities have been detected within these conditions. Previous and ongoing studies have described concrete communities as being seeded by their precursor materials and that key microbes may be bioindicators of infrastructural integrity. In my research, I aim to obtain geographic-specific data to contribute to the collaborative SCIENCE HOORAY project: Self Cleaning Infrastructure Engineering Concrete Environments – HydrOcarbon & Oil Remediation Across Years. Our data will be used to compare relative abundances of bacteria and assess how those may vary regionally, seasonally, and over time. My research project focuses on performing a standardized DNA extraction protocol on samples collected from the Colorado Rocky Mountain Region of the USA. Concrete samples have very low biomass, so an extensive and highly specialized DNA extraction protocol is required for accurate analysis. Over the course of three days, microbial DNA within concrete samples is extracted, purified, and evaluated. Taxonomic 16S amplicon sequencing and bioinformatical analysis on extracted DNA will reveal relative abundances of key microbes and allow cross-comparisons. Concrete is the most utilized building material in the world, so greater insight into its microbial inhabitants can contribute meaningful data to potentially develop more effective damage detection and mitigation methods, and microbe-mediated repair, while also contributing to the earth microbiome project.

Land Use and Precipitation Effects on Legume Richness in Midwestern Prairies

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Dorothea Summers*[1], Dr. Susan Magnoli[2], Dr. James Bever[3]
[1]The University of Kansas and Haskell Indian Nations University, [2]The University of Kansas, [3]The University of Kansas

Abstract: Prairies across Midwestern United States are home to thousands of prairie plants and can be incredibly diverse. Numerous prairies have been overturned for farming, commercial use and a variety of other human constructions, though in recent years many of these lands are in the process of being restored. Past research has shown a decreased species richness in disturbed prairies compared to nearby native prairies with some evidence this is in part to degradation of the soil microbial communities which plants interact with. Increased precipitation has also been shown to increase species richness in both native and disturbed prairies. Here we explore whether legumes, which make up a large percentage of the prairie community, aid in nitrogen fixation, and provide food and habitat for wildlife, follow these general patterns. In a study of forty native and disturbed sites we found legume richness did not change across the precipitation gradient. However, legume richness was higher in native sites compared to the disturbed sites. The legumes' response to habitat disturbance could reflect degradation of the soil microbial communities on which legumes depend. Reintroducing these microbial communities, and in particular rhizobia, could facilitate restoration of the much needed legume.

Testing the role of Bruno1 in metabolic function and fat regulation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Tyler Shambaugh*[1]and Tania Reis[2]

[1]Bates College, [2]University of Colorado Anschutz

Abstract: Genetics are a largely implicated in obesity, however proportionally very few genes have been studied and found to be part of energy homeostasis. Drosophila melanogaster provide a useful model to study genetics, metabolism, and obesity. We used Drosophila larvae to test the role of an RNA-binding protein, Bruno1. Bruno1 is most commonly known for its role in transcriptional regulation during oogenesis and Bruno-like genes have been identified in mammals—like CELF1 in humans. CELF1 is a differentially-spliced gene associated with the disease Myotonic Dystrophy 2. My project examines the role of Bruno1 in Drosophila metabolic function and regulatory mechanisms, including differential expression of Bru1 isoforms in different tissues upon different diet challenges. Previous data taken during a pilot screen of RNA-binding proteins has indicated that Bruno1 is a fat regulatory gene in Drosophila . We used secondary screening assays to test this hypothesis. Based off additional preliminary, we also investigated the differential expression of different Bru1 isoforms in different diets. This study will provide preliminary insight on the role of Bru1 and its different isoforms in Drosophila metabolism. This is important research for humans to destigmatize obesity and learn more about how our genetics play into fat regulation.

Manipulation of host translation machinery by coronavirus nonstructural protein nsp2

Discipline: Life Sciences
Subdiscipline: Microbiology

Brynn Roman*[1]and Lars Plate [2]
[1]Vanderbilt University, [2]Vanderbilt University

Abstract: Nonstructural proteins (nsps) play a crucial role setting up RNA viral replication in the infected host cell. Exerting control over host translation machinery is necessary during the viral life cycle to slow endogenous host protein synthesis while promoting viral protein translation. However, the underlying mechanisms by which viral nsps regulate protein translation are not well-understood. SARS-CoV nsp2 has been identified as a viral protein that interacts with host translation repressors 4EHP and GIGYF2. SARS-CoV-2 nsp2 does not strongly interact with 4EHP or GIGYF2, despite the nsp2 homologs having a sequence similarity of 79.1%. We have identified the general GIGYF2/4EHP binding region in SARS-CoV nsp2 using SARS-CoV nsp2 truncations and SARS-CoV and SARS-CoV-2 chimeras. In addition to identifying the binding region it is important to determine how the nsp2 homologs are manipulating the host translation machinery. To this end, we utilized biorthogonal noncanonical amino acid tagging (BONCAT) to investigate and compare the effects of SARS-CoV and SARS-CoV-2 nsp2 on host translation rates. Significant differences in the translation rates of individual host proteins between SARS-CoV and SARS-CoV-2 nsp2 indicate the homologs are targeting different host proteins. In the event nsp2 promotes viral translation in addition to impacting host translation, we developed a reporter to measure viral frameshifting efficiency. While it appears neither nsp2 protein impacts viral frameshifting efficiency, the data suggest the presence of nsp2 may increase translation initiation. Ultimately our finding provide insight into the functions of SARS-CoV and SARS-CoV-2 nsp2.

Computational Design of Cytokine Receptor Agonists

Discipline: Life Sciences

Subdiscipline: Biochemistry

Muna Yase*[1], David Baker[2], Joseph Harman[3]
[1]University of Washington, [2]University of Washington, [3]University of Washington

Abstract: Cytokine therapies using Interleukin-7 (IL-7), show promise for addressing immunosuppression that arises from cancer tumors: IL-7 increases circulating T cells while exhibiting reduced toxicity than other cytokine therapies that trigger adverse effects. Although decades worth of research and human clinical trials have been conducted, IL-7 has yet to show objective responses in clinical settings. I aim to overcome this limitation by designing de novo versions of IL-7 that exhibit stronger signaling properties while retaining low toxicity. De novo protein design will allow for more control over protein properties and, as a result, signaling outcomes. We have designed high-affinity protein binders for the IL-7Rα and gamma common (γc) receptors. My goal is to fuse receptor minibinders in different geometries to explore the effect of receptor geometry on signaling output. I will pass the designs through a series of networks developed in the lab to predict protein structure and sequence and evaluate using the AlphaFold2 (AF2) protein structure prediction network which predicts the structures of de novo proteins with high accuracy. After computationally evaluating these designs, I will experimentally characterize top-scoring designs using mass spectroscopy to confirm protein size. I will analyze binding of designs to the target receptors using octet binding analysis and phospho-flow cytometry to measure design signaling through the receptor complex. Our goal is that these designs will lead to new agonists with biochemical and signaling properties that exceed those of natural cytokines, paving the way for the development of a new and highly effective class of cancer therapeutics.

Developing new tools for early detection of Botrytis cinerea on strawberry fruit

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Dilasha Shenaz*[1], Dr. Barbara Blanco-Ulate[2], Saskia Mesquida Pesci[3], Lolita Adkins[4]
[1]University of California, Davis, [2]University of California, Davis, [3]University of California, Davis, [4]University of California, Davis

Abstract: Strawberries (Fragaria x ananassa) are a soft fruit crop that gets easily damaged along the market supply chain through handling and processing. Physical damage increases their susceptibility to fungal pathogens, particularly to B. cinerea , resulting in moldy fruit which faces consumer rejection and significant economic losses. The present study aims to develop new tools to detect the fungal infection in its early stages to prevent fruit loss and reduce food waste by combining two different methodologies: profiling volatile organic compounds and multispectral imaging. For volatile compound profiling, we inoculated fresh strawberries with B. cinerea and collected volatile compounds at early time points after inoculation. Volatile compounds will be analyzed via gas chromatography coupled with mass spectrometry to find those specific to B. cinerea -infected strawberries. For multispectral imaging, we monitored visual changes of B. cinerea -inoculated and healthy fruit at early time points after treatment using the VideometerLab®. Light reflectance profiles will be compared to identify areas of the light spectrum with potential for B. cinerea detection. Additionally, we collected infected and healthy strawberry tissue to perform RNAseq that will reveal genes and biochemical pathways involved in strawberry fruit interaction with B. cinerea . Our future research will continue to investigate the outcomes of this study to develop applied solutions to early detect B. cinerea and reduce food and economic losses.

Modelling p53 allelic heterogeneity using precision genome editing

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Diego Pomales Matos*[1]and Francisco J. Sánchez-Rivera [2]
[1]University of Puerto Rico, Rio Piedras, [2]Massachusetts Institute of Technology

Abstract: Genomic studies have shown there exists a heterogeneous collection of cancer-associated mutations, which include known and druggable oncogenic mutations, as well as many variants of uncertain significance (VUS) whose function remains unknown. One method for characterizing single nucleotide VUS is using precision genome editing to perform functional analysis on cellular and animal models. For instance, base editors can be used to install targeted point mutations in the absence of double strand breaks or exogenous DNA templates with high efficiency and precision. Here, we describe a novel system that integrates precision genome editing in combination with either Cre/loxP or RNA interference technologies to engineer defined mutations in an inducible and reversible manner. As proof-of-concept, we show that a panel of cancer-associated p53 alleles can blunt p53-mediated tumor suppression in pancreatic, lung, and hepatocellular carcinoma cells with a potency that varies depending on the precise nature of the mutation. Current studies are focused on elucidating the cellular and molecular mechanisms by which these and other cancer-associated p53 alleles functionally impact p53-mediated tumor suppression across a variety of in vitro and in vivo contexts. We anticipate that this approach will be widely useful to investigate the mechanisms by which cancer-associated alleles in p53 and other driver events impact tumorigenesis and disease progression.

The Diatom Genus Gyrosigma as a Test for Marine Microbial Regional Endemicity

Discipline: Life Sciences
Subdiscipline: Microbiology

Khazmyne Kawamoto*
University of Guam

Abstract: A prevailing hypothesis of microbial biogeography is that “Everything is Everywhere” (EIE hypothesis) is now being challenged with recent evidence from freshwater diatoms in Australia and in the marine Licmophora floras of Guam. Other genera of diatoms, such as Mastogloia seem to be mostly pantropical, with little evidence of regional endemicity to date. Several new species of Gyrosigma with unusual pitting in the valves have been found in samples from Micronesia, so this genus has the potential for regional endemicity. Two new species with pits were reported from China in 2020, neither of which has been seen here yet. Samples of mangrove mud and biofilm habitats from Guam, Yap, Palau are being studied primarily with scanning electron microscopy (SEM), plus LM to survey our samples. Although diatoms of coral reef habitats have been studied in Guam and Micronesia, no Gyrosigma species have been reported from the region. With recent LM and SEM studies, I have found various new species in the genus within the region. This genus has thus far led to a high ratio of regional endemicity.

Understanding the role of Condensin II in genome compartmentalization.

Discipline: Life Sciences
Subdiscipline: Genetics

Brenda L Ramos Villanueva*[1], Randi Isenhart[2], Son Nguyen[3], Leah Rosin[4], Olivia Crocker[5], Eric Joyce[6]
[1]University of New Mexico, [2]University of Pennsylvania Biomedical Graduate Studies, [3]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, [4]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, [5]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, [6]Department of Genetics, Perelman School of Medicine, University of Pennsylvania

Abstract: Understanding 3D genome organization is crucial to the understanding of how our genomes function in normal development and in disease. One widespread feature higher-order chromatin organization in the nucleus is the compartmentalization and spatial separation of transcriptionally active (A) and silent (B) regions of the genome. However, it remains unclear how this level of organization is achieved. Previous studies in our lab and others have found that the protein Cap-H2, a component of the Condensin II complex, is essential for the regulation of large-scale chromatin folding. We aim to determine whether this involves the disruption of A/B compartments. First, we will be using custom chromosome paints to image A/B compartments in Drosophila nuclei after Cap-H2 knockdown to determine how the size, shape and behavior of different chromatin types are being disrupted in individual cells. In addition, to test a compartment interaction directly, we will use the Drosophila bw D mutation, which is a position effect variegation (PEV) assay that requires a long-range B-B compartment interaction for its transcriptional silencing. We will test whether Condensin II depletion disrupts this interaction and the silencing of the bw gene in the developing fly eye. Together, these experiments will determine if Condensin II is a critical component of genome compartmentalization, which would represent one of the only complexes implicated in this level of organization.

Follicle density in a guinea pig model of polycystic ovarian syndrome (PCOS): a pilot study.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Rosalia Tanori*[1], Cecily V. Bishop[2], Juriana E. Barboza Sagrero[3]
[1]Oregon State University, [2]Oregon State University, [3]Oregon State University

Abstract: Our research group has begun to determine if guinea pigs (Cavia porcellus), a rodent with a long-lived corpus luteum (CL), are a suitable model for androgen excess/PCOS (Barboza Sagrego et al., 2022). Determining follicle density is an important consideration in models of PCOS due to the disorder's tendency to promote the growth and development of numerous smaller follicle types within the ovary. Therefore, the objective of this analysis was to determine the relative abundance of each follicle type within a cross-section of 20-week-old guinea pig ovarian tissue. Ovarian tissues were collected from seven guinea pigs treated with cholesterol implants (vehicle, n=4) or testosterone implants (n=3). Tissues were processed for embedding in paraffin, cut into serial sections (5 μm wide), and placed onto glass slides (1 section/slide). Every fifth slide was chosen for the staining process to observe ovarian/follicular morphology. Tissues were stained with Mayer's hematoxylin and eosin Y/phloxine B. Stained slides were viewed at 4x magnification with a fluorescent microscope. Images were captured of the 5 μm wide sections at a scale of 930 μm. Follicles of interest were primordial, primary, multi-layer, antral, and CL. Length, width, and area measurements were taken of the field of view, within ImageJ, of the ovaries in micrometers. Data will be analyzed by follicle number and type per area of tissue. All

follicle types were found in all the ovaries imaged and some CL. These should provide needed baseline analyses for future experiments employing guinea pigs as a model of PCOS.

Developing a peptide tagging strategy to improve tethering in optical tweezers

Discipline: Life Sciences
Subdiscipline: Biochemistry

Paola Miranda Castrodad*[1], Hannah Haller-Hidalgo [2], Christian Kaiser[3]
[1]University of Puerto Rico at Cayey, [2]Johns Hopkins University, [3]Johns Hopkins University

Abstract: Optical tweezers (OT) is a powerful technique that is used to measure sub-nanometer changes associated with protein folding and unfolding. Applying force to a protein acts like a denaturant that is more directed and better controlled than typical methods, which enables reversible single-molecule measurements. Manipulation with OT requires tethering the protein of interest by its ends to molecular handles for force application. Chemical coupling has been a prevalent tethering method, but it can cause protein modification that can affect measurements. A better alternative is peptide tags that spontaneously form covalent bonds to attach the protein of interest to molecular handles. We aim to develop a method to tether proteins efficiently using orthogonal tags. The Kaiser lab has previously demonstrated that the SpyTag/SpyCatcher (Sp/SpC) system is effective for forming tethers in OT experiments by attaching the protein being studied to DNA handles. Since the SnoopTag/SnoopCatcher (Sn/SnC) system is orthogonal to Sp/SpC, we hypothesize that combining both these systems will facilitate sample preparation for OT experiments. To evaluate our hypothesis, we are developing a modular tethering strategy that involves preparing SnC DNA handles and performing OT experiments using an N-terminally Sn-tagged and C-terminally Sp-tagged protein. Preliminarily experiments indicate that purified SnC robustly reacts with a Sn-tagged model protein to form a covalent bond. The Sn/SnC system thus seems like a useful addition to the OT sample preparation toolkit. We expect the approach to be highly efficient, making it particularly attractive for multimeric complexes and proteins that cannot be obtained in biochemical quantities.

The Effects of Temperature and Nutrition on The Growth and Development of Pedal Lacerates in the Tropical Anemone Aiptasia: a Model to Understand the Future of Coral Bleaching

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kali Sivula*[1], Jun Cai [2], Virginia Weis[3]
[1]Oregon State University, [2]Oregon State University, [3]Oregon State University

Abstract: Aiptasia are a species of tropical anemones, which form a mutualistic symbiotic bond with dinoflagellate species of the family Symbiodiniceae, commonly found in corals. This makes Aiptasia a great model for the study of coral-algal symbiosis. They can also reproduce both sexually and asexually through the development of pedal lacerates. These are a portion of the foot or pedal disk separated from the adult organism, which typically develop into juvenile stages within 7 days. Our project specifically focuses on the effects of nutrition and temperature on the development of pedal lacerates into juvenile animals. Given the negative effects of global bleaching and climate change, we initially hypothesized that heat-stressed lacerates would develop at a slower rate than non-stressed lacerates, and nutrition would play an important role in development. In our experiment, lacerates are produced by cutting from adults. They are divided into three nutritional treatments: (starved, fed control, and enriched feeding) and two different temperatures (control at 25C and heat stress at 32C). We measured the developmental responses of Aiptasia to the different treatments over a 21-day period. Daily development was measured through tentacle counts, size quantification by compound microscope imaging, and measuring algal density through the use of hemocytometers. Our results suggest that temperature played a more important role in development than nutritional differences. Contrary to our hypothesis, heat stress caused higher tentacle growth in the initial 7 days of regeneration. This could be the result of metabolic increases and resilience of juvenile animals to moderate heat stress.

Aberrant endosomal trafficking in cancer results in dependency on STAMBP

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Paloma Bravo*[1]and Jason Kwon[2]
[1]Carleton College, [2]Broad Institute

Abstract: The lack of effective therapies contributes to the high cancer mortality rates. Precision medicine will help identify new therapeutic strategies to target specific cancer contexts. There have recently been large efforts to systematically identify novel therapeutic targets by deploying genome-scale CRISPR-Cas9 loss-of-function screens across multiple cancer cell models. Systematic analysis of this dataset identified the gene STAMBP, involved in the deubiquitination of internalized receptor cargo which results in degradation, as a novel selective dependency. Upon knockdown of STAMBP in dependent cells we observed decreased cell viability and endosome accumulation which could be a promising target for therapeutics. However, STAMBP dependence is variable and difficult to detect. Our goal is to identify biomarker features for cancer contexts where STAMBP is required. We found that the absence of VPS35L, a protein involved in receptor recycling in cells, was the top correlated feature of STAMBP dependency, and that overexpression of VPS35L rescues STAMBP dependency and aberrant endosomal trafficking upon STAMBP knockdown. Further analysis identified absence of the endosomal trafficking protein, SNF8, as a potential additional biomarker for STAMBP dependency in downregulated VPS35L cancers. To investigate if SNF8 can functionally rescue the cell in the absence of STAMBP, we knocked down STAMBP and overexpressed SNF8 and are measuring cell viability. We plan to study endosomal accumulation of ubiquitinated cargo proteins to determine if SNF8 is involved in endosomal receptor degradation or recycling. A better understanding of endosomal trafficking pathways as biomarkers of STAMBP dependency will support the development of more effective targeted therapeutics.

Characterizing Deep-sea Coral Communities in ROV Footage of the Musicians Seamounts

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Abigail Fritz*[1]and Dr. Deanna Soper[2]
[1]University of Dallas, [2]University of Dallas

Abstract: CAPSTONE Expedition 1708 of the National Oceanic and Atmospheric Administration (NOAA), conducted in the Musicians Seamounts region of the Pacific Ocean in 2017, used bathymetry mapping to describe the topography of the seafloor while 20 remotely operated vehicle (ROV) dives collected video footage, environmental data, and samples from 17 geological features at depths between 290 and 3,854 meters. The information gathered through these efforts offers an opportunity to increase understanding of deep-sea coral communities in the region, which are believed to play a vital role in local ecosystems due to their provision of substrate and sustenance to a wide range of species; however, prior to analysis, ROV footage must be processed to create a quantitative data set. Initial annotation of the raw footage was performed by experts at NOAA, who identified the taxa present and gave population estimates for each. Undergraduate students used CVision AI's Tator software to localize annotations by drawing boxes around every individual and linking them to the relevant identifications. Environmental variables like water temperature, salinity, and oxygen saturation were then integrated by matching timestamps to those of localized annotations. Thus far, 13 out of the 20 dives from the expedition have been processed in this manner. The resulting data set is being used to identify distinct coral communities within and across dives and to investigate potential drivers of diversity, composition, and distribution. Preliminary analysis suggests that these may include: depth; environmental variables; and the type and makeup of geological features on which they were observed.

Succession and Reef Accretion of Crustose Calcifying Red Algae on Recruitment Cubes

Discipline: Life Sciences

Subdiscipline: Marine Sciences

Raianne Quichocho*[1]and Tom Schils [2]

[1]University of Guam, [2]University of Guam

Abstract: Crustose calcifying red algae (CCRA) are dominant benthic organisms on tropical reefs. Through the deposition of calcium carbonate in their thalli, CCRA build reef and cement substrates together. CCRA identification requires specialized techniques for morpho-anatomical investigations and suffers from the frequent lack of reproductive structures and similarities in overall habit morphology. To investigate the floristic diversity and the contribution to reef accretion of CCRA in microhabitat environments, an experimental setup of replicate units of recruitment cubes was installed in the holding tanks of a flow-through seawater system. The floristic diversity, changes in community composition, and calcium carbonate accretion will be monitored over time using DNA barcoding, image analysis, and 3D scanning. Three discrete microhabitats are represented within each experimental unit: (1) exposed surfaces with high water flow and direct sunlight, (2) exposed surfaces with high water flow and indirect sunlight, and (3) cryptic surfaces with reduced water flow and low irradiation. A previous study has shown that CCRA communities on coral recruitment tiles were species-rich and homogeneous across tiles, but this study was not designed to address differences related to microhabitat diversity. We predict that environmental differences at the scale of microhabitats will affect the composition of CCRA communities. Knowledge of the floristic diversity, community composition, succession, and reef accretion of CCRA assemblages at small spatial scales fills an important gap in our understanding of ecological processes on coral reefs.

Computational Analysis of Interleukin-4 and its Potency As a Therapy for Autoimmunediseases

Discipline: Life Sciences

Subdiscipline: Biology (general)

Tyrece Frater*[1], Dr. Lawrence A. Stern[2], Mr. John Fynn[3]
[1]Polk State College, [2]University of South Florida, [3]Polk State College

Abstract: Intereleukin-4(IL-4) is a cytokine that initiates type 2 helper-T cell pathways and mediates lymphocyte differentiation. Interleukin-4 is prized for its ability to suppress pro-inflammatory responses. Interleukin-4 is not a heavily engineered protein despite its notable impact in relieving autoimmune diseases such as psoriasis (Yang et. Al). Our approach to interleukin-4 was to increase its affinity for interaction without jeopardizing its stability. We ran a command called Analyse Complex to understand the thermodynamic values that constitute interleukin-4. These values are important because it is no use to engineer a brilliant protein that cannot withstand the body's internal environment. We ran two commands called Position Specific Scoring Matrix(PSSM) and Build Model. These commands applied mutagenesis to interleukin-4's ligand, and receptor. Position Specific Scoring Matrix mutated the amino acids on the ligand that interact with the receptor. Build Model mutated the thermodynamic values of the non-interacting amino acids found on the receptor. After mutation, the thermodynamic values of a protein change, as did ours. We used this data to create heat maps in Microsoft Excel that allowed us to target segments of our cytokine that are suitable for bioengineering. Our heat map results from PSSM suggest that we may not be able to improve IL-4's affinity for interaction without compromising structure. Our results from Build Model suggest that there are many mutations that we can make to IL4's non-binding interface to improve its potency as a therapy for autoimmune diseases. Collectively, our results provide great incentive for further research.

Utilizing Split GFP Technique to Assess Hepatitis Delta Virus Replication

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Veronica Sanchez Gonzalez*[1], Susannah Stephenson-Tsoris[2], Jake Liang[3]
[1]University of Puerto Rico- Rio Piedras, [2]Liver Diseases Virology Lab, National Institute of Diabetes and Digestive and Kidney Diseases, National Institute of Health, Bethesda, MD, USA, [3]Liver Diseases Virology Lab, National Institute of Diabetes and Digestive and Kidney Diseases, National Institute of Health, Bethesda, MD, USA

Abstract: An estimated 257-291 million people are chronically infected with the hepatitis B virus (HBV) worldwide, putting them at greater risk for cirrhosis and hepatocellular carcinoma (HCC). Co-infection with hepatitis delta virus (HDV), which affects nearly 5% of people living with HBV globally, can accelerate the progression of liver disease and cancer. The HDV RNA encodes for the hepatitis delta antigen (HDAg), which is composed of the small form (S-HDAg) and the large form (L-HDAg). While it is known that these two forms of HDAg interact with the HDV RNA to play a vital role in HDV replication and infection, it is still mostly unknown which host factors HDV RNA and HDAg interact with during replication. The purpose of this study is to perform shRNA genome-wide gene-knockout screening to determine which genes affect HDV replication, with the end goal of understanding the interactions of HDV with different host factors. To this end, the Split GFP technique is being used. This method uses GFP 1-10 and GFP 11, two parts of GFP that are non-fluorescing on their own, but when combined form GFP, a fluorescent molecule, that can be used to assess HDV replication. Site-directed mutagenesis was used to append GFP11 to the C-terminus of the S-HDAg. Gateway cloning and the piggyBac Transposase method will be used to create a Huh 7 cell line that expresses GFP 1-10 constitutively. Together, the

GFP11 HDV and GFP1-10 Huh7 cell lines will be used to assess HDV replication levels when treated with shRNA.

: Developing an RNA-targeted therapeutic for microsatellite repeat expansion disorders using catalytically dead Cas13d

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Valerie Gonzalez*[1]and Gene Yeo [2]
[1]University of California San Diego, [2]University of California San Diego

Abstract: Microsatellite repeat expansion (MRE) diseases are caused by repetitive DNA sequences that can produce toxic RNA and protein products. Examples of MRE diseases include Huntington's disease, caused by a CAG repeat expansion in the Huntingtin (Htt) gene, and myotonic dystrophy type 1 (DM1), caused by a CTG repeat expansion in the DMPK gene. Knocking down the MRE-containing RNAs is an attractive therapeutic strategy for treating these conditions. However, previous work has largely relied on Cas13d, a protein with high levels of off-target RNA cleavage. In an effort to design a robust system for knocking down MRE-containing RNA, we have utilized PIN endonuclease fused to catalytically dead Cas13d (dCas13d). Our system takes advantage of Cas13d's RNA-targeting capabilities while avoiding the unwanted off-targeted effects associated with its native endonuclease domain. To test our system, we transfected human embryonic kidney (HEK293T) cells with three plasmids encoding 1) PIN-dCas13d, 2) a guide RNA (gRNA) targeting CAG repeats, and 3) exon 1 of the Htt gene containing 74 CAG repeats. We then quantified the CAG repeat RNA using RNA dot blots. We saw that both fusion orders (N-terminal or C-terminal PIN) resulted in a strong knockdown of CAG repeat RNA when compared to a non-targeting gRNA. We are now testing our system's efficacy in HEK293T cells expressing 105 CTG repeats, the MRE implicated in DM1. Our preliminary results demonstrate that PIN-dCas13d could be an effective research tool and/or therapeutic system for knocking down MRE-containing transcripts.

Tracing the Energy Pathways of Macroinvertebrates in Saltmarsh Food Webs Using Carbon and Nitrogen Stable Isotopes

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Yuleny Gomez*[1]and Paola López-Duarte, PhD [2]
[1]University of North Carolina at Charlotte, [2]Assistant Professor

Abstract: Macroinvertebrates have key trophic positions in saltmarsh food webs and the creation of saltmarshes is known to increase the biodiversity of new habitats. The effects on food web interactions at the macroinvertebrate level, however, are less understood. The gap in knowledge suggests the need for additional research concerning the trophic differences and similarities between newly-created and natural saltmarshes. Macroinvertebrates (ants, amphipods, midges, springtails, bristle worms, ticks, and crabs) were sampled at two different habitats: two newly-created and one naturally established saltmarsh located in the Lake Hermitage Marsh Creation area in Louisiana. Stable isotope analysis (SIA) of δ13C (energy source) and δ15N (trophic position) was used to trace the trophic pathways throughout each marsh and compare the trophic connectivity to neighboring marshes to determine whether newly-created marshes can sustain similar food webs as naturally established saltmarshes. We hypothesize that newly created saltmarshes do not sustain the same food webs as naturally established saltmarshes. Higher biodiversity is associated with a more complex food web. Therefore, newly-created marshes may sustain simpler food webs before they become well-established. Similarly, those newly-created marshes may contribute less macroinvertebrate organisms to neighboring habitats than natural marshes. Understanding the contributions of macroinvertebrate communities is important because they are at the base of saltmarsh food webs and not as well studied as higher trophic levels. The SIA data can provide valuable information for decision making processes for the creation of future saltmarshes.

Automated Image Analysis Tool Development for Diabetic Retinopathy

Discipline: Life Sciences
Subdiscipline: Biochemistry

Anne Martin*[1], Lauren Wilcox [2], Miguel Reyes[3], Madison Whitekiller[4], Dr. Joshua Butcher [5], Dr. Cammi Valdez[6]
[1]Northeastern State University, Tahlequah, [2]Biology Program, Department of Natural Sciences, Northeastern State University, [3]Chemistry Program, Department of Natural Sciences, Northeastern State University, [4]Chemistry Program, Department of Natural Sciences, Northeastern State University, [5]Department of Physiological Sciences, College of Veterinary Medicine, Oklahoma State University and Harold Hamm Diabetes Center, University of Oklahoma Health Sciences Center, [6]Chemistry Program, Department of Natural Sciences, Northeastern State University and Harold Hamm Diabetes Center, University of Oklahoma Health Sciences Center

Abstract: Diabetic retinopathy is the leading cause of blindness in working-aged adults. Affecting one third of people with diabetes, diabetic retinopathy is a complication of diabetes that leads to retinal vascular degradation and ultimately vision loss. While visual impairment primarily manifests in late stages of diabetic retinopathy, one of the earliest signs of the complication is the loss of retinal pericytes, which make up the outer layer of the capillary, the smallest of the blood vessels; endothelial cells comprise the inner layer of capillaries. Pericyte dropout can be detected by isolating the retinal vasculature and manually counting the pericytes and endothelial cells based on cell morphology. In the human retina, the ratio of endothelial cells to pericytes is 1:1, but due to pericyte dropout in diabetics, that ratio shifts to 1:4. Manual analysis of these images is time consuming, particularly challenging in mice, and may include human bias. In order to identify this ratio in cells in an expedited, rigorous, and unbiased manner, our lab has developed an automated image analysis program to detect and quantify cells in mouse retinal vasculature, isolated via elastase digest. Our automated image analysis program uses CellProfiler to identify cells, eliminating cells on the border of the image as well as any overlapping cells. Then, our algorithm distinguishes the cells as either endothelial cells or pericytes for quantification. Using this automated image analysis program, we will be able to better characterize mouse models of diabetic retinopathy, shedding light on the early progression of the disease.

The Evolutionary Basis of Sensory-Motor Integration through CRISPR/Cas 9

Discipline: Life Sciences
Subdiscipline: Genetics

Samantha Zaninelli*[1], Erik Duboué [2], Alexandra Paz[3]

[1]Harriet L. Wilkes Honors College of Florida Atlantic University, [2]Assistant Professor of Biology, [3]Graduate Student

Abstract: Startle response and locomotive activity are evolutionarily conserved behaviors that play a key role in the daily necessities of an animal, including sleep, foraging, searching for mates, and predator avoidance. While the neuronal mechanisms underlying startle responses and locomotive activity are well understood, less is known about the evolutionary mechanisms that modify these behaviors . This study places a focus on uncovering the evolutionary genetic basis of sensory-motor integration through the analysis of startle response behavior. We address these questions using the emerging evolutionary model, Astyanax mexicanus , which consists of 2 different populations: a river-dwelling surface fish and a cave-dwelling fish. These populations drastically evolved differential traits due to their environment, and distinctly differ in pigmentation, mechanosensory function, sleeping patterns, and visual necessities. We are studying the genes extracellular leucine-rich repeat and fibronectin type III domain containing 1 (elfn1), cytoplasmic FMR1 interacting protein 2 (cyfip2), and CUB and Sushi multiple domains 1 (csmd1) to analyze their impact on sensory-motor behaviors utilizing the CRISPR/Cas 9 gene-editing technique. Together, this study could reveal genetic mechanisms underlying the evolution of conserved sensory-motor behavior. Startle response behaviors are evolutionarily fundamental assets to life, and understanding the role genetics plays in this will assist us with identifying a continuous circuit of genes with significant roles in sensory overload and their relationship with commonly inherited disorders in humans, such as Schizophrenia.

Going with the flow and using bubbles to escape threats: microhabitat use for anti-predator behavior in Anolis aquaticus.

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Diana Cordero*[1], Lindsey Swierk[2], Alexandra Martin[3], Alva Mihalik[4]
[1]California State University, San Marcos, [2]Binghamton University, [3]Binghamton University, [4]University of Florida

Abstract: Antipredator behavior is an energetically costly tactic that many organisms use to aid survival. In ectotherms, antipredator behavior can be incredibly costly due to their reliance on environmental conditions, which can greatly affect their behaviors. Anolis aquaticus is a semi-aquatic lizard found near tropical rivers in Central America. This species uses various strategies to avoid predation, such as running away, swimming, and even diving into the water. A. aquaticus has been observed “rebreathing” air bubbles while diving, which allows them to remain underwater for more than 15 minutes at a time. We collected a representative sample of A. aquaticus from Rio Java at the Las Cruces Biological Station in San Vito de Coto Brus, Costa Rica, and quantified in the lab how diving is affected by environmental conditions. We aim to discover whether A. aquaticus’ dive duration is affected by water flow rate and the dissolved oxygen content of water and whether males and females perform differently in these microhabitats, as indicated by dive duration and bubble retention. We predict that in faster flowing water, A. aquaticus will have a shorter dive duration due to disruption of the rebreathing bubble. We also predict that in water with higher dissolved oxygen, A. aquaticus will have a longer dive duration because oxygen may be diffused into the air bubble. We hope that this research will help us better understand the mechanics of this rebreathing behavior as well as the preferred environmental conditions of A. aquaticus in a rapidly changing global climate.

Tetrahymena and Aquatic Virus Transfer

Discipline: Life Sciences
Subdiscipline: Biology (general)

Qootsvenma Denipah-Cook*[1], Katherine Deets[2], Nels Elde[3]
[1]Fort Lewis College, [2]University of Utah, [3]University Of Utah

Abstract: Aquareoviruses cause hepatitis and other forms of pathogenic disease among fish, contributing to mortality in fish populations. Viral transfer, however, is not fully understood in aquatic settings. Tetrahymena thermophila , a unicellular eukaryotic organism that resides within the same aquatic habitats as fish and aquareoviruses, are often consumed by juvenile fish and may act as an aquatic viral vector. Recent studies showed that T. thermophila increases the infectious titre of chum salmon reovirus (CSV) through the process of endocytosis and exocytosis. However, the mechanism responsible for increased infectivity is unknown. Because protease treatment increases infectivity of other aquareoviruses, we hypothesize that proteases within T. thermophila vacuoles play an essential role in the observed increase in CSV infectious titre. To test our hypothesis, we will determine if inhibition of protease activity in T. thermophila limits the increase in infectious CSV. However, we need to first understand the impact of various protease inhibitors and virus media on T. thermophila survival . T. thermophila were incubated with varying concentrations of three common protease inhibitors and found that undiluted Roche cOmplete exhibited 99% T. thermophila viability after 24 hours. As a follow-up experiment, we are optimizing an assay to quantify protease inhibition in T. thermophila. Next, we determined if T. thermophila were able to sustain and replicate within virus media. Ciliates in virus media with added iron had 70% viability compared to 10% without iron. These optimization experiments allow us to test the role of T. thermophila proteases in the increase of CSV infectivity.

Diversity and distribution of Fusarium sp. in soil and leaf litter of a premontane rainforest of southern Costa Rica

Discipline: Life Sciences
Subdiscipline: Microbiology

Zia Cryster*[1]and Terry J. Torres-Cruz[2]
[1]University of Guam, [2]Pennsylvania State University

Abstract: Fusarium is a soil-borne, filamentous fungus with a worldwide distribution. While this genus has been extensively studied for its critical role in agriculture as a plant pathogen causing crop diseases and major economic losses, the diversity and potential benefits of this genus within tropical forests is still poorly understood. Our goal is to bridge that gap by surveying the diversity and distribution of Fusarium species in soil and leaf litter of three different habitats within Las Cruces Biological Station, San Vito, Costa Rica. Soil and leaf litter samples were collected from primary forests, secondary forests (10–25 yrs.), and abandoned pastures (0–10 yrs.). Fusarium was isolated using a selective medium (Nash-Snyder Agar) and pure cultures were obtained. A total of 112 fungal isolates were attained and categorized in at least 50 morphotypes. Morphological traits will be used to identify specific Fusarium species using Carnation Leaf Agar. In this study, we predict that 1) given the heterogeneity and old growth of host plants, primary forest will have the highest diversity of Fusarium , 2) while secondary forests have been reforested, the habitat may be an intermediate zone between primary forest and abandoned pastures, and 3) abandoned pastures will have the lowest amount of diversity of Fusarium species due to the previous practice of monoculture. Our findings will help shed light

on the ecological relationships and diversity of the genus in uncultivated areas where plant life is species rich as well as in two habitats undergoing various reforestation approaches at different stages.

Evaluating hippocampal injury and plasticity following a neonatal rat cardiac arrest model

Discipline: Life Sciences
Subdiscipline: Neurosciences

Shay Kathiresh*[1], Nidia Quillinan[2], Erika Tiemeier[3], Danae[4]
[1]University of Colorado Denver, [2]University of Colorado Anschutz Medical Campus, [3]University of Colorado Anschutz Medical Campus, [4]University of Colorado Anschutz Medical Campus

Abstract: Neonatal hypoxic-ischemic encephalopathy resulting from sudden cardiac arrest (CA) is an unfortunate and devastating condition, which leads to long-lasting neurological impairments. However, little experimental data on the pathophysiology of neonatal CA is currently accessible due to the lack of animal models. A novel experimental model of neonatal cardiac arrest and cardiopulmonary resuscitation (CA/CPR) was developed utilizing postnatal 9-11 day rats. Cardiac arrest durations of 8, 10, 12, and 14 minutes were observed and evaluated. Hippocampal CA1 and striatal neuronal injury were quantified 3 days after resuscitation with NeuN and Fluoro-Jade B staining. Blood analysis for circulating troponin levels were evaluated at 2 hours after CA/CPR. Neonatal rats exhibited a lack of Fluoro-Jade B positive neurons in both CA1 hippocampal and striatal neurons following an 8 minute CA/CPR. Increasing ischemia time to 10 min or greater CA/CPR resulted in an increase in hippocampal injury in neonatal rats. We detected increases in blood troponin levels indicating myocardial injury associated with CA/CPR. This is the first report of a cardiac arrest and CPR model of global cerebral ischemia in term-equivalent neonatal rats. Therefore, the neonatal rat CA/CPR model we developed is unique and will provide as an important new tool to the research community for the study of neonatal brain injury. Future studies will focus on the functional outcomes of neonatal CA/CPR.

Salinity tolerance of Colletotrichum fructicola associated with the Maga flower

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Gabriela Canizares*[1], Leslie Ann Eaton-Ocasio[2], Katerina Toyos-Quinones[3], Ariana Unda-Rivera[4], Emmanuel Ojeda-Vega[5], Ivelisse Irizarry-Caraballo[6]
[1]Universidad del Sagrado Corazon, San Juan, [2]Universidad del Sagrado Corazon, [3]Universidad del Sagrado Corazon, [4]Universidad del Sagrado Corazon, [5]Universidad del Sagrado Corazon, [6]Universidad del Sagrado Corazon

Abstract: Flowers are temporary plant organs that harbor microorganisms. The microbiota of Maga tree flowers (Thespesia grandiflora) , Puerto Rico's national flower, is still unknown. Our objective was to identify the microbiota of the Maga flower and study whether sodium chloride (NaCl) influences their growth. We hypothesized flowers host microorganisms whose growth is impacted by NaCl. Fungi were initially isolated from pollen and stigmas on potato dextrose agar (PDA). Morphology, sequencing of the internal transcribed spacer (ITS) gene, and BLAST analysis identified two isolates as Colletotrichum fructicola . A maximum parsimony phylogenetic analysis was done using MEGA software with sequences of Colletotrichum species. C. fructicola GC02 and KT02 were grown on PDA with a range of concentrations of NaCl at 25 ° C in a triplicate and their colony diameter was measured. Statistical analysis showed a significant difference in the average colony diameter of strains GC02 and KT02 on PDA with 0-350mM NaCl after 96 hrs. The colony diameter increased when GC02 was grown on PDA with 50mM-300mM NaCl after 96 hrs. The greatest average colony diameter of KT02 after 96 hrs was observed on PDA with 50mM NaCl (60mm) indicating that a slight concentration of NaCl stimulated fungal growth. Our findings suggest that the growth of C. fructicola from Maga flowers is influenced by NaCl and tolerates a range of concentrations up to 350mM of NaCl. The microorganisms that colonize T. grandiflora could impact its health and reproduction. Studying Maga flowers' microbiota is essential for conserving this endemic plant.

Evaluating the intraspecific variation of Corynactis californica in response to marine heatwaves

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ricardo Hernandez*[1], Amelia Ritger[2], Gretchen Hofmann[3]
[1]Georgia State University, [2]University of California Santa Barbara, [3]University of California, Santa Barbara

Abstract: In recent decades, experts have recognized that anthropogenic activities have drastically increased global temperatures, resulting in significant damage to our planet. One byproduct of anthropogenic climate change is an increasing frequency and intensity of marine heatwaves (MHWs). These heatwaves can be categorized by their frequency, intensity, and duration, typically ≥3°C above ambient temperatures and lasting for at least three consecutive days. Consequently, numerous species, as well as various marine and terrestrial ecosystems, have become susceptible to MHWs. In this study, we will observe the effects of different MHW simulations on a corallimorpharian, Corynactis californica , located off the coast of the Santa Barbara Channel. Previous research on the species have mentioned that C. californica may act as a site of refuge for macroalgae and marine invertebrates from predation, indicating ecologically-significant interspecific relationships. To understand the effects of MHWs on these organisms, we ask whether C. californica exhibits phenotypic plasticity and whether genets vary in their susceptibility to warming events. In this experiment, we identify the temperature at which C. californica experienced 50% mortality (LT50). We will place 12 ramets of 6 genets in one of four temperature treatments, ranging from 17°C (ambient) to 26°C in +3°C increments. Polyps will be removed after 24 hours, 3 days, 1 week, or 1 month and observed for recovery. This study is presently ongoing, with results expected to inform future laboratory studies regarding the importance of intraspecific variation in species responses to climate change.

Synthesis of Vitexin-inspired 4-quinolone scaffold against colorectal cancer

Discipline: Life Sciences
Subdiscipline: Biochemistry

Will Smither*[1], Taotao Ling[2], Fatima Rivas[3]
[1]Louisiana State University, Baton Rouge, [2]Research Assistant Professor, [3]Assistant Professor

Abstract: Vitexin and isovitexin are naturally occurring flavonoids with promising anticancer properties found in many terrestrial plants such as oak, buckwheat, and cannabis. Their exceptional chemical potential as antioxidants or pro-oxidants is due to their electron relay, which facilitates multiple reactions. For instance, they can promote reactive oxygen species

(ROS) to induce apoptosis in cancer cells while displaying no cytotoxicity against surrounding healthy cells. Our objective is to develop a synthetic strategy to a 4-quinolone system to mimic these natural products but exploit them to enhance their bioactivity and bioavailability properties against colorectal cancer cell models. Utilizing this 4-quinolone system, we intend to develop a thorough derivative library investigating the anti-inflammatory, antioxidant, and antiproliferative effects of various hydrophilic moieties at the C2, C3, and C8 positions of the quinolone core structure. Our methodology includes organic synthesis, structure elucidation using nuclear magnetic resonance (NMR) and high-resolution mass spectroscopy (HRMS), and cytotoxicity assays using colorectal cancer cell lines. Preliminary studies in our group have shown these compounds to have significant antiproliferative effects by inhibition of cyclin-dependent kinases (CDKs), and we envision that the addition of glycoside, halogen, and hydroxamic acid substituents will improve the activity of these scaffolds against designated biological targets. This study has the potential to provide an efficient synthetic protocol to a biologically active molecular scaffold as well as a diverse variety of novel, potential anticancer compounds. Investigating the anticancer effects of these 4-quinolone derivatives and elucidating their modes of action could provide valuable chemical tools for anticancer drug discovery.

Using Zebrafish as a Model System to Study the Effects of Microplastic Ingestion on Fecal Microbiomes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jessica Sklar*[1]and Fang Wang [2]
[1]California State University, Dominguez Hills, [2]California State University, Dominguez Hills

Abstract: Microplastics (MPs) are a major pollution issue in aquatic ecosystems that impact aquatic life, and some land animals. However, studies on how MPs affect vertebrates’ health, especially at the cellular or molecular level, are limited. Our lab uses zebrafish as a model organism to investigate the effects of chronic microplastic ingestion. In this project we focus on identifying zebrafish fecal microbiome changes caused by MPs. To conduct this experiment, zebrafish from the same parents, born on the same day, will be separated into one control group (0 mg/L) and three treatment groups with MP concentrations mimicking locations in Los Angeles County: 1.0 mg/L (West Catalina site), 2.5 mg/L (Palos Verdes and San Pedro Channel sites), and 5.0 mg/L (LA Harbor). Fecal samples will be collected at 1,2,3,4 months post fertilization, and DNA will be isolated. Then, 16S sequencing libraries will be created and sequencing will be performed using the Illumina MiSeq. Finally, the microbiome sequencing data will be analyzed through web-based platform Nephele. We expect to identify fecal microbiome changes in zebrafish treated with MPs compared to the control group, which will illustrate an important connection between MP ingestion and animal health. Our results can also be applied to other aquatic organisms and animals consuming aquatic organisms. Since the MP conditions used are similar to the environments in Los Angeles County, our discoveries will be relevant to our local communities and can help find solutions.

Hungry Hungry Spiders: How feeding state modulates jumping spider response to visual stimuli

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Meridia Jane Bryant*[1], Lin Yan [2], Damian O. Elias[3]
[1]University of Kansas, [2]University of California Berkeley, [3]University of California Berkeley

Abstract: Animal senses serve to translate external stimuli into internal representations. Jumping spiders (Family Salticidae) are a model for studying sensory perception because they perceive the environment using multiple sensory modalities for key processes such as predation and courtship. Previous studies focus on Salticids' ability to distinguish external stimuli, however, there are few studies on how internal factors modulate responses to the environment. Responding properly to prey is tightly bound to survival, thus, predation is an effective context to study the interaction between Salticid internal state and its behavior. In the present study, I exposed Habronattus formosus males in hunger and satiated states to an animated stimulus and measured their orienting behavior to determine if hunger state modulates jumping spider responses to a prey stimulus. I hypothesize that Habronattus formosus males under a hunger state would orient to the stimulus resembling prey more often than spiders in satiated state, which would suggest hunger regulates responses to stimuli. Alternatively, hungry and satiated spiders may react similarly to cues resembling prey, implying that responses to stimuli may not be modulated by hunger. Ultimately, I will explore the role of internal state in the behavioral response to prey items in a jumping spider, shedding light on the integration of internal and external signals in animals.

Recognition of Pseudomonas syringae effector protein HopZ1a in Nicotiana benthamiana depends on specific residues of the pseudokinase ZED1

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Helena Heiberger*[1], Nathan Diplock [2], Mael Baudin[3], Jennifer D. Lewis[4]
[1]University of North Alabama, [2]Department of Plant and Microbial Biology, University of California, Berkeley, [3]Department of Plant and Microbial Biology, University of California, Berkeley, [4]Department of Plant and Microbial Biology, University of California, Berkeley; Plant Gene Expression Center, United States Department of Agriculture, Agriculture Research Service, Albany CA

Abstract: Plants rely on an innate immune system to defend against pathogens. Plant disease-causing bacteria such as P. syringae , inject type III secreted effectors (T3SEs) into the plant cell to promote virulence. However, plants possess nucleotide-binding leucine-rich repeat receptors (NLRs) that can recognize T3SEs and induce effector-triggered immunity (ETI). ETI is often associated with a form of programmed cell death known as the hypersensitive response (HR). HopZ1a is a T3SE from P. syringae that acetylates the Arabidopsis thaliana receptor-like cytoplasmic kinase HOPZ-ETI-DEFICIENT1 (ZED1). The NLR known as HOPZ-ACTIVATED RESISTANCE1 (ZAR1) senses the acetylation of ZED1 by HopZ1a and mediates HR. We hypothesize that specific residues in ZED1 are important for the recognition of HopZ1a through ZAR1. We selected 29 mutations in ZED1 that are likely important for ETI, and characterized these mutations using the Agrobacterium tumefaciens transient gene expression system in Nicotiana benthamiana . We tested each ZED1 mutant for HR with A. thaliana ZAR1 or N. benthamiana ZAR1 in the presence or absence of HopZ1a. We identified several residues in ZED1 that are important for ETI. Our findings contribute to understanding the indirect recognition of HopZ1a by ZAR1 from two plant species. Expanding our understanding of how ZAR1-mediated

ETI occurs on a molecular scale may lead to innovations in engineering plant resistance to bacterial pathogens.

Zebrafish Models of Fibrodysplasia Ossificans Progressiva

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Olusola Babalola*[1], Pamela C. Yelick[2], Weibo Zhang[3], Rowan Cutler[4]
[1]Harvard University, [2]Tufts University, [3]Tufts University, [4]Tufts University

Abstract: Fibrodysplasia Ossificans Progressiva (FOP) is a rare disorder characterized by progressive, heterotopic bone formation, and an arginine to histidine (R206H) mutation in the human receptor ACVR1. This mutation induces upregulation of bone morphogenetic protein (BMP) signaling and increases phosphorylation of the downstream signaling partner, Smad1/5. Zebrafish express an ortholog of the human ACVR1 receptor, acvr1l. However, in Acvr1l, the equivalent R203H mutation does not trigger the upregulated BMP signaling seen in human FOP. To investigate this unexpected molecular mechanism, we established: 1) a transgenic zebrafish line expressing mCherry-tagged human ACVR1 R206H under a heat-shock (HS) promoter; 2) a transgenic zebrafish line expressing HS inducible mCherry-tagged zebrafish Acvr1l R203H; and 3) zebrafish expressing Acvr1l R203H under their endogenous promoter. The mCherry-tagged lines expressed red fluorescence in heat-shocked zebrafish. Endogenous R203H zebrafish were identified by PCR amplification, followed by Hha1 restriction enzyme digestion. Wild-type Acvrl1 contains an Hha1 restriction site at amino acid 203 and digests into 2 fragments, while the R203H mutant Acvr1l does not and remains uncut. To investigate BMP signaling, we conducted western blot analysis to detect phosphorylated Smad1/5 (pSmad1/5) expression in each zebrafish FOP line. Results showed HS R206H lines expressed higher levels of both mCherry and pSmad1/5 compared to controls. Conversely, HS R203H zebrafish expressed mCherry, but only very weak pSmad1/5 expression. Endogenous R203H lines produced similar weak pSmad1/5 expression. This novel finding suggests that amino acid differences between human ACVR1 R206H and zebrafish Acvr1l R203H may be responsible for the differences observed in BMP signaling.

Enabling Hepatoxicity Assays in HepG2 Spheroids Using Centrifugal Hydrogel Synthesis

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Daisy Belmares-Ortega*[1]and Rama Gullapalli[2]
[1]The University of New Mexico, [2]The University of New Mexico

Abstract: Hepatotoxicology assays are fundamental elements in drug development studies. Modern platforms to investigate hepatotoxic effects of drugs and environmental xenobiotics are increasingly in demand. Existing cell scaffolding models are two-dimensional and do not offer a physiologically relevant environment exhibited in spheroid cell culture. The two major experimental components of this project include the generation of the centrifuge-based microdroplets for the embedding of model liver cell lines of HepG2, and the utilization of biomarker assays to analyze effects of toxicants of heavy metal exposure including cadmium. Production of microdroplets made of calcium-alginate involved systematic testing of optimal centrifugal rotation speeds (50-1,250 rpm) across 1, 2, and 3 percent weight by volume alginate

viscosities into a calcium chloride catch solution. Alginate solutions were prepared using sodium alginate powder from brown algae and calcium chloride (Sigma-Aldrich). HepG2 cells have been encapsulated at ideal density ranges of 2,500-5,000 cells per microliter of sodium alginate and DMEM media composite. HepG2 spheroids will be cultured inside a Rotary Cell Culture System (RCCS). Upon one week after incubation, cell viability assays will be conducted with Alamar Blue protocol. CYP450 gene expression will be measured using qPCR including metabolic assessment of CYP450 functionality using 4-Hydroxycoumarin fluorescence to compare results to two-dimensional cell culture. Cells and tissues function in a three-dimensional space across all organisms. Cell scaffolding in the third dimension presents an optimal option to assess biologically significant outcomes of hepatoxicity testing platforms. We developed a novel, low-cost approach to create a relevant hepatotoxicity analysis method.

Characterization of Transcript Wide Genetic Associations to Systemic Lupus Erythematosus and Rheumatoid Arthritis

Discipline: Life Sciences
Subdiscipline: Genetics

Adriana Payan-Medina*[1]and Ayshwarya Subramanian [2]
[1]University of Utah, [2]Broad Institute of MIT and Harvard

Abstract: Autoimmune diseases, where the immune system’s response to self-antigens induces tissue damage or dysfunction, impact 23.5 million Americans. Systemic Lupus Erythematosus (SLE) and Rheumatoid Arthritis (RA) are two highly prevalent autoimmune diseases that cause widespread inflammation in affected tissues or joints respectively. Understanding the fundamental mechanisms modulating autoimmune disease is imperative to optimize treatment and prevention strategies. Though these autoimmune diseases cause adverse health morbidity, their direct disease origins are unknown. However, several studies have hypothesized that potential mechanisms of autoimmune disease could include genetic factors. We aim to compare the transcriptomic profiles of diseased and control cells to elucidate genetic associations of autoimmune disease. Specifically, we aim to use single-cell RNA sequencing (scRNA-seq) data from RA and SLE cases and controls to compare differential gene expression (DGE) across each autoimmune disease. The scRNA-seq data from each autoimmune disease was UMAP computed to cell subtypes. Pseudobulk profiles on each cell subtype were derived to leverage bulk RNA sequencing DGE analysis methods. DGE analysis on pseudobulk profiles identified upregulated genes between diseased and non-diseased cell types. Through this DGE analysis across SLE and RA autoimmune diseases, we anticipate that we will gain a more thorough understanding of the genetic factors that affect autoimmune disease incidence. Characterization of the underlying transcriptomic mechanisms in autoimmune disease guides the direction for the development of a more personalized approach to disease screening and treatment.

Exploring Microfungal Diversity on Impatiens marianae at Las Cruces Biological Station in Costa Rica

Discipline: Life Sciences
Subdiscipline: Microbiology

Julianna Harden*[1]and Terry J. Torres-Cruz [2]
[1]Howard University, [2]The Pennsylvania State University

Abstract: Fusarium is a diverse group of microfungi notorious for affecting agricultural crops. Even though Fusarium is widely known for its pathogenic behavior, recent studies have identified species in this group with environmental benefits. There is an abundance of Impatiens marianae (Balsaminaceae) at the Las Cruces Biological Station in San Vito, Costa Rica. Although this plant is distributed worldwide, there are no studies on its fungal diversity. Our study explores the diversity of microfungi on the leaves, rhizomes, and roots of I. marianae in a selectively logged primary forest at the Las Cruces Biological Station aiming to discover potential new species of Fusarium with novel applications, such as mycoremediation. Full plants were collected in triplicate from three different sites at Las Cruces. Tissues (roots, rhizomes, and leaves) were washed with tap water, rinsed 3x with distilled water, and five 2x2mm pieces of each tissue were put onto Nash-Snyder Agar and incubated at room temperature. Pure cultures were transferred to PDA. A total of 106 fungal cultures have been isolated, 36 from roots, 33 from rhizomes, and 37 from leaves; representing 24 morphotypes. Isolates will be identified morphologically to make inferences about their distribution in I. marianae and identify potential novel species that could have potential for mycoremediation. It is vital to explore fungal diversity in underexplored regions of the world. Species discovery could lead to groundbreaking scientific information being revealed that is potentially useful for conservation decision making and environmental bioremediation efforts.

Investigation of Opioid Transporters in the Blood-Retina Barrier

Discipline: Life Sciences
Subdiscipline: Biology (general)

Glenda Torres Lopez*[1], Jozsef Vigh [2], Casey-Taylor Berezin[3]
[1]University of Northern Colorado, [2]Faculty/Staff, [3]PhD Candidate

Abstract: As of 2020 opioids were the leading cause of overdose deaths (68,630) in the US. In order for opioids to exert their analgesic and addictive effects, they must first reach their relevant brain targets. Opioid delivery to the brain is mediated by ATP-binding cassette (ABC) transporters expressed at the blood-brain barrier (BBB). Systemically delivered opioids have also been shown to accumulate in the vitreous humor of the eye, which is separated from circulation by the blood-retina barrier (BRB). In the retina, the expression of two ABC transporters - P-glycoprotein (P-gp) and Multidrug resistance protein 2 (Mrp2)- have been confirmed by quantitative reverse-transcription PCR (qRT-PCR). Importantly, vitreous samples are used in forensic evaluation of opioid metabolites in cases of suspected overdose. The aim of this study was to confirm the expression of P-gp and Mrp2 at the BRB with immunohistochemistry in vertical cryosections of the mouse retina, using fluorescent confocal microscopy. The blood vessels of the BRB were labeled with an antibody against occludin, a tight junction marker abundantly expressed in blood vessels. The P-gp antibody labeled retinal blood vessels and colocalized with occludin, as determined by Costes' approach. However, although the Mrp2 antibody also produced immunolabeling of retinal cells, that label was never associated with blood vessels. In conclusion, in the mouse retina, opioid transport through the BRB is primarily mediated by P-gp, and not Mrp2.

Detection of Related Genes in Ocular Melanoma Using cBioPortal

Discipline: Life Sciences
Subdiscipline: Biology (general)

Nicole Rivera Acevedo*[1], Nicole Rivera Acevedo [2], Elizabeth Padilla, Ph.D.[3], Bianca Lopez Rosado[4], Nathan Reyna, Ph.D. [5]
[1]InterAmerican University of Puerto Rico Aguadilla Campus, [2]InterAmerican University of Puerto Rico Aguadilla Campus, [3]InterAmerican University of Puerto Aguadilla Campus, [4]InterAmerican University of Puerto Rico, [5]Ouachita Baptist University

Abstract: Uveal melanoma is a disease in which cancerous (malignant) cells are found in the part of the eye called the uvea. When uveal melanoma becomes metastatic, treatment options are limited and often extrapolate from medications for cutaneous melanoma, even though patients with uveal melanoma are routinely excluded from clinical trials. The aim was to investigate genes involved in uveal melanoma by using the cBioPortal for Cancer Genomics open-source database for the interpretation of clinical genomic data. We hypothesize that the genes GNAQ, GNA11, BPA1, SF3B1 and EIF1AX manifest Uveal Melanoma. TCGA's Firehose Legacy was identified as a research paper since they studied over eighty samples, providing a comprehensive analysis. Through the selection, the query of the genes with the highest amount of mutation and frequency related to Uveal/Ocular Melanoma was established: GNAQ, GNA11, BAP1, SF3B1 and EIF1AX. The results showed that GNAQ and GNA11 exhibited higher mutation percentages with a 49.37% and a 45.57%. Also GNA11 was the only one to reflect an amplification frequency, SF3B1 was the only one that exhibited the Deep Deletion frequency, and EIF1AX exhibited a low mutation percentage with a 12.5%. Through the mutations that cover the various protein domains, we derive that they are linked to the development of uveal melanoma. Therefore, the mutated or altered versions of the GNAQ, GNA11, BPA11, SF3B1 and EIF1AX genes contribute to the manifestation of uveal melanoma and that there is no literature on the gene pathways since they have not yet been classified as oncogenic genes.

Modulation of DEGS1 Exon 2 Identity Using Antisense Oligonucleotides

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Martin Gutierrez*[1], Victor Tse [2], Guillermo Chacaltana[3], Arcelia Gonzalez Jimenez[4], Michael Stone [5], Jeremy Sanford[6]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz, [4]University of California, Santa Cruz, [5]University of California, Santa Cruz, [6]University of California, Santa Cruz

Abstract: Pre-mRNA splicing is critical for accurate gene expression of most human protein-encoding genes. Many disease-causing mutations frequently induce aberrant splicing. We recently identified a mutation near the 5' splice site of DEGS1 exon 2. This mutation correlates with aberrant mRNA transcripts in patients with hypomyelination leukodystrophy. Splicing reporter assays demonstrated this mutation induced aberrant splicing in vivo. Antisense oligonucleotides (ASOs) can correct aberrant splicing and ameliorate human inherited diseases. We screened a library of ASOs to identify splicing regulatory elements in DEGS1 exon 2. This approach revealed splicing enhancers and silencers that influence splicing efficiency. We used chemical probing to determine how the mutation impacts DEGS1 pre-mRNA structure. MAP-Seq revealed substantial differences in accessibility of the 5' and 3' ss in the mutant. Our results illuminate unexpected impacts of disease-causing mutations on RNA structure and function.

Utility or Decor: The Influence of Plant Communities on Painted Turtle (Chrysemys picta) Habitat Use

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Paige Boban*[1]and Beth Reinke [2]
[1]Northeastern Illinois University, [2]Northeastern Illinois University

Abstract: Plant and animal biodiversity is under threat due to our rapidly changing climate. Understanding the role of plant communities in animal habitat selection and use can inform strategies for mitigating declining animal populations. The painted turtle is a widespread freshwater species in North America that inhabits a variety of habitats. Visual surveys by kayak were used to determine how painted turtle space occupation was impacted by vegetation in a northern Wisconsin lake system. We found that the space occupied by turtles could be predicted by the distribution of key plant species and this relationship changed throughout the active season. Plant communities can strongly influence the spatial distribution and overall behavior of freshwater turtle populations that are declining due to habitat loss and climate change and should be considered when making conservation decisions.

Genetic Mechanisms of Aggression in Three-spined Stickleback

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Meg Tucker*[1], Dr. Alison M. Bell [2], Colby Behrens[3]
[1]Parkland College, [2]University of Illinois, Urbana-Champaign, [3]University of Illinois, Urbana-Champaign

Abstract: The scientific breakthroughs of genome sequencing pushed modern biology closer to understanding the genetic and molecular basis of complex traits. By capitalizing on evolutionary divergence of behavioral traits within ecotypes of the same species, we are able to identify the genetic mechanisms influencing aggression, a trait which directly contributes to organismal fitness and survival. To address the genetic basis of aggressive traits, my lab uses the three-spined stickleback, (Gasterosteus aculeatus). In this species, males build nests and defend established territory from intruding males through behaviors like biting. Aggression in three-spined stickleback has been extensively studied by early ethologists. Two ecotypes of Nova Scotian stickleback, which vary extensively in a variety of traits, have also been reported to vary in aggression. Due to the polygenic and complex genetic architecture of aggression, one tactic to examine its underlying genetic mechanisms is using quantitative trait locus (QTL) mapping. Our on-going project uses QTL mapping to associate aggressive behaviors with genomic loci. To do this, we generated a reciprocal cross of F1 hybrids in 2019, followed by an F2 mapping population in 2020. In 2021, I phenotyped the aggressive behaviors of n=150 individual male F2 fish in two successive trials. Upon completion of assays, DNA was extracted from collected tissue samples, and processed for RAD-seq. Preliminary results indicate aggression has high repeatability (W=0.454) and that the phenotype is amenable to QTL mapping.

Interannual Patterns of Species Diversity in Guánica Dry Forest

Discipline: Life Sciences
Subdiscipline: Environmental Science

Yamilet Feliciano-González*[1]and Stefanie L. Whitmire [2]

[1]University of Puerto Rico at Arecibo, [2]Clemson University

Abstract: Guánica Dry Forest, located on the southern coast of Puerto Rico, is one of the most extensive tropical dry coastal forests in the world with 8,630 acres. This forest provides important habitat for a wide variety of species. However, because of the low rainfall (~840 mm/yr), the changes in climate, and increasing disturbance (hurricanes) understanding what vegetation needs to adapt to extreme conditions. In this study, we retrieved data from NSF's National Ecological Observatory Network (NEON) to answer questions about the interannual patterns of plant biodiversity in Guánica, specifically what abiotic or biotic factors contribute to these patterns. Annual species presence data was downloaded, processed, and Shannon and Simpson diversity indexes were calculated for all vegetation plots (10m 2 and 1m 2) from 2015 to 2020. We also retrieved and are processing NEON data related to precipitation, soil moisture, and soil biogeochemistry to analyze the biodiversity patterns. As expected, Guánica has high plant diversity, but it does vary across years. The highest Shannon diversity measured was in 2018 (H'= 4.15 ± 0.05) and lowest in 2015 (3.47 ± 0.04) in the 10m 2 plots. Higher diversity seems to be tied to higher rainfall during the rainy season of the year previous to the presence measurements. Thus, the higher diversity in 2018 is likely due to the high rainfall that occurred in 2017, likely due to hurricane María. Soil moisture data will be examined to verify the role of water availability in changes to community composition and biodiversity in Guánica.

Investigating the role of phosphorylation of the synaptonemal complex protein SYP-1 during meiosis in the nematode Pristionchus pacificus

Discipline: Life Sciences
Subdiscipline: Genetics

Paloma Pérez*[1], Renzo S. Adilardi PhD[2], Abby F. Dernburg PhD[3]
[1]University of California, Santa Cruz, [2]Department of Molecular and Cell Biology, University of California, Berkeley; Howard Hughes Medical Institute, [3]Department of Molecular and Cell Biology, University of California, Berkeley; Howard Hughes Medical Institute

Abstract: Sexual reproduction enables organisms to produce genetically diverse offspring, a significant evolutionary advantage. This genetic diversity arises through the specialized cell division process of meiosis, in which a single cell divides twice to produce gametes, each containing one set of chromosomes that carry genetic information. During meiosis, each chromosome pairs with its homolog, the matching copy from the other parent. Homologous chromosomes are held together by the synaptonemal complex, a protein assembly that also regulates genetic recombination. A major open question is how meiotic cells regulate the formation of the synaptonemal complex and ensure that all chromosomes undergo synapsis. Recent studies in the nematode C. elegans have shown that phosphorylation of the synaptonemal complex protein SYP-1 is important for this regulation. Once phosphorylated, SYP-1 recruits a Polo-like kinase (PLK-2) to the synaptonemal complex, and thus promotes progression of the meiotic cell cycle. I am testing whether this regulation is conserved in the distantly related nematode Pristionchus pacificus . While P. pacificus shares many anatomical features with C. elegans , the regulation of meiosis is very different between the two species, and comparative studies may help reveal the fundamental, shared aspects of meiotic regulation. Using CRISPR/Cas9, I am engineering SYP-1 mutants that are unable to be phosphorylated. I plan to analyze their fertility and the frequency of chromosome missegregation during meiosis. I will also examine the effects of these mutations on synapsis and meiotic progression through

cytological analysis. Understanding these dynamics will advance our knowledge of meiotic regulation and its evolution.

Isolation of single cell cardiomyocytes from adult zebrafish atria

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Jade Underwood*[1], Natalia Torres [2], Martin Tristani-Firouzi[3], Christopher Kauffman[4]

[1]Fort Lewis College, [2]University of Utah, [3]University of Utah, [4]University of Utah

Abstract: Zebrafish are an emerging model to study heart development and cardiovascular disease due to its functional similarities to human hearts. Zebrafish presents additional advantages as an animal model in cardiac research, including fast reproduction, transparent embryos, and a capability for genetic manipulation. The most commonly used protocols for cardiomyocyte isolation from adult zebrafish heart use ventricle or whole heart. Our objective was to design a protocol to isolate single cardiomyocytes from zebrafish atria that could be then used to study cell functionality related to atrial disorders such as atrial fibrillation. We explanted hearts from adult zebrafish and separated the ventricles and atria. Atria were incubated in the cardiomyocyte isolation solution from the Pierce Primary Cardiomyocyte isolation kit at 32ºC. To find the optimal digestion time, we varied the incubation time in different samples from 30 to 45 minutes, in 5 minutes increments. A buffer containing 10% fetal bovine serum was used to stop the enzyme activity. Individual cells were obtained by gently mechanical disruption using a pipette tip. An identical protocol was applied to ventricles. The resulting cardiomyocytes were stained with an antibody targeting myosin (MF20, DSHB) to evaluate the preservation of the myofilaments. We found 35- and 40-minutes incubation to be the optimal time for the atria and ventricle respectively. The cells had the reported shape and a preserved myofilament structure indicative of cardiomyocytes. These single cells isolated from adult zebrafish atria can be used in future functional studies to investigate mechanisms behind cardiovascular disease, such as atrial fibrillation.

Functional analysis of ZNF143 in zebrafish craniofacial development.

Discipline: Life Sciences

Subdiscipline: Developmental Biology

Isaiah Perez*[1], Anita M. Quintana, Ph.D. [2], Nayeli G. Reyes-Nava[3]

[1]The University of Texas at El Paso, [2]The University of Texas at El Paso, [3]The University of Texas at El Paso

Abstract: ZNF143 is a sequence-specific DNA binding protein that modulates the expression of protein-coding genes and small RNA molecules. In humans, ZNF143 interacts with HCFC1, a transcriptional cofactor, to regulate the expression of downstream target genes, including MMACHC , an enzyme involved in cobalamin (cbl) metabolism. Mutations in HCFC1 or ZNF143 cause a multiple congenital anomaly syndrome characterized by abnormal cbl metabolism, intellectual disability, seizures, and mild to moderate craniofacial abnormalities. However, the mechanisms by which ZNF143 mutations cause disease are unknown. Defects in metabolism and craniofacial development are hypothesized to occur as a result of decreased expression of MMACHC . Yet, whether the abnormal craniofacial development in patients with ZNF143 mutations is directly related to MMACHC expression is currently unknown. Therefore, in the present study, we implemented a loss of function analysis to uncover the function of ZNF143 in craniofacial development using the developing zebrafish. The knockdown of znf143b, one zebrafish paralog of ZNF143, caused a phenotypic spectrum with different severity, which included shortened and cleaved Meckel’s cartilage, loss of ceratobranchial arches, and a distorted ceratohyal. In tandem, preliminary data suggest downregulation of mmachc in knockdown animals utilizing quantitative real-time PCR. We hypothesize the abnormal craniofacial development is associated with the downregulation of mmachc ; consequently, providing a mechanism by which mutation of ZNF143 causes mild to moderate facial dysmorphia in humans.

Indigenous Native American Representation in National Park Documents

Discipline: Life Sciences
Subdiscipline: Environmental Science

Christopher Kalman*[1], Rachael Vannatta [2], Rachael Vannatta[3]
[1]The Ohio State University, [2]The Ohio State University, [3]The Ohio State University

Abstract: Western paradigms have long dominated natural resource management discourse. Since the advent of national parks in the U.S., the removal of Indigenous populations from these spaces has led to a disregard for Indigenous knowledge, lack of communication between stakeholders, and jurisdictional fragmentation of vulnerable ecosystems. As other countries have institutionalized the significance of Indigenous populations and knowledge in natural resource management, it is unknown where the United States stands in attempts to reconcile Indigenous and Western ontologies, particularly through the National Park Foundation. The purpose of this research, through boundary work and co-management theories, is to examine the ways in which U.S. national parks collaborate with Indigenous populations, using qualitative content analysis and multi-value qualitative comparative analysis to code and interpret publicly available foundation documents. Though limited to the non-Indigenous perspective, this research will provide important insights into Western/Indigenous dichotomies, and, ultimately, how to better represent Indigenous interests in U.S. natural resource management.

Microscopy of GFP-Tagged HLH-25 Transcriptional Repressor in Caenorhabditis elegans at Different Stages of Development

Discipline: Life Sciences
Subdiscipline: Genetics

Leona Jafari*[1]and Casonya Johnson [2]
[1]James Madison University, [2]James Madison University / National Science Foundation

Abstract: HLH-25 is a transcriptional repressor found to phenotypically manifest reduced brood size, unfertilized oocytes, and abnormal gonad morphology in embryonic development of Caenorhabditis elegans (C. elegans). Overall, our goal is to understand the mechanisms by which HLH-25 regulates transcription, and previous studies examined HLH-25 expression driven by a transcriptional fusion of the HLH-25 promoter to Green Fluorescent Protein (GFP). While the transcriptional fusion provided details of the timing and location of the production of HLH-25 mRNA, other studies suggest that the protein may function in cells that do not produce the mRNA. My goal in this project is to use a translational fusion of the HLH-25 protein to GFP to determine where HLH-25 protein accumulates over the developmental life cycle of C. elegans , using confocal microscopy. These expression data will then be correlated with data from gene expression analysis to determine which genes are transcriptionally repressed by HLH-25 in different cells at distinct developmental stages.

The Effect of Mitomycin C and its Analog on Cell Cycle Arrest

Discipline: Life Sciences
Subdiscipline: Pharmacology

Hannah Tetreault*[1]and Shu-Yuan Cheng [2]
[1]CUNY John Jay College of Criminal Justice, [2]CUNY John Jay College of Criminal Justice

Abstract: Mitomycin C (MC) is an antibiotic with DNA alkylating properties and is used in chemotherapy to treat cancers with p53. Its analog Decarbamoyl mitomycin C (DMC), unlike MC, shows stronger effects on cancers with p53 mutation. MC and DMC form cross-linkages in DNA which stop DNA replication from occurring, but the cross-linkages have opposite stereochemistry. By stopping DNA replication, the cell cannot proliferate, which stops the growth of cancer. If MC and DMC stop cell division, then they could potentially be causing cell arrest at some point in the cell cycle. This study aims to see if Mitomycin C and Decarbamoyl mitomycin C, synthesized in Dr. Champeil's lab, cause cell arrest during the S-phase of the cell cycle. Changes in DNA replication during S-phase were detected by the Click-iT plus EdU assay using flow cytometry, in order to analyze the number of cells in each stage of the cell cycle after being treated with MC, DMC, or the negative control, methanol. The results showed that MC caused cell cycle arrest in the S phase for MCF-7 breast cancer (p53 proficient) cells and the G2 phase for MDA MB-468 cells. DMC appears to follow the same pattern, causing cell cycle arrest during the S phase for MCF-7, but G2 for MDA MB-468 triple-negative breast cancer cell (p53 mutation). Determining which phase of the cell cycle MC and DMC cause cell arrest could elucidate the discrepancies in the molecular pharmacological mechanism of MC and DMC in-vitro systems.

Genetic diversity and pattern of infection of Spiroplasma in the alpine ground beetle, Nebria ingens species complex

Discipline: Life Sciences
Subdiscipline: Genetics

Robert Hall*[1], Yi-Ming Weng [2], Sean D. Schoville[3]
[1]University of Wisconsin, Madison, [2]University of Wisconsin, Madison, [3]University of Wisconsin, Madison

Abstract: Insect endosymbionts have been found in more than half of insect species. The roles these microorganisms play in their host could vary from parasitism to mutualism but have not been well explored due to the high diversity of insects and their extremely heterogeneous life histories. In general, common endosymbionts, such as Wolbachia and Spiroplasma , could be beneficial to their host by increasing the number of offspring, or by increasing the resistance of their hosts against other parasites. Conversely, endosymbionts can cause male killing processes or post-mating cytoplasmic incompatibility in offspring, which could negatively impact the host population. Here we aim to understand the role of Spiroplasma sp. NR in their host—the Nebria ingens species complex—by scanning the prevalence of infection, genetic diversity, geographic distribution, and associating the infection rate with environmental factors as well as the physiological, morphological, and molecular characteristics of the beetles. Initial results show a relatively high (57%) and geographically widespread infection rate of Spiroplasma throughout the Nebria ingens species complex. Both host and microbe populations show a similar trend of gradual genetic divergence across geographical space, but Spiroplasma appears to have longer

dispersal distance. Also, findings show Spiroplasma in sympatric species of Nebria at different altitudes. Our next step will be to utilize Local PCA, sNMF functions, and geographic distribution to elucidate their genetic structures. Our ongoing research utilizes population genomic variation of all species, including the beetle mtDNA, to identify inheritance patterns and assess the ecological role of Spiroplasma in this insect host.

Exploring Imatinib's Affinities and Specificities for Tyrosine Kinases Using Molecular Dynamics Simulations

Discipline: Life Sciences
Subdiscipline: Biochemistry

William Troxel*[1], Chia-en Chang [2], Jianan Sun[3], Talant Ruzmetov[4]
[1]University of California, Riverside, [2]University of California, Riverside, [3]University of California, Riverside, [4]University of California, Riverside

Abstract: Computational proteomics lets us study drug-protein interactions in ways conventional assays cannot. Most drugs target one protein, but some affect multiple proteins. Imatinib inhibits the ABL kinase to treat chronic myeloid leukemia, and while protein assays show it inhibits other kinases to treat different illnesses, the atomistic mechanisms are not known. Although complex structures are available, binding dynamics and protein functions are not shown. Imatinib has differential kinase affinities, ABL and SRC share 50% similarity, but a 3000x affinity difference. In contrast, ABL and KIT have strong imatinib affinities despite sharing 30% similarity. My objectives are to model free protein and imatinib-bound states for ABL, KIT, and SRC kinases using 100 ns Molecular Dynamics (MD) simulations to survey the non-covalent interactions and protein conformational dynamics over time. Root-mean-square-deviation and fluctuation (RMSD and RMSF) analyses show the systems equilibrate by 40 ns, but the flexible regions differ for the three systems. This is important for kinase activity as proteins need to be flexible to fold into the correct conformations for cellular signaling. Key binding-site salt bridges form in the ABL complex and break in the KIT complex. ABL has one hydrogen bond (H-bond) between MET84 and imatinib for 20.4 ns. KIT has three H-bonds with imatinib, one between CYS109 for 16.8 ns and both oxygens of GLU76 for 11.4 ns. SRC has no major H-bonds with imatinib. These findings show that imatinib’s multi-kinase promiscuity cannot solely be explained by general protein homology and requires a more nuanced analysis of non-covalent interactions.

Genetic Barcoding of All Amphidromous and Freshwater Nerite and Thiarid Snails Native to Guam

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Louise Pascua*[1]and Dr. Daniel P. Lindstrom [2]
[1]University of Guam, [2]University of Guam

Abstract: Streams on Guam are home to nineteen putative species of amphidromous gastropods which are presumed to be native. Of these nineteen, fourteen belong in the family Neritidae (Clithon corona, C. oualaniensis, C. sowerbiana, Narita auriculata, N. petitii, N. pulligera, N. squamaepicta, N. turrita, N. variegata, Neritodryas subsulcata, Septaria cumingiana, S. lineata, S. janelli and S. porcellana) and five belong in the family Thiaridae (Tarebia granifera, Melanoides tuberculata, M. riquetii, Stenomelania plicaria and Thiara scabra). None of these species had been analyzed and confirmed using genetic barcoding techniques. The goal of this project was to remedy this important information gap which will open up myriad research and conservation avenues. It is hypothesized that all these species are native to Guam and may even represent presently undescribed cryptic endemic species. Ten individuals of each species were collected from various locations in Guam's southern streams. All individuals were photo-documented, biopsied, and preserved. Genomic DNA targeting the Cytochrome-Oxidase I gene was extracted, purified, PCR amplified and sequenced to produce genetic barcodes which were then compared to those in GenBank to confirm or refute species affinities. In the course of genetic barcoding all specimens, two cryptic species were identified (Neritina delestennei and N. stumpffi). Confirmation of all species present in Guam's streams and their native and/or endemic status is essential before planned future population genetics research and conservation planning can be conducted.

Ground dwelling invertebrate community responses to bison and prescribed fire management in tallgrass prairies

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Maricela Alaniz*[1], Nicholas A. Barber[2], Samantha Padilla[3], Holly P. Jones[4], Sheryl C. Hosler[5], Melissa Nelson[6]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University, [4]Northern Illinois University, [5]University of Illinois at Chicago, [6]Northern Illinois University

Abstract: Disturbance events are important drivers of ecosystem function and can play consequential roles in shaping ecological communities. In the central U.S., fire and grazing by bison are disturbances which historically shaped tallgrass prairies. These disturbances have been greatly disrupted but remain important management tools in the little prairie habitat that remains or has been restored. Fire and grazing effects on plant communities and vegetation-dwelling invertebrates are well studied, but less is known about their effects on ground-dwelling invertebrates. We examined how bison grazing and prescribed fire affect the abundance, diversity, and community composition of ground-dwelling invertebrate groups in restored and remnant prairies. We collected ground-dwelling invertebrates using pitfall traps in May and June of 2017 and 2018 and identified them to order or family. Surprisingly, invertebrate diversity was reduced when bison were present and was unaffected by fire or the fire–bison interaction. Bison, and to a lesser extent fire, caused differences in community composition while individual invertebrate groups varied in their responses to both disturbances. Bison presence may amplify the abundances of the most abundant groups, such as ground beetles and dung beetles, that outcompete other invertebrates and reduce diversity. Understanding these effects may help land managers choose management strategies that promote desirable invertebrate-driven ecosystem processes.

Defining the Role of Mitochondrial Dynamics in Regulating Pancreatic Ductal Adenocarcinoma Cell Sensitivity to ERK Inhibition

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Amber Amparo*[1], Kristina Drizyte-Miller[2], Claire Gates[3], Kirsten L. Bryant[4], Channing J. Der[5]

[1]The University of North Carolina at Chapel Hill, [2]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA, [3]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA, [4]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA; Department of Pharmacology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA, [5]Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA; Department of Pharmacology, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is driven by oncogenic activation of KRAS in over 95% of patients. Recent evidence suggests that mutant KRAS activation rewires cancer cell metabolism, altering mitochondrial morphology and function. Specifically, activation of the downstream RAF-MEK-ERK effector signaling pathway leads to phosphorylation of mitochondrial fission protein DRP1, which drives mitochondrial fragmentation to support PDAC growth. In contrast, pharmacological inhibition of ERK signaling, using a selective ERK1/2 inhibitor (ERKi, SCH227984), causes mitochondrial fusion and inhibits PDAC cell growth. However, the mechanistic basis by which mitochondrial fragmentation supports PDAC proliferation remains unknown. Furthermore, it is unclear whether mitochondrial fusion is required for ERKi-mediated growth suppression. We hypothesized that preventing mitochondrial fusion by silencing mitochondrial fusion proteins OPA1 and MFN1 will yield resistance to inhibition of ERK signaling. To test this, we used two unique siRNAs targeting OPA1 or MFN1, which caused a hyper-fragmented mitochondrial phenotype. Interestingly, we found that loss of OPA1 or MFN1 in Pa14C cells prevented ERKi-induced mitochondrial fusion and increased the GI50 concentration of ERKi by ~40% compared to control-treated cells. This suggests that PDAC cells with hyper-fragmented mitochondria may be slightly resistant to ERKi. However, the other PDAC cell line tested (HPAC) displayed, on average, no significant changes in the GI50 concentration of ERKi despite having a hyper-fragmented mitochondrial phenotype. Future studies are focused on further characterizing the impact of altered mitochondrial dynamics on PDAC cell sensitivity to inhibition of KRAS downstream effectors.

Fibronectin Exposes a Targetable DHPS/SLC3A2 Vulnerability that Can Be Leveraged to Decrease Cytoplasmic Levels of eIF5A1/2 and Proliferation/Survival in TNBC

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ranel Tuplano*[1], Jonathan Kelber[2], Cameron Geller[3], Joanna Maddela[4], Joseph Cantor[5]
[1]California State University, Northridge, [2]Professor of Biology, [3]Ph.D Candidate, [4]Research Assistant, [5]Assistant Professor of Medicine

Abstract: Metastatic breast cancer is the leading cause of cancer-related deaths in women in the United States decreasing survival to ~20%. This emphasizes the need to investigate mechanisms that govern metastasis in triple-negative breast cancer (TNBC). Our lab previously found that eukaryotic initiation factor 5A 1/2 (eIF5A1/2) regulates PEAK1, a pro-tumorigenic protein, which acts as a non-canonical switch for TGFβ, a hallmark of epithelial to mesenchymal transition. Our 2019 BBRC publication demonstrated that the pharmacological inhibition of eIF5A1/2 with GC7 blocking TGFβ/fibronectin induced metastasis to the lungs. Moreover, intratumoral heterogeneity is known to confer treatment resistance. We then assessed the effect of genomic alteration of eIF5A1/2 pathway markers and heterogeneity markers. We discovered a correlation between elevated solute carrier 3A2, SLC3A2, and decreased survival in TNBC patients with

amplified SMAD3, a TGFβ transcription factor. We hypothesize that SLC3A2 and eIF5A1/2 cooperatively promote tumorigenesis in TNBC. We conducted immunofluorescence to assess the subcellular localization where we discovered TNBC eIF5A1/2 and SMAD3 shift localization to cytoplasmic and nuclear, respectively. After performing Flow Cytometry and analyzing TNBC cell cycle profile, we found SLC3A2 to be important in cell viability and proliferation. Ongoing work aims to observe 3D formation and aggregation as well as cyclic immunofluorescence for intratumoral heterogeneity of TNBC in association with eIF5A 1/2 and SLC3A2. This work has the potential to identify possible therapeutic approaches to inhibit TNBC progression.

The Role of ELF4 in T-cell Immunity and Autoinflammation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Faiad Alam*[1], Molly Bucklin [2], Carrie Lucas[3]
[1]Yale University, [2]Yale University, [3]Yale University

Abstract: Autoinflammation occurs due to a dysregulated inflammatory response that can result in diseases such as Inflammatory Bowel Disease (IBD) and other forms of colitis. The ELF4 gene encodes an ETS transcription factor that we have previously demonstrated to be a key regulator in the inflammatory capacity of several T-cell lineages; however, mechanisms are still unknown. Our lab strives to find novel ELF4 variants in IBD patients and explore how ELF4 impacts inflammatory regulation in T helper type 1 (Th1) cells. Our prior discovery of a novel autoinflammatory disorder, Deficiency in ELF4, X-linked (DEX), revealed that ELF4 is required in humans to protect from mucosal inflammation and inflammatory bowel disease-like symptoms. To validate loss-of-function mediated by genetic variants in ELF4, we used a luciferase reporter assay and Western blotting. We found that variants in the ETS DNA-binding domain or those that cause a frameshift significantly hamper transcription factor activity of ELF4, despite robust protein expression detected by the Western Blots. In addition, we used mice genetically engineered to delete ELF4 from T cells (Elf4-floxed; CD4-cre mice) and found that splenic T cells produce elevated interferon gamma (IFNg), an inflammatory cytokine, in supernatants after in vitro Th1 differentiation, highlighting increased inflammatory response. Mechanisms for upregulated cytokine expression in Th1 T-cells are currently being defined. Ultimately, our investigation of the ELF4 gene can provide insight into previously unknown inflammatory processes.

wnt16 is necessary for zebrafish spine mineralization and notochord morphology

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Maria Rojas*[1], Weishene Joyce Tang [2], Ronald Young Kwon[3]
[1]University of Washington, [2]University of Washington, [3]University of Washington

Abstract: Understanding how genetic variation contributes to skeletal traits is critical in order to better understand the underlying mechanisms of musculoskeletal diseases. A previous genome wide association study identified the CPED1-WNT16 locus as a region harboring genetic variants that are co-associated with bone mineral density (BMD) and total-body lean tissue mass in children. A recent study by Watson et al. (2021) revealed that wnt16 w1001 zebrafish (Danio rerio) mutants have reduced vertebral bone mass. This study also found that wnt16 is expressed in the developing notochord; however, the mechanism by which the wnt16 w1001 mutant allele alters vertebral bone mass is unknown. We hypothesized that the wnt16 w1001 allele is a null allele, and that wnt16 acts through the notochord to influence zebrafish spine development. To test this, we isolated wnt16 w1008 and wnt16 w1009 alleles with predicted loss-of-function in wnt16 and compared the effects of these alleles with wnt16 w1001 on spine development. We found that wnt16 w1001 mutants exhibited reduced and delayed spine mineralization, as well as a shorter and more slender notochord. Moreover, similar alterations were found in wnt16 w1008 and wnt16 w1009 mutants, supporting the notion that all three alleles are null alleles. Our studies suggest that loss of wnt16 alters spine mineralization dynamics and notochord morphology. Together, these findings could have relevance to understanding how genetic variants act through WNT16 to influence musculoskeletal traits in pediatric populations.

Competition in A. aegypti according to size and food type

Discipline: Life Sciences
Subdiscipline: Biology (general)

Melanie Szasz*
Illinois State University

Abstract: In mosquito larvae, competition between individuals for resources may result in density-dependent effects on adult body size. We define synchronous hatching as individuals of the same age who possess similar competitive abilities, while asynchronous hatching as individuals of different ages who possess different competitive abilities. We want to test whether or not the asynchronous individuals are more efficient at obtaining food. We hypothesize that synchronous and asynchronous hatching has an effect on the competition in the A. aegypti mosquito species. This experiment utilized small vials to contain mosquito larvae, and after pupating, were transferred to micro-capsules to allow pupae to emerge. We predict that the results will show a difference in the effects of competition, such as delayed emergence or varying adult size. Specifically, we predict that there is greater competition occurring under asynchronous hatching conditions. My underlying prediction is that asynchronous hatching will have a greater impact on competition because individuals who are larger will dominate the majority of the food due to survival instincts. This is relevant as mosquitos are present in different habitats where synchronous or asynchronous hatching may occur. This could lead us to more information about how to improve mosquito control.

A Camelid Nanobody Affinity Ligand for the Purification of Monoclonal Antibodies

Discipline: Life Sciences
Subdiscipline: Biochemistry

Yazmine Bedolla*[1]and Dr. Cory L. Brooks [2]
[1]California State University, Fresno, [2]California State University, Fresno

Abstract: Monoclonal antibodies have emerged as vital instruments in the diagnosis and treatment of diseases such as cancer. Despite their significant value in clinical and laboratory settings, the lengthy process and high cost associated with antibody purification continues to be a bottleneck in antibody processing. Nanobodies, a class of single domain antibodies, are the smallest known autonomous antigen-binding fragment (Fab). Nanobodies are characterized by high stability, solubility, and antigen affinity, which enables nanobodies to serve as an effective ligand for affinity chromatography. To facilitate an efficient and cost-effective method of antibody purification for IgG and Fab formats, we have constructed an affinity chromatography column using a nanobody specific for the human antibody kappa light chain. To fabricate this affinity column, the sequence for the nanobody (called Kappa VHH) was deduced from a published X-ray structure, and the gene produced by gene synthesis and cloned into pET22b(+) vector. The protein was extracted from the periplasm and purified using Nickel Affinity Chromatography. Purified Kappa VHH was covalently immobilized to aldehyde activated resin by reductive amination. Subsequently, purification of a human IgG by this affinity column was confirmed by SDS-PAGE. Further testing of this affinity column will evince its capability to purify all antibodies possessing a human kappa light chain. Ultimately, this Kappa VHH affinity chromatography column will serve to rapidly purify human monoclonal antibodies.

The Role of Arbuscular Mycorrhizal Fungi (AMF) in Sustainable Rice Farming

Discipline: Life Sciences
Subdiscipline: Biology (general)

Amber Born*[1]and Catherine Propper [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: In order to feed the growing population, many forms of agricultural intensification have been introduced into rice farming systems. One commonly used form of agricultural intensification is the application of pesticides to reduce pests and weeds. The impact of these chemical inputs may influence the plant microbiome, including arbuscular mycorrhizal fungal (AMF) symbionts in agricultural plants such as rice. Fungi like AMF form symbiotic relationships with crop plants and influence plant health and overall crop yields. Our research compares AMF and other fungal colonization abundances in rice plant roots from both organic and conventional fields. We hypothesize that different farming types will alter plant and AMF associations. We collected rice plant samples at different stages of growth from organic and conventional farms near Chico, California and scored them in the lab at Northern Arizona University. Preliminary data suggests that there is a significant stage-by-field type interaction, and that differences in agricultural practices may influence important microbiome-plant interactions. Further research into the impact of these shifts in AMF interactions in rice roots may lead to implementation of farming practices necessitating fewer chemical inputs while simultaneously having a neutral or even positive effect on yield.

Role of environmental variation in sky island pines in response to climate change

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Daniela Tirado Barva*[1]and Amy Whipple [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: It is important to understand how climate change will affect populations of trees so we can prevent their extinction. Southwestern white pine (Pinus strobiformis) is one of many species that are being threatened by climate change and has a limited distribution across the United States. The purpose of this study was to determine if drought decreases leaf mass per area (LMA) in sky island pines. Pines in these areas are more vulnerable because they are surrounded by desert and at the highest elevation and therefore cannot migrate. We focused on leaf mass per area (LMA) because it’s a morphological trait widely used as an indicator of healthy plant function. To understand the relationship between LMA and drought, seeds of Southwestern White Pine (SWWP) maternal trees from 60 different sites in New Mexico, Arizona, and the mountains of central Mexico were collected, then planted into two common gardens at the north rim of the Grand Canyon. These common gardens were used to minimize environmental variation to facilitate the investigation of genetic differences. Within these common gardens we used a high water and drought treatment to investigate phenotypic plasticity. Trees with maternal seeds from colder sites had higher LMA than those with maternal seeds from warmer sites. However, under the drought treatment, this difference among seed source temperatures disappeared. These results suggest that genetic variation will not matter as much for LMA if SWWP is experiencing drought. Additionally, these results present how sky island pines will respond to drought and climate change.

Differential expression of immediate early genes and neural correlates in severity of impulsive endophenotypes

Discipline: Life Sciences
Subdiscipline: Neurosciences

Brandon León*[1], Lee Peyton [2], Hesham Essa[3], Doo-Sup Choi[4]
[1]Mayo Clinic Department Molecular Pharmacology and Experimental Therapeutics Track, [2]Mayo Clinic Department of Molecular Pharmacology and Experimental Therapeutics, [3]Mayo Clinic Department of Molecular Pharmacology and Experimental Therapeutics, [4]Mayo Clinic Department of Molecular Pharmacology and Experimental Therapeutics

Abstract: Individuals exhibiting high waiting impulsivity, the inability to withhold a behavioral response to a rewarding stimulus, is a behavioral endophenotype and an established risk factor for many neuropsychiatric disorders. Immediate early genes (IEG) encode transcription factors that modulate neuronal physiology by regulating the expression of downstream target genes and thereby extensively used as indirect markers of neuronal activity. We aim to map the expression of IEGs in high and low impulsive mice to uncover brain-wide neural activation patterns since we hypothesized that different impulsive endophenotypes may be correlated with IEGs expression. To screen mice for impulsive endophenotypes, we employed the 5-choice serial reaction time task (5-CSRTT). After 5-CSRTT acquisition, mice were screened with 3 extended intertrial interval (ITI) sessions and stratified into high and low impulsive groups. Mice then performed an impulsivity test using a differential reinforcement of low rates of responding (DRL) operant schedule. Our results demonstrated that combining the 5-CSRTT and DRL operant schedule separates high and low impulsive mice. After sacrifice, we will serially section brains and stain for three IEGs: c-Fos, Egr1, and Egr2. Slices will be registered to the mouse Allen Brain Atlas for bioinformatic analysis. We aim to discover differentially activated and novel brain regions recruited between impulsive endophenotypes. We also aim to identify IEGs that uniquely distinguish high and low impulsive endophenotypes. These results will provide a map to uncover the unique circuits and IEG transcriptional programs that underly the mechanisms through which high impulsivity predisposes individuals to neuropsychiatric disorders.

Inference of bacterial pathogen load in US rivers from shotgun metagenomic sequencing

Discipline: Life Sciences
Subdiscipline: Biology (general)

Alyssa Cruz*[1], Derick Singleton [2], Mikayla Borton[3], Rebecca Daly[4], Kelly Wrighton [5], Christopher S. Miller[6]
[1]University of Colorado Denver, [2]University of Colorado Denver, [3]Colorado State University, [4]Colorado State University, [5]Colorado State University, [6]University of Colorado Denver

Abstract: Pathogenic bacteria from environmental sources pose a significant risk towards public health. Surface waters have been shown to contain potential human pathogens, but their sources and breadth of distribution remain understudied with modern methods. For example, wastewater treatment plant (WWTP) effluent points serve as potential reservoirs for human pathogens surviving the conventional activated sludge (CAS) method. CAS is a secondary removal step done to remove nutrients and organic material, but particle-pathogen interactions have shown to negatively affect the success of wastewater disinfection. Utilizing high-throughput DNA sequencing methods like metagenomics, large-scale microorganism identification can be completed. In addition, metagenomics provides the metabolic potential of these communities, and may offer insight into the way pathogens persist in surface waters. Using hundreds of surface water samples from the Genome Resolved Open Watersheds project, we are characterizing the pathogenic potential of samples taken from freshwater ecosystems impacted by a range of human activities, including WWTP effluent. High throughput metagenomics was conducted, the sequences were assembled, and protein-coding genes were inferred. Biological sequence similarities are being found using BLASTP against the Virulence Factor Database for medically significant pathogenic bacteria, and MetaPhlAn 3.0 is being used for microbial composition profiling. It is hypothesized that the microbial composition at sites most impacted by human activities will include larger amounts of bacterial pathogens. This study offers insight into microbial surveillance at scale for human pathogens in freshwater ecosystems.

An Examination of Marine Fungi’s Ability to Degrade Plastic Pollution

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ronja Steinbach*[1]and Anthony Amend [2]
[1]University of Hawaiʻi at Mānoa, [2]University of Hawaiʻi at Mānoa

Abstract: Plastics are a prevalent and persistent pollutant in the marine environment. With plastic production continuing to increase, finding ways to break down the plastics in the ocean is of great importance. Several fungi have demonstrated potential in degrading various types of plastic. Since plastics are widespread in the oceans, we hypothesized that fungi isolated from the marine environment would demonstrate high success rates in degrading polyurethane (PU) and polyethylene (PE). To test this, visual degradation assays were performed by inoculating 1% PU-medium and ultra-high-density PE-medium plates with 68 unique cultured fungal strains. The area of clearance of the fungus was measured periodically, to determine a relative degradation rate. Of the 68 fungal strains, 41 demonstrated the ability to degrade PU. Reliably determining the areas of clearance on the PE plates was not viable, so liquid medium containing pieces of PE were inoculated with the 68 strains and possible degradation will be determined using IR methods. The 11 fastest PU degraders underwent experimental evolution through serial inoculations into liquid media with increasing concentrations of PU. The original and “evolved” fungi were then raced, and preliminary results suggest that the “evolved” fungi degrade PU faster. Additionally, interactions between the 7 fastest degraders were tested by inoculating one plate with two different fungi, so that every isolate was grown with every other isolate. Competitively dominant species were of special interest for future work. Marine fungi show promise in helping remediate our oceans of plastic pollution.

The Migration of Microplastics: From urban creeks to the Pacific Ocean

Discipline: Life Sciences
Subdiscipline: Environmental Science

Benjamin-Rafael Mingoa*[1]and Christine Case [2]
[1]Skyline College, [2]Skyline College

Abstract: Microplastics originate from many urban sources, including the degradation of tires and synthetic fabrics. Our hypothesis is that these plastics wash into storm drains, where they flow into streams and accumulate in lakes and rivers before being deposited into the ocean. The aim of this study is to analyze the microplastic concentrations along an urban stream to determine the degree of plastic accumulation from city streets. Water samples were taken from different locations along Belmont Creek, which receives stormwater runoff from various streets along its three-mile course. These samples were filtered and selectively stained with Nile Red (0.01 mg/mL), which allows for fluorescent microscopy analysis to quantify microplastic concentrations as the creek flows to San Francisco Bay and the Pacific Ocean. Microplastics were found to be at a higher concentration (2.8-4 particles/mL) upstream in comparison to downstream (0.8-2 particles/mL), which indicates that microplastic concentrations decreased as the creek approaches San Francisco Bay. These findings, which were taken during the COVID-19 lockdown, are being validated due to the return of human activity in the area. We are currently investigating the hydrologic factors that might deposit microplastics prior to reaching the ocean. In addition, we are expanding our research to measure microplastics in the gastrointestinal tract (<40 particles/g) and gills (<10 particles/g) of local fish species.

Mouse Strain Variations in Drug-Induced Lung Stromal Responses

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Carlos Leon*[1], Zheng Gong [2], Qing Li[3], Jiayuan Shi[4], Wulin Zuo [5], Muneer G. Hasham[6], Lenny Shultz[7], Sheng Li[8], Guangwen Ren[9]
[1]The Jackson Laboratory Cancer Center, [2]The Jackson Laboratory Cancer Center, [3]The Jackson Laboratory Cancer Center, [4]The Jackson Laboratory Cancer Center, [5]The Jackson Laboratory Cancer Center, [6]The Jackson Laboratory Cancer Center, [7]The Jackson Laboratory Cancer Center, [8]The Jackson Laboratory Cancer Center, [9]The Jackson Laboratory Cancer Center

Abstract: Chemotherapy significantly improves the survival of cancer patients. However, the differential treatment responses remain a clinical issue. It is imperative to understand the molecular mechanisms underlying treatment failure among patients. It is not feasible to map the responsible genetic variants within millions of single-nucleotide polymorphisms in the human genome with a limited number of subjects and insufficient genomic information. Genetically diverse mice models overcome the limitations in clinical studies for host drug responses requiring genetic susceptibility and resistance factors. The host regenerative response upon chemotherapy “injury,” regarded as an intrinsic host mechanism to repair damaged tissues, may be exploited by tumor cells for their local recurrence or metastases. We used a lung injury model to determine how drug-induced lung stromal wound healing responses differed among eight inbred mouse strains (BALB/cJ, NSG, C57BL/6J, CH3/HeJ, CBA/J, SJL/J, A/J, and NOD/ShiLtJ). Upon either cisplatin or doxorubicin stimulation, the wound healing-associated genes Il-6 , Spp1 , Cxcl1, and Ccl2 were upregulated in lung stromal cells but showed a great variation across different strains. We performed single-cell RNA sequencing on the lung stromal cells and immune cells isolated from three selected mouse strains (BALB/cJ, C57BL/6J, and NOD/ShiLtJ) without and with doxorubicin treatment in vivo. The transcriptomic analyses revealed strain-specific and non-specific therapy-elicited gene signatures in the lung tissue cells. Our results signify an association between genetic backgrounds and drug-induced host responses in mice. Next, we aim to understand how genetic diversity impacts drug-induced lung tissue regeneration, lung inflammation, and post-therapy tumor relapse or lung metastasis.

Novel Genome wide Screen to Identify Translational Regulators and Potential Drug Targets

Discipline: Life Sciences
Subdiscipline: Genetics

Tara Antee*[1], Travis Lantz [2], Maria Barna[3]
[1]ChEM-H/IMA Postbac Researcher at Stanford University School of Medicine, [2]PhD Student in Chemical and Systems Biology at Stanford University School of Medicine, [3]Associate Professor in the Department of Genetics at Stanford University School of Medicine

Abstract: Dysregulated translation is a hallmark of a diverse range of diseases from neurological and congenital anemias (decrease in global protein synthesis) to cancer (increase in global protein synthesis). Mounting evidence suggests that these diseases can be treated by restoring global protein synthesis to a normal level. In fact, translational inhibitors are currently being used clinically to treat many different cancer types. However, translational activators have remained largely unexplored due to the lack of known protein targets to develop drugs against. To identify novel proteins that control global protein synthesis, we developed a screen that inhibits or activates expression of every gene, termed CRISPRi or CRISPRa respectively. Global protein synthesis will then be measured directly using a fluorescent reporter assay to determine the gene's role in global protein synthesis. By using this unbiased genome wide CRISPRi/a screen coupled with the reporter assay, we will not only identify novel targets for drug development but also to better understand the pathways, components, and mechanisms by which translation is regulated. A drug screen can then be completed on the targets from this screen to identify potential drugs that can be used to inhibit or activate these targets. The outcome of this project will uncover fundamental mechanisms responsible for regulating gene expression, global protein synthesis, and disease.

Role of the Substantia Nigra to Dorsal Lateral Striatum Circuit in the Acquisition and Maintenance of Voluntary Physical Activity is Sex-Dependent

Discipline: Life Sciences
Subdiscipline: Neurosciences

Nadja Brown*[1], Benjamin Greenwood [2], Margaret Tanner[3], Alyssa Hohorst[4], Esteban Loetz [5]
[1]University of Colorado Denver, [2]University of Colorado Denver, [3]University of Colorado Denver, [4]University of Colorado Denver, [5]University of Colorado Denver

Abstract: Understanding neural circuits that contribute to the maintenance of exercise, particularly rapid escalation of exercise behavior in female rats, could maximize exercise benefits. We have previously observed that the rapid acquisition of voluntary exercise in female, versus male, rats is dependent on activity in the dorsal lateral striatum (DLS). Females have greater evoked dopamine (DA) activity and develop habits more readily than males. This may be evidenced by the role of the substantia nigra (SN) to DLS projections in acquisition and maintenance of voluntary exercise. The goal of the experiment is to determine the role of the SN-to-DLS circuit in the acquisition and maintenance of voluntary exercise and identify sex differences. We hypothesized that SN-DLS circuit activity is responsible for habitual exercise and rapid escalation to habitual running displayed by females. An intersectional chemogenetic approach silenced the SN-DLS circuit daily during acquisition and maintenance of running in both sexes. This is the first time a circuit-specific approach was used to investigate circuits underlying exercise behavior. The effect of SN-DLS inhibition was robust during the maintenance phase when nightly running reaches high, stable levels. Females' running distance was reduced by SN-DLS inhibition on the first day of wheel access, whereas SN-DLS circuit inhibition reduced males' running behavior on the fifth day. This suggests that the SN-DLS circuit is necessary for the development of stable running "habits" in both sexes and the rapid development of exercise habits in females. The SN-DLS circuit therefore represents a novel target for increasing exercise participation.

Assessing Interspecies Metabolic Complementation Mediated by Pyrimidine Exchange

Discipline: Life Sciences
Subdiscipline: Microbiology

Randy Garcia*[1], Catherine Wakeman[2], Hafij Al Mahmud[3], Jiwasmika Baishya[4], Alexsis Garcia[5]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University, [5]Texas Tech University

Abstract: In polymicrobial communities, members participate in various metabolic interdependencies, which can be found within the nutrient-rich environments of chronic infections like cystic fibrosis. This often leads these microorganisms to overcome growth retardation due to auxotrophy through resource sharing with the surrounding microbial community. Cooperation/synergy in an infectious microbial community can be detrimental, as this can lead to microbial tolerance to antibiotic treatment and the host immune response. In our earlier study, members of our research group demonstrated that the usually competitive Pseudomonas aeruginosa and Staphylococcus aureus can, when undergoing a bi-directional purine exchange, mediated from the release of eDNA, adopt more cooperative tendencies. In this follow-up study, we wanted to further verify our results by studying a potential pyrimidine exchange. Therefore, I selected pyrimidine deficient transposon mutants of P. aeruginosa and grew them alone or together with wild-type S. aureus in RPMI media supplemented with 1% casamino acid. The results showed that P. aeruginosa mutants can be rescued by S. aureus . To validate the pyrimidine exchange, I determined whether enzymatically digested or undigested exogenous DNA can rescue the growth of the mutants. Indeed, the mutants had experienced an increase in cell growth in the presence of eDNA. Overall, our data suggests that, in polymicrobial infection, eDNA containing both purine and pyrimidine can be secreted by neighboring pathogens without cell lysis and these can be exchanged between classical competitors to establish cooperation. By better understanding sources of microbial synergism during infection, we can learn how to disrupt this problematic phenomenon.

Variation in thermosensitivity of meiosis within and between species using 2 species from the genus Saccharomycees as a model

Discipline: Life Sciences
Subdiscipline: Genetics

Mili Gallardo*[1], Lauren Bailey[2], Caiti Smukowski Heil[3]

[1]North Carolina State University, [2]Graduate Student, [3]Assistant Professor

Abstract: Meiosis is required for the formation of gametes in all sexually reproducing species, however meiosis can fail under certain conditions. For example, the optimal temperature for successful meiosis varies between species of plants and animals. This suggests that meiosis is temperature sensitive, and that natural selection may act on variation in meiotic success as organisms adapt to different environmental conditions. To understand how temperature alters the successful completion of meiosis, we surveyed two metrics of meiosis, sporulation efficiently and spore viability, in the cryotolerant species Saccharomyces uvarum and the thermotolerant species Saccharomyces cerevisiae. We induced meiosis for 6 strains of S. uvarum and 6 strains of S.cerevisiae for 7 days at three different temperatures, 15℃ , 23°C, and 30℃. Sporulation efficiency was assessed by counting the proportion of cells that successfully formed spores. Spore viability was assessed through tetrad dissection of 24 meioses for each strain at each temperature and recorded as the number of alive spores from the total of spores dissected. Our results indicate that there is variation in both sporulation efficiency and spore viability within and between S. uvarum and S. cerevisiae species. In S. uvarum, the threshold of meiotic failure is between 25℃ C and 30℃, while meiosis proceeds normally at 30℃ for strains of S. cerevisiae. We interpret these results to indicate that selection may be acting on meiotic machinery within species. This has implications for the distribution of species ranges and may be important in the divergence of populations into separate species.

Tracking Real-time Changes in House Mouse Centromere Satellite Architecture during Inbreeding

Discipline: Life Sciences
Subdiscipline: Genetics

Kimberly Heath*[1], Beth L. Dumont[2], Uma P. Arora[3], Aditya Mahadevan Iyer[4], Christopher Baker[5], Beth Sullivan[6], Michael Nachman[7]
[1]The Jackson Laboratory for Mammalian Genetics, [2]The Jackson Laboratory for Mammalian Genetics, [3]The Jackson Laboratory for Mammalian Genetics, [4]The Jackson Laboratory for Mammalian Genetics, [5]The Jackson Laboratory for Mammalian Genetics, [6]Duke University School of Medicine, [7]University of California, Berkeley

Abstract: Mammalian centromeres are satellite-rich, multi-megabase chromatin domains that direct kinetochore assembly and chromosome segregation. Although they execute highly conserved and fundamental processes, centromeres are subject to high rates of structural mutation and are rapidly evolving. Our recent work uncovered significant variation in centromere sequence and architecture among house mice (Mus musculus) , including notable differences between wild-caught and inbred mice. In particular, wild mice harbor fewer centromere satellite repeats and higher levels of satellite sequence heterogeneity compared to inbred strains. These observations have prompted us to hypothesize that the intense bottleneck imposed by inbreeding may promote selfish transmission of larger, more homogenous centromeres. To test this possibility, we are leveraging a unique mouse resource comprised of genetically diverse inbred wild-derived mouse strains paired with tissue samples from their wild-caught progenitors to track changes in centromere organization during the course of inbreeding. Utilizing centromere-associated k -mer frequencies and long-read whole-genome sequences, we are currently contrasting estimates of centromere satellite heterogeneity and copy number between wild-caught mice and their derivative inbred strains. These on-going genomic investigations will be coupled with chromatin profiling of a key centromere-associated protein, CENP-A, to identify one potential functional outcome of inbreeding-associated changes in centromere architecture: shifts in the CENP-A sequence association landscape. Overall, it is anticipated that this work will provide a real-time snapshot into the rapid, dynamic evolution of the centromere, exposing the incredible power of centromere drive in the context of inbreeding.

Dam the Wildfires: How Beavers Respond to Megafire Events

Discipline: Life Sciences
Subdiscipline: Environmental Science

Brandon Osorio*[1], Dr. Emily Fairfax[2], Joseph Miller[3]
[1]California State University Channel Islands, [2]California State University Channel Islands, [3]California State University Channel Islands

Abstract: In recent years megafires (wildfires burning more than 100,000 acres) have become common, rapidly burning through millions of acres across the American West each year. Extreme autumn fire weather conditions have increased since the 20th century, with models suggesting continued warming and seasonal drying trends will likely result in further increases in extreme fire weather conditions in the future. Wildfires cause billions of dollars of damage and cost billions more to fight, highlighting the need for an effective but cheap alternative to help reduce wildfire drivers and burn severity: e.g. beavers. Beavers significantly reshape riparian wetlands and alter the hydrological cycle. Their work in riparian zones brings many benefits to the ecosystem by supporting the growth of abundant vegetation. Beaver dams slow and store water which helps maintain riparian vegetation health through both regular dry seasons and extended droughts. We characterize the influence of beaver dams on riparian vegetation conditions - before, during, and after the 2020 Rocky Mountain megafires and use that to understand how beaver activity influences fuel conditions. We use Google Earth Pro to map out beaver dams within three Rocky Mountain megafire perimeters (East Troublesome, Cameron Peak, and Mullen Fires); then use the remotely sensed Normalized Difference Vegetation Index (NDVI) to quantify how green and lush vegetation is in riparian areas with and without beaver dams, before, during, and after the fires. Our study provides important data for a variety of local, state, federal, and private land management agencies exploring new strategies for wildfire risk reduction.

Proposed life cycle of the snow algae Chlainomonas sp. from Washington, USA

Discipline: Life Sciences
Subdiscipline: Environmental Science

Maya Matsumoto*[1], Robin B. Kodner[2], Trinity L. Hamilton[3], Stacy A. Krueger-Hadfield[4], Clare Hanneman[5]
[1]Western Washington University, [2]Western Washington University, [3]University of Minnesota, [4]University of Alabama at Birmingham, [5]Western Washington University

Abstract: Chlainomonas is one of the three genera of true snow algae known to produce large pink or red blooms in alpine snow annually. There are currently two named species in this genus – Chlainomonas rubra (Stein et Brooke) and C. kolii (Hardy et Curl) – and another described, but none of these species have been successfully cultured in the laboratory, rendering studies of the life cycle difficult as it is challenging to decipher the order of individual stages. We have observed seasonal blooms of a Chlainomonas sp. from May through June across 5 years on a snow-on-lake habitat in the alpine Bagley Lakes Basin in the North Cascade Mountains of Washington, USA. Cells across different developmental stages were observed in field-collected samples and an additional stage was induced in the laboratory by holding samples in the dark for at least 2 months. We suggest this species is distinct from the three previously reported species based on morphology seen in microscopy images and rbcL sequences. Moreover, these observed stages suggest sexual cycling interspersed with asexual replication. We propose two hypotheses for the life cycle of this species, linking stages to seasonally available habitat. The life cycle is the most fundamental biological feature of an organism, with direct consequences for evolutionary processes. For microbial taxa, we often lack this information, but temporal studies, such as we report here, may be key to creating testable life cycle hypotheses, which for snow algae, may assist in tracking the pace of global warming.

The Effects of Trash on Javelina (Pecari tajacu) Abundance and Wildlife Species Richness in Tucson, Arizona

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Nadira Mitchell*[1], Michael Bogan[2], Alexandra Burnett[3]
[1]University of Arizona, [2]University of Arizona, [3]University of Arizona

Abstract: As urbanization increases, wildlife is prone to human interactions and contact with trash from illegal dumping and littering. The level of trash, actual number of trash items found, and how it accumulates in an area can have negative or positive effects for wildlife. Plastics, Styrofoam, and human food inadvertently consumed can cause harm. Our research aimed to learn more about how wildlife navigates urban environments with differing levels of trash to inform land-use decisions and minimize human-wildlife conflict. We hypothesized that elevated levels of trash increase the relative abundance of javelina (Pecari tajacu), increases the average group number of javelina, and increases overall wildlife species richness. Wildlife cameras were placed across an urban and suburban landscape in Tucson, Arizona (USA). Trash surveys were conducted at each site to determine trash levels. Photo data was analyzed with TimeLapse, and statistical analysis was completed with the software program R. Results indicate that javelina abundance and group size did not increase when there was a higher level of trash nor did we find a significant relationship between the level of trash and overall wildlife species richness, the number of species in a community. Trash does not increase or decrease fitness, the ability of an organism to pass on its genetic material to its offspring, which has important evolutionary and management implications. Expanding the scope of the study to include more sites with a high abundance of trash would be beneficial to further explore this topic.

Investigation of Antimicrobial Activity of Anemopsis californica

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Monica Mendoza*[1], Christine Case[2], Brinda Govindan[3]
[1]Skyline College, [2]Skyline College, [3]San Francisco State University

Abstract: The discovery of penicillin in 1928 sparked an active period of natural-product antibiotic discovery, which positively impacted the human lifespan. Modern medicine has employed antibiotic drugs to treat bacterial infections. However, the widespread misuse of antibiotics has led to antibiotic-resistant bacteria while the list of infections continues to rise. This dilemma fuels efforts to find novel sources of antibiotics that can be effective against today’s antibiotic-resistant pathogens. Throughout history, plants have been sources of natural-

product antibiotics and continue to be viable sources. For example, many Native American tribes in the southwestern United States used Anemopsis californica (Saururaceae) as a disinfectant and topical antiseptic. In this study, a methanol extract of A. californica roots and rhizomes (210.1 mg/mL to 215.3 mg/mL) inhibited the growth of Bacillus cereus bacteria with zones of inhibition ranging from 10 to 14 mm. Experiments are underway to determine the minimal inhibitory concentration of the extract and its efficacy against other gram-positive bacteria and fungi. These findings contribute to the research required to identify new sources for novel antibiotics and shed light on the unique contributions Native American tribes have made to the field of antimicrobial discovery.

Impacts of Ungulate Grazers on Plant Root Associated Fungi in Tallgrass Prairie

Discipline: Life Sciences
Subdiscipline: Microbiology

Rissa Gracia-Prudencio*[1], Dr. Lydia Zeglin [2], Nico Vega Anguiano[3]
[1]Kansas State University, [2]Kansas State University, [3]Kansas State University

Abstract: Once the dominant and most influential grazer on the great plains, the plains bison (Bison bison) are now a minority in their homelands. Cattle currently outnumber bison 200:1. The near eradication of the keystone species bison, and introduction of cattle into the plains has caused many changes within ecosystem relationships. This project focuses on the impacts of Native and non-native ungulate grazers on symbiotic root mycorrhizal fungi-vegetation relationships, in an area of native tallgrass prairie, at the Konza Prairie, KS, USA. Plant roots and soil core composites were gathered along replicate transects in bison grazed, cattle grazed and ungrazed watersheds. DNA extraction, PCR amplification, and chloroform fumigation were performed to assess the fungal species presence, diversity, and abundance. We predicted that fungal biomass and diversity in soil and root-associated samples would be higher in grazed areas due to animal dispersal of spores, and that bison and cattle would have different effects on fungal communities. Previous work has shown that plant root growth is lower in bison grazed areas as a result of grazing-promoted fertility, and that fungi have a higher average carbon:nitrogen ratio than bacteria. The data in hand suggest that lower plant root growth could reduce total microbial biomass in both bison and cattle grazed areas, but that cattle may change the relative abundance of soil fungi as compared to native prairie with native ungulate grazers. DNA extraction and PCR for the fungal sequence library preparation is complete, and diversity data will inform our final predictions.

Optimization of endospore production and purification from Bacillus cereus

Discipline: Life Sciences
Subdiscipline: Microbiology

Tatiana Serrano-Zayas*[1], Carlos Ríos-Velázquez [2], Carlos González-Lugo[3], Luis Mercado-Pérez[4]
[1]University of Puerto Rico at Mayaguez, [2]University of Puerto Rico at Mayaguez, [3]University of Puerto Rico at Mayaguez, [4]University of Puerto Rico at Mayaguez

Abstract: Bacterial endospores are resistant structures produced as a defense mechanism to adverse conditions. The endospores can maintain themselves dormant for longer periods of time, until conditions are optimal for germination. Bacillus cereus is a gram-positive bacteria and foodborne pathogen that can cause vomit and diarrheal symptoms on humans and animals; due to their endospores production it’s harder to eliminate in the food industry. B. cereus endospores are resistant to radiation, heat, and chemical treatments. Their detection is harder due to their small size, which can range from 0.95±0.11μm wide and 1.31±0.17μm long. Therefore, to study them it’s necessary to produce high concentrations of viable endospores while reducing the vegetative cells. The research seeks to optimize the production and purification protocols of endospores; to have representative data for further detection experiments. The production optimization included growth in different culture media and incubation temperatures. Also, a growth curve to evaluate the endospores and vegetative cells in different growth phases, was also done. The best endospores purification procedure was chosen by comparing chemical, physical and enzymatic methods. The endospores were detected by using the Schaeffer-Fulton staining. B. cereus growth in Brain-Heart Infusion Agar showed an increased in endospores production. The chemical purification method showed the highest quantities of single endospores when ethanol concentration was increased, obtaining a 15:1 ratio of endospores to vegetative cells respectively. The strategies development to increase isolation of viable endospores will be useful in detection assays developments to further study these structures.

Resilient Lagoon: Density dynamics of harmful dinoflagellate Ceratium furca in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Elizabeth M. González Cruz*[1], Marión S. Benítez Silvera, [2], Alba Cruz Alicea[3], Yogani Govender[4], Melaury Hernández Ortiz [5], Arianah Z. Montijo Hernández[6], Karina M. Rodríguez Torres[7], Coral J. Torres Maldonado[8], Odalys Velázquez Montes[9]
[1]Inter-American University of Puerto Rico, Metropolitan Campus, [2]Inter-American University of Puerto Rico, Metropolitan Campus, [3]Inter-American University of Puerto Rico, Metropolitan Campus, [4]Inter-American University of Puerto Rico, Metropolitan Campus, [5]Inter-American University of Puerto Rico, Metropolitan Campus, [6]Inter-American University of Puerto Rico, Metropolitan Campus, [7]Inter-American University of Puerto Rico, Metropolitan Campus, [8]Inter-American University of Puerto Rico, Metropolitan Campus, [9]Inter-American University of Puerto Rico, Metropolitan Campus

Abstract: Globally, Ceratium furca has been associated with harmful algal blooms. In Puerto Rico, it is found associated with the economically important bioluminescent dinoflagellate Pyridium bahamense which in recent years has been on the decline. Understanding the population density dynamics after hurricanes will help improve management strategies for Biobays in Puerto Rico. Our study investigated the effects of hurricanes on C. furca density in Laguna Grande de Fajardo. Field sampling was carried out monthly at 6:00-8:00 pm from 2016 to 2021, at the edge and middle (0m, 2m) of lagoon. Samples were collected and stored in 1 L bottles and preserved with 20 mL of formalin. To determine density, 1ml of sample was examined under the microscope using a Sedgwick slide. The densities of C. furca significantly increased by month (F= 8.5, =< 0.001) and by year from 2016 to 2021 (F=128, p <0.001). The middle of the lagoon (0m ,2m) had higher densities than sites at the edge (F=16.8, p <0.001). Density was highest in the rainy season with a peak in November. Our results show a spatial temporal change in density after the hurricanes. We suspect that density increases are associated with increased nutrient inputs immediately after the Hurricanes from leaf fall and debris. Although algal bloom of C.furca was documented, it did not negatively impact the tourism industry and economy. Continued monitoring is warranted to better understand the mechanism underlying the control of bloom outbreaks in Puerto Rico.

Project Safe Flight: Evaluating the Impact of Georgia State University Campus Buildings on Birds

Discipline: Life Sciences

Subdiscipline: Biology (general)

Alejandra Tapia Batres*[1], Amy Reber[2], Rebekah Chapman[3], Raquel Gonzalez[4], Ricardo Hernandez[5]

[1]Georgia State University, [2]Georgia State University, [3]Georgia State University, [4]Georgia State University, [5]Georgia State University

Abstract: Building collisions are a major anthropogenic threat to birds, with estimates of 100 million to 1 billion killed annually in the United States. Previous research indicates bird collisions are strongly correlated with the percentage of glass comprising building facades because birds will often mistake reflections of vegetation for the real thing. With over 300 high-rise glass buildings, Atlanta poses a serious potential threat to bird migrations. However, few studies have been done in downtown Atlanta to identify specific buildings of concern. This study examines the frequency of bird-building collisions at Georgia State University's Atlanta campus. The objectives of this study are: 1) identify which buildings on campus experience the greatest number of bird collisions and 2) determine which bird species are most affected. To assess the impact of campus buildings on birds, student interns and volunteers conducted morning patrols to geotag collision events with ArcGIS Collector and collect impacted birds. Preliminary results show differences between campus buildings in the number of collisions, with the College of Law building experiencing the highest proportion of events. Results also suggest a greater impact on migratory species than year-round residents, with the ruby-throated hummingbird and cedar waxwing being the most frequently impacted species. Overall it appears that certain buildings on the Atlanta campus pose a greater threat to migratory birds than others. Ongoing data collection will be used to encourage campus managers to retrofit problematic buildings with bird-safe films and promote "lights out" campaigns to reduce collision incidents.

Isolation of Novel Antibiotic-Producing Bacteria from a Botanical Garden in the Desert Southwest

Discipline: Life Sciences

Subdiscipline: Biology (general)

Luis Saucedo*[1], Dr. Robin Cotter[2], Lindsey Duran[3], Ilian Rico-Chavez[4], Maria Camargo Arredondo[5], Reilly Bendon[6], Maria Soto Fuentes[7], Jessica Mondragon[8]

[1]Phoenix College, [2]Phoenix College, [3]Phoenix College, [4]Phoenix College, [5]Phoenix College, [6]Phoenix College, [7]Phoenix College, [8]Phoenix College

Abstract: According to the Centers for Disease Control and Prevention around 2.8 million people per year will become infected with antibiotic-resistant bacteria and fungi, with more than 35,000 of these cases becoming fatal, and costing an estimated $4.6 billion USD to treat. As nearly two-thirds of antibiotics used in medicine today originated from soil, we were interested in performing drug-discovery studies using local soil samples. Working in collaboration with the Tiny Earth Research Network, we hypothesized that bacteria able to produce novel antimicrobial compounds would be present in soil samples collected from a local desert botanical garden. Students at a 2-year Hispanic Serving Institution collected soil samples from eight different regions of a desert botanical garden on land ancestrally held by the Akimel O'odham, or Upper

Pima People, and the Hohokam. Upon collection, serial dilutions of the soil were plated on trypticase soy agar to generate colony counts. Soil isolates were then tested for antimicrobial activity against known pathogens and characterized using biochemical and genetic testing. In total, 22 out of 64 isolates from the botanical garden soil samples demonstrated the ability to inhibit the growth of two indicator bacteria: Escherichia coli and Staphylococcus epidermidis . These findings warrant the need for further studies that will focus on collection of samples from additional sites, seasonal comparison of samples, and chemical analyses of the antimicrobial compounds produced by these soil isolates in an attempt to address the looming antibiotic resistance crisis.

Investigating the molecular mechanism of PCH-2 during Meiosis I

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Valery Ortiz*[1], Anna Elizabeth Russo[2], Needhi Bhalla[3]
[1]University of California, Santa Cruz, [2]University of Califorina, Santa Cruz, [3]University of California, Santa Cruz

Abstract: Meiosis is a specialized form of cell division that produces haploid gametes such as sperm and eggs. Errors in meiosis can lead to gametes that inherit an incorrect number of chromosomes (aneuploidy), which can result in infertility, miscarriages, and genetic disorders such as Down Syndrome. We are interested in how meiotic prophase events such as pairing, synapsis, and crossover recombination are coordinated so that chromosomes segregate correctly. Pachytene Checkpoint Protein 2 (PCH-2) is a highly conserved regulator of meiotic fidelity and mutations in the human ortholog of PCH-2 (TRIP13) have been linked with infertility. However, its molecular mechanism during meiosis is poorly understood. Previous evidence has shown that PCH-2 interacts with HORMA-domain containing proteins (HORMADs). We hypothesize that this interaction involves conformationally remodeling HORMADs to regulate and coordinate pairing, synapsis, and recombination. Using the nematode C.elegans as a model organism, we used genetic and cytological experiments to test this hypothesis. With CRISPR/Cas9 gene editing, we created a hypomorphic allele of one meiotic HORMAD, htp-1, that limits its ability to adopt its active conformation and tested whether this allele genetically interacts with pch-2 null mutations. We report that htp-1(G97T) mutants have recombination defects and we are currently generating the htp-1(G97T);pch-2 double mutants to test for a genetic interaction, consistent with our hypothesis that PCH-2 and HTP-1 cooperate to regulate recombination. These experiments provide a model for how different conformers of HTP-1, and their regulation by PCH-2, control and coordinate meiotic prophase events to promote accurate meiotic chromosome segregation.

Isolation of polyhydroxybutyrate-degrading marine microorganisms to mitigate oceanic plastic pollution

Discipline: Life Sciences
Subdiscipline: Microbiology

Alessandra Valdivia*[1], Madison Cohen[2], Dr. Alyson Santoro[3], Natalie Dornan[4], Chance English[5], M. Ofelia Aguirre Paden[6]

[1]University of California, Santa Barbara, [2]University of California, Santa Barbara, [3]University of California, Santa Barbara, [4]University of California, Santa Barbara, [5]University of California, Santa Barbara, [6]University of California, Santa Barbara

Abstract: Every year, 300 million tons of plastic are produced, 14 million of which end up in our oceans. Despite this staggering data, only about 1% of all plastics produced are “ecofriendly” bioplastic, however, the fate of these biopolymers in marine environments is not well understood. Previous experiments have shown certain marine microorganisms have the ability to use the biopolymer polyhydroxybutyrate (PHB) as a carbon and energy source. Therefore, PHB has been a biopolymer of interest to replace petroleum-based plastics to reduce the time that plastic would remain in the ocean. For this project, we sought to cultivate marine microorganisms responsible for the degradation of PHB and obtain preliminary degradation rates. Samples were collected at the University of California, Santa Barbara Lagoon and Campus Point, and grown on PHB media plates. The microorganisms that demonstrated degradation were observed by the visible clearing of the opaque PHB media and further isolated to single colonies. Preliminary degradation rates of PHB in natural seawater were calculated in the laboratory to be 1.6 x 10-3 d-1. Future experiments will involve using these microorganism isolates to further investigate the dynamics of PHB degradation in conditions that reflect various oceanic environments. Ultimately, these data can aid in the future design of bioplastic products that will integrate marine microorganism isolates to customize the degradation of the product itself.

Anti-metastatic effect of the Rac1 inhibitor MBQ-168

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Derealise Garcia-Almedina*[1], Julia Medina Velázquez [2], Suranganie Dharmawardhane[3], Eliud Hernández O’farril[4], Cornelis Vlaar Stoop [5]

[1]University of Puerto Rico Río Piedras Campus, [2]University of Puerto Rico, Medical Sciences Campus, School of Medicine, San Juan, PR, [3]University of Puerto Rico, Medical Sciences Campus, School of Medicine, San Juan, PR, [4]University of Puerto Rico, Medical Sciences Campus, School of Pharmacy, San Juan, PR, [5]University of Puerto Rico, Medical Sciences Campus, School of Pharmacy, San Juan, PR

Abstract: Metastasis is the primary cause of breast cancer-related death. The first step of the metastatic process is initiated by the homologous Rho GTPases Rac and Cdc42, which regulate cytoskeletal dynamics required for cell migration. Therefore, targeting the activation of Rac and Cdc42 is a strategy to block cell migration, and thus metastasis. Our group has characterized MBQ-167 as a potent dual inhibitor of Rac and Cdc42 with IC 50 s of 103 nM and 78 nM. To develop more potent inhibitors of Rac and Cdc42, we designed MBQ-167 derivatives maintaining the original carbazole group with a triazole group as the center core with alterations in the aliphatic and aromatic groups. From our screening analysis, we elucidated MBQ-168, a derivative of MBQ-167, with a similar anti-metastatic profile in a mouse model. This project tested the hypothesis that MBQ-168 inhibits cell viability in the MDA-MB 231 human triple-negative cell line, using clonogenic assays. After treatment of 24 hr with 250 nM of MBQ-167, we re-seeded the cells and allowed the formation of colonies for approximately 7 days. Results show that colony formation is inhibited by both MBQ-167 and MBQ-168 at 250 nM when compared to non-treated cells. This data validates the development of MBQ-168 as an inhibitor of triple-negative breast cancer progression.

Native and Non-Native Terrestrial Gastropods in Natural Communities around Atlanta, Georgia

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Raquel Gonzalez*[1], Donata Borsos [2], Christy C. Visaggi[3], Jann E. Vendetti[4]
[1]Georgia State University, [2]Georgia State University, [3]Georgia State University, [4]Los Angeles County Museum of Natural History

Abstract: Land snails and slugs impact ecosystem function through calcium cycling and decomposition. Due to their limited movement over their lifetime, they can serve as indicators of site conditions and environmental health. Research on land snails and slugs in Georgia has primarily focused on species distribution at larger geographic scales. This study aims to examine assemblages of land snails and slugs as they correspond to different natural community types in the Piedmont region of Georgia. Natural community types are formed as a product of weathered rock that determines soil composition, moisture, depth, and contributes to slope-direction/angle. Terrestrial gastropod assemblages are expected to vary between communities due to differences in diversity of plants and soil composition. Three natural community types in the Piedmont were the focus of this research: Mesic Forests, Oak-Pine-Hickory Forests, and Pine-Oak Woodlands. Thirteen localities have been studied to date through fieldwork and analysis of existing observations in iNaturalist. Over 250 observations have been examined yielding 19 genera overall (13 native genera, 5 non-native genera, and one genus with both native and non-native species in the region). The presence of non-native taxa, some yet to be formally reported in Georgia, is concerning given that they may negatively impact native species or become invasive with cascading effects on the ecosystem. Data collection is still ongoing; more research is needed to determine the extent to which snail and slug assemblages reflect natural community types and any impacts from human activities at these localities.

Classical music promotes neurobehavioral and cognitive recovery after experimental traumatic brain injury

Discipline: Life Sciences
Subdiscipline: Neurosciences

Andrew Victoria*[1], Vincent Vozella [2], Eleni Moschonas[3], Tyler Ranellone[4], Rithika Reddy [5], Piper Rennerfeldt[6], Jessica Jarvis[7], Ericka Fink[8], Jeffery Cheng[9], Dr. Corina Bondi[10], Dr. Anthony Kline [11]
[1]University of Pittsburgh, [2]University of Pittsburgh, [3]University of Pittsburgh, [4]University of Pittsburgh, [5]University of Pittsburgh, [6]University of Pittsburgh, [7]University of Pittsburgh, [8]University of Pittsburgh, [9]University of Pittsburgh, [10]University of Pittsburgh,[11]University of Pittsburgh

Abstract: Traumatic brain injury (TBI) is a leading cause of disability worldwide. Pharmacological interventions to treat TBI have not successfully translated to the hospital, thus strongly advocating for the need to assess novel, safe, nonpharmacological strategies. Music may hold an untapped potential for improving neurobehavior after TBI as limited clinical reports in CNS-injured adults showed that music-based interventions improved cognitive and emotional functioning. Basic science data in non-TBI rats also show that music enhances cognition. The aim of this study was to test the hypothesis that providing classical music to adult rats after TBI would ameliorate TBI-induced deficits in cognition and neurobehavior. Anesthetized adult male rats (n=5 per group) received a cortical impact of moderate severity (2.8 mm impact at 4 m/s) or sham injury and 24 h later were randomized to classical music or ambient room noise for 3 h/day from 19:00-22:00 for 32 days (last day of behavior). Motor (beam-walk), cognitive (acquisition of spatial learning and executive function), anxiety-like behavior (evaluated via open field and shock probe defensive burying tasks), as well as histopathology (lesion volume), neuroplasticity (BDNF) and neuroinflammation/plasticity (Iba1, CD-68, and CD-163). The data were analyzed by ANOVAs, followed by the Newman-Keuls post-hoc test. Music improved motor, cognitive, and anxiety-like behavior vs. no music. Music also reduced cortical lesion volume and increased hippocampal BDNF expression and markers of neuroplasticity vs. no-music. These preliminary findings provide strong support for music as a potential rehabilitative therapy for experimental TBI and perhaps clinically as well.

Nucleopolyhedrovirus Effects on Mating Success of Agraulis vanillae Butterflies

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Yuriani Palomino*[1], Arietta Fleming-Davies [2], Wilnelia Recart Gonzalez[3]
[1]University of San Diego, [2]University of San Diego, [3]University of San Diego

Abstract: Host-pathogen interactions are an aspect of ecosystems but the rapid change of the environments has challenged organisms to adapt quickly. In my research, I investigated how nucleopolyhedrovirus (NPV) affects the reproduction of the Gulf Fritillary Butterfly, Agraulis vanillae , on drought-stressed Passiflora caerulea . NPV infects individuals at larval stage, when larvae consume the virus on contaminated P. caerulea leaves. Larvae grew in controlled environments where they were selected at random for a diet of high water or drought-stressed plants. We then infected larvae with one of four virus doses. Pupae were collected and survivors mated within their diet and infection treatment groups after they emerged as butterflies (n= 27 females and n= 17 males). Male and female mating success was determined as a binomial (yes/no) trait, based on whether a mating led to laying of fertile eggs. We found that in the absence of the virus, there was no difference in female mating success between butterflies raised on drought-stressed plants and those raised on high-water plants. However, in the presence of the virus, female butterflies raised on drought-stressed plants had higher mating success (logistic regression, virus by water treatment interaction effect= 19.58, LR= 4.72, p=0.03). This experiment has shown that pathogens and the effects of climate change in the form of drought can influence mating success and oviposition in a butterfly. Thus, the presence of pathogens negatively influences population growth of butterflies through increases in larvae mortality, butterflies that survive exposure see an increase in fitness.

Does Reclaimed Water Affect Plant Growth and Mycorrhizal Colonization?

Discipline: Life Sciences
Subdiscipline: Environmental Science

Ivory Bacy*[1], Anita Antoninka [2], Catherine Propper[3], Nancy Johnson[4]
[1]Northern Arizona University, [2]Assistant Research Professor, [3]Professor, [4]Regents Professor

Abstract: Arbuscular mycorrhizal fungi (AM fungi) are obligate biotrophs, supporting the majority of plants by providing limited soil nutrients in exchange for fixed carbon from plant hosts. AM fungi also support plants experiencing high salinity and drought stress. Cities are utilizing reclaimed water (RW) for irrigation in agriculture and snowmaking. In this short experiment, we asked if RW affects corn growth and mycorrhizal colonization in roots. We collected soil along with RW and melt-water from natural snow from a ski resort in northern Arizona, and watered the plants with the two types of water for 11 weeks. We hypothesized that plant growth and mycorrhizal colonization would be altered by RW because of high nutrient and salt content. Plants were harvested to measure biomass and root colonization. Our results showed a 17% increase in AM fungal hyphae in roots watered with RW compared to snow-melt. Otherwise, RW did not impact corn biomass or other AM fungi structures (arbuscules, coils, vesicles). Nutrient analysis showed higher S and Al in RW treatments but no other differences in soil nutrients. Because there were no significant nutrient differences that increased plant biomass and decreased AM fungi colonization, our research hypothesis was not supported. These results were only from corn but we have on-going studies using native plants as well. Longer term exposures to RW could have different effects. These findings contribute information about the potential influences of RW irrigation in agriculture.

Differential Transcription Effects of Leishmaniasis donovani’s Gene Expression When Challenged with Various Natural Compounds.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kai Brantley*[1], Dr. David Blake [2], Dr. Joslynn Lee[3], Dr. Kenny Miller[4]
[1]Fort Lewis College, [2]Fort Lewis College, [3]Fort Lewis College, [4]Fort Lewis College

Abstract: Title: Differential Transcription Effects of Leishmaniasis donovani’s Gene Expression When Challenged with Various Natural Compounds. Leishmania donovani (LD) is a species of protozoans that cause the highly lethal vector born disease Visceral Leishmaniasis (VL). The current treatments for VL infections are small molecules such as amphotericin B (AmpB). While AmpB can be effective, it has low selective toxicity, and has increasing drug resistances. The grave prognosis of untreated VL infections and lack of safer alternatives are the why these drugs remain in use. There are currently no vaccines or novel drugs available. New small molecule treatments are urgently needed. Plant metabolites that increase reactive oxygen species (ROS) can be quite effective anti-leishmanials and several of these compounds pose minimal toxicity to human cells. We tested two plant compounds, deoxyalpinoid B (DAB) and sulforaphane (SUL) by incubating them with human macrophages infected with LD to understand the differential expression patterns of the parasite. Using RNA-seq technologies, we can understand the genes that are essential during infection and how RNA expression patterns change when in the presence of natural compounds. The primary goal of this project is to identify which genes are necessary (host-associated and parasite associated) for successful infection and to determine the extent to which different natural products change gene expression, possibly leading to clearance or inhibition of parasite growth. The work presented here is the bioinformatics workflow performed on this data set. This data will contribute to the larger investigation on Leishmaniasis infection in humans.

Multimodal Approaches for Assessing Cognitive and Emotional Disturbances After Experimental Brain Trauma

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ann Marie Robles*[1], Dr. Corina Bondi [2], Dr. Anthony Kline[3], Nicholas Race[4], Eleni Moschonas [5], Piper Rennerfeldt[6], Rithika Reddy[7], Tyler Ranellone[8], Ellen Annas[9], Mathew Bertocchi[10], Jeffrey Cheng [11]

[1]University of Pittsburgh, [2]Safar Center for Resuscitation Research, University of Pittsburgh, [3]Safar Center for Resuscitation Research, University of Pittsburgh, [4]Safar Center for Resuscitation Research, University of Pittsburgh, [5]Safar Center for Resuscitation Research, University of Pittsburgh, [6]Safar Center for Resuscitation Research, University of Pittsburgh, [7]Safar Center for Resuscitation Research, University of Pittsburgh, [8]Safar Center for Resuscitation Research, University of Pittsburgh, [9]Safar Center for Resuscitation Research, University of Pittsburgh, [10]Safar Center for Resuscitation Research, University of Pittsburgh,[11]Safar Center for Resuscitation Research, University of Pittsburgh

Abstract: Traumatic brain injury (TBI) causes cognitive disability, which may result from acetylcholine (ACh) dysregulation. Thus, restoring cholinergic function may restore cognition. Our hypothesis is that chronic administration of NS-1738, a novel α7 nicotinic ACh receptor (α7-NAChR) allosteric modulator, will improve sustained attention post-TBI and the effect will be augmented when combined with environmental enrichment (EE). Moreoever, blocking α7-NAChRs with methylycaconitine (MLA) will attenuate the benefits of NS-1738. Methods used were training adult male rats in 3-choice serial reaction time task (3-CSRT) before cortical impact or sham injury and then randomized to NS-1738 (3 mg/kg) or saline (1 mL/kg) given sub-acutely (7d) or chronically (28d). The chronic paradigm coupled with daily EE (6h/d) was subjected to daily α7-NAChRs blockade via MLA (3 mg/kg) injections. Western blot assessed the cholinergic markers acetylcholinesterase (AChE), choline acetyltransferase (ChAT), and α7-NAChR in the medial prefrontal cortex (mPFC). Microarray analysis examined inflammatory gene expression. Statistical analysis utilized ANOVAs with Newman-Keuls post hoc tests. Results show TBI impaired sustained attention versus shams (p<0.05), which was improved by chronic (p<0.05) but not by sub-acute NS-1738 (p>0.05) treatment. NS-1738+EE rendered an additive effect on lowering behavioral omissions and inflammatory markers (p<0.05) including triggering receptors expressed on myeloid cells-1 and interleukin-1 receptor antagonist. TBI decreased mPFC ChAT and AChE (p<0.05) with partial restoration by subacute NS-1738. TBI groups that received MLA demonstrated a reinstatement of performance deficits. Overall, the data support the hypotheses that enhancing cholinergic transmission after TBI enhances sustained attention and systemic inflammation.

Computational Bioprospecting: Identification of Novel Cas Proteins In Metagenomic Datasets of Microbiomes in Puerto Rican Ecosystems

Discipline: Life Sciences

Subdiscipline: Biology (general)

Gabriel Jimenez-Pagan*[1], Diego Detrés Martínez [2], Carlos Ríos Velázquez[3]

[1]University of Puerto Rico - Mayaguez Campus, [2]University of Puerto Rico - Mayaguez Campus, [3]University of Puerto Rico - Mayaguez Campus

Abstract: CRISPR-Cas9 technology has become one of the most groundbreaking discoveries of the 21st century. As a gene editing tool, CRISPR-Cas9 allows for sequence-specific targeting, which scientists have exploited to alter and remove genes in almost all eukaryotic cells. In spite of its implications in research, CRISPR-Cas9 has important limitations. Particularly, Cas9 interacts with a specific DNA recognition site, known as the protospacer adjacent motif (PAM). Without the correct PAM sequence, Cas9 is unable to bind DNA and cannot perform its endonuclease

function. Our current understanding of Cas9 and other CRISPR-associated proteins is deficient, and the characterization of novel PAM sequences will continue to improve the applications of CRISPR technology. Throughout this project, we aim to use functional metagenomics as a vehicle for bioprospecting novel CRISPR-Cas systems within different environmental samples of Puerto Rico. We analyzed two metagenomic datasets from the microbial and functional diversity of distinct water systems: the Guajataca water reservoir, and the Clara Cave and Empalme Sinkhole waters. Sequencing data was analyzed regarding CRISPR-Cas analogy through CRISPR databases via CRISPRCasFinder and NCBI-BLAST. Multiple sequence alignments were conducted to describe conserved regions in Cas genes using the ConSurf server. Several CRISPR-Cas-like regions were identified within the metagenomic datasets. Candidate prospects will be analyzed concerning Cas protein identity and function with in vivo and in vitro approaches. Throughout this approach, we expect to unravel new CRISPR-Cas systems, as well as characterize Cas protein orthologs within these environments respecting PAM sequence specificity and other functional and structural characteristics.

The Effects of Early Life Manganese Exposure on Dopaminergic Proteins in the Prefrontal Cortex and Striatum

Discipline: Life Sciences
Subdiscipline: Microbiology

Nelida Robles*[1], Donald Smith[2], Ellie Fisher[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: Elevated early life manganese (Mn) exposure is associated with attentional deficits in children and adolescents. Affected individuals often live in communities disproportionately impacted by higher levels of environmental manganese. Our rodent model studies have shown developmental Mn exposure disruptions in the catecholaminergic system function in the prefrontal cortex (PFC) and striatum (Str). In this study, we exposed male Long-Evans rats to Mn (50 mg/kg/d) during early development (P1 - 21) and were tested with a series of attention tasks in adulthood. We then imaged the animals using Positron Emission Tomography (PET) for functional dopamine D2 receptor (D2R) binding potential (BP) in the PFC and Str in the absence or presence of methylphenidate (MPH) challenge. PET imaging showed no measurable differences in D2R levels between Mn and control animals but higher levels of MPH-induced synaptic dopamine levels in the PFC of the Mn animals. To further elucidate the results from our PET scans, we developed an immunohistochemistry fluorescence microscopy method to quantify D2R and dopamine transporter (DAT) levels in the PET-imaged animals. Samples were cryosectioned (20 microns) and stained with D2R and DAT primary antibodies. Brain sections were imaged using Widefield Fluorescence Microscopy, and protein levels were quantified using Autoquant and Imaris software. With these results, we hope to understand the underlying mechanisms by which early Mn exposure affects attentional disfunction and provide insight into the use of MPH as a potential treatment for these neural deficits.

Coexpression of Wnt1 and WLS in 3T3 Cells Induce Filopodia

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Megan Voss*

San Francisco State University

Abstract: Humans function effectively with each other through communication, whether verbal or through pheromones to communicate implicit behaviors. Likewise, cells communicate by sending chemical signals from the “talking” cell to the “listening” cell. Cell communication is regulated by signaling molecules like Wnt (Wingless-related integration site) and WLS (Wntless), critical proteins in the Wnt signaling pathway. Wnt proteins are crucial in embryonic development and tissue homeostasis. Dysregulation of the Wnt pathway has been shown to cause embryonic defects, cancer, and neurological diseases. WLS is an essential integral membrane protein that binds to Wnt allowing for intracellular transport of Wnt to the cell membrane and filopodium. Inducing the Wnt signaling pathway in target cells requires Wnt transportation from Wnt producing to Wnt receiving cells. Current data illustrates filopodia’s critical role for Wnt intercellular transport. We have previously determined overexpression of WNT1 and WLS in chick neural crest cells and in HEK293T cells induce filopodia. Therefore, I hypothesize that the overexpression of WNT1 and WLS in 3T3 cell will induce filopodia. To test my hypothesis, I have successfully overexpressed WNT1 and WLS in mammalian cells, which have been confirmed through immunofluorescence assay. Using confocal microscopy, I will perform image analysis on transfected cells to determine the length and the amount of filopodia. I expect the WNT1 and WLS expressing 3T3 cells will induce filopodia; compared to the WNT1 and WLS non-expressing control 3T3 cells. If successful, I will have established a new model system for studying the induction of filopodia by WNT1 and WLS.

Climate change and plant-microbe interactions: water-availability influences the direction and specificity of microbial effects on plants

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jakob Joachin*
Cal Poly Humboldt

Abstract: Soil microbes are a key force behind plant community dynamics, and their effects on plants are often context-dependent and influenced by abiotic factors. Understanding how altered abiotic conditions affect plant-microbe interactions will help us better predict the consequences climate change will have on plant community structure and composition. In our study, we worked with a pathogenic soil fungi (Fusarium sp .), 3 native coastal prairie plant species, and 3 invasive plant species found in Houston, Texas. We manipulated water availability to simulate drought, average rainfall, and flooding conditions as our climate change treatment. Considering the plasticity of plant-microbe interactions, we hypothesized that the effect of Fusarium would differ by water availability, by host species identity, and by a combination of species-specificity and water availability. Each plant species was grown separately, with or without the presence of Fusarium , per watering treatment for 7 weeks, and we recorded weekly and final plant biomass. We tested treatment effects on total plant biomass by fitting generalized linear models with the fixed effects of plant species, watering availability, presence of Fusarium , and all possible interactions followed by a three-way ANOVA. The model most notably revealed significant microbial effects by host species identity (F 5, 324 = 5.89, P < 0.0001) and by a combination of host species identity and water availability (F 10, 324 = 2.93, P < 0.002). Our results highlight the complexity of plant community dynamics and that the species-specificity of microbial effects will be affected by a changing climate.

Identification and Analysis of a Cortical Subpopulation in a Mouse Model of DDX3X Syndrome

Discipline: Life Sciences
Subdiscipline: Neurosciences

Michael Flores*[1], Marta Garcia-Forn[2], Silvia De Rubeis[3], Alexa Von Mueffling[4], Praise Ola[5]
[1]Icahn School of Medicine at Mount Sinai, [2]Icahn School of Medicine at Mount Sinai, [3]Icahn School of Medicine at Mount Sinai, [4]Barnard College, [5]Alcorn State University

Abstract: DDX3X syndrome is a rare neurodevelopmental disorder primarily affecting females. It is caused by mutations in the X-linked gene DDX3X , yet its neurobiological mechanisms remain elusive. Ddx3x mutant mice (Ddx3x +/- females) exhibit developmental and behavioral deficits closely resembling the clinical phenotype of DDX3X syndrome. Further, Ddx3x +/- pups (postnatal day 3; P3) show excess glutamatergic neurons co-expressing molecular markers that lead to opposite cellular identities: CTIP2 for subcortical neurons and BRN1 for intracortical neurons. Little is known about this cortical subpopulation and how it is altered in Ddx3x +/- mice. We examine the co-expression timeline of CTIP2 and BRN1 by immunostaining cortices from Ddx3x +/- and control mice (Ddx3x +/+ females) across postnatal time points. We define the window of neurogenesis for CTIP2+BRN1+ neurons by marking progenitors with bromodeoxyuridine across embryonic time points. To identify targets innervated by CTIP2+BRN1+ neurons, we inject a fluorescent retrograde virus into cortical and subcortical areas of Ddx3x +/- and Ddx3x +/+ mice. We observed excess CTIP2+BRN1+ neurons in the primary motor cortex of adult Ddx3x +/- mice, in line with our previous observations at P3. CTIP2+BRN1+ neurons are decreased in premotor and primary somatosensory cortices of Ddx3x +/- mice. This imbalance might be due to changes in neurogenesis. We expect this imbalance to also be reflected at earlier postnatal time points. Finally, we expect CTIP2+BRN1+ neurons in Ddx3x +/- mice to display altered projections. These alterations may underlie the developmental and behavioral impairments caused by DDX3X syndrome.

Uncovering molecular mechanisms for rescuing FXN expression in FRDA utilizing programmable DNA binding molecules.

Discipline: Life Sciences
Subdiscipline: Genetics

Rocio Cisneros*[1], Tim MacKenzie[2], Graham Erwin[3], Ananya Vadlakonda[4], Michael P. Snyder[5]
[1]Stanford University, [2]Stanford University, [3]Stanford University, [4]Case Western Reserve University, [5]Stanford University

Abstract: Friedreich's ataxia (FDRA) is a rare, fatal, neurodegenerative disease characterized by the dysfunction of the peripheral and central nervous systems, critically affecting organs like the heart and pancreas. This condition is an inherited autosomal recessive disorder caused by an abnormal trinucleotide repeat expansion located in the first intron of the frataxin gene (FXN) that prevents transcription. Recently developed synthetic transcription elongation factors (Syn-TEFs) like Syn-TEF1 are a class of polyamide molecules that are programmable to bind to specific DNA sequences and have the capability of interacting with the transcription elongation machinery. Treatment of cells derived from FRDA patients rescues expression of the FXN gene, overcoming the silencing associated with the tandem repeats. However, Sny-TEF1 is a cumbersome molecule to work with in a clinical setting and the mechanisms of action are still unresolved. We hypothesize that chromatin remodelers are involved in both silencing the mutated FXN and in the rescued expression upon Syn-TEF1 treatment. The focus of our research is on locus specific isolation of proteins associated with the FXN gene. We will be developing a locus-specific chromatin isolation technique of reverse-ChIP followed by mass spectrometry to study the FXN locus in a cell line model system from a sibling derived FRDA positive and negative B-lymphocytes (GM15850 and GM15851). By identifying the proteins that change association with the locus in healthy and FRDA positive cells upon treatment with Syn-TEF1, we will begin to build a mechanistic understanding of how FXN expression is rescued leading to new therapeutic approaches.

Evaluation of Performance Between Machine-Learning Models and CARD to Predict Antibiotic Resistance in Bacteria

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

John Matthew Suntay*[1]and Pleuni Pennings [2]
[1]San Francisco State University, [2]San Francisco State University

Abstract: Antibiotic resistance among bacteria is an ongoing global health threat. To combat this threat, the Comprehensive Antibiotic Resistance Database, CARD, has been widely used to determine whether a specific strain would have antimicrobial resistance genes. A limitation of CARD is that data on each bacterial strain must be known before referencing. However, machine-learning models do not. By training the models with already known core and accessory genomes of a bacteria, machine-learning can be used to predict whether a new strain would be antibiotic resistant or susceptible. Currently, we have created four different machine-learning models, Random Forest, Gradient Boosted Trees, Logistic Regression, and Deep Learning to predict antibiotic resistance of E. coli. Our goal is to have our models identify, classify, and predict antibiotic resistance in bacteria and result in higher accuracies than CARD without much information on the new strain. Of the models that were created, Random Forest and Gradient Boosted Trees had resulted in accuracies upward of 90% after parsing through the dataset. For future directions, we will focus on hyperparameter tuning all of our models to see which machine-learning model would be the most efficient and yields the highest accuracy when compared to CARD. Afterwards, we plan to implement CARD with the same dataset and measure performance, via accuracy, and compare it to the multiple machine-learning models. We hope our analysis will convince physicians and pharmaceutical companies that machine-learning is a viable tool in automating diagnoses of patients creating effective patient plans.

Using machine learning to identify novel circadian behaviors

Discipline: Life Sciences
Subdiscipline: Neurosciences

Blanca Perez*[1], Larissa Rays Wahba [2], Erik Herzog[3], Jeff Jones[4]
[1]Brown University, [2]Washington University in St. Louis, [3]Washington University in St. Louis, [4]Texas A&M University

Abstract: Organisms have evolved circadian rhythms in behavior to anticipate daily opportunities and challenges such as mating and predation. However, the ethological investigation of behavioral rhythms has been traditionally limited to studying easy-to-measure behaviors on a circadian timescale or difficult-to-measure behaviors with limited temporal resolution. Manual scoring of recorded videos is commonly used to study behavior, but this method can be inaccurate, variable across researchers, and time-consuming. Here, we tested the hypotheses that circadian genotype and sex affect daily patterns of motor behaviors. We used a novel machine-learning classifier, DeepEthogram (Bohnslav et al. 2021), to automatically score eight complex behaviors from millions of video frames of singly-housed mice. We recorded movies from 32 male and female wild-type mice and vasoactive intestinal peptide (VIP)-deficient mice, which lack a neuropeptide critical for circadian synchrony and thus exhibit deficits in circadian wheel-running behavior. Our model uses convolutional neural networks to identify movement, extract features from raw pixel values of individual frames, and classify these features into temporally sequenced behaviors. DEG predictions for each behavior were highly correlated with videos labeled by five trained human classifiers. Using our model, we observed several phenotypes that were consistent with previous locomotor activity results. We also identified phenotypes that had not been previously reported including sex-specific differences in "nesting" and "digging" rhythms. These results demonstrate that machine learning can be used to study circadian behaviors that were previously difficult or impossible to observe and will allow for the rapid circadian phenotyping of mice with different genotypes or disorders.

Identifying underlying molecular mechanisms and corrective drug treatments in a mouse model of CTNNB1 Syndrome

Discipline: Life Sciences
Subdiscipline: Neurosciences

Leeanne Vazquez Ramirez*[1], Jonathan Alexander[2], Michele H. Jacob[3]
[1]University of Puerto Rico at Cayey, [2]Tufts University, [3]Tufts University

Abstract: β-catenin (CTNNB1) is a ubiquitously expressed protein that regulates synaptic density, maturation, plasticity, and skeletal muscle function. Its key role in cadherin-based adhesion complexes and canonical Wnt signaling transduction is important for the proper development and function of the brain. Haploinsufficiency caused by partial or complete deletion of one CTNNB1 allele in humans results in CTNNB1 syndrome, a developmental disorder characterized by intellectual disabilities and reduced motor capabilities. There are no treatments because the pathophysiological mechanisms are poorly defined and few murine model studies of CTNNB1 haploinsufficiency extend beyond embryogenesis. Thus, we generated a CTNNB1 heterozygous mouse line with full-body haploinsufficiency via deletion of one allele. Preliminary studies of the CTNNB1 mice showed reduced cognitive and motor capabilities, relative to littermate controls. Our goal is to identify molecular changes and treatments to correct these deficits. We hypothesized that drug treatments that target β-catenin regulators will normalize β-catenin levels and ameliorate the phenotypes caused by the haploinsufficiency. Drug #1, which targets a β-catenin regulator, normalized β-catenin levels and significantly improved muscle grip strength and associative learning of CTNNB1 heterozygotes that closely resemble wild-type littermates. However, Drug #2, which targets another regulator, did not significantly alter β-catenin levels and the motor and cognitive disabilities, suggesting specificity of the molecular targets. Overall, our CTNNB1 mouse exhibits motor and learning disabilities, similar to individuals with CTNNB1 syndrome. Using this preclinical in vivo model, we provide proof-of-concept for the potential of pharmacological approaches to remedy this disorder by showing that Drug #1 corrects disease-relevant phenotypes.

The Heterogeneity and Plasticity of Memory CD8 T Cell Clones

Discipline: Life Sciences

Subdiscipline: Physiology/Pathology

Mollie Black*[1], Kamir Hiam-Galvez[2], Ansuman Satpathy[3], Katalin Sandor[4]
[1]Stanford University, [2]Stanford, [3]Stanford University, [4]Stanford University

Abstract: When exposed to a pathogen, T cells proliferate, expand, and then contract after pathogen clearance; leaving behind a memory pool. These memory T cells provide potent protection against secondary exposure. Each T cell contains a T cell receptor (TCR) that recognizes a specific antigen. Little is known about the plasticity and differentiation trajectories of individual memory T cell clones (T cells with the same TCR). We hypothesize that individual memory T cell clones have fixed proliferative capacities and differentiation trajectories. To test this we have established an in vivo mouse model system to trace the same T cell clones across different hosts. To comprehensively test clonal memory T cell differentiation plasticity, we first infected donor mice with Lymphocytic choriomeningitis virus (LCMV), then transferred memory T cells from a single donor into multiple new congenic hosts and rechallenged with LCMV. Using paired single cell RNA and TCR sequencing, we characterized clonal transcriptional states in different hosts and found similar gene expression profiles. We further found that clonal proliferative capacity is fixed across multiple hosts. Between different clones, we found substantial heterogeneity in expansion and transcriptional profiles. We next looked at how the same memory clones behave in chronic versus acute LCMV infection and preliminary results suggest that donor memory cells are more resistant to exhaustion than primary host cells. Understanding the heterogeneity of clonal T cell differentiation can help us discover the mechanisms that drive optimal T cell function to help create better vaccines and adoptive T cell therapies.

The Impact of Nutrition on Fecal Odors and Intraspecific Olfactory Communication in Gromphadorina Portentosa

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Samone Donald*[1], Steven A. Juliano[2], Katherine G. Evans[3]
[1]Illinois State University, [2]Illinois State University, [3]Illinois State University

Abstract: Olfactory cues play a large role in aggregation and social communication in the order Blattodea (roaches and termites). Previous research postulated that roaches could communicate geographical heredity through gut bacteria shed in feces due to the reflection of the local environment on a colony's gut bacteria, which creates a distinguishable odor. Hence, roaches producing favorable fecal odors would elicit the strongest aggregational response. This study tests whether fecal olfactory cues influence aggregation preferences in a currently unresearched species, Gromphadorhina portentosa the Madagascar hissing cockroach, and whether those preferences are related to nutrition. A four-choice behavioral assay was used to differentiate the directional responses shown in a colony of G. portentosa when presented with fecal olfactory cues produced by conspecifics provisioned on diets composed of greater vs. lesser nutritional value and familiar vs. unfamiliar food. Pairwise analysis revealed G. portentosa can identify scent differences in feces produced by conspecifics and are significantly attracted to feces derived from diets of the greatest relative nutrition (X2(2, N=80)=66.325, p=< .00001). Based on these results, we propose that relative nutrition of foods consumed is likely more important for the formation and longevity of cockroach aggregations than a familiar colony scent, as previously suggested. To expand this research, microbial analysis would determine if G. portentosa's ability to distinguish nutritional density in feces is related to the specific odor caused by gut bacteria

acquired from the local environment. Findings that would provide a new perspective on symbiotic gut bacteria and fecal based communication strategies.

Use of Bioinformatics to Distinguish H. sapiens, H. Denisova, and H. Neanderthalensis through the lens of miRNA

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Gabriel Gonzalez*[1]and Nathan Lents [2]
[1]John Jay College of Criminal Justice, [2]John Jay College of Criminal Justice

Abstract: Evolutionary genetics aims to identify changes in genes that lead to the evolution of a species. With the use of genomic comparisons and analysis, the genome of modern humans can be compared to that of Neanderthals and Denisova hominins in order to reveal specific differences that may have been crucial to the unique evolutionary trajectory of each species. In this project, we specifically focus on the evolution of microRNA genes in these three lineages. We use BAM/SAM tools to align the genomes and extract the full gene sequence of every single microRNA gene that's been annotated. We detect all the changes among the three genomes and categorize them into “entire microRNA gene”, the “mature siRNA sequence” or “the seed region” of the microRNA. We then examine the list of microRNAs that are distinct in each species and assemble the gene expression regulatory networks in which these microRNAs participate. This work aims to build a full picture of the unique function of these species-unique microRNAs in each lineage. Within each lineage, we identified 20-24 microRNAs that have evolved uniquely in that species. So far, our analysis indicates that the gene regulatory networks most impacted by the recent evolution of microRNA genes in these human species are those involved with the embryonic development of the nervous system. These discoveries shed light on the genetic events that facilitated our unique evolutionary fate.

Phage Therapy for Apple-Tree Fire Blight Control

Discipline: Life Sciences
Subdiscipline: Microbiology

Katherine Vignona*[1]and Nana Ankrah [2]
[1]State University of New York at Plattsburgh, [2]State University of New York at Plattsburgh

Abstract: Apple trees are important to the agricultural industry in New York State and having healthy viable trees is critical to the success of this industry. The bacterium Erwinia amylovora is the causative agent of “fire blight”, a destructive disease that forms cankers on apple trees and results in severe reductions in apple yields. The purpose of this study was to isolate bacteriophage (viruses that infect bacteria) capable of killing Erwinia amylovora. We hypothesized that bacteriophage capable of infecting and killing Erwinia amylovora would be abundant in the soil around diseased fire blight apple trees. To isolate Erwinia-infecting bacteriophage, fire blight infected leaves were collected from an apple orchard on Long Island, NY and incubated on tryptic soy agar plates. Eight unique bacteria were isolated from the fire blight infected leaves to use as hosts for bacteriophage enrichment and isolation. DNA samples of all eight microbes have also been submitted for identification by Sanger sequencing. Bacteriophage enrichments were generated by incubating the eight isolated bacteria with the supernatants of soil samples collected from the apple orchard. We have currently isolated eight unique bacteriophages capable of infecting and killing bacteria isolated from fire blight leaves.

The newly isolated bacteriophage will be used to set up a host-phage infection system to streamline the methodology for using bacteriophage to control fire blight in apple orchards. Altogether, data from this study will help provide the methodology to adopt bacteriophage as an alternative therapy to treat diseases caused by bacterial infections in economically important plants.

Respiration of the biopolymer polyhydroxybutyrate by marine microorganisms for the development of bioplastic materials

Discipline: Life Sciences
Subdiscipline: Microbiology

Madison Cohen*[1], Alessandra Valdivia [2], Dr. Alyson Santoro[3], Natalie Dornan[4], Chance English [5], M. Ofelia Aguirre Paden[6]
[1]University of California, Santa Barbara, [2]University of California, Santa Barbara, [3]University of California, Santa Barbara, [4]University of California, Santa Barbara, [5]University of California, Santa Barbara, [6]University of California, Santa Barbara

Abstract: Petroleum-based plastics make up a large portion of oceanic plastic pollution, and it is estimated that by the year 2050 the weight of plastic in the ocean will outweigh that of fish. Biopolymers are being investigated because while they have the capability to replace some of these petroleum-based plastics, it is not well understood how viable of a choice they are in marine environments. Since a carbon and energy source for some marine microorganisms can be found in the biopolymer polyhydroxybutyrate (PHB), isolates of these microorganisms gathered from multiple marine locations at the University of California, Santa Barbara are being jointly investigated with different PHB sources in order to obtain preliminary degradation rate measurements. These rates were calculated in the laboratory using an automated biological oxygen demand sensor to observe the drawdown of oxygen as a proxy for respiration to measure the rate of PHB degradation. The preliminary calculations show a degradation rate for PHB by microorganisms found in natural seawater to be 1.6 x 10 -3 d -1 under experimental conditions, which suggests that it would take approximately 8 years to degrade 2 kg of the compound. Future experiments will involve measuring respiration and degradation rates at temperatures that mirror different marine environments while using different forms and concentrations of PHB. This data can further be used to aid in the development of bioplastic materials that will more quickly degrade in marine environments with the help of naturally-occurring marine microorganisms.

Microplastic Abundance Across Trophic Levels in Freshwater Streams in South Central Pennsylvania

Discipline: Life Sciences
Subdiscipline: Environmental Science

Aaliyah Pabon*[1], Joellina Stewart [2], Kiel Vega[3], Jessica Nolan[4], Bridgette Hagerty [5], Karl Kleiner[6]
[1]York College of Pennsylvania, [2]York College of Pennsylvania, [3]York College of Pennsylvania, [4]York College of Pennsylvania, [5]York College of Pennsylvania, [6]York College of Pennsylvania

Abstract: Plastic pollution is pervasive and has negative effects on freshwater environments. Microplastic particles (< 5mm) infiltrate freshwater streams through inconspicuous sources (e.g., household washing machines) and the breakdown of macroplastics. Additionally, they may be transferred through the food web by aquatic organisms that mistake them for viable food sources. The impacts of microplastics may also differ based on abundance, which is influenced by land use. We addressed these concerns by comparing the abundance of microplastics in two second-order streams, Tyler Run and Hollow Creek, that have different levels of urbanization in York County, Pennsylvania. Tyler Run is heavily impacted by urbanization while Hollow Creek is impacted by agriculture. Both streams are in the Chesapeake Bay watershed, where research on the impacts of plastic pollution is limited. We hypothesized that Tyler Run would have a significantly higher abundance of microplastics than Hollow Creek among all matrix types. We quantified microplastics in stream water, macroinvertebrate, and small fish. Macroinvertebrates (family Ephemeroptera) were sampled using standard kick-net protocols and fish were sampled opportunistically using seine and kick nets. Animal tissues were digested using hydrogen peroxide. All samples and controls were filtered and microplastic particles were counted and confirmed with multiple observers. Our results demonstrated that microplastic fibers were present across all matrix types, with a greater abundance in the urban creek with the interesting exception of the fish. This study can help raise awareness of the severity of microplastic pollution in small streams, which ultimately contributes to plastic pollution in the Chesapeake Bay.

Genital Papilla Morphogenesis in Gravid Female Blue-banded Gobies, Lythrypnus dalli

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Shanna Barber*[1], Katrina White [2], Devaleena Pradhan[3]
[1]Idaho State University, [2]Idaho State University, [3]Idaho State University

Abstract: Female genitalia have been largely neglected in studies of genital evolution, perhaps due to the long-standing assumption that they are relatively invariable and therefore taxonomically and evolutionarily uninformative in comparison with male genitalia. Here, we investigated this idea in Lythrypnus dalli, a bi-directionally hermaphroditic fish, that exhibits complex and sexually dimorphic reproductive behaviors. The external genital papilla (GP) undergoes dramatic morphogenesis concurrent with physiological changes associated with sex change. Males have a longer, tapered GP with length:width ratio (L:W) >1.6, female to male transitioning fish have a conical GP with L:W 1.4-1.6, and females have a L:W <1.4. In this study, we hypothesized that the variation in female GP shape is associated with the gravidity state of females. We investigated the GP L:W of sexually mature female L. dalli of variable sizes (N=250). The standard length of fish was not related to gravidity; thus smaller fish were gravid as larger fish. There was an inverse relationship between GP L:W and gravidity, such that a wider GP was associated with more gravid females. We categorized the shape of GP as ‘rounded’ if they were not gravid versus “flattened” for gravid fish. It is possible that a wider morphology allows for a more efficient release of mature vitellogenic eggs. Interestingly, we also discovered females whose GP had a ‘tubular’ appearance; these could be fish that have recently transitioned from male to female. Differences in steroid hormone sensitivity via receptor expression might underlie morphological changes in GP in gravid females.

New Insight Into The Molecular Mechanism Of Obesity-Associated Metabolic Inflammation: A Novel Cross-Talk Between Autophagy And NF-κB Pathways

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Kristy Philogene Philogene*[1]and Zulema Cabail [2]
[1]State University of New York, Old Westbury, [2]State University of New York, Old Westbury

Abstract: A significant underlying cause of insulin resistance induced by obesity is a chronic low-grade systemic inflammation. This meta-inflammation results from the infiltration of immune cells into the adipose tissue (AT), driving a pro-inflammatory environment. However, the cellular and molecular mechanisms responsible for the initiation and maintenance of the inflammatory response in AT are not completely understood. The goal of this study is to investigate how such metabolic-induced inflammation is chronically sustained. Our lab have shown that macrophages stimulated with saturated fatty acids (SFA) polarized toward a pro-inflammatory state via NF-κB pathway and this was accompanied by decrease levels of autophagy, a normal physiological process that maintains homeostasis, and regulates inflammation. We hypothesize that a link between NF-κB and autophagy plays a significant role in sustaining metabolic inflammation. We addressed this hypothesis using the macrophage cell line, RAW264.7, and exposed them to a lipid-rich microenvironment to mimic the obese AT metabolic inflammation. To test the crosstalk between NF-κB and autophagy, we utilized an inhibitor of NF-κB, BOT-64. We found that the interplay between NF-κB and Autophagy pathways is mTOR-mediated as indicated by a significant gain in the levels of the autophagy marker LC3 after NF-κB activation was blocked with BOT-64, and this was accompanied by the recovery of TSC1 activity and the decrease of phospho-mTOR in the presence of NF-κB inhibitor. These results are significant because they provide new insights into the molecular underpinnings of the obesity-induced AT inflammation, which is an essential cause of insulin resistance and Type 2 Diabetes.

Evaluating Pesticide Resistance of Sumithrin in Hyalella azteca

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexandra Figueroa*[1]and Helen Poynton [2]
[1]University of Massachusetts Boston, [2]University of Massachusetts Boston

Abstract: In 2019, there were outbreaks in Massachusetts of Eastern Equine Encephalitis (EEE), a rare, but lethal virus that was transferred through infected mosquitoes. Due to the outbreaks in specific towns, there were spray events with a pesticide having two chemicals, Sumithrin and piperonyl butoxide (PBO), to reduce the spread of EEE in mosquitoes. Although the levels of chemicals were low in drinking water post-spray events, there is limited information on the effects of Sumithrin, especially in non-target species like Hyalella azteca , a freshwater amphipod with known high pesticide sensitivity. It is hypothesized that samples from exposed sites have mutations, which is an indicator of environmental exposure in highly polluted areas for adaptation. There was a collection from exposed sites within the Bristol-Plymouth region and a control site outside all spray zones, followed by samples undergoing a DNA Isolation and Genotyping Assay protocol. The second component of the project consisted of attending the MA Mosquito Control Task Force (MCTF) sessions. After analyzing sequences, there was a mutation detected in the I936 region in 11/24 controls samples, compared to no mutations among the 21 exposed sites samples. The MCTF's top, final recommendations that passed with full support include Best Practice BP-5: Statewide Education on Mosquito Management, BP-12: Monitoring and Evaluations After Spraying, and Learning Engagement-1: Online system for requesting property exclusions and property opt-outs, which were the most impactful for proper utilization

and usage of pesticides. Future work includes a toxicity test and continuing regulating pesticides to prevent excess chemical inputs.

Modeling fallopian tube-induced tumorigenesis and the influence of increased number of ovulations

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Alfredo A Carrero*[1], Joanna Burdette [2], Angela Russo[3]
[1]University of Illinois at Chicago, [2]University of Illinois at Chicago, [3]University of Illinois at Chicago

Abstract: High-Grade Serous Ovarian Cancer (HGSOC) is the most common and letal histotype of ovarian cancer and its high mortality is due to the difficulty of detecting the disease at an early stage. Previous studies have shown evidence of HGSOC originating from the fallopian tube epithelium rather than from the ovaries. Therefore, studying early tumorigenesis from the fallopian tube may help develop a novel strategy for the early detection of HGSOC. Retrospective investigations of human patients have shown evidence that the inhibition of ovulation reduces the risk of developing ovarian cancer, thus we aim to investigate how an increased number of ovulations affects early tumorigenesis. Previous studies have shown that the factors secreted during ovulation might damage the DNA of the fallopian tube epithelial cells suggesting they may play a role in tumorigenesis, however, the role of the increased number of ovulations on fallopian tubes has not been studied. We identified the proteoglycan Versican, as the critical component of murine ovarian secretion inducing migratory and invasive properties of FTE cells. We also show, consistent with previous studies that Versican secretion is increased close to ovulation time. Herein, we manipulated a transgenic mouse model of FTE-derived tumorigenesis to study changes in versican expression as well as genetically modified cells to study the role of versican on invasion and metastasis. The results from our study will provide new insights into the early events occurring during FTE tumorigenesis and metastasis to the ovary.

The On-going Arms Race between Host Cell Antiviral Factors and Viral Antagonists

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Magdalena Sotelo*[1]and Adam P. Geballe [2]
[1]The University of Washington, [2]Fred Hutchinson Cancer Center

Abstract: Protein kinase R (PKR) is a host antiviral factor that shuts off translation in response to double-stranded RNA that accumulates during viral infection. Many viruses, including cytomegaloviruses (CMVs), encode proteins that inhibit PKR and rescue viral protein synthesis in infected cells. In the case of CMV, the “terminal repeat short 1” (TRS1) protein antagonizes PKR. Analyses have shown that PKR has been evolving under positive selection among primates, likely to evade viral factors such as TRS1. Consequently, the ability of TRS1 encoded by different CMVs to block PKR is quite species-specific in human and Old-World monkey (OWM) cells. Thus, it is surprising that TRS1 encoded by a New World monkey (NWM) virus, squirrel monkey CMV (SqCMV), antagonizes hominoid and OWM PKR. I hypothesize that SqTRS1 has broad activity against diverse PKRs because it interacts with a conserved domain that is different from the region bound by the TRS1 gene from human and OWM CMVs. To test this hypothesis, I first tested PKR function using a reporter gene-transfection assay and demonstrated all PKRs inhibited translation, and that SqTRS1 was able to block all the PKRs, consistent with my hypothesis. Unexpectedly, TRS1 from HCMV, was also able to counteract the effects of SqPKR. ----These results were confirmed using viral replication assays. Thus, human and SqTRS1 may share binding sites on PKR. Understanding the evolution and molecular mechanisms that have diverged in the ongoing “arms race” between host and viruses can reveal insights into the risks and barriers to cross-species transmission of viruses.

How the Tfh Response in Neonates Fed Breast Milk Devoid of Maternal Antibodies Impacts the Composition and Function of Intestinal Microbes

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Stephanie Torres*[1], Dr. Meghan Koch [2], Bingjie Wang[3]
[1]University of Washington, [2]University of Washington, [3]University of Washington

Abstract: Breast milk is essential to a child’s health as it contains immune-modulating factors, including antibodies that shape infant immune responses to pathogenic and beneficial microbes (such as the gut microbiota). However, infant formula lacks maternally derived immune modulators such as antibodies. Using a mouse-model, our group previously discovered that breastmilk antibodies help establish mutually beneficial relationships between the gut microbiota and immune system in infants. Specifically, we found that offspring lacking breastmilk antibodies mount dysregulated immune responses to the microbiota characterized by the expansion of CD4T follicular helper(Tfh) cells and associated germinal center(GC) B cells in gut associated lymphoid tissues. Tfh driven immune responses can alter the composition and function of the microbiota. One such function is colonization resistance, whereby the microbiota competes with pathogens to resist host infection. I hypothesize that the increase in Tfh and GC-B cells in pups lacking maternal antibodies fundamentally alters the function of the intestinal microbiota. To test this hypothesis, I first optimized a system to ablate Tfh and associated GC-B cell responses in offspring lacking maternal antibodies by treating weanlings with anti-ICOSL. Next, I infected Tfh-ablated and control animals that received or not receive breastmilk antibodies with Salmonella typhimurium, a bacterial pathogen that must compete with the microbiota to successfully colonize the host. I found no significant difference in susceptibility to Salmonella typhimurium between the maternal antibody sufficient or deficient groups that were ablated of Tfh-cells or not. Overall, my work aids in our understanding of how breastmilk antibodies shape long-term host health.

Environmental Escherichia coli Harbors Multidrug Resistance Region that is Distributed Among Diverse Taxa

Discipline: Life Sciences
Subdiscipline: Biology (general)

Camryn Zurita*[1], Luis Mota-Bravo [2], Iván Muñoz-Gutiérrez[3]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: By the year 2050, antibiotic resistant bacterial infections will cause more global deaths annually than cancer. We hypothesize that aquatic environments are reservoirs of antibiotic resistance genes (ARGs) and propose that horizontal gene transfer events are disseminating these genes. In this project, the genome of environmental Escherichia coli SW3232 was analyzed for its antibiotic resistance profile. Isolate SW3232 was collected from Rock Creek Pond in Kensington, Maryland and identified as E. coli by MALDI-TOF. Its resistance phenotype was determined by disk diffusion tests. Plasmid annotation was completed using PATRIC, CGE, ISfinder and NCBI databases. Isolate SW3232 displayed resistance to six classes of antibiotics. The sequenced and assembled plasmid shows that the isolate contained one 127 kbp plasmid, encoding a novel multidrug resistant region (MDR) containing nine ARGs flanked by more than twenty transposases. Bioinformatic analysis shows that sections of the MDR are described on plasmids of different incompatibility types in diverse genera with 100% nucleotide similarity. This suggests that transposases are facilitating the insertion of ARGs into DNA molecules. Additionally, the spread of these genes across different genera supports the idea that conjugation is responsible for the dissemination of resistance plasmids. The examination of this E. coli genome shows the role that transposition and conjugation have in antibiotic resistance. Surveying the environment for drug resistant bacteria helps us understand the reservoirs of genes conferring resistance to multiple drug classes.

Effect of Fast Transcription on Nucleosome Landscape

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Olivia Lopez*[1], Srinivas Ramachandran [2], Irma Zenteno[3]
[1]Metropolitan State University of Denver, [2]University of Colorado School of Medicine, [3]Metropolitan State University of Denver

Abstract: Transcription by RNA polymerase II (RNAPII) is much more efficient on naked DNA templates compared to DNA wrapped around histones in vitro . Only a small percentage of RNAPII can transcribe across nucleosomes. The main focus of this project is to ask the extent to which RNAPII elongation is involved in disrupting the nucleosomal barrier in vivo . To ask how much RNAPII itself influences nucleosome disruption, we used a mutant RNAPII that has a faster polymerization rate compared to wild type. Our lab has developed tools that use genomics to infer the structure of nucleosomal intermediates in cells. Using micrococcal nuclease treatment followed by sequencing (MNase-seq), we are mapping nucleosomal intermediates in vivo . We are now performing the sequencing and analysis of these completed MNase-seq experiments. We predict faster RNAPII to result in more transient nucleosomal intermediates or in other words, a decrease in intermediate structures. If this proves to be true, our results would show that RNAPII has a major role in setting the chromatin landscape rather than the chromatin landscape setting RNAPII activity. Further, this would show that the chromatin landscapes we observe in active genes is a function of RNAPII elongation speeds.

Boosting Plant Immunity to Parasitic Nematodes through CRISPR Gene Editing

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Andrea Romero*[1], Damaris Godinez-Vidal [2], Simon Groen[3]
[1]University of California, Riverside, [2]University of California, Riverside, [3]University of California, Riverside

Abstract: Ten to twenty percent of crop plant yield is lost each year due to attack of plant roots by microscopic nematode worms, contributing to economic hardship and food insecurity in tropical and sub-tropical regions. The main culprit is the root-knot nematode (Meloidogyne incognita) , whose parasitic infection is defined by the root galls it creates at feeding sites. Galling prevents water and nutrient uptake, resulting in reduced plant fitness, quality, and yield. Tomato (Solanum lycopersicum) is particularly vulnerable to M. incognita since this nematode

has evolved resistance-breaking phenotypes in response to cultivars harboring the Mi-1 gene, which is used to trigger effective plant resistance upon nematode detection. Previous work in the model plant Arabidopsis thaliana identified a G-type lectin receptor kinase as a negative regulator of plant resistance to M. incognita . When this kinase is rendered inactive, plants show heightened immunity to nematodes. Thus, we hypothesize that we could locate a similar negative regulation gene in tomatoes. Using Agrobacterium-mediated delivery of CRISPR/Cas9, we have knocked out the functionality of the orthologous gene in tomato and successfully identified gene-edited lines through PCR screening of progeny plants. Plants that were homozygous for the knock-out mutation were inoculated with nematodes to determine the role of the ortholog in plant resistance. This poster will report the findings to date of this ongoing study. Our approach not only expands knowledge on the genetic basis of plant immunity, but could kick-start more efficient management practices of nematode pests in agriculture.

Impact of host stroma on the anti-tumor effects of metronomic chemotherapy

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Laura Ronquillo Silva*[1], Hector Padilla [2], Alejandro Sanchez[3], Ryley Stewart[4], Serina Batson [5], Guido Bocci[6], Giulio Francia[7]
[1]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas,
[2]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas,
[3]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas,
[4]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas,
[5]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas,
[6]Dipartimento Di Medicina Clinica e Sperimentale, Università Di Pisa, Pisa, Italy, [7]Border Biomedical Research Center, University of Texas at El Paso (UTEP), El Paso, Texas

Abstract: Metronomic chemotherapy is the continuous low dose administration of chemotherapy, and it has shown anti-tumor activity in preclinical models as well as in the clinic. A number of mechanisms of action of metronomic chemotherapy include immune activation in addition to inhibition of tumor angiogenesis. We set out to test the hypothesis that in immunodeficient mice the response of prostate xenografts to metronomic cyclophosphamide should be equivalent in nude mice and in SCID mice. To test this, PC3 human tumor cells were implanted subcutaneously into nude mice and SCID mice (n=5 mice/group). Cyclophosphamide was added to the mice drinking water once they had established tumors so that the dosage would be 25mg/kg/day. Our results show that over months of tumor monitoring by twice-weekly caliper measurements, PC3 tumors initially responded in nude mice and shrank, then after 2 weeks they relapsed under continuous therapy. In contrast, no tumor regression was observed in SCID mice, where metronomic therapy only caused a significant tumor delay. Since nude mice and SCID mice have a few differences, including the presence of B cells absent in SCID mice, these results indicate that the anti-tumor effect of metronomic chemotherapy is impacted by host immune and/or stromal components that can be observed even in immunodeficient mice. The impact of these results is that they shed light on how the host can contribute to the effectiveness of metronomic chemotherapy. Our conclusion is that tumor regression by metronomic chemotherapy involves a host component possibly related to the B cell population.

Prediction of Antimicrobial Resistance Profiles in Escherichia coli Using Machine Learning and ResFinder

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Kristiene Recto*[1]and Pleuni Pennings[2]
[1]San Francisco State University, [2]San Francisco State University

Abstract: Antimicrobial resistance (AMR) is a global health threat. To fight against antibiotic-resistant pathogens, it is essential to identify the strains that are resistant or susceptible to antibiotics. ResFinder relies on literature for well-studied AMR mechanisms to accurately predict resistance/susceptibility profiles. The aim of this study is to evaluate the performance of Machine Learning against ResFinder in predicting antibiotic resistance profiles in Escherichia coli (E. coli). Machine-learning learns from input data and does not require prior knowledge to make predictions. We set out to create multiple machine learning models and compare the prediction results of each model against multiple antibiotics with the ResFinder program. From these models, we saw that Gradient Boosted Trees performed better than Random Forest because this classifier combined many decision trees in order to reduce overfitting. This in turn increased the accuracy of the model because this model does not learn from previously used trees. Our expected result is that machine-learning will yield higher accuracy than ResFinder when predicting the resistance profiles of E. coli. For future directions, we will add hyperparameters to increase the accuracy of our models, test Resfinder against our machine-learning models, and apply the models to multiple bacterial species. Our project can improve machine learning for predicting antibiotic resistance during an outbreak which will ultimately improve patients' health.

Identification of Lethal Mutation in D. melanogaster via Complementation Analysis

Discipline: Life Sciences
Subdiscipline: Genetics

Trevor Kotchman*[1]and Tracy Dohn[2]
[1]Waynesburg University, [2]Waynesburg University

Abstract: There are many similarities in the genomes of Drosophila melanogaster (fruit flies) and humans. As such, the Drosophila genome can be used to help understand and detect genetic diseases in humans. Complementation analysis is a common process in genetics in which multiple test crosses are performed between a specimen with an unknown deficiency and specimens with known deficiencies. If the deficiencies are in the same gene, then the offspring will be unable to survive (as they will not have a functional copy of the essential gene). In this experiment, complementation analysis is used to map the gene responsible for a recessive lethal phenotype in D. melanogaster . Out of the lines being tested, current evidence suggests that presently examined lines are complementary to the lethal mutation. Additional lines are now being examined to find the gene noncomplementary to the lethal mutation. By characterizing the lethal mutation, it can be determined what biological process is disrupted and how the gene is necessary to that process, which would provide genetic insights applicable to Drosophila as well as to humans. This data is useful for characterizing genes, and knowledge of this deficiency will allow greater understanding of genetic diseases and potentially help discover treatments for them.

Developing a homemade dry/wet deposition sampler using Raspberry Pi.

Discipline: Life Sciences

Subdiscipline: Environmental Science

Damian Santiago-Sosa*[1], Bryan E. Rosado Maldonado [2], Pedro Maldonado[3], Natasha DeLeon-Rodriguez[4]

[1]Inter American University Of Puerto Rico , Metropolitan Campus, [2]Inter American University Of Puerto Rico, Metropolitan Campus, [3]Inter American University Of Puerto Rico, Metropolitan Campus, [4]Inter American University Of Puerto Rico , Metropolitan Campus

Abstract: Weather forecasting in Puerto Rico can be highly unpredictable and depends on the availability of the Doppler radar. Atmospheric studies, specifically bioaerosols, rely on sterile sampling devices and the forecast's accuracy to collect wet or dry aerosols deposition. Commercial dry/wet deposition samplers are not cost-effective and require space for their setup. For that reason, an automated wet deposition sampling system was designed and assembled to isolate bioaerosols present in rainwater. The important aspect of this equipment is that it is partially autonomous as it closes and opens when it detects rain. The automatization of the sampler aids to maximize the sampling method, which is prone to contamination due to human error. A Raspberry Pi computer was used to program a series of sensors for rain detection and an automated arm to obtain the samples when it rains and closes when it stops. It can also support a wireless mechanism that sends text messages to let the user know when the sample is collected. This project aims to build a low-budget but precise automated sampling system with proficiency in aseptic techniques to understand bioaerosols associated with rainwater.

Defined power limits prevent cellular damage during longitudinal in vivo 3-photon imaging of mouse cortical gray and white matter

Discipline: Life Sciences

Subdiscipline: Neurosciences

Alexandra Ramirez*[1], Ethan Hughes, PhD [2], Michael Thornton[3]

[1]University of Colorado, Denver, [2]University of Colorado, Anschutz Medical Campus, [3]University of Colorado, Anschutz Medical Campus

Abstract: In vivo 2-photon microscopy (2P) allows for longitudinal tracking of individual cells over time; however, this method is limited to depths of ~400 μm into the mouse cortex. The development of in vivo 3-photon microscopy (3P) increases this depth limit to ~1200 μm, which includes the subcortical white matter. Because 3P requires high pulse energy, the potential for tissue damage is significantly higher than 2P, and such effects are magnified with longitudinal imaging. In this study, we tracked individual oligodendrocytes over ~3 months with longitudinal 3P imaging. Following the study, we used correlative post-hoc immunostaining of longitudinally imaged brain regions to assess multiple markers of cellular and molecular stress. We found that, within our empirically determined laser power limits, longitudinal in vivo 3P imaging did not significantly increase the fluorescence intensities of markers of cellular reactivity in oligodendrocytes, microglia, astrocytes, or neurons when compared to contralateral controls. Then, we analyzed the intensity of molecular markers of oxidative stress and phototoxicity specifically in oligodendrocytes and similarly found no differences between imaged and contralateral cortical hemispheres. In contrast, we found increased markers of cellular reactivity, oxidative stress, and phototoxicity in tissues exposed to elevated laser power limits that resulted in laser-induced tissue damage. Our results broaden the understanding of region-specific differences in oligodendrogenesis and prove that longitudinal in vivo 3P imaging over multiple months is sustainable without inducing laser damage and cellular stress. These experiments provide important imaging and analysis guidelines for future studies employing longitudinal 3P imaging in the mouse brain.

Investigating Free-Living and Symbiotic Functions of ExoS/ChvI Target Genes in Sinorhizobium meliloti

Discipline: Life Sciences
Subdiscipline: Biology (general)

Kristen Abe*[1]and Esther Chen [2]
[1]California State University, Fullerton, [2]California State University, Fullerton

Abstract: Nitrogen is required for the growth and function of all living organisms, but the Earth's supply of atmospheric nitrogen is inaccessible to plants until it is reduced, or fixed, by the process of nitrogen fixation. Synthetic nitrogen fixation methods are used in the agricultural industry but contribute to environmental pollution, prompting research into biological nitrogen fixation. The process of nitrogen fixation by the microbe Sinorhizobium meliloti is performed in an endosymbiosis with legume plants. The ExoS/ChvI two-component signaling pathway is essential for this symbiosis to occur and also regulates other bacterial functions such as motility and biofilm formation. However, many other transcriptional target genes of ExoS/ChvI have functions that are currently unknown. Our research aims to characterize ExoS/ChvI target genes with unknown functions by studying their symbiotic and free-living bacterial phenotypes. For this study, phenotypes of overexpression and knockout strains will be observed and compared to a wild-type strain using growth assays of free-living bacteria in various media and symbiotic assays with a plant host. So far, we have successfully constructed knockout and overexpression plasmids for an ExoS/ChvI target gene. Once introduced into S. meliloti strains, we expect that these knockout and overexpression strains will have different phenotypes compared to wild type, indicating a role for the gene in bacterial and symbiotic processes. By investigating the functions of ExoS/ChvI target genes in S. meliloti , we will gain insight into the molecular mechanisms involved in biological nitrogen fixation.

Stimulation of the substantia nigra to dorsal lateral striatum circuit during fear extinction reduces fear relapse

Discipline: Life Sciences
Subdiscipline: Neurosciences

Rebecca Han*[1], Benjamin Greenwood [2], Esteban Loetz[3], Erik Oleson[4], John Wiseman [5]
[1]University of Colorado Denver, [2]University of Colorado Denver, [3]University of Colorado Denver, [4]University of Colorado Denver, [5]University of Colorado Denver

Abstract: Exposure therapy targeting fear extinction is often used to treat anxiety and post-traumatic stress disorders, but the long-term efficacy of exposure therapy is limited due to relapse phenomena such as fear renewal. Fear renewal occurs when fear responses return in contexts different from where extinction was learned. Substantia nigra (SN) dopamine (DA) activation during fear extinction promotes fear extinction and protects against fear renewal, but the specific postsynaptic targets where SN DA is acting to reduce renewal are unclear. Fear extinction supported by SN DA activation is associated with neural activity in the dorsal lateral striatum (DLS), a region implicated in habit learning processes which are resistant to contextual modulation. Therefore, the goal of the current experiment was to determine whether activation of the SN-DLS circuit during fear extinction can reduce renewal. Adult Long-Evans male rats received either control virus or AAV-Chr2-hSyn-mCherry bilaterally into the SN and bilateral optic ferrules in the DLS to optogenetically stimulate SN terminals in the DLS during fear extinction. Expression of neural activation marker cFos was used to verify the effectiveness of optogenetic stimulation. Activation of SN terminals in the DLS during fear extinction reduced fear renewal in a novel context without improving the fear extinction recall in the extinction context. The data suggest that the SN-DLS circuit is a novel target for freeing fear extinction memory from contextual modulation.

Characterizing a Locus Linked to Beech Bark Disease

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Mohamed Elgallad*[1], Suzy Strickler[2], Adrian Powell[3]
[1]Hunter College, [2]Cornell University, [3]Cornell Univeristy

Abstract: American beech (Fagus grandifolia) is an ecologically and economically important native species. This species has high-quality wood used for furniture, flooring, and firewood, and its beech nuts are a vital nutrition source for many species ranging from birds to deer and black bears. American beech trees are seriously threatened since their smooth bark makes them susceptible to Beech Bark Disease (BBD). BBD is caused by an insect-fungal complex attack that begins with scale insects (Cryptococcus fagisuga) that attack the tree to feed on its sap. Insect feeding in turn creates points of entry for the fungal pathogens that cause BBD. When American beech trees are evaluated for BBD, some individuals show signs of resistance; this resistance was previously genetically linked to a chromosomal locus. For this project, we gathered samples from infected individuals from Arnot forest for genome sequencing using Nanopore technology. This data was analyzed using a combination of software (guppy, racon, medaka) and was compared to previously collected and sequenced samples from both resistant and susceptible trees, in an attempt to characterize a locus that provides beech trees with resistance to this insect-fungal attack. Through this analysis, we identified a candidate locus containing a deletion mutation that confers resistance to Beech Bark Disease. These findings will help future conservation and breeding efforts and contribute to the restoration of ecosystems afflicted with BBD. Without intervention, BBD would continue to impact a large number of organisms that depend on this native tree species to survive.

TNFSF11 Mutants Support the Potential for Zebrafish to Model Genetic Determinants of Human Bone Mineral Density

Discipline: Life Sciences
Subdiscipline: Biology (general)

Priscilla Boatemaa*[1], Ronald Kwon[2], Jyoti Rai[3]
[1]University of Washington, Seattle, [2]University of Washington, [3]University of Washington

Abstract: Osteoporosis is a disease that increases risk of bone fractures and affects more than 200 million people worldwide. Bone mineral density (BMD), a key indicator for diagnosing osteoporosis, has a strong genetic component. Human genetic studies have identified thousands of genes potentially contributing to BMD; however, knockout mice have been generated for less than 10% of those genes. Zebrafish are an emerging model organism for biomedical research due to their capability for high-throughput genetic approaches. However, their potential to model the genetic component of human BMD is largely unknown. Tumor necrosis factor super family member 11 (TNFSF11) is a gene essential for bone resorption in humans. TNFSF11 encodes for receptor activator of nuclear factor kappa-B ligand (RANKL). When this ligand binds its receptor RANK, this stimulates osteoclast formation and activity, and bone resorption occurs. The purpose of this study was to determine if the function of T NFSF11 is conserved in zebrafish. We hypothesized that zebrafish with loss of tnfsf11 would exhibit high BMD, due to a decreased level of Rankl. To test this, CRISPR-based gene editing was used to create loss-of-function mutations in tnfsf11 . Wildtype and mutant fish were scanned using microcomputed tomography to analyze their BMD and microarchitecture. We found significant differences in bone density measurements between wildtype and mutant fish; the bones in the mutants were hyper-mineralized. These data indicate that the function of TNFSF11 in humans is conserved in zebrafish, which supports the potential for zebrafish to model genetic determinants of human BMD.

Whole Genome Sequencing and PCR Validation of Transgenic C. elegans

Discipline: Life Sciences
Subdiscipline: Genetics

Kianna Butts*[1]and Dr. Casonya Johnson[2]
[1]James Madison University, [2]National Science Foundation/James Madison University

Abstract: HLH-25 is a transcriptional repressor found in Caenorhabditis elegans (C. elegans) that affects embryonic development. Our overarching goal is to understand the molecular mechanisms by which HLH-25 regulates transcription. We previously used a combination of gene editing techniques to develop transgenic C. elegans strains that inducibly and ectopically express HLH-25. My goal was to use whole-genome sequencing to confirm the sites of insertion for these strains, and to determine if any other chromosomal abnormalities, insertions, or deletions were introduced into the genomes. To accomplish my goal, I completed NEB Next End Library Prep, conducted PCR to amplify my libraries, and performed whole-genome sequencing using a Mini-Seq Illumina DNA Sequencer. For the final analysis, I used Cryverse R and MACGene to assemble the genomes. Surprisingly, I discovered that the expected insertion was not present in the genome. To validate this result, I used PCR with primer specific to the array sequences to detect the transgene. Based on these data, we are repeating the sequencing and PCR validation with a new transgenic line. The sequenced strains and the annotated genomes will be made available to the C. elegans community.

T-bet-expressing CD11c+ myeloid cells are indispensable for pathogen clearance and host resistance against acute Toxoplasma gondii infection

Discipline: Life Sciences
Subdiscipline: Microbiology

Madison Schanz*[1]and Américo H. López-Yglesias[2]
[1]Indiana State University, Terre Haute and Indiana University School of Medicine, Terre Haute,
[2]Indiana University School of Medicine, Terre Haute

Abstract: The intracellular protozoan parasite, Toxoplasma gondii , is the causative agent of toxoplasmosis and chronically infects over 2 billion individuals worldwide. T. gondii can cause severe illness and even death in infected immunocompromised patients and fetuses.

Unfortunately, current treatment regimens for acute toxoplasmosis consist of repurposed medicines that can lead to severe side effects. Thus, our research focuses on how the host immune response results in rapid parasite elimination. Immunity against T. gondii is characterized by myeloid cell-derived IL-12, which mediates a CD4+ T cell (Th1)-derived interferon-gamma (IFN-g) response necessary for host survival. The molecule T-bet is classically considered as the lineage-defining transcription factor required for the effector function of Th1s; however, recent findings from our lab have demonstrated that T-bet is dispensable for Th1-derived IFN-g and T-bet-deficient mice succumb to infection significantly faster than mice lacking T cells. These findings suggest T-bet-expressing myeloid cells are essential for host survival. We hypothesize that T-bet-expressing myeloid cells are critical for innate host defense during acute T. gondii infection. To test our hypothesis, we used genetically modified mice and flow cytometry to identify and determine the role of T-bet-expressing myeloid cells during acute parasite infection. We have identified a novel subpopulation of T. gondii -mediated T-bet-expressing CD11c+MHCII- myeloid cells during parasite infection. Our data reveals this population possesses the highest frequency of intracellular parasites and kills T. gondii during infection. Furthermore, we demonstrate that T-bet-expressing CD11c+MHCII- myeloid cells are indispensable for parasite clearance and host survival during acute T . gondii infection.

Diurnal Photosynthetic Study in Allium Species

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Christopher Gomez*[1], Joseph Wood[2], Ivette Guzman[3]
[1]New Mexico State University, [2]New Mexico State University, [3]New Mexico State University

Abstract: Onion (Allium spp.) is the second most cultivated horticultural crop in the world for dietary consumption. Onion growth and life cycle are predominantly dependent on photoperiod light responses and are classified by the amount of light needed for bulbing: short day (8-12 hours), intermediate day (13-14 hours), and long day (15+ hours). The objective of this study was to determine the time of day when onions were at peak photosynthesis. The hypothesis was that the time of peak photosynthesis would be between 11:00 A.M. and 12:00 P.M. Four varieties, two bunching, He Shi Ko (Allium fistulosum) and Red Welsh (Allium fistulosum), and two bulbing, Ailsa Craig (Allium cepa), and Yellow Sweet Spanish (Allium cepa), were grown from seed in a controlled environment for a six-month period. The methods included a diurnal experiment utilizing an LI-6800 portable photosynthesis system. Photosynthesis rates and light adapted fluorescence (PhiPSII) of two onion plants per varieties were measured every hour from 10:00 A.M. to 1:00 P.M. Results indicated that for all four onion varieties' peak photosynthesis occurred between 10:00 - 11:00 A.M. The highest photosynthetic rate was 22.528 µmol $m^{-2}s^{-1}$ and the highest PhiPSII was 0.377 for the He Shi Ko variety at 10:00 AM. Photosynthetic rate averages ranged from 10.513 to 22.231 µmol $m^{-2}s^{-1}$. In conclusion, this diurnal study's optimal photosynthetic results for onion are imperative to conduct further onion physiology photosynthetic research for yield and quality crop output improvement.

Effect of Slow Transcription on Nucleosome Landscape

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Irma Zenteno*[1], Srinivas Ramachandran[2], Olivia Lopez[3]

[1]Metropolitan State University of Denver, [2]University of Colorado Colorado School of Medicine, [3]Metropolitan State University of Denver

Abstract: Eukaryotic Genomes are tightly packed in nucleosomes to provide regulation and protection of DNA. This tight packing involves protein units known as histones that help regulation of genome transcription. RNA Polymerase II (RNAPII) is a protein involved in transcription of RNA that must unwind DNA that is tightly wrapped around these histones to proceed. After transcription, DNA must be wrapped back into these histones and respective nucleosomes for compaction and protection. In vivo , it is still unclear how these transitions take place. We hypothesize that the RNAP II enzyme plays a major role in chromatin landscaping due to its role in unraveling of histones. Our lab has developed tools that use genomic data to infer structure of chromatin and identify the nucleosomal intermediates involved in transcription elongation using Micrococcal nuclease treatment followed by sequencing (MNase-seq). We are determining changes in nucleosomal intermediates when RNAPII is slowed down in comparison with wild type RNAP II in Saccharomyces cerevisiae. We have performed MNase treatments of yeast cells and purified the DNA fragments. We are currently performing sequencing and analysis of these experiments. The nucleosomal intermediates we will map are hexasomes, an intermediate with six histones instead of eight. If RNAPII disrupts elongation in vivo during transcription, we predict an increased number of hexasomes near transcription sites when RNAPII transcribes slower than the WT. We can not only identify the effect of the RNAPII enzyme itself on nucleosome disruption in vivo but also if RNAPII sets the nucleosomal landscape.

Genes Involved in Renal Clear Cell Carcinoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Paola Rosa Crespo*[1], Yarielis Torres Alers [2], Nathan Reyna[3], Elizabeth Padilla[4]
[1]Interamerican University of Puerto Rico, Aguadilla Campus, [2]Interamerican University of Puerto Rico, Aguadilla Campus, [3]Ouachita Baptist University, [4]Interamerican University of Puerto Rico, Aguadilla Campus

Abstract: Renal clear cell carcinoma is a type of kidney cancer that originates in the lining of the proximal convoluted tubule, a part of the very small tubes in the kidney that transports primary urine. This cancer is the most common type of kidney cancer in adults, responsible for approximately 90-95% of cases and is among tumors that are the most resistant to systemic therapy. Cancer is caused by changes or mutations in DNA within cells. Through this research, multidimensional genomic data of cancer was performed, specifically renal cell carcinoma. The cBioPortal platform for Cancer Genomics made possible to identify and localize the genes involved in this type of cancer, through it we studied those that can mutate and alter others. The VHL, MET, and TFE3 genes were selected because they are the most common in renal clear cell carcinoma. A comparison of the manifestation of Renal Clear Cell Carcinoma in different ethnic categories was carried out. Through this comparison, another common gene was found between Hispanics/Latinos and non-Hispanics/Latinos, PBRM1. According to studies, we concluded that the VHL gene has a frequency of 44.92% in 354 cases, being the most present in both Hispanic/Latino and non-Hispanic/Latino patients related to kidney cancer known as renal clear cell carcinoma.

Industrial Hemp in Oklahoma: A Case Study

Discipline: Life Sciences

Subdiscipline: Other Life Sciences

Alexandria Howard*[1], Tracey Payton-Miller[2], James Arati[3], Newton Nyairo[4]
[1]Langston University - Langston, [2]Langston University Department of Agriculture, [3]Langston University Department of Agriculture, [4]Langston University Department of Agriculture

Abstract: Although hemp has been around for thousands of years, the ability to mass-produce hemp for seed or stalk for various products is a modern concept. Since the legalization of industrial hemp, there have been negative remarks from producers regarding low seed germination, the inability to maintain uniformity, and weed control in their fields. Variability can cause female-dominant fields, illegal levels of tetrahydrocannabinol (THC), and complications with harvest. Infield studies were conducted with Cannabis sativa var. 'Yuma Crossbow' near Ponca City, Oklahoma, a region with many large agricultural producers. Many producers growing industrial hemp in this area expressed those complaints, and this study was conducted to either validate or refute the producers' claims. Measurements, taken as height in inches, were made across eight weeks. Each set of measurements consisted of 20 samples. The samples were distributed evenly between both males and females. Weeds and pests were also notated. Following completion of the study, it was shown that the overall height trends were linear; however, there were slight discrepancies. It was also seen that the ranges in height between both females and males were significant. There was a mass die-off of males following the pollination of the female plants. The large presence of johnsongrass also posed a serious risk to the crop, shading out the smaller plants. Following the conclusion of the study, it was found that the farmers' claims were legitimate. The seed's variability is abundant, and the threat from other weeds is also a factor.

An RNAi Screen to Determine Genetic Interactions Between Spliceosomal Factors Using Caenorhabditis Elegans

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Orazio Bagno*[1], Kenneth Osterhoudt[2], Alan Zahler[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: Precursor-messenger RNA (pre-mRNA) splicing is a process in eukaryotic cells that catalyzes the excision of non-coding RNA sequences (introns) from an mRNA transcript. The spliceosome locates the 5' and 3' splice sites, excises the intron from the transcript and ligates the surrounding exons together. Some introns contain multiple 3' splice sites, leaving the spliceosome with a choice of where to cut and splice the RNA. The process by which the spliceosome identifies and maintains the specificity of 3' splice site selection throughout the splicing cycle is still largely unknown, with mutations in certain spliceosomal proteins leading to the selection of the incorrect site, which can be deleterious. To study how certain spliceosomal proteins interact in order to maintain 3' splicing specificity, we are performing an RNA interference (RNAi) screen on 12 splicing proteins. Of the 12, slu-7, sacy-1, and mog-5 are of most interest because of their confirmed involvement in 3' splice site selection. Each RNAi depletion will be done in four different strains of Caenorhabditis elegans with mutations in spliceosomal RNA helicases sacy-1 (G533R), mog-5 (E608K), or emb-4 (G833R), and a wildtype control. Once we have performed RNAi on all strains, phenotypic observations and examination of splicing patterns will be made. In preliminary RNAi experiments, we see stronger phenotypes

when mog-5 RNAi is induced on the sacy-1 strain, suggesting that these proteins have overlapping roles.

Enteric glia regulates the expression of neutrophil inflammatory factors during acute inflammation

Discipline: Life Sciences
Subdiscipline: Neurosciences

Darwing Santiago Padilla Rolon*[1], Brian D. Gulbransen[2], Jacques Gonzales[3], Wilmarie Morales Soto[4], Jonathon McClain[5]
[1]University of Puerto Rico at Cayey, [2]Michigan State University, [3]Michigan State University, [4]Michigan State University, [5]Michigan State University

Abstract: Inflammation in the gastrointestinal tract is a detrimental event in inflammatory bowel disease. Crosstalk between the immune and enteric nervous system leads to this proinflammatory occurrence. Recent advances in our understanding of the enteric nervous system indicate that enteric glial cells modulate immune cells in the gastrointestinal tract. Previous single-nuclei multiomic analysis data has shown that genes that encode for and influence neutrophil function are highly changed in enteric glia during peak colitis. Therefore, we hypothesize that enteric glia regulates the expression of neutrophil modulating factors during acute inflammation. We tested our hypothesis using the acute dinitrobenzene sulfonic acid colitis model, which involves a major neutrophil immune response. Animal body weight and gross macroscopic damage were recorded as indications of overall inflammation and tissue was harvested for immunohistochemical analysis. Enteric glia were labeled with antibodies against glial fibrillary acid protein for confirmation and Neutrophil cytosolic factor 4 and C-X-C motif chemokine ligand 5 as possible evidence of immunological markers. Results suggested no significant difference in labeling for immunological markers of neutrophils in enteric glial cells, which rejects our hypothesis of an increase in neutrophil infiltration to the colon in dinitrobenzene sulfonic acid treated mice by these cells, in comparison to saline controls. However, results showed significant labeling for some neurons that may or may not be specific. These studies will contribute to further understand how immune responses are regulated in the gut and impact the general knowledge there is regarding the gastrointestinal health and its disease processes.

Vpr-dependent degradation of macrophage-specific transcription factors enhances viral spread during HIV-1 and SIV infection of human macrophages

Discipline: Life Sciences
Subdiscipline: Microbiology

Thomas Chen*[1], Kathleen L. Collins[2], Maria C. Virgilio[3], W. Miguel Disbennett[4], Joshua D. Welch[5]
[1]The University of Michigan, Ann Arbor, [2]The University of Michigan, Ann Arbor, [3]The University of Michigan, Ann Arbor, [4]The University of Michigan, Ann Arbor, [5]The University of Michigan, Ann Arbor

Abstract: Approximately 39 million people live with Human Immunodeficiency Viruses (HIV) worldwide, many from minority and socioeconomically-deprived populations. Unlike most viral infections, HIV-1 is able to overcome the host's innate and adaptive immune response to establish a lifelong infection in nearly every infected person, primarily through the use of several viral accessory proteins. One of these accessory proteins, Vpr, is highly conserved among HIV

variants as well as evolutionarily-related viruses including Simian Immunodeficiency Virus (SIV). Vpr is necessary for optimal spread in macrophages, but the mechanism of action is poorly understood. Using single-cell RNA sequencing, our group has demonstrated that Vpr selectively enhances viral spread in macrophages by modulating the transcriptional landscape of the infected cell when Vpr is present compared to infections that lacked Vpr. Closer examination of the genes downregulated in the presence of Vpr lead to our hypothesis that HIV Vpr can directly target host transcription factors (TF) for degradation, inhibiting gene expression of downstream TF targets. We confirmed our findings in infected monocyte-derived macrophages by measuring a decrease in specific TF levels when HIV Vpr was present using flow cytometric analysis and western blotting. Our findings are also reproducible in cell line model systems when TFs and Vpr are provided in trans . Whether the relationship between our TFs of interest and Vpr is conserved in SIV infections affecting non-human primates is currently under investigation. Our initial results suggest a subset of SIV Vpr variants behave similarly to HIV-1 Vpr. Studies to confirm these findings are ongoing.

Pseudo-cooperation Between Pseudomonas aeruginosa and Staphylococcus aureus Mediated by Purine Exchange

Discipline: Life Sciences
Subdiscipline: Microbiology

Alexsis Garcia*[1], Catherine Wakeman [2], Hafij A. Mahmud[3], Jiwasmika Baishya[4]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University

Abstract: Chronic infections like cystic fibrosis (CF) are commonly associated with polymicrobial biofilm communities which often provide a nutrient rich environment that can lead to these organisms to be interdependent metabolically to one another. These metabolic cross feeding between microorganisms can help them overcome bacterial growth retardation due to autotrophy, evade host immunity and avoid antibiotic threat. Therefore, in this study, we were interested in investigating whether an essential nutrient such as purine could be exchanged between Pseudomonas aeruginosa and Staphylococcus aureus in support of possible metabolic complementation between these general competitors. To achieve this, we selected several purine-deficient transposon mutant strains of P. aeruginosa and S. aureus in addition to their wild-type counterparts, which we grew in co-cultures and monocultures. We found a bi-directional exchange of metabolite between purine defective mutant of P. aeruginosa and wild type S. aureus, and also between purine defective mutant of S. aureus and wild type P. aeruginosa. However, while the presence of S. aureus may have rescued the purine deficient P. aeruginosa, we assumed that the extracellular DNA (eDNA) freed by the lysis of S. aureus may have contributed to the partial complementation. The CF lung is usually comprised of a high amount of extracellular DNA and from our data, the purine-deficient strains have displayed that, with adequate levels of eDNA, they are capable of rescuing the growth of purine deficient of P. aeruginosa . Similar metabolic interdependencies between co-infecting pathogens could indicate the primary stages of evolution of cooperative interactions in polymicrobial communities.

Monitoring Biodiversity with eDNA in the Sierra de Manantlan, México

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Isaac Aguilar*[1], Arthur Middleton [2], Juan Pablo Esparza Carlos[3], Rachel Meyer[4]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]Universidad de Guadalajara, [4]University of California, Santa Cruz

Abstract: Global protected areas provide a network of landscapes for biodiversity conservation, scientific research, and responsible public use. The Sierra de Manantlan Biosphere Reserve is a global biodiversity and cultural hotspot located in Jalisco-Colima, México inhabited by a quarter of all Mexican mammals and providing ecosystem services for over a quarter million humans. Since being designated as a biosphere reserve in 1988, activity in the Sierra de Manantlan landscape has developed from natural resource management and extraction to include conservation and ecological research initiatives. Quantifying biodiversity can prove to be a challenging task, especially in remote locations. Environmental DNA (eDNA) metabarcoding is an innovative tool for providing comprehensive biodiversity assessments that has never been used in this region. We expect differences in the number of taxa detected between the eDNA analysis and an existing camera trap network. Additionally, this study will evaluate the effectiveness of eDNA studies and sampling methods in the nearctic realm across temporal and geographic scales. This novel eDNA biodiversity assessment in the region will provide a comprehensive list of present taxa and may be used to inform management and policy strategies for endangered species conservation, sustainable natural resource use, and future research.

Identification of miRNAs associated with neuropathic pain in Hispanic patients with rheumatoid arthritis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Veronika Zenkeviciute*
John Jay College of Criminal Justice

Abstract: Epigenetic mechanisms are directly involved in the regulation of biological processes. These mechanisms represent changes in gene expression that can be impacted by environmental factors and can also be inherited through cell division leading to different phenotypes and potentially impacting development of disease. Racial and ethnic minority groups in the United States experience worst health outcomes for several diseases including rheumatoid arthritis (RA). To learn more about RA in Hispanics, we conducted a pilot study to measure exosomal miRNA levels in 27 Hispanic RA patients. 8 miRNAs were identified that significantly differed ($p \leq 0.05$) between RA patients with different clinical pain (ID pain) symptoms. For the analysis we created low (LP) and high pain (HP) categories by using the mean ID pain measure (4) in our population. The top three miRNAs with the largest difference identified in this analysis were hsa-miR-373-3p (LP (<4) = 27.45 vs HP (>4) = 20.44, p-value=0.0491), hsa-miR-376b-3p (LP (<4) = 27.69 vs HP (>4) = 20.19, p-value=0.0314), and hsa-miR-489-3p (LP (<4) = 27.21 vs HP (>4) = 19.46, p-value=0.0269). To predict possible pain signaling pathways, we used the identified miRNAs and the miRDB, miREalk and TargetScan databases. We identified 429 targets and carry out an analysis using the Kyoto Encyclopedia of Genes and Genomes (KEGG) to identify 10 pathways as the most likely affected by deregulation of these miRNAs. Several pathways on this list, including cAMP are related to clinical pain. These findings have a potential to help us better understand pain in Hispanic RA patients.

Modified bispecific antibodies blocking both PD-L1 and PD-L2 engagement of PD-1 show higher ADCC potential and in vivo anti-tumor response

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ashley Gelin*[1], Anupallavi Srinivasami [2], Coline Agnes Couillault[3], Shweta Mahendra Hegde[4], Qinying Liu [5], Michael Curran[6]
[1]The Pennsylvania State University, [2]University of Texas MD Anderson Cancer Center, [3]University of Texas MD Anderson Cancer Center, [4]University of Texas MD Anderson Cancer Center, [5]University of Texas MD Anderson Cancer Center, [6]University Of Texas MD Anderson Cancer Center

Abstract: Antibody immune checkpoint (ICP) blockade has shown superior efficacy to improve the outcome of a fraction of patients in some cancers. ICP blockade increases the proportion of tumor-infiltrating lymphocytes and their functionality, including cytotoxicity, proliferation, and cytokine production. Programmed Cell Death-1 (PD-1) blockade, for instance, inhibits the interaction between PD-1 and its receptors PD-L1 and PD-L2. PD-L1 itself can be targeted to address both engagements to PD-1 and B7-1, although PD-L1 blockade alone fails to address the engagement between PD-L2 and PD-1. Unlike monospecific antibodies, bispecific antibodies (BsAbs) provide dual ligand specificity, allowing blockade of multi-inhibitory pathways. This presentation will report the comparison of the efficacy and specificity of BsABs that target PDL1/2 with clinical anti-PD-L1 antibodies, as well as their in vivo efficacy. The efficacy and specificity of the anti-PD-L1/2 BsAbs with a modified Fc receptor (GASDIE) is determined by the induction of antibody-dependent cell-mediated cytotoxicity (ADCC) using an in vitro assay, flow cytometry competition assay, and an analysis of tumor growth and survival of mice implanted with a colon cancer cell line treated with BsAbs or an anti-PD-1. My findings suggest that BsAbs targeting PD-L1 and PD-L2 and bearing the Fc modification promote superior ADCC activity against target cells that express either ligand by effector cells expressing Fc receptors. It also suggests that our BsAbs mostly share the same epitope as clinical antibodies. Finally, BsAbs possess higher in vivo efficacy than a reference anti-PD-1 therapeutic antibody, supporting the therapeutic potential and molecular target specificity of anti-PD-L1/PD-L2 BsAbs.

Identifying Candidate Immunogenic Epitopes for Developing Therapeutics

Discipline: Life Sciences
Subdiscipline: Genetics

Bailee Alonzo*[1], Rene Welch [2], Jess Vera[3], Jason Weinfurter[4], Cindy Zuleger [5], Mark Albertini[6], Matt Reynolds[7], Irene Ong[8]
[1]Texas Tech University, [2]University of Wisconsin-Madison, [3]University of Wisconsin-Madison, [4]University of Wisconsin-Madison, [5]University of Wisconsin-Madison, [6]University of Wisconsin-Madison, [7]University of Wisconsin-Madison, [8]University of Wisconsin-Madison

Abstract: Cancer is a major public health problem worldwide and is the third leading cause of death in the United States. Immune checkpoint inhibitors (ICIs) can achieve durable responses, but only in some tumors. The challenge of designing CAR T-cell therapies or vaccines that can be used in combination with ICIs to improve immune response is in predicting which neoantigens will be immunogenic. Tumors hold unique collections of somatic mutations that can be processed and presented as neoantigens, however identifying which mutations are immunogenic is difficult. We hypothesize that tumor-promoting mutations that confer a selective advantage to the tumor cell (aka driver mutations) may serve as important neoantigen targets. Here we utilized the DRAGEN platform to identify tumor-specific somatic mutations from a melanoma patient with a durable response to immunotherapy. Of 5,785 somatic mutations identified, 189 drivers were predicted using the machine learning method AI-Driver from OncoVar, a platform to decipher oncogenic driver variants. Variants with an AI-Driver score > 0.95 and association to melanoma were chosen, which narrowed results to a list of 9 top drivers. The amino-acid variants were provided as input into a human genomic variant search engine and annotation tool, Varsome, to verify pathogenicity. The results here are used to prioritize peptide array results that detect binding of MHC Class I HLA-A2 to peptides from tumor neoepitopes.

Valley fever spreads beyond endemic regions

Discipline: Life Sciences
Subdiscipline: Biology (general)

Brianne Cooke*[1], Marieke Ramsey[2], Daniel Kollath[3], Dr. Bridget Barker[4], Dr. Anita Antoninka[5]
[1]Northern Arizona University, [2]Northern Arizona University, [3]Northern Arizona University, [4]Northern Arizona University, [5]Northern Arizona University

Abstract: Valley fever is a fungal infection that is caused by two species in the genus Coccidioides . Infection occurs when mammals inhale airborne spores that are discharged from contaminated soil. Valley fever is thought to be endemic to the Southwestern United States, but in the past decade, the range of Valley fever has been suspected to have increased. Climate change has been implicated in this range expansion from hyper-endemic regions such as Southern Arizona to Northern Arizona. Climate fluctuations associated with the spread of Valley fever are higher temperatures, lower precipitation, and drier soils. Due to this reemergence, there is an urgent need to understand the ecological niche and determine the extent of the spread of Coccidioides spp. in the Southwestern United States. Our objective is to determine the extent of the spread of Valley fever due to climate fluctuations. We took eight years of environmental surveillance data from various sites throughout Arizona that were confirmed positive through qPCR analysis. Using this data, we also created an ecological niche model to predict the current and future range of Coccidioides spp. The results showed an increase in endemicity in Arizona, spreading from Southern Arizona to previous non-endemic regions of the Western United States. The knowledge gained from soil sampling and ecological niche modeling will lay the foundation to better understand disease surveillance and how global climate change will exacerbate this and other environmentally-acquired pathogens in the coming decades.

Progress toward the synthesis of a new cobalt(III) coordination complex with 5-methyl-1H-indazole ligands

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Amber Herrod*[1], Dr. Aimee M Morris[2], Milo A Adams[3]
[1]Fort Lewis College, [2]Fort Lewis College, [3]Fort Lewis College

Abstract: Co(III) complexes have been proposed as low cost prodrugs in chemotherapeutics with potentially favorable and tunable properties. However, the use of octahedral, low-spin Co(III) complexes with only monodentate ligands as prodrugs remains a relatively unexplored area in cancer research. Utilizing the known complex, trans -dichlorotetrakis(pyridine)cobalt(III) chloride, under reflux conditions in the presence of excess 5-methyl-1 H -indazole, a new coordination complex was reproducibly obtained via ligand exchange albeit in low yields. 1 H and 13 C NMR studies allowed for structural elucidation of a new complex with partial substitution of the pyridine ligands. Interestingly, the two 5-methyl-1 H -indazole ligands appear to bind to the octahedral cobalt(III) metal center through a deprotonated carbon atom in the third position of the indazole ring. Addition of either strong or weak bases prior to reflux conditions did not result in any significant increase in product yields. Work continues in order to optimize the reaction conditions to produce high yields of a new Co(III) coordination complex with 5-methyl-1H-indazol-3-yl ligands. Future studies will focus on the full structural characterization and biological relevance of this new complex for potential medicinal applications.

Structural and Functional Characterization of Phospholipase C β3

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kennedy Outlaw*[1], Isaac Fisher[2], Kaushik Muralidharan[3], Angeline Lyon[4]
[1]Purdue University, [2]Purdue University, [3]Purdue University, [4]Purdue University

Abstract: Phospholipase C β (PLCβ) plays an important role in cardiovascular diseases and opioid analgesia. PLCβ catalyzes the hydrolysis of the inner membrane lipid phosphatidylinositol-4,5-bisphosphate (PIP 2) to inositol-1,4,5-triphosphate (IP 3) and diacylglycerol (DAG). IP 3 and DAG are crucial secondary messengers that activate multiple signaling pathways to change cellular behavior. PLCβ is a downstream effector of G-protein coupled receptors (GPCRs) and is activated by the heterotrimeric G protein subunits Gα q and Gβγ. We and others have reported that PLCβ is more flexible in solution as compared to crystal structures of the protein. In small-angle X-ray scattering (SAXS) experiments, the solution structure of PLCβ had additional density unaccounted in crystal structures. We hypothesize the open state represents a low activity conformation. To test this hypothesis, we used cryo-electron microscopy (cryo-EM) to determine the solution structure of full-length PLCβ3 to 4.08 angstroms. PLCβ3 primarily existed in a closed confirmation under these conditions. We also mutated residues in PLCβ3 at intramolecular interfaces to disrupt the contacts and measured changes in basal and Gβγ-stimulated activity. These mutations only decreased apparent activation by Gβγ. These results suggest PLCβ may adopt a different conformation when interacting with the membrane and Gβγ. We are currently working to determine the structure of PLCβ3 on membrane mimetics to investigate this further.

Are midbody remnants bona fide extracellular vesicles?

Discipline: Life Sciences
Subdiscipline: Genetics

Ashley-Grace Dureke*[1]and Ahna Skop[2]
[1]University of Wisconsin-Madison, [2]University of Wisconsin-Madison

Abstract: Extracellular vesicles (EVs) are lipid bound vesicles that are secreted by cells into the extracellular space. EVs are abundant in the human body and during cancer they are shed into the bloodstream, often serving as markers for cancer. There are three main classes of EVs: 1) exomes (type 1), 2) microvesicles (type 2), and 3) midbody remnants (MBRs) (type 3). Extracellular vesicles are important for intercellular communication, and this occurs via the transfer of nucleic acids, including RNA, microRNAs and lncRNAs, to other cells. Since MBRs have recently been identified as a type III extracellular vesicle, the biogenesis of the MBR with regard to extracellular biology is unclear. Our lab is particularly interested in when and where the canonical EV markers localize during the cycle with regard to the midbody/MBR marker, MKLP1, a kinesin unique to MBRs. To determine this, we are using antibodies against a few tetraspanins (CD9, CD81 and CD63), canonical extracellular vesicle markers. The goal of my proposed project is to determine where extracellular vesicle markers localize during cell cycle and where in the cell these are found, with regard to MKLP1, during late-stage mitosis. This goal will be accomplished by culturing HeLa cells, subsequent immunocytochemistry, high-resolution microscopy, and then I will analyze my data using GraphPad PRISM. Preliminary data has revealed that CD63 localizes to the cleavage furrow membrane, in addition to the centrosome during mitosis.

RNA Sequencing For The Masses

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kelsey O'Brien*[1], Amy Toth [2], Katherine Geist[3]
[1]Iowa State University, [2]Iowa State University, [3]Iowa State University

Abstract: RNA sequencing (RNAseq) is an increasingly valuable tool for evolutionary biologists and ecologists because it provides a snapshot of gene regulation to environmental conditions. RNAseq uses short-read sequencing to identify the presence and quality of RNA in a tissue at a given moment. The challenges for new users include the choice and implementation of RNA extraction protocol. Reviewing published RNAseq studies from 2015-2021 from the field of entomology, we find the majority of RNA extraction methods for RNAseq employed either a commercial kit or a TRIzolTM-only extraction method. A smaller fraction of studies combined TRIzolTM with a spin column kit. These studies spanned ten insect orders with over 80% coming to these three orders; Diptera, Hymenoptera, Lepidoptera, and Hemiptera. Here we assess these three RNA extraction protocols for insect brains and larvae using the non-genomic model species Bombus impatiens. We compare purity and total yield among these three extraction methods to determine the best practice for RNAseq. We find that TRIzolTM based methods including those with a spin column kit produced higher overall RNA yield. However, this increased yield may result from form increased RNA degradation as determined by 2100 Bioanalyzer. Insects are known to have non-canonical RNA Profiles, making the assessment of RNA purity challenging since Bioanalyzer software is tuned for other eukaryotes. Thus, we also present a novel method for assessing RNA purity from Bioanalyzer electropherogram to address this challenge.

Inhibition of p300/CBP Acetyltransferase and BRD4 Attenuates Transcriptional Synergy in Endothelial Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alexander Martinez Lopez*[1], Jonathan D. Brown, M.D. [2], Ronan Bracken[3], Selma Z. Elsarrag, Ph.D.[4]
[1]Vanderbilt University, [2]Vanderbilt University, [3]Vanderbilt University, [4]Baylor College of Medicine, Houston TX

Abstract: Signaling by proinflammatory cytokines plays a major role in the pathogenesis of atherosclerosis. Specifically, interferon-gamma (IFN-γ) and tumor necrosis factor-alpha (TNF-α) orchestrate the influx of immune cells into the vessel wall. We hypothesized that IFN-γ and TNF-α synergistically induce proatherogenic gene products in vascular endothelial cells (ECs) via p300 and BRD4-dependent mechanisms. To test our hypothesis, we used RNA-sequencing to identify synergistically induced genes. RNA was isolated from immortalized human aortic ECs (HAECs) after 1-hour treatment with vehicle, IFN-γ (50 ng/uL), TNF-α (25 ng/uL) or both cytokines. Poly-A selected mRNA libraries were sequenced with PE150 reads. These results were confirmed by real-time quantitative polymerase chain reaction (RT-qPCR). HAECs were also stimulated with synergy cytokines and either a highly selective inhibitor of p300/CREB Binding Protein (CBP) acetyltransferase (A-485) or a BET bromodomain inhibitor (JQ1) to assess the role of p300 and BRD4 in the synergy response. Results identified that dual cytokine treatment in HAECs synergistically induced chemokines CXCL9, -10, -11 compared to stimulation with individual cytokines. Synergistic cytokine stimulation resulted in a 7,600-fold CXCL10 induction compared to control, as determined by RT-qPCR. Co-treatment of HAECs with A-485 or JQ1 completely abrogated maximal cytokine induction of CXCL10 . Our data demonstrate that IFN-γ and TNF-α synergistically induce atherogenic genes including chemokines in HAECs. Inhibition of p300/CBP or BRD4 disrupts transcriptional synergy responses. Additional investigation into the mechanisms of how these transcriptional coactivators function in synergistic gene induction could lead to novel therapeutic strategies in atherogenesis.

The Plant Hormone Ethylene in Stress Responses in the Liverwort Marchantia polymorpha

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Lizbeth Sanchez*[1], Caren Chang[2], Priyanka Bharadwaj[3], Divine Enyi[4]
[1]University of Maryland, College Park, [2]University of Maryland, College Park, [3]University of Maryland, College Park, [4]Eleanor Roosevelt High School

Abstract: Environmental stressors, such as high temperature and salinity, are increasing due to climate change and can negatively impact plant growth. Ethylene is a gaseous plant hormone important for many aspects of growth and development, and plays a role in responses to abiotic and biotic stresses. In angiosperm models, ethylene signaling has a protective role against abiotic stress. However, little is known about ethylene's role in stress responses in non-seed plants, and consequently the evolutionary history of ethylene in stress response is also unknown. The liverwort, Marchantia polymorpha, is a non-seed plant with one of the earliest land plant ancestors (~400 million years ago). Therefore, M. polymorpha is valuable for determining whether the protective role of ethylene signaling in abiotic stress is conserved in plants. We used existing M. polymorpha knockout mutants, Mpctr1 and Mpein3, in the ethylene signaling pathway to determine ethylene's role in stress responses. It was previously shown that Mpctr1 displays constitutive ethylene responses, and Mpein3 has ethylene insensitivity. The stressors used were increased heat (29°C and 30°C), salinity, and far-red light. Studies for salinity and far-red light are currently ongoing. When treated with heat stress, Mpein3 mutant plants showed more severe growth inhibition than the wild type and Mpctr1 plants, indicating that ethylene plays a protective role in M. polymorpha. Ethylene therefore has a protective role in response to temperature stress in M. polymorpha, similar to angiosperms. The protective role of ethylene in heat stress suggests conservation of this role through at least 400 million years.

High Evolutionary Conservation of Dsor1 as Compared to Roc1a

Discipline: Life Sciences

Subdiscipline: Biology (general)

Bridgiet Alvarado*[1], Lindsey Long [2], Tanner German[3]
[1]Oklahoma Christian University, [2]Oklahoma Christian University, [3]Oklahoma Christian University

Abstract: The understanding of signaling pathways in cells have been of interest in the scientific community for many years. The Insulin/TOR pathway is relevant in medical research due to its role in the regulation of metabolism, cell growth, and ageing. By enhancing the genomic understanding of this pathway, we can expand our foundation for future research. To study this pathway, the genome of Drosophila species, fruit flies, were used considering its high similarity to humans. In this project, we studied the evolutionary constraints of several genes in the Insulin/TOR pathway, specifically Roc1a and Dsor1. We hypothesized that Dsor1 would be more conserved than Roc1a based on the interactions that each gene possesses. Roc1a has 7 interactions while Dsor1 interacts with 77 proteins. It is thought that as the number of physical interactions increases, the greater the evolutionary constraint will be on that gene. We used bioinformatic genomic data to annotate these genes in several Drosophila species using Drosophila melanogaster as the reference species. Divergence was measured after annotation by taking various factors into account including genomic copies, gene structure, genomic neighborhood, protein sequence identity, protein sequence similarity, and nucleotide sequence identity. We found that Dsor1 was more conserved than Roc1a which diverged at a faster rate. Differences included variation in the genomic neighborhoods and disappearance of an isoform past D. melanogaster. As this project continues, it would be wise to compile information on the environmental factors that favored Dsor1 over Roc1a as well as other relevant genes.

GDF15 DEFICIENFY IN BROWN ADIPOSE TISSUE DOES NOT AFFECT THERMOGENESIS, BUT EXACERBATES DIET-INDUCED OBESITY

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Luis Garcia-Pena*[1], Renata O. Pereira [2], Jayashree Jena[3], Kevin Kato[4]
[1]University of Iowa, Carver College of Medicine, [2]University of Iowa, Carver College of Medicine, [3]University of Iowa, Carver College of Medicine, [4]University of Iowa, Carver College of Medicine

Abstract: Obesity is a global public health issue. Activation of brown adipose tissue (BAT) function have emerged as a therapeutic strategy to increase energy expenditure and counteract obesity. Thermogenic stimuli and high-fat feeding (HFD) induces BAT’s GDF15 in mice. To test whether BAT-derived GDF15 is necessary to mediate thermogenesis and systemic adaptations to diet-induced obesity (DIO), we generated mice lacking BAT-specific GDF15 by crossing Gdf15 floxed mice with mice harboring the Cre-recombinase under the control of the Ucp1 promoter (GDF15 BAT KO). KO mice were treated with the β-adrenoreceptor agonist CL316,243 (CL) for 5 days, cold-exposed for 3 days, or HFD-fed for 12 weeks to induce thermogenesis. A significant induction in Gdf15 mRNA levels was observed in CL-treated mice, however, serum GDF15 levels were similarly induced in both WT and KO mice. CL-induced activation of thermogenic genes in BAT was comparable between genotypes, and UCP1 protein levels were equally induced in BAT of WT and KO mice in response to cold exposure. Accordingly, core body temperature was unchanged between CL-treated or cold-exposed WT and KO mice. After 12 weeks of HFD, KO mice had significantly increased body weight and fat mass relative to WT mice. However, food intake, locomotor activity and energy expenditure were unchanged between genotypes. Although glucose tolerance was unchanged between genotypes, insulin sensitivity was impaired in KO mice. Our data indicates that BAT-derived GDF15 is largely dispensable for CL and cold-induced BAT Thermogenesis. However, BAT-derived GDF15 seems to be required to regulate diet-induced weight gain and insulin sensitivity.

Hippocampal CA1 Place Cell Activity in a Alternate Reward and No Reward Paradigm

Discipline: Life Sciences
Subdiscipline: Neurosciences

Anyu Cao*[1], Mark Sheffield [2], Seetha Krishnan[3]
[1]The University of Chicago, [2]The University of Chicago, [3]The University of Chicago

Abstract: Reward expectation is an internal state of associative learning between external cues and reward. At the cellular level, external cues in an environment are represented by the firing of hippocampal place cells. How internal states of reward expectation affect place cell firing is unknown. In this project, we aim to test how place cell activity changes when mice learn to expect and not expect a reward in the same environment. We hypothesize that place cells will be more stable in laps where reward is expected compared to unexpected laps. Wildtype mice were trained to run in a VR environment consisting of a linear track, at the end of which they were teleported back to the start of the track, thereby completing a lap. Mice were given a water reward at the end of each alternating lap and trained to expect alternating rewards. After 3 weeks of training, mice learned the paradigm by displaying pre-emptive licking in the rewarded laps but not in the unrewarded laps. When well-trained animals were shown a novel VR with alternate rewarded laps, they displayed similar pre-licking and running behavior to the training VR, indicating that they had learned the paradigm. To investigate place cell activity, Thy1-GCaMP6f transgenic mice were implanted with an imaging cannula above the hippocampus. Hippocampal place cells are imaged using a two-photon microscope. Analysis of place cells is ongoing. Results from this study will be important to understand how reward expectation influences memories of external environments that lead to rewards.

Male nuptial food gifts as a Trojan horse for manipulating reproduction: a genetic dissection in gift-giving crickets

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Megan Grant*[1], Benjamin Sadd [2], Scott Sakaluk[3], Bert Foquet[4], Jack McKermitt [5], John Hunt[6]
[1]Illinois State University, [2]Illinois State University, [3]Illinois State University, [4]Illinois State University, [5]Illinois State University, [6]Western Sydney University

Abstract: In many species, males and females have opposing interests regarding reproduction, leading to sexual conflict. Males often attempt to manipulate female behavior to enhance their share of paternity. One avenue of such manipulation is the nuptial food gift, which gives males access to a female’s physiology. Male decorated crickets (Gryllodes sigillatus) offer females a spermatophylax, an unusual food gift comprising part of the male’s spermatophore, at mating. Consumption of the gift extends the period of sperm transfer, which increases a male’s paternity and possibly decreases females’ subsequent sexual receptivity. The spermatophylax comprises about 30 proteins in addition to other substances, but the function of these proteins remains unclear. I hypothesized that they function to enhance the gustatory appeal of the spermatophylax or to diminish female receptivity to remating. Two spermatophylax proteins, SPX4 and SPX6, are of special interest because of their similarity to other proteins in insects (a protease inhibitor and a growth factor, respectively) and therefore might mediate these effects.

In this experiment, I tested the above hypothesis using RNA interference (RNAi) to knock down the expression of genes encoding these proteins. I will record changes in mating behaviors including gift acceptance, feeding duration, and tendency to remate in females mated with SPX4 or SPX6 knockdown male crickets in comparison with control males. This research is ongoing and will not only help improve our understanding of the evolution of nuptial gifts but will also contribute to a broader understanding of the molecular mechanisms underlying sexual conflict.

Analytical Method for the Determination of Pharmaceuticals and Drugs of Abuse in River Water

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Viviana Chavez*[1], Marta Concheiro Guisan[2], Natalie Fernandez[3]
[1]John Jay College of Criminal Justice, [2]Professor, [3]Student

Abstract: Analytical Method for the Determination of Pharmaceuticals and Drugs of Abuse in River Water Pharmaceuticals and drugs of abuse have been detected in water and are increasingly recognized as a contaminant of emerging concern. Once these substances enter the environment, the ecotoxicological effect on non-target organisms is often unknown. Several studies have identified negative effects of pharmaceutical exposure on behavior, reproduction, and development of aquatic organisms. The goals of this study were to develop and validate a comprehensive analytical method for the determination of 24 pharmaceuticals, drugs of abuse, and metabolites in river water by liquid chromatography-tandem mass spectrometry (LC-MSMS). Fifty mL of sample were centrifuged and acidified before being extracted by cation exchange solid phase extraction. The chromatographic separation was performed by reversed-phase. The linearity ranged from 5 to 1000 ng/L, and the limit of detection was 1-5 ng/L, depending on the analyte. The precision of the low-quality control was acceptable for most of the compounds under 20%, except for ranitidine, atenolol, and methadone with values of 22.4, 20.6, and 39.3 respectively. The high-quality control values were also under 20%, except for ranitidine which showed a value of 23.1. Most of the bias criteria range between +/- 20%, except for clonidine and methadone, giving values of 27.2 and 21.0 respectively. We developed a sensitive and specific method that was applied to authentic samples collected from the New York/ New Jersey estuary to identify particular areas where drugs reach concentrations that may pose a risk to target aquatic organisms.

Acylcarnitine-Induced Insulin Resistance in Brown Adipose Tissue

Discipline: Life Sciences
Subdiscipline: Biochemistry

Mae Hurtado-Thiele*[1], Dr. Judith Simcox[2], Helaina Von Bank[3]
[1]University of Wisconsin - Madison, [2]University of Wisconsin - Madison, [3]University of Wisconsin - Madison

Abstract: Levels of circulating acylcarnitines are increased in metabolic diseases such as type 2 diabetes, cardiovascular disease, and inborn errors of metabolism. In these diseases, acylcarnitines have been implicated as a disease driver causing insulin resistance and inflammatory responses. Acylcarnitines are also necessary for survival during cold exposure in mammals, as a fuel source for nonshivering thermogenesis mediated by brown adipocytes. Understanding the functional role of circulating acylcarnitines in the selective pressure of cold

exposure will allow us to better understand their role in disease etiology. We hypothesize that acylcarnitines cause insulin resistance in brown adipocytes to reduce glucose utilization and promote lipids as a primary fuel source. Our proposed cellular study aims to determine if acylcarnitines induce insulin resistance in brown adipocytes and if this insulin resistance is necessary for thermogenesis. Levels of insulin resistance will be quantified using in vitro models of immortalized brown adipocytes and skeletal myocytes that have been treated with acylcarnitines and insulin.Western blots of Akt phosphorylation are used as a primary measurement of insulin signaling. A secondary readout will be qRT-PCR of genes that are downstream of the FOXO1, a target of insulin action. Lastly, a fluorescent dye for mitochondrial membrane polarization (ERThermAC) will be used to measure thermogenic capacity of the cells. This study will inform on the mechanisms through which acylcarnitines provide a selective advantage in cold exposure, providing a better understanding of their role in metabolic dysfunction and insulin resistance associated with disease.

Rethinking parameters for gauging divergence: the missing isoform of rictor

Discipline: Life Sciences
Subdiscipline: Genetics

Christelle Urujeni Wa-Mana*[1], Dr. Lindsey Long [2], Melissa Testut[3], Dr. Laura Reed[4]
[1]Oklahoma Christian University, [2]Oklahoma Christian University, [3]Oklahoma Christian University, [4]Genomics Education Partnership (GEP)

Abstract: Improving the prognosis and treatment of disease requires an understanding of complicated molecular interrelationships. The complex Insulin/TOR signaling pathway is involved in growth, stress response, blood glucose regulation, and aging. Recognizing the impact of aberrations within this pathway is critical to developing new treatments for diseases such as diabetes, obesity, and cancer. Drosophila is a powerful model for examining the divergence of genes within the Insulin/TOR pathway because we can measure how genes in this pathway evolve across several species. In this study, the conservation of the gene rictor across multiple Drosophila species was examined. Because mutations of rictor can affect genes further down the pathway, determining its degree of divergence between species better illuminates how genes impact one another as they change. We found a missing isoform in rictor across several species. We hypothesized that because the missing isoform occurred due to fused exons, the effect on the Insulin/TOR pathway was negligible and, thus, rictor is a relatively well-conserved gene in the pathway. As a future direction, we would like to apply an adjusted divergence score calculator (DSC) to other genes in the pathway that have circumstances similar to rictor .

ER Stress Inhibition Protects C57 Mice from High Fat Diet-induced Weight Gain

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Josh Peterson*[1], Cally Tucker [2], Sanmati Thangavel[3], Renata Pereira[4], Marcelo Correia [5], Evan Dale Abel[6]
[1]The University of Iowa, [2]The University of Iowa, [3]The University of Iowa, [4]The University of Iowa, [5]The University of Iowa, [6]The University of Iowa

Abstract: Dynamin related protein-1 (DRP1) mediates mitochondrial fission in diverse tissues, including skeletal muscle. Previously we have investigated the metabolic effects of a skeletal muscle-specific knockout of (DRP1 KO) in C57 mice. DRP1 KO mice are resistant to weight gain induced by high fat diet related to a reduction in adipose tissue, and are more tolerant to glucose challenge associated with lower insulin levels. Gene expression of ATF-4, a transcription factor associated with endoplasmic reticulum (ER) stress activation was elevated in DRP KO mice. Furthermore, DRP1 KO mice have increased gene expression and plasma levels of GDF15 and FGF21, which we hypothesized was downstream from an increase in ER stress. To test this hypothesis, we chronically treated wildtype and DRP1 KO mice with tauroursodeoxycholic acid (TUDCA), which is a bile acid that has been shown to alleviate ER stress. As opposed to the anticipated results, TUDCA did not rescue the weight phenotype in DRP1 KO mice and indeed substantially protected wild type mice from weight gain and glucose intolerance associated with high fat diet for 12 weeks. We now hypothesize that ER stress might have a bidirectional effect on weight and gluco-homeostasis. It is possible that different pathways of the ER stress response might have distinct impacts on adiposity regulation.

Effectiveness of tissue clearing method ClearT2 in 3D cortical microtissues

Discipline: Life Sciences
Subdiscipline: Neurosciences

Harrison Katz*[1], Rafael D. González-Cruz[2], William K. Renken[3], Liane L. Livi[4], Diane Hoffman-Kim[5]

[1]Brown University, Department of Biology, [2]Brown University, Department of Neuroscience, Carney Institute for Brain Science, Center for Biomedical Engineering, Center for Alternatives to Animals in Testing, [3]Brown University, Department of Neuroscience, [4]Brown University, Department of Neuroscience, [5]Brown University, Department of Neuroscience, Carney Institute for Brain Science, Center for Biomedical Engineering, Center for Alternatives to Animals in Testing

Abstract: Variations in molecular refractive indexes of biological tissue result in light scattering, and thus the inability to visualize biological components in thicker tissue samples. Visualizing biological tissue beyond surface level is essential for observation of cellular morphologies within inner tissue layers. Previous research in our lab revealed that ClearT2 allowed full visualization of 3D cortical microtissues 104.6 microns in diameter. Here our goal was to evaluate the depth of tissue visibility from ClearT2 in larger microtissues. We explored ClearT2 tissue clearing methods of varying durations in 3D cortical microtissues 140+ microns in diameter. Scaffold-free self-assembled spheroidal microtissues of 4000 cells each were derived from postnatal rat cortical tissue. Spheroids were fixed at day 14 and stained for ionized calcium-binding adapter molecule 1 and either glial fibrillary acidic protein or 4’,6-diamidino-2-phenylindole. Prior to imaging, spheroids were exposed to clearing reagents for 75 minutes, 7 hours, 12 hours, or 17 hours. After 75 minutes of exposure, tissue depth of visibility was 146.9 microns compared to 70.9 in control. Tissue depth of visibility in 7-, 12-, and 17-hour groups exceeded average spheroid diameters of 163.1, 144.2, 164.2 microns respectively. Experimental groups with longer exposure to clearing reagents required increases in confocal laser intensity and high voltage for immunohistochemistry visualization, indicating suboptimal long-term fluorescence preservation. However, we have shown that clearing with ClearT2 for just 7 hours can achieve extensive depth of tissue visibility. Future work will focus on clearing larger microtissues and investigating alternative solvent-free clearing methods. Funding: NIEHS U01ES028184, US ONR N000142112044

Determining the Synthetic Lethality of Cancer Related Mutations with Methyl and Ethyl Paraben in Drosophila melanogaster

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Nicole Bañuelos*[1], Zainab Rizik [2], Blake Riggs[3], Lela Legesse[4]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University, [4]San Francisco State University

Abstract: The aim of our project is to determine the synthetic lethality of methyl and ethylparaben on Drosophila melanogaster with cancer-causing related mutations, specifically tumor suppressor mutations. Parabens are found in our everyday lives and act as xenoestrogens that cause the over-proliferation of cells. Tumor suppressor genes code for tumor suppressor proteins that maintain the role of preventing the over-proliferation of cells. When there is a loss-of-function mutation in a tumor suppressor gene, cells excessively divide. In our research, we are analyzing two specific tumor suppressor genes. These genes are Brca2 and P53. Brca2 is a tumor suppressor gene that provides instructors for making a tumor suppressor protein and is involved in repairing DNA damage. Mutations in the Brca2 gene are associated risk of breast, ovarian, and fallopian tube cancers. P53 is a tumor suppressor gene that prevents the over-proliferation of cells. Mutations in the p53 gene are involved in over 70% of all cancer cases. To study the effects of exposure to parabens on Drosophila melanogaster with tumor supressor mutations, we dissolved parabens in anhydrous ethanol in varying concentrations of 2000, 3000, 4000, and 5000 mg/L and added 0.5mL of the solution to 5mL of fly food. We determined the synthetic lethality by counting the number of surviving organisms over total organisms. Overall, there is no concentration-dependent survivability. Overall, there is no concentration-dependent survivability found in tumor suppressor mutants with methylparaben.

Investigating the Impact of Climate Change on Microbe-Phage Interactions in Lake Champlain

Discipline: Life Sciences
Subdiscipline: Environmental Science

Ashley Barkley*[1]and Nana Ankrah [2]
[1]State University of New York at Plattsburgh, [2]Assistant Professor

Abstract: Climate fluctuations in the Earth's atmosphere are part of the natural processes that bring the planet into periods of warming or cooling. However, the normal patterns of these fluxes have been altered by substantial increases in greenhouse gas production from anthropogenic sources post the industrial revolution. At the base of all trophic levels is the microbial community and we hypothesize that the microbial response to the effects of climate change will determine how resilient members of higher trophic levels are to changes in our climate. Our primary objective for this study was to isolate a large diversity of bacteria and their infecting bacteriophage from Lake Champlain and set up microbe-phage infection systems to investigate the impact of changes in climate on microbe-phage interactions in aquatic systems. Currently having isolated and brought into culture over 30 unique bacteria and have isolated over 10 unique bacteriophages capable of infecting our bacterial hosts. Using these microbe-phage systems we are setting up experiments where the host microbe is incubated at 1°C increments over a 5°C range to determine the impact of an increase in temperature on host growth and phage infection dynamics. Our initial results show that increases in temperature increase microbial growth rate and experiments are currently underway to determine the impact of such changes in microbial growth on bacteriophage infectivity. Altogether, data from our experiments will provide better insight into the impact of climate change on microbe-phage interactions in freshwater ecosystems and provide a framework for understanding microbe-phage dynamics in aquatic systems.

Comparing body sizes of dolphins using land- and aerial-based LiDAR photogrammetry

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Emily Cano*[1]and Dara Orbach [2]
[1]Texas A&M University-Corpus Christi, [2]Texas A&M University-Corpus Christi

Abstract: Unmanned aerial vehicles (UAVs) are becoming increasingly used to research marine mammals that may reside in remote or inaccessible waters. In the past decade, UAVs have been applied to ascertain the health status, population estimates, behavioral patterns, identity, genetics, and hormone concentrations of a variety of species of cetaceans (whales, dolphins, and porpoises). Unlike boats, which produce underwater noise, UAVs are considered noninvasive if flown at a minimal altitude. However, cetaceans may be aware of the presence of UAVs and sometimes behave evasively. In contrast, land-based research is completely noninvasive, although used less frequently in recent years as proximity to animals is thought to increase observational capacity. We present the novel application of a land-based tool to measure the body size of free-swimming dolphins off Port Aransas, Texas, and compare data with measurements simultaneously collected by a UAV flown over the same dolphins. A terrestrial LiDAR (light detecting and ranging), which is usually applied to collect topographic data, was adapted to scan dolphins surfacing to breathe from a rooftop platform. A custom-built LiDAR was affixed to a UAV with a high-quality video camera. Preliminary results indicate that both techniques can be used to extract body size measurements of dolphins, indicating important possibilities to collect data on free-swimming dolphins without any invasive aspects. Applications of land-based LiDAR for cetacean research are discussed.

Distinct Patterns of Aneuploidization Impact the Structure and Stability of the Yeast Genome

Discipline: Life Sciences
Subdiscipline: Environmental Science

Hyatt Vincent*[1]and Lydia Heasley [2]
[1]Colorado State University, [2]Colorado State University

Abstract: The frequencies and patterns by which cells gain new genomic mutations profoundly shape their evolutionary trajectories and phenotypic potential. Recently, we established that several classes of large-scale structural genomic mutation, including whole chromosome copy number alterations (e.g. aneuploidies), are acquired by cells via at least two distinct modes: the well-established neo-Darwinian pattern of gradual accumulation, during which single aneuploidies are acquired independently over time, and a burst-like pattern characterized by transient episodes of punctuated systemic genomic instability (pSGI), during which multiple aneuploidies are acquired simultaneously. The coexistence of such disparate tempos of aneuploidization has critical implications for our current paradigms of genome stability and evolution, yet, the incidence of each mode, as well as the molecular mechanisms underlying these different patterns of aneuploidization remain poorly understood. Using Saccharomyces cerevisiae cells, we have defined the frequencies at which gradual and pSGI-class aneuploidization events occur in populations, and in doing so have also characterized a third distinct class of aneuploidization. This third pattern is characterized by chromosome-specific uniparental disomy (UPD), a copy-neutral karyotypic alteration which results in the concurrent loss of one homolog and gain of the other. Interestingly, we have found that different yeast chromosomes display unique aneuploidization spectra, suggesting that chromosome-intrinsic features influence the propensity of a given chromosome to become aneuploid by a gradual, pSGI, or UPD-type mechanism. Together, these studies define a comprehensive model of aneuploidization, and inform on the intrinsic and extrinsic sources which may contribute to the stochastic patterns by which cells acquire de novo aneuploidies.

Native seed production in a changing climate: concerns for thornforest restoration in the Rio Grande Valley of Texas

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexa Escobedo*[1], Gisel Garza [2], Jon Dale[3], Teresa Patricia Feria Arroyo[4]
[1]University of Texas Rio Grande Valley, [2]American Forests, [3]American Forests, [4]Empowering Future Agricultural Scientists (EFAS)

Abstract: Texas' Rio Grande Valley (RGV) features native Tamaulipan thornforests, a biodiverse woodland composed of subtropical shrubs and trees. Thornforests have experienced severe fragmentation and less than 10% of the original ecosystem remains, threatening local wildlife. For over 40 years, ecological restoration of these woodlands has ensued to combat habitat loss. These efforts are based on seed collection from over 30 species found in remaining forest fragments. In 2021, many restoration species showed changes in phenology compared to historical records. A prominent species within restoration efforts is the Texas ebony (Ebenopsis ebano), a leguminous tree used extensively by native wildlife. Here, we present our observations on Texas ebony's phenology at 7 collection locations in the RGV from summer 2021 through spring 2022. Typically, this species produces fruits throughout the summer months, but we observed delayed production at all sites into spring 2022. Given the ongoing effects of climate change and forest restoration's role in realizing both climate resilience (e.g., carbon sequestration) and biodiversity conservation, observations like these have wider implications for future planning among restoration practitioners and land managers.

Characterizing the Role Fever Plays in Antibiotic Efficacy

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Gabriela Martinez*[1]and Autumn Henderson [2]
[1]University of California, Irvine, [2]University of California, Irvine

Abstract: Millions of people develop urinary tract infections (UTIs) on a yearly basis. One of the organisms causing these infections is uropathogenic Escherichia coli (UPEC). UPEC has become problematic due to its ability to develop antibiotic resistance. This generates a large economic burden on the healthcare system. One symptom present in humans upon contracting a UTI is fever (38°-40° C). Fevers are classified by an increase in body temperature above 37°C. Growing E. coli at high temperatures (42.2°C) has been previously shown to decrease the effectiveness of antibiotics due to genetic mutations that can help E. coli survive in the presence of antibiotics. However, there is a lack of information as to how fevers may influence the evolution of antibiotic resistance in UPEC. This project focuses on analyzing the role of heat stress on antibiotic effectiveness in order to better understand stressors that may lead UPEC to evolve antibiotic resistance. Through susceptibility assays, high throughput sequencing, and evolutionary rescue experiments, we observed how different antibiotics and different levels of heat shock interact. We hypothesize that fevers affect UPECs susceptibility to antibiotics by affecting survival rate. These changes in survival can ultimately influence the development of antibiotic resistance. Research in this area will help to develop more effective treatments for UTIs and increase our knowledge on how bacteria adapt to a given environment.

Using a Single Sequence Repeat (SSR) Fingerprinting Set to Characterize the U.S. National Ribes Collection

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Anton Alvarez*[1], Nahla Victor Bassil [2], Kim E. Hummer[3], Jill M. Bushakra[4], April Nyberg [5], Ryan King[6], Jaimie Green[7]

[1]Oregon State University, [2]USDA National Clonal Germplasm Repository, [3]USDA National Clonal Germplasm Repository, [4]USDA National Germplasm Repository, [5]USDA National Clonal Germplasm Repository, [6]USDA National Clonal Germplasm Repository, [7]USDA National Clonal Germplasm Repository

Abstract: The Ribes (currants and gooseberries) germplasm collection at the US Department of Agriculture, National Clonal Germplasm Repository (NCGR) in Corvallis, Oregon includes containerized, protected cultivation and field-grown plants as well as seeds of wild relatives. The objective of this study was to use a Ribes Single Sequence Repeat (SSR) fingerprinting set to develop baseline genetic profiles for the Ribes collection. SSRs are small repetitive DNA sequences in plant genomes. SSR genotyping uses these short repeats as targets for assessing the genetic variation among closely related samples and for confirming identity using parentage analyses. Discrepancies that can be resolved using this technique include cultivars with known pedigree, plants that have the same name but are phenotypically different, others that share the name and come from different locations, as well as plants that have very similar names in different languages but have identical appearance. Leaf samples from each of the sample plants were collected in cluster tubes, flash frozen, and stored at −80 °C until DNA extraction. This was followed by a DNA extraction protocol and standardized dilutions for all samples. Polymerase chain reaction (PCR) amplification was then performed, and PCR products were confirmed with gel electrophoresis. The PCR products were separated by capillary electrophoresis and GeneMarker software was used to determine product sizes. This anticipated genetic data will be used to confirm the identities of the Ribes samples. This will help the NCGR staff to more efficiently and accurately manage the Ribes collection.

Metallothionein-1 as a Targetable Selective Dependency in Acute Myeloid Leukemia

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Patricia Colom Diaz*[1], Chih-Hsing Chou [2], Jayna J. Mistry[3], Khan Mohammad Daud[4], Nathan Salomonis [5], H. Leighton Grimes[6], Jennifer J. Trowbridge[7]

[1]The Jackson Laboratory, [2]Division of Immunobiology, CCHMC, Cincinnati, USA., [3]The Jackson Laboratory, Bar Harbor, ME, [4]Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, United States., [5]Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, United States., [6]Division of Experimental Hematology and Cancer Biology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH., [7]The Jackson Laboratory, Bar Harbor, ME

Abstract: Adult de novo acute myeloid leukemia (AML) is a blood cancer with poor prognosis and the highly heterogeneous nature of this disease motivates targeted gene therapeutic investigations. To understand molecular mechanisms underlying AML development and progression, our lab developed the first mouse model with independently inducible mutations in Dnmt3a and Npm1 , two commonly co-mutated genes in human AML. Single-cell RNA-sequencing was performed to identify differentially expressed transcripts in Dnmt3a;Npm1 -mutant mouse AML progenitor cells compared to wild-type mouse progenitor cells. An upregulated transcript identified in this work was Metallothionein-1 (MT1), which has an important role in protection against heavy metal toxicity, inflammation, oxidative stress, and has been implicated in cancer progression. We hypothesize that MT1 is critical for growth and survival in Dnmt3a;Npm1 -mutant AML. In murine and human DNMT3A;NPM1 -mutant AML cells, we find that MT1 is over-expressed at the RNA, gene and protein levels. Furthermore, we designed a CRISPR-mediated MT1 knockout strategy for Dnmt3a ; Npm1 -mutant AML cells to test the extent to which loss of MT1 can inhibit growth. In conclusion, our study provides further insight into the use of MT1 for targeted treatment and prevention of DNMT3A;NPM1 -mutant AML.

Investigating the stress counteracting effects of exercise in female mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

Charmi Desai*[1], Karina Alviña [2], Samantha Vilarino[3], Jonah Juergensmeyer[4]
[1]University of Florida, [2]University of Florida, [3]University of Florida, [4]University of Florida

Abstract: Stress leads to anxiogenic behaviors and hippocampal-dependent memory impairment. Exercise induces the release of myokines such as Irisin from skeletal muscles which can have neuroprotective effects. We previously showed that exercise reverses the effects of acute stress in male mice. However, whether exercise can counteract stress-induced anxiety behaviors and memory impairment in female mice has not been shown. To test how exercise can be neuroprotective in female mice, we used adult wildtype female mice divided into two groups: control and exercise. The exercise mice swam for 20min daily for 20 days, while the control mice remained sedentary. After this swimming protocol, mice underwent a combined open field (OF) and novel object recognition (NOR) test with two identical objects. After this, mice were randomly assigned to undergo acute 3h restraint stress protocol (stress group) or to be returned to their home cages (control group). After 3h stress or home cage, each mouse completed the second session of OF/NOR test with one different object. Video tracking analysis software was used for data quantification. Our results show that unlike male mice, the exercised female mice did not lose weight over time. Furthermore, stressed sedentary mice showed more anxiety behaviors compared to unstressed sedentary groups. Exercise mice also showed increased rearing behavior, which coupled with more time in the center of the OF suggests reduced anxiety. Overall, our study suggests that exercise does have anxiolytic effects in female mice when subjected to acute stress.

Inferring the Evolutionary Genomic Recombination Rates of Arctic Wolves and the Domestic Dog

Discipline: Life Sciences
Subdiscipline: Biology (general)

Pedro Perez*[1]and Tina Del Carpio [2]
[1]University of California, Los Angeles, [2]University of California, Los Angeles

Abstract: Recombination is an evolutionary process that impacts genetic diversity and fertility. Since dogs and wolves lack functional PRDM9 genes, which influence recombination hotspots, we expected them to have similar recombination rates r. However, mean wolf r values are 18 times greater than dogs. Here, we examine this disparity by simulating genetic data to approximate pug and arctic wolf (AW) genomes. With msprime, we simulated forty dog and AW 20MB chromosomes (n=15, r=1e-8 per bp per generation, mu=4.5e-9 per bp per generation). Using pyrho and each group's demography, we inferred r values that are similar between AW and dogs (4.5e-09 vs 5.1e-09 per bp per generation, respectively) but lower than the true value. When simulating under a static demography of the harmonic mean of each population's demographic history, AW and dogs had mean r values of 3.7e-9 vs 6.8e-9 per bp per generation, respectively. Simulating chromosomes using a static demography of recent population sizes resulted in similar r values of 9.0e-9 vs 9.2e-9 per bp per generation for dogs and AW, respectively. Since breed dog genomes often have runs of homozygosity (ROHs), we simulated dog genomes with ROHs. This resulted in an estimated mean r of 5.6e-09 per bp per generation, similar to that without ROHs. While there are differences between dogs and AW under these scenarios, none mimic the empirical differences between these groups. Further analysis will investigate how mutation rates, recombination rates, and ROHs impact the canid genome.

Abnormal radial glial cells development caused by missense mutation of hcfc1a in zebrafish

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Valeria Virrueta*[1], David Paz [2], Anita Quintana[3]
[1]University of Texas at El Paso, [2]University of Texas at El Paso, [3]University of Texas at El Paso

Abstract: cblX syndrome is an inborn error of vitamin B12 (cobalamin) characterized by metabolic deficits, abnormal brain development, craniofacial dysmorphia, and intractable epilepsy. cblX is caused by mutations in the HCFC1 transcriptional cofactor. Previous studies have shown that HCFC1 regulates brain development and neural precursor cell (NPC) proliferation/differentiation in a vitamin B12 independent manner. However, there are no studies that demonstrate a role for HCFC1 in radial glial cells (RGCs), which are a sub-population of the larger NPC population. In this study we used a germline mutant of hcfc1a, one ortholog of HCFC1 to study the effect of missense mutation on the number and function of RGCs during development. We will demonstrate decreased expression of glial fibrillary acidic protein (gfap), one marker of RGCs in zebrafish, in homozygous mutant larvae. We hypothesized that decreased expression of gfap was the result of decreased overall numbers of RGCs. To test this, we used flow cytometry and a transgenic reporter animal (Tg(gfap:GFP)) to measure the total number of RGCs in mutant larvae. Interestingly, we found a significant decrease in the total number of Gfap positive cells, which validate using immunohistochemistry. Future experiments

will determine the proliferation and survival of RGCs after mutation of hcfc1a . Our results will provide further insight into the underlying mechanisms of how mutation of HCFC1 regulates multi-potent progenitor cells and brain development.

Extraction of Antibiotic producing bacteria from soil sample

Discipline: Life Sciences
Subdiscipline: Microbiology

Opeoluwa Adesola*[1]and Dr. Meda Higa [2]
[1]York College of Pennsylvania, [2]York College of Pennsylvania

Abstract: The war against antimicrobial resistant (AMR) bacteria is at a critical point. Even minor infections that could be treated with antibiotics could become lethal as the bacteria become resistant to already-in-use antibiotics. A strategy for possible control or elimination of AMR is the attempt to discover novel antibiotic-producing bacteria. In this research, we extracted antibiotic-producing bacteria from soil in York, Pennsylvania. We characterized bacterial isolates by performing a Gram stain and sequencing their 16s rRNA genome to determine the type of bacteria our isolates are. We also performed a Kirby Bauer test to determine the antibiotic resistance of our isolates. Preliminary results showed that bacterial isolate 3OA18 was Gram-positive and a part of the Bacillus genus. Isolate 3OA19 was Gram-negative and a part of the Pseudomonas genus. TheKirby-Bauer test showed that 3OA19 was resistant to cell wall synthesis antibiotics, suggesting that this could be the function of the antibiotic it produces. Isolate 3OA18 showed resistance to the 50s ribosomal subunit inhibitor antibiotics, suggesting it might produce a similar antibiotic. Genome sequencing confirmation of the isolates are currently in progress. Transposon mutagenesis experiment will be done to identify gene(s) responsible for the production of the antibiotics. Taken together, this strategy could identify novel antibiotics that are effective against antibiotic-resistant pathogens. In the long run, we hope to use this information to improve antibiotic production and increase the effectiveness of these antibiotics, progressing the fight against AMR.

Quantifying phenotypic outputs of Protein Kinase A in S. cerevisiae in response to nutrient inputs

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Nicole Carmiol*[1], Michael Plank [2], Andrew Capaldi[3]
[1]University of Arizona, [2]University of Arizona, [3]University of Arizona

Abstract: The Protein Kinase A (PKA) pathway is highly conserved across eukaryotes, where it acts as a key regulator of cell growth and metabolism. Previous research in the model organism, S. cerevisiae's PKA pathway, generally assumes that the pathway's activation and resulting stimulation of cell growth only occur in presence of glucose. Here we report that the model is inaccurate. Proliferation assays and phosphoproteomics demonstrate PKA is active in the presence of poor carbon sources (such as glycerol), and is activated to different levels depending on quantity and timing of glucose stimulus, which directly correlates with proliferation rate. More generally, this data shows that the pathway elicits graded control over its signaling outputs and cell growth across a wide variety of carbon sources and cell growth, instead of acting as an "on/off switch" like some other kinases. Further research is in progress to determine details of PKA's role in different stages of the cell cycle. Analysis pipelines to quantify the data extracted from DIC microscopy images have been developed (involving neural network processing, custom Python scripts, image analysis software, etc.), which report on budding indices and cell size measurements. Our findings on PKA impact the current view of kinase function, with some exhibiting a fine-tune control mechanism instead of acting as global switches for their signaling outputs.

Phylogenetic analysis of chloramphenicol resistance catA2 gene in Klebsiella pneumoniae shows mobilization from Morganella morganii

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cristabel Portillo*[1], Dr. Luis Mota-Bravo [2], Dr. Andrei Tatarenkov[3]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Bacterial resistance to chloramphenicol is encoded by the catA2 gene and previous research in our lab suggests that catA2 may have originated in Morganella morganii. We hypothesize that the catA2 found in an environmental Klebsiella pneumoniae isolate was originally mobilized from M. morganii. The objective of our study was to investigate the taxonomic, geographical, and plasmid distribution of the catA2 gene. A K. pneumoniae (SW4861), collected in the Mississippi River, contained a catA2 gene. Resistance profile was established with disk diffusion tests (DDTs). Plasmids were analyzed using PATRIC, CGE, and MEGAX. The isolate contained a 121 kb long plasmid (p121) encoding three antibiotic resistance genes: catA2, tet(D), and sul2. The catA2 gene in P121 was enclosed by insertion sequences IS26 making a composite transposon, which could explain possible mobilization. Comparison with Genbank data found this region to be on plasmids of several incompatibility types, in diverse bacterial species and worldwide geographical distribution. Plasmid-borne catA2 gene showed considerable diversity with divergence up to 11% among 7 alleles which formed 3 major groups based on a haplotype network. A phylogeny of these alleles and 33 M. morganii chromosomal catA2 genes indicated that the plasmid-borne catA2 resulted from three independent mobilizations from M. morganii. Plasmid catA2 were surrounded by MGEs such as IS26 and ISKpn13 that were consistent with these mobilizations. Our study exhibits the dissemination and evolutionary history of catA2 in K. pneumoniae isolate via MGEs mobilization. Studying these mobile genetic elements can aid in deterring the dispersion of antimicrobial resistance genes.

Are Neurotransmitters Conserved Among Species?

Discipline: Life Sciences
Subdiscipline: Neurosciences

Megan Hampton*[1], Ray L. Hong [2], Heather R. Carstensen[3], Juan Cardenas[4]
[1]University of California, Northridge, [2]Biology Professor and mentor, [3]Research Scientist, Lab Manager, [4]Undergraduate Research Scientist

Abstract: The nematode, Pristionchus pacificus , serves as a model organism for studying development and evolution. Its free-living and host dependent life cycles provide insight into independent and commensalistic lifestyles. Like Caenorhabditis elegans, P. pacificus has a simple nervous system allowing for direct single cell comparisons between these species and providing a molecular and cellular basis for behavioral comparisons. P. pacificus has an attraction to ZTDO, the oriental beetle’s sex pheromone, but the molecular factors driving this response are unidentified. The obi-1 mutant is hypersensitive to ZTDO, becoming paralyzed when exposed. By performing a non-biased genetics screen for suppressors of this paralytic response in the ZTDO hypersensitive obi-1 mutant, the gene Ppa-cat-1 was identified as a candidate. Utilizing CRISPR/cas9, Ppa-cat-1 mutants were produced and tested revealing that Ppa-cat-1 alone may not suppress the ZTDO attraction pathway. We therefore continue to characterize the function of Ppa-cat-1 believed to be homologous to dopamine and serotonin transporters in C. elegans . Ppa-cat-1 mutants express an egg laying defect (egl); this phenotype may be attributed to defects in serotonin transport. With the addition of exogenous serotonin, the egl phenotype is rescued; subsequent 2-way ANOVA of the Ppa-cat-1 mutant (n=68-72) showed significance (p<0.0001). Determination of dopamine phenotypes is required for further analysis. Using Gibson Assembly, we produced a reporter construct to visualize the expression patterns of Ppa-cat-1 . Identifying the role of the Ppa-cat-1 gene is necessary to demonstrate homology, but initial results reflect similarities between C. elegans and P. Pacificus prompting further research .

Investigation of pH induced epileptiform activity in Drosophila MDH2 mutants.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Frank Sigui Sigui*[1], Roberto X. Hernandez [2], Gregory T. Macleod[3]
[1]Wilkes Honors College, Florida Atlantic University, [2]Florida Atlantic University, [3]Florida Atlantic University

Abstract: Neuroexcitability is highly sensitive to changes in pH. This is a consequence of pH-sensitive proteins that regulate the ionic gradients that establish membrane potential and neuronal excitation. Surprisingly, mechanisms that link acid-base imbalance and neurological disorders have yet to be elucidated and the manner in which pH contributes to conditions such as epileptic seizures remains unclear. Despite this knowledge gap, drugs targeting pH regulatory proteins have been effective for treating epilepsy and migraine. Recently, it has been reported that children containing point mutations within the gene that encodes the citric acid cycle enzyme, mitochondrial malate dehydrogenase (MDH2) exhibit symptoms of hypotonia, lactic acidosis and epilepsy. To date, no treatment exists for this disorder and the cellular conditions leading to epilepsy caused by a loss of function in MDH2 needs further investigation. Here we investigate how lactic acid associated pH changes contribute to the manifestation of epilepsy in these patients. To elucidate the possible connections between pH imbalance and epileptic seizures in children who have MDH2 mutations we used CRISPR technology to introduce the same MDH2 mutations to the genetic model organism, Drosophila . With the use of confocal microscopy, we investigated cytosolic pH concentration, mitochondrial function, and mitochondrial density in neurons of 3 rd instar larval Drosophila . The results of these experiments will help explain the physiological conditions responsible for symptoms such as epilepsy in children with MDH2 mutations. Furthermore, this will shed light on how acid-base imbalance may lead or contributes to neurological disorders with no current treatment.

Unique Multi-Drug Resistant Region Mobilized by an IS26 Composite Transposon within Environmental Citrobacter freundii Plasmid

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Isabel Vargas*[1], Luis Mota-Bravo [2], Andrey Tatarenkov[3]

[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Although deemed a rare healthcare-associated pathogen with low virulence, Citrobacter freundii has emerged as a multidrug-resistant (MDR) pathogen, thus its potential risk in clinical settings urges a better understanding of how antibiotic resistance genes (ARGs) are mobilized. We hypothesize that the aquatic environment serves as a reservoir for antibiotic resistance genes, which can be disseminated among bacteria via plasmids and mobile genetic elements (MGEs). The objectives of this study are to characterize plasmids from a C. freundii isolate and identify ARGs, including their genetic environment, in order to further examine their dissemination. This isolate was obtained from the Harlem River in New York, New York, and was identified as C. freundii using MALDI-TOFF. Its resistance profile was determined via disk diffusion tests which were followed by extraction of plasmid and genomic DNA. These genomes were then sequenced, assembled, and annotated using PATRIC, CGE, ISfinder, and NCBI databases. The analyses revealed that the C. freundii isolate is resistant to 6 antibiotic drug classes and harbors a 151,817bp nonconjugative plasmid. Analyses revealed a unique 27.9kb IS 26 composite transposon containing 6 resistance genes. This composite transposon shared 80% similarity with 35 sequences pertaining to different sources, species, and incompatibility types, thus emphasizing the role of MGEs in the rearrangement and mobilization of genes within plasmids. Reorganization of this MDR region due to the IS 26 composite transposon indicates how ARGs are disseminated in the environment. Because similar samples were sourced from clinical settings, this demonstrates C. freundii's increasing threat in healthcare.

Characterizing the role of glutamate in decision-making behavior

Discipline: Life Sciences
Subdiscipline: Neurosciences

Gianina Pontrelli*[1]and Dr. Gareth Harris [2]
[1]California State University, Channel Islands, [2]California State University, Channel Islands

Abstract: Glutamate signaling is a key neurotransmitter involved in complex behaviors across the human brain. Glutamate signaling has been implicated in pain sensing, olfaction, learning, memory and decision-making. Despite understanding the appreciation of glutamatergic transmission in complex behavioral strategies, our understanding of the molecular mechanisms and brain circuits that are shaped by glutamate signaling is still not fully understood. Our project uses the invertebrate worm, C. elegans, to characterize how glutamate controls decision-making behaviors associated with the sensation of odors and the processing of food related cues. We used a behavioral paradigm that examines escape responses from food when paired with a repulsive volatile odorant, 2-nonanone. We found that glutamate signaling mediates, 1) food recognition, while worms reside on a food patch, and 2) the dynamics of food leaving during exposure to repellents. We have identified key roles for glutamate based on using mutant analysis, to examine worms that lack glutamate transmission of downstream glutamate receptors in the worm's 'brain'. We have identified a role for glutamate signaling in spontaneous food related behavior on a food patch, and we identified a role for glutamate and multiple glutamate receptors that mediate 2-nonanone-dependent food leaving. We hope that our findings provide a platform to continue our investigation of how key human relevant neurotransmitters control complex decision-making behaviors.

Retinoic Acid Induced 14 Drives Pancreatic Cancer Progression and Metastasis

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Luke Tomaneng*[1]and Jonathan Kelber [2]

[1]California State University, Northridge, [2]California State University, Northridge

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is associated with very poor outcomes - fewer than 10 percent of patients survive beyond five years after diagnosis. Hurdles facing PDAC patients and clinicians include early dissemination, a lack of therapeutic targets and desmoplasia that renders the primary tumor refractory to chemotherapy. We previously reported that pseudopodium-enriched atypical kinase 1 (PEAK1) and integrin α1 (ITGA1) mediate gemcitabine resistance and metastasis in PDAC. To identify new mechanisms of PDAC progression, we mined the Cancer BioPortal and Human Cell Map BioID databases for additional pseudopodium-enriched (PDE) proteins that predict poor patient outcomes, correlate with PEAK1 and ITGA1 expression in PDAC, and interact with PEAK1 and ITGA1. Here, we identify Retinoic Acid Induced 14 (RAI14) as a new candidate driver of PDAC. Silencing of RAI14 in KRas mutant PDAC cells impaired adhesion-dependent proliferation/survival in vitro and tumor growth and metastasis in vivo. Cyclic immunofluorescence (CycIF) was used to identify subpopulations of PDAC cells supported by RAI14. By using a bioinformatics pipeline in combination with proteomic and immunofluorescence data on the composition of ITGA1-dependent adhesion complexes in PDAC cells, we identified Polo-Like Kinase 1 (PLK1) as a candidate that may control RAI14 function and adhesion-regulated mitosis during PDAC progression. The potency of volasertib, a PLK1-specific inhibitor, was reduced in RAI14 knockout cells, supporting a model in which RAI14 mediates PLK1 functions in PDAC. These studies uncover a mechanism for RAI14-driven PDAC progression and the development of strategies to increase chemotherapy sensitivity, reduce primary/metastatic tumor burden and improve patient outcomes.

Periodontal Disease as Risk Factor for Oropharyngeal Cancer in Puerto Rican PLWH

Discipline: Life Sciences

Subdiscipline: Cancer Biology

Yabdiel Ramos*[1], Josue Perez-Santiago [2], Coral Martes[3], Pedro Medina Cuevas[4], Alejandra Ballester [5], Ana P. Ortiz-Martinez[6], Ramon Gonzalez Garcia[7]

[1]University of Puerto Rico Comprehensive Cancer Center, [2]University of Puerto Rico Comprehensive Cancer Center, [3]University of Puerto Rico Mayagüez, [4]1University of Puerto Rico Medical Science Campus, [5]University of Puerto Rico Rio Piedras, [6]University of Puerto Rico Comprehensive Cancer Center, [7]University of Puerto Rico Medical Science Campus, School of Dental Medicine

Abstract: Oral Human Papillomavirus (HPV) infection remains one of the main risk factors for oropharyngeal cancers, particularly in people living with HIV (PLWH). Puerto Rico has a high burden of HPV-related cancers and is also characterized by socioeconomic disadvantage, which is a social determinant of oral health disparities and can potentially affect oral HPV risk. Periodontal disease is a chronic inflammatory condition associated with oral HPV infection and cancer in PLWH but has not been evaluated in the context of HIV in Puerto Rico. We evaluated periodontal disease in 19 virologically suppressed sexually active PLWH (men and women ≥21 and <65 years old), in relation to sociodemographic, behavioral, HPV knowledge, and HPV vaccine awareness. Adequate HPV knowledge was defined as a score of ≥70% of correct responses on a 13-item knowledge scale. A clinical full-mouth periodontal assessment was performed following the NHANES protocol where periodontitis and gingivitis were defined according to the CDC. Participants' mean age was 47.4±13.4 years, and 94.7% of participants were men. Only 36.8% of the participants had adequate HPV knowledge, 10.5% were vaccinated, and 21% were previously diagnosed with HPV. The prevalence of periodontitis and gingivitis as defined in the study was 72.2% and 16.7% respectively. Understanding how periodontal disease could facilitate HPV infection and other comorbidities in PLWH is crucial for the development of cancer prevention and reducing the burden of HPV-associated malignancies in PLWH. Furthermore, HPV vaccine-oriented and oral health educational interventions should target this high-risk group.

Understanding the Establishment of TWIST Neural Crest Gene Regulatory Systems and Their Evolutionary Significance in Chordates

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Austin Katzer*[1]and Daniel Medeiros [2]
[1]University of Colorado Boulder, [2]University of Colorado Boulder

Abstract: This project focused on the evolutionary aspect of the neural crest in chordate organisms and addressed the question of how the neural crest emerged. The twist gene is essential in chordate development and encodes a basic transcription factor that plays an important role in the development of embryos. An experiment was conducted to determine what kind of mutations may have integrated twist in the neural crest gene network. This project focuses specifically on mutations within twist cis-regulatory elements (CREs), non-coding DNA sequences that regulate transcription of genes, that may have facilitated its involvement in neural crest cells. A new CRE would consist of a novel sequence that is not present in invertebrate chordates and only acts in neural crest cells. Alternatively, an existing CRE could have been modified to permit twist expression in a novel tissue other than the ancestral mesodermal pattern. By identifying putative CREs using conserved teleost sequences outside of the coding region for twist it is possible to functionally test these elements using standard transgenic techniques. The putative cis-regulatory element sequences of around 1000-2000 base pairs in length were tested functionally within zebrafish using the gateway cloning method to introduce the fragments into the reporter construct pGreene, which has a cFos basal promoter and eGFP flanked by Tol2 recombination arms. Injecting these constructs along with transcriptase into single-cell embryos highlights twist CRE activity by driving fluorescent signals in a given region of the embryo revealing how the neural crest gene network was co-opted.

Elucidating the Structure of the CLN5:GPD Complex

Discipline: Life Sciences
Subdiscipline: Biochemistry

Andy Hims*[1], Uche Medoh [2], Monther Abu-Remaileh[3]
[1]Stanford University, [2]Stanford University, [3]Stanford University

Abstract: CLN5 Batten’s disease is a lysosomal storage disorder that arises from a mutation of the CLN5 lysosomal protein, resulting in accumulation of lysosomal material in neuronal cells and neurodegeneration. The CLN5 protein has been shown to bind to and transfer glycerophosphodiesters (GPDs), a lipid metabolite, out of the lysosome. CLN5 is hypothesized to dock onto intralysosomal vesicles (ILVs) by utilizing an amphipathic helix. When CLN5 is bound to GPDs, a conformation change may result in dissociation from the ILVs and allow CLN5 to transfer GPDs to other lysosomal proteins for further export. Currently, a known crystal

structure of the CLN5 has contributed to our understanding of the CLN5:GPD binding site. However, a structure detailing changes in the CLN5:GPD structural complex has yet to be resolved. Human CLN5 protein was expressed and purified from mammalian cell cultures using 6xHisTag affinity and size-exclusion chromatography, followed by glycosidase treatment and GPD incubation. The purified protein is then crystallized onto trays whereby X-ray crystallography techniques allow us to resolve the crystal structure. This presentation will report the crystal structure of the CLN5:GPD complex and compare changes in protein conformation to unbound CLN5, such as shifts of the amphipathic helix that would allow for the undocking of CLN5 from ILVs. Resolving the crystal structure of the CLN5:GPD complex will further aid in our understanding how CLN5 interacts with structures within the lysosome and provide evidence for a metabolite export pathway involving CLN5 to maintain lysosomal function and physiology.

Angiotensin receptor blocker ameliorates elevated systolic blood pressure and poor glucose tolerance in OLETF rats fed a high cholesterol diet

Discipline: Life Sciences
Subdiscipline: Biology (general)

Eira Jardines*[1], Rudy M. Ortiz [2], Jessica Wilson[3], Dora Mendez[4]
[1]University of California, Merced, [2]University of California, Merced, [3]University of California, Merced, [4]University of California, Merced

Abstract: Metabolic Syndrome (MetS) affects nearly 60% of Hispanic adults over the age of 60 and more than 30% of the US population. MetS is a cluster of conditions, which include elevated arterial pressure and poor glucose tolerance with or without insulin resistance. Unmanaged, MetS can lead to lethal conditions like type II diabetes. A high cholesterol diet (HCD) is known to promote cluster-factor conditions of MetS like dyslipidemia. A common therapy to treat hypertension is disruption of the renin-angiotensin system that includes blockade of the angiotensin receptor (ARB), which our lab has shown to attenuate cluster factor conditions in a model of MetS. However, the effectiveness of ARB during a HCD remains unclear. Otsuka Long Evan Tokushima Fatty (OLETF) rats (a MetS model) were given a HCD and at presentation of elevated arterial pressure, they were treated with ARB (10 mg olmesartan /kg/d x 3 wks by oral gavage). Blood pressure was monitored real time with surgically implanted radio telemeters. ARB reduced systolic blood pressure by 15±1mmHg (11%; p<0.05) in HCD OLETF. Additionally, ARB reduced AUC glucose by 28% (p<0.05) and tended to reduce fasting blood glucose by 19% (p=0.06) compared to OLETF+HCD. However, ARB did not affect static fasting insulin levels. These findings demonstrate that chronic treatment with ARB can effectively ameliorate MetS-associated hypertension despite the additional insult of a HCD.

Investigating TTLL Enzyme Redundancy in Caenorhabditis elegans Male-mating Responses

Discipline: Life Sciences
Subdiscipline: Genetics

Naileny Rodriguez*[1], Nina Peel [2], Danielle Ayoub[3]
[1]The College of New Jersey, [2]The College of New Jersey, [3]The College of New Jersey

Abstract: Microtubule (MT) glutamylation is a post-translational modification where glutamates are reversibly attached to microtubules. This process is required for proper cilia function in C. elegans and other organisms. In humans, cilia dysfunction is associated with deafness, infertility,

and polycystic kidney disease, and a mutation that causes dysregulation of glutamylation is associated with infantile-onset neurodegeneration. Investigating the function of glutamylation in C. elegans will help us to better understand how glutamylation regulates microtubule function in the cilia. This project aims to explore if redundancy occurs within the five TTLL enzymes expressed in C. elegans and if so, to what extent. In C. elegans, cilia function is necessary for proper male-mating behavior. C. elegans expresses five glutamylating enzymes TTLL-4, TTLL-5, TTLL-9, TTLL-11, and TTLL-15. Loss of individual TTLL enzymes does not seem to cause cilia dysfunction, however, the ttll-4; ttll-11; ttll-5 triple mutant does show defects in male mating, and preliminary data of the ttll-15, ttll-5, him-5 mutant shows little to no difference in male mating responses. This indicates that redundancy may exist between the enzymes, whereby the loss of one enzyme can be compensated for by the presence of others. To begin to explore the redundancy of these enzymes, our lab generated all ten double mutant combinations of the TTLL enzymes, I am analyzing male mating responses of the double mutants and will present a complete analysis of any redundancies between the TTLL enzyme double mutants. This work will help to determine which TTLL enzymes are most essential in C. elegans.

Bioinformatic and Experimental Evaluation of Otx2 and Oc1 Transcription Factor Binding Site Conservation and Specificity in the ThrbCRM1 Retinogenesis Enhancer Element

Discipline: Life Sciences

Subdiscipline: Genetics

Mykel Barrett*[1], Mark Emerson [2], Sacha Sulaiman[3], Denice Moran[4]

[1]The City College of New York, [2]The City College of New York, [3]The City College of New York, [4]The City College of New York

Abstract: In retinal progenitor cells, the transcription factors, Otx2 and Oc1 interact with the ThrbCRM1 enhancer to regulate Thrb expression. Interestingly, ThrbCRM1 contains Otx2 and Oc1 binding site sequences that deviate from the sequences that the factors prefer binding in vitro . HT-SELEX data suggest that Otx2 and Oc1 prefer binding “ T AATCC,” and “AAATC R AT” sequences, respectively; however, in ThrbCRM1, “ A AATCC” and “AAATC A AT” sequences are conserved in almost all vertebrate genomes. To test the hypothesis that nucleotide substitutions within transcription factor binding sites affect enhancer function, plasmid reporter vectors were electroporated into developing chick retinal cells. ThrbCRM1 was placed upstream of GFP or TdT reporter genes, which allowed for the modification of its Otx2 and Oc1 binding sites, and for the functional affects of variant sites to be quantitated using flow cytometry. “AAATCCAT” and “AAATCTAT,” Oc1 binding site variants abrogate ThrbCRM1 activity, and statistical tests show the expression pattern of cell populations containing the “AAATCGAT,” mutant Oc1 site do not significantly differ from populations containing the “AAATCAAT,” wild type sequence (p = 0.9100). Finally, our data suggest that the “TAATCC,” Otx2 binding site variant drives a significant, non-discrete increase in enhancer activity, compared to the wild type “AAATCC,” version (p < 0.0001). Our findings spotlight the failure of in vitro assays to recapitulate important molecular variables that are present within the authentic physiological setting, and support the potential use of designer enhancer elements in the quantitative control of delivered, therapeutic gene expression.

Can A Change In Temperature Affect The Distribution Of Drosophila Species Diversity?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kayla Scott*[1], Joanna Vondrasek[2], Anne B. Allison[3]
[1]Piedmont Virginia Community College, [2]Piedmont Virginia Community College, [3]Piedmont Virginia Community College

Abstract: Fruit flies are tiny ectothermic invertebrates, belonging primarily to the Drosophila genus, that cannot regulate body temperature independently. Drosophila species must rely on external heat sources and employ physiological mechanisms to maintain an ideal internal temperature. Temperature change is an essential variable influencing species distribution since organisms must respond with adaptations. This study aims to investigate how the distributions of Drosophila species vary over a season change. It is hypothesized that as the average temperature decreases during the autumn months, the diversity of Drosophila species will increase. In five collection periods from September 2022 to November 2022, Drosophila samples were captured using various techniques at a local apple orchard in Central Virginia. Each collection vial was humanely euthanized, sorted, and then counted by species using a dissecting microscope. The temperature change was recorded via local meteorological reports, and species diversity was compared via a chi-squared analysis. It was found that only three out of approximately ten locally common Drosophila species were consistently observed: Drosophila melanogaster/simulans, D . Indianus, and D. Suzuki. Results suggest that a change in the distribution of species with decreasing temperature was not detected; however, interestingly, when temperatures fell below 43 degrees, no samples could be collected. A more extended collection period would allow for a more robust analysis of seasonal change in distribution. Future studies could confirm the species identity of flies, and genetic sequencing could investigate population structure. Altogether, these studies will help describe rapid population variations on seasonal time scales.

Examining the Impact of Nicotine on Place Cell Activity for Encoding Contextual Spatial Memories

Discipline: Life Sciences
Subdiscipline: Neurosciences

Zinnia Saha*[1]and Seetha Lakshmi Krishnan[2]
[1]University of Chicago, [2]Postdoctoral researcher

Abstract: Chronic nicotine abuse and addiction is a result of neuroadaptations in brain circuits that produce positive reinforcement during abuse and negative reinforcement during withdrawal. Learned associations between spatial contexts and nicotine rewards are a major cause of craving and often leads to relapse amongst smokers when returned to said contexts. This presentation will report the effect of nicotine on neural mechanisms for encoding spatial memories. Contexts are encoded by place cells in the hippocampus. Using two-photon microscopy and virtual reality contexts (VR) we will study the effect of a water reward versus a nicotine reward on place cell activity. We have established a behavioral paradigm to train mice to associate a VR with nicotine reward and another VR with water reward. In trained mice, two-photon imaging of hippocampal cells labeled with calcium indicator will be performed to investigate place cell activity in the nicotine-associated VR versus the water-associated VR. We hypothesize that place cells will display properties associated with better spatial tuning, like higher reliability, lower out of field firing and greater stability across days in the nicotine-associated VR. Furthermore, we expect higher place cell overrepresentation around the rewarded zone compared to the rest of the track for nicotine-associated VR. Finally, we will investigate the effect of withdrawal on place cell activity by placing the animals back in the VR without a nicotine reward. We hope to understand how nicotine affects hippocampal encoding of contextual spatial memories to understand the neurobiology of learning and addiction.

Evaluation of the antagonistic activity of bacteria isolated from London Rocket against three agricultural pathogens

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kaihre Brightwater*[1]and Soum Sanogo [2]
[1]New Mexico State University, [2]New Mexico State university

Abstract: London rocket is a ubiquitous weed that displays resiliency in the extreme environments of New Mexico. It is hypothesized that endophytic bacteria might afford London Rocket this resiliency. Endophytic bacteria were isolated from London Rocket collected in agricultural and non-agricultural areas around Las Cruces. Multiple experiments consisting of diffusion well and volatile tests were conducted to evaluate the antagonistic activity of endophytic bacteria from London Rocket against three plant pathogens, Phytophthora capsici, Fusarium oxysporum, and Sclerotium rolfsii isolated from chile, cotton, and peanut, respectively. Results showed that bacteria isolated from London Rocket produced volatiles that reduced mycelium growth of all three pathogens, with the greatest reduction recorded in S. rolfsii and P. capsici. Further experimentation will utilize these endophytic bacteria for protection of crops against these pathogens.

Genetic Barcoding of all Diadromous Shrimp Native to Guam

Discipline: Life Sciences
Subdiscipline: Genetics

Antoni Badowski*[1]and Daniel Paul Lindstrom Ph.D. [2]
[1]University of Guam, [2]University of Guam

Abstract: Guam is home to at least seven species of native shrimp presumed to be amphidromous. Amphidromy is a diadromous life history pattern where newly hatched larvae are carried from streams to the sea and drift among plankton for up to nine months. They recruit to streams as pre-juveniles, mature and spawn in freshwater. Six species have been described in the family Atyidae: Atyoida pilipes, Caridina brachydactyla, C. mertoni, C. typus, C. weberi, and C. serratirostris and one in the family Palaemonidae: Macrobrachium lar . No genetic confirmation/refutation of these shrimp on Guam have been performed. The first step before future research and conservation efforts can be conducted will be to confirm species identifications. We collected multiple specimens of all known and unknown species of amphidromous shrimp native to the island of Guam from as many watersheds as possible. All individuals were photo documented prior tissue biopsy and specimen preservation. Genomic DNA was extracted from biopsied tissue, PCR amplified, and subsequently sequenced of the "Barcode" mitochondrial gene Cytochrome-Oxidase I. Sequences were compared to the extensive GenBank database to confirm species affinities. All six of the previously known shrimp species were confirmed and three yet to be described, genetically distinct, species were

identified and await further taxonomic analysis. Confirmation of species in Guam's streams and their native/endemic status will be key in future research and conservation. This information will allow more extensive genetic analyses to be conducted in future population genetic studies and serve as a guide for effective conservation efforts .

Analyzing Genetic Variability and Diversity of Microbial Communities in Geothermal Hot Springs using Metagenomic Read Recruitment

Discipline: Life Sciences
Subdiscipline: Microbiology

Juan Gomez*[1]and Jose de la Torre [2]
[1]San Francisco State University, [2]San Francisco State University

Abstract: Metagenomics has overcome the limitation of studying uncultured microorganisms by allowing direct extraction and sequencing of entire genomes from microbial communities present in the environment. Our model organism Nitrosocaldus yellowstonensis HL72 contains an integrating mobile genetic element (iMGE), but it is unknown if other strains contain this (iMGE), analyzing metagenomic data can determine if they are present in other strains. My research focuses on metagenomes that were collected and sequenced from a single terrestrial geothermal system known as the Great Boiling Spring (GBS) located in northern Nevada. This geothermal system harbors microbial communities growing over a temperature gradient of 60℃, 70℃, & 85℃. My research aims to understand the genetic variability and diversity that are indicative of genetic adaptation to the local physical environment that is influenced by the temperature in these springs. One commonly used approach to study this data is metagenomic read recruitment, by matching individual short sequences from the metagenome, known as reads, to the genomes of our key reference organism HL72. The reads can then be plotted onto a graph based on the match's location and the percent identity to the reference genome, giving information on regions of genetic variability known as genomic islands within the natural population. I have used these results to identify genomic regions that vary between the reference organisms and the population present in the spring. In summary, this study can help us understand the adaptation and evolution of uncultured microbial communities that have a key role in the nitrogen cycle.

Male mate choice contributes to species boundaries in Cyprinodon spp. from inland lakes in The Bahamas

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jonathan Enriquez Madrid*[1], Rhiannon west [2], Estrella Gonzalez[3]
[1]Northern New Mexico College, Espanola., [2]Northern New Mexico College, [3]University of New Mexico

Abstract: Several factors can contribute to speciation. Examples include physical barriers and differences in seasonal sexual receptivity, both capable of disrupting gene flow. A different factor is reproductive isolation through assortative mating. Assortative mating dictates the direction of gene flow and can lead to speciation. As females are generally the investing sex, most research has focused on female choice but a growing body of literature indicates male choice exists and may contribute to speciation. We utilize a group of Cyrpinodon ssp . pupfish from The Bahamas to examine the importance of male choice in maintaining species boundaries. Reckley lake holds one species (C. variegatus), while Crescent lake holds all three (C. variegatus , C. desquamator , and C. brontotheroides). These species do not interbreed in the wild. We hypothesize that mate choice by both sexes contributes to species boundaries. We performed binary choice sexual preference trials with C. variegatus as our focal fish. Our results show that females from both lakes do not show a preference for either lake or species type ($F_{1,98} = 0.01$, p =.941) ($F_{1,50} = 0.01$, p =.924). Reckley males prefer C. variegatus females from Crescent over C. desquamator ($F_{3,96} = 4.54$, p =.005), and Crescent males showed a non-significant preference for Reckley females over their own lake ($F_{1,48} = 3.72$, p =.060). We show support for male choice contributing to species boundaries in these lakes. More work is needed to understand why females lack a preference.

Investigating the role of maternal wnt16 in axial elongation in zebrafish

Discipline: Life Sciences
Subdiscipline: Genetics

Sumaya Addish*[1], Joyce Tang [2], Ronald Kwon[3]
[1]University of Washington, Seattle, [2]University of Washington, Seattle, [3]University of Washington, Seattle

Abstract: Understanding how genetic variation contributes to musculoskeletal traits could help identify new treatments for orthopaedic disorders. Previous human genetic studies have found that genetic variants near the WNT16 gene are associated with altered bone and lean mass in children. How genetic variants might act through WNT16 to influence these traits is unknown. Our lab previously showed that loss of wnt16 results in reduced axial bone length and muscle mass in zebrafish due to defects in axial elongation during embryonic development. In many organisms, the influence of Wnts on axis patterning originates through maternal transcripts, i.e., transcripts already present in an unfertilized egg that are subsequently degraded during the maternal-to-zygotic transition. The purpose of this study was to determine whether maternal wnt16 contributes to axis patterning. We hypothesized that the absence of maternal wnt16 would disrupt axial patterning in the early zebrafish embryo. To test this, we compared the effects of loss of zygotic wnt16 to loss of both maternal and zygotic wnt16 on embryonic axial patterning. Our findings revealed similar embryonic axial patterning defects in wnt16 zygotic mutants and wnt16 maternal zygotic mutants, indicating that there was no observable consequence of loss of maternal wnt16 . Thus, our studies indicate that maternal wnt16 transcripts do not contribute to bone and lean mass in zebrafish, suggesting it may be dispensable in other vertebrates including humans.

Organelle Size Scaling Regulation in Saccharomyces cerevisiae Optogenetically Grown to Immense Cell Size

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Brenda Garibay*[1], Yee-Hung Mark Chan [2], Ryan Joseph Acbay[3]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University

Abstract: The yeast Saccharomyces cerevisiae has organelles that serve as biochemical reactors in the cell; specifically, the vacuole maintains pH, ion homeostasis, and degrades proteins. The lysosome found in plant and animal cells is homologous to the vacuole, which regulates size and count, and attributes to disease when unbalanced. Previous studies found that the vacuole also shows a scaling trend with cell size, suggesting a size-coordination regulating mechanism. Inheritance plays a significant role in organizing vacuole size. Yeast strains defective in vacuole inheritance, vac8Δ and vac17Δ , result in a loss of vacuole to cell size scaling compared to wildtype. In this study, we work to uncover how vacuole inheritance contributes to a change in size-scaling through optogenetics. I will use a cell line that optogenetically blocks Bem1, creating a significantly larger cell with enlarged vacuoles. This cell line paired with vac8Δ and vac17Δ will allow me to study size regulation. A possible outcome of this experiment is an enhanced size defect because the cell can no longer transfer its vacuoles. Understanding the cellular mechanisms present during a cell’s response to excess vacuole and size contributes to advancing the knowledge of biological systems and translating new therapeutic approaches to clinical practice.

The role of the RNA helicase DDX6 in L-body RNP granules

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

June Winters*[1], Dr. Jessica Otis [2], Dr. Kimberly Mowry[3]
[1]Brown University, [2]Brown University, [3]Brown University

Abstract: In Xenopus oocytes, RNA localization occurs through the formation of RNA-protein condensates known as L-bodies, a newly discovered biomolecular condensate that functions in the localization of maternal mRNAs to the vegetal cortex of the developing oocyte. RNA-dependent DEAD-box helicases, which may promote phase separation and condensate disassembly, represent a potential mechanism to regulate mRNA localization by modulation of RNA-protein and RNA-RNA interactions within L-bodies. These helicases have the capacity to unwind double-stranded RNA and act within many RNA-containing phase-separated mRNP granules to promote RNP complex assembly and disassembly and to remodel RNA-protein interactions. The RNA helicase DDX6 has emerged as an ideal candidate for such roles in L-body RNP granules, which are localized to the vegetal cortex during oogenesis and released from the cortex at the end of oogenesis. I have hypothesized that DDX6 regulates the anchoring and disassembly of L-bodies through RNP remodeling. To determine whether DDX6 regulates L-body RNA anchoring and disassembly, I am carrying out experiments to spatially mis-express DDX6, as well as experiments to express a mutated form of DDX6 lacking helicase activity. I will use confocal imaging to determine whether DDX6 can modulate L-body anchoring and disassembly. My research will contribute to the understanding of RNA helicase function, biomolecular condensate dynamics, and dysregulated RNA granule disassembly, which has been linked to several neurological disorders.

Using tongue-flicking to determine prey preference chemosensory behavior in juvenile Lake Chapala (Thamnophis eques obscurus) and checkered (Thamnophis marcianus marcianus) garter snakes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Itzel Somarriba*[1], Rita Mehta [2], Elsie Carrillo[3]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz, [3]University of California, Santa Cruz

Abstract: Chemosensory behavior, or using taste and smell to forage for prey is an important aspect of snake foraging ecology. Chemosensory studies have been used to determine prey preference of individuals of different life history stages. We question whether there are interspecific and intraspecific differences in prey preference in juvenile garter snakes, which are great models for studying diet. For our comparison, we selected two species of garter snakes, the semi-aquatic Lake Chapala (Thamnophis eques obscurus) and the more terrestrial checkered (Thamnophis marcianus marcianus) which are closely related but have different lifestyles. For our methods, we will prepare a variety of terrestrial and aquatic prey stimuli including: pinky mice, nightcrawler worms, minnow fish, mosquito fish, silver side fish and distilled water for our control. To determine prey preference, we will quantitatively compare 1) number of attacks, 2) attack latency (time to attack), 2) number of tongue flicks. We predict that the 10 individuals of the more aquatic Lake Chapala garter snake will have a greater number of attacks, reduced attack latency, and greater number of tongue flicks on aquatic prey items compared to the 7 individuals of the more terrestrial checkered garter snake, indicating a preference for prey of a similar lifestyle. As the foraging ecology in the Lake Chapala has not been well-studied, our project on prey preference is novel. This experiment will enable us to understand if these species have a preference for particular prey and how much individuals vary in their chemical preference for terrestrial versus aquatic prey.

A Comparison of the Lateral Pallium in Muraenidae Species to Determine the Relationship Between Spatial Cognition and Habitat Complexity

Discipline: Life Sciences
Subdiscipline: Neurosciences

Harleen Kaur*[1], Dr. David Lent[2], Kayla Trevino[3], Kiara Brown-West[4], Breana Pulido[5]
[1]California State University, Fresno, [2]Associate Professor, Department of Biology, California State University, Fresno, [3]Undergraduate Student, [4]Undergraduate Student, [5]Undergraduate Student

Abstract: Based on their diversity and wide range of habitats, eels can provide insight into environmental pressures affecting ocean inhabiting organisms. Furthermore, eels are efficient model organisms to analyze spatial navigation and effects of environmental pressures on brain morphology. However, there are gaps in literature of moray eel neuroanatomy and their general biology. Eel species belonging to the Muraenidae family are typically found in both marine and freshwater environments at a range of depths, climates, and habitat spatial complexity. This study focuses on the relation between the level of habitat spatial complexity and the relative size of the lateral pallium, a brain region in teleost fish which may be important for spatial navigation. Furthermore, the lateral pallium, a brain structure in the telencephalon in teleost fish (homologous to hippocampus in mammals), has been associated with spatial cognition through previous studies of observing the effects of lesions to the lateral pallium in teleosts. It's hypothesized that there would be a positive correlation between the ratio of the lateral pallium to the telencephalon (the brain region containing the lateral pallium) and the level of habitat spatial complexity. A cross species morphology examination of species living in either "simple" or "complex" environments will be performed with comparison to the Anguillidae eel family. Species from more complex habitats are expected to experience selective pressures that would favor higher spatial navigation abilities and thus a larger ratio of the lateral pallium. A histological method is utilized to observe specific anatomical features through staining sectioned neurological tissue.

Isolating and Identifying Novel Antibiotics from Soil Bacteria

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Taylor Rossiter*[1]and Meda Higa [2]
[1]York College of Pennsylvania, [2]York College of Pennsylvania

Abstract: The antimicrobial resistance crisis is one of the greatest concerns among the scientific and healthcare communities. Common infection-causing bacteria (known as the ESKAPE pathogens) are becoming increasingly untreatable using established antibiotics. Therefore, there is a need for the discovery of novel antibiotics or new ways to increase antibiotic efficiency to try and solve this crisis. To achieve this, we isolated bacterial samples from soil and plated them against different ESKAPE pathogen safe relatives to screen for antibiotic zones of inhibition. We further characterized these isolates using Gram stain, 16s rRNA amplification and sequencing, and a Kirby-Bauer assay to determine the nature of the antibiotic being produced. Preliminary BLAST results of the 16s rRNA sequence indicated that isolate 3TR12 is from the genus Arthrobacter, and isolates 3TR5 and 3TR15 are Paenarthrobacter nicotinororans. Verification of these results will provide information on the bacteria responsible for producing antibiotic resistance. Future studies would include transposon-directed mutagenesis to identify genes involved in antibiotic production. Taken together, these results could ultimately lead to the identification of the antibiotics each isolate is producing, and potentially the identification of a novel antibiotic that could be used against ESKAPE pathogens.

An improved auxin degron system for endogenous tagged protein degradation in Drosophila melanogaster.

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Yingshan Bi*[1], Tom Kornberg [2], Wanpeng Wang[3]
[1]University of California, San Francisco, [2]University of California, San Francisco, [3]University of California, San Francisco

Abstract: The auxin-inducible degron(AID) system is composed of auxin receptor F-box protein, a degron tagged to the target protein, and plant hormone auxin class such as indole-3-acetic acid (IAA) to induce the degradation of the protein through the ubiquitin-proteasome pathway in non-plant cells. A previous study discovered that a combination of mutated F-box protein OsTIR F74A and an auxin derivative 5-Ad-IAA demonstrated increased degradation efficiency by 1000 fold. Meanwhile, another study reported that the F-box protein AtAFB2 and short degron miniIAA7 showed minimal basal degradations, as well as rapid auxin-inducible depletion of endogenous proteins. We aim to combine the degradation efficiency provided by the F74A/5-Ad-IAA with the low basal degradation conferred by the F-box protein AtAFB2 to establish an improved auxin degron system to study morphogen signaling in the Drosophila melanogaster cell lines and whole animal. We've generated cell lines and flies that express the F-box proteins OsTIR, OsTIR-F74A, AtAFB2, and AtAFB2-F74A. To tag our proteins of interest for degradation, we used the CRISPaint method to knock in universal donors with degron tags mini-AID or miniIAA7. We targeted cytoplasmic components such as actin and tubulin as proof of concept. We will apply the improved auxin degron system to our proteins of interest in Drosophila trachea development and contact-based signaling. The system will enable bio-orthogonal disruption of protein function in a reversible fashion and allow live imaging.

Environmental Escherichia coli ST131 Carries Conjugative Plasmid With Multi-Drug Resistance Region

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Celeste Sanchez*[1], Dr. Luis Mota-Bravo[2], Dr. Andrey Tatarenkov[3]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: The dominant multidrug-resistant (MDR) extraintestinal pathogenic Escherichia coli lineage is sequence type 131(ST131). Bacteria can acquire resistance through horizontal gene transfer in which antibiotic resistance genes (ARG) carried on plasmids are exchanged between bacteria. We hypothesize that the natural environment serves as a potential reservoir for ARGs. The objective of this study was to determine the genotype and phenotype of a bacterial isolate from a freshwater environment and characterize the ARGs as well as their global spread. The isolate SW4578 collected from the Mississippi River, was identified as E. coli using MALDI-TOF mass spectrometry. Resistance phenotypes were studied through Disk Diffusion Tests. Plasmid and chromosomal genome of this isolate were sequenced, assembled, and analyzed using PATRIC, CGE, and ISFinder. The isolate was confirmed to be ST131 and displayed resistance to 10 antibiotics from 5 different antibiotic classes. One IncF plasmid, named p135, was found to be conjugative and harbored 8 ARGs arranged in a compact 22kb MDR region. This region is divided into subregions bordered by insertion sequences, resulting in potential mobilizable units. These subregions were found in multiple plasmid types in NCBI Genbank accessions, indicating that the MDR region of SW4578 p135 was formed by the activity of mobile genetic elements. Highly similar MDR regions were found in four K. pneumoniae and 56 E. coli isolates of 15 different sequence types other than ST131. Our study demonstrates the way bacteria like E. coli ST131, isolated from the environment, can disseminate ARGs with mobile genetic elements via horizontal gene transfer.

Determining the cis-regulatory elements controlling a stochastic cell fate choice in the Drosophila eye

Discipline: Life Sciences

Subdiscipline: Developmental Biology

Yaniris Molina*[1], Robert J. Johnston Jr.[2], Elizabeth Urban[3], Alison Ordway[4], Lukas Voortman[5]
[1]Johns Hopkins University, [2]Johns Hopkins University, [3]Johns Hopkins University, [4]Johns Hopkins University, [5]Johns Hopkins University

Abstract: Stochastic gene expression is a poorly understood mechanism that generates cellular diversity. Disruption can lead to human diseases, including vision impairment and lymphoma. I aim to study stochastic gene expression using the Drosophila melanogaster eye as a model. The fly eye contains 800 unit eyes, each with eight photoreceptors (R1-8). Two subtypes of R7 photoreceptor are defined by expression of Rhodopsin 3 (Rh3) or Rhodopsin 4 (Rh4), and are randomly patterned across the eye. This stochastic pattern is controlled by the transcription factor Spineless (Ss). When Ss is off, Rh3 is expressed. Alternatively, when Ss is on, Rh4 is expressed. The genetic elements that influence when and how Ss is expressed, and how it controls fate decisions in R7s are poorly understood. I hypothesize that cis- and trans -acting elements associated with the gene have roles in regulating ss expression and R7 subtype fate decisions. My goal is to use CRISPR-Cas9 to mutate cis -acting elements in the ss locus. Specifically, I aim to mutate two enhancers required for ss expression in R7 precursor cells and terminally differentiated R7s. By targeting the enhancers, I expect to identify putative transcription factor binding sites. Using CRISPR, I will create deletions within the endogenous enhancers that retain local chromatin environment inputs. Then, I will examine cis -element mutants for changes in Rh3:Rh4 expression. We anticipate that sub-regions in the enhancers will determine expression of ss . Our work will provide mechanistic understanding of the precise elements that govern stochastic Ss expression during development.

Suppressing the CXCL12-CXCR4 chemokine axis at the fetal-maternal interface during implantation alters expression of this axis in ovine placenta at mid and late gestation.

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

mariah leonard*[1], Ryan Ashley[2], Jillian Hughes[3], Cael Alderete[4]
[1]New Mexico State University, [2]New Mexico State University, [3]New Mexico State University, [4]New Mexico State University

Abstract: Placental formation is a key component for healthy fetus development during early gestation. Many maternal and fetal pregnancy complications stem from problems arising during placental development. Chemokine ligand 12 (CXCL12) and its receptors CXCR4 and CXCR7 are expressed in placental tissues and dysregulated signaling of this axis is implicated in pregnancy complications. However, the precise roles of CXCL12/CXCR4/CXCR7 signaling during placental formation are not clear. We hypothesized suppressing CXCL12/CXCR4 signaling during placental formation would result in compromised placental development with lasting effects to the CXCL12/CXCR4/CXCR7 axis and mid and late gestation. The goal of this study was to investigate CXCL12 induced actions in placental development using an in vivo sheep model. The similarity in fetal placenta vascular structure coupled with fetal maturity at birth allows sheep to serve as an unsurpassed animal model of placental formation. On Day 12 post-breeding, osmotic pumps were surgically installed in 37 ewes to deliver CXCR4 inhibitor (AMD3100) at 1X dose, (n=8), 1.5X, (n=8), 3X, (n=8) or saline (n=13) into the uterine lumen ipsilateral to the corpus luteum for 14 days during placental formation. At mid (d90) and late (d135) gestation, placental tissues were collected and separated into maternal (cot) and fetal (car) components. The placenta reaches its maximum growth around day 90 of gestation and average gestation length in sheep is 150 days. Tissues were snap frozen in liquid nitrogen and stored prior to RNA isolation and cDNA synthesis. Gene expression for CXCL12, CXCR4, and CXCR7 in the placenta were analyzed using real-time qPCR.

Examining Interactions of the Periplasmic Binding Protein, FecB, with Ferric-Siderophores and MmpS4 from Mycobacterium tuberculosis

Discipline: Life Sciences
Subdiscipline: Biochemistry

Vanessa Saldivar*[1], Celia W. Goulding[2], Rodger de Miranda[3], Jessica Mendoza[4]
[1]University of California, Irvine, [2]University of California, Irvine, [3]University of California, Irvine, [4]University of California, Irvine

Abstract: Mycobacterium tuberculosis (Mtb) is the species of bacteria responsible for the disease tuberculosis, the leading cause of death worldwide from a single pathogenic organism. Current treatment strategies involve a cocktail of antibiotics taken for at least six months, leading to patient non-compliance and a rise in antibiotic resistance. Consequently, new treatment strategies to combat tuberculosis are desperately needed. It is essential for Mtb to acquire iron from the human host, and as such, Mtb iron uptake pathways are attractive therapeutic targets. One avenue Mtb utilizes to acquire host iron is siderophore-mediated, which involves biosynthesis and export of two Mtb siderophores, carboxymycobactin and mycobactin. Presently, little is known about the mechanism to shuttle apo- or ferric-siderophores to and from the host environment to the Mtb inner membrane. Mtb has two periplasmic binding proteins, one of which (FecB), we hypothesize shuttles ferric-carboxymycobactin (Fe-CMB) through the periplasm. We have shown using fluorescence titration that FecB preferentially binds to Fe-CMB. We have also shown that FecB potentially interacts with one of the apo-CMB export proteins, MmpS4. To further probe the FecB residues involved in Fe-CMB binding, we performed mutagenesis studies and observed mutant affinity to Fe-CMB compared to wild-type. We have also carried out FecB-MmpS4 direct protein-protein interaction experiments. We will discuss herein the results of FecB binding to Fe-CMB and its interactions with siderophore-export proteins. These data suggest that FecB is involved in Mtb siderophore-mediated iron uptake; however, the precise role that FecB plays within this pathway requires further investigation.

The Effect of the Extracellular Matrix on the Proliferation, Fusion, and PAX7 Maintenance of Human Skeletal Muscle Stem Cells

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Michael Torres Espinosa*[1], Devin Gibbs[2], April D. Pyle[3], Victor Gutierrez-Garcia[4], Rachelle H. Crosbie-Watson[5]

[1]University of California, Los Angeles, [2]University of California, Los Angeles, [3]University of California, Los Angeles, [4]California State University, Northridge, [5]University of California, Los Angeles

Abstract: Duchenne muscular dystrophy (DMD) is a disease in which the loss of dystrophin results in muscle fiber degeneration. Skeletal muscle stem cells, known as skeletal muscle progenitor cells (SMPCs) during fetal development or satellite cells (SCs) postnatally, conduct skeletal muscle growth and repair. Unlike SCs, progenitors derived from induced pluripotent stem cells (iPSCs) fail to engraft into their niche and lose PAX7 expression, which is indicative of losing their stem cell state. For iPSC-SMPCs to be a viable DMD therapy, they must be matured to an SC-like state. scRNA-seq showed a key difference between iPSC-SMPCs, SMPCs, and SCs was the ECM genes they expressed. We hypothesized that the ECM drives late stage human skeletal muscle development and matures SMPCs to fully functioning SCs. ECM myoscaffolds were made by decellularizing human skeletal muscle from different developmental timepoints. SMPCs were cultured on these myoscaffolds to investigate ECM-SMPC interactions. Myoscaffolds from late stage fetal tissue promoted proliferation, decreased myofiber fusion, and maintained PAX7+ identity. We performed quantitative mass spectrometry on human skeletal muscle tissues across development and identified the individual ECM proteins that composed the myoscaffolds. From these proteins, we investigated in vitro the potential candidates that maintain PAX7+ identity. These experiments showed that specific ECM factors expressed during late fetal development maintain PAX7+ identity and spur proliferation of SMPCs in vitro .

Defining the role of SOX10 in cranial neural crest cell formation and migration

Discipline: Life Sciences

Subdiscipline: Developmental Biology

Carly Adamson*[1]and Crystal Rogers [2]

[1]University of California, Davis, [2]University of California, Davis

Abstract: Neural crest cells (NCCs) use different mechanisms to develop across the anterior-posterior axis. Specifically, the expression, timing, and localization of transcription factors and cadherin proteins change depending on the axial position, even within the same stage of development. Although SOX10 is one of the most common markers used to study NCC development, we still lack significant understanding of its actual function at early NCC developmental stages. I hypothesized that excess chicken SOX10 (cSOX10) would increase NCC-derived oligodendrocyte and Schwann cell formation in the chicken central and peripheral nervous systems at the cost of NCC-derived craniofacial derivatives. To define the role of SOX10 in cranial NCC development, I investigated its necessity and sufficiency to drive NCC formation, migration, and differentiation using gain and loss of function methods in avian embryos. My data shows that cSOX10 overexpression increases markers of glial and neuronal differentiation in chicken, but drives premature migration in quail embryos. These differences in response to cSOX10 overexpression suggest that either SOX10 has different functions in these two closely related bird species or that the downstream targets respond to exogenous cSOX10 differently in the two birds. Future work will define organism-specific protein-protein interactions and will use perturbation followed by RNA sequencing to elucidate the genes downstream of SOX10 during cranial NCC development in chicken and quail embryos. This study will provide the groundwork for future experiments in additional organisms where SOX10 may play a different role.

Decolonizing Sustainability Science and Indigenous Practices: Promoting Environmental Health and a Sustainable Future, using Kanaka Maoli Traditions as a Case Study.

Discipline: Life Sciences

Subdiscipline: Environmental Science

Sommer Kimokeo*[1]and Lori Lei Ishikawa, PhD [2]

[1]University of Hawaii Maui College, [2]University of Hawaii Maui College

Abstract: Using ʻike Hawaiʻi (ancestral Hawaiian knowledge) approaches Kānaka ʻŌiwi methodologies (Oliveira & Wright, 2016) as a case study of Indigenous culture, we can decolonize sustainable science and Indigenous approaches to land management to promote a collaborative global effort for environmental health and a sustainable future. The worldview of sustainable science has changed to include culture and place-based systems (Jarvis et al., 2021). In this time of history, we have changed what we knew as Indigenous people to modern technology and sciences, which simplified and quantified conveniences to include new approaches to specific topics and yet desired to return to indigenous cultural considerations as an internal part of the system rather than external. With a shifting extent of respect for Indigenous presence, and consultation on environmental management (Garnett et al., 2018), Indigenous peoples are still challenging contemporary global capitalism to protect the environment and resources (Dhillon, 2018). Breaking barriers to communication and knowledge exchange need to be overcome and defining the potential misperceptions born of colonialism and cultural suppression by power structures to increase collaborative efforts for sustainability. Recognizing Indigenous knowledge systems and approaches to conservation can spark collaborative efforts for worldwide resource conservation (Garnett et al., 2018). By exploring ʻike Hawaiʻi approaches and their connections to sustainable science, we can decolonize these concepts to communicate and build the present and future collaborative efforts in the global goal of survival on Earth and keep the spiritual and physical connection of all people with the environment for future generation's needs.

Chromosome scale genome assembly and historical changes in the effective population size of two marine fishes from the Philippines

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jordan Rodriguez*
Texas A&M University-Corpus Christi

Abstract: One of the greatest challenges facing humanity today is our ability to understand the impact humans have on the natural resources we rely on for our existence. Overharvesting and environmental degradation have led to declines in fish populations of tropical regions, yet there is little genetic evidence of this. Here, we utilize modern genomic tools, such as in situ Hi-C, to explore the previously unprecedented ability to evaluate genetic diversity and infer changes in it. We test for historical changes in the effective population size (Ne) of two marine fishes targeted by the NSF funded Philippines PIRE Project: Salarias fasciatus and Sphaeramia nematoptera. Using in situ Hi-C, we output a de novo chromosome scale genome assembly for the S. fasciatus species using only Illumina short read 2 x 150 bp paired end shotgun and Hi-C libraries. To validate our approach, we compare the quality metrics of our de novo assembly to the published assembly. By mapping contemporarily collected individuals of both targeted species to the reference genomes, we will estimate linkage disequilibrium and thus infer changes in historical Ne over the past five centuries. Our research suggests that the incorporation of in situ Hi-C libraries in de novo genome assemblies may improve the accuracy and validity of chromosome-scale assemblies and enable scientists to better understand population genomics spanning many generations. Such understanding would allow us to better conserve and protect vital resources for future use. Choosing a successful resource management strategy ensures sustainability of resources for present and future generations.

An immunohistochemistry-compatible FISH method for testing protein and DNA co-localization

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Hannah Gilbonio*[1], Leila E. Rieder[2], Gwyn Puckett[3]
[1]Emory University, [2]Emory University, [3]Emory University

Abstract: When investigating interactions between proteins and DNA, it is often necessary to determine whether a protein is binding to a specific DNA locus. This is commonly achieved through DNA fluorescent in situ hybridization (FISH) which aims to mark a particular genomic location using microscopy. Unfortunately, this protocol is limited due to its interference with protein detection by antibodies (immunofluorescence). This occurs because DNA FISH requires a denaturation step that can reverse chemical crosslinks and denature protein epitopes, making it incompatible with fluorescent antibody staining of proteins. In order to address this technical issue, we seek to develop an alternative strategy using RNA FISH probes that bypasses the denaturation process and combines RNA localization with immunohistochemistry on Drosophila polytene chromosomes. We hypothesize that RNA transcripts concentrate around their source

gene, thus providing a potential alternative method to obtain genetic location data. The objectives of this project are threefold: 1) Test the ability of RNA FISH probes to mark genomic loci; 2) Determine if single molecule (sm)RNA probes are hybridizing to local RNA or DNA; 3) Combine RNA FISH with immunohistochemistry. Ultimately, our goal is to engineer a protocol that combines protein and DNA loci information as a broadly applicable laboratory technique for investigating protein binding.

Characterizing Antibiotic-Producing Bacteria from Soil Samples in York, PA

Discipline: Life Sciences
Subdiscipline: Microbiology

Jacob Wingard*[1]and Meda Higa [2]
[1]York college of Pennsylvania, [2]York College of Pennsylvania

Abstract: Since the discovery of antibiotics, scientists have been warning the world about the potential of antibiotic resistant strains that would become invincible and render current treatments useless. Unfortunately, commonly resistant bacteria (known as ESKAPE pathogens) have already appeared. Our goal was to identify and isolate bacteria that produce novel antibiotics that can be used to fight these ESKAPE pathogens.To do this, we have isolated bacteria from soil samples, tested isolates against safe relatives of ESKAPE pathogens, and screened for antibiotic zones of inhibition and categorized the extent of antibiotic zones. We also tested LB and R2A growth conditions on antibiotic production,to determine differences of metabolism. Selected isolates were characterized via Gram stain and 16s rRNA gene was amplified by PCR and sequenced. We also conducted a Kirby-Bauer assay against our antibiotic-producing candidates to determine if isolates were resistant to certain families of antibiotics. The goal was to identify potential mechanism(s) of actions of the antibiotics that were produced. Preliminary results yielded 3 bacterial isolates producing antibiotics, two of which are likely Gram negative. Isolate 3RB1_21 was identified by 16s sequencing as belonging to the genus Serratia. Sequencing from isolates 3MM22_21, and 3MM23_21 was inconclusive and thus we are currently repeating 16s PCR and sequencing. Confirming these results will characterize the general bacteria and give us a solid background for further research. Hopefully these results will lead us to finding a novel bacteria.

fire!in the savanna--how a decade of fire shapes flowering plant abundance

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ovya Venkat*[1], Toby SantaMaria [2], Lars Brudvig[3]
[1]Michigan State University, [2]Michigan State University, [3]Michigan State University

Abstract: Humans have altered ecosystems by changing the disturbance regimes that ecosystems normally experience.This is especially true with regards to fire and its exclusion from ecosystems. Fire is a huge disturbance in any ecosystem; however, not all ecosystems respond to fire in the same way. Grass-dominated ecosystems, such as grasslands, prairies, and savannas, have evolved over millennia to be fire-adapted. However, global burned area has decreased 25% in the last twenty years with ~90% of this decrease occurring in savannas.This has caused grass-dominated systems to undergo environmental degradation on a global scale, converting many savannas into woody shrublands. Grass-dominated ecosystems account for 40% of terrestrial land cover and 30% of global primary production; b ecause of their size, restoring the structure and biodiversity of grass-dominated systems is on the rise and involves

reintroducing fire to these systems. Despite recognition that altered fire regimes have caused ecosystem shifts away from flowering forbs and grasses and towards trees, we lack critical understanding of how fire suppression followed by reintroduction affects plant community structure. Here, we measured the ten dominant flowering plant species in savannas undergoing restoration by prescribed burning, restoration by tree cutting and prescribed burning, or savannas undergoing no restoration action. Because the savannas which has undergone restoration have been burned 3-5 times in the last decade, we expect that flowering plants will be most numerous and have the most flowering heads per plant in the savanna with the most intensive restoration actions [tree cutting and prescribed burns].

Differential Expression of Lung Cancer Biomarkers for Early Detection

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Breanna James*[1], Jennie Williams [2], Barbara Nemesure[3], Shrey Thaker[4]
[1]State University of New York Stony Brook University, [2]Stony Brook Medicine, [3]Stony Brook Medicine, [4]SUNY Stony Brook University

Abstract: Lung cancer is the leading cause of cancer related death in the United States. Although lung cancer incidence rate has steadily declined over the last decade, differences in lung cancer risk contribute to disproportionate incidence and disease outcome in racial/ethnic groups. Studies have shown that African Americans have a higher risk for lung cancer compared to Caucasian Americans, while Hispanic Americans have the lowest risk. Studies suggest that environmental, socioeconomic, and behavioral factors alone do not fully explain these differences and suggest a role for tumor biology. Our hypothesis is that the underlying genetic components of racial and ethnic populations may influence lung cancer development. From our preliminary discoveries, we are validating the potential diagnostic biomarkers Cytokeratin-7, Napsin-A, Thyroid Transcription Factor-1, and Ceruloplasmin by performing immunohistochemical and immunofluorescent analyses of normal adjacent and lung tumor tissue. These results will ultimately reveal drivers of lung cancer associated with increased susceptibility of racial and ethnic groups.

Developing Zebrafish Mutants Using Cas9 Gene Editing to Assess Metabolic Pathways

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Chantel Tsosie*[1]and Matthew Salanga [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: Activation of the nuclear receptor, Pregnane X Receptor (PXR) is a first step toward the detection and removal of foreign substances in the cells of many vertebrate species, including humans, rodents and zebrafish. In rodents and human cells, PXR binds to foreign chemicals, then activates detoxification by inducing expression of the detoxifying enzyme CYP3A. Gene activation studies suggest this is the case in zebrafish too, but recent loss-of-function (LOF) studies hint that PXR may be dispensable for CYP3A induction in zebrafish. The drug, pregnenolone, is a potent activator of PXR in zebrafish, and under normal conditions, pregnenolone exposure will lead to CYP3A transcription, presumably a result of transactivation by PXR. We hypothesize that nonsense mutations in exon 3 or exon 6 will ablate or attenuate the

CYP3A response. To test our hypothesis, we used CRISPR-Cas9 to create presumptive LOF mutations in exons 3, and 6 of the PXR locus, which notably contains regions of DNA binding and ligand binding, respectively. Genotypes of PXR mutant zebrafish have been confirmed by DNA sequencing; however, we have not yet created purified (single allele) homozygous null mutants, which are essential for LOF experiments. Here we report on our genotyping efforts and preliminary results from pregnenolone exposure studies.

Optogenetic Inactivation of CEP Sheath Glia Hampers Memory in C. elegans

Discipline: Life Sciences
Subdiscipline: Neurosciences

Angel Garcia*[1], Rashmi Chandra [2], Noelle L'Etoile[3]
[1]University of California, San Francisco, [2]University of California, San Francisco, [3]University of California, San Francisco

Abstract: Experience-dependent learning and memory are vital to our ability to survive in diverse conditions. Research shows simple organisms, such as the nematode Caenorhabditis elegans , can retain memory, which we can observe at a synaptic level. Through subjecting the C. elegans to a training regime that pairs an innately attractive odor with a negative stimulus, we show that they can be trained to be repulsed by that same odor. We can then perform a memory assay which allows us to quantify the worms' memory over time. Studies in mammals suggest glia may play important roles in memory, but the systems lack the cellular and molecular mechanisms behind it. C. elegans provide a platform to study this relationship, as their neural circuits are completely mapped out. Additionally, they have a variety of glia, such as the CEP sheath (CEPsh) glia, which resembles vertebrate astrocytes in several ways. Does glia play a role in long-term memory retention, and if so, what are the mechanisms behind it? To answer these questions, we have expressed the plant-derived protein, miniSOG, in the CEPsh glia of the worm, which inactivates the glia when exposed to blue light. We found that if the CEPsh glia is inactivated during memory consolidation, the animals do not retain memory. Whole-brain calcium imaging of the worm suggests that inactivating the CEPsh cells results in wide-scale neuronal disruption of calcium transients. Further experiments are being conducted to investigate if inactivating different glia has a similar effect, or if it is CEPsh specific.

First U.S. Report of Environmental Escherichia coli carrying tetM gene commonly found in Gram-positive and Gram-negative bacteria

Discipline: Life Sciences
Subdiscipline: Genetics

Sophia Aredas*[1], Andrey Tatarenkov [2], Luis Mota-Bravo[3]
[1]University of Califofornia, Irvine, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Few antibiotic resistance genes (ARGs) are known to be shared by both Gram-positive and Gram-negative species, including tetracycline ribosomal protection protein gene, tetM . Horizontal gene transfer is common among bacteria of the same family and order but rare between highly diverged phyla. We hypothesize that aquatic environments serve as a potential reservoir for bacteria to acquire ARGs. The objectives of this study were to 1) analyze the plasmid carrying tetM and its genetic neighborhood in an Escherichia coli isolate (SW4712) and 2) conduct comparative analysis of tetM to characterize its diversity as well as taxonomic, genomic, and geographic distributions. Isolate SW4712 was collected from the Mississippi River, Louisiana, and identified as E. coli by MALDI-TOF. Disk diffusion tests were employed to determine the phenotypic resistance profile. SW4712 was then sequenced, assembled, and analyzed using Unicycler, NCBI databases, and PATRIC. The bacterium contained 4 plasmids with the largest being 90 bp (p90). Analysis of 206 plasmid-borne tetM genes discovered they were quite divergent with 29 different haplotypes. The haplotype network confirmed and illustrates the dissemination of tetM among Gram-positive and Gram-negative species. Some haplotypes were restricted to one phylum each while others were shared by Gram-positive and Gram-negative bacteria which suggests current interspecies genetic exchange. By studying what elements are driving genetic exchange we will be able to better understand the evolution of antibiotic resistance. At the time of writing, this study marks the first report of environmental E. coli carrying tetM in the United States.

Spatial and temporal changes of osteoblast distribution during development in parentally Benzo[a]pyrene-exposed Japanese medaka (Oryzias latipes)

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alexis Trujillo*[1], Rijith Jayarajan[2], Frauke Seemann[3], Frauke Seemann[4]
[1]Texas A&M University Corpus Christi, [2]Texas A&M Corpus Christi, [3]Texas A&M Corpus Christi, [4]Texas A&M Corpus Christi

Abstract: Reports in the literature and our preliminary data indicate contributions of parental polycyclic aromatic hydrocarbons exposure to reduced bone health and increased fracture risk in the offspring. Our lab has demonstrated that parental exposure to benzo[a]pyrene (BaP) at environmentally relevant doses impairs bone formation in the offspring of exposed Japanese medaka (Oryzias latipes), a widely utilized and tractable ecotxicology fish model. In a multi-biological level approach, vertebra compression (development) and reduced bone thickness (adult male) at the tissue level were likely associated with reduced osteoblast differentiation and activity. Using the unique twist:rfp/collagen10a1:gfp transgenic medaka line mesenchymal stem cells (twist+) and osteochondral progenitors (collagen10a1+) development was assessed in the parentally BaP exposed (1µg/L for 21 days) F1 embryos and larvae until 30 days post fertilization (dpf) through fluorescent microscopy. Fluorescence intensity and fluorescent area of the anterior, middle and posterior section of the vertebra were monitored to analyze the spatial and temporal distribution of these osteblast populations in response to parental BaP exposure. The posterior vertebral bone section seemed to be more affected and showed reduced fluorescence for both cell populations in the parentally exposed F1 sample. The presented data will allow to pinpoint the developmental onset of the parental exposure induced bone phenotype and provide a scientific basis to reassess the impact of environmental BaP on public and environmental health, foreshadowing strategies for early detection of ancestral exposure.

Determining the Mechanism of Chaperone Function for the Yeast Derlin Dfm1

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jasmine Jung*[1], Rachel Kandel[2], Dr. Sonya Neal[3]
[1]University of California, San Diego, [2]University of California, San Diego, [3]University of California, San Diego

Abstract: Protein aggregates are a common feature of diseased and aged cells. Membrane proteins comprise a quarter of the proteome, and yet, it is not well understood how aggregation of membrane proteins is regulated and what effects these aggregates can have on cellular health. We have determined in yeast that the derlin Dfm1 is has a chaperone-like holdase activity for preventing misfolded membrane proteins from entering aggregates. We establish that this function of Dfm1 does not require recruitment of the ATPase Cdc48 and it is distinct from Dfm1's previously identified function in dislocating misfolded membrane proteins to the cytosol for degradation. Additionally, we assess the cellular impacts of misfolded membrane proteins in the absence of Dfm1 and determine that misfolded membrane proteins are toxic to cells in the absence of Dfm1 and cause disruptions to proteasomal and ubiquitin homeostasis.

Observing Programmed Cell Death in C. elegans following Transdifferentiation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Martín Koch*[1], Joel Rothman [2], Tsunghan Yeh[3]
[1]University of California, Santa Barbara, [2]University of California, Santa Barbara, [3]University of California, Santa Barbara

Abstract: Cancer remains one of the leading causes of death worldwide. Our body produces cancer cells extremely often, but these cells undergo programmed cell death (PCD) before they initiate tumorigenesis. The analysis of the genes that trigger this PCD could lead to a further understanding of the underlying mechanisms our body uses to protect itself from its own cancerous cells. The widely studied model organism Caenorhabditis elegans has many homologous genes with humans and contains pharyngeal and uterus cells which can be reprogrammed into cells found in the intestinal lining of the worm by utilizing the JR3642 strain to overexpress the elt-7 transcription factor. We analyzed if transdifferentiate stress causes PCD in these regions by heat-shocking JR3642 and quantifying the post heat-shock corpses at different time points. To allow for accurate quantification, the heat-shock strain was crossed with strains which have a fluorescent tag on proteins expressed only when a cell corpse is being engulfed. The fluorescent silhouette which forms around the cell is used as a marker for PCD. Cell corpses were found consistently in young (L1) and adult worms following transdifferentiation, and we are currently attempting to identify which specific cells are consistently undergoing PCD to analyze their gene expression, which can then be translated to which genes are expressed during programmed cell death in humans. We hypothesized that if elt-7 overexpression is triggered by heat-shocking JR3642, then the transdifferentiate stress will induce programmed cell death in specific cells within the pharynx of C. elegans.

The Effects of Sleep Deprivation on Metabolic Health Within Drosophila Melanogaster

Discipline: Life Sciences
Subdiscipline: Biology (general)

Grace Keirn*[1], Dr. Laura K. Reed [2], Cole Kiser[3], Anna Grace Price[4], Jhilam Dasgupta [5]
[1]The University of Alabama, [2]The University of Alabama, [3]The University of Alabama, [4]The University of Alabama, [5]The University of Alabama

Abstract: According to the CDC and Hirode (2020), more than 30% of individuals in the United States suffer from metabolic syndrome. Metabolic syndrome is a risk factor for many diseases including cardiovascular disease, diabetes, and hypertension. Furthermore, we know that disruptions to sleep can contribute to the risk of obesity and metabolic disease in humans. Drosophila melanogaster is an established model organism that can be used to illustrate the effects of sleep deprivation on metabolism and obesity. To study these effects, Drosophila were placed in an apparatus known as the “Flybrator.” It vibrates and flashes LED lights at random time intervals for a total of twelve hours per night until all flies have died or five weeks have passed. This experiment is ongoing and seeks to determine whether sleep deprivation is a factor involved in metabolic health, longevity, and fecundity in Drosophila. We previously found an increased rate of fecundity in the sleep-deprived female flies and decreased longevity in sleep-deprived male flies. This experiment hopes to replicate these findings. Due to the conservation of gene function between Drosophila and humans, results will likely be useful in determining the relationship between sleep and metabolic health in humans.

The Cultivation and Characterization of Soil Bacterium in Navajo Nation to Identify the Natural Soil Biome and Understand Impact of Abandoned Uranium Mines and Remediation

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Nizhoni Hatch*[1]and Phillida A. Charley[2]
[1]Colorado State University, [2]Colorado State University

Abstract: From 1944 to 1986, nearly 30 million tons of uranium ore were extracted from Navajo lands. Today the mines are closed, but a legacy of uranium contamination remains, including over 500 abandoned uranium mines. Present-day, the Navajo Nation is still dealing with the side effects of uranium mining and different stages of remediations. Abandoned uranium mines caused major disruptions to the soil that can affect the natural soil biome and continues to this day. There has been very little study on the interaction of soil remediation with the soil biome. This study will identify the culturable and non-culturable bacteria found in Navajo Nation soils. Also, bacteria collected from soil samples in areas of remediation or open abandoned mines in the Sweetwater chapter community will be characterized. We have identified several bacteria from natural and contaminated soil at uranium mine sites that have anti-fungal and anti-bacterial properties. The project will extend the current abandoned uranium mine study, which involves livestock water testing for arsenic and social impact interviews with the Navajo community. This research is essential to understanding the impact of uranium contamination on Navajo Nation soil and provides crucial information for the remediation process.

Investigating how signaling pathways are activated by Epstein-Barr Virus and participate in the regulation of microRNA to cause B cell lymphomas in Posttransplant Lymphoproliferative Disorder

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Christian Cepeda*[1]and Olivia Martinez[2]
[1]Stanford University, [2]Stanford University

Abstract: Epstein-Barr Virus (EBV) is a common herpesvirus that has infected more than 90% of the human population and is linked to the development of Post-Transplant Lymphoproliferative Disorder (PTLD) in organ transplant recipients. Recently my lab analyzed the microRNAs that are controlled by EBV in host B cells and how they lead to the production of the cytokine IL-10. My lab also showed that the PI3K/Akt/mTOR pathway is important in IL-10 production. My study will determine how the PI3K/Akt/mTOR pathways are involved in EBV control of miRNA. I will isolate microRNA and use quantitative PCR to measure microRNA to answer the question: How does EBV use host cell signaling pathways and alter microRNA to promote the development of B cell lymphomas, and how would drug inhibitors affect these in EBV positive B cell lymphomas? To answer this, I will be learning techniques to precisely isolate miRNA from EBV positive B cell lymphomas treated with and without pathway inhibitors and to use RT-PCR and qPCR to measure microRNA. I will be analyzing five human cell lines, four from our lab that are derived from EBV-positive PTLD patients, and one control cell line, Toledo, that is EBV-negative. I will also analyze three different drug inhibitors that have been known to inhibit the signaling pathways used by Epstein-Barr Virus: AZD2014, MK-2206, and GDC-0941.

The Characterization of Remodeling and Non-Remodeling Craniofacial Defects in Pre-Metamorphic Xenopus laevis tadpoles

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jay-Miguel Fonticella*[1], Kelly McLaughlin [2], Emilie Jones[3], Michael Levin[4]
[1]Tufts University Center for Regenerative & Developmental Biology, [2]Tufts University Center for Regenerative & Developmental Biology, [3]Tufts University Center for Regenerative & Developmental Biology, [4]Tufts University Center for Regenerative & Developmental Biology

Abstract: The regulatory networks coordinating cell proliferation, migration, and differentiation in craniofacial (CF) development are highly conserved between vertebrate species. The level of intricacy in the processes involved in the formation of CF structures results in an elevated likelihood of creating CF defects. In this study, we examined the ability of pre-metamorphic Xenopus laevis (African clawed-toed frog) tadpoles to correct CF defects through tissue remodeling, a process defined as the renovation of existing tissues. Our previous research demonstrated that tadpoles with abnormal, but not missing, CF defects exhibited cartilage correction abilities prior to metamorphosis. Because the underlying processes that mediate the remodeling of head structures have not been well-studied, characterizing the self-correction of malformed structures is our focus. Interestingly, in other species, the eyes are associated with early CF development and cell migration processes. Thus, we investigated a possible role for eye tissue during CF remodeling in our system. To test this hypothesis, we exposed X. laevis embryos to Thioridazine, resulting in eye disfigurations, and Ivermectin, resulting in primarily ventral defects. We found an interesting correlation between the presence of eye-defects and the ability to remodel malformed structures. Specifically, Ivermectin-induced defects showed no significant eye displacement and no sign of tissue remodeling. In contrast, the remodeling process was observed among Thioridazine-treated tadpoles, which demonstrated substantial eye disfigurations. Since the eyes have been postulated to act as a potential organizer in early CF development, our findings suggest a possible link between the organizational role of eyes in later stages of CF development.

Passivation of Fluorescent Nanosensor for In Vivo Sensor Development

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jalen Crespo*[1], Ryan Williams [2], Pooja Gaikwad[3]
[1]CUNY City College of New York, [2]Graduate Center, City University of New York, PhD in Chemistry Program, New York, NY, [3]Graduate Center, City University of New York, PhD in Chemistry Program, New York, NY

Abstract: Advances in the sciences have created implantable nanosensors to detect cancers at early stages of development. Fluorescence optical properties of single-walled carbon nanotubes are used as a tool for detection of biomarkers which indicates early-stage cancer. In breast cancer for example, the 5-year survival rate at the distant stage, on the SEER scale of breast cancer development, is 28%. The Estrogen Receptor Alpha protein plays an important role in the progression and development of breast cancer. The survival rates can be increased with the use of nanosensors to detect the spread of cancers at early stages of development. The limitation of nanosensor application often is the risk of non-specific interactions with other proteins. This compromises the selectivity with which the biomarker of interest can be detected. In our research, we are focusing on improving the selectivity of Estrogen Receptor Alpha (ERA) nanosensors. The ERA nanosensor is designed to detect ERA protein as an analyte of interest. We have performed studies with the base construct of this nanosensor. We use base construct of this nanosensor SWCNT-TAT6 as a model system for evaluating success of different passivating agents reducing the nonspecific interactions. Protein based and polymer based passivating agents were used. BSA and PEG were the chosen candidates from each of these groups. Our studies indicate that BSA is the better candidate for passivation than PEG. With this in mind, using these optimized agents will help increase the SWCNTs' selectivity to detect the biomarker of interest, thus finding cancers early in development.

Analysis of the role of WNT1 and WNT3A in filopodia induction

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jordan Burnett*[1], Laura W Burrus [2], Lisa M Gali[3]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University

Abstract: Wnt morphogens regulate the development of organisms by controlling the proliferation, specification, and migration of cells in embryos. As such, dysregulation of Wnt signaling can lead to birth defects. There are nineteen different Wnt proteins in metazoans, which are transported from one cell (the producing cell) to a neighboring cell (the receiving cell). Although the mechanism by which Wnts are transported is poorly understood, accumulating evidence suggests a critical role for filopodia. The Burrus lab has shown that co-expression of WLS, a Wnt cargo transporter, along with WNT1 causes a redistribution of WNT1 from the endoplasmic reticulum into filopodia. In addition, preliminary evidence suggests that co-expression of WLS and WNT1 induces new filopodia in embryos and in cultured cells. Because WNT1 and WNT3A are functionally redundant, I hypothesize that overexpression of WLS with WNT3A will also induce new filopodia. To test this hypothesis, I will overexpress WNT3A proteins along with WLS into tissue culture cells (3T3 cells, mouse fibroblast cell line). I will then image the filopodia, measure the length of the filipodia, and count the number of filipodia induced. To date, I have generated all of the experimental and control expression constructs needed for the experiment. If my hypothesis is correct, I expect that the filopodia induction will be highest in cells that overexpress the Wnt3A protein with Wntless.

Detection & Quantification of smalINA species in Bacteroides fragilis vs. Secretory Outer Membrane Vesicles: Potential Effects on Colorectal Cancer Pathogenesis

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Alysia Martinez*[1], Jospeh Taube[2], Leigh Greathouse[3]
[1]Baylor University, [2]Baylor University, [3]Baylor University

Abstract: Colorectal cancer (CRC) is the third most common cancer worldwide and accounts for the second-highest number of cancer-related deaths. Further, the development of CRC is highly correlated with an imbalanced intestinal microbiota composition. Functional studies in animal models have pinpointed the roles or several bacterla in colorectal carcinogenesis, including Bacteroides fragilis . Bacteroides fragilis is usually found as a commensal organism, Non-Toxigenic Bacteroides fragilis (NTBF). However, Enterotoxigenic Bacteroides fragilis (ETBF) is strongly associated with occurrence of inflammatory bowel disease, colitis-associated colorectal cancer, and colorectal cancer. Recent studies have identified enterotoxigenic Bacteroides fragilis as an important CRC candidate pathogen. Further, OMVs produced by Gram-negative bacteria and their RNA content have recently recieved increasing attention as novel communicators of host-pathogen intercellular and interspecies communication. Using OMV enriched DeSeq analvsis transcripts, we aimed to compare the selective smalRNA content of whole cell (WC) Bacteroides fragilis and their secreted OMVs to understand their role in governing microbe-host communication and colorectal cancer.

Insights into the health risk imposed by bacteria associated with Saharan dust events through the understanding of the pathogenic pathways and antibiotic resistance genes

Discipline: Life Sciences
Subdiscipline: Microbiology

Travis Santana*[1], Natasha DeLeon-Rodriguez[2], Alexandra M. Torres Maisonet[3]
[1]Interamerican University of Puerto Rico, Metropolitan Campus, [2]Interamerican University of Puerto Rico, Metropolitan Campus, [3]Interamerican University of Puerto Rico, Metropolitan Campus

Abstract: Antibiotic resistance has become a global public health crisis that is influenced by a wide variety of factors, ranging from misuse and overuse of antimicrobial agents to environmental alterations caused by anthropogenic events. Every year, Saharan dust travels over 500km from the Saharan Desert to the Caribbean, saturating the atmosphere in Puerto Rico with a wide variety of bioaerosols, which include bacteria, pollen, and fungi. These Saharan Dust events cause a public health dilemma in Puerto Rico, given that the island has among the highest rates of asthma in the world. Since these yearly events deteriorate Puerto Rico’s public health, we wondered what specific species of bacteria can travel among the Saharan dust, and not only cause upper respiratory problems, but can also contribute to other public health concerns. We have applied our recent research in literature to design a project that will identify and analyze the microbial population that is associated with Saharan dust and how it affects the atmosphere in Puerto Rico. In addition, the analysis of bacterial genomes to identify genetic and pathogenic pathways of certain bacterial species will be performed to potentially pinpoint specific contributors to antibiotic resistance. Specifically, we aim to identify if Saharan dust may be a hotspot for horizontal gene transfer of antibiotic resistance genes. This research aims to provide insight in the field of aerobiology and genomics that can potentially supply knowledge of how Saharan dust can have an impact on public health

Responses of mangrove and salt marsh in Corpus Christi Bay after the Feb. 2021 hard freezes

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Phillip Rivera*[1], Edward Proffitt [2], Donna Devlin[3]
[1]Texas A&M Corpus Chirsti, [2]Texas A&M Corpus Christi, [3]Texas A&M Corpus Christi

Abstract: Since the last freeze in 1989, populations of black mangroves (Avicennia germinans) have rapidly increased throughout coastal Texas. Some sites are dense shrub thickets that reduce light penetration, lowering salt marsh abundance; causing large-scale ecological regime shifts along with segments of the Texas coast. Two consecutive nights of below-freezing temperatures in Feb. 2021 provided an opportunity to study the effects of a catastrophic disturbance on the regime shift in Corpus Christi Bay. We are using observational data to test the hypothesis: That recovery of mangroves will be faster on Mustang Island than on Ward Island because Mustang is nearer the Gulf of Mexico which may provide for more mangrove propagule colonizers from locations outside the bay and also may have been a little warmer due to thermal buffering by the Gulf. We established paired 3x3 m plots on each Island near the seaward edge of the intertidal vegetation and 5-11m further inland. We quantified shrub mortality, survivor resprouting, seedling recruitment, and marsh cover. Data from October 2021 shows there was adult shrub recovery via epicormic resprouting and seedling recruitment in most plots, while marsh cover expanded in most plots due to mangrove canopy reduction. Nine months post freeze Ward had a mean = 1.16 (2.6 SD) total seedlings per m 2 and Mustang had a mean = 40.8 (22.8 SD) seedlings. In 2019, Ward had a mean = 5 (1.1 SD) seedlings per m 2 and Mustang had a mean = 4.3(1.1 SD) seedlings per m 2 .

Somatic Mosaicism of a PDGFRB Activating Variant in Aneurysms of the Intracranial, Coronary, Aortic, and Radial Artery Vascular Beds

Discipline: Life Sciences
Subdiscipline: Neurosciences

Daphne Toglia*[1], Dr. Manuel Ferreira [2], Dr. Carolina Parada[3], Fatima M. El-Ghazali[4], Dr. Manuel Ferreira [5]
[1]University of Washington, [2]University of Washington, [3]University of Washington, [4]University of Washington, [5]University of Washington

Abstract: Somatic Mosaicism of a PDGFRB Activating Variant in Aneurysms of the Intracranial, Coronary, Aortic, and Radial Artery Vascular Beds Activating variants in platelet-derived growth factor receptor beta (PDGFRB), including a variant previously described (p.Tyr562Cys [g.149505130T>C [GRCh37/hg19]; c.1685A>G]), have been found related to the development of multiorgan pathology, such as aneurysm formation. In order to find the relation between the allele fraction genotype and histopathologic phenotype, we conducted an evaluation of post-mortem normal and aneurysmal tissue specimens from the formerly reported index individual (Karasozen et al., 2019). DNA was extracted from a total of 80 post-mortem tissues and alternate allele fractions (AAF) of PDGFRB were determined using digital droplet PCR. Radiographic and histopathologic results, along with genotype expression of PDGFRB were then correlated in aneurysmal tissue and compared to non-aneurysmal tissue. The PDGFRB variant was identified in the vertebral artery, basilar artery, and P1 segment aneurysms (AAF: 28.7%, 16.4%, and 17.8%, respectively). It was also identified in the coronary and radial artery aneurysms (AAF: 22.3% and 20.6%, respectively). In phenotypically normal intracranial and coronary artery tissues, the PDGFRB variant was not present. The PDGFRB variant was absent from lymphocyte DNA and normal tissue, confirming it to be a non-germline somatic variant.

The Effect of Aging on the Lactate Receptor GPR81 and Metabolic Inflexibility

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Marvin Miller*[1], José Adan Arevalo [2], José Pablo Vázquez-Medina[3]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]University of California, Berkeley

Abstract: Metabolic inflexibility is the inability to switch between energy sources, carbohydrates (CHO) and free fatty acids (FFA). Metabolic inflexibility increases with age and is associated with declining muscle mass (atrophy). Lactate signaling through the lactate receptor, GPR81 , inhibits FFA lipolysis. It is not known, however, if lactate receptors levels change with age progression. Therefore, we explored the effect of aging on GPR81 protein abundance. We hypothesized that GPR81 abundance is higher in skeletal muscle cells(myoblasts) derived from young than old humans . To test our hypothesis, myoblast cell cultures from two individuals, one young (18 y/o) and one old (69 y/o), were obtained from Cook MyoSite and the GPR81 protein abundance was measured by Western Blot. Our preliminary results show that GPR81 is more abundant in cells derived from young humans, suggesting that lactate receptor levels decrease with age. Further work is needed to confirm this effect and to disentangle the contributions of GPR81 to aging-induced metabolic inflexibility.

Effect of Tegument Protein UL25 on Human Cytomegalovirus Latency and Infection Cycle

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Asa Laskie*[1]and Caroline Kulesza [2]
[1]Fort Lewis College, [2]Fort Lewis College

Abstract: Human cytomegalovirus (hCMV) is a betaherpesvirus that is the leading infectious cause of congenital birth defects in the U.S., and has a 50-95% seroprevalence in the U.S. adult population depending on the region. In neonates, hCMV infections cause sensory neural hearing loss as well as other neurological issues. In addition, hCMV infections are challenging to avoid during organ transplants, where an immunocompromised individual receives an organ from a donor harboring hCMV. hCMV is problematic to treat because it has two different phases on infection: the latent/dormant phase, and the lytic/infectious phase. Since hCMV can become latent in some cells, where no viral particles are produced, it is challenging to completely clear hCMV from someone's system. As a result, there is much need to understanding the molecular mechanisms that transition hCMV from a latent phase to a lytic phase of infection. One such candidate is the tegument protein UL25, which has previously been reported to associate with cellular chromatin and well as the crucial tumor supressor protein p53. To study the potential effects of UL25 on hCMV replication cycles, we have designed UL25 knockouts via homologous recombination of BACs (bacterial artificial chromosomes) in both human and mouse CMV strains. To analyze the difference in infectivity between strains, we performed TCID-50 plaque assays to create viral infection curves. We will also be performing qPCR on hCMV marker genes in different strains to assess infectivity. Afterwards, we will perform several p53 assays to further elucidate UL25's function in the latent-lytic cycle of hCMV.

Autism-associated δ-catenin G34S mutation promotes GSK3β-mediated degradation and social deficits

Discipline: Life Sciences
Subdiscipline: Neurosciences

Hadassah Mendez-Vazquez*[1]and Seonil Kim [2]
[1]Colorado State University, [2]Colorado State University

Abstract: Social impairment is key symptom in several mental disorders, including autism spectrum disorder, depression, and schizophrenia. However, cellular and molecular factors underlying social behavior remain poorly understood. δ-catenin is a post-synaptic scaffolding protein that is important for AMPA GluA2 subunit localization through the δ-catenin-n-cadherin-GRIP/APB complex. In humans, mutations in δ-catenin gene are linked to severely impacted ASD patients from multiple families. A glycine to serine mutation at residue 34 (G34S) in the n-terminal region of δ-catenin has been identified in humans as an ASD-associated missense mutation. The G34S mutation, according to the Group-based Prediction System, is an added target for GSK3-mediated phosphorylation. Transfected human neuroblastoma (SH-SY5Y) cells expressing WT and mutant δ-catenin were found to have significantly lower G34S δ-catenin levels compared to WT δ-catenin. The same cells treated with lithium chloride to inhibit GSK3β activity, had a significant increase in both WT and G34S δ-catenin levels indicating GSK3β-mediated degradation. We used a δ-catenin G34S knockin loss-of-function mouse model to investigate the effects of G34S δ-catenin mutation on social interaction. We used the three-chamber sociability test in 3-month-old male and female δ-catenin KI mice to discover social impairment. Males showed normal sociability, but females were found to have impaired sociability as compared to the WT; however, female G34S mice had normal social novelty preference while male G34S mice showed atypical social novelty preference as compared to the WT. We believe G34S δ-catenin induces GSK3β-mediated δ-catenin degradation, and G34S δ-catenin mutation causes impaired sociability and social novelty with sex specific deficits.

Batrachochytrium dendrobatidis infection dynamics in heavily human populated areas of Honduras, Costa Rica and Panama

Discipline: Life Sciences
Subdiscipline: Microbiology

Marina De Leon*[1]and Jonathan A. Eisen [2]
[1]University of California, Davis, [2]University of California, Davis

Abstract: Chytridiomycosis is a fatal skin disease of amphibians. Epizootics have occurred throughout Central America but Bd endemism is also likely to occur in the same regions, accounting for observed enzootic patterns. Analysis of Bd genomic data in Central and North America would give insight into Batrachochytrium dendrobatidis (Bd) lineages allowing us to form hypotheses about Bd endemism or arrival based on phylogenetic relationships. We investigated the lineages of Bd samples throughout Central America by observing fine-scale genomic variation in order to better infer the origin of Bd over multiple, large spatial scale datasets from three neotropical countries. Non-invasive amphibian skin swabs were collected from Honduras, Costa Rica, and Panama where Bd has been reported and profound amphibian declines are associated with chytridiomycosis. We show current Bd presence within Central America and report endemic vs. invasive lineages. Sequencing specific gene markers of Bd - positive samples collected across this spatial scale followed by phylogenic assessment to test whether the Bd strains are endemic or invasive, or a combination of the two is an imperative step in reconstructing more accurate epidemiological data regarding Bd endemism and dissemination throughout the region. Bd in Central America has led to severe amphibian population declines, especially in heavily trafficked areas. Understanding the genetic history and virulence of Bd and relationships between Bd lineages and human traffic will help us understand the chytridiomycosis pandemic and ultimately help drive conservation actions based on endemism or invasive species concepts.

Elucidating the role of the Notch signaling pathway in Sonic hedgehog-mediated oligodendrocyte fate specification

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Luuli Tran*[1], Santos J. Franco [2], Caitlin C. Winkler[3]
[1]University of Colorado, Anschutz Medical Campus, [2]University of Colorado, Anschutz Medical Campus, [3]University of Colorado, Anschutz Medical Campus

Abstract: Neural progenitor cells in the developing brain generate many different neuronal and glial cell types that each have unique and important roles in the neural circuits that allow us to sense, think, and act. A fundamental challenge in developmental neurobiology is understanding how this cellular diversity is achieved from a common pool of neural progenitor cells. After making neurons, progenitors in the dorsal part of the forebrain produce oligodendrocytes, glial cells that wrap axons with myelin membrane to enhance axon conduction. Failure to form myelin causes severe neurological dysfunctions, so identifying the mechanisms that produce oligodendrocytes is an essential step toward a more complete understanding of brain development and disease. We discovered that the Sonic hedgehog (Shh) signaling pathway initiates oligodendrocyte production, but the mechanisms by which Shh acts to instruct progenitors to the oligodendrocyte lineage remain unknown. We analyzed a single-cell RNA sequencing dataset of the developing mouse neocortex, which revealed Notch signaling activity in Shh-responding progenitors that appear committed to the oligodendrocyte lineage. Pharmacological and genetic approaches to block Notch signaling in vivo inhibited the formation of oligodendrocyte precursor cells (OPCs). Furthermore, we show that adding Shh ligand to brain slice cultures stimulates OPC production, but pharmacologically blocking Notch signaling strongly attenuates this effect. We hypothesize that Notch signaling promotes oligodendrocyte specification by enhancing progenitor responses to Shh in the developing dorsal forebrain. This work will contribute to a better understanding of oligodendrocyte development and provide insight on therapeutic strategies to treat demyelinating diseases, such as multiple sclerosis.

Modulation of the Innate Immune Sensor Cyclic GMP-AMP Synthase (cGAS) by Chikungunya virus (CHIKV)

Discipline: Life Sciences
Subdiscipline: Microbiology

Jeury Veloz*[1]and Ana Fernandez-Sesma [2]

[1]Icahn School of Medicine at Mount Sinai, [2]Icahn School of Medicine at Mount Sinai, Department of Microbiology

Abstract: Chikungunya virus (CHIKV) is a virus of the Alphavirus genus in the Togaviridae family with a plus sense single-stranded RNA (+ssRNA) genome known to cause periodic explosive epidemics. CHIKV is further classified into the Semliki Forest (SF) antigenic complex clade of ‘Old-World’ alphaviruses, which are viruses generally associated with rheumatic disease. Although infection with CHIKV is associated with low mortality rates, an estimated 80% of patients infected experience disabling polyarthralgia in the acute phase which may persist for months or years in chronic cases. Cytosolic immune sensing of viruses is an important component of innate human cellular immunity against infection, including CHIKV. These pathways recognize pathogen-associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs) that are generated during virus infection and trigger transcriptional induction of type-I interferon (IFN) and subsequent production of antiviral interferon-stimulated genes (ISGs). Mounting evidence from our lab and others demonstrate evidence for non-canonical antiviral functions of the DNA sensor cyclic GMP-AMP synthase (cGAS) in response to RNA viruses, including CHIKV. Recently, we published that CHIKV is able to circumvent host innate immune sensing by targeting cGAS. Here, we demonstrate that CHIKV infection leads to the degradation of cGAS and that recovery of cGAS is observed in CHIKV infected cells chemically and genetically inhibited of autophagy. We hypothesize that CHIKV specifically hijacks host autophagy machinery to mediate cGAS trafficking to autolysosomes during infection. Results from this study will further elucidate novel mechanisms of modulation of cGAS by CHIKV and possibly other +ssRNA viruses.

ERα Mediated Recovery of Synaptic Plasticity in Juvenile Female Mice After Global Cerebral Ischemia

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jose Vigil*[1], Nidia Quillinan [2], Paco S Herson[3], Erika Tiemeier[4], Nicholas E Chalmers [5], Rob Dietz[6], James Orfila[7]

[1]University of Colorado Anschutz Medical Campus, [2]University of Colorado Anschutz Medical Campus, [3]Ohio State University, [4]University of Colorado Anschutz Medical Campus, [5]University of Colorado Anschutz Medical Campus, [6]University of Colorado Anschutz Medical Campus, [7]Ohio State University

Abstract: We have previously shown that global cerebral ischemia (GCI) in juvenile male mice results in cognitive impairments and corresponding hippocampal long-term potentiation (LTP) impairments which endogenously recover within 30 days. It is also important to determine if the juvenile female brain undergoes endogenous recovery and the mechanisms by which this recovery occurs. Therefore, we hypothesize that GCI in juvenile female mice results LTP impairments that endogenously recover as a result of estrogen signaling that increases during puberty. Female mice were subjected to cardiac arrest (CA) or sham procedure at p21-25 and ovariectomy (OVX) performed 5-7-days later. At time of OVX, hormone replacement (E2, DPN, PPT) was performed via subcutaneous osmotic pumps. 30-days after CA, hippocampal slices were prepared and LTP recordings were performed. GCI in juvenile female mice produces acute deficits in LTP that endogenously recover on a timescale that coincides with the onset of sexual maturity. LTP in sham animals reaches 145.3±6.9% of baseline while GCI animals only reach 118.3±7.25% (p< 0.05 vs. shams) 7-days after GCI. Interestingly, 30-days after GCI, LTP returns to 143.2±7.13% of baseline (p>0.05 vs. shams). Endogenous recovery was ablated in OVX animals (130.6±6.9%), however, OVX and prolonged hormone replacement therapy increased LTP (E2= 45.8±7.48; DPN=160.0±12.6%) with the ERα agonist PPT restoring LTP to the greatest extent (170.4±12.1%; p<0.05 vs sham). This suggests that endogenous recovery of LTP in the juvenile female brain after GCI is mediated by the surge of sex hormones that occurs during the onset of puberty by acting upon ERα receptors.

The roles of interleukin-18 and gasdermin-D in APP/PS1 mice

Discipline: Life Sciences

Subdiscipline: Neurosciences

Stephanie Becker*[1], Douglas Golenbock[2], Michael Heneka[3], Kensuke Futai[4], Gail Germain[5], Te-Chen Tzeng[6]

[1]University of Massachusetts Chan Medical School, [2]University of Massachusetts Chan Medical School, [3]Luxembourg Centre for Systems Biomedicine, [4]University of Massachusetts Chan Medical School, [5]University of Massachusetts Chan Medical School, [6]University of Massachusetts Chan Medical School

Abstract: Alzheimer’s disease (AD) is a neurodegenerative disease featuring chronic inflammation and seizures induced by amyloid beta. The innate immune system responds to amyloid beta by initiating a Nod-like receptor protein 3 (NLRP3) inflammasome-mediated proteolytic cascade that produces active interleukin-18 (IL-18) and -1b, secreted through gasdermin-D (GSDMD) pores. Interestingly, IL-18 plays a protective role at an early stage of AD, reducing excitatory synaptic transmission in APP/PS1 mice. In the brain, resting microglia secrete mature IL-18 and express GSDMD. However, the role of GSDMD and the main source of IL-18 in the brain are unknown. Previously published data suggest that astrocytes are a potential main source of IL-18. Therefore, glial IL-18 production and maturation, as well as the proteolytic cascade upstream IL-18 maturation, were observed by western blot. We found that resting astrocytes produce pro IL-18 but not mature IL-18 while microglia produce both pro and mature IL-18. To investigate the role of GSDMD in AD, we bred Gsdmd [-/-] mice into APP/PS1 mice. These mice (APP/PS1/ Gsdmd [-/-]) show increased mortality and a severe deficit in spatial memory formation compared to Gsdmd [-/-] and WT mice. Like APP/PS1/ Il-18 [-/-] mice, these data indicate that APP/PS1/ Gsdmd [-/-] mice remain unprotected from AD. Further studies are warranted to determine if and how astrocytes can produce mature IL-18, as well as the reason for the deleterious effects of GSDMD deficiency in APP/PS1 mice.

Comparison of native amphidromous freshwater snail Vittina variegata vs. native live-bearing freshwater snail Melanoides tuberculata

Discipline: Life Sciences

Subdiscipline: Animal Sciences/Zoology

Khanh Ly*[1]and Dr. Daniel P. Lindstrom[2]

[1]University of Guam, Guam, [2]University of Guam

Abstract: This study compared two native freshwater gastropod species on Guam, showing contrasting life-history traits. An amphidromous nerite, Vittina variegata, lives as an adult and reproduces in freshwater. Veliger larvae hatch in freshwater but are transported to the marine planktonic environment, where they develop before recruiting back into freshwater as juveniles. This life-history characteristic allows dispersal and a potentially wider geographic distribution. In contrast, a thiarid Melanoides tuberculata broods and gives live birth in freshwater, limiting its dispersal potential and likely leading to genetic isolation. It is postulated that these contrasts in dispersal ability will be reflected in population genetic patterns. This study discerned the population structure of these species across Guam's 14 watersheds. It was hypothesized that V. variegata would show less genetic heterogeneity across rivers than M. tuberculata . Individuals of each species were collected from inhabited streams in Southern Guam. They were photo-documented, biopsied, and preserved. The freshly biopsied tissue was used in genomic DNA extraction and used as a template in a PCR targeting the COI gene and sequenced. Genetic sequences were edited, aligned, and analyzed. The data supported the hypothesis that limited dispersal ability resulted in greater genetic intraspecific heterozygosity. Freshwater resources on populated and isolated islands, including the living resources they support, are threatened worldwide. To effectively conserve these resources, the species' life-history traits must be considered. Those with greater genetic diversity, like M. tuberculata, should be managed on a watershed-by-watershed basis. More genetically connected, like V. variegata , require a broader geographic management plan.

Characterizing the Role Fever Plays in Antibiotic Efficacy

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Autumn Henderson*[1]and Gabriela Martinez [2]
[1]University of California, Irvine, [2]University of California, Irvine

Abstract: Antibiotic resistant bacteria are a major global health concern. One concerning organism is uropathogenic Escherichia coli (UPEC), the most common species involved in urinary tract infections (UTI). This organism has become problematic to treat, as UPEC often evolves resistance to antibiotic treatments. One of the symptoms of UTI in humans is fever, characterized by an increase in body temperature above 37°C. It is known that culturing E. coli at high temperatures (42.2 °C) can decrease antibiotic efficacy through genetic mutations that help bacteria survive better in antibiotics. However, there is a knowledge gap as to the role fever plays in UPEC’s ability to evolve resistance. In this project, we have characterized the role that heat stress from simulated fever plays in antibiotic efficacy to help us understand the stressors that modulate UPEC to evolve resistance. We have identified combinations of heat stress and antibiotics that promote tolerance to antibiotics. We examined what occurs when heat stress and antibiotic treatments interact by using a combination of susceptibility assays, evolutionary rescue experiments, and high throughput sequencing. Based on previous and preliminary data, we show that fever modifies UPEC’s susceptibility to antibiotics through changes in survival and this differential survival in turn influences the probability of the emergence of antibiotic resistance. This study provides a better understanding of how heat stress influences bacteria’s ability to evolve antibiotic resistance to provide more effective antibiotic treatments for UTIs and gain better understanding of how host physiology may influence UPEC’s response to antibiotics .

Exploring how aging-associated changes in autophagy dictate the development of lung cancer or leukemic disease

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Amy Briggs*[1]and James V DeGregori [2]
[1]University of Colorado, Denver --Anschutz Medical Campus, [2]University of Colorado, Denver --Anschutz Medical Campus

Abstract: While mutations are important for lung cancer development, our lab also factors in the microenvironment. Under the adaptive oncogenesis model, insults such as aging and smoking can dramatically alter the tissue microenvironment thus leading to selection for adaptive oncogenic mutations that otherwise would not be selected for in an unperturbed environment. Additionally, autophagy is a metabolic process has been seen to deteriorate as we age, affecting tissue maintenance and homeostasis. Many studies have shown premature aging due to autophagy inhibition in different model organisms. Thus, we hypothesize that there is a strong relationship between autophagy and oncogenesis through the decline of tissue maintenance and increase in positive selection of potentially harmful clones in the changing microenvironment. To begin to test this, I have used a mouse model with an inducible, systemic, and mosaic inhibition of autophagy followed by intranasal instillation of an adenovirus-CRISPR system which causes an oncogenic fusion protein called EML4-ALK. In young mice, autophagy inhibition is initiated and maintained throughout the experiment, after two months the oncogene is introduced and the lungs are harvested six weeks later. The mice with decreased autophagy were seen to have larger adenomas than their control littermates (p<0.05). This indicates autophagy is protective and when decreased it creates an environment that is favorable for cells harboring an oncogene. With this project, I hope to illustrate the effect of autophagy decline in old lungs, reveal the mechanism of decreased autophagy in oncogenesis, and determine if increased autophagy in old age can protect against oncogenesis.

Electrospun Scaffolds with Rhamnolipids to Treat Depleted-Uranium Contaminated Wounds

Discipline: Life Sciences
Subdiscipline: Biology (general)

Brenda Padilla*[1], Taylor R. Gilmore [2], Marjorie A. Nguyen[3], Dominic D. Dominguez[4], Desirae E. Enriquez [5], Chett J. Boxley[6], Jeanne E. Pemberton[7], Robert S. Kellar[8]
[1]Northern Arizona University, [2]Northern Arizona University, [3]Northern Arizona University, [4]Northern Arizona University, [5]Northern Arizona University, [6]Glycosurf, Salt Lake City, UT, [7]University of Arizona, [8]Northern Arizona University

Abstract: Depleted uranium (DU) is a metal by-product produced after the enrichment of natural uranium to lower its radioactivity for military use. Although most of the radioactive isotopes have decayed, DU remains both toxic and a health hazard when ingested or inhaled. Over 500 abandoned uranium mines are located in the American Southwest that not only pose a threat to the surrounding environment but the population’s health through the ingestion of contaminated water. Previous literature demonstrated exposure to DU has negative effects on the wound healing process through a variety of cytotoxic mechanisms; however, current literature lacks a healing therapeutic to counteract this issue. Therapeutics, such as novel wound coverings, have been developed to promote wound healing by treating wounds with three-dimensional biomaterials made to mimic the extracellular matrix. These biomaterials are applied to effectively promote cellular migration and proliferation. In the current study, novel electrospun wound healing scaffolds are impregnated with unique chemistries to facilitate delivery into the wound bed to neutralize or de-contaminate the tissue from DU exposure. An in vitro wound model was prepared using human dermal fibroblasts in combination with rhamnolipids, a biosurfactant with known environmental contaminant binding properties. Using this in vitro wound model, cells contaminated with DU and treated with rhamnolipids had an increased closure rate over cells only contaminated with DU. These preliminary findings provide proof of concept for the continued exploration of using rhamnolipids as a treatment for DU-contaminated wounds. Future work will focus on incorporating rhamnolipids into novel electrospun wound healing scaffolds.

A Therapeutic Platform for X-linked Intellectual Disabilities

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Casiana Gonzalez*[1], Julian Halmai [2], Kyle Fink[3]
[1]University of California, Davis, [2]University of California, Davis, [3]University of California, Davis

Abstract: There are over 140 known intellectual disabilities linked to genes on the X chromosome, with approximately 38 genetic conditions predominantly affecting females, a targetable therapeutic platform for the X chromosome is needed. CDKL5 , MECP2 and CASK constitute a portion of those 38 X-linked intellectual disabilities (XLID), associated with CDKL5 deficiency disorder, Rett Syndrome and CASK-related intellectual disability, respectively. These disorders are typically the result of loss of function mutations, and have convergent phenotypes such as learning disabilities, epilepsy, developmental impairments and motor dysfunction. As females have two X-chromosomes, disease causing mutations in these genes are diluted out by the mosaicism of X-chromosome inactivation (XCI), which allows for affected females to survive past birth. Previously, the Fink lab has shown the ability to target CDKL5 in human neuron-like cells and reactivate the XCI-silenced healthy allele using our dual CRISPR/dCas9 epigenetic approach. Our current goal is to test if this approach is able to have wide-spread application across other monogenetic XLIDs. We aim to answer this by creating a screening platform for our customizable dCas9 constructs and apply it to MECP2 and CASK. To achieve this, we will clone our construct to target specific genetic sites and validate the efficacy of the construct through Next-Generation and bisulfite sequencing. Downstream molecular effects will be measured through RT-qPCR and Western Blot. Results show the ability to target and alter gene expression and methylation status within multiple genetic settings. This project allows for a therapeutic platform that could be applied to over 38 XLIDs.

Deep in the subsurface, land use decisions and climate drive altered soil development and nutrient flows

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

annalise guthrie*[1], Pam Sullivan [2], Terry Loecke[3], Matthew Kirk[4], Micah Unruh [5], Sharon Billings[6]
[1]University of Kansas, Kansas Biological Survey and Center for Research, [2]Oregon State University, [3]University of Kansas, Kansas Biological Survey and Center for Research, [4]Kansas State University, [5]University of Kansas, Kansas Biological Survey and Center for Research, [6]University of Kansas, Kansas Biological Survey and Center for Research

Abstract: Over half of habitable land in the world is used for agricultural purposes. While impacts of agriculture on surface soil physical structure are well-researched, effects of these impacts and altered rooting patterns on biogeochemical cycling, especially in deeper subsurfaces, are less understood. We investigate how soil pore water is modified by agriculture across a precipitation gradient. Pore water chemistry reveals both biotic and abiotic processes, and can be linked to soil structural characteristics. Past research focusing on biogeochemical effects of agriculture were limited to shallower soils, typically less than 30cm in depth. Here, we analyze soil water dissolved organic carbon, nitrate, phosphate, calcium, and potassium collected every two weeks using vacuum lysimeters in which the soils' structure has undergone dramatic transformation with land use change, throughout 2m of their yet-deeper profiles. Lysimeters are installed at depths of 10cm, 40cm, and 120cm in agriculture, restored, and native prairie sites in Kansas across a region representing a doubling of mean annual precipitation (~500 to ~1000mm y-1). We demonstrate where root abundance has changed and soil structure has modified soil pore networks, soil water retention time has likely changed and resulted in modified patterns of weathering, biological activity, and soil nutrient release. Results serve to model future responses of soil to land-use decisions in the context of changing evapotranspiration, soil pore geometry, and microbial activity. These efforts aim to increase understanding of the degree to which humans influence soil processes in unexpected ways and the resulting future economy of farmers and food security.

Surveying the dynamic phenotype of tumor infiltrating immune cells in a murine breast cancer model

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Nicole Couturier*[1], Gregoire Lauvau [2], Marie Boutet[3], Wenjun Guo[4]
[1]Albert Einstein College of Medicine, [2]Albert Einstein College of Medicine, [3]Albert Einstein College of Medicine, [4]Albert Einstein College of Medicine

Abstract: Breast cancer is the second leading cause of death in women of all ages each year. Thus, a deeper understanding of the molecular determinants promoting tumor development and suppressing anti-tumor immune responses is greatly needed. With our collaborators, we developed a preclinical breast cancer mouse model that harbors frequently associated cancer driver mutations including the functional loss of the tumor suppressor genes p53 and MLL3, and constitutive activation of PI3 kinase. Loss of MLL3 drives more aggressive tumor growth as "MP5" tumors with all three mutations (Mll3 -/- p53 -/- PIK3 CA) onset and grow significantly faster than "P5" tumors (p53 -/- PIK3 CA). Therefore, we hypothesized that loss of MLL3 establishes a distinct microenvironment in MP5 tumors compared to P5 tumors. To characterize this preclinical tumor model, we developed a 30-color high dimensional spectral flow cytometry panel to phenotype tumor-infiltrating leucocytes. We observed that Ly6C + monocytes and regulatory T (Treg) cells infiltrated MP5 but not P5 tumors concomitantly with high numbers of CD169 + F4/80 + macrophages. We also observed that these macrophages express high levels of MHC-II and CD86, suggesting that they may present tumor antigen and promote Treg cell expansion in the MP5 tumors, contributing to the rapid establishment of a highly immunosuppressive tumor microenvironment in MP5 compared to P5 tumors. By connecting key tumor mutations to specific facets of the immune response in the tumor microenvironment, we expect to reveal novel therapeutic targets for better-personalized breast cancer treatments.

Flavonoids, Total Phenolic Content, and Antioxidant Activity of Hibiscus sabdariffa and Hibiscus rosa-sinensis

Discipline: Life Sciences

Subdiscipline: Plant Sciences/Botany

Maegan Marie Delfin*[1]and Mari Marutani [2]

[1]University of Guam, [2]College of Natural and Applied Sciences, University of Guam

Abstract: Hibiscus sabdariffa and H. rosa-sinensis, known to possess antioxidant properties in their flowers and leaves, are used in traditional medicine as a treatment for oxidative-stress related diseases. H. rosa-sinensis is an ornamental plant and H. sabdariffa is grown as a specialty crop for their pigmented calyx of its flower. For the introduction of new crops in the Pacific Islands, nine accessions of H. sabdariffa (Accession: PI256039, PI265319, PI273389, PI275413, PI275414, PI291128, PI500706, PI500713, PI500724) were examined for their biochemical properties in their calyxes and leaves and were compared to red petals of H. rosa-sinensis . Calyxes, leaves, and flower petals of Hibiscus spp. were collected, freeze-dried, and ground. Aqueous extracts were prepared by placing powdered samples into acidified ethanol (80:2:18 of ethanol:acetic acid:water). Seven flavonoids, including two phenolic acids (protocatechuic acid, chlorogenic acid), four anthocyanins (delphinidin 3-sambubioside, delphinidin 3-glucoside, cyanidin 3-sambubioside, cyanidin 3-glucoside), and one flavonol (quercetin) were identified using high-performance liquid chromatography (HPLC). Total phenolic content was determined by the Folin-Ciocalteu assay. Antioxidant activity was determined by two free-radical scavenging activity assays, using the ABTS and the DPPH assay. Results demonstrated that the quantity of flavonoids varied among accessions, with anthocyanins being the most abundant flavonoid in highly pigmented flower parts. The highest amount of total phenolic content and antioxidant activity was exhibited by H. rosa-sinensis petals, followed by H. sabdariffa accessions with highly pigmented calyxes. These results suggest that Hibiscus spp . flower parts have the potential to be used as a source of antioxidants.

Impact of prenatal exposures to per- and polyfluoroalkyl substances (PFAS) on the developing neonatal immune system

Discipline: Life Sciences

Subdiscipline: Other Life Sciences

Darline Castro Melendez*[1], Kristin Scheible [2], B. Paige Lawrence[3], Nathan Laniewski[4], Xing Qiu [5], Qiuyi Wu[6], Thomas O'Connor[7], Todd Jusko[8]

[1]University of Rochester, [2]University of Rochester, [3]University of Rochester, [4]University of Rochester, [5]University of Rochester, [6]University of Rochester, [7]University of Rochester, [8]University of Rochester

Abstract: Per- and polyfluoroalkyl substances (PFAS) are persistent synthetic chemicals widely used in industrial processes and consumer goods, and are ubiquitous in the environment and people. Epidemiological studies have associated exposure to PFAS with detrimental effects on the immune system, yet how these chemicals alter the immune response is not fully understood. Fetuses and infants are particularly susceptible to environmental exposures due to their rapid growth and developing systems. During fetal development each immune cell type develops in layers at a different gestational stage, thus perturbations during pregnancy could alter the normal establishment of these immune layers. There is strong evidence of PFAS-associated immunotoxicity and its effects on vaccine responses; however little attention has been drawn to how these compounds affect fetal T cell development. Here we hypothesize that maternal PFAS exposure during pregnancy disrupts infant T cell development. Using a systems immunology approach, our data reveal the phenotypic and time-dependent complexity within the CD4 + and CD8 + T cell pool at birth, 6 and 12 months of age. We show the presence of 36 unique CD4 + and 14 unique CD8 + clusters of cells identified through high-dimensional analysis and how these clusters change over time. We further identify specific clusters associated with PFAS exposure during pregnancy. Our data gives us further insight into the complexity of the immune response, the importance of controlling maternal exposures during pregnancy, and how these antenatal exposures may reshape the fetal developmental program.

A Non-canonical Mechanism of Complement 4-Driven Cortical Synaptic Loss

Discipline: Life Sciences
Subdiscipline: Neurosciences

Rhushikesh Phadke*[1], Alberto Cruz-Martin [2], Luke Fournier[3], Alison Brack[4], Ashley Comer [5], Yen Yu Liu[6], Ezra Kruzich[7], Connor Johnson[8], Ines Picard[9], Maria Salgado[10]
[1]Boston University, [2]Boston University, [3]Boston University, [4]Boston University, [5]Boston University, [6]Boston University, [7]Boston University, [8]Boston University, [9]Boston University, [10]Boston University

Abstract: Synaptic connections enable neural networks to orchestrate functions underlying complex behaviour and are disrupted in many neurological disorders. Several lines of evidence indicate that immune molecules are expressed in the brain and can regulate synaptic connectivity. Our group has recently shown that increasing the levels of the complement component 4 (C4) – an immune molecule shown to be linked with schizophrenia –decreases the connectivity of developing cortical neurons. A long-standing dogma in the neuroimmune field is that cells in the brain can release complement proteins into the extracellular space, where they modify the connectivity of neurons through the activation of complement receptors and recruitment of microglia. However, our preliminary data shows that overexpression of C4 via in utero electroporation (IUE) in transgenic mice lacking the microglia C3 receptor (CR3-KO) still leads to a decrease in the density of postsynaptic dendritic spines of layer (L2/3) prefrontal (PFC) pyramidal neurons. Our data supports that C4 contributes to synaptic loss through a non-canonical, CR3-independent mechanism. Using co-immunoprecipitation in HEK293T cells, we also show that C4 interacts with Sorting Nexin 27 (SNX27), a protein shown to be an important regulator of endocytosis and protein trafficking. Importantly, IUE of both C4 and SNX27 together leads to an increase in density of dendritic spines of L2/3 PFC neurons, undistinguishable to that of controls, indicating that increased levels of SNX27 could rescue C4-induced hypo connectivity. Taken together, our results suggest an intracellular, non-canonical mechanism of C4 action in neurons, via inhibition of SNX27 function.

Grip Strength as a Potential Biomarker for Insoluble Tau Accumulation

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Bryan Alava*[1], Jose Abisambra [2], Karyn Esser[3]
[1]University of Florida, [2]University of Florida, [3]University of Florida

Abstract: Alzheimer’s Disease (AD) is associated with muscle weakness, but the molecular basis of this association is unknown. Beyond motor function, skeletal muscle is a highly metabolic endocrine organ, that crosstalks with other systems. Therefore, disruptions in skeletal muscle may influence physiology in AD. Accumulation of insoluble tau that forms neurofibrillary tangles

(NFTs) is a hallmark of AD. Neurodegeneration could negatively impact muscle function; dysfunctional skeletal muscle can also influence the environment of tau pathogenesis. Therefore, changes in muscle function relative to insoluble tau accumulation would suggest skeletal muscle can contribute to the progression of tau pathology. Inducible muscle specific Bmal1 knockout mice were used to model muscle weakness. Intracerebroventricular injections with adeno-associated viral (AAV) vector encoding P301L human tau (n= 15) and controls (n=18) were done at postnatal day 0. Grip strength, rotarod, and body composition were measured at 16 weeks. At 18 weeks, intraperitoneal injections were performed with either tamoxifen (n=8 tau, 11 control) or corn oil (n=7 tau, 7 control) to delete Bmal1 in muscle. Brains were harvested at 24 weeks. Soluble and insoluble tau were biochemically measured. Grip strength was reduced at 16 weeks in the tau mice, two weeks before induced muscle weakness, and 10 weeks before NFTs are reported. Insoluble tau was detected at 24 weeks. Changes in grip strength preceded NFTs in this tauopathy model. This suggests that a) muscle weakness may serve as a biomarker and b) that disrupted skeletal muscle health may be capable of contributing to tauopathy progression.

The eIF2 kinase PERK facilitates Keratinocyte Collective Cell Migration via regulation of ECM and cytoskeletal dynamics

Discipline: Life Sciences
Subdiscipline: Biochemistry

Miguel Barriera Diaz*[1], Ronald C. Wek[2], Dan F. Spandau[3]
[1]Indiana University School of Medicine, [2]Indiana University School of Medicine, [3]Indiana University School of Medicine

Abstract: Cutaneous wound healing has become an essential topic of research, as the cases of chronic (non-healing) wounds keep rising in America due to Diabetes. A key stage of normal wound healing is the re-epithelialization phase which involves the collective migration of keratinocytes as an epithelial sheet, also known as keratinocyte collective cell migration (KCCM). Failure to properly invoke and regulate KCCM is thought to facilitate chronic wounds. The Integrated Stress Response (ISR) is a major mechanism for cell adaptation to acute stress . We hypothesize that the ISR protein kinase PERK (EIF2AK3) is central for KCCM. To test this hypothesis, we compared immortalized human keratinocytes (NTERT cells) with NTERTs depleted of PERK using CRISPR (PERK-KO) for differences in KCCM dynamics using in vitro models of wound healing. We found that PERK-KO NTERTs showed a significant delay in KCCM compared to WT NTERTs. Cytoskeletal analysis using immunofluorescence (IF) techniques showed that PERK-KO NTERTs have a lack of F-actin organization. Furthermore, immunoblot and IF analysis also showed that PERK-KO NTERTs have disrupted cell-ECM dynamics, as measured by fibronectin overexpression and lack of α5β1 integrin expression. These results suggest that PERK is involved in key mechanisms that drive KCCM. Therefore, we propose that an appropriate window of regulation of PERK and the ISR is critical for proper wound repair and that these processes may be an important target for the treatment of chronic non-healing wounds.

The role of histone acetyltransferase activity in alcohol-induced neuroadaptations

Discipline: Life Sciences
Subdiscipline: Neurosciences

Airined Montes*[1], Carolina Dasta-Cruz[2], Leonardo Ramos-Rodríguez[3], Christian D. Del Valle-Colón[4], Madhavi Kuchibhotla[5], Jose L. Agosto[6], Alfredo Ghezzi[7]

[1]University of Puerto Rico, Rio Piedras, [2]University of Puerto Rico, Rio Piedras, [3]University of Puerto Rico, Rio Piedras, [4]University of Puerto Rico, Rio Piedras, [5]University of Puerto Rico, Rio Piedras, [6]University of Puerto Rico, Rio Piedras, [7]University of Puerto Rico, Rio Piedras

Abstract: Excessive alcohol consumption is one of the most prevalent disorders among individuals in our society. Alcohol consumption causes a homeostatic imbalance in the organism followed by the development of adaptations in the brain leading to alcohol tolerance and physiological dependence, or addiction. Recent evidence suggests that epigenetic mechanisms regulating gene expression and chromatin states are involved in such alcohol-induced neuroadaptations. However, most of these mechanisms are still unknown. The goal of this study was to determine the role of histone-modifying enzymes in behavioral responses and gene expression dynamics associated with alcohol tolerance. We hypothesize that the histone acetyltransferase Tip60 activity in neurons mediates transcriptional dysregulation associated with alcohol tolerance. Tip60 is the mammalian homolog of Kat5, in the Drosophila melanogaster model organism, and has been linked to gene expression in neurons. We employed Tip60 knockdown using RNAi and the GFP marker in neurons using the UAS-Gal4 system to generate two lines of transgenic flies. To measure alcohol tolerance, we observed the difference in the rate of sedation between mock-treated and ethanol-sedated, female adult flies. Our findings showed that Tip60 knockdown flies did not acquire alcohol tolerance. Furthermore, to identify genome-wide transcriptional changes in these flies, we performed a high throughput mRNA quantitation (RNA-seq) of the whole brain. This study revealed significant differential expression of genes of Tip60 knockdown flies exposed to alcohol. Collectively, our data can provide us with new insights into how neurons adapt to alcohol through histone acetylation mechanisms.

Adams Oliver Syndrome-associated RBPJ variants cause phenotypes by impairing DNA binding and sequestering the Notch signaling molecule

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Alyssa Solano*[1], Lisa Gutzwiller[2], Ellen K. Gagliani[3], Rhett A. Kovall[4], Brian Gebelein[5]
[1]University of Cincinnati College of Medicine, [2]Cincinnati Children's Hospital Medical Center, [3]University of Cincinnati College of Medicine, [4]University of Cincinnati College of Medicine, [5]Cincinnati Children's Hospital Medical Center

Abstract: Adams Oliver Syndrome (AOS) is a rare genetic disorder characterized by scalp and skull defects (aplasia cutis congenita) and transverse terminal limb defects of variable severity. AOS patients can also have cardiovascular problems, brain and eye anomalies, developmental delays, and skeletal anomalies with variable penetrance. AOS pathogenesis is not yet well understood. Previous sequencing of a large AOS cohort identified allelic variants in several components of the highly conserved Notch signaling pathway, including the ligand DLL4, the receptor NOTCH1, and the transcription factor RBPJ (known as Suppressor of Hairless (Su(H)) in Drosophila). Six dominantly inherited autosomal missense mutations were identified in or near the DNA-binding domain of human RBPJ. The goal of this project is to describe the pathogenesis of autosomal dominant AOS variants in RBPJ using a combination of quantitative biochemical assays and animal models. Our current biochemical studies support the hypothesis that RBPJ AOS variants cause dominant phenotypes by weakening DNA binding but not binding to the Notch signaling molecule. Using analogous mutations in Drosophila Su(H) and mouse RBPJ, we further show that both flies and mice with AOS variants develop autosomal dominant

phenotypes consistent with a dominant-negative protein function. These findings suggest that AOS-associated RBPJ variants cause phenotypes by interrupting Notch signaling via a sequestration mechanism. Importantly, we are now using our novel mouse models of AOS-associated RBPJ variants to investigate both the tissue types and temporal windows involved in AOS pathogenesis.

"Jumping" into gene regulation: Understanding the regulatory adaptation of transposable elements and their effect on gene expression in maize

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Merritt Khaipho-Burch*[1], Taylor Ferebee[2], Michelle Stitzer[3], Edward Buckler[4]
[1]Cornell University, [2]Cornell University, [3]Cornell University, [4]USDA-ARS and Cornell University

Abstract: With the onset of climate change, developing crop varieties adapted to future environments is paramount in maintaining plant productivity. Breeding a crop like Zea mays (maize) for future environments requires that we understand how all 35,000 genes are regulated in the genome. In the 1950s, Barbara McClintock hypothesized that transposable elements - so-called "jumping genes" - could be responsible for controlling the individual activity of genes and could lead to the specialized evolution and adaptation of gene regulatory grammar in their host genomes. We now know that genes are heavily impacted by the nearly 350,000 transposable elements that comprise 85% of the maize genome sequence. We hypothesize that transposable elements have played a key role in adaptation to new environments and, on a smaller scale, provided an abundant source of regulatory information that can impact gene expression. To test this hypothesis, we used gene expression data from 7,500 maize varieties and 600 wild relatives related to maize. We built models that quantify how transposable elements impact gene regulation and adaptation to new environments. We identified numerous transposable element insertions regulating or disrupting gene expression, enriched transposable-element derived motifs in environmentally responsive genes, and described other genomic features associated with these expression changes. These patterns can be used to guide plant breeders on how to design high-yielding maize varieties more suited to new environments and conditions.

Targeted Proteomics to Elucidate the Malaria Parasite Plastid DNA Repair Proteins

Discipline: Life Sciences
Subdiscipline: Biochemistry

Nicholas Nieto*[1], Scott W. Nelson[2], Joshua R. Beck[3]
[1]Iowa State University, [2]Iowa State University, [3]Iowa State University

Abstract: Malaria is an ancient disease caused by unicellular protists of the genus Plasmodia with P. falciparum responsible for most severe disease and deaths in humans. Plasmodium spp . contain a relict plastid called the apicoplast (AP) that is critical to parasite metabolism and is an important drug target. Like other endosymbiotic organelles, the apicoplast contains its own genome that must be replicated and repaired for parasite survival. Although the minimum required components of AP DNA replication machinery have been identified and individually characterized, AP DNA repair remains poorly understood and several expected repair pathway components have not been identified, likely due to the divergent nature of this early branching eukaryote. We have developed a targeted proximity-labeling approach that fuses a promiscuous biotin ligase to known AP DNA replication/repair enzymes such as AP DNA polymerase (apPOL) to identify repair-associated proteins. We utilized a CRISPR-Cpf1 gene editing strategy to generate a parasite line bearing a DiCre-recombinase inducible C-terminal TurboID fusion to the endogenous apPOL gene. To establish a labeling control, an AP-targeted version of TurboID was integrated into a benign locus of same cell line and conditionally expressed under the same promoter as apPOL. Results from gDNA PCR, Western blot, and indirect fluorescent assays demonstrate successful editing of each locus and inducible labeling of apicoplast. Preliminary results from proteomics suggest apPOL-TurboID successfully labels AP proteins in a targeted manner. Promising candidates from proteomics and efforts to identify unknown proteins through structural homology searches are discussed.

The Multisensory Coding of Flavor in Freely Moving Rats

Discipline: Life Sciences
Subdiscipline: Neurosciences

Thomas Gray*[1], Donald Katz [2], Jian-You Lin[3], Daniel Svedberg[4], Isaac Goldstein [5]
[1]Brandeis University, [2]Brandeis University, [3]Brandeis University, [4]Brandeis University, [5]Brandeis University

Abstract: Title: The Multisensory Coding of Flavor in Freely Moving Rats Smell and taste are highly interdependent, but how activity in olfactory and gustatory circuits impact one another in real-time remains unclear. Previous work has demonstrated that activity in the gustatory cortex (GC) can influence odor encoding in the piriform cortex (PC) and that GC is required for retronasal odor discrimination (the smell of food in the mouth, which generally accompanies eating). The aim of my study is to identify the temporal dynamics of information transmitted from GC to PC in a dynamic manner to mediate retronasal odor perception. By comparing the temporal response profiles of retronasal odor responses in the two areas, we can determine if there is a unique relationship between each area’s sensory responses in the context of retronasal olfaction. To look at these two regions simultaneously in freely behaving animals we have developed and successfully tested an easily produced 3D printed drivable electrode array that targets both PC and GC. In addition, we have developed a paradigm where we can disrupt activity in either of these areas with optogenetics and observe altered responses. These electrophysiological recordings and manipulations provide insights to the characteristics and relationships between GC and PC retronasal odor responses. We will further dissect these relationships by comparing different ways in which GC processing specifically influences odor discrimination in the piriform cortex.

The Role of Magi-1 Scaffold Protein in Joint Afferent Neurons and its Effect on Osteoarthritis Pain.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Raider Rodriguez*[1]and Arin Bhattacharjee [2]
[1]University at Buffalo, SUNY., [2]University at Buffalo, SUNY

Abstract: Persistent pain is the main clinical factor that leads to disability in osteoarthritis (OA) patients. Current clinical treatment for chronic OA pain includes Intraarticular injection of glucocorticoids, however, their long term use leads to loss of cartilage volume. Nonetheless, it remains clear that a local approach is far more desirable to manage joint pain due to less adverse effects, However, this requires the identification of specific targets at peripheral joint terminals. Our previous studies identified protein Magi-1 as an important scaffold for ion channels in nociceptive neurons. Our studies showed that Magi-1, through the regulation of Na V 1.8 channel membrane localization and protein stability, affected sensory neuronal excitability. Here we aimed to characterize Magi-1 expression in subchondral bone joint nociceptors, and its effect on OA-associated pain transduction. Our immunostaining analysis of subchondral bone have indicated that Magi-1 and Na V 1.8 channel are both expressed in joint nociceptor terminals. Such results have led us to elucidate the effects of joint nociceptor Magi-1 deficiency on noxious mechanosensation associated with OA. To do so, we have used a chemically-induced knee OA model in mice to replicate progressive joint degeneration and chronic pain. In these mice, in vivo sciatic nerve transfection was used to knockdown Magi-1 expression in joint afferents. Behavior assays were used to assess the effects of Magi-1 deficiency on OA pain development. Altogether, this study seeks to expand the current knowledge on the complex heterogenous mechanism of OA pain, and identify novel analgesic targets to treat OA.

From seed to seedling: following the distribution and fates of piñon seedlings (P.edulis)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Diana Macias*[1]and Will Pockman [2]
[1]University of New Mexico, [2]University of New Mexico

Abstract: The long-term stability and resilience of our forests depends on tree reproduction. Understanding and predicting demography is critical to determine whether reproduction can balance increasing mortality and facilitate range shifts to track suitable habitats. This is particularly challenging for plant species with highly variable reproduction, known as “mast seeding.” Using a 27-year reproduction dataset on P .edulis from the Sevilleta Long Term Ecological Research (LTER) and newly germinated seedlings data, we examined the plant seed to seedling transition. Specifically, we asked (1) Are seedling hotspots spatially distributed near super seed producers? (2) Which micro-conditions are important for seedling survivorship? Four-hundred seedlings were tagged, measured, and censused from September 2021 until present. We find that seedlings are spatially aggregated near super seed producers, but seedling survival is trait and micro-environment dependent. For example, seedlings in environments with greater litter cover and moderate canopy openness have a higher survival rate than seedlings with less litter cover and either extensive or minimal canopy openness Additionally, we find that seedlings that died had smaller heights and smaller diameters during the initial survey suggesting that these seedlings were showing early signs of stress. Plant reproduction is expected to become more variable and less predictable in a changing climate. For plant species that have episodic reproduction such as “mast seeders” this means even smaller seed crops spaced over multiple years. Tracking the fate of seedlings allows researchers to understand the benefits of masting on seedling recruitment and make predictions on the long-term stability of forests.

Metabolite Sensing by the BumSR Two-Component Signal Transduction System of Campylobacter jejuni

Discipline: Life Sciences
Subdiscipline: Microbiology

Nestor Ruiz*[1]and David Hendrixson [2]
[1]University of Texas Southwestern Medical Center, [2]University of Texas Southwestern Medical Center

Abstract: Campylobacter jejuni is a commensal bacterium of the lower intestinal tract of avian species and a leading cause of bacterial diarrheal disease in humans. Differences in colonization and virulence may be attributed to how C. jejuni senses and responds to the gut environment, however the mechanisms that drive these responses have not been well studied. We identified the BumSR two-component signal transduction system (TCS) as the first bacterial TCS to sense exogenous butyrate. After sensing butyrate, the TCS alters transcription of colonization and virulence factors essential for infection. Paradoxically, butyrate does not alter the in vitro phosphatase activity of BumS which we know is important for signal transduction. We then discovered that the branched short-chained fatty acids (BSCFAs) isobutyrate and isovalerate influenced transcription of the same virulence and colonization genes as butyrate. In vitro biochemical and biophysical assays provided evidence that BumS directly binds both isobutyrate and isovalerate leading to an inhibition of BumS phosphatase. These data suggest that isobutyrate and isovalerate are direct cues sensed by BumS while butyrate is an indirect cue. To understand the role of the response regulator, BumR, we used a combination of physiological and genetic manipulation techniques, which suggest that it is phosphorylated by endogenous high-energy phosphometabolites generated by one or more metabolic pathways to alter transcription of specific C. jejuni virulence and colonization genes. Further analysis of this unusual bacterial TCS should provide insight into how bacteria sense intestinal metabolites and mediate signal transduction for proper colonization and virulence responses.

Pitx2 Regulates Intestinal Stem Cell Differentiation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Brian Aguilera*[1]and Natasza Kurpios [2]
[1]Cornell University, [2]Cornell University

Abstract: The homeodomain transcription factor Pitx2 has been traditionally studied during embryogenesis where it establishes the left-right (LR) body plan and directs asymmetric morphogenesis of all visceral organs including the gut and its vasculature. Specifically in the intestine, Pitx2 has been shown to direct looping and patterning through its expression in the Dorsal Mesentery (DM), a mesodermal tissue that suspends the gut and is a reservoir for developing smooth muscle. Interestingly, Pitx2 expression is not limited to the DM during embryonic development – Pitx2 is also robustly expressed in the embryonic intestinal endoderm and Pitx2 epithelial lineage contribution is maintained throughout life suggesting continuous expression of Pitx2 in undifferentiated endodermal cells and mature intestinal stem cells. Intriguingly, I have recently discovered that Pitx2 loss in adult mice results in defects in the differentiation of intestinal stem cells with a dramatic increase in secretory tuft, Paneth and goblet cells and sex specific weight loss in females. Furthermore, Pitx2 has also been implicated in the regenerative process following injury and may play a similar role during regeneration of intestinal tissues in the context of disease. Based on these exciting preliminary findings, I will test the hypothesis that Pitx2 is necessary for the absorptive function, homeostasis, and regeneration of the postnatal intestinal epithelium. In summary, my research will uncover the novel role for Pitx2 in the postnatal intestinal epithelium and provide tools to address its function in the context of debilitating intestinal metabolic and inflammatory diseases.

Characterization of a filarial nematode muscarinic acetylcholine receptor as a putative antiparasitic target

Discipline: Life Sciences
Subdiscipline: Biology (general)

Kendra Gallo*[1], Nicolas J Wheeler[2], Kathy Vaccaro[3], Abdifatah M Elmi[4], Mostafa Zamanian[5]
[1]University of Wisconsin- Madison, [2]University of Wisconsin- Madison, [3]University of Wisconsin- Madison, [4]University of Wisconsin- Madison, [5]University of Wisconsin- Madison

Abstract: Neglected tropical diseases are infectious diseases of poverty endemic to underdeveloped and exploited countries that account for 26 million disability-adjusted life years with nearly half of these caused by parasitic worm (helminth) infections. Current control mechanisms for helminth infections rely upon mass drug administration with a limited arsenal of antiparasitic drugs (anthelmintics). Lymphatic filariasis (LF) is a debilitating disease caused by mosquito-transmitted filarial nematodes that infects over 50 million people. Anthelmintics used for LF treatment are suboptimal and the threat of anthelmintic resistance underscores a need for new treatments. G protein-coupled receptors (GPCRs) are established drug targets in human medicine but remain unexploited as potential anthelmintic targets. There are significant challenges in exploring the druggability and pharmacology of helminth GPCRs, including the genetic intractability of helminths and difficulties in establishing reliable heterologous expression of receptors in single-cell systems. We identified a muscarinic acetylcholine receptors (Bma-gar-3) from Brugia malayi, an etiologic agent of LF, and determined its spatiotemporal expression profile. We established new endpoints for GPCR expression in the model nematode Caenorhabditis elegans . We expressed Bma-gar-3 in three discrete C. elegans tissues and optimized plate-based and high-throughput assays that enabled receptor deorphanization and pharmacological profiling. We show Bma-gar-3 is responsive to acetylcholine and other classic muscarinic compounds including the selective agonist oxotremorine. Fundamental knowledge of novel helminth drug targets is crucial for the future control and elimination of LF and other neglected diseases. These approaches progress the characterization and screening of a lucrative class of proteins with anthelmintic target potential.

Characterizing T cell exhaustion profiles in ovarian cancer ascites

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Mayra Betancourt Ponce*[1], Manish Patankar[2], Lisa Barroilhet[3], Jenny Gumperz[4]
[1]University of Wisconsin, Madison, [2]University of Wisconsin, Madison, [3]University of Wisconsin, Madison, [4]University of Wisconsin, Madison

Abstract: Ovarian cancer is the deadliest gynecologic cancer in the United States with more than 22,000 patient deaths every year. Due to a lack of effective screening methods, most patients are diagnosed at late stages, limiting their treatment options and survival. In the past decades, immunotherapies have emerged and provided a new avenue of treatment for cancer patients. Unfortunately, these have not proven effective in ovarian cancer clinical trials. Given the chronic nature of this disease, we hypothesize that one of the factors that might be preventing immunotherapies from being successful in this context is the presence of hypo- or dysfunctional immune cells with low antitumorigenic activity in ovarian cancer microenvironments. We have previously shown that innate immune cells, particularly natural killer cells, have decreased function when exposed to ascites, or peritoneal fluid, of ovarian cancer patients. Ascites accumulation is thought to be linked to inflammatory responses, making it an ideal substrate for the study of ovarian cancer microenvironments. In this project, we characterized the phenotypic and functional states of adaptive immune cells, namely T cells, in human ascites. Through flow cytometry analyses, we identified inhibitory receptors linked to T cell exhaustion, including PD-1, LAG-3, TIM-3, TIGIT, and CTLA-4. The different T cell subsets were further studied via functional assays. These results can help inform strategies to overcome or circumvent T cell exhaustion to help promote T cell antitumorigenic effects and, thus, advance immunotherapy efforts.

Investigating the Impacts of Multiple Stressors on an Urban Aquatic Ecosystem

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Nicole Doran*[1]and Mark Scheuerell[2]
[1]University of Washington, [2]U.S. Geological Survey Washington Cooperative Fish and Wildlife Research Unit, University of Washington School of Aquatic and Fishery Sciences

Abstract: Urban freshwater ecosystems are impacted by multiple anthropogenic stressors resulting from climate change, urban development, and introduced species. In recent decades there has been increased interest in understanding how these stressors interact to affect important top-down and bottom-up processes. In some cases, quantitative approaches have been used to estimate the direction and magnitude of various effects, but these studies have multiple limitations that make them unsuitable for data-poor systems. We provide a framework for studying multiple interacting stressors in an understudied freshwater ecosystem, Lake Sammamish, located in western Washington, where a genetically distinct population of Kokanee salmon (Oncorhynchus nerka) has experienced drastic declines from numerous synergistic causes. These include loss of spawning and rearing habitat, increased temperature and decreased dissolved oxygen regimes owing to climate change, and introduced piscivorous fishes such as Smallmouth bass (Micropterus dolomieu) and Walleye (Sander vitreus). However, the degree to which each of these factors affects Kokanee and inhibits recovery is unknown. Here we describe a framework for combining multiple complementary approaches to address these shortcomings in our knowledge. In partnership with local citizens, tribes, non-governmental organizations, and government agencies, we are undertaking a set of observational and comparative studies, which include assessments of predator diets, stable isotope analyses of food web structure, and life cycle modeling. By leveraging the complementary strengths of different stakeholder groups, we can better tease apart the interactions among multiple stressors to understand their combined impact on the Lake Sammamish Kokanee population.

Role of Wnt in pHi Regulated Stem Cell Differentiation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Harnoor Virk*[1], Dr. Todd Nystul[2], Dr. Diane Barber[3]
[1]San Francisco State University, [2]University of California San Francisco, [3]University of California San Francisco

Abstract: Intracellular pH (pHi) is an emerging factor contributing to the regulation of cell fate decisions. Increased pHi is required for differentiation in both mouse embryonic stem cells (mESCs) and Drosophila follicle stem cells (FSCs) while its regulatory role remains unclear. However, studies in other cell types revealed how responses to changes in pHi are mediated by

pH-sensing proteins. Previously, we showed that increased pHi attenuates Wnt signaling by permitting the ubiquitin-mediated degradation of a key Wnt pathway effector, β-catenin. Our preliminary analysis suggests that β-catenin binding to another Wnt pathway effector, BCL9, is also pH-dependent. Dysregulated Wnt signaling impairs development and plays an important role in regulating mESC and FSC differentiation. Thus, we hypothesize that pHi dynamics regulate both mESC and FSC self-renewal by modulating Wnt signaling. To test this in mESCs, we are immunoprecipitating β-catenin and co-precipitating BCL9, which we predict will be more abundant at the lower pHi of naïve cells and less abundant at the higher pHi of differentiated cells. Additionally, we will test whether pH-dependent regulation of β-catenin binding to BCL9 promotes mESC self-renewal. In FSCs, we found that expression of a constitutively protonated β-catenin mutant disrupts differentiation and causes tissue dysplasia. We are now testing whether pHi dynamics regulate Wnt signaling and self-renewal in the FSCs. These studies will reveal the mechanisms for how underlying pH-sensing by β-catenin and BCL9 regulate Wnt pathway activity to promote stem cell differentiation, thus strengthening our understanding of pHi-dependent embryonic and adult stem cell fate decisions.

Plasma and Adipocyte-Conditioned Media from Obese Asthmatic and Non-Asthmatic Patients Undergoing Bariatric Surgery Induce Augmented Secretion of Inflammatory Cytokines by Human Bronchial Airway Epithelial Cells

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Paola Pena Garcia*[1], Matthew E. Poynter [2], Anne E. Dixon[3], Madeleine M. Mank[4], Olivia Johnson [5]
[1]University of Vermont, [2]University of Vermont, [3]Univeristy of Vermont, [4]University of Vermont, [5]University of Vermont

Abstract: Obesity is an increasingly prevalent healthcare crisis that affects the outcome of airway diseases, with obese asthmatics showing poor asthma control and increased airway reactivity despite treatment. The most effective means of improving symptoms in obese asthmatics is through weight loss, with a 5-10% loss in body mass necessary and sufficient to lead to clinically relevant improvements. The reduction in adipose tissue mass accompanying weight loss suggests that adipocytes may alternately function as pathogenic and protective participants in obese asthma. A previous study showed that adipocyte-derived products from obese mice augment pro-inflammatory responses of murine airway epithelial cells and that this effect is largely reversed by weight loss. Whether similar effects occur in humans remains largely unstudied. We hypothesize that elevated circulating adipocyte-derived factors in human obesity augment airway epithelial cell pro-inflammatory responses. We utilized samples collected from a 12-month longitudinal study of obese subjects undergoing bariatric surgery for weight loss who were non-asthmatic, allergic asthmatic, and non-allergic asthmatic. Human bronchial airway epithelial cells were exposed to either patient plasma or conditioned-media from cultured visceral adipose tissue with or without stimulation with agonists including house dust mite extract. Cell supernatants from plasma exposure showed augmented secretion of pro-inflammatory cytokines including IL-8 and CCL20 at baseline as compared to subsequent visits. Whereas exposure to adipocyte-conditioned media also augmented inflammatory responses, there were no differences between groups. These data show that bariatric surgery and subsequent weight loss beneficially change the circulating factors that augment airway epithelial cell pro-inflammatory responses.

Do invasive plants alter soil microbiome: The case of blackberry in Galapagos

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Lorena Benitez Rivera*[1], Pleuni Pennings [2], Jaime Chaves[3], Dario Xavier Ramirez[4], Camila Alejandra Contreras Guerrero [5]
[1]San Francisco State University (SFSU), [2]San Francisco State University, [3]San Francisco State University, [4]Universidad San Francisco de Quito, [5]Universidad San Francisco de Quito

Abstract: Title: Do invasive plants alter soil microbiome: The case of blackberry in Galapagos Non-native blackberry (Rubus niveus) is incredibly invasive to the Galapagos islands. It currently covers up to 85% of the agricultural lands and easily replaces native vegetation threatening endemic species such as the iconic Giant Diasies (Scalesia pedunculata). Blackberry has shown to be almost impossible to control and soil microbiome analysis can facilitate the understanding of the effect this invasive has on the ecosystem, by comparing the soil microbiota between sites with native, invasive, and non-invasive plants. In this project, 76 local Galapagos residents have become fundamental in the collection of soil samples. DNA was extracted from soil, sequenced on nanopore Minion sequencer using 16S ribosomal RNA (rRNA), and analyzed with the programming language R. Soil samples were collected from three main Galapagos islands: San Cristobal, Santa Cruz and Isabela, and at both sea level and highlands, to control for island and climatic factors. Our null expectation is to find similar soil microbiome composition and abundance from samples corresponding to native, invasive, and non-invasive plant ecosystems across the three islands. Identifying soil microbiome associations with R. niveus will provide insights on whether or not this invasive plant alters soil bacteria composition, and thus above ground biodiversity. In the future, we could contribute to the R. niveus control efforts by restoring blackberry-free soil for native species to thrive.

The role of Tubulin β-III in neural crest cell formation and migration

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Camilo Echeverria*[1]and Dr. Crystal Rogers [2]
[1]University of California, Davis, [2]University of California, Davis

Abstract: Neural crest (NC) cells are an embryonic stem cell population that creates craniofacial bone and cartilage, peripheral and enteric neurons, and various other adult cell types. These cells undergo an epithelial-to-mesenchymal transition (EMT) and migrate through the embryo to their final differentiation sites. EMT is the process in which cells transition from tightly packed epithelial cells to mesenchymal cells that lose their apical-basal polarity and alter cell-cell adhesion molecules. Abnormal NC migration is associated with disorders such as cleft palate and heart defects, which can have devastating lifelong, social, and health consequences. Although many studies focus on the role of transcription factors in this process, transcriptional control of cell adhesion is a slow process during such dynamic cell transitions. Therefore, cells also use methods like intracellular protein trafficking to transport epithelial and migratory cell adhesion molecules to and from the membrane during EMT. β-III tubulin (TUBB3) is a microtubule subunit primarily expressed in neurons, but it is also expressed in premigratory NC cells. I hypothesize that TUBB3-dependent microtubule-mediated trafficking regulates rapid changes in cadherin protein localization and cytoskeletal rearrangements, driving NC EMT. Loss of function experiments have identified that in the absence of TUBB3, NC cells migrate prematurely and maintain cell-cell adhesions similar to epithelial premigratory NC cells. Future

work will identify the mechanisms downstream of TUBB3 that directly regulate cadherin localization during NC EMT. When completed, our work will define a mechanistic framework linking cytoskeletal elements to changes in cell-cell adhesion, NC EMT, and formation of cranial NC derivatives.

Changes in phylogenetic diversity of rainforest moth communities following hurricane disturbance

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Aura Alonso-Rodriguez*[1], Pablo E. Gutiérrez-Fonseca[2], Catherine M. Hulshof[3], Scott E. Miller[4], Taylor H. Ricketts[5]
[1]University of Vermont, Burlington., [2]University of Vermont, [3]Virginia Commonwealth University, [4]Smithsonian Institution, [5]University of Vermont

Abstract: Climate-driven disturbances are expected to increase in frequency and severity under global change, yet knowledge is limited on the potential response and stability of biological communities amid these rapidly changing conditions. Extreme climatic events such as hurricanes may result in communities with increased phylogenetic relatedness (i.e., decreased phylogenetic diversity), as closely related species may possess similar traits that influence their sensitivities and resilience to disturbance. However, most studies have traditionally focused on measuring taxonomic diversity metrics, ignoring other dimensions of community structure. In this study, we assessed the impacts of category 4 Hurricanes Irma and María on the phylogenetic diversity (PD) of moth communities at the Luquillo Mountains in Puerto Rico. Moths were sampled monthly in Tabonuco and Sierra Palm forests in the 5 months before and 6 months after the passage of the hurricanes in September 2017. We conducted DNA barcoding on a subsample of the collection to construct a maximum likelihood phylogenetic tree. We then extracted the tree terminal branch lengths to quantify various PD metrics, such as Faith’s PD and the net relatedness index. We found decreased moth PD after hurricane disturbance, mainly driven by the loss of larger-sized species. This decrease was consistent in both forest types, but more pronounced in Palm forests. Thus, old-growth Tabonuco forests may be vital for conserving phylogenetic biodiversity in an otherwise decimated forest. Our findings highlight how hurricanes and ensuing forest regeneration dynamics can have cascading effects on lower trophic levels such as insect communities, which are already declining worldwide.

Dissecting the Function of the Microtubule-Associated Protein, Doublecortin

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Regina Agulto*[1]and Kassandra Ori-McKenney[2]
[1]University of California, Davis, [2]University of California, Davis

Abstract: Microtubule-associated proteins (MAPs) regulate microtubule dynamics, bundling, and motor transport for specific cellular processes important for cellular function and health. Mutations in the MAP Doublecortin (DCX) lead to defects in neuronal migration causing the neurodevelopmental diseases subcortical laminar heterotopia (SCLH), in females, and lissencephaly in males. Despite this understanding, the actual function of DCX and how disease mutations alter its function during neuronal migration are open areas of investigation. DCX, and other proteins in its superfamily, contain conserved tandem microtubule-binding domains connected by a linker region. We recently published a study on Doublecortin-like kinase 1, one of the members of the DCX superfamily where we investigated how this DCX superfamily member self-controls its function by regulating its microtubule-binding affinity via autophosphorylation of these tandem microtubule-binding domains. These observations led to new hypotheses about the roles of the highly conserved tandem domains and linker sequence in the function of DCX and other proteins in the superfamily. I have since cloned and purified twelve different DCX constructs to study the complicated cooperative binding behavior of this protein and identified the linker region as being especially important for DCX cooperativity using in vitro single molecule assays. I am currently working on how decreased cooperativity affects DCX function and alters its interactions with other proteins relevant to microtubule dynamics. Overall, this project will provide significant insight into how DCX behaves on the microtubule to regulate diverse microtubule processes within the cell and how its function becomes altered in disease.

Identifying the role of COX2 signaling in neurulation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Tess Leathers*[1], Crystal Rogers [2], Crystal Rogers[3]
[1]University of California, Davis, [2]University of California, Davis, [3]University of California, Davis

Abstract: During neurulation, the ectoderm-derived neural plate undergoes cytoskeletal rearrangements and folds until its borders meet and fuse at the dorsal side of the embryo, forming the neural tube. Differential gene expression in the ventral and dorsal neural tube then patterns these tissues into separate lineages, the central nervous system (CNS) and neural crest (NC) cells. Though neural tube defects are the second most common congenital malformations in humans, the molecular mechanisms regulating neural tube closure and patterning are poorly understood. Additionally, dietary and environmental perturbations increase the risk of neural tube closure defects. Use of non-steroidal anti-inflammatory drugs (NSAIDs) during embryonic development is linked to a greater risk of neural tube defects, but the mechanistic reasons are unclear. NSAIDs inhibit cyclooxygenase (COX) enzymes, which synthesize the hormone-like lipid, prostaglandin E2 (PGE2). To uncover the mechanistic pathway by which COX signaling inhibition leads to neural tube defects, we have characterized the expression of Cox genes and the genes encoding tissue-specific PGE2 receptors, Ep3 and Ep4 , during neurulation. Cox1 expression is ubiquitous in early embryos, but Cox2 is expressed in the anterior and trunk ectoderm. Ep3 is localized to the developing neural tube, while Ep4 is expressed in developing intermediate mesoderm. Knockdown of COX2 and EP3 signaling impedes neural tube patterning and closure, expanding the NC population at the expense of CNS progenitors. Our work has identified a previously uncharacterized role of an enzymatic and lipid-based pathway in neurulation: COX2 signaling via EP3 is necessary for neural tube closure and patterning.

Examining Mitochondrial and Innate Immune Function in Drosophila

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Angshita Dutta*[1]and Adrienne Wang [2]
[1]Western Washington University, [2]Western Washington University

Abstract: Mitochondrial dysregulation has long been implicated in the process of aging. More recently, findings point to innate immune-mediated inflammation as a critical regulator of age and age related diseases such as Alzheimer’s disease (AD). Depletion of mitochondrial DNA (mtDNA) has been observed with age and neurodegeneration. Though severe mtDNA depletion is lethal, studies suggest that moderate mtDNA depletion can induce mitochondrial stress responses that act as a signaling hub for innate immune activation. Understanding the effects of mtDNA depletion on mitochondrial function and innate immune signaling, will further our understanding of age driven changes that remain conserved across organisms. To understand the effects of mtDNA depletion on mitochondrial function and innate immune signaling, we will use a Drosophila melanogaster model of mtDNA depletion. This model fly expresses a nuclease, UL12.5, that depletes mtDNA. Prior data from our laboratory demonstrates these flies have higher levels of immune signaling than control flies. We will conduct a bacterial challenge and subsequent lifespan analysis assay to determine differences in lifespan between the UL12.5 fly model and controls. Additionally, imaging analysis should demonstrate differences in mitochondrial morphology that occur when mtDNA is depleted. Our goal is to explore the connection between mitochondrial dysfunction and innate immune activation to better understand the effects of mitochondrial stress on aging.

Targeting breast cancer stem cells with oncolytic virus

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Natasha Roman*[1], Pranav Danthi [2], Julie Ostrander[3]
[1]University of Minnesota Twin Cities, [2]Indiana University, [3]University of Minnesota Twin Cities

Abstract: Breast cancer is the second leading cause of cancer deaths among women in the United States. Estrogen receptor positive [ER+] breast cancer has a more favorable prognosis, however patients can experience recurrence for many years after initial diagnosis. Breast cancer stem cells (BCSC), which are dormant and exist as a minority sub-population (0-5%), drive recurrence, metastasis and resistance to therapies that primarily target rapidly proliferating tumor cells. Current treatments are insufficient to cure metastatic ER+ breast cancer and there are no specific therapeutics that target BCSC. Mammalian orthoreovirus (MRV) is a virotherapeutic tested in clinical trials for many cancer types including metastatic breast cancer. MRV was found to be safe, but efficacy limited as a monotherapy. In our studies we compared several laboratory MRV strains to the strain used clinically (T3D). Our studies suggest that T3D is less effective in killing ER+ breast cancer cells and BCSCs. We propose to generate a novel MRV strain with enhanced BCSC-targeting capacity using forward genetic approaches by serially passaging MRV strains in BCSC enriched 3D tumorsphere cultures of MCF-7 paclitaxel resistant (TaxR) cells to generate a selective oncolytic virus. Preliminary data has shown that serially passaged (SP) MRV strains are more effective in decreasing cell viability and inhibiting tumorsphere formation compared to the parental strains and T3D. We anticipate these studies will lead to an improved MRV virotherapeutic that will be combined with clinically relevant inhibitors to prevent and treat therapy-resistant ER+ breast cancer.

CRISPR-mediated gene silencing with MBD proteins

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Maria Torres-Colon*[1]and James K. Nuñez [2]
[1]University of California, Berkeley, [2]University of California, Berkeley

Abstract: Current epigenetic editing tools are based on the use of catalytically dead CRISPR–Cas9 (dCas9) fused to different chromatin-modifying proteins for either silencing or activating genes.

Epigenetic-mediated gene silencing entails DNA or histone modifications that lead to condensed chromatin states. Three main proteins mediate this process: writers, readers and erasers. Methyl-CpG-binding-domain (MBD) proteins function as readers by binding to methylated DNA (DNAme) and recruiting transcriptional repressors through their transcriptional repressor domain (TRD). Current epigenetic editing technologies are limited by their large size, which limit their delivery into mammalian cells. For this reason, we aim to generate new smaller epigenetic editors based on MBD domains fused to dCas9. We generated four different MBD designs and tested their efficiency in gene silencing in mammalian cells. Flow cytometry results after 5 days of transfection show that one of the MBD constructs effectively silenced the target gene with 32.5% of median fluorescence when compared to cells transfected with dCas9 only (1.4% median fluorescence). These results show that CRISPR-MBD constructs can be used for transcriptional tuning as gene silencing is effectively induced for a specific period of time. After 9 days of transfection, the gene expression reverts back to its unperturbed levels, suggesting that the MBD proteins do not program epigenetic memory of silencing. In conclusion, our data highlight the a new CRISPR approach for transcriptional repression based on the MBD proteins and their potential for use in basic research and therapeutic applications.

Determining the Antimicrobial Susceptibility and the Presence of Antibiotic-Resistant Genes in Staphylococcus Aureus Isolated from Bovines with Mastitis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Yarilys Bonilla*[1], Gladys M. Varela Agront[2], Dahiana Blas Cortes[3]
[1]Interamerican University of Puerto Rico, Aguadilla, [2]Interamerican University of Puerto Rico, Aguadilla, [3]Interamerican University of Puerto Rico, Aguadilla

Abstract: Antibiotic resistance in bovine mastitis is one of the main problems affecting the dairy industry in PR where, despite antibiotic treatment, mastitis may become a recurrent disease in the same bovine. Staphylococcus aureus , a common pathogen associated with mastitis, has the ability to acquire genes that increase its pathogenicity and provide survival mechanisms to resist antibiotic treatment, thus being a potential culprit for recurrent mastitis cases. To improve the therapeutic approaches used in dairy farms, we seek to understand how the genetic composition of Staphylococcus aureus influences its phenotypic resistance mechanisms in bovine mastitis. First, we determined the antimicrobial susceptibility of Staphylococcus against three beta-lactam antibiotics commonly used by dairy farmers to treat mastitis: Go-Dry (penicillin G), ToDay (cephapirin sodium), and Spectramast (ceftiofur hydrochloride). From 36 collected mastitis milk samples from dairy farms in Hatillo, Puerto Rico, 9 where positive for S.aureus as detected by Mannitol Salt Agar, Gram Staining, and catalase test. Kirby-Bower tests were performed to determine antibiotic resistance in those samples. Based on inhibition zone diameter, all of the samples exhibited resistance to ToDay while 55% exhibited resistance to Go-Dry. Our data shows that S.aureus is resisting these common mastitis treatments which may lead to further mastitis infections in these bovines and the subsequent loss of milk production by dairy farmers. As our sample size increases and we detect the presence of beta-lactam resistant genes in S.aureus , we intend to share this information with dairy farmers so that they may optimize their treatment options.

EXPRESSION OF THE PALMOPLANTAR SKIN-SPECIFIC KERATIN K9 DURING POSTNATAL DEVELOPMENT

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sarah Steiner*[1]and Pierre A. Coulombe [2]
[1]University of Michigan Medical School, Ann Arbor, [2]University of Michigan Medical School, Ann Arbor

Abstract: Skin epithelia provides a multimodal barrier that protects us against the external world, essential for water retention, mechanical protection, and immune surveillance. Skin on the ventral aspect of the feet and hands, known as palmoplantar skin, bears higher mechanical stress in daily life; however, the cellular and molecular components that mediate mechanical resilience in palmoplantar skin are only partially understood. The epidermis of palmoplantar skin maintains a complex architecture and an intricate pattern of keratin expression. Importantly, the type I keratin 9 (KRT9 /K9) is specifically and robustly expressed in differentiating keratinocytes of the epidermis in human and mouse palmoplantar skin. In this study, we aim to define the regulation of Krt9 /K9 expression in developing palmoplantar skin; we hypothesize that Krt9 /K9 expression is regulated in response to postnatal mechanical stress. We collected paw-pad skin from WT and Krt9 -/- mice at multiple stages of pre- and perinatal development, as well as from 3.5- and 6-week-old mice, to quantitatively examine the pattern of Krt9 /K9 expression at the mRNA transcript (RT-qPCR, RNAScope) and protein levels (indirect immunofluorescence (IF), western blotting). Krt9 transcript levels are low in E18.5 skin, and K9 is undetectable at the protein level via IF on days E18.5 to P1. However, robust K9 expression is noted by IF and western blot at 3.5 weeks of age, and Krt9 -/- mice display tissue fragility at 10 days of age. We conclude, based on preliminary findings, that Krt9 /K9 is regulated by mechanical stress in perinatal life.

Does soil stoichiometry affect leaf litter amphibian and reptile abundance, biomass, and community structure in tropical wet forests?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alondra Medina Charriez*[1]and Kelsey E. Reider [2]
[1]James Madison University, [2]James Madison University

Abstract: Understanding the mechanisms behind species patterns of diversity and abundance is one of the major goals of ecology. Studies have shown that biogeochemical gradients driven by soil stoichiometry can shape community structure of tropical leaf litter invertebrates. However, few studies have addressed whether organisms in higher trophic levels are also influenced by soil nutrients. Research on tropical secondary consumers, such as the mega-diverse leaf litter herpetofauna, has primarily focused on describing broadscale patterns of species distribution and abundance, rather than testing specific mechanisms driving the observed patterns. In this study, I will determine if limiting soil nutrients and leaf litter habitat structure affect herpetofauna abundance, biomass, and community structure in lowland tropical wet forests of Costa Rica. I will conduct standardized leaf litter surveys in alluvial and residual soils to measure amphibian and reptile abundance, biomass, and community assemblage. I will collect soil samples from each plot and will measure soil total phosphorus, nitrogen, carbon, magnesium, calcium, and potassium. Because invertebrate prey abundance is positively associated with higher levels of limiting nutrients, I expect that soils with higher nutrient concentrations should

support a greater abundance of amphibian and reptile consumers. My study will be the first to examine the role of soil nutrient stoichiometry as a mechanism driving patterns of leaf litter amphibian and reptile abundance and community composition and will provide much needed insight into how bottom-up resource limitation affects the diversity of herpetofauna, a vulnerable yet ecologically important taxonomic group, in the lowland tropics.

Structural-functional study of HAP40 and its role in Huntingtin regulation

Discipline: Life Sciences
Subdiscipline: Neurosciences

Amanda Solbach*[1]and Sheng Zhang [2]
[1]The University of Texas MD Anderson Cancer Center UTHealth Graduate School of Biomedical Sciences, Houston, TX, [2], MD Anderson Cancer Center & UTHealth Graduate School of Biomedical Sciences (GSBS), Institute of Molecular Medicine (IMM)(

Abstract: Huntington's disease (HD) is a fatal neurodegenerative disease caused by the disturbance of HD gene Huntingtin (HTT)'s normal functions and a gained toxicity from expanded polyglutamine tract in mutated HTT protein. In Drosophila , our lab has isolated a novel protein as one of the strongest binding partners of HTT and further demonstrated that it is the fly ortholog of Htt-associated protein 40 (HAP40), a known HTT interacting protein. We also demonstrated that HAP40 is a highly conserved and strong modulator of HTT, affecting its protein stability, normal physiological functions and the toxicity of mutant HTT in Drosophila HD models. Despite the significant sequence divergence between fly and human HAP40 proteins, HAP40 is functionally conserved from Drosophila to humans, we therefore hypothesize that HAP40 sequences that are highly conserved between these two evolutionarily distant species are most important for HAP40's normal functions. We further hypothesize that while the majority of the conserved HAP40 sequences are involved in its direct physical interaction with HTT; those not involved in direct binding are the ones likely playing a regulatory role on HAP40 and its functional interaction with HTT. Using established model systems, I am testing this hypothesis by engineering transgenic Drosophila and mammalian cell lines expressing a serial of HAP40 deletions to examine their effect on protein stability, subcellular dynamics, their association with HTT and on HTT's cellular activities, and lastly on HD pathogenesis. I expect to identify and elucidate the regulatory mechanism governing HAP40's activity and its functional association with HTT.

How Many Bacterial Samples Do We Need to Make a Good Predictive Machine Learning Model?

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Meris Johnson-Hagler*[1], Jameel Ali [2], Faye Orcales[3], John Matt Suntay[4], Kristiene Recto [5], Lucy Mocteczuma[6], Fayeeza Shaikh[7], Pleuni Pennings[8]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University, [4]San Francisco State University, [5]San Francisco State University, [6]San Francisco State University, [7]San Francisco State University, [8]San Francisco State University

Abstract: Antibiotic resistance has become a worldwide threat. People who are suffering from bacterial infections are being prescribed antibiotics that are less effective due to evolving bacterial strains. Currently, traditional assays are being used that don't provide quick treatment for patients. Machine learning algorithms have been proposed as a method because of its ability to predict antibiotic resistance in a quick and efficient manner. However, it is not known how many samples are needed to create highly accurate predictions. In this project, we aim to see if different sample sizes will affect predictive accuracy in machine learning models. The algorithms will process publicly available whole genome sequences of E.coli strains. Each model will be tested with varying sample sizes. All models will be compared to see which one retains the highest predictive accuracy overall with each change in sample size. We expect to find that larger population sizes will have the best performance. We aim to use what has been found in this study to create a diagnostic tool to determine antibiotic resistance.

Intertidal Canopy Formers: How Much Cover is Enough?

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Angelina Zuelow*[1]and Sarah Henkel [2]
[1]Oregon State University, [2]Oregon State University

Abstract: Canopy-forming seaweeds provide shade for smaller algae and invertebrates in intertidal communities, ameliorating low tide stressors such as ultraviolet radiation, desiccation, and temperature variability. Conversely, canopies can negatively affect understory organisms by limiting settlement, causing physical disruption, and trapping sand. At SACNAS 2020, I presented the results of manipulative experiments conducted in southern California and northern Washington demonstrating that the canopy-forming kelp species, Egregia menziesii , did not always act as a foundation species when its cover was low (<30%). I aim to identify the amount of canopy cover that correlates with a statistically significant community difference for each understory associated with two common Oregon intertidal canopy species (Egregia menziesii and Hedophyllum sessile). I hypothesize canopy formers will only have a significant impact on the understory community when they are extremely abundant (>70% cover). In January 2022, at three northern Oregon field sites (Boiler Bay, Yaquina Head, and Seal Rock), I set up observational plots at five levels of naturally occurring canopy cover (0%, 10-30%, 40-60%, 70-90%, 100%) with four replicates at each site. I have conducted community surveys of algae and sessile and mobile invertebrate cover for one season (Winter 2022) and will conduct surveys for three additional seasons this year (Spring, Summer and Fall). The community data will be transformed as necessary and multivariate analyses will be conducted with JMP 16 and Primer 7. I expect differences in understory communities at different levels of canopy cover for each species (Egregia and Hedophyllum).

Investigating The Role of Resident Microbes in Pancreatic Disease

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Diane Hernandez*[1], Charles Murtaugh [2], June Round[3], Jennifer Hill[4]
[1]University of Utah, [2]University of Utah, [3]University of Utah, [4]University of Utah

Abstract: The gut microbiota affects many aspects of host-physiology involved in the prevention and promotion of cancers. However, little is known about how the microbiome affects pancreatic cancer (PC) initiation, particularly its role in PC-promoting inflammation. This is particularly relevant as the pancreas is intimately connected to the intestinal tract and in contact with the gut microbiome. Pancreatitis, inflammation of the pancreas, represents a significant risk factor for PC. Mouse models have shown that inflammation greatly exacerbates cancer initiation and

progression. Our preliminary data suggests bacteria are required to promote these disease processes in mice. Therefore, we sought to ask are bacteria required for the inflammatory and recovery processes during pancreatic injury. Using an inducible drug model of acute and chronic pancreatitis, we have found that ablation of the microbiome with antibiotics significantly ameliorates acute injury in the pancreas and delays the regeneration process in the chronic model. To further understand how bacteria exacerbate pancreatic injury, we have utilized an ex-vivo model of acinar cells, the primary cell type in the pancreas, to evaluate gene expression changes in the presence of pattern-recognition receptor (PRR) agonists. PRRs elicit inflammatory signals in response to a wide range of microbial products. We have found that acinar cells variably express pro-inflammatory cytokines and antimicrobial peptides (AMP) in response to these agonists. These studies aim to understand the mechanism underlying microbe-driven inflammation in the pancreas and provide a new avenue for early detection methods and treatments for these painful and untreatable conditions.

Insight on the evolution of pallial and vocal learning circuits from spatial and cellular transcriptomic mapping of the songbird brain

Discipline: Life Sciences

Subdiscipline: Neurosciences

Carlos Orozco*[1], Devin P. Merullo [2], Genevieve Konopka[3], Todd F. Roberts[4]

[1]University of Texas Southwestern Medical Center, [2]University of Texas Southwestern Medical Center, [3]University of Texas Southwestern Medical Center, [4]University of Texas Southwestern Medical Center

Abstract: The brain of songbirds contains well-characterized, specialized regions for learning and producing complex vocalizations. Single-nucleus RNA-sequencing (snRNA-seq) has recently been used to map the cell-types from three of these regions residing in the dorsal ventricular ridge (DVR) or striatum. To build a wider understanding of the organizational principles of the songbird forebrain and evolution of song circuits, we conducted large-scale mapping of the male zebra finch brain using snRNA-seq and spatially resolved transcriptomics. We first tested if the cell-types of the DVR are conserved in other pallial areas by mapping the cell-types in another major region of the avian forebrain, the hyperpallium, which is thought to share a developmental origin with the mammalian neocortex. We next used spatial transcriptomics on whole sagittal tissue slices. We mapped differential gene expression patterns in the brain to build a high-resolution spatial transcriptomic atlas of the zebra finch brain. Preliminary analysis reveals that spatial transcriptomic profiles clearly define anatomically recognized sub-regions of the avian pallium and subpallium including some song nuclei. Lastly, because differences in cell-type composition and function likely underlie transitions through developmental sensitive periods for song learning, we have also begun to analyze the development of song circuitry using similar methods. Our analysis shows that cellular transcriptomics provides a sensitive read-out of neuronal maturation and how experience influences circuit development. By integrating spatial and cellular transcriptional data, we aim to build a framework for understanding the cell-type composition of vertebrate brain regions involved in orchestrating complex suites of behavior, like vocal learning.

Characterization of the P450 17A1-V366M mutation to probe for the biochemistry of the 17,20 lyase reaction

Discipline: Life Sciences
Subdiscipline: Pharmacology

Neikelyn Burgos-Tirado*[1]and Richard Auchus [2]
[1]The University of Michigan, [2]University of Michigan

Abstract: Steroidogenesis is the process by which cholesterol is metabolized via different enzymes into biologically active steroid hormones. Steroidogenic enzyme cytochrome P450 17A1 is essential for all androgen biosynthesis in the adrenal glands and the gonads. P450 17A1 catalyzes the 17-hydroxylase reaction, which is required for cortisol synthesis, and the 17,20-lyase reaction, which is a crucial step for androgen precursor synthesis. The 17,20-lyase activity requires the cofactor cytochrome b5 to enhance the reaction. P450 17A1 is the target of abiraterone acetate, an approved treatment for advanced prostate cancer. However, a major disadvantage of abiraterone acetate is that the drug inhibits both activities of P450 17A1, and 17-hydroxylase inhibition shifts steroid production from cortisol to mineralocorticoids. A previous study identified a patient with the P450 17A1 mutation V366M which is selectively deficient for the 17,20 lyase activity. We hypothesize that by studying the biochemical mechanisms of this mutation in in vitro systems it might provide information to guide the development of selective inhibitors of the 17,20-lyase activity. An initial screening assay was done with HEK-293T cells followed by expression in E. coli. purification, and reconstitution for activity assays. The V366M variant demonstrated a significant loss of the 17,20-lyase activity in transfected HEK-293T cells, 3% product formation, and preserved 17-hydroxylase activity. Yet, the reconstituted mutation V366M exhibited similar 17,20-lyase activity as wild-type P450 17A1. Our study highlights the importance of comprehensive assessment of P450 mutations in several relevant assay systems.

Identification of Influential Features Analyzed by Machine Learning Models to Predict Antibiotic Resistance in E. Coli

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jameel Ali*[1], Meris Johnson-Hagler, B.S. [2], Faye Oracles, B.S.[3], John Matt Suntay[4], Kristiene Recto [5], Lucy Monteczuma, B.S.[6], Fayeeza Sheikh[7], Pleuni Pennings, Ph.D.[8]
[1]San Francisco State University, [2]San Francisco State University, [3]San Francisco State University, [4]San Francisco State University, [5]San Francisco State University, [6]San Francisco State University, [7]San Francisco State University, [8]San Francisco State University

Abstract: Clinics have cataloged a rise in antibiotic drug resistance in bacteria resulting in a global public health concern. Researchers have found the key to controlling the spread of resistant strains of bacteria is accurate and efficient detection. However, the current method to establish drug resistance profiles are time-consuming culture-based assays based on known local bacterial populations. In order to address the need for a better detection method, machine learning models have been applied as an alternative. The models require predictive factors, such as genomic data, in order to perform their analyses. However, it is not understood what predictive factors hold the most influence in identifying drug resistance strains. By understanding which factors are most influential, we can optimize models to identify drug resistant strains with greater accuracy. Our goal is to rank the most influential factors used by the machine learning models to identify drug resistant strains. Using a publically available E. Coli WGS dataset, we will extract factors that will be used to train and test the models. We will then compare the predictive performances of the models to determine the best performing model. From the best performing model, we will rank the factors based on their predictive influence in the analysis. We expect to find well-characterized and less characterized genes that are associated with drug resistance will hold the most influence. We aim to use this study to add to the growing body of research where machine learning is used to improve patient outcomes.

Ecology of invasion: Potential for parasite spillover in Abert's squirrels (Sciurus aberti) and endangered Mt. Graham red squirrels (Tamiasciurus fremonti grahamensis)

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Deandra Jones*[1]and John L. Koprowski [2]
[1]University of Arizona, [2]University of Wyoming

Abstract: Invasive species are among the leading global threats to native wildlife and are a factor in the decline of 42% of threatened and endangered species. Invasive species can influence ecosystem health through parasite loads that they introduce during establishment in new areas. In the 1940s, Abert's squirrels (Sciurus aberti) were introduced to the Pinaleño Mountains in southeastern Arizona where they now co-occur with endemic endangered Mount Graham red squirrels (Tamiasciurus fremonti grahamensis) . Parasite loads between invaders and imperiled endemic species are poorly understood, including S. aberti and T. f. grahamensis; we identified and quantified parasites in this important system. We hypothesized that spillover of parasites occurred between S. aberti to T. f. grahamensis . We also hypothesized that presence/absence of parasites might be affected by host-linked factors and extrinsic factors. Genetic analyses through PCR amplification revealed two species of helminths from single nematode DNA: Citellinema sp. and Trypanoxyuris (Rodentoxyuris) sp. Our results demonstrated the potential for spillover of Trypanoxyuris (Rodentoxyuris) sp. between S. aberti and T. f. grahamensis . Body mass influenced presence/absence of endoparasites and males are more likely to have presence of ectoparasites than females in Abert's squirrels. Two species of fleas and one species of louse were found on Abert's squirrels . One species of flea and one species of mite from the Glycyphagidae family were found on Mt. Graham red squirrel. Our data highlighted the importance of developing future management and conservation strategies for similarly threatened or endangered species.

Comparing the effects of antibiotics and alternatives used in the dairy cattle industry and their affects on the soil microbial community

Discipline: Life Sciences
Subdiscipline: Environmental Science

Kameron Richardson*[1], Michael Strickland [2], Amanda Bauer[3]
[1]University of Idaho, [2]University of Idaho, [3]University of Idaho

Abstract: Antibiotics are commonly used in the dairy industry to prevent and treat disease in cattle. Previous research has shown that manure from treated cattle, when applied as an organic fertilizer, influences the soil microbial community and carbon cycling. Increased use of antibiotics has also led to a rise in antibiotic resistance bacteria, so there is a need for alternatives to antibiotics. One alternative that has recently been created is a product called AHV. AHV's mode of action is to inhibit quorum sensing, the ability of bacterial cells to communicate with one another, and treat dairy cattle with udder mastitis. The effects of AHV on the soil microbial community, however, has not been tested. In this experiment, we compared the use of two antibiotics that are commonly used to treat udder mastitis, clindamycin and cephalexin, and the product AHV. Two field sites located in North Carolina and Washington were chosen for this experiment. Weekly additions of the two antibiotics and AHV were made at both sites for 12 weeks and soil respiration measurements were taken weekly. After 12 weeks, samples were harvested for pH, carbon mineralization, substrate induced respiration, microbial biomass, and DNA extraction for microbial community analysis. Results will be compared between treatments at each site and between the two sites to compare the effect of the AHV product on the soil microbial community.

No Ka Lāhui: Using IUCN Data to Inform Recovering Imperiled Species of Hawai‘i, for Hawai‘i

Discipline: Life Sciences
Subdiscipline: Environmental Science

Brissa Christophersen*
University of Hawai‘i at Mānoa

Abstract: Extinction rates have been increasing over the past century and this trend is likely to continue with the growing prevalence of threats such as climate change and invasive species. Hawai‘i is nicknamed the “extinction capital of the world”, with 586 species listed as either threatened or endangered according to state and international listings (IUCN Red List). Collaborative efforts that integrate multiple knowledge systems, communities and approaches are critical, yet conservation efforts are often siloed among taxonomic groups, ecosystems, and land owners (e.g., state, federal, private, non-profit), limiting potential for collaboration and increased efficiency in resource allocation when addressing threats that impact multiple taxonomic groups or adjacent ecosystems. My overarching objective is to identify potential synergies and collaborative solutions for proactive conservation management across taxonomic groups and conservation communities in Hawai‘i. To achieve this, I will utilize the IUCN Red List data regarding at-risk species in the Hawaiian Islands to: (1) evaluate threats and potential solutions across taxonomic groups; (2) discern whether recovery actions to address the threat of climate change are explicitly addressed in Red List data; (3) explore the incorporation of Indigenous knowledge and values in the IUCN Red List data. Expected outcomes will allow for resource managers to have a better understanding of how to allocate limited resources to achieve ‘āina momona (thriving and abundant landscapes and communities) .

Behavioral changes and tau pathology in response to Traumatic Brain Injury

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kailea Wiese*[1], Roilea Maxson[2], Christine Smoyer[3], Kassandra Ori-Mckenney[4]
[1]University of California, Davis, [2]University of California, Davis, [3]University of Kansas Medical Center, [4]University of California, Davis

Abstract: Traumatic brain injury (TBI) is a disruption of normal brain function that results from mild to severe impacts to the head, and can affect memory, as well as behaviors such as anxiety, aggression, and depression. TBI is the leading risk factor for late onset neurodegenerative diseases such as Alzheimer’s Disease. Both TBI and Alzheimer’s Disease are associated with the presence of hyperphosphorylated tau in the brain and cerebrospinal fluid. In a healthy brain, tau is a microtubule associated protein that controls microtubule based processes. Upon

hyperphosphorylation, tau forms aggregates called neurofibrillary tangles (NFTs)— thought to contribute to neurodegeneration. Events that cause tau hyperphosphorylation and NFT formation post-injury, and how these contribute to neurodegeneration are not well established. We utilize a high impact method to subject flies expressing 2N4R human tau pan-neuronally to TBI to study the contribution of tau phosphorylation and oligomerization to neurodegeneration and behavioral decline. In the 24 hours after inflicting TBI on 1 week old virgin males, pan-neuronal expression of tau increased inter-male aggression. We have screened a variety of specific drivers for neuronal types involved in mating and aggressive behaviors, and have identified dopaminergic and serotonergic circuits as contributors to increased aggression. Additionally, we are using immunohistochemical and biochemical techniques on fly brains from 24 hours and 1 week post-injury to determine if there are any differences in tau localization, phosphorylation, or neurodegeneration. Ultimately, we hope to elucidate how different molecular states of tau contribute to neurodegeneration and lead to alterations in brain function and behaviors.

Assessing the use of pre-germinated and soaked seed of native plants species for badland restoration: lab and field trials

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alyssa Calalo*
University of Guam

Abstract: The effects of erosion are very prominent in Southern Guam which comprises fourteen watersheds. Big erosion scars cause land degradation and add sediment to our coral reefs. Erosion is most prominent during periods of heavy rain, causing degradation of native terrestrial and marine ecosystems. Watershed restoration, more specifically expanding our erosion scar restoration techniques, is crucial to stop this erosion to ensure our natural ecosystems continue to thrive for future generations to enjoy. In efforts to restore the land, we used native plants such as Pandanus dubius - Påhong and Pandanus tectorius - Kafu. Both Pandanus species are well known for their endurance to harsh conditions, such as drought and heat. As these native plants are important to the CHamoru culture, ethnobotanical and cultural uses were documented and integrated in our conservation strategies. The effectiveness of different germination methods were initially tested in control trials in 4x4 cinder block plots filled with badland soil. 90 Pandanus dubius - Påhong seeds and 90 Pandanus tectorius - Kafu seeds were used in total, with 30 of each being pre-germinated, soaked in water, and as a control. Pre-germinated Pandanus tectorius had the most effective results. We recorded high survival and growing rates. In June, we conducted a field trial, with pre-germinated Pandanus tectorius at Ugum Watershed. The results concluded that the planting of pre-germinated Pandanus tectorius is an effective method of watershed restoration technique.

Studies of small aromatic compounds as inhibitors of quorum sensing in the pathogenic bacterium Pseudomonas aeruginosa.

Discipline: Life Sciences
Subdiscipline: Microbiology

Alice Wambua*[1], Josephine Chandler[2], Kate Woods[3], Kade Townsend[4], Rhea Abisado[5]

[1]University of Kansas, [2]University of Kansas, [3]University of Kansas, [4]University of Kansas,
[5]University of Kansas

Abstract: The multidrug drug-resistant and opportunistic pathogen Pseudomonas aeruginosa commonly results in severe infections in immunocompromised and cystic fibrosis patients. P. aeruginosa utilizes quorum sensing, a population density-dependent cell communication that regulates gene expression. In P. aeruginosa, quorum sensing involves the production of acyl-homoserine lactone signaling molecules that bind to the transcription factor LasR causing it to activate the transcription of specific genes. Quorum sensing activates the production of virulence factors, antibiotic resistance, and biofilm formation; thus, there is intense interest in developing quorum sensing inhibitors as a potential novel treatment for P. aeruginosa infections. Several related benzaldehyde derivatives have been reported to inhibit P. aeruginosa LasR. Here, we use a cell-based heterologous Escherichia coli system to characterize several benzaldehyde derivatives, such as O-vanillin, to block LasR activity. The system involves a plasmid expressing LasR and another plasmid carrying the LasR-regulated lasI gene promoter fused to the lacZ transcriptional reporter gene. A plasmid expressing lacZ from a constitutive promoter served as a control. Dose-response curves were generated to determine the efficacy of each inhibitor compound. Results showed that many of the small aromatic compounds inhibit the expression of the lasI-lacZ transcriptional reporter at a half-maximal concentration of about 1mM. However, most compounds also inhibit the transcription of the constitutive lacZ control at less than 2-fold higher concentrations. These results suggest that these benzaldehyde compounds might not be as LasR-specific as previously believed. The continued study and development of quorum sensing inhibitors may lead to new therapies for P. aeruginosa infections.

NACHO Mediates Expression of Dα7 in Drosophila Model

Discipline: Life Sciences
Subdiscipline: Neurosciences

luciano Cantu*[1]and Susan Tsunoda[2]
[1]Colorado State University, [2]Colorado State University

Abstract: Neuronal homeostatic plasticity (HSP) is an essential process for maintaining balance of neuronal activity from increases or decreases in action potentials. The growing field of HSP aims to understand the intrinsic and synaptic scaling changes of neural circuits that are thought to maintain homeostasis. In previous studies, inactivation of nicotinic acetylcholine receptors (nAChRs) resulted in a homeostatic increase of Drosophila α7 (Dα7)– nAChRs . Current research and preliminary data in our lab suggest NACHO mediates (Dα7)– nAChRs expression. NACHO is a localized ER integral membrane protein that acts as a chaperone to initiate protein folding, assembly, and surface expression of α7 nAChRs. Furthermore, mammalian alpha7 nAChRs have been expressed in cell lines with NACHO. However, it is unknown as to how assembly proteins such as NACHO mediate Dα7 nAChRs in vivo. Here we attempt to analyze levels of Dα7 in Drosophila transgenic lines in the absence of NACHO using Western Blots to quantify protein levels and immunostaining for subcellular localization. We predict that the absence of NACHO will greatly reduce the levels of Dα7. Our preliminary data confirms that we can detect Dα7-Mcherry in control flies by Western Blot analysis, we are in the process of developing our experimental lines which will have NACHO-null mutation. These findings will allow us to elucidate the role of NACHO in mammalian models. For example, α7 nAChRs have been implicated in mediating synaptic homeostasis in Alzheimer Disease. Thus, understanding how

NACHO mediates α7 expression could also give insight in developing new neurodegenerative disease models.

From Ridges to Reefs: Using Environmental Indices of the Belizean River Watershed to Establish Ecosystem Conditions and Connectivity with the Mesoamerican Reef

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ignacio Rueda*[1]and Dr. Keisha Bahr[2]
[1]Texas A&M University-Corpus Christi, [2]Texas A&M University-Corpus Christi

Abstract: Belize is one of the most biologically diverse nations containing part of the second largest barrier reef and sharing the largest proportion of forested areas in Central America. The Mountain Pine Ridge Forest Reserve contains riparian rivers that discharge materials that support the ecology of surrounding riparian environments while simultaneously transporting organic material, suspended inorganic particles, and freshwater into the Caribbean Sea supporting coral reefs. However, there are no standardized criteria to correlate the ecosystem health of this region's terrestrial and marine habitats. Therefore, over two weeks, undergraduates at Texas A&M University-Corpus Christi conducted fieldwork in both terrestrial and marine habitats using infiltrometers, velocity meters and transects to interpret the various environmental factors contributing to coral reef and river ecosystem health. Results indicated that water quality, water flow, and structural complexity are essential for plant and animal welfare in their respective ecosystems. The sites sampled did not directly influence one another, however, there were similar characteristics that each environment shared, making it possible to quantify and correlate healthy ecosystems. Understanding the changes in health for coastal marine and riparian river systems is important for determining the degree of dynamic balancing occurring for biological systems to be efficient. The applications of this study can be used to create a criterion for assessing favorable environmental conditions by creating a health index to understand the optimal states that make up the Belizean Rivers and the Mesoamerican reef environment.

The potential role of P-JNK in metastatic breast cancer dormancy

Discipline: Life Sciences
Subdiscipline: Biology (general)

Alejandra Cardenas Montañez*[1], Alessandra I. Riggio[2], Alana L. Welm[3]
[1]University of Puerto Rico at Bayamón, [2]University of Utah, [3]University of Utah

Abstract: A major concern of breast cancer is metastatic recurrence when clinically disease-free patients relapse and die as a result of lack of curative therapy. This multistep process involves a population of disseminated tumor cells (DTCs) which escape primary tumors and seed into secondary sites. To further study the concept of dormancy, as there is a long latency period of months to decades between tumor removal and relapse, we combined an ex vivo HER2 + /ER + rapid autopsy (RA) model with in vitro proliferative D2A1 and dormant D2OR breast cancer cell lines model. A protein of interest, i.e. P-JNK, was previously found through spatial proteomics to be upregulated in regions of grossly uninvolved (GU) tissue that contained DTCs when compared to those without them in the RA study. To test our hypothesis that P-JNK could be involved in breast cancer dormancy/reawakening, we performed a mIF for HER2/P-JNK/Ki67/CC3 where P-JNK seems to be expressed at the cell membrane along cancerous tissue, while the expression pattern in GU tissue involves progressional P-JNK expression as DTC clusters become larger and form micro-mets. To characterize P-JNK expression in vitro, western blots were performed for 2D culture and 3D tumorsphere assay conditions. P-JNK seems to be expressed differently with higher expression by D2OR in 2D setting but by D2A1 in 3D which better models self-renewal capability and stemness viability. We aim to better understand the mechanisms of tumor dormancy/reawakening as it would help us tackle its re-emergence to improve survival of breast cancer patients.

Investigation of potential trade-offs associated with immunity and reproduction in the northern star coral, Astrangia poculata

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Natalie Villafranca*[1], Sofia Diaz de Villegas [2], Isabella Changsut[3], Haley Womack[4], Koty Sharp [5], Lauren E. Fuess[6]
[1]Texas State University, [2]Texas State University, [3]Texas State University, [4]Texas State University, [5]Roger Williams University, [6]Texas State University

Abstract: Most living organisms face ubiquitous pathogenic threats in natural environments. Consequently, organisms have evolved a complex defense system to protect against potential invaders, commonly known as the immune system. However, the components of the immune system are physiologically costly to maintain and engage, often drawing resources away from other expensive organismal processes such as growth and reproduction. Many studies have sought to increase understanding of trade-offs between two costly traits (i.e. growth, reproduction, immunity) in a diversity of systems. However, few studies have investigated these topics in cnidarians, which include key ecosystem engineers such as hard corals. Here, we characterize trade-offs between constitutive immunity and reproduction in the facultatively symbiotic coral Astrangia poculata . We hypothesized that there would be trade-offs between constitutive immunity and reproduction. Further, we expected variation in energetic budget resulting from differences in symbiotic state to impact these trade-offs. Colonies underwent ex situ spawning and reproductive output was quantified by counting gametes. We then correlated reproductive output to immune metrics including melanin production, antioxidant production, and antibacterial activity. We found no significant associations between reproductive output and immunity, but did document a positive association between melanin production and symbiont density, in agreement with past studies. The lack of trade-offs found point towards complexities in energetic budgets, and highlight the importance of characterizing multiple complex traits when considering these questions. Our results provide a preliminary framework for future studies to understand immune trade-offs in cnidarians.

Investigation of gene knockdown efficiencies of CRISPR/Cas13d and Cas7-11 in zebrafish

Discipline: Life Sciences
Subdiscipline: Genetics

Divya Proper*[1], Saba Parvez, PhD [2], Chelsea Herdman, PhD[3], Dr. H. Joseph Yost, PhD[4], Dr. Randall T. Peterson, PhD [5]
[1]College of Charleston, [2]University of Utah, [3]University of Utah, [4]University of Utah, [5]University of Utah

Abstract: Gene knockdown is a powerful approach to investigate gene function. CRISPR-based technologies have made targeted gene knockdown in several model systems more facile and accessible. Cas13d, a class 2 type VI CRISPR-Cas RNA endonuclease, has recently been shown to effectively induce mRNA knockdown in the zebrafish model. However, in addition to its on-target activity, Cas13d also has ‘collateral’ activity that results in significant off-target effects. Thus, there is a need to develop targeted gene knockdown approaches with minimal off-target activity. mRNA knockdown by Cas7-11, a type III CRISPR-Cas RNA endonuclease, was recently shown to be successful in target knockdown in mammalian cells without non-specific activity and negative effects on cell viability. However, the efficacy of this technique has not been assessed in zebrafish. In order to compare the effectiveness of RfxCas13d and DiCas7-11 for RNA knockdown in zebrafish, DiCas7-11 was cloned into pT3TS. Next, in-vitro transcription of both RfxCas13d and DiCas7-11 was conducted. Guide RNAs (gRNAs) targeting several genes with known mutant phenotypes in zebrafish embryos were generated as controls to assess knockdown efficiency. After injecting zebrafish embryos at the one-cell stage with the mRNA encoding for either RfxCas13d or DiCas7-11 and the gRNAs, embryos were screened for phenotypes several hours post injection. I discovered that RfxCas13d mediated gene knockdown results in significant deformities in the injected embryos, likely due to Cas13d ‘collateral’ activity. This study aims to provide a direct comparison of two CRISPR knockdown technologies in order to develop approaches for effective gene knockdown with reduced off-target effects.

Population Genetics of Two California Species of Checker Lily (Fritillaria)

Discipline: Life Sciences
Subdiscipline: Biology (general)

Andrew CARDENAS*[1], Katherine Waselkov[2], Jacklyn Fajardo[3], Arshnoor Kaur[4], Chris Winchell[5]
[1]California State University, Fresno, [2]California State University, Fresno, [3]California State University, Fresno, [4]California State University, Fresno, [5]Ecologist at Novaterra Biological Consulting, Arcadia, CA

Abstract: Our project focuses on the genetics of two species of wildflowers called checker lilies, Fritillaria atropurpurea and F. pinetorum. Fritillaria is a genus that consists of approximately 140 perennial plants and is known for its huge genome (30-80 Gb of DNA). Two local California species of checker lily wildflowers, Fritillaria atropurpurea and F. pinetorum, are morphologically very similar but are currently listed as two different species. Aside from slight and inconsistent morphological differences, both species are generally found in different but contiguous parts of California. F. pinetorum is listed as rare by the California Fish and Wildlife Society. This research focuses collecting data about whether F. atropurpurea and F. pinetorum are the same or different species by utilizing the chloroplast DNA via DNA extractions, PCR, and gel electrophoresis. I have tested out a few different primers, and the results so far show that primers for the chloroplast region trnH-psbA amplify well in both species. Those DNA sequences were cleaned and then sent to Eurofins Genomics for Sanger sequencing. The sequencing alignment showed an indel of (TCTTA) from #352-357 bp for one population of F. atropurpurea, with the same insertion in three F. pinetorum populations. However, the insertion was not observed in 3 other populations of F. atropurpurea. The implications of this work could affect conservation decisions involving F. pinetorum: if these two species cannot be differentiated genetically, then it would imply that they are still exchanging genes and would not be two different species according to the Biological Species Concept.

Impact of Nucleic Acid Sequence and Structure on the Composition and Magnitude of TLR-Mediated Innate Immune Signaling Outcomes

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Laurie Agosto*[1], Margaret Lange-Osborn[2], William Schulze[3]
[1]University of Missouri, [2]University of Missouri, [3]University of Missouri

Abstract: Toll-like receptors are pattern recognition receptors (PRRs), which recognize a variety of pathogen-associated molecular patterns (PAMPs). When a PAMP interacts with a PRR, it triggers an intracellular signaling cascade, resulting in proinflammatory or antiviral responses. Toll-Like Receptor 9 (TLR9), which recognizes CpG DNA, induces differential signaling responses dependent upon the class of CpG DNA ligand utilized. For example, class A CpG DNAs are described to generate primarily antiviral signaling responses, while class B CpG DNAs generate primarily proinflammatory signaling responses. Despite these observations, the transcriptomics profiles for the different classes of CpG DNA have not been well defined. Here, we examined three different CpG DNA classes to determine the diversity of genes that are differentially expressed. We treated both a Burkitt's lymphoma cell line (Ramos) and HEK-Blue hTLR9 cells with CpG DNAs from class A, class B, or class C. Following stimulation, bulk RNA sequencing was performed on samples enriched for polyA RNAs using the Illumina NovaSeq. Sequences were aligned, and differential expressions of genes were analyzed using R scripts. Our results suggest that each CpG DNA induces a specific gene expression signature and are consistent with prior findings that class A CpG DNAs induce primarily interferon responses, while class B CpG DNAs induce predominantly proinflammatory responses. Notably, we observed both antiviral and proinflammatory signaling for each CpG, although the specific genes induced were often distinct. These results suggest that there is more to learn about the responses induced by each CpG class and the mechanisms responsible for differential induction.

Use of competitive growth between bacteria and fungi for the purpose of antimicrobial discovery

Discipline: Life Sciences
Subdiscipline: Microbiology

Stephanie Valdez*[1], Dr. Catherine Wakeman[2], Hafij Al Mahmud[3]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University

Abstract: Chronic infections often contain multiple species of pathogens. The complex interactions between these co-infecting pathogens play an important role in disease outcome and progression. These interactions can be either competitive or cooperative. Antimicrobial molecules can be discovered through studying the competitive interactions of microbes. In fact, most of the currently available antibiotics are derivatives of naturally occurring molecules produced by microbial competitors. Pseudomonas aeruginosa, a common chronic infection pathogen, often found to be competitive against other co-inhabiting pathogens. This bacterium typically outcompetes the surrounding community not only through production of its own well characterized antimicrobials but, we hypothesize, also via expression of defensive mechanisms protecting it against the antimicrobial compounds secreted by co-infecting microbes. To test this hypothesis, we have developed both liquid and solid media competition assays between P. aeruginosa and the fungal pathogen, Cryptococcus neoformans, and demonstrated that C. neoformans does possess antibacterial activities. Using a transposon insertion mutant library of P. aeruginosa, we found several P. aeruginosa genes required for competitive growth in the

presence of C. neoformans. Some of these mutants lack multi-drug efflux pumps, indicating that there is a secreted molecule from C. neoformans that is no longer able to be exported from the cells. We are now fractionating the active cell extracts of C. neoformans that are likely to contain the hypothetical secreted antimicrobial compound to further determine the identity of this molecule. The secreted molecule from C. neoformans may represent a novel antimicrobial agent that could be developed further for clinical use.

Defining a cryptic species, Portunus pelagicus, using morphometric and phylogenetic analysis

Discipline: Life Sciences
Subdiscipline: Genetics

Jerome Wolfgang Isaac Uy*[1], David T. Gauthier[2], Christopher E. Bird[3], Robert S. Guino-o[4], Nadia Palomar-Abesamis[5]
[1]Eckerd College, [2]Old Dominion University, [3]Texas A&M University - Corpus Christi, [4]Silliman University, [5]Silliman University

Abstract: Portunus pelagicus , a commercially important swimming crab species widely distributed throughout the Indo-Pacific region, is currently managed as a single species in the Philippine archipelago. Recent taxonomic work, however, indicates that P. pelagicus comprises a five-member species complex, one of which is an undescribed Portunus species from Japan. Two members of the complex are hypothesized to occur in the waters of the Philippine archipelago, P. pelagicus sensu stricto and the undescribed Portunus species, but more sampling effort is needed to identify independently evolving lineages. This study aims to assess the presence of these two Portunus species in the Philippine archipelago. We collected specimens from fish markets found in different locations around Negros and Panay Island, Philippines and conducted morphometric, geomorphometric, and genetic barcoding analyses to identify and quantify cryptic diversity in the Portunus spp. Only male specimens were used to avoid sexual dimorphism during the geomorphometric analysis. Muscle samples were collected from the pereopods for use in DNA barcoding and phylogenetic analysis. I will present an analysis of the congruence between the morphometric, geomorphometric, and phylogenetic barcoding data to determine if there is additional cryptic diversity present. This study provides the foundation for further characterization of the undescribed Portunus sp. using the quantitative analysis of its body form. Furthermore, the results of this study can be used to develop accurate identification keys for use in Portunus fishery management, governance and scientific research.

Gene Expression Biomarkers in Feline Injection-Site Sarcomas

Discipline: Life Sciences
Subdiscipline: Biology (general)

Thalia Dien*[1]and Stephen Ramsey[2]
[1]Oregon State University, [2]Oregon State University

Abstract: Feline injection-site sarcoma (FISS) is an invasive soft tissue tumor that develops at the site of injection or vaccination in cats. The tumor can appear as early as 4 weeks to as late as 10 years after vaccination and is the most serious adverse effect a cat could get following vaccination. Some scientists theorize that local chronic inflammation, possibly triggered by vaccine adjuvants and genetic predisposition, could be linked to FISS development. However, the exact pathogenesis of FISS is unknown. Our goal is to identify key differentially expressed genes

in FISS to provide the basis for further research and treatment. Some genes known as microRNAs (miRNAs) regulate gene e xpression by binding to their target genes (mRNAs) and degrading them. The dysregulation, or changes in the expression, of miRNAs contribute to many cancers because they can degrade important genes involved in suppressing cancer . Thus, we hypothesize that the imbalance of gene expression levels of certain miRNAs and their target genes could contribute to FISS formation by disrupting homeostasis and inducing chronic inflammation at the injection site. We use bioinformatics analysis tools, such as STAR and R software, to quantify gene expression levels in FISS versus normal tissue samples in cats. The analysis demonstrated that MiRNA-21-5p, an important regulator of cell proliferation and apoptosis, is upregulated in FISS compared to normal tissues, while its target gene, TP63, is extremely downregulated. TP63 plays an important role in gene regulation and its dysregulation is known to contribute to sarcoma formation in humans.

Investigating the effects of sex hormones, chromosomes, and gonads on the regulation of the Krüppel Like Factor 14 (KLF14) trans-eQTL network

Discipline: Life Sciences
Subdiscipline: Genetics

David Gragirenes*[1], Yonathan Aberra [2], Mete Civelek[3]
[1]University of Puerto Rico, Cayey, [2]University of Virginia, [3]University of Virginia

Abstract: Obesity is a complex disorder where excessive adipose tissue accumulation presents a risk to health. Several genetic variants on chromosome 7 upstream of the gene encoding transcription factor Krüppel Like Factor 14 (KLF14) have been robustly associated with metabolic pathologies, such as Type 2 Diabetes (T2D), obesity, and unhealthy lipid profiles. Additionally, these genetic variants regulate the expression of KLF14 in cis and 385 other genes in trans . Associational and functional follow up studies of KLF14 establish that KLF14 has a sex-biased function. In females only, KLF14 deficiency detrimentally leads to (1.) abdominal obesity, (2.) insulin resistance, (3.) poorer clearance of non-esterified fatty acids and triglycerides. Despite these advances, the mechanism explaining the sex-biased KLF14 phenotypes remain unknown. To investigate this, we conducted a comprehensive analysis of publicly available adipose tissue bulk and single cell RNA sequencing data. Using differential gene expression analysis and other statistical genetics approaches, we investigated the contribution of sex chromosomes, sex hormones, and sex organs to the regulation of the KLF14 trans -genetic network. Our preliminary results show that the trans network is regulated by sex hormones and gonads, but not by sex chromosomes. By completing single-cell RNA-Sequencing data analysis in adipose tissues, we will be able to propose specific testable hypotheses to discover the basis of the sex-biased function of KLF14. Taken together, our results point to the importance of hormones and gonads in the regulation of the KLF14 trans network.

Engaging in a 2-week creativity camp boosts positive emotional tone and authenticity during imagination in adolescents with depressive symptoms

Discipline: Life Sciences
Subdiscipline: Neurosciences

Yeritmary Rodriguez Delgado*[1], Olivia Edoigiawerie [2], Michaelle DiMaggio-Potter[3], Laura Padilla[4], Yuko Taniguchi [5], Bonnie Klimes-Dougan[6], Kathryn Cullen[7], Wilma Koutstaal[8]

[1]University of Puerto Rico at Cayey, [2]University of Minnesota, [3]University of Minnesota, [4]University of Minnesota, [5]University of Minnesota, [6]University of Minnesota, [7]University of Minnesota, [8]University of Minnesota

Abstract: This multiphase intervention study aims to examine if inviting adolescents with depressive symptoms to participate in a two-week creativity camp enhances their imagination and redirects their negative thoughts. The creativity camp consisted of mental agility, creative writing and design exercises. To test this, we administered newly-developed fMRI-based imagination tasks before and after the camp, followed by post-scan written reflection tasks. The reflection tasks were evaluated using a psycholinguistic application known as the Linguistic Inquiry Word Count (LIWC-22). This application categorizes words into various semantic categories and four summary variables: analytical thinking, clout, authenticity and emotional tone. We hypothesized that participating in a variety of creative activities would promote a more hopeful and beneficial outlook. Preliminary LIWC analyses on the Phase 1 reflective written task (N = 14 adolescents, aged 12-17) revealed an increase of authenticity and positive emotional tone in the participants. In contrast, a standardized neuropsychological measure of verbal fluency showed little or no change. These findings suggest that engaging in a creativity camp may improve the participants' emotional outlets, candor and hopefulness. In conclusion, engagement in broader creative behavioral repertoires during the two-week creativity camp may positively impact adolescents' flexible thinking despite depressive symptoms.

Isolation of hydrocarbon degrading bacteria from soil samples, and identification of their alkb gene

Discipline: Life Sciences
Subdiscipline: Environmental Science

Maricarmen Rodríguez*[1]and Elizabeth Padilla Crespo [2]
[1]Interamerican University of Puerto Rico, [2]Interamerican University of Puerto Rico

Abstract: Fuel contamination poses a threat to mangroves: 1-5% of these ecosystems are disappearing due to oil spills. For that reason, soil samples were collected from mangrove areas near the Guajataca River in Isabela, Puerto Rico, with the goal to isolate and characterize hydrocarbon-degrading bacteria, specifically kerosene. Using standard microbiological techniques and Bushnell Hass Agar with 1% of kerosene, we isolated 8 strains of bacteria capable of growing in kerosene as their only carbon source. All our isolates were gram-positive cocci and were further characterized via biochemical. Screening via PCR with the primers alk B fd and alk BR d confirmed the presence of the alkb gene in six of our isolates which encodes the key enzyme involved in bacterial alkane degradation. Further analysis suggests that our isolated kerosene degrading- bacteria are from the CMNR group (Corynebacterium , Mycobacterium , Nocardia , and Rhodococcus), commonly associated with n -alkanes degradation. Through this, we expect to establish a microbial consortium that can be used in bioremediation applications for the cleanup and restoration of contaminated sites. Our results are of ecological importance, because as far as we know the Guajataca mangrove area is not anthropogenically impacted by fuel, therefore it shows the natural presence of these microorganisms in pristine environments, or it may indicate that an unknown source (or past contamination) occurred in the area. Sequencing efforts are undergoing to know more about the diversity of these isolates.

Characterization of novel bacteriophages for Pseudomonas aeruginosa

Discipline: Life Sciences
Subdiscipline: Microbiology

Karagen Rojas*[1], Lisa Bono[2], Fahareen Mosharraf[3], Austen Rowell[4], Jeffrey Bernard[5]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University, [5]Texas Tech University

Abstract: Pseudomonas aeruginosa is a known pathogen that chronically infects patients suffering from cystic fibrosis . The purpose of our research is to isolate bacteriophage from various freshwater lakes around Lubbock, TX and see how human disturbance correlates to the presence of P. aeruginosa -infecting bacteriophage in these lakes. We hypothesize that phage collected from more disturbed lakes would tend to infect P. aeruginosa -strains associated with human infection while the host range of phage from less disturbed water sources would contain environmental host strains. We identified a series of playa lakes that varied in distance from human activities, including parks, hospitals, etc. These samples underwent a series of dilutions and filtration steps, and afterwards they were then triple plaque purified. Phage host range was assessed by spotting on a variety of P. aeruginosa hosts, including clinical samples collected from hospital patients and environmental isolates. We incubated these plates over a range of temperatures from room temperature to human body temperature. Additionally, the morphology of the phage were characterized using TEM. In the future, the phage will be assessed as candidates for phage therapy.

“Understanding nanoparticle-leaf surface interactions using magnetite (Fe3O4)”

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Kevin Rodriguez*
University of Puerto Rico in Cayey

Abstract: This summer I will be working with the Connecticut Agricultural Experiment Station on projects related to the use of nanoparticles to inhibit Fusarium disease in plants and enhance plant nutrition while taking note of the environmental effect. We are currently working with different morphologies and surface charges of metal-based nanoparticles to see the best mechanism to enhance the defenses against diseases. One of the projects seeks to understand the underlying chemistry governing the interaction between nanomaterials and a unique hydrophobic biological surface, for example, the leaves. In this experiment, we are using ferric oxide (Fe 3 O 4) nanoparticles of variable surface charges to treat tomato plants that are either healthy or infected with Fusarium oxysporum . The goal of the study is to determine if nano-sized ferric oxide could increase the tomato plant’s disease resistance ability. Another project we are working on is the use of nanoscale copper(II) sulfide for soybean plants’ nutrition, disease suppression, and food safety. In this experiment, we are using nanoscale copper(II) sulfide with different morphologies such as sheet and rod, as well as nanoscale copper(II) oxide with morphologies such as spike, flower, and sheet. The last experiment I am forming has a similar methodology as the one mentioned before, but the main target of the investigation is the watermelon and the expected results of both experiments are to find an efficient nanoparticle that can enhance the productivity of the plants and defense against diseases, while not posing a serious threat to the environment.

Oncological comparison of the TTN gene via bioinformatic approaches using cBioPortal.

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Axwel Deliz*[1], Nathan Reyna Ph.D [2], Elizabeth Padilla-Crespo Ph.D[3]
[1]Interamerican University of Puerto Rico- Aguadilla Campus, [2]Ouachita Baptist University, [3]Interamerican University of Puerto Rico- Aguadilla Campus

Abstract: The TTN gene encodes a large abundant protein of striated muscle and has been used as a biomarker in different cancers. Its mutations have the potential to determine if treatment would work in a patient or not. To understand the genomic proprieties of this gen, we used the TCGA database research of the PanCancer Atlas for Prostate Adenocarcinoma which has 489 patients/samples. Using cBioPortal for Cancer genomics we collected TTN mutational data and compared it to 4 other genes with known oncogenic genomic on prostate adenocarcinomas: SPOP, PIK3CA, MUC16 y TP53. Our findings show that TTN has a co-occurrence with PIK3CA and MUC16. Also, TTN presented mainly missense mutations showing 68 of 81 mutations in 47 mutation samples. TTN has been previously demonstrated, along with a co-mutation in TP53, to predict chemotherapy response in lung cancer for men and women. Further efforts will be concentrated in comparing the survival rate of patients with the mutations in the TTN gene (usig other databases), an evaluating TTN co-occurrence with PIK3CA or MUC16 to see if this could result in a higher incidence of prostate adenocarcinoma.

Understanding the Binding Preferences of WAGO Clade Argonaute Proteins

Discipline: Life Sciences
Subdiscipline: Biochemistry

Rosa Sanchez*[1], Leah Braviner [2], Leemor Jushua-Tor[3]
[1]University of California, Santa Cruz, [2]Cold Spring Harbor Laboratory, [3]Cold Spring Harbor Laboratory

Abstract: RNA interference (RNAi) is a method for regulating gene expression. Argonaute proteins bind a small RNA, which guides the protein to regulate a target RNA. The Argonaute family can be divided into three clades based on phylogenetic analysis: Agos, PIWIs, and WAGOs. While the Ago and PIWI clades are found in all known organisms, the WAGO clade is specific to worms. It is known that Agos and PIWIs are each specific for one type of small RNA. However, it is unknown whether this is true for WAGO clade proteins, as it has been suggested that WAGOs may bind several types of small RNA. We hypothesize that WAGO proteins bind to one small RNA type, and that binding pockets in the protein interact strongly with these specific small RNAs. We will test this hypothesis by purifying WAGO proteins, conducting affinity assays and obtaining a structure of our proteins though cryo-EM. Biochemical analysis will determine whether WAGOs are specific to one type of small RNA or different small RNAs. A structure of the Argonaute will show the molecular interactions within the small RNA-protein complex, highlighting what makes the interactions strong or weak. We have overexpressed WAGO Argonautes in SF9 insect cells and purified them by removing cellular components through affinity chromatography, ion exchange, and gel filtration. We have commenced preparation of cryo-EM samples and collected preliminary data, which is now being processed. Additionally, we are developing a limited proteolysis assay to test affinity of our proteins to each small RNA.

Comparing RNA quality from Oyster gill and mantle tissues utilized in EecSeq for exome surveying.

Discipline: Life Sciences
Subdiscipline: Genetics

Hector Santiago Alvarez*[1], Jonathan B. Puritz [2], Jacob M. Green[3]
[1]University of Rhode Island, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: In the field of seascape genomics, the last two decades have provided many insights into the adaptation and evolution of non-model species to anthropogenic climate change. Yet, there's still space for improving the molecular and bioinformatic protocols that are used to explore these topics. Reduced representation sequencing approaches, such as targeted capture sequencing, allow evolutionary biologists to survey the genome of non-model species efficiently but commercial approaches to developing capture probes are cost-prohibitive. The development of efficient and cost-effective methods for surveying the genome, like Expressed Exome Capture Sequencing (EecSeq), are becoming increasingly more important for the scientific community. Eecseq develops target capture probes de novo from organismal mRNA to survey the exome of any organism, even without a reference genome. This project aims to explore the differences in RNA quality and quantity post-extraction from different Oyster (Crassostrea virginica) tissue samples (gill and mantle). Tissue-specific RNA profiles may alter the composition of EecSeq probes used for surveying the exome. We assessed RNA quality and quantity with Qubit fluorometer assays and an Agilent Tapestation fragment analyzer. In addition, we can measure tissue-specific probe capture specificity and efficiency after hybridization and sequencing of target captured gDNA. Our goal is to stress-test and refine the EecSeq protocol to provide a tool for exome sequencing of nonmodel species that allows researchers to cost-effectively approach the exome for genes under selection. Our project will inform studies seeking to explore exome adaptation by providing a new sequencing tool that does not require previous genomic resources.

Human Voice Recognition in Exotic Cats

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Felix Berrios- Ortega*[1], Molly McGuire [2], Jennifer Vonk[3], Taylor Crews[4]
[1]University of Puerto Rico Humacao, [2]Zoo Miami, [3]Oakland University, [4]Oakland University

Abstract: The ability to differentiate between familiar and unfamiliar voices has been demonstrated in many species, both wild and domestic. However, this social ability is often linked to domestication. Little is known about human voice recognition in members of the Felidae family. The purpose of this study is to determine if wild cats respond differently to familiar, less familiar, and unfamiliar voices. We predict that increased familiarity and the inclusion of the animal's name will result in greater attention and responsiveness to the vocal cues measured by latency and frequency of their responses. We examined 8 individuals from 5 species (Panthera tigris sumatrae, Puma concolor coryi, Acinonyx jubatus, Leptailurus serval, and Lynx rufus) using audio playbacks from 3 different degrees of familiarity to the cats (unfamiliar, less familiar, and most familiar) with and without the cat's name. We recorded and examined the difference in response by coding for behaviors such as ear, head and body orientation, movement towards or away from the sound, and response vocalizations. With wild cats being common species found in managed care, information on how they respond to vocal cues could have broad applications to their management and care.

Combining Habitat Use and Dietary Biomarkers to Recreate Marsh-Dependent Fish Life History

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kathryn Brinegar*[1]and Dr. Paola López-Duarte [2]
[1]University of North Carolina at Charlotte, [2]University of North Carolina at Charlotte

Abstract: Several fish enter estuaries during the larval stages and remain in there throughout the juvenile stage, where they feed and grow before returning to coastal areas as adults. In contrast to these transient fish, we also find permanent residents that complete their life cycle within estuaries. The first objective of this study is to compare diets of transient and resident fish in southern Louisiana salt marshes. To that end, fish were collected from three sites at varying distances from the coast. Muscle tissue samples from two transient species at the juvenile stage: spot [Leiostomus xanthurus] (n=18), and sand seatrout [Cynoscion arenarius] (n=7) and one permanent resident at juvenile and adult stages, Gulf killifish [Fundulus grandis] (n=57) were stable isotopes indicative of diet (13C: energy source; 15N: trophic position, and 34S: source and trophic level identification). Preliminary isotopic results suggest that sand seatrout exhibit more marine signatures and a higher trophic position than the killifish and spot. The second objective of this study is to determine whether dietary signatures reflect habitat use. We anticipate fish with more marine dietary markers are more recent arrivals in the marsh, and would have signatures that differ from the marsh resident fish. To evaluate habitat use, we will examine the otolith microchemistry signatures for the same samples. Through the integration of otolith microchemistry and dietary stable isotopes, the life history of the fish will be reconstructed which provides insight into habitat use patterns across the salinity gradient.

Using Biotin Ligase to Label Tumor Cells

Discipline: Life Sciences
Subdiscipline: Neurosciences

Abraham Lopez*
Case Western Reserve University

Abstract: Targeted anticancer therapies have the potential to more effectively attack cancer cells with reduced toxicity, but they are limited by the similarity in surface marker expression between cancer cells and healthy cells. Most cancer biomarkers are also expressed to some extent in healthy cells, which can cause side effects such as rash, cardiac dysfunction, thyroid dysfunction, hypertension, and others. One distinguishing feature of tumors is that the tumor microenvironment has elevated levels of extracellular ATP (~1000-fold compared to healthy tissue). We aim to take advantage of this by using ATP-dependent enzymes to facilitate cancer cell targeting. Biotin ligases (when modified to eliminate substrate specificity) use a molecule of ATP n to attach a biotin molecule to nearby proteins. Zhao et al. developed a variant, UltraID, that is smaller and more efficient than other biotin ligases. We attached a nanobody against a cancer cell biomarker to the UltraID enzyme so that upon binding, it biotinylates the surface of the target cell. Since extracellular ATP is highly regulated in normal tissue, the ATP-dependent enzyme would only label cells within the tumor. The biotin molecules will act as a label to distinguish cancer cells from healthy cells that could potentially be used for targeted therapy, identification, and diagnostics.

A role for Rhamnolipids in Treating Depleted Uranium-Contaminated Skin Wounds

Discipline: Life Sciences
Subdiscipline: Biology (general)

Taylor Gilmore*[1], Robert S. Kellar, PhD [2], Brenda Padilla, B.S.[3], Marjorie A. Nguyen, M.S.[4], Dominic D. Dominguez, M.S. [5], Desirae E. Enriquez, M.S.[6]
[1]Northern Arizona University, [2]Associate Professor of Practice, [3]Master's Student, [4]Previous Master's Student, [5]Previous Master's Student, [6]Previous Master's Student

Abstract: Depleted uranium (DU) is a prevalent heavy metal by-product that has leached into soil and groundwater within the Southwest United States due to abandoned uranium mines. Native populations face numerous health disparities which could be linked to elevated uranium levels found in unregulated water sources. Previous research demonstrates that DU impairs key processes in wound healing, including delayed cell proliferation and hindered cell migration; furthermore, current research reveals the lack of therapeutics that can potentially alleviate these negative effects. Rhamnolipids are a naturally occurring biosurfactant with known biofilm-disrupting, anti-adhesive, and contaminant binding activities. Cellular migration/wound assays used fibroblasts grown to appropriate confluency in T75 flasks. These cells were sub-cultured into 12-well plates and pre-treated with their respective treatments of rhamnolipids and DU for 24 hours. The monolayer was scratched/wounded to mimic a contaminated wound site and subsequent images were collected over 24 hours, for analysis. The incorporation of these rhamnolipids as a treatment in these wound assays have demonstrated a significant increase in wound closure rate (migration) as a result of sequestering the harmful effects of DU. Even at lower concentrations of rhamnolipids (6.25 μM) the negative effects of DU were mitigated in the wound assays; higher concentrations of the rhamnolipids (50 μM) achieved results in half the time. These preliminary, proof of concept, results indicate that rhamnolipids can be used as a natural treatment for DU-contaminated wounds. Future work will focus on the incorporation of rhamnolipids into electrospun wound healing scaffolds for direct delivery into the wound bed.

An Immune Profiling of Spleen Tissue From Schistosoma Infected Mice

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Mohammad Alsheikh*[1], Afzal Siddiqui [2], Aryandra Arya[3]
[1]Texas Tech University, [2]Texas Tech University Health Sciences Center, [3]Texas Tech Universty Health Sciences Center

Abstract: Schistosomiasis is a helminth infection caused by Schistosoma spp. The mode of transmission is skin contact from contaminated freshwater. The disease is second only to malaria with an estimated 240 million people affected and 700 million people living in endemic areas. Current therapeutic treatment is limited to Praziquantel. With the emergence of new resistant strains, a protective prophylactic vaccine is of critical need. Currently, there are few vaccines available for helminth infections, and due to the variety of hosts, different larval stages, and widespread chronic disease of these multicellular pathogens, vaccination against helminth parasites requires an extensive cognizance of the immunology of the host-parasite relationship. Without the proper comprehension of the immunological relationship, there is a risk of amplifying certain immunopathogenic responses and the invocation of ineffective immune mechanisms. Therefore, a thorough immune profiling of infection can help us understand how to research suitable vaccine candidates and understand the immunological parameters of

protection in Schistosoma infection. For this, we can perform immune profiling using RT PCR and flow cytometry. RT PCR allows for the detection and quantification expression profiling of specific genes. Flow cytometry, on the other hand, can be used to characterize different immune cell types within heterogeneous samples. Principally, to oppose this impairing and fatal disease, a comprehensive understanding of the schistosome immunological relationship is imperative for the development of treatment.

Examining the immunoepigenetic-gut microbiome axis in self-esteem of Native Hawaiians and other Pacific Islanders

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Celyna Becerra*[1], Braden P. Kunihiro [2], Riley K. Wells[3], Rosa H. Lee[4], Lesley Umeda [5], Nina P. Allan[6], Noelle C. Rubas[7], Chandler K. L. Nunokawa[8], Krit Phankitnirundorn[9], Rafael Peres[10], Alika K. Maunakea [11]

[1]John A. Burns School of Medicine, University of Hawaii at Manoa, [2]John A. Burns School of Medicine, [3]John A. Burns School of Medicine, [4]John A. Burns School of Medicine, [5]John A. Burns School of Medicine, [6]John A. Burns School of Medicine, [7]John A. Burns School of Medicine, [8]John A. Burns School of Medicine, [9]John A. Burns School of Medicine, [10]John A. Burns School of Medicine,[11]John A. Burns School of Medicine

Abstract: Native Hawaiians and other Pacific Islanders (NHPIs) experience disparities in mental health. While existing literature describes social determinants of mental health in this population, little is known about the biological mechanisms that underlie the disproportionately higher rates of low self-esteem/depression among NHPIs. Herein, we investigated the immunoepigenetic-gut microbiome axis in a cohort enriched with NHPI participants who completed the Rosenberg Self-Esteem Scale questionnaire and provided blood and stool samples. We observed that individuals with low self-esteem exhibited significantly higher plasma concentrations (pg/ml) of proinflammatory cytokines IL-1β (P=0.039), IL-6 (P=0.040), IL-8 (P=0.023), TNF-α (P=0.008), and the chemokine MCP-1 (P=0.020). Using 16S-based sequencing, we identified associations of specific gut bacteria with self-esteem yet surprisingly individuals with low self-esteem exhibited a significantly higher microbial diversity relative to those with normal self-esteem (P<0.05). From monocytes enriched from blood samples, we identified 108 CpGs using Illumina EPIC array that were significantly differentially methylated between normal and low self-esteem groups and were preferentially located at genes involved in cancer, gastrointestinal, and immunological diseases. Interestingly, the methylation levels at 8 of these CpGs exhibited a highly significant correlation with self-esteem scores (R>0.34 or R<-0.33 and P<0.001). This included cg25450121 (in ATP5G1) and cg16274205, loci previously implicated in depression and suicide ideation, respectively. Altogether, these data reveal for the first time differences in the immunoepigenetic-gut microbiome axis that associate with self-esteem among NHPIs and implicates this axis in the pathology of mental health conditions including depression, which warrants further study.

The Role of COX2 Signaling in Neural Crest Cell Migration

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Jessica Pacheco*[1], Crystal D. Rogers [2], Tess A. Leathers[3]

[1]California State University Northridge, [2]University of California, Davis, [3]University of California, Davis

Abstract: Nonsteroidal anti-inflammatory drugs (NSAID), such as ibuprofen and naproxen, are commonly used to treat headaches, fevers, and body pain. These medications work by inhibiting the cyclooxygenase (COX) isomerase signaling pathway. COX enzymes ultimately drive the conversion of arachidonic acid to the prostaglandin, PGE2. PGE2 binds to the receptors EP1-4, and preliminary work from the Rogers lab identified that the EP3 receptor is expressed at the right time and place to be involved in neural tube and neural crest cell formation and migration. NSAID use during the first trimester is linked to an increased risk in developmental defects in neural crest cell-derived tissues including heart defects and craniofacial anomalies. Neural crest cells are migratory multipotent stem-like cells that give rise to many derivatives including bones and cartilage of the face and the peripheral nervous system. They undergo an epithelial to mesenchymal transition (EMT) to migrate out of the neural tube and travel long distances to form these derivatives. We aim to understand the role of the COX enzymatic pathway in neural crest cell formation and migration. Based on our preliminary findings, we hypothesize that knocking down the EP3 receptor downstream of COX2 will result in reduced neural crest cell formation and migration, causing abnormal development of neural crest-derived tissues. We will knock down EP3 using a translation-blocking morpholino and will perform immunohistochemistry to define changes in quantity and migration distance of neural crest cells. If successful, our findings will improve the understanding of NSAID exposure and neural crest cell-related birth defects.

Dietary Blueberries to Improve Oral Dysbiosis in C57BL/6J Mice

Discipline: Life Sciences
Subdiscipline: Microbiology

Nizhoni Porter*[1]and Anandh Velayutham [2]
[1]University of Utah, [2]University of Utah

Abstract: The gut and oral cavity are the two largest microbial habitats and are closely connected through the digestive pathway. Evidence indicates microbial transmission (oral-to-gut and gut-to-oral) regulates pathogenesis of diseases such as cancer and is mediated through the 'oral-gut microbiome axis'. An imbalance in the oral microbes (dysbiosis) is implicated in oral diseases and systemic diseases (inflammatory bowel disease, cardiovascular disease, and Alzheimer's disease). Our lab recently showed that dietary supplementation of blueberries improves diabetes-induced gut dysbiosis. Dietary blueberries increased the abundance of commensal microbes and decreased the opportunistic microbes in diabetic mice. In the proposed study, we will evaluate whether supplementation of blueberry improves high-fat diet (HFD) and antibiotics-induced oral dysbiosis in a preclinical model. Mice will be divided into 4 groups: Control (C), HFD-fed (HF), HFD-fed mice treated with antibiotics in drinking water (HFA), and mice fed with HFD supplemented with blueberries and treated with antibiotics in water (HBA). We will analyze oral and gut microbiome using 16s rRNA amplification. Phytochemicals such as anthocyanins found in blueberries act as a prebiotic and promote the growth of beneficial gut microbes. Due to the probiotic effect of anthocyanins and the translocation of bacteria between the oral and gut microbiota, this correlation could help replenish the gut and oral microbiome once destroyed or altered and therefore aid in creating a healthier immune system. Our study will identify whether dietary blueberries improves oral dysbiosis by modulating 'oral-gut microbiome axis'.

Solvothermal carbonization of polypropylene for the creation of nanomaterials

Discipline: Materials Research
Subdiscipline: Other Materials Research

Elvin Cordero Figueroa*[1], Deidre O'Carroll[2], Nasir Javed[3]
[1]University of Puerto Rico-Humacao, [2]Rutgers, [3]Rutgers

Abstract: Plastic is one of the most used and discarded materials on the planet and one of the big problems to recycle plastic is to find an efficient method to obtain valuable materials that can be reused. The objective of this project is to convert waste plastic into carbon dots (CDs) by solvothermal carbonization. CDs are a new class of luminescent nanomaterial that possess properties such as photoluminescence, high quantum yield, and low toxicity. The purpose of this project is to demonstrate and study the carbonization mechanisms of polypropylene (PP), a common consumer plastic. A recipe was created for initial carbonization studies that involves (1) dissolving PP, (2) heating PP solution under high temperatures, and (3) characterization. To dissolve PP, 30mg and 100mg of PP pellets is added to 10mL of toluene and heated at 100˚C for 1h. The solution is placed in an autoclave and heated in a vacuum oven at temperatures between 200˚C to 300˚C. Chemical changes are observed through UV-Vis absorption spectroscopy. Absorption peaks are found between the wavelength ranges 300nm to 400nm. The solution containing 30 mg of PP that is exposed to 260˚C for 15h shows the most intense absorption peak at a wavelength of 325nm. The results show that the higher the temperature of exposure to the solution, the stronger the UV absorption peaks. However, further characterization by infrared spectroscopy is needed to determine the extent to which the solution is carbonized. Sulfonation is also being investigated to increase the degree of carbonization of PP.

Optimizing the Synthesis of Lipid Nanoparticles

Discipline: Materials Research
Subdiscipline: Materials Research

Stephanie Ramirez*[1]and David Johnson[2]
[1]Rio Hondo College, [2]University of Southern California

Abstract: Over the years, lipid-nanoparticles (LNPs) have become an instrumental component in drug delivery, most notably exemplified in modern COVID-19 vaccines. Not only are they relevant in drug delivery, but they serve as a tool to study cell membranes by breaking down this complex system in-vitro into a tunable membrane-mimic. The lipids that make up these LNPs are soluble in nonpolar solvents (e.g chloroform or methanol) but are sensitive to their presence when transferred to an aqueous environment where they self-assemble into LNPs. Therefore, the assembly is a delicate process, and it is important to take into account the environment of the lipids. Because of this, the solvent has to be completely removed before adding the lipids to an aqueous environment, because it could ultimately have an influence on the vesicle preparation. By examining the intrinsic and extrinsic properties of the membrane using dynamic light scattering (DLS) and fluorescence anisotropy in the presence of residual solvents, we can understand the effects of solvent on LNP formation. Preliminary results show that even small amounts of residual solvent have a direct impact on membrane phase transition temperature, fluidity, and resulting diameter. Therefore, we hypothesize that the presence of residual solvent affects the LNP’s formation and properties. Overall, this work will increase understanding of LNP formation for membrane-mimic systems in research and industry applications as they garner increased popularity and function in modern medicine.

Hydrogenation of Sb_2Te_3 and $(Sb_2Te_3)_{1-x}(MnSb_2Te_4)_x$ Thin Films

Discipline: Materials Research
Subdiscipline: Materials Research

Amy Lopez Navarro*[1], Maria C. Tamargo [2], Candice Forrester[3], Kaushini Wickramasinge[4]
[1]CUNY College of Staten Island, [2]CUNY The City College of New York, [3]CUNY Lehman College, [4]CUNY The City College of New York New York

Abstract: Topological Insulators (TI), such as Sb_2Te_3, are a class of materials with unique, highly conducting metallic surface states and insulating bulk regions. They are of interest for quantum computing and thermoelectric devices, as well as provide test beds to explore novel physics like Majorana fermions. The surface states have locked spin and momentum and are protected by time reversal symmetry leading to their exotic properties. When magnetic impurities are added, the symmetry breaks, a gap appears in the surface states and the system becomes a magnetic topological insulator (MTI). Previously, it was shown that the electronic and magnetic properties of the 3D topological insulators could be changed by a process known as hydrogenation. For hydrogenation, the samples are dipped in 0.5M solution of hydrochloric acid for different amounts of time, and Hall measurements are used to measure the electrical and magnetic properties. Molecular beam epitaxy, a high vacuum deposition technique, was used to grow the TI materials Sb_2Te_3 and $MnSb_2Te_4$. For characterization, Hall effect focuses on the electrical and magnetic properties of the material before and after hydrogenation. Hydrogenation is expected to reduce the background doping, affecting the fermi level of the material. By tuning the fermi level of TIs the unique properties of their surface states can be investigated. Here we study the effect of hydrogenation on the bulk carrier density of Sb_2Te_3, with the aim to investigate the effect of hydrogenation on the magnetic properties of $(Sb_2Te_3)_{1-x}(MnSb_2Te_4)_x$, which are predicted to change from ferromagnetic to antiferromagnetic.

Relationship Between $(Sb_2Te_3)_{1-x}(MnSb_2Te_4)_x$ Molecular Beam Epitaxy Growth Conditions and Curie Temperatures

Discipline: Materials Research
Subdiscipline: Materials Research

Adrián Rúa*[1], Maria Tamargo [2], Candice Forrester[3]
[1]University of Puerto Rico-Mayaguez, [2]Department of Chemistry, The City College of New York, CUNY, New York, NY 10031, [3]Department of Chemistry, Lehman College, CUNY, Bronx, NY 10468

Abstract: Topological Insulators (TIs) have garnered much interest due to their unique properties including highly conducting surface states, spin-momentum locking, and time reversal symmetry. When magnetic impurities are added to a TI, time reversal symmetry is disrupted and a gap at the Dirac point appears; these materials are called magnetic topological insulators (MTI). MTIs are a step closer to the realization of exotic physical phenomena, such as the quantum anomalous Hall effect (QAHE), which offers quantized conductance and lossless transport without the need for an external magnetic field. However, the experimental observation of the quantum effects has been limited to very low temperatures (a few Kelvin). Since the spontaneous magnetism only occurs below the Curie temperature (Tc), applications of the unique properties of these materials become realistic only if the Tc could be significantly

raised. The highest recorded Tc value for this material is 30-45K. In this work we report the properties of MTI $(Sb_2Te_3)_{1-x}(MnSb_2Te_4)_x$ films grown by molecular beam epitaxy (MBE) using different growth conditions. Several characterization techniques are utilized to understand the systems, such as X-ray diffraction (XRD), atomic force microscopy (AFM) and Hall effect. We analyzed how changes in growth rate and manganese (Mn) beam equivalent pressure (BEP) used during growth affects the Tc of the samples. We measured Tc values ranging from 40-100K depending on the growth conditions used. This result shows great promise for higher temperature quantum devices.

Exploring the Defects of CVD Grown Graphene

Discipline: Materials Research
Subdiscipline: Other Materials Research

Lesley Tolentino*[1], Xingzhou Yan [2], Dr. James Hone[3]
[1]CUNY Lehman College, [2]Columbia University, [3]Columbia University

Abstract: Graphene is a 2D, monolayer allotrope of carbon derived from graphite. The honeycomb lattice structure and unique Dirac cone band structure give rise to extraordinary physical properties, such as exceptionally high mechanical strength, thermal and electronic conductivity, and impermeability to all gases, making it highly attractive to a wide variety of applications, including high-performance electronics, photonics, protective coatings, and barrier films. Chemical vapor deposition (CVD) has proven to be a scalable mechanism for manufacturing large area graphene films but it is highly susceptible to defect and contamination which is a critically unresolved issue with detrimental impacts on graphene's intrinsic properties and performance qualities. Intrinsic defects such as grain boundaries(1D) and point defect(2D) result from misaligned nucleation and incomplete growth. Other potential defects are extrinsic contamination such as amorphous carbon that may deposit on the graphene surface during the growth. Both categories of defect can lead to electron scattering and uncleanliness which limits the performance of graphene. Exploring methods to characterize defects to improve the CVD growth inorder to diminish impurities is an important area of current research. understanding what leads to different defects will pave the way for these synthetic methods. My research focuses on developing different methods to elucidate defects in CVD grown graphene via Raman spectroscopy to distinguish structural defects in terms of hybridization, Oxidation test to denote the presence of grain boundaries and point defects, and Atomic Force Microscopy (AFM) to highlight any extrinsic defects such as contamination as well as the presence of amorphous carbon.

Preparation and characterization of chitosan-coffee silverskin composites

Discipline: Materials Research
Subdiscipline: Materials Research

Yetzzel Cortes*[1]and Oscar Marcelo Suárez [2]
[1]University of Puerto Rico at Mayagüez, [2]University of Puerto Rico at Mayagüez

Abstract: Coffee is a widely consumed beverage whose economic worth has grown over time. Due to its production, several derivatives are produced, leading to significant waste generation. These wastes are discarded or incinerated, negatively impacting the environment and human health. Thus, researchers are interested in developing new eco-friendly materials derived from these coffee production by-products. These by-products contain several components, such as reinforcement fibers or fillers that could enhance materials. Natural fillers combined with

polymers have the advantages of low production costs, being lightweight, and having excellent mechanical properties. Our interest is to evaluate the feasibility of a novel biocomposite consisting of chitosan (CH) and coffee silverskin (CS) obtained from coffee production by-products. CS is a solid waste lignocellulosic and renewable material, while CH is a biodegradable polymer with significant biological and chemical characteristics. The casting protocol involves dissolving CH with an acetic acid solution followed by mechanical agitation, adding CS component, and drying until CH/CS films solidify. X-ray powder diffraction (XRD) and Fourier Transformed Infrared Spectroscopy (FTIR) techniques were used to evaluate the CH, CS, and composite samples. XRD patterns showed CH characteristic peaks, and adding CS showed the presence of lignocellulosic material, which resulted in more amorphous patterns. Analysis of the CS/CH composites with FTIR showed lignocellulosic components present in CS. The produced composite may provide benefits for water purification. Hence, this research intents to encourage scientists and engineers to use inexpensive and eco-friendly materials to create new sustainable-based materials and prevent wastes from damaging the environment.

Synthesis of Flavonoid Iron Nanoparticles

Discipline: Materials Research
Subdiscipline: Materials Research

Damaris Rodriguez-Deluna*[1], Yuping Bao[2], Lucas Prestianni[3]
[1]University of Texas at San Antonio, [2]Department Graduate Program Coordinator, [3]graduate student

Abstract: One of the major obstacles in the treatment of cancers is the development of drug resistance of tumor cells during chemotherapy. In addition, the lack of efficient and safe tracking protocols also hinders understanding of the treatment process. Due to their biocompatibility, iron-based materials have been developed as contrast agents for magnetic resonance imaging, drug delivery, and therapy. The natural flavonoids rutin, quercetin, and luteolin were used as a coordination ligand for the preparation of the nanoparticles. Rutin, as well as other flavonoids, is known as an anticancer agent and has the potential to inhibit cell proliferation and cause apoptosis in cancer cells. However, its poor solubility has limited its uses in biomedical research. Here, we plan to overcome this limitation by forming flavonoid-Fe complex nanoparticles. Specifically, the effects of reaction pH, flavonoid-to-Fe ratio, and buffers on the formation of nanoparticles were studied using dynamic light scattering, ultraviolet visible light spectroscopy, and transmission electron microscopy. These novel iron nanostructures will have the potential of overcoming drug resistance in cancer treatment and serve as imaging nanoprobes.

Lubricants for outer space: properties of nickel doped molybdenum disulfide

Discipline: Materials Research
Subdiscipline: Materials Research

Elsa Vazquez*[1], Enrique Guerrero[2], David A. Strubbe[3]
[1]University of California, Merced, [2]University of California, Merced, [3]University of California, Merced

Abstract: Layered two-dimensional materials have several physical properties arising from their special crystal structures, giving them popularity in materials science. One such material is MoS_2, a transition-metal dichalcogenide, used for solid lubrication. MoS_2 performs well in vacuum, and NASA uses it for motorized instruments in space. Its lubricity has been experimentally shown to increase with Ni in the structure. This computational study evaluates the frictional properties of layered and bulk phases of Ni-doped MoS 2 by sliding or shearing the material in two directions. The material is doped by substituting a molybdenum or sulfur atom or inserting Ni between the layers (intercalation). Intercalation leads to two structures (octahedral or tetrahedral). Using density-functional theory we find the potential energy surfaces (PES), then analyze the contributions from the stacking of the layers and breaking/forming bonds. The structures are relaxed using different constraints to understand the effect of structural changes during the process. The PESs for the substituted sites have similar patterns but the S substituted case switches locations of the stable and meta-stable sites relative to that of the pristine. At certain positions in the sliding/shearing, the octahedral site can convert to structures with four or five bonds. The PESs for all four structures have extrema at common points of high symmetry stackings. As NASA plans more long-distance and long-duration space exploration, it needs to reduce power requirements with higher mechanical efficiency. This work provides insights into mechanisms of lubrication in Ni-doped MoS 2 and how it can be improved.

Spin structures and cation intermixing in the perovskite heterostructure LaCoO3/SrFeO3

Discipline: Materials Research

Subdiscipline: Materials Research

David González*[1]and Juan A. Santana Palacios [2]

[1]University of Puerto Rico, Cayey, [2]University of Puerto Rico, Cayey

Abstract: Perovskite heterostructures are remarkable materials because of their broad electrical and magnetic properties. Characterization of doped models is one aspect of these systems that have not been explored in much detail. We have studied the stability and effects of spin-orientation in fourth magnetic structures of the perovskite heterostructure LaCoO 3 /SrFeO 3 . Calculations were performed with the PBE+U (U d -Fe = 5.5 eV) method as implemented in VASP. The energetics, magnetic moments, and spin-densities were analyzed for (LaCoO 3) 1 /(SrFeO 3) 2 . To study the magnetic structures of these systems, we use various models. The results show that there are various stable spin configurations. Calculations indicate that the configurations where the Fe-layers have opposite spin orientation are more stable than with parallel orientation. The results of our calculations can help identify new spin-orientation in perovskite heterostructures.

Marginal Costs of Sunburn Prevention Methods in Apple Orchards

Discipline: Materials Research

Subdiscipline: Materials Research

Daniel Chaidez*[1]and Dr. Michael Brady [2]

[1]California Polytechnic Humboldt, [2]Washington State University

Abstract: In the midst of current climate change there have been developments to adapt agricultural sectors to endure the drastic changes in temperature. Sunburn in apples causes an annual loss in yield. The average loss of total production is about ten percent. There have been a few methods used to mitigate the losses due to sunburn. Two of these methods are shade netting and evaporative cooling. The shade netting method prevents some of the solar radiation from reaching the trees and evaporative cooling prevents sunburn by misting water over the trees to ensure that the temperature is not over a certain threshold. The threshold in which sunburn occurs varies with each variety of apple. For this study I used data collected for the crisp

pink and honey crisp varieties. The average threshold of sunburn for each of these varies is 43 and 46 degrees celsius respectively. A portion of the data used came from the annual enterprise budgets for specific orchards. The purpose of this experiment was to create a model to compare the costs of using these methods to their efficiency in preventing sunburn. Being that a budget is a previously observed occurrence, the model uses a trend of forecasted days that sunburn will occur. The goal from creating such a model would be as a tool for decision makers to gain the knowledge of the marginal cost of setting up each of these systems in comparison to the prevention of losses in yields due to sunburn.

The Extent of Hydrophobic Recovery on Nitrogen and Water Vapor Plasma Treated Silk Films

Discipline: Materials Research
Subdiscipline: Materials Research

Ashley Keobounnam*[1], Morgan J. Hawker[2], Chase Lenert-Mondou[3]
[1]California State University, Fresno, [2]California State University, Fresno, [3]California State University, Fresno

Abstract: Silk, derived from the bombyx mori cocoon, is a natural polymer that is widely studied for its mechanical strength, biodegradability, and non-immunogenic properties in biomedical applications. However, inducing specific interactions between silk and cells in vivo is challenging because of its hydrophobic nature. Therefore, modification must be performed to increase surface hydrophilicity. Plasma modification is a polymer modification method that is simple, economical, and solvent-free. Nitrogen and water vapor are both recognized plasma modifications that increase polymer surface polar functional groups. However, plasma-modified polymers often undergo hydrophobic recovery: rearrangement of modified polymer chains from a higher surface energy state to a lower one. This results in negating the plasma modification effects. The hydrophobic recovery of plasma-modified silk has not been previously studied. The goal of this study was to systematically evaluate hydrophobic recovery of nitrogen and water vapor plasma-treated silk films. Films were prepared by dropcasting. After drying, films were plasma modified using optimized plasma parameters. Interactions between plasma-treated silk films and water were examined using water contact angle goniometry. Untreated silk films displayed water contact angles of 69+/-1° while the nitrogen and water vapor plasma-treated films exhibited water contact angles of 35+/-1° and 25+/-2°, respectively, demonstrating a decrease in hydrophobicity. Treated films were aged up to 6 weeks under ambient conditions and analyzed after aging for 7 days, 21 days, and 42 days. Nitrogen and water vapor plasma-treated silk film water contact angles remained consistent throughout the 42 day aging period, suggesting minimal hydrophobic recovery occurred.

Synthesis of Nanostructured FeWO4 Thin Films for Efficient Photoelectrochemical Water Splitting

Discipline: Materials Research
Subdiscipline: Materials Research

Alfred Vargas*[1], Matt Law[2], Logan Brennan[3]
[1]University of California, Berkeley, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: Photoelectrochemical (PEC) water splitting is a prospective method to directly utilize solar energy to produce carbon-free hydrogen fuel. Semiconductor photoelectrodes used in PEC

water oxidation must absorb the energy of photons higher than 1.23 eV to meet the thermodynamic limit for water oxidation and harness a significant portion of the solar spectrum. However, under the oxygen evolution reaction (OER), many semiconductor photoelectrodes are not stable in an aqueous solution because of dissolution and lack of photoactivity during photoillumination. Therefore, in this study, we demonstrate a synthesis procedure that utilizes earth-abundant metals to produce FeWO 4 nanocrystalline thin films that encompass a suitable band gap for water splitting and absorb photons in the ultraviolet-visible (UV-vis) region that are stable in alkaline solutions during OER. This presentation reports efforts to control the morphology and thickness of nanostructured FeWO 4 thin films by tuning spin speeds during the spin coating fabrication and duration of the calcination process to enhance absorptivity. Films are characterized by scanning electron microscopy, x-ray photoelectron spectroscopy, x-ray diffraction crystallography, and UV-vis spectroscopy. Moreover, a bismuth precursor incorporated into the FeWO 4 molecular ink can be used in the synthesis procedure to tune the resulting films. These films will ultimately be electrochemically assessed to measure the activity and stability in order to evaluate the efficacy of the nanostructured Bi-doped FeWO 4 thin films for PEC water oxidation.

p-Wasserstein Distance between High-Dimensional Point Clouds via Persistent Homology

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Liu Zhang*
Yale-NUS College, National University of Singapore (going to start PhD in Applied and Computational Mathematics at Princeton University)

Abstract: Topological Data Analysis (TDA) is a recent field that emerged from various works in applied algebraic topology and computational geometry. The aim of TDA is to extract and analyze relevant topological and geometric features of real-world data, which are often high-dimensional and have complex underlying geometric structures. Our project is motivated by the question: how can high-dimensional point clouds be compared based on their topological structures? To this end, we proposed an approach to compare point clouds based on the p-Wasserstein distance of their topological fingerprints. We illustrated the approach with a concrete application in studying the neural population responses in the primate visual system to different visual stimuli. Each neural population response was represented as a high-dimensional point cloud. Our approach allowed us to quantify the pairwise similarity of the neural population responses in terms of their topological structures. Specifically, we investigated the topological structure of each neural population response to different stimuli (low-frequency gratings, high-frequency gratings, 1- and 3-dot negative flows, and 1- and 3-dot positive flows) and compared each against synthetic data sampled from 2-sphere and torus. Our results showed that in terms of topological structures, the neural response to low-frequency gratings is significantly different from all other types of flow stimuli, which suggests that further investigation in neuroscience could potentially uncover new understanding of the primate visual system.

Displacement Partitions of Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Lucas Chaves Meyles*[1], Ethan Spingarn [2], Richter Jordaan[3], Sam Sehayek[4]
[1]University of California, Los Angeles, [2]Amherst College, [3]Massachusetts Institute of Technology, [4]University of California, Santa Barbara

Abstract: Parking functions are a rich field of study in combinatorics, relating to a myriad of other combinatorial objects such as maximal chains in noncrossing partitions, labeled plane trees, and labeled Dyck paths. Of particular interest is how the displacement vector of a parking function—a vector which records how far each car parked from its preference—relates to these combinatorial objects. Let the displacement partition of a parking functoin be an integer partition wherein one removes all the zeroes from the displacement vector and arranges it in nonincreasing order. In a recent paper by P. Harris, et al., the authors produced a bijection between parking functions of length n with a displacement partition of 1 and ideal states in the Tower of Hanoi game. Our paper generalizes this result. Consider the set of parking functions of length n with displacement partition $1 + \cdots + 1$, with k 1s. Then, this set is in bijective correspondence with the set of surjective functions from $[n]$ to $[n - k]$. The bijection arises by sending component prime parking functions in the original parking function to the number of prime parking functions already uncovered. Moreover, we establish relationships between the displacement partition of a parking function and the number of tree inversions of a labeled plane tree on $n + 1$ vertices.

Enumerating the Superstable Configurations of Path Graphs by the Even Ordered Fibonacci Numbers

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Ava Mock*[1], Gordon Rojas Kirby [2], Susanna Fishel[3], Lucy Martinez[4], Cara Bennett [5], Robin Truax[6]
[1]Wellesley College, [2]Arizona State University, [3]Arizona State University, [4]Rutgers University, [5]Georgia Institute of Technology, [6]Stanford University

Abstract: Parking functions are a well-studied combinatorial family of objects with many meaningful generalizations of parking functions in recent years. In our work, we focus on a generalization known as G -parking functions, which relate to the theory of chip-firing and sandpile models. For a graph G with designated sink vertex q , the G -parking functions can be directly related to chip firing configurations on the graph G –they are precisely the set of superstable configurations of G . In this poster, we focus on the family of examples when the defining graph G is the product P n * q of a path graph and a single vertex, and we establish that the G -parking functions are enumerated by the set of even ordered Fibonacci numbers F 2n .

Near Term Climate Forcers and Interactions with Tipping Points

Discipline: Mathematics
Subdiscipline: Other Mathematics

Riley May*[1], Hannah Back [2], Steffen Eikenberry[3]
[1]Utah State University, [2]University of Iowa, [3]Arizona State University

Abstract: The global earth system is at a precarious state. The actions of mankind are critical to address the upcoming effects of climate change. It is largely agreed by the scientific climate community that there are certain thresholds, such as a 1.5 degrees Celsius change of temperature of the Earth, that when crossed will cause irreversible damage to various ecosystems. Carbon dioxide reduction to net zero in the coming years is critical to avoid major tipping points and various feedbacks. The major feedback into the carbon cycle that this paper analyzes is the permafrost melt. One of the key factors that is largely undervalued is the impact of near term climate forcers on the path to avoid tipping points and feedbacks. Carbon is a millennial gas that has detrimental effects, but many near term climate forcers are overlooked although they have significant radiative forcing. We analyze specifically the impacts of methane reduction pathways to avoid various feedbacks and largely reduce warming. Methane reductions do not substitute for the other efforts to limit carbon emissions. This paper will analyze the significance of methane reduction on protecting the environment. We utilize various RCP scenarios to simulate the emissions of others gases while controlling the emissions of methane. In our research we used the BEAM model to analyze the ocean chemistry and analyze the flow of carbon between sinks.

Convexity of Neural Codes with up to 4 maximal codewords

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Deanna Perez*[1], Anne Shiu[2], Federico Ardila[3], Gustavo Flores[4], Osiano Isekenegbe[5]
[1]California State University, Fullerton, [2]Texas A&M, [3]San Francisco State University, [4]Carleton College, [5]Florida State University

Abstract: A central problem of neuroscience is deciphering the neural code, or identifying the relationship between neural activity and stimuli. We use combinatorial neural codes to record neural activity as a set of codewords. A code is called convex if it can be realized by a family of convex open sets in Euclidean space. Though detecting convexity in arbitrary codes is an NP-hard problem, local obstructions and wheels have been identified to eliminate convexity. Loosely speaking, a local obstruction is incontractible and a wheel has a realization which bends. Items that are incontractible or bend or both violate convexity. It is known that for codes with at most 3 maximal codewords that the absence of local obstructions is equivalent to convexity. This presentation focuses on codes with 4 facets. The nerve lemma allows us to focus our attention to simplicial complexes on 4 vertices where each vertex corresponds to a facet from our code generated by the family of open convex sets. Previous research has shown that certain 4-maximal codes are convex if and only if they do not have local obstructions. We aim to extend this result by classifying the convexity of all 4-maximal codes. Furthermore, we present results in the direction of showing that local obstructions and wheels are the only criterion preventing convexity for such codes.

Racial Bias and Over Policing In Chicago Traffic Stops

Discipline: Mathematics
Subdiscipline: Statistics

Jasmine Hope*[1], Tim Hannifan[2], Amanda Kube[3], Nathalie Valenzuela[4], Antoinette Raggs[5]
[1]North Carolina State Universitty, [2]University of Chicago, [3]University of Chicago, [4]California State University, Fresno, [5]University of Illinois, Chicago

Abstract: Despite being an extremely diverse city, Chicago is one of the most segregated cities in the United States. Due to this segregation, there can be an increase in racial bias and profiling. For example, African Americans make up only 30% of Chicago’s population however, they account for 65% of traffic stops within the city. This would suggest that racial profiling could play a role when deciding to stop someone for a traffic violation. Our study aims to pinpoint the extent of racial bias when it comes to traffic stops and searches as well as determine which districts may be responsible for over policing. In our project we are conducting the veil of darkness analysis based on our calculated inter-twilight period for Chicago to determine if the proportion of African Americans stopped is different when it is light than when it is dark. We will also be using hypothesis testing of hit rates versus search rates to determine the extent of over policing. We are currently in the process of creating the function of time for the inter-twilight period, which will then be used for our analyses. The results of our study will go to BPI Chicago who is a nonprofit that works towards police accountability.

BPI Traffic Stops

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Nathalie Valenzuela*[1], Amanda Kube[2], Tim Hannifan[3], Jasmine Hope[4], Antoinette Raggs[5]
[1]California State University, Fresno, [2]UChicago, [3]UChicago, [4]North Carolina State University, [5]University of Illinois, Chicago

Abstract: In Chicago, African Americans make up roughly 30% of the population. However, they make up for over half of the traffic stops in the city. Our research will look at traffic and pedestrian stops made by police officers in the town to assess the racial bias of the police officers when traffic stops occur. We will analyze the data from districts with higher stop rates, which racial groups are being stopped, and the reasoning behind the stops. The data we will analyze was collected from the Illinois Department of Transportation (IDOT). One method we will be using is the veil of darkness test. This test will help us assess the extent of this bias by looking at the difference in racial stats of the offenders compared to when it is sunny or dark outside. The main idea is that the officers on duty cannot as easily identify the driver's race at night, which will help us with our findings. With the results of our research, we could help improve policing and address the racism and systemic oppression which have led to inequities and injustices in Chicago from the Police department.

Estimating Chromatin Accessibility and Epigenetic Erosion from Single-cell ATAC-seq

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Jorge Lopez-Nava*[1], Alex Lenail[2], Manolis Kellis[3], Gisselle Velez-Ruiz[4]
[1]Swarthmore College, [2]Massachusetts Institute of Technology, [3]Massachusetts Institute of Technology, [4]Broad Institute of MIT and Harvard

Abstract: Transcription factors regulate transcription by cooperatively configuring chromatin loci to be either recalcitrant to or amenable to RNA polymerase engagement. The current best approach for identifying and studying open chromatin regions in the genome at single cell resolution is Single-cell Assay of Transposase Accessible Chromatin sequencing (scATAC-seq). However, there is no current consensus on the best approach to analyze scATAC-seq data. Recently, studies have reported epigenetic erosion, where aging causes degradation of the epigenetic integrity of cells -- this causes previously inaccessible regions to become accessible and vice versa. The goal of this project was to investigate how epigenetic erosion, responsible for changes for chromatin accessibility, can be modeled using epigenetic data from scATAC-seq data. Alignment was performed using an existing tool named Cell Ranger ATAC, a computational pipeline developed by 10xGenomics. Using the outputed fragments file and reference ATACseq peak files, we analyzed a scATAC-seq dataset of the prefrontal cortex in the human brain with

designed metrics. Chromatin accessibility was found to change over the course of aging, and epigenetic erosion was more prevalent in samples with neurodegenerative diseases. The transcription factor footprints were identified in the scATAC-seq dataset. Our approach therefore has potential for uncovering transcription factor combinations required to reverse the effects of epigenetic erosion. Future models will integrate scATAC-seq analysis with that of scRNA-seq to induce target epigenetic and transcriptional phenotypes.

Using Neural Networks and Iterative Methods to Solve Inverse EIT Problems

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Nick Wharff*[1], Dr. Malena Espanol[2], Mason Manning[3], Shelby Horth[4], Jose Alanis[5], Sol Farber[6]
[1]Drake University, [2]Arizona State University, [3]Arizona State University, [4]Wake Forest University, [5]Sacramento State University, [6]Freed Hardeman University

Abstract: Electrical Impedance Tomography (EIT) is a low-cost, portable, and noninvasive imaging system that does not use ionizing radiation. It has many potential applications including the continuous monitoring of lungs, detection of cancerous regions in the body, and industrial uses beyond what is typically recognized in human medicine. EIT formulates a very challenging, nonlinear, highly ill-posed problem. In this project, we investigate, develop, and implement new regularization methods and deep neural network (NN) approaches for solving the EIT inverse problem. In particular, we explore the use of Krylov methods, various regularization operators, and distinct neural network architectures. We compare our approaches with traditional methods and show the benefits of each technique with respect to improvement in spatial resolution as well as computational cost.

Finding Number Sequences in Sets of Flattened Insertion Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Izah Tahir*[1], Pamela Harris[2], Jennifer Elder[3], Amanda Verga[4], Zoe Markman[5]
[1]Georgia Institute of Technology, [2]University of Wisconsin-Milwaukee, [3]Rockhurst University, [4]Trinity College, [5]Swarthmore College

Abstract: A flattened permutation is a permutation in which the leading terms of each run are in increasing order. Unlike permutations, parking functions allow for repeated numbers, and in our research we extend the notion of “flattened” from permutations to parking functions by allowing the leading terms of each run to be in weakly increasing order. To better understand this topic, we focus this presentation on a subclass of flattened parking functions called “flattened insertion parking functions.” These combinatorial objects can be obtained from a permutation of the numbers 1 through n by inserting i numbers between 1 and n to get a parking function of length n+i. Once we provide this insertion, we check if the obtained parking function satisfies the needed condition on weakly ascending runs, which implies that the parking function is flattened. We implemented Sage code to compute the total flattened insertion parking functions when a single digit is inserted into a permutation. Based on these computations, we discovered that the number of flattened insertion parking functions with certain properties are enumerated by the Eulerian numbers, and from this we provided a bijection between our combinatorial objects and set partitions of {1,2,...n}. We will provide some directions for further study in which one can extend our results to explore patterns in insertion parking functions when varying the amounts of numbers inserted into a permutation.

Flattened Parking Functions: Combinatorial Interpretations and Computation

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Zoe Markman*[1], Izah Tahir [2], Amanda Verga[3], Pamela E. Harris[4], Jennifer Elder [5]
[1]Swarthmore College, [2]Georgia Institute of Technology, [3]Trinity College, [4]University of Wisconsin Milwaukee, [5]Rockhurst University

Abstract: Permutations with the quality of being “flattened,” that is, permutations with the leading terms of consecutive ascents in increasing order, are well studied objects in the field of combinatorics. We introduce the new concept of flattened parking functions, which are parking functions for which the leading terms of consecutive ascents are in weakly increasing order. In our work, we study the number of flattened parking functions of length n, and aggregated by the number of runs. After writing and implementing Python and Sage code to produce the patterns present in flattened parking functions, we have discovered a connection to the Eulerian numbers and the Catalan numbers, both of which are some of the longest existing entries in the Online Encyclopedia of Integer Sequences. We introduce and prove a new enumerative result establishing that flattened parking functions with 1 run are enumerated by the Catalan numbers. We also establish that flattened parking functions with two runs, that have exactly one duplicated value of 1 while all other numbers appear exactly once, are enumerated by the Eulerian numbers. This last result follows from a bijective proof between our combinatorial objects and the number of permutations of length n with one ascent.

Displacement in Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Ethan Spingarn*[1], Gordon I. Rojas Kirby [2], Lucas Chaves Meyles[3], Richter Jordaan[4], Sam Sehayek [5]
[1]Amherst College, [2]San Diego State University, [3]University of California, Los Angeles, [4]Massachusetts Institute of Technology, [5]University of California, Santa Barbara

Abstract: A parking function is a sequence of integers of positive integer length n whose entries take values ranging from 1 to n, such that, if you rearrange the sequence into ascending order, the ith entry is less than or equal to i. A helpful heuristic goes as follows: suppose n cars want to park in n consecutive parking spots along a one-way street and each car has a preferred parking spot. Each car initially tries to park in its preferred spot. However, if that spot is already occupied, then the car will park in the next available spot. Parking functions are preference assignments that result in every car being able to park. Given a parking function, a car’s displacement is the difference between that car’s preferred spot and the spot where the car parks. The parking function’s displacement partition is the partition of the total displacement k into the sum of the cars’ nonzero displacements. From these definitions, a question arises; given a length and an integer partition, how many parking functions are there with that length and displacement partition? In this presentation, we give a partial answer that addresses the case when the partition of k is $1+...+1$ k times. We provide a bijection between parking functions of length n with this type of displacement partition and surjections from the set $[n]$ to the set $[n-k]$. In addition, we give formulas for other infinite families of displacement partitions, such as when exactly one or two cars are displaced.

Statistics of Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Juliet Whidden*[1]and Gordon Rojas Kirby [2]
[1]Vassar College, [2]San Diego State University

Abstract: A parking function p is a sequence of positive integers (a_1,a_2,...,a_n) such that p contains at least i values less than or equal to i for all i \in {1,2,...,n} . These are well-studied combinatorial objects that are a superset of permutations. We extend the study of statistics on permutations to parking functions and enumerate parking functions that satisfy certain constraints. We focus on ascents, where a_i<a_{i+1} , descents, where a_i>a_{i+1} , and ties, where a_i=a_{i+1} , and look at how often they occur and where they are most likely to appear. Specifically, we explore the number of parking functions of length n with k ascents/descents for k>0 , which has yet to be completely enumerated. We give formulas for how many parking functions exist with a certain number of descents or a fixed set of indices where descents occur while drawing connections to other objects such as Dyck paths and Prüfer codes.

Modeling Environmental Factors Effects on Valley Fever Incidence Rates

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Jacob Caraccilo*[1]and Mario Banuelos [2]
[1]Fresno State University, [2]Fresno State University

Abstract: Coccidiomycosis , also known as Valley Fever, is a disease caused and transmitted by the fungi Coccidioides immitis and Coccidioides posadasii . The disease affects the lungs and is endemic to arid regions within the southwest United States. While studies have been conducted to analyze disease severity and quantify risk factors, few focused on creating a mathematical model to study and quantify specific environmental parameters which affect transmission. Valley fever is not typically spread from person to person, so understanding environmental factors which affect transmission can help us better predict future occurrences of the disease. Using publicly available data from the last two decades, we construct mathematical models which consider factors such as air quality, water temperature, wildfires, and climate change in our study. Specifically, we use decision trees and deep learning to investigate patterns between those specific environmental parameters and case occurrences. With this research, our goals include better informed future predictions of case occurrences based on these environmental factors and identifying possible non-environmental factors which could serve as the basis of future studies.

Metrics on Ideals and the Hausdorff Distance

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Zoe Batterman*[1]and Konrad Aguilar [2]
[1]Pomona College, [2]Pomona College, Mathematics Department

Abstract: Calculating distances between sets has led to many breakthroughs in imaging, metric geometry, and object recognition. One of the main methods used to calculate these distances employs the Hausdorff distance. In general, it is computationally demanding to calculate this distance explicitly due to its analytic structure. However, there is a new metric introduced by Aguilar that is topologically equivalent to the Hausdorff distance on certain spaces that uses a discrete and therefore, more manageable structure. In particular, Aguilar's metric calculates distances between ideals of approximately finite-dimensional algebras. When the algebra is commutative, it is isomorphic to a space of complex-valued continuous functions on a compact metric space, (X, d). The ideals in this case are in bijection with the closed subsets of X, which induces a metric on the closed subsets of X, which is Aguilar's metric. To understand this new metric in an explicit way, we calculated distances using Aguilar's metric and found enlightening comparisons with the Hausdorff distance. This has also led us to develop and introduce our own metric between subsets of certain spaces. Thus, this presentation focuses on these calculations and their proofs as well as their comparisons.

The Three Rows Game: Repetitions in the Pak-Stanley Labels for Path Graphs

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Robin Truax*[1], Gordon Rojas Kirby[2], Susanna Fishel[3], Pamela Harris[4]
[1]Stanford University, [2]Arizona State University, [3]Arizona State University, [4]Williams College

Abstract: Given a simple graph G, one can define a hyperplane arrangement called the G-Shi arrangement. The Pak-Stanley algorithm labels the regions of this arrangement with G-parking functions. When G is a complete graph we recover the full Shi arrangement, and the Pak-Stanley labels give a bijection with ordinary parking functions. However, for proper subgraphs $G \subset K_n$, while the Pak-Stanley labels still include every $(G * 0)$-parking function, they may repeat a parking function multiple times. These repetitions are a topic of interest in the study of G-Shi arrangements and G-parking functions, and since G-parking functions are connected to many other combinatorial objects, these repetitions have implications for the study of those objects as well. We develop a classification theorem for repetitions in the Pak-Stanley labels of the regions of G-Shi arrangements, where G is a path graph. To do so, we translate the problem into a combinatorial model about patterns of moves in what we call ``The Three Rows Game". Analyzing the histories of this game and the ways in which they can induce the same outcomes allows us to characterize the repetitions in the Pak-Stanley labels. This characterization yields many interesting results, including which parking functions appear only once, which parking functions appear the most often, and so on. Finally, we discuss the implications of this work, and how other families of graphs can be analyzed using similar techniques.

Geometric Framework for Statistical Analysis of Eye Tracking Heat Maps, with Application to a Tobacco Waterpipe Study

Discipline: Mathematics
Subdiscipline: Statistics

David Angeles*
The Ohio State University

Abstract: Health warning labels have been found to increase awareness of the harmful effects of tobacco products. An eye tracking study was conducted to determine the optimal placement of a health warning label for hookah pipes. Three areas of interest (AOIs) were considered for comparison: water bowl, stem and hose. Participants viewed images that contained one of four waterpipes, one of three warning labels, and placed in one of the AOIs. Typically, summary statistics such as total dwell time, duration score, and number of fixations on an AOI have been the focus for determining such placement. However, these summary statistics fail to capture the complete variability of eye movement over the entire image domain. Instead, we propose heat map estimation of eye coordinates via kernel density estimation, which are nonparametric, bivariate pdfs. For statistical analysis of heat maps, we use the Riemannian-geometric framework based on the Fisher-Rao metric. This metric-based framework enables efficient comparisons of heat maps, statistical summarization and exploration of variability of a sample of heat maps through the Karcher mean and principal component analysis, and metric-based clustering.

Bond Lattices and Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Bianca Teves*[1]and Susanna Fishel [2]
[1]Haverford College, [2]Arizona State University

Abstract: Parking functions are a well-studied combinatorial object with numerous connections to other structures like trees and posets. Parking functions can also be seen in the maximal chains of the noncrossing partition lattice NC_{n}, an important partially ordered set (poset) that relates all noncrossing set partitions on the integers 1 through n. Just as there are $(n+1)^{(n-1)}$ parking functions of length $n-1$, there are $(n+1)^{(n-1)}$ maximal chains in NC_{n}. What happens when we focus on a subposet of the noncrossing partition poset? In 1964, Rota introduced a family of posets called bond posets, each of which corresponds to a graph. It turns out that the bond lattice of a certain family of graphs, the triangulation graphs, is always a subposet of NC_n and therefore encodes a particular subset of the parking functions of length $n-1$. We describe how a triangulation graph determines what parking functions are expressed and not expressed in its bond lattice. We also explore how the bond lattice shows up in other settings related to parking functions, such as rooted forests. A paper from a previous REU group found that the bond posets of certain triangulation graphs have the same number of maximal chains as there are ordered cycle decompositions on n integers. Anders and Archer showed that each ordered cycle decomposition corresponds to a rooted unimodal forest. Although there exist many bijections between parking functions and rooted forests, we want to find the mapping between unimodal rooted forests and parking functions that appear in the bond lattice.

The Future of Southern Rockhopper Penguins in the Face of Climate Change

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Nina Pyron*[1], Amanda Laubmeier [2], Emily Svetlik[3], Bridgette Epps[4]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University

Abstract: Southern Rockhopper Penguins are a well known species, as they are featured prominently in zoos and various media sources. This makes these penguins an ideal species to observe when addressing the effects of climate change on a local population, as their husbandry and behavioral patterns are well studied. S. Rockhoppers rely on krill as their main source of prey, which has been majorly impacted by the effects of climate change. We hypothesize that as air temperatures increase, the amount of krill will decline and penguin populations will

plummet. To investigate how temperature changes will affect S. Rockhopper penguins, we created a mathematical model that would replicate S. Rockhopper decline with fluctuations of temperature. This model consisted of two sets of equations: continuous differential equations and discrete differential equations. Our continuous model described the decline of the species during the winter foraging period, with krill being consumed and penguins dying from either natural causes or starvation, influenced by the availability of the krill. The discrete model described growth of krill and penguins during the summer mating months, which is directly dependent upon temperature. As a consequence of ice caps melting in the Southern Ocean, local waters begin to chill. Lower water temperatures stunt krill growth and cause a penguin food shortage. Using our model, we demonstrate that krill decline due to low temperatures will cause S. Rockhopper penguins to experience exponential decline. Thus, we demonstrate that climate change directly contributes to the demise of S. Rockhopper penguins.

Assessing the Correlation between Bird Migrations, Climate, and West Nile Virus

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Daniela Rodriguez-Chavez*[1], Morgan Gorris [2], Andrew Bartlow[3]
[1]Cornell University, [2]Los Alamos National Laboratory, [3]Los Alamos National Laboratory

Abstract: West Nile virus (WNV) is the largest cause of mosquito-borne illness in the contiguous US and primarily circulates between birds and mosquitoes. Passerine birds, such as American Robins and Blue Jays, are amplifying hosts and can act as super-spreaders of the disease, especially along migration routes. With climate change causing earlier, warmer springs that are changing the timing of bird migration, understanding how changes in seasonal patterns of bird arrival affect outbreaks of WNV will be crucial for public health. Earlier arrivals of highly competent species may lead to an increased spillover window, causing more WNV cases. Alternatively, the increased presence of other, less competent bird species over time may provide a dilution effect, lowering case counts. County-level preliminary analysis was conducted on Arizona from 2001-2020 due to their high prevalence of WNV. We used climate data from PRISM Climate Group at Oregon State University, American Robin sightings from the Global Biodiversity Information Facility, and neurodegenerative WNV cases from the US Centers for Disease Control and Prevention. We chose robins due to their wide distribution and high transmission competence. From these data, we confirmed significant positive correlations between temperature and cases, and significant negative correlations between temperature and robin migration arrival date. Because relationships between arrival date and cases may be influenced by the addition of other Passerines, like the American Crow, we are actively expanding this analysis to include such species and analyzing the contiguous US over the past two decades, which will aid in predicting future outbreaks.

Preferential and k-Zone Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Christopher Soto*[1], Pamela E. Harris [2], Parneet Gill[3], Pamela Vargas[4]
[1]Columbia University, [2]Williams College, [3]Fresno State, [4]Smith College

Abstract: Parking functions are vectors that describe the parking preferences of n cars that enter a one-way street containing n parking spots numbered 1 through n. A list of each car’s preferences is also compiled into vectors in which we denote as (a_1, ..., a_n), such that a_i is the parking preference for car i. The classical parking rule allows cars to enter the street one at a time going to their preferred parking spot and parking, if that space is unoccupied. If it is occupied, they then proceed down the one-way street and park in the first available parking spot. If all cars can park, we say the vector (a_1, ..., a_n) is a parking function. We introduce new variants of parking function rules with backward movement called k-Zone, preferential, and inverse preferential functions. We study the relationship between k-Zone parking functions and I-Naples parking functions and count the number of parking functions under these new parking rules which allow cars that find their preferred spot occupied to back up a certain parameter. One of our main results establishes that the set of non-increasing preference vectors are k-Naples if and only if they are k-Zone. For one of our findings we provide a table of values enumerating these new combinatorial objects in which we discover a unique relationship to the order of the alternating group A_{n+1}, numbers of Hamiltonian cycles on the complete graph, K_n, and the number of necklaces with n distinct beads for n! bead permutations.

Generalized Splines over Complete Graphs

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Makayla Hall*[1]and Naomi Krawzik [2]
[1]Sam Houston State University, [2]Sam Houston State University

Abstract: Consider a graph G with edges defined by ideals in the polynomial ring R for two variables with coefficients from a field. A generalized spline was introduced by Gilbert, Polster, and Tymoczko as a label on the vertices in such a way that the difference between any two adjacent vertices determines the ideal of the edge label. For a graph, the collection of splines forms an R-module. This talk explores methods of creating a basis for the R-module of generalized splines when the graph G is a complete graph.

On Permutation Invariant Parking Sequences

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Gabriel Sargent*[1], Eric Pabón-Cancel [2], Douglas Chen[3], Juan Carlos Martinez Mori[4], Pamela Harris [5]
[1]University of Notre Dame, [2]University of Puerto Rico, Mayagüez Campus, [3]Johns Hopkins University, [4]Cornell University, [5]Williams College

Abstract: Suppose n cars of various sizes seek to park on a one-way street. Let x be a vector that contains the preferred parking spots for each car. A car is able to park at a spot k if, beginning with k, there are enough consecutive open spots for it to fit (based on the car's size). The cars take turns parking, and each initially tries to park at its preferred spot; if it is unable to do so, it continues driving forward in the street until it is able to park. If all cars are able to park in this process, we say that the preference vector x is a parking sequence. When the lengths of all cars are exactly one, parking sequences are exactly the set of parking functions. Therefore parking sequences are a natural generalization of parking functions which allow cars to have positive lengths greater than or equal to 1. While parking functions have the property of permutation invariance--any permutation of a parking function is also a parking function--parking sequences do not always have this property. In this work, we contribute to the theory of permutation invariant parking sequences and study the necessary and sufficient conditions for parking sequences to have this property. In particular, we provide a characterization of permutation invariant parking sequences in the special case where all cars have the same length.

A Combinatorial Proof for the Enumeration of Certain u-Parking Functions

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Douglas Chen*[1], Eric J. Pabón-Cancel[2], Gabriel Sargent[3], Juan Carlos Martinez Mori[4], Pamela E. Harris[5]
[1]Johns Hopkins University, [2]University of Puerto Rico, Mayagüez Campus, [3]University of Notre Dame, [4]Cornell University, [5]Williams College

Abstract: Let u be a non-decreasing sequence of n positive integers. A u-parking function is a sequence x of n positive integers such that its non-decreasing arrangement satisfies the following: every term in the non-decreasing arrangement is at most the corresponding term in u. We study the enumeration of u-parking functions when u is an arithmetic progression, say with first term a and common difference b. The number of such u-parking functions is a times a+bn raised to the n-1 power (Foata and Riordan, 1974; Yan, 2000). In our work, we consider an alternative combinatorial proof of this counting formula employing the "circular parking lot" argument used by Pollak (Pollak, 1974) in his classical proof enumerating the number of parking functions of length n.

Exploring the Effect of a Mutation in Ducci's Four-Number Game

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Anish Suresh*[1], Dominic Klyve[2], Kieran Cook[3], Tasha Fellman[4], Mason Fishell[5]
[1]Rutgers University Honors College - New Brunswick, [2]Central Washington University, [3]Central Washington University, [4]University of Illinois at Urbana-Champaign, [5]Kenyon College

Abstract: Ducci's Four-Number Game is a fun introduction to number theory starting simply with a square game board that has four positive integers on each corner. The game begins by labeling the midpoints of each side and taking the positive difference between the corresponding edge's two corners. Finally, the midpoints are connected and the game repeats. Our team explored how much information can be learned about this straightforward game. This includes the final convergence values (if any exist), the speed of convergence, and extension of the game to rational, negative, and even complex numbers. However, let us consider a slightly more complex problem. What if there is a chance that one side's positive difference is off by a value at every iteration? How does this affect our previous questions? In order to learn more, running simulations and repeated trials of the game was key. After running over 100,000 randomly generated starting values between 1 and 2 32 , a few conclusions were reached: 1. If there is a guaranteed error every iteration, then the values never converge to (0,0,0,0), the only proven convergence point for the original game, and 2. All plots were exponential decay, with error rate being 50% and the error value being +1. Our goal is to study this behavior and understand how the half-life depends on the chance for error and the error value. This presentation will summarize these and other results of the CC-REU NSF summer REU experience (DMS-2050692) where these questions were explored.

Some Results of k-almost τ(n)-primes

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Dario Cruzado*[1]and Dr. Reyes Ortiz Albino [2]
[1]University of Puerto Rico, Mayagüez, [2]University of Puerto Rico, Mayagüez

Abstract: The theory of τ (n) -factorizations and τ (n) -products were first introduced and defined by Anderson and Frazier in 2006. As an example in the Theory of Generalized Factorizations they used the relation τ (n) , which is the equivalence relation modulo n on the non zero, non invertible integers as a restriction on the multiplicative operation. That is, a τ (n) -product is the product of elements that are related under τ (n) . In 2007, Hamon characterized the form of the integers known as the τ (n) -primes. In 2021, Ortiz and Cruzado introduced the notion of the semi τ (n) -primes which are integers that are a result of the usual product of exactly two τ (n) -primes and provided a characterization of their form. This ongoing work further studies such elements and extends the notion, as a generalization, to the k -almost τ (n) -primes; an integer is called a k -almost τ (n) -prime if it has k (not necessarily distinct) τ (n) -prime factors. We provide some examples and properties of them. Moreover, we use known results related to the distribution of prime numbers (respectively k -almost primes) to analyze the distribution of the τ (n) -primes (respectively the k -almost τ (n) -primes).

The Study of t(n)-primes

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Eric Pabon-Cancel*[1]and Reyes M. Ortiz-Albino [2]
[1]University of Puerto Rico, Mayagüez Campus, [2]University of Puerto Rico, Mayagüez Campus

Abstract: The theory of t(n)-factorizations was first defined in 2006 by Anderson and Frazier; since 2007, Hamon, Juett, among others have developed this theory. Many results have been obtained in terms of algebraic structure classification, but very little about some types of elements that have arisen. For example, is the concept of t(n)-prime elements, which are analogue to the primes in the usual product. Unfortunately, the only properties we know is a characterization of their form. And the fact that each t(n)-factorization into t(n)-primes is unique if it exists. In our recent work, we focused on studying the distribution of t(2)-primes and t(3)-primes, respectively. This gave us an idea on the structure of t(n)-primes distribution for other values of n. We noticed that if k is a t(2)-prime, then each equivalence class modulo k contains at least one t(2)-prime. This property also holds when k is a t(3)-prime and t(6)-prime as well. We suspect this also occurs in a more general form. This is analogue to the idea that the prime numbers are distributed among all equivalence classes modulo a prime. Therefore, we have studied the equivalence classes modulo k that contain t(n)-primes. From this, possible results regarding the Euler totient function may arise in the theory of t(n)-products. We show examples and ongoing results.

Pokemon GO: Best Raid Boss Attacker

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Pablo Castro*[1]and Jonathan Brown [2]
[1]Bakersfield College, [2]Bakersfield College

Abstract: We expanded on previous work on the game theory of Pokemon GO and made an interface. This app will allow users to access lists of the best Pokemon to use against a particular

raid boss based on information provided by the user (Information such as the name of the raid boss, current weather conditions in the area, etc.). These lists are generated by novel mathematical models we have built and models built by previous research groups.

Numerical and Experimental Aspects of Electrochemical Corrosion Damage Modeling

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Patrick McDonough*[1], Sheradyn Ruef[2], Cynthia Flores[3], Scott Feister[4]
[1]California State University Channel Islands, [2]California State University Channel Islands, [3]California State University Channel Islands, [4]California State University Channel Islands

Abstract: In corrosive environments, materials can experience electrochemical damage that couples with the propagation of cracks. There are multiple numerical codes, but none support electrochemical models of corrosion. Peridigm (originally created by Sandia National Laboratories) is a computational peridynamics code for multi-physics simulations. Since it is designed for coupling, it can be extended to model crack propagation and material damage due to the electrochemical corrosion process. However, installing Peridigm is remarkably difficult. Another peridynamic code is Peripy, which allows for better dissemination of our model to industry. Our preliminary work is performed on the Cori supercomputing cluster at the National Energy Research Scientific Computing Center (NERSC). The proposed model accounts for both mechanical and electrochemically-induced damage. The combination of these causes corrosion and their coupling causes challenges for simulations, necessitating a solution such as peridynamics. Results are focused on writing a new input deck and modifying an existing code by adding a new subsystem that computes the mechanics of the corrosion penetration scalar field. This captures the dynamics of damage due to the electrochemical effects of corrosion in the numerical simulation. Currently, these tools are used in conjunction with input decks such as “tensile stress,” “fragmenting cylinders,” “waves in bar,” and industrial applications. Our model’s correctness can be demonstrated by comparing results with physical simulations.

MERG

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Serina Cabrera*[1], Omayra Ortega[2], Geoffrey Knoll[3], Dirk Tolson[4], Dustin Yan[5]
[1]Sonoma State University, [2]Sonoma State University, [3]Sonoma State University, [4]Sonoma State University, [5]Sonoma State University

Abstract: An ordinary differential equations based model for Sonoma State University (SSU) is proposed. The model is based on SEAIRV including both vaccinated and unvaccinated individuals. Simulations were conducted using R to explore the effectiveness of higher or lower vaccine uptake in the community. Special focus will be placed on Vaccination rates to help better the SSU community to move forward with opening up the campus. We monitored vaccination rates through October 2021-February 2022 and compared the differences. When conducting our model, being boosted was not accounted for and we do not differentiate between the different vaccines but assume that each has received a full dosage of the respective vaccine they have chosen.

SARS-CoV-2 mitigation measurements using epidemiological modeling

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Adrian Marquez*[1]and Maytee Cruz Aponte [2]
[1]University of Puerto Rico at Cayey, [2]University of Puerto Rico at Cayey

Abstract: The COVID-19 pandemic has taught us how lethal infectious diseases can be, as mortality figures seem to increase rather than decrease. As a relatively novel virus, it is clear we do not understand its complexity and underlying mechanisms. However, through advances in Mathematical Epidemiology, we can usually study disease behaviour at a multi-scale level and COVID-19 is no exception. In this work, we focus on explaining the fundamental principles of how epidemiological models can help us describe disease spatial spreading and the pivotal role of “human mobility parameters” in these models. We also discuss our approach for calculating mobility parameters in the models, which will be of crucial importance to building a “metapopulation model”. The purpose is to apply these methods to our ongoing research and discover through mathematical simulations effective ways to slow down COVID-19 spread in Puerto Rico, or any other region by applying interventions such as social distancing and vaccination. In doing so, we would like to develop a general metapopulation epidemiological model that accounts for human mobility, so it serves as a foundation to simulate future diseases and raise awareness to the community.

Sonoma State University Covid-19 Model Disparities on African-American Community

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Dirk Tolson*[1], Serina Cabrera [2], Geoffrey Knoll[3], Dustin Yan[4], Dr. Omayra Ortega [5]
[1]Sonoma State University, [2]Sonoma State University, [3]Sonoma State University, [4]Sonoma State University, [5]Sonoma State University

Abstract: A model for Covid-19 infection within the Sonoma State University (SSU) community is proposed. This simplified differential equation-based model considers a closed population of students, faculty, and staff at SSU in Rohnert Park, CA. Positive cases on Sonoma State's campus were tracked and a visualization of the prevalence over time was created. A SEAIRV and VEAR model which includes both vaccinated and unvaccinated individuals, as well as, asymptomatically and symptomatically infected individuals is proposed. A basic reproductive number R Naught (Ro) of 3.3427 is calculated for the system using the next-generation matrix method and without intervention, the virus would spread in the population. Simulations in R were conducted to explore the effectiveness of higher or lower vaccine uptake in the community. With regulations and policies changing throughtout the year, the continuing use of masks and social distancing is recommended and increasing the proportion of vaccinated individuals on campus to 100%, which is a stated goal of the university, would also serve to reduce the total number of cases in the population. In addition, a model for disparities of Black People/African Americans in Sonoma County is also implemented into analyzing the correlation of Covid-19 for Black/African-American students, faculty, and staff on campus at Sonoma State University. Our goal is to analyze the causes and effects Covid-19 has on the Black People and to understand the different disparities in order to bring awareness to the community.

A Bayesian Nonparametric Model for Analyzing Freely-Diffusing smFRET Data

Discipline: Mathematics
Subdiscipline: Other Mathematics

Jared Hidalgo*[1]and Roberto Rivera Santiago [2]
[1]University of Puerto Rico - Mayaguez Campus, [2]University of Puerto Rico - Mayaguez Campus

Abstract: Experiments using single-molecule Förster resonance energy transfer (smFRET) techniques have greatly contributed to studies regarding conformational states of significant biological molecules. Such progress allows further examination of complex dynamics of highly flexible systems such as intrinsically disordered proteins. The goal of our work is to capture the conformational dynamics during a freely-diffusing smFRET experiment. This is accomplished by representing a Hierarchical Dirichlet Process (HDP-HMM) framework in a way that distinguishes between photon-bursts (enzyme is in front of the camera) and background noise (enzyme is not in front of the camera). We present a Python code that can model surface-immobilized smFRET experiments and discuss how a Markovian model with an auxiliary background state will be used to extend the Python algorithm to also capture conformational dynamics from freely-diffusing smFRET experiments.

Accounting for the effect of reporting delays in estimation of infectious disease dynamics using pathogen genetic sequences

Discipline: Mathematics
Subdiscipline: Statistics

Catalina Medina*[1], Vladimir Minin [2], Julia Palacios[3], Lorenzo Cappello[4]
[1]University of California, Irvine, [2]University of California, Irvine, [3]Stanford University, [4]Universitat Pompeu Fabra

Abstract: The ongoing pandemic demonstrated that fast and accurate analysis of continually collected infectious disease surveillance data is crucial for estimating key parameters of infectious disease dynamics. Phylodynamic analysis uses genetic sequences of the pathogen to estimate changes in its genetic diversity in a population of interest, which can be interpreted as changes in disease prevalence – the number of infections in the population. Phylodynamics is an important tool because it offers a data source free from sampling biases other surveillance data suffer from (e.g., preferentially testing symptomatic individuals). Unfortunately, it takes weeks or months to deposit the sampled pathogen genome into a database. This reporting delay limits current analyses to a time window up to a date the researchers believe most, or all sequences would have been reported by. Here we present a method to facilitate reliable estimation of the prevalence trajectory closer to the time of data collection, allowing for dynamic health policy decisions based on more recent data, with a better understanding of the limitations and uncertainties of such estimation. Our work uses readily available historic times between sampling and sequencing for a population of interest, and incorporates this information into the sampling intensity model to mitigate the effects of reporting delay in real-time analyses by adjusting for the proportion of samples actually known at a given time. We illustrate our methodology on simulated data and on SARS-CoV-2 sequences collected in California during 2020-2021.

An Approximation of the Modulus of the Family of Edge Covers

Discipline: Mathematics

Subdiscipline: Applied Mathematics

Adriana Ortiz Aquino*[1]and Nathan Albin [2]
[1]Kansas State University, [2]Kansas State University

Abstract: Modulus on graphs is a very flexible and general tool for measuring the richness of families of objects defined on a graph. It has been shown that the modulus of special families generalizes classical network theoretic quantities such as shortest path, max flow/min cut, and effective resistance. Our focus is on the p -modulus of the families of edge covers, specifically on the family of fractional edge covers on an unweighted, undirected graph. Direct computation of the modulus can be expensive because these families tend to be exponentially large, leading to a large number of constraints for the modulus problem. Furthermore, computing the modulus of edge covers is difficult (no known efficient algorithm), but if we could compute the modulus of fractional edge covers we obtain an upper bound for the modulus of edge covers. Through the theory of Fulkerson blocking duality, every family of objects has a corresponding dual family, whose modulus is closely related to the modulus of the original family. Our results show that the dual family of fractional edge covers is the family of stars, which greatly reduces the number of constraints for the p -modulus problem and allows us to calculate the modulus of fractional edge covers. Our goal is to give an approximation for the modulus of edge covers using the modulus of fractional edge covers, and to study the complexity of calculating the modulus over these families of graph objects.

Synthetic aperture radar inverse scattering reconstruction using convolutional neural networks

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Jacqueline Alvarez*[1]and Roummel F. Marcia [2]
[1]University of California, Merced, [2]University of California, Merced

Abstract: Synthetic aperture radar (SAR) is a remote sensing technique used to obtain high-resolution images and one of the main challenges is the reconstruction of these images. We present a study to address the reconstruction of SAR images using machine learning. From previous work, we utilize a single, fully-connected layer to learn the sensing matrix of the forward scattering problem by using a set of reflectivites as the inputs and the SAR measurements as the outputs. Using this result, we estimate the reflectivity of the SAR measurements by applying the conjugate transpose of the learned sensing matrix to the SAR measurement data. Then we further improve the reconstructions of the reflectivity using convolutional layers. Employing a training set made up of 50,000 images of randomly placed point scatterers as the reflectivities, we simulate SAR measurement data using a physical model for the sensing matrix. The model is trained to reconstruct images containing a single target. We find that the resulting reconstructions are sharper images than those from the initial estimate from applying the conjugate transpose of the learned sensing matrix. In particular, we find that the background noise is significantly decreased. In addition, we test this model on a different dataset with multiple targets as reflectivities. Similar to previous results, and with no additional training, the model applied to data with multiple targets also demonstrated improved reconstructions of reflectivities.

How Inconsistent Patterns of Healthcare System Usage Impact Statistical Analyses in Censored Time-to-Event Settings with Application to Indian Health Services Data

Discipline: Mathematics
Subdiscipline: Statistics

Kyle Conniff*[1], Dan L Gillen [2], Luohua Jiang[3], Joan O'Connell[4]
[1]University of California Irvine, [2]University of California Irvine, [3]University of California Irvine, [4]University of Colorado Denver

Abstract: Electronic health records (EHRs) have grown in popularity for healthcare research in the recent decade. While they provide cheap access to large amounts of observational health data, they also come with a long list of potential biases, including but not limited to confounding bias, selection bias, informed-presence bias, and misclassification bias. An unstudied bias results when patients utilize multiple healthcare systems (referred to as "system migration" hence forth). Since system migration patterns are typically unknown in EHR data, the time of disease onset can be unclear for a given patient. This bias is of particular concern in, for example, studying risk factors of the time-to-dementia onset in the Indian Health Services (IHS) EHR data. Many American Indian and Alaskan Native (AI/AN) patients using the IHS also have access Medicare, Medicaid, and/or private insurances, which offer them flexibility in choosing a healthcare system. This flexibility results in two different patterns of system-usage: 1) patients who routinely use IHS and 2) patients who migrate between systems. Ignoring the system migration of select patients will bias effect estimates toward the null. We propose extending the Cox proportional hazards model—a regression method for analyzing the relationship between covariates and time-to-event in the censored survival data setting—to (1) identify potential cases of system migration and (2) map migrated patients' IHS diagnosis times to a routine system visit time. Simulation studies and an application to IHS data highlight how our model reduces bias and is instrumental in producing valid and replicable research in AI/AN healthcare.

Multi-fidelity information fusion for modeling ocean acidification

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Anna Diaz*[1], George Karniadakis [2], Xuhui Meng[3]
[1]Heritage University, [2]Professor in the Department of Applied Mathematics, [3]Department of Applied Mathematics

Abstract: We propose to improve the predicted accuracy of ocean acidification by multi-fidelity modeling using a mixture of high-fidelity (high resolution) data and low-fidelity (low resolution) data in order to assess pH levels in Boston Harbor, Massachusetts. The marine ecosystem and the global environment are strongly affected by ocean temperature/acidification. To accurately predict ocean acidification, big data of high quality are required, which is impractical. Meanwhile, plenty of low-fidelity data which are cheap (e.g., satellite data), are available. Updating the model with low-fidelity data in regions with high uncertainty will improve the prediction accuracy of sea surface temperature (SST). Multi-fidelity Gaussian process regression (MF-GPR) makes use of both the low and high-fidelity data to enhance the model's predicted accuracy and produce a low error. We apply the MF-GPR using the satellite and in-situ data to advance the understanding of the effect of ocean temperature/acidification on the marine ecosystem and the global environment. Using mathematical models in conjunction with a combination of the available data (satellite, in-situ measurements) to predict the mean SST as a function of space and time and analyze its corresponding uncertainty. We demonstrate that the multi-fidelity model is able to approximate SST with good accuracy by fusing the high-fidelity and low-fidelity data.

Rockhopper Penguins and Illegal Fishing

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Bridgette Epps*[1], Amanda Laubmeier [2], Emily Svetlik[3], Nina Pyron[4]
[1]Texas Tech University, [2]Texas Tech University, [3]Texas Tech University, [4]Texas Tech University

Abstract: Human activity is causing a drastic decline in the population of Southern Rockhopper Penguins in the Falkland Islands. In addition to climate change and loss of habitat, illegal krill fishing may contribute to Rockhopper Penguin decline. Limits on krill fishing in the Falkland Islands are poorly enforced. High fishing rates can cause mass starvation rates of Rockhopper Penguins, because krill makes up 80% of their diet. We hypothesize that increased krill fishing rates will cause Rockhopper Penguins to die at a rapid pace. To study this, we developed mathematical models for Rockhopper Penguin populations. Using ordinary differential equations, we describe krill consumption, adult and juvenile death rate, the starvation rate of adults and juveniles based on krill available, and the fitness of the adult Rockhoppers. Using discrete difference equations, we describe the birth pulse of krill, adults, and juveniles. In Matlab, we simulated the model using three different fishing rates: one for legal fishing, one for the actual rate that is being fished, and one for the potential increase of future fishing. We found that if fishing rates continue to increase, then the Rockhopper population will continue to decrease drastically. We also show that if the Falkland Islands enforce the fishing limit more strictly, then it is possible that the population of Rockhoppers will return to a healthy population. We therefore conclude that the increased krill fishing causes the Rockhoppers to decline in numbers and that the Falkland Islands must strictly regulate fishing to avoid Rockhopper decline.

Partial Ordering and Properties of Neural Codes Preserved Under Morphisms

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Yasmeen Shaw*[1], Anne Shiu [2], Federico Ardila[3], Saber Ahmed[4], Gradmar Maldonado Marti [5], Mateo Morales[6]
[1]University of Texas at Dallas, [2]Texas A&M, [3]San Francisco State, [4]University of Texas at Arlington, [5]University of Puerto Rico, Mayagüez, [6]University of California Berkeley

Abstract: Neural codes are a tool that can be used to understand neural activity and the behavior of a group of neurons. There are significant biological implications when we are able to study these neural codes and determine properties of them. The study of neural codes is a fairly new field, in which most papers exploring properties of neural codes focus primarily on open convexity. In our research, we concentrate more on closed convexity and non-closed convexity in relation to partial orderings arising from morphisms. We use algebraic methods to generalize a result from Amzi Jeffs, proving that properties that are closed under finite intersections are preserved under morphisms. Furthermore, we prove that if a code has up to k maximal codewords, the image under a morphism has also up to k maximal codewords by utilizing trunks. We also describe results in the direction of finding minimally non-closed convex codes that are open convex. We conclude with open questions left to be explored.

Morphism of Neural codes

Discipline: Mathematics

Subdiscipline: Mathematical Biology

Mateo Morales*[1], Yasmeen Shaw [2], Gradmar Maldonado[3], Federico Ardila[4], Anne Shiu [5], Saber Ahmed[6]

[1]University of California, Berkeley, [2]University of Texas, Dallas, [3]University of Puerto Rico, Mayagüez, [4]San Francisco State University, [5]Texas A&M University, [6]Hamilton College

Abstract: Title: Morphisms of Neural Codes Our work is in the intersection of Biology and Mathematics. We study neural codes that are motivated by the place cells found in the hippocampus of small animals in confined spaces. Neural codes are a combinatorial representation of such spaces. We further the work done in morphisms of neural codes. We have written proofs for theorems that have been presented without proof. We also generalize previous results that touch upon the properties that are preserved. An example is Amzi Jeffs theorem that the image of a open convex code under a morphism is open convex, which we generalize so that we have the same results for closed convexity and other properties. We investigate the minimally non-closed convex family of isomorphism classes of codes. Using algebraic methods and properties from topology, we have found that morphisms as defined by trunks can preserve nice properties of neural codes. We are building towards finding an exhaustive list of properties that are of interest to those studying neural codes through morphisms.

Convexity of Neural Codes with up to Four Maximal Codewords

Discipline: Mathematics

Subdiscipline: Mathematical Biology

Osiano Isekenegbe*[1], Federico Ardila [2], Anne Shiu[3], Saber Ahmed[4]

[1]Florida State University, [2]San Francisco State University, [3]Texas A&M University, [4]University of Texas, Arlington

Abstract: In 2014, John O'Keefe was awarded a Nobel Prize in Physiology or Medicine for discovering place cells, neurons in the hippocampus that determine an organism's sense of location. Place cells are linked to place fields, locations in an environment in which the cells fire upon the entry of the organism. These firing patterns can be recorded as codes, which are sets of strings called codewords. Codewords represent intersections of firing neurons. An important neuroscientific problem is determining the convexity of neural codes, where a code is called convex if it can be realized by a family of convex open sets in Euclidean space. We would like criteria that allow us to quickly determine the convexity of a code. To date, topological objects called local obstructions and wheels have been identified as precluding convexity, and it is known that for codes with at most 3 maximal codewords, the absence of local obstructions is equivalent to convexity. We look at codes with 4 maximal codewords, also called 4-maximal codes. Owing to the nerve lemma, we may examine convexity by studying the simplicial complexes of the topologically equivalent nerve of facets of a neural code, where the facets correspond to codewords that are maximal concerning set inclusion in the code. We show that certain 4-maximal codes are convex if and only if they do not have local obstructions and aim to classify the convexity of all 4-maximal codes. We anticipate that local obstructions and wheels are the only convexity criteria for such codes.

Using Operations on Chemical Reaction Networks to analyze Deficiency and Absolute Concentration Robustness

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Elijah Leake*[1], Jordy Lopez Garcia [2], Anne Shiu[3], Federico Ardila[4], Caelyn Sobie [5], Awildo Gutierrez[6]
[1]Depaul University, Chicago, [2]Texas A&M University, [3]Texas A&M University, [4]San Francisco State University, [5]Arizona State University West, [6]Hamilton College

Abstract: Chemical reaction networks are made up of sets of species, complexes and reactions. Realized as a graph, complexes serve as nodes made up of different species, and edges represent reactions that send a complex to another complex within the network. We evaluate the network’s properties, such as deficiency and Absolute Concentration Robustness, before and after we apply operations that are known to preserve multiple steady states and periodic orbits. The deficiency is described to be the dimension of a linear subspace and is an important invariant. We calculate the deficiency of a network before and after applying these operations. Each operation may or may not have its own unique effect on the network’s deficiency and there are fruitful discoveries that can be made out of this evaluation. A network has ACR, if the concentration of a species stays the same for any steady state the network may have. One of our motivations to look at the relationship between ACR and deficiency comes from a 2010 result of Shinar and Feinberg that states that if there exists a positive steady state in a network and the deficiency of a network is 1, then ACR exists. We also describe more relationships like this and other interesting relationships between ACR and deficiency before and after we apply operations.

Convexity of 1-dimensional 4-maximal Neural Codes

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Gustavo Flores*[1], Federico Ardila [2], Anne Shiu[3], Saber Ahmed[4], Deanna Perez [5], Osiano Isekenegbe[6]
[1]Carleton College, [2]San Fransisco State University, [3]Texas A&M University, [4]University of Texas at Arlington, [5]California State University, Fullerton, [6]Florida State University

Abstract: A central challenge facing neuroscientists is deciphering neural code, or understanding the relationship between stimuli and neural activity. A motivating example comes from hippocampal place cells observed in rats, which fire when the animal is in specific regions of its environment. To represent the stimuli-neural activity relationship mathematically, we use combinatorial neural codes, which record neural activity as a set of binary strings called codewords. This allows us to survey the intrinsic properties of neural codes. Convex codes can be realized by a family of convex open sets in Euclidean space. Detecting convexity in arbitrary codes is an NP-hard problem, so we wish to find to find simple convexity criteria. Past research has identified combinatorial local obstructions to convexity, and it is known that for codes with at most 3 maximal codewords that convexity is equivalent to the absence of local obstructions. We look at codes with 4 maximal codewords, also termed 4-maximal codes. A topological result known as the nerve lemma lets us focus on simplicial complexes on 4 vertices. We show that 4-maximal codes with 1-dimensional simplicial complexes are convex if and only if they do not have local obstructions, adding to the knowledge on convexity of families of neural codes. We aim extend this result by classifying the convexity of other 4-maximal code families that depend on the presence of local obstructions.

Detecting Wheels in the Neural Ideal

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Loan Tran*[1], Federico Ardila [2], Anne Shiu[3], Natasha Crepeau[4], Elijah Washington [5], Luis Gomez[6]
[1]San Francisco State University, [2]San Francisco State University, [3]Texas A&M, [4]U Washington, [5]Williams College, [6]University of Arkansas

Abstract: Neural codes are a set of codewords that indicate patterns of neural activity. A neural ideal is a set of pseudo-monomials generated by characteristic functions of codewords not contained in the code. Codewords can be used to make realizations. We are interested in the convexity of these realizations. Local obstructions have been the main tool used in detecting non-convexity in neural codes. A new tool is called wheels, which can cause non-convexity even without the presence of local obstructions. This word will serve as an umbrella term that includes wheels, partial wheels, wire wheels, sprockets, and wheel frames. All of which have their own set of conditions. This presentation focuses on how to detect an algebraic signature of a wheel in the neural ideal of a code. This will enable us to detect non-convexity (caused by wheels) without the need for realizations. We first look at multiple codes containing wheels and compute the neural ideal using an algorithm made by researchers of a previous related topic. We make use of the receptive field relation types in order to translate conditions from the code onto the neural ideal. We also translate the wheel conditions onto the canonical form of the neural ideal and the Stanley-Reisner ideal as well. The results shed new light on how neural codes and ideals are related to one another.

A model for the mean global surface temperature of an Earth-like planet derived from the geological history of Earth.

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Carlos Ortiz-Quintana*[1], Abel Méndez [2], Karen N. Delgado Vega[3], Alanice Agosto Reyes[4], Vanelie Olivieri Encarnación [5]
[1]University of Puerto Rico, Mayagüez, [2]Planetary Habitability Laboratory at University of Puerto Rico, Arecibo, [3]University of Puerto Rico, Arecibo, [4]University of Puerto Rico, Mayagüez, [5]University of Puerto Rico, Mayagüez

Abstract: Proxy data from the geological record shows large variability in the mean global surface temperatures and greenhouse effect of Earth in the last 750 million years. We propose a model to predict the mean global surface temperature derived from the contribution of land to ocean ratios of an Earth-like planet calibrated with Earth in the last 750 million years. We have fit the model to theoretical and experimental data from proxies using a Markov chain Monte Carlo (MCMC) method. We found that past land-ocean fractions contributed around ± 2°C change from the current mean global temperature of ~15°C. Moreover, corrections for a variable normalized greenhouse reproduced the surface temperatures of the Phanerozoic with a range between 0.37 to 0.47. Thus, we suggest that an Earth-like planet with a similar stellar flux and atmospheric composition should have a greenhouse between 0.3 to 0.5 to support similar terrestrial temperatures. Our model presents a new empirical approach to estimate the evolution of a rocky planet’s mean global surface temperature based on its surface and general atmospheric properties. Such a model could validate results from General Circulation Models (GCMs) and characterize the habitability of exoplanets.

Hunting for supersymmetric dark matter in high-energy photon-photon collisions

Discipline: Physics & Astronomy
Subdiscipline: Physics

Kimberly Long*[1], Simone Pagan Griso[2], Aleksandra Dimitrievska[3]
[1]University of California, Berkeley, [2]Lawrence Berkeley National Laboratory, [3]Lawrence Berkeley National Laboratory

Abstract: The theory of supersymmetry (SUSY) is believed to unlock many of the mysteries of the universe, such as providing a viable candidate for dark matter. Unfortunately, SUSY has yet to be discovered despite many world-wide efforts over the past couple of decades. We investigate a new method of detecting SUSY particles. We use the Large Hadron Collider (LHC), a high-energy proton-proton collider, as an indirect photon-photon collider by analyzing the ultraperipheral (skimming) proton interactions. SUSY particles may be produced in these processes and “detectable” if their masses fall within the energy scales accessible to the collider. Although these particles cannot be detected directly as they decay “instantly”, they decay into known and detectable particles with specific kinematic properties. We study background processes that may lead to similar decay products and make selections on their kinematic properties, aiming to suppress their contributions (predominantly quark-quark and photon-photon induced). Using a Monte Carlo Simulation, we emulate ATLAS’s sensitivity to SUSY particles in the proposed mass range. Upon showing that ATLAS is sensitive to SUSY particles in the mass range under study, we propose to the ATLAS Collaboration that we initiate the search for SUSY using our algorithm on the latest LHC Run 3 data.

Simulating Planetary Systems Imager (PSI) Observations for Terrestrial Exoplanets

Discipline: Physics & Astronomy
Subdiscipline: Physics

Ezequiel Contreras Martinez*[1], Paul Robertson[2], Steph Sallum[3]
[1]University of California, Santa Barbara, [2]University of California, Irvine, [3]University of California, Irvine

Abstract: The telescope is an extension of the eye that will soon allow us to answer one of humanity’s greatest questions: “are we alone in the universe?”. In order to do so, there exist several exoplanet detection and characterization methods such as direct imaging, radial velocity, and transit photometry with different advantages and disadvantages. As such, there exist ongoing efforts to push direct imaging to closer angular separations so that astronomers can access planets once typically detected via radial velocity and transit photometry. Astronomers would then be able to acquire high-contrast images of terrestrial planets to characterize the atmospheres and terrains of these foreign exoplanets. This includes the search for possible biomarkers - signs of life or the possibility to host life. However, this will require extremely large telescopes (ELTs) such as the Thirty Meter Telescope (TMT) and the Planetary Systems Imager (PSI). My goal with this research project is to develop a realistic PSI instrument simulator to generate mock observations for terrestrial planets. This will, in turn, explore PSI’s ability to detect and characterize different rocky planet systems. I will inject models of realistic systems into these mock datasets and recover them to understand what kind of terrestrial planet

systems should be detectable with PSI once it exists. Ultimately, I expect to generate figures that accurately represent the expected science yield for PSI observations of realistic rocky exoplanetary systems.

A Study of Gas Outflows in MaNGA Galaxies

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Brandon Villalta Lopez*[1], Aleks Diamond-Stanic [2], Jade Emerald Pinto[3], Mariana Kaluba[4]
[1]Bates College, [2]Bates College, [3]Bates College, [4]Bates College

Abstract: Star formation in galaxies is a very inefficient process, with most of the available material not being used for the production of new stars. This disagreement between expectations and observations raises the question: why are galaxies not forming as many stars as they could? One of the potential reasons is the gas outflows that are observed in many disk galaxies, which deplete the interstellar medium from star-forming gas. Therefore, our research attempts to identify the cause of these outflows by examining the relationship between outflow signatures and physical parameters like stellar mass and star formation rate (SFR). We study galaxies in the MaNGA (Mapping Nearby Galaxies at Apache Point Observatory) Data Release 17 from the Sloan Digital Sky Survey, which includes more than 10,000 galaxies from which we selected the ~900 disk galaxies with an edge-on orientation. Using spatially resolved spectroscopy, we classified these galaxies as outflow candidates by looking for asymmetries in their velocity maps. This classification is studied as a function of stellar mass and SFR, as well as used for analyzing the distribution of these and other SFR-related parameters. We find that outflow candidates lie higher on the SFR vs stellar mass plot, and we find statistically significant differences in the distribution of SFR-related values like the SFR surface density. These results indicate that galaxies with higher, more concentrated SFR are more likely to present outflow signatures, which has important implications for how star formation is self-regulated in galaxies.

Heat treatment of quartz optical fibers for nEXO

Discipline: Physics & Astronomy
Subdiscipline: Physics

Sara Ellingsworth*
Skyline College, San Bruno

Abstract: The nEXO experiment, currently under development, is designed to challenge the Standard Model via the detection of neutrinoless double beta decay. One of the ongoing R&D activities for nEXO involves measuring the electron lifetime in liquid xenon (LXe) in the presence of candidate detector construction materials. For these measurements, pulses of 266 nm UV laser light are sent down a quartz optical fiber into a special device for measuring electron lifetime in LXe called the xenon purity monitor (XPM). A long electron lifetime in LXe is important because it makes it possible to drift electrons over long distances in LXe, which is essential to the detection of the neutrinoless double beta decay candidate events. As the quartz optical fiber is repeatedly illuminated with 266 nm light during XPM operation, defects known as color centers are formed in the quartz fiber and its ability to transmit UV light is degraded. It has been theorized that the application of heat can remove the color centers. In previous experiments, 375 nm light, the only available wavelength at the time, was used to characterize the UV transmissivity of the fiber as it was being subjected to heat treatment. No significant reversal of fiber transmissivity degradation was observed. In the present experiment, 266 nm

light is used to characterize the quartz fiber UV transmissivity instead of 375 nm light. This will make it possible to check the prior result using UV light of the same wavelength that is used in the working XPM.

Investigating Fast Frequency Scanning for Thermally Driven Instabilities in Kerr-Microresonator Optical Frequency Combs

Discipline: Physics & Astronomy
Subdiscipline: Physics

Marie Angelli Ruiz*[1], Tara Drake [2], Emilio Pérez de Juan[3], Gabriel Colación[4], Lala Rukh [5]
[1]New Mexico State University, [2]University of New Mexico, [3]University of New Mexico, [4]University of New Mexico, [5]University of New Mexico

Abstract: Kerr-microresonator optical frequency combs are useful for a wide spectrum of applications, ranging from optical frequency synthesis and metrology to spectroscopy and ranging. These microscopic devices exploit a Kerr nonlinearity to facilitate frequency comb formation via four-wave mixing (FWM). Frequency comb generation is achieved by sweeping a tunable external cavity diode laser (EDCL) pump that is coupled through a waveguide into an optical microresonator, which confines the light to micron-scale volumes via internal reflection. However, a challenge in generating and sustaining low-noise frequency combs is overcoming the thermally driven instabilities that exist in small photonic waveguides and microresonators with high optical intensities. Here, we present a solution by constructing an apparatus based on an electro-optic modulator that drives rapid optical frequency scans. The fast frequency scan is achieved by pairing an arbitrary waveform generator (AWG) with a voltage controlled oscillator (VCO) to create and control optical sidebands generated from the EDCL pump using an intensity modulator (IM). To characterize the sweep rates, we use a Mach-Zehnder interferometer together with a digital oscilloscope and an optical spectrum analyzer. We measure laser scanning rates of up to 10 MHz/ns, which increases the scanning rate 1,000 times beyond standard EDCL tuning rates. We anticipate that the fast frequency scan will allow us to mitigate thermal instabilities in order to deterministically and consistently generate low-noise frequency combs. Reliable Kerr-microresonator comb formation is an essential step towards the realization of compact, low-cost frequency combs for applications beyond the optics laboratory.

A Computational Study of Ground State Conductivity in One-Dimensional Simulated Crystalline Solids

Discipline: Physics & Astronomy
Subdiscipline: Physics

Sobhan Sayadpour*[1]and Ettore Vitali [2]
[1]California State University, Fresno, [2]California State University, Fresno

Abstract: In quantum mechanics, computer simulations can provide valuable insight into studying complex systems and predicting their behaviors starting from the fundamental equations of quantum mechanics, which is a significant challenge with extensive applications, including but not limited to condensed matter physics, atomic physics, and even quantum information. Our computational experiment aims to design and perform Quantum Monte Carlo simulations of a collection of interacting fermions in the ground state of the one-dimensional Fermi-Hubbard model to study the behavior of electrons in a crystalline solid. Furthermore, we studied and assessed the two quantities, quantum metric tensor and localization length, as computational probes that can distinguish between a conductor and an insulator and their sensitivity in detecting a metal-insulator phase transition only relying on the ground state physics. These ground state probes measure how the fermions scatter in the system depending on the system's parameters. We compute and compare these values with the exact values of the charge gap of the system as a function of the interaction strength. The preliminary results in two dimensions will also be presented. This study is particularly relevant in a strongly correlated system as most current approaches rely on response functions that involve the entire manifold of the excited states of the system, thus making the theoretical and computational approach a formidable task. *This material is based upon work supported by the CSU-LSAMP program funded by NSF under grant #HRD-1826490, CSU Office of the Chancellor, and Fresno State.

Reprogramming organelle sequestration via phosphorylation of synapsin-rich liquid droplets

Discipline: Physics & Astronomy
Subdiscipline: Physics

Roman Leyvas*[1], Peter Chung [2], Christian Vaca[3]
[1]Rio Hondo College, [2]University of Southern California, [3]Rio Hondo College

Abstract: Intrinsically Disordered proteins (IDPs) persist in the neuron as unfolded biopolymers at physiologically-relevant concentrations, and are associated with nearly every major neurodegenerative disease. The IDP synapsin coacervates into protein-rich liquid droplets in the neuron, which leads to the inhibition of homeostatic neurotransmission. Peter Chung's lab at the University of Southern California aims to understand the neuronal dysfunction of the IDP synapsin, as well as reprogram the ability of synapsin to sequester organelles through phosphorylation. The phosphorylation of synapsin changes its ability to interact with other organelles from structural dissolution to phase behavior. By merging a RF1-deficient E. Coli cell line with a phosphoserine Genetic Code Expansion (GCE) translation system, expression and purification of phospho-protein is possible. High proteolytic activity in the cytosol has been proven to decrease protein yeilds, therefore production of synapsin is thought to increase in the periplasm of E. Coli bacterial cells, where proteolytic activity is decreased. Through fusion with a small metal-binding protein (SmbP) and a signal sequence from the protein PelB, it is thought that production of synapsin in the periplasm will be possible . With the ability to produce high yeilds of phosphorylated synapsin in the periplasm of E.Coli, we hope to better understand the dysfunction of IDPs and its relation to neurodegenerative disease

The Influence of the Andromeda Galaxy on the Milky Way Galaxy and its Satellites

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Ludia Adhikary*[1], Joshua Tan [2], Nicolas Garavito-Camargo[3], Emily Cunningham[4]
[1]The City College of New York, [2]Professor, [3]Postdoc at Simons Foundation:Center for Computational Astrophysics, [4]Postdoc at Simons Foundation: Center for Computational Astrophysics

Abstract: Our galactic home, the Milky Way (MW) is a member of a group of galaxies known as the Local Group. The Local Group consists of the MW, the Andromeda Galaxy (also known as M31), and their satellite populations, which are lower-mass galaxies orbiting the more massive galaxies. Both the MW and M31 are embedded in massive halos of dark matter. While the nature of dark matter remains a mystery, we can observe its presence indirectly by studying the motions of the satellite galaxies, which feel the gravitational influence of the dark matter halos. However, most studies of MW satellite motions neglect the presence and influence of M31. Our goal is to study the orbits of MW satellites accounting for the gravitational influence of M31. We construct models for the gravitational potentials of MW and M31 in python, modeling the disk, bulge, and halo components of each galaxy. Taking the present-day positions and velocities of MW satellites, we integrate their orbits back in time (4 billion years) using Gala, a python toolkit for galactic dynamics. Through this study, we determine which MW satellites have orbital histories that are affected by M31, constraining M31's influence on the past and future orbits of the MW satellites as well as the MW's dark matter distribution.

Phosphorescence Measurements of Organic Semiconductors at Room Temperature

Discipline: Physics & Astronomy
Subdiscipline: Physics

Soledad Figueroa*[1], Dalia Maraoulaite[2], David Laman[3]
[1]Heritage University, [2]Heritage University, [3]Heritage University

Abstract: Abstract The topic of our research is room temperature phosphorescence measurements of different types of samples with organic semiconductors. We are attempting this at room temperature, which is a relatively new method as triplet state spectroscopy is usually performed at cryogenic temperatures. Phosphorescence applications include solid-state lighting, optical storage, and displays. More knowledge is needed to optimize performance of these devices. The purpose of this study is to obtain at room temperature strong phosphorescence spectra of organic semiconductors embedded in a polymer matrix and perform photon counting experiments to obtain the decay curve. When phosphorescence decay rate is dependent on the population of the triplet state, the decay curve is logarithmic. At longer decay times, the number of excited states has decreased, and deviation from logarithmic decay curve shape indicates that the rate of disappearance of phosphorescence becomes independent of the triplet state population. Initial samples are prepared with anthracene as a target molecule ad TOPAZ polymer as the matrix, with the addition of hexabromocyclododecane (HBCD) to enhance non-radiative decay. Chloroform is used as the solvent that is evaporated after thorough mixing of the components, leaving behind a solid-state sample. By changing sample composition and preparation parameters, we aim to maximize radiative decay (light emission) and minimize non-radiative decay (e.g. heat). In applications, this knowledge would allow to enhance phosphorescence device performance and improve device efficiency.

The Cosmic Web and Effects on Galaxy Properties Through Cosmological Stimulations

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Alyssa Abeyta*[1], Joe Burchett[2], Priscilla Holguin Luna[3], Farhanul Hasan[4]
[1]New Mexico State University, [2]New Mexico State University, [3]New Mexico State University, [4]New Mexico State University

Abstract: Star formation in galaxies can be altered by conditions within the host galaxy and in the environment surrounding the galaxy. The amount of gas in and around a galaxy affects star formation rates (SFR) and vice versa. In this investigation, I study filament structures in the cosmic web that may impact galaxy properties due to their proximity to various features in identified filaments. By utilizing CosmoVis, a 3D interactive visualization tool for cosmological hydrodynamical simulations, I have identified and analyzed features marked by the gaseous physical conditions, such as temperature and entropy, in the intergalactic medium within filament structures. Once such features are identified, I investigate how SFR and other galaxy properties evolve over a range of redshifts. Tracking these effects over time in context with these cosmic web features reveals their joint evolution. Having analyzed the star formation histories for a large number of simulated galaxies and determining their positions relative to filaments in the cosmic web, I will highlight the interconnectedness between the two. My results have shown common occurrences for stimulated galaxy data, such as a positive relationship of SFR as a function of stellar mass in galaxies. Further analysis includes exploring relationships such as the specific star formation rate as a function of a ratio of gas mass to stellar mass within a galaxy. In my presentation, I will discuss my findings connecting the evolution of cosmic web gas conditions to the galaxies residing within.

Design and Construction of Muon Detector for Cosmic Muon Detection

Discipline: Physics & Astronomy
Subdiscipline: Physics

Faith Beall*[1]and Dr. Jeffery Spirko[2]
[1]Texas A&M University Corpus Christi, [2]Texas A&M University Corpus Christi

Abstract: Muons are elementary particles listed in the Standard Model. Muons are produced when high energy cosmic rays collide with the Earth’s atmosphere, resulting in showers that rain muons upon the Earth’s surface. The muon has a rest lifetime merely a fraction of a second long. However, the high energy at which muons are produced cause them to reach a relativistic speed, allowing them to reach the Earth’s surface for detection. CosmicWatch is a cost-effective, compact, and portable muon counter applying plastic scintillator as the muon target and a silicon photomultiplier (SiPM) for light detection. The easy construction and data collection provided by CosmicWatch’s simplistic design allows for inexpensive particle physics research at an undergraduate level. We intend to build a second muon detector to determine direction and position of incoming muons. Possible future experiments with the two detectors can be used as a direct proof of concept by showing the muon flux as a function of the incident angle with respect to the zenith, which is approximated as the intensity of the flux times the cosine of the angle squared.

Accretion Variability in Transitional Disk Host-Stars: Constraints on Second-Minute Timescale H-alpha Variability from the Giant Accreting Protoplanet Survey

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Julio Morales*[1]and Katherine B. Follette[2]
[1]University of Massachusetts Amherst, [2]Amherst College

Abstract: The accretion process is the defining characteristic of young stellar objects (YSOs). The process by which stars accrete their circumstellar disks is that of magnetospheric accretion—in which the magnetic field truncates the inner disk material along field lines, and crashes on to the photosphere. Models and observations of YSOs undergoing accretion have shown that the in-flow of material produces an excess of Hα emission, which has caused the atomic line to become

a popular tracer of accretion. Accretion onto the central star and protoplanets embedded within the disk are thought to carve out large gaps (~10-100's of AU) between the central star and disk, creating the subset of objects known as transitional disks. While accretion in transitional disks is not well-understood on theoretical grounds, observations have shown that these objects are still actively accreting despite their large cavities. This is a surprising fact since the large cavities in between the central star and the outer disks of transitional objects would immediately suggest otherwise. Accretion studies on YSOs with transitional disks are few, and time-domain studies are even scarcer. As a result, we have a limited understanding of the timescales of accretion variability in transitional systems. This project seeks to inform the conversation of accretion variability in transitional systems by producing light-curves for 15 of the most well-studied transitional disk bearing stars (GAPlanetS Survey). We then perform a time-series analysis to search for and constrain variability due to changes in accretion rate on second-minute timescales over the course of 5 years.

Efficiently Imaging Accreting Protoplanets from Space: Reference Star Differential Imaging of the PDS 70 Planetary System with the HST/WFC3 PSF Library

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Aniket Sanghi*[1], Yifan Zhou [2], Brendan P. Bowler[3]
[1]The University of Texas at Austin, [2]The University of Texas at Austin, [3]The University of Texas at Austin

Abstract: Accreting protoplanets provide key insights into how planets form within their natal protoplanetary disks. The direct detections of Hα emission from newly formed planets have constrained planetary-mass accretion rates and enabled quantitative studies of accretion physics, planet-disk interactions, and planetary luminosity evolution. Recently, Zhou et al. 2021 used angular differential imaging (ADI) with Hubble Space Telescope's Wide Field Camera 3 (HST/WFC3) to recover the young accreting planet PDS 70 b in F656N (Hα) at a signal-to-noise ratio (S/N) of 7.9. Here we demonstrate the applicability of reference star differential (RDI) with the same dataset. We compile a reference library from the database of WFC3 point-spread functions (PSFs) provided by Space Telescope Science Institute and develop a set of morphology-significance criteria for pre-selection of reference frames to improve RDI subtraction. We explore different implementations of RDI by varying the library size, reference star subsets, and subtraction regions to find the optimal setups for planet detections with HST/WFC3. RDI with this PSF library results in a detection of PDS 70 b at a S/N of 5.3, opening up the possibility of imaging accreting planets more efficiently than with ADI. The lower detection significance with RDI is attributed to the ~100 times lower S/N of the reference PSFs compared to the ADI PSFs. Building a high-quality reference library with WFC3 will enable unique opportunities to monitor planetary accretion variability and efficiently search for actively accreting protoplanets in Hα around targets inaccessible to current ground-based adaptive optics systems, such as faint transition disk hosts.

Alma Band 7 Imaging and Analysis of the Luminous Infrared Galaxy ESO 203-IG001

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Miguel Montalvo*[1], Devaky Kunneriath [2], Loreto Barcos-Muñoz[3]

[1]University of California, Berkeley, [2]National Radio Astronomy Observatory - CV, [3]National Radio Astronomy Observatory

Abstract: Local Ultra/Luminous Infrared Galaxies (U/LIRGs) host one of the best laboratories to study star formation in extreme environments. Specifically, U/LIRGs showing compact emission (concentrated within the central kpc), with extremely high obscuration, and high star formation rates may represent a brief transition stage between powerful starbursts and optically visible QSOs. We present Atacama Large Millimeter/submillimeter Array (ALMA) Band 7 (~340 GHz) observations of the dense gas tracers HCN (4-3) and HCO+ (4-3) in one of the most obscured local LIRG, ESO 203-IG001, that is part of the Great Observatories All-sky LIRG Survey (GOALS), to map and extract physical properties of the circumnuclear interstellar medium, including its dense gas and dust components. Emission was detected and values for dust and molecular gas mass were calculated. We find enhanced HCN emission, relative to HCO+, but it is unclear if it is due to AGN presence as some studies suggest. We observe different kinematics for the rotating disk between HCN and HCO+ and observe tentative evidence of outflows, but further analysis must be performed with deeper observations and using different tracers, to understand the dynamics of the galaxy better and verify our preliminary results.

SIMULATING & PREDICTING COMPLEX EVOLUTIONARY HISTORIES USING THE WRIGHT-FISHER MODEL & BAYESIAN INFERENCE

Discipline: Physics & Astronomy
Subdiscipline: Physics

Uchenna Nwaege*[1]and Dr. John Barton [2]
[1]University of California, Riverside, [2]University of California, Riverside

Abstract: Living things evolve to increase their chances of survival within their environment. The same process also occurs for pathogens such as viruses or bacteria within a host. Better understanding of the evolution of antibiotic resistance or how pathogens escape from immune responses may inform the design of treatment techniques and vaccines. Evolutionary models such as the Wright-Fisher model can simulate such processes. The Wright-Fisher model though simple, can accurately simulate evolutionary data given an initial population. However, the Wright-Fisher model depends on knowing detailed properties of a pathogen, such as its mutation rate and the fitness or selection coefficient. Since these evolutionary properties are not readily known, we study how such properties can be inferred from data, in particular, genetic sequences collected over time from a population. First, we wrote code to simulate evolution following the Wright-Fisher model for multiple scenarios expected with real world data, including different levels of selection and different mutation rates. We collected virtual samples from these simulations to closely reflect sampling constraints found in real world data. We then developed a program to implement the Marginal Path Likelihood (MPL) method, a statistical technique to determine the fitness effects of mutations from evolutionary data based on changes in mutant frequencies over multiple generations of a population. Our results demonstrate that the MPL can still reliably infer selection even when samples are collected with large or irregular gaps in time and limited numbers of sequences.

Defect-Induced Noise in Photonic Crystal Fiber

Discipline: Physics & Astronomy
Subdiscipline: Physics

Verenise Martinez Lopez*[1]and Ryan Behunin [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: The ability to precisely control quantum systems promises a new era powered by high-performance computers and unconditionally secure communications. However, the relatively short lifetime of quantum states poses critical challenges to the wide-scale application of quantum technology. In a variety of systems, the core mechanism of this challenge has to do with noise induced by so-called two-level tunneling states (TLS) that occur during critical temperatures below 1K. Recent work shows that this form of noise may be radically altered in reduced dimensional structures such as waveguides, membranes, or resonators. Here, we explore how TLS physics is changed within photonic crystal fiber (PCF) waveguides in a matter where we characterize the interaction of defects with confined electromagnetic waves and acoustic excitations in order to correlate and control the noise induced defect dynamics with its geometry. Using a finite element solver (COMSOL Multiphysics), we simulate stimulated Brillouin scattering in a SiO2 PCF to obtain the optical and mechanical properties, enabling detailed calculations of the noise and dissipation produced by TLSs in these highly confined waveguides. By looking for drastic changes in the temperature scaling laws for dissipative and dispersive shifts in frequency compared to bulk systems, we fine tune tunneling state theories accounting for phonon confinement. Our results uncover the impact phonon confinement has on TLS physics, advancing our understanding of this critical form of noise and dissipation.

The Nature of X-ray Sources in the Andromeda Galaxy

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Erika Marentes*[1]and Blagoy Rangelov [2]
[1]Texas State University, San Marcos, [2]Texas State University

Abstract: Even though over 1,000 X-ray sources are cataloged in the Andromeda (M31) galaxy, only a small fraction (less than ~1/4) of those have reliable astrophysical classifications. The goal of this research is to study the X-ray source populations M31 using a robust, systematic methodology. To achieve this goal, we will utilize archival data from the Hubble Space Telescope and the Chandra X-ray Observatory to cross-correlate the positions of X-ray sources with those of their possible low-energy counterparts, and to extract the multi-wavelength parameters for thousands of X-ray sources. Here we present preliminary results of our findings.

TNO or Comet? The Search for Activity and Characterization of Distant Object 2009 MS9

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Erica Molnar-Bufanda*[1]and Karen Meech [2]
[1]University of Hawaii, Manoa, [2]University of Hawaii, Manoa

Abstract: When gas was present in the solar system during its first few million years a local chemical signature was imprinted on small planetary bodies (e.g. comets and asteroids). This is why it is important to study these primitive remnants - they are vehicles for us to learn about how the solar system formed. Small bodies can be separated into classes based on their orbits. Trans-Neptunian objects (TNOs) occupy a region just beyond Neptune's orbit. Long period comets (LPCs) by contrast are from the Oort Cloud (trillions of miles away). 2009 MS9 is an object whose orbit straddles the boundary between TNOs and LPCs. It's unique orbit motivated us to study this target with the hypothesis that it would become "active" (out-gassing on the surface) like a comet. We show that 2009 MS9 exhibits activity as predicted based on our measurements of its brightness over time and its color changes. We execute methods involving image reduction and analysis to assess activity of this target using over a decades' worth of data collected with professional telescopes. We show that a fraction of the surface is out-gassing with CO or CO 2 based on gas models. We place strong limits on the amount of dust lifted off of the surface during out-gassing using stacked images of the target. Our results suggest out-gassing may explain color changes observed in other TNOs. This work has been submitted as a benchmark paper for the PI's thesis as it exhibits tools she uses to characterize other comets.

Refining the Redial Velocity Method to Precisely Locate Earth-Like Exoplanets

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Lianys Feliciano*[1], Lily Zhao [2], Megan Bedell[3]
[1]City University New York (Cuny) New York City College of Technology, [2]Center of Computational Astrophysics at Flatiron Institute, [3]Center of Computational Astrophysics at Flatiron Institute

Abstract: Of the 5,000 discovered exoplanets only a small fraction are Earth-like. However, with instruments like the Extreme Precision Spectrograph (EXPRES) many smaller exoplanets can be detected using the radial velocity method. The radial velocity method is a technique that exploits the fact that stars do not remain stationary when orbited by a planet. We use EXPRES observation to analyze specific segments of spectra produced by star HD26965. Segments from the same observation should return the same radial velocities. However, we have found that the segments are not similar which suggests that there may be a form of interference such as stellar activity instead of an orbiting planet. By analyzing the segments of the spectrum we determine the radial velocity of the exoplanet at various positions in its orbit, identify any interference from stellar activity, and achieve greater precision to locate more Earth twins. I will present my analysis as to why these segments are not identical and how that is linked to stellar activity. Through the investigation of these spectra segments, we will learn more about the interaction between exoplanets and their host star. This will refine the method to discover more Earth-like planets with greater precision.

Response of Cell Cycle Oscillator to Temperature

Discipline: Physics & Astronomy
Subdiscipline: Physics

Ernesto Flores*[1], Qiong Yang [2], Franco Tavella[3]
[1]The University of Texas at San Antonio, [2]The University of Michigan, [3]The University of Michigan

Abstract: Temperature is known to affect the cell cycle in vivo. However, we do not know how it affects the core signaling network driving cell cycle oscillations. Additionally, theoretical studies suggest that positive feedback affects period and amplitude tunability. The cell cycle is a well-known positive feedback oscillator. We hypothesize that inhibiting the positive feedback mediated by the protein Wee1 will decrease the period tunability and increase the amplitude tunability based on theoretical results. For that purpose, we analyze how the period and amplitude of a cell cycle oscillator centered around cyclin-dependent kinase (Cdk1) responds to changes in temperatures when the positive feedback is inhibited. We encapsulate cycling Xenopus laevis egg extract in cell-sized microfluidic droplets and study cell cycle oscillations at different temperatures. First, we characterized the temperature response of the core signaling networks driving cell cycle oscillations. The oscillations were tracked using fluorescence microscopy and image segmentation algorithms. The shift in temperature was shown to increase the overall period of the cell cycle oscillations in agreement with previous observations. However, it is challenging to measure the response of the system for several temperatures: intrinsic variations in biological samples prohibit measuring the response at different temperatures on different experimental days. To solve this, we develop a microscope stage made of copper that creates a gradient in the space where the samples are imaged. Using this device we are in the process of characterizing the response of the system to multiple temperatures and the role of positive feedback on its behavior.

Structural and Magnetic Characterization of MnPdSb

Discipline: Physics & Astronomy
Subdiscipline: Physics

julissa Cesareo*[1]and Nelson Moreno [2]
[1]University of California, Santa Barbara, [2]University of California, Santa Barbara

Abstract: Interest in fast and nonvolatile mass storage memory devices has led to the investigation of properties in magnetic materials. Specifically, MnPtSb has been discovered to be a half-metallic Heusler alloy that possesses such qualities for spin-transport based devices. This understanding motivated us to progress our research to another isoelectric compound, MnPdSb. MnPdSb powder will be synthesized and structurally characterized with x-ray diffraction (XRD). Zero field-cooled and field-cooled measurements will be done with a magnetic property measurement system (MPMS). By calculating intensities at different angles, we are able to determine the structure and purity of our material through XRD. For the MPMS analysis, a device cooled by liquid helium measures the change of magnetic flux. We can analyze the magnetic properties of our material such as the change of entropy under different environments through certain temperatures and fields. We predict that MnPdSb will have a similar electronic structure to MnPtSb and aim to discover if MnPdSb is half-metal ferromagnetic. A full characterization of MnPdSb has not been done yet therefore we plan to structurally and magnetically characterize MnPdSb. Our research will contribute to the overall manipulation of these samples to fit the demand for more advanced memory technology.

Assessing the Quality of Articles Chosen for a Systematic Review on Patient-Provider Prenatal Satisfaction

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

Vianey Quaney*[1]and Ophra Leyser-Whalen [2]
[1]University of Texas at El Paso, [2]University of Texas at El Paso

Abstract: Patient satisfaction is useful in establishing the quality of care that is provided to patients, regardless of their condition. In this case, prenatal patient satisfaction ensures that primary care physicians have provided their patient with the support needed to appropriately navigate through any symptoms that may arise during their pregnancy. However, it is important to note that some physicians may not address all patient concerns. Additionally, some patients have reported less satisfaction with their prenatal care visits because they felt as if their concerns had been dismissed. A systematic review, sometimes referred to as secondary research, utilizes a compilation of existing studies to provide a condensed analysis about a given topic. Studies that are typically analyzed for systematic reviews include those that employ qualitative and quantitative analysis, as well as mixed method articles that make use of both qualitative and quantitative research methods. Systematic reviews are crucial in understanding the limitations of certain studies as well as the benefits of refining the mechanisms used to clarify a topic. To understand the type of care that expectant mothers necessitate, studies that evaluate women's perception of provider care and how this contributes to their satisfaction were assessed for quality by assigning a score out of ten to each article using a series of questions that have been previously established by researchers.

Employer and Student Disparities: Undergraduates' Perceptions and Knowledge of Essential Skills in the Workplace

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Sofia Christofi*[1]and Jennifer Dyer-Seymour [2]
[1]California State University, Monterey Bay, [2]California State University, Monterey Bay

Abstract: According to recent surveys of employers conducted by the National Association of Colleges and Employers (NACE), about 25-45% of employers do not find new-collegiate hires very proficient in the essential skills of the workplace such as communication, critical thinking, and teamwork. It is unclear whether current psychology majors recognize the extent to which they need to match the skills they learned in college with those desired by employers. It is not even clear whether current students know which skills employers consider essential. In the present study we measured students' knowledge of the essential skills that employers value. As part of a larger experiment, 343 participants, (51% Latino), were asked to name four essential skills that employers value most from new collegiate hires with a B.A in psychology. The responses were coded to see which ones fit into the six essential skills valued by at least 80% of employers, as determined by NACE. Results revealed that about 47% of students did not name one of the six essential skills. Communication was the most frequently named skill (16%), followed by professionalism (13.5%), critical thinking (11.5%), and teamwork (10%). Fewer than 3% of students named equity and inclusion or technology as essential skills.Findings may lead us to create institutional change for undergraduates seeking a B.A. in psychology. A better understanding of the extent to which students know which skills employers consider essential may help us influence better outcomes for students, and overall job performance in the psychological sciences.

Deliberative Cues within the Context of Religious Communities

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Andrea Mullin*[1], Michael Nick Stagnaro [2], David Rand[3]
[1]University of Central Florida, [2]Massachusetts Institute of Technology, [3]Massachusetts Institute of Technology

Abstract: Recent research in the field of the Cognitive Science of Religion has indicated a negative relationship between the willingness of an individual to engage in deliberation and religious belief. A number of potential mechanisms driving this relationship have been investigated; however, here we focus on the communal and interpersonal aspects of religious

life. Specifically, we ask how religious individuals perceive and treat religious community members who signal a strong inclination to engage in deliberation. If those more inclined to deliberate are also more inclined to push back on religious/ ideological ideas, they may receive disproportionate social costs in their religious communities. We will conduct an experiment that systematically manipulates the perceptions of a target individual's thinking style while holding their reported religious belief constant. The study will recruit 1,000 individuals to take part in a two-condition (deliberative target vs non-deliberative target), between-subjects design. Participants will rate how dedicated the target is to their religious belief and how well they would be able to follow the religious teachings and traditions. Further, all participants will be asked how much they like the target individual. We hypothesize that both religious and non-religious participants will view the target individual described as being more deliberative, and will be perceived as being less dedicated to, and less able to comply with, their religious belief compared to the non-deliberative individual. Further, we predict that religious participants will show a much stronger liking for the non-deliberative target, compared to the deliberative target individual.

The Mediating Role of Social Support in Mindfulness and Depressive Symptoms Among Underrepresented Minority University Freshmen

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Cathy Quach*[1], Dr. Yolanda Vasquez-Salgado [2], Felicity Gutierrez[3], Fenan Kifleyesus[4], Dr. Shu-Sha Angie Guan [5], Dr. Yolanda Vasquez-Salgado[6]
[1]California State University, Northridge, [2]California State University, Northridge, [3]California State University Northridge, [4]California State University Northridge, [5]California State University, Northridge, [6]California State University, Northridge

Abstract: Prior studies have demonstrated the positive role of mindfulness and social support in college student's mental health. However, these constructs have not been examined together among underrepresented minority (URM) students. The purpose of this study is to examine associations between mindfulness, social support, and depressive symptoms in a sample of URM university freshmen. We hypothesize that (1) higher levels of mindfulness and social support will be associated with lower levels of depressive symptoms, and (2) the link between mindfulness and low depressive symptoms will be explained or mediated by higher levels of social support. One hundred and seventy-three URM freshmen (Mage = 18.03, SD = .41; 67% female) completed an online survey that examined mindfulness (10-items; e.g., "I am easily distracted"), social support (11-items; e.g., "I get useful advice about important things in life") and depressive symptoms (8-items; e.g., "I felt sad") during their first semester at a four-year university. The data from this study is from a larger, on-going longitudinal study surrounding sociocultural experiences and adjustment during the transition to college. Hierarchical linear regressions revealed that mindfulness and social support predicted lower levels of depressive symptoms, b = -.54, SE = .07, p < .001, and, b = -.32, SE= .07, p < .001, respectively. Bootstrap mediation modeling revealed evidence of partial mediation (ps = .001 - .006; 95% CI [-.10, -.01]). Our results, confirming our hypotheses, illustrate the protective and interconnected nature of mindfulness and social support in URM students' mental health. Implications for intervention will be discussed.

COVID-19 Testing and Beliefs Among a Sample of People Who Use Opioids

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Zoe Chang*[1], Kate Elkington[2], Alwyn Cohall[3], Renee Cohall[4], Peter G. Gordon[5], Corianna E. Sichel[6], Patrick Wilson[7], Daniel Winetsky[8]

[1]Hunter College, [2]NewYork-Presbyterian / Columbia University Irving Medical Center, [3]Columbia University Medical Center, [4]Mailman School of Public Health Columbia University, [5]Columbia University Department of Medicine, [6]Columbia University and New York State Psychiatric Intitute, [7]Columbia University, [8]Columbia University Medical Center

Abstract: This presentation will describe COVID-19 testing and beliefs among the sample recruited for the COVID Warriors NYCstudy. The goal of this study was to increase COVID-19 testing uptake among people who use opioids. Our sample data (n=477) found that 70% reported being Hispanic, Latinx, or Spanish, and 22% were African-American. Discussion on COVID-19 testing and beliefs will describe aspects such as testing barriers and challenges, trust in COVID-19 sources, and other personal beliefs and outcomes on COVID-19 Funded by the RADx-Underserved Populations NIH initiative, the study aims to recruit individuals who use opioids for rapid COVID-19 testing and interviews to expand and assess COVID-19 testing for underserved populations. Data collected in New York City has shown that in the first wave, communities prone to poverty with high rates of substance and opioid use are at increased risk for poor COVID-19 outcomes. Social networking strategies have proven to efficiently engage with more elusive populations, including users of substance. The two following strategies were used to engage our target population: credible messenger and chain-referral. These strategies were implemented at two community-based organizations in New York City: Argus Community Inc. and Alliance for Positive Change. Through leveraging the two outreach methods, the goal is to increase COVID-19 testing among those who use opioids within underrepresented communities. Findings from COVID-19 testing and beliefs survey data will provide information on what efforts can be done to address and maximize education and resources within marginalized communities to increase COVID-19 testing and vaccines.

Predictors of HIV testing among adolescent sexual minority men aged 13-17 years

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Christel Adhemar*[1], Tyrel Starks[2], Trey Dellucci[3], Travis Lovejoy[4], Sarah Feldstein Ewing[5], S. Scott Jones[6]

[1]City University of New York of Hunter College, [2]Hunter College of the City University of New York, [3]Doctoral Program in Health Psychology and Clinical Science, Graduate Center of the City University of New York, [4]Oregon Health & Science University, [5]University of Rhode Island, [6]Hunter College of the City University of New York

Abstract: Sexual minority males (SMM), which include gay, bisexual and other men who have sex with men, disproportionately account for new HIV infections in the US. The Centers of Disease Control and Prevention recommends HIV testing every 3-6 months as essential to HIV prevention among those at the highest risk of infection. There has been extensive research examining predictors of HIV testing among adult SMM, but research is limited among adolescents and has overlooked developmental impacts on HIV testing. This study examined factors associated with HIV testing among adolescent SMM aged 13-17, including whether HIV testing was associated with relationship status. Participants were recruited through social networking and dating applications popular among SMM. Interested participants who clicked on the advertisement were directed to an online survey. The sample was 1,641 cisgender male adolescents taken from a larger sample of SMM. A multigroup ordinal-regression model evaluated associations between predictor variables and HIV testing frequency. Predictors included relationship status (single, partnered monogamous, partnered non-monogamous), and Condom Anal Sex (CAS) with casual partners. Sixty percent of adolescent SMM tested less than annually for HIV while 13% reported testing every 3 months. Moreover, being in a non-monogamous relationship was associated with more frequent HIV testing, while being in a monogamous relationship was associated with less frequent HIV testing. Having CAS with a casual partner was associated with a 1.46 odds of HIV testing. These rates of HIV testing are lower than what is usually seen among adult SMM and may reflect specific barriers adolescents experience.

Ultra-long term blood pressure variability and neighborhood factors across race-ethnicity in a sample of older adults.

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Giovanni Marquez*[1]and Melissa Ann Flores, PhD [2]
[1]The University of Arizona, [2]University of Arizona

Abstract: Recent literature suggests that ultra-long term blood pressure variability (BPV) is a strong predictor of future cardiovascular disease. Further, neighborhood social and structural factors are associated with cardiovascular health and disease. However, little is known whether BPV may be a pathway through which neighborhood factors contribute to disease. In the current study, we seek to understand the association between ultra-long term BPV and neighborhood residential stability and cohesion in a sample of older adults. We hypothesized that lower BPV would be associated with longer neighborhood residency and greater neighborhood social cohesion. Using a subset of the National Social Life, Health, and Aging Project (NSHAP) we assessed 15-year, ultra-long term BPV in sample of older adults (N = 1,554). BPV was calculated using the standard deviation of three blood pressure measurements across three waves. Multiple linear regressions were estimated with BPV as the outcome, and baseline neighborhood factors and relevant health covariates as predictors. Preliminary results showed neighborhood residency nor neighborhood social cohesion were associated with ultra-long term BPV. However, both systolic and diastolic (all Fs(5, 1387) > 2.66, all ps < 0.020) BPV varied across race-ethnicity such that African American/Black older adults had greater systolic (b = 3.18; 95% CI(1.94, 4.43)and diastolic (b = 1.25; 95% CI(0.55, 1.96)BPV. American Indian/Alaskan Native older adults also had greater systolic BPV (b = 6.05; 95% CI(0.50, 11.60), than their non-Hispanic white counterparts. Next steps include assessing whether race-ethnicity moderates the association between neighborhood factors and BPV. Results may inform current health equity research.

Type 2 Diabetes in a Developing Rural Town in Costa Rica vs. a First World Country, with a Focus on Socioeconomic Class

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Alexandra Acevedo*[1]and Sara Shuger Fox [2]

[1]CUNY Bernard M. Baruch College, [2]Central College

Abstract: Type 2 diabetes has been increasing globally and affecting developing countries such as Costa Rica. As the world westernizes, consequently, we see major shifts in culture and specifically dietary intake. In Uvita, Costa Rica ecotourism and foreign migrants bring major changes to local culture. Our study aims to show how the level of risk for type 2 diabetes varies by socioeconomic status, physical activity, and nutritional habits. We will measure each participant's risk of type 2 diabetes based on survey answers and CDC recommended guidelines for each indicator of metabolic dysfunction. This study will examine the correlation of socioeconomic status and the risk of developing type 2 diabetes in Uvita. Additionally, a comparison will be conducted between metabolic dysfunction indicators of Uvita residents and Americans. Results are pending as we gather data this summer as part of the REU program at Las Cruces. We expect risk of developing type 2 diabetes in Uvita to vary by socioeconomic status as it does in the U.S. We also expect our results to indicate the risk factor for Uvita residents and Americans to be extremely similar due to how the influence of westernization and ecotourism changed their culture. Gaining a better understanding of these relationships is beneficial to guide future research in this area of metabolic dysfunction and to help healthcare practitioners better understand cultural barriers preventing their patients from successfully self-managing. This research is especially pertinent with the context of Costa Rican healthcare capacities to handle a problem at this scale.

Trauma Exposure and Disclosure in Underrepresented Populations at Clinical High Risk for Psychosis

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Sam Barans*[1], Bess Friedman[2], Justine L Saavedra[3], Annette Crisanti[4], David Lardier[5]
[1]Michigan State University, [2]University of New Mexico, [3]University of New Mexico, [4]University of New Mexico, [5]University of New Mexico

Abstract: A consistent relationship between a diagnosis of Clinical High Risk for Psychosis (CHR) and trauma repeatedly presents in research, with estimates of trauma in CHR populations ranging from 54% to 97%. Thus far, Hispanics and Native Americans lack representation in this research. The present study aims to identify discrepancies in self and clinician reports of trauma in a sample of CHR patients enrolled in a Coordinated Specialty Care program (N = 52) and observe whether rates of reporting differ by race/ethnicity. Clinician reports of trauma are being identified through a A review of Electronic Medical Records searching for key words related to Adverse Childhood Events (ACE) in clinical notes – with a total ACE generated ranging from 0 to 10. Preliminary findings (N = 45) indicate limited self-report of trauma at the beginning of treatment (58%) relative to clinician-reports of trauma throughout treatment (87%) with a mean ACE score of 2.02 (sd = 1.44). The most common types of trauma experienced include parental divorce (51%), familial mental illness (44%), and emotional abuse (31%). We found a significant difference between ethnic groups in the complete sample, with Hispanic patients disclosing a history of trauma less frequently than Non-Hispanics (p = 0.03). We are in a unique position to address the limitations of the current research, with 50% and 11.2% of the population of New Mexico (the location of this study) being Hispanic or Native American, respectively. The clinical implications of these findings and ideas for future research will be discussed.

Investigating the role of Implicit Statistical Learning in the Acquisition of Morphology

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Joemari Pulido*[1]and Joanna Morris [2]
[1]Providence College, [2]Providence College

Abstract: Implicit statistical learning (ISL) or the mechanisms that enable humans to pick up on patterns in the environment have been shown to be associated with variability in reading accuracy, however, there is still no clear explanation for these links. To understand the links between ISL and reading accuracy we need to make sense of the role of ISL in the acquisition of morphology and whether individual differences in readers' ISL make a difference during the extraction of the morphological structure of words. Reading and writing are essential skills, especially in the world today. Still, there are learning disorders, such as dyslexia, that make it difficult for individuals to acquire these much-needed skills. By understanding the role that ISL plays in the acquisition of morphology and the extent to which individual differences influence this process, we will have a better understanding of how to aid individuals, such as those with dyslexia, to acquire the highly in-demand skills of reading and writing. This study plans to measure reader's lexical representation quality, sensitivity to the internal structure of words, and the ability to notice statistical patterns in visual sequences. These behavioral measures will then be correlated with event-related potentials (ERPs) to identify neural signals of ISL and determine if similar neural signals are used during the decomposition of complex words. Our goal in these efforts will lead to a better understanding of the role of ISL in morphological decomposition which will allow us to design effective ways for individuals to learn to read.

Investigating activity-dependent myelination following viral encephalitis and seizures in the Theiler’s Murine Encephalomyelitis Virus (TMEV) mouse model of viral-induced epileptogenesis.

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Arianna Fritz*[1], Dr. Karen Wilcox [2], Laura Bell[3]
[1]University of Illinois Urbana Champaign, [2]University of Utah, [3]University of Utah

Abstract: Viral infection is a major source of seizures and epilepsy, yet the mechanisms underlying the development of epilepsy following infection remain largely unknown. Seizures occur when there is an imbalance of inhibitory and excitatory neurotransmission in the brain resulting in too much excitability. Oligodendrocyte precursor cells (OPCs) are known to strengthen active circuits in the brain through their differentiation into myelinating oligodendrocytes. However, recent studies suggest that this process can become maladaptive in the process of epileptogenesis, contributing to synchronicity and generalization of seizure activity over time.These findings lead me to hypothesize that viral-induced seizures result in maladaptive myelination which may contribute to the progression of epilepsy. The TMEV mouse model of viral-induced epileptogenesis is used as a preclinical model of seizures and epilepsy. Previous work shows that glial cells, such as microglia and OPCs, become reactive and proliferate at the primary injury site of the hippocampus following infection. Preliminary data from mice at 6 days post-infection suggests that there may be increased myelination in the hippocampus after TMEV infection, particularly in the CA3 region. To assess whether OPCs contribute to myelination following viral infection, I use immunohistochemistry for the myelin-specific protein (MBP) to compare the amount of myelin between TMEV-infected mice and saline-injected controls throughout a time course following TMEV infection. The results of this study will contribute to our understanding of activity-dependent myelination in the brain following viral encephalitis and seizures and may identify a novel target for preventing or treating the development of epilepsy following viral infection.

Investigation of Positive and Negative Emotional Responses in Relation to Alcohol Use Disorder Severity across Gender

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Stephen Coutu*[1], Nicole Holland Weiss [2], Silvi Goldstein[3]
[1]University of Rhode Island, [2]University of Rhode Island, [3]University of Rhode Island

Abstract: Emotional responses are linked to risk for alcohol use disorder severity (Weiss et al., 2018). Notably, however, expectations of emotional responses vary across men and women, linked to gender norms established by society (Parker et al., 2021). Therefore, we hypothesize that alcohol use disorder severity across gender will vary based on differing emotional responses. Participants were 314 trauma-exposed, substance-using adults (women n = 150, men: n = 164) who were recruited from Amazon’s Mechanical Turk (MTurk) platform, a crowdsourcing website that facilitates online data collection. The average age of study participants was 35.79 and the majority identified as white (81.6%). Following informed consent, participants completed a series of validated self-report measures, including the Emotional Avoidance Questionnaire (Taylor et al., 2004) to assess negative and positive emotional avoidance and the Alcohol Use Disorder Identification Test (Saunders et al., 1993) to assess alcohol use disorder severity. Bivariate correlations revealed among men, negative and positive emotional avoidance was significantly correlated with alcohol use disorder severity. However, among women, positive but not negative emotional avoidance was significantly correlated with alcohol use disorder severity. Our study revealed that avoidance of positive emotions was similarly related to alcohol use disorder severity in men and women, whereas avoidance of negative emotions was significantly associated with alcohol use disorder severity for men but not women. Future studies may consider exploring these relations among other gender identities not captured here (e.g., trans) to parse out further differences in emotional avoidance.

Achievement guilt and well-being among first-generation Latinx college students: Does familism influence this relationship?

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Summer Herrera*[1]and Rosa Toro [2]
[1]California State University, Fresno, [2]California State University, Fresno

Abstract: Numerous first-generation college students (FGCS) experience a sense of achievement guilt, feeling responsible for leaving their family behind to pursue a greater opportunity than the rest of their family, throughout their college life. Due to the impact of the transition to college, achievement guilt is associated with increased depression and anxiety amongst FGCS. Current literature has studied the influence of the cultural value of familism, having a strong and supportive relationship with family members, on first-generation college students and its role in reducing depression and anxiety. It has been shown to help reduce depression and anxiety in students, which occur when having achievement guilt. The purpose of this study is to get a better understanding of the relationship between achievement guilt and well-being and the moderating influence of familism. It is expected that achievement guilt will be positively associated with stress, depression and anxiety. Also, when students have strong familism values, it will buffer the impact of achievement guilt. Participants included 256 (75% females) Latinx college students and completed an online survey. Preliminary results show emerging support for the proposed hypotheses. First, regression analyses indicated that achievement guilt was positively associated with stress, depression, and anxiety. Similarly, regression analyses indicated that familism was negatively associated with stress, depression, and anxiety. The findings of this research bring awareness to the difficulties Latinx college students face when transitioning to college and the importance of providing resources to support this student population.

Social withdrawal after trauma exposure and relationships with brain activity during social reward-related decision-making: a functional magnetic resonance imaging (fMRI) study

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Blair Chase*[1]and Elizabeth Olson [2]
[1]Amherst College, [2]McLean Hospital

Abstract: Anhedonia—blunted reward processing— is a prominent feature of post-traumatic stress disorder (PTSD). Recent literature emphasizes the role of social rewards in shaping social interactions. Prior research used neuroeconomic games (including the trust task) to investigate social anhedonia but has not related trust task behavior to real-world social functioning. We hypothesize that altered activity in social reward processing regions (e.g., ventral striatum (VR)) during the trust task will be associated with social withdrawal. Women (N=95: 35 non-trauma-exposed controls, 60 exposed to interpersonal trauma) completed structured psychiatric interviews, self-report questionnaires including the Social Network Index, and an fMRI version of the trust task. Whole-brain images were collected on a 3T Siemens Prisma scanner, including high-contrast T1-weighted MPRAGE images and gradient echo T2*-weighted echoplanar images. Results are pending in Summer 2022. fMRI scans are preprocessed using fMRIprep. We will build first-level models in SPM12 to extract brain activity from the VR. Using R, we will use regression to test relationships between brain activity in the VR and social network size, diversity, and embeddedness. We hypothesize that we will find that lower VR responsivity to social reward is correlated with lower social network size, diversity, and embeddedness. This would suggest that social anhedonia is a driver of social withdrawal following trauma exposure, highlighting the importance of social anhedonia as a central feature of PTSD in women. Identifying abnormal social reward processing in PTSD might ultimately generate new and creative modalities of effectively treating post-traumatic stress.

Are more reflective children less likely to gender stereotype?

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Caleigh Vanecek*[1], Isaac Cortez [2], Margaret Verne[3], Ruth "Breckie" Church[4], Andrew Young [5]

[1]Northeastern Illinois University, [2]Northeastern Illinois University, [3]Northeastern Illinois University, [4]Northeastern Illinois University, [5]Northeastern Illinois University

Abstract: Stereotyping is the tendency to attribute fixed and simple characteristics to social groups (e.g., racial or gender groups). Prior research suggests adults with greater cognitive reflection (the use of deliberative vs. intuitive thinking) engage in less stereotyping, however this relationship has not been investigated in children. The present study examines the relationship between cognitive reflection and stereotyping in a diverse sample of 5- to- 12-year-old children. Online over Zoom, we measure children's cognitive reflection through a verbal problem set, and gender stereotyping via direct questions about typically gendered activities. Data collection is ongoing. We hypothesize that children with greater cognitive reflection will engage in less gender stereotyping. We additionally expect that children's cognitive reflection will increase and stereotyping will decrease with age. Results from this study will clarify the developmental role of cognitive reflection in stereotyping. Furthermore, our findings may reveal cognitive reflection as a critical target for intervention to reduce harmful stereotyping.

The Effects of Transcutaneous Electrical Nerve Stimulation on Pain Perception During Isometric Exercise

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Cecil Ehirindu*[1]and Dr. Black[2]
[1]University of Oklahoma, Norman, [2]University of Oklahoma, Norman

Abstract: The treatment of choice for chronic pain has been opioid drugs, a pharmaceutical agent that is highly addictive. Transcutaneous Electrical Nerve Stimulation (TENS) is an inexpensive, non-addictive, alternative therapy that uses low voltage electrical current to provide pain relief. These electrical impulses alter how the nervous system transmits pain signals to the spinal cord and brain. In previous studies, TENS has also been shown to alter one's pain perception by stimulating the production of endorphins in the body. The purpose of this study was to gain a deeper perspective on the effects of several durations of TENS alone or in combination with exercise. This study will focus on 12-15 female participants between the ages of 18-24. We expect the use of TENS to increase one's pain sensitivity following exercise. Participants were familiarized with pain threshold testing, TENS application, and exercise protocols. Pressure pain threshold was determined by applying pressure to each person's upper leg until they deem it painful. This was performed before and immediately following one of four TENS/exercise protocols: 1) TENS only for 20 min, 2) isometric knee exertion exercise at 25% of their maximum voluntary contraction (MVC) until fatigue, 3) isometric exercise at 25% MVC plus TENS, and 4) high-intensity electrical stimulation at 25% of MVC time matched to voluntary exercise. Through these protocols, we hope to learn more about the factors that influence pain sensitivity and explore the efficacy of alternative treatments to opioids.

Prosocial youth purpose in Peruvian adolescents during the pandemic: a mixed-methods study

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Rebecca Avina*[1], Lucia Magis-Weinberg[2], Yailin Alvarez[3]
[1]University of Washington,Seattle, [2]University of Washington, [3]University of California, Berkeley

Abstract: Adolescents with prosocial purpose focus on their friends, family and community to develop their identity and maintain positive future expectations. During the COVID-19 pandemic, prosocial purpose may have acted as a source of resilience for teens, especially Peruvian adolescents who faced extreme stress during a uniquely strict lockdown. The aims of this mixed-methods study are to 1) quantitatively investigate gender and school-grade differences in prosocial youth purpose across adolescence and 2) qualitatively describe whether Peruvian adolescents perceive that the pandemic transformed their sense of purpose. A total of 988 adolescents from low- and middle-income in Peru, ages 11 to 17, completed the Prosocial Youth Purpose Scale. Adolescents chose their top 3 goals out of a list of 10 goals that included 5 beyond-the-self oriented (BYSO) and 5 self-oriented (SO) goals and reported on their level of commitment to each of their chosen goals. Adolescents also qualitatively reflected on whether the pandemic changed their goals. Findings show that girls had higher commitment to BYSO goals than boys but there were no school-grade differences in terms of frequency of endorsement of SO or BYSO goals. Half the students reported that the pandemic shifted their goals and perspectives. Additionally, I found 8 themes that emerged in relation to pandemic impacts on goals with three main themes of: (1) Self-Perspective Shift, (2) Self-Centered Goal-Oriented, (3) Negative impact. These findings provide further information on the long-term impacts of COVID-19 on adolescent development in underserved populations like Peru.

Niche modeling of two vulnerable and endemic ferns in the Hawaiian Islands

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Krystalyn Edwards-Calma*[1], Laura Jimenez [2], Rosana Zenil-Ferguson[3], Miles Thomas[4], Carrie Tribble [5]
[1]University of Hawaiʻi at Mānoa, [2]University of Hawaiʻi at Mānoa, [3]University of Hawaiʻi at Mānoa, [4]Herbarium Pacificum at Bernice Pauahi Bishop Museum, [5]University of Hawaiʻi at Mānoa

Abstract: Hawaiʻi is recognized for its botanical biodiversity, evolutionary history, and unique ecology. In this context, studying the ecology of endangered ferns is important because learning more about their ecology allows us to understand how these ferns were able to survive in invaded habitats, as well as, how to care for them so that they can become non-endangered. In particular, two ferns Doryopteris decipiens and Doryopteris decora are of interest because they are prime examples of endemic and endangered ferns of Hawaiʻi. These species reside in dry, warm habitats located on popular and accessible touristic hikes, making their populations more vulnerable. In this work, we propose studying the modern distribution of D. decipiens and D. decora by examining existing collections in the Herbarium Pacificum Department of Natural Sciences at the Bishop Museum, and the occurrences of these two species in the Pteriodophyte Collections Consortium (PCC), Global Biodiversity Information Facility (GBIF), and iNaturalist. Using their recorded occurrences we propose an ecological niche modeling approach that uses fine resolution climatic databases created by the Geography department at the University of Hawaiʻi at Mānoa for the modern distributions of D.decipiens and D. decora. The niche models fitted in this project find high probability areas where vulnerable species could be located and allows us to compare observed vs. realized niches of ferns in the islands. We find that the ecological niche model predicted the possible limited habitats of D. decipiens and D. decora need to have an increased awareness due to their modern vulnerable habitats.

Perceptions of Familism on Kinship Adoption in South Texas

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Yara Green-Jordan*[1]and Robert F. Villa [2]
[1]Texas A&M University- Kingsville, [2]Texas A&M University- Kingsville

Abstract: What is the influence of familism in perceptions of kinship adoption? Previous studies have found that the attachment as experienced in kinship care is higher than other forms of care. Limited studies have a focus on a comprehensive understanding of the experience of kinship care. The present exploratory study focuses on the influence that familism has on attitudes, values, and beliefs of kinship adoption. Participants from a South Texas university will be asked to fill out an online questionnaire covering demographics and perceptions of familism and kinship care. This study will explore kinship perceptions, adoption factors, motivation to adopt, and awareness of adoption. The study anticipates having a convenience sample of N = 50 participants and will analyze data through a convergent design using descriptive statistics, analysis of recurrent themes in the qualitative data, and in order to merge quantitative and qualitative data, the researcher will then use grounded theory methods to expand on existing theory. The goal of the study is to explore the perceptions of familism on kinship adoption from which a more in-depth study can be initiated in the future. The researcher anticipates high levels of familism within participants who perceive kinship adoption positively. There will be higher levels of this value among ethnic minority groups. Also, a younger generation will be less likely to relate to familism due to lack of cultural awareness. Lastly, participants will be familiar with familism on kinship adoption. Key Words : kinship adoption, adoption, familism, Mixed Methods, grounded theory

Social Anxiety & The Peak-End Rule

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Aleah Brown*[1]and Dr. Erin Tone [2]
[1]Spelman College, [2]Georgia State University

Abstract: The peak-end rule is a well-researched phenomenon in which memories of distressing experiences are biased by the most intense (peak) or very last (end) point of the experience (Kahneman et al., 1993). Originally, the peak-end rule was researched in the context of medical procedures, but some studies suggest the peak-end rule also extends into social interactions (Fredrickson, 2000). Little research exists, however, examining individual differences, like social anxiety, that could impact the peak-end rule. Social anxiety and the peak-end rule should be explored together because research indicates that socially anxious people may be more biased than their less-anxious counterparts to remember negative experiences (e.g., Krans, de Bree, & Bryant, 2014). It is unknown whether people with higher social anxiety are susceptible to more intense peak-end effects during experiences that are not uniformly negative or positive than people with lower social anxiety. To investigate this, 122 college students completed self-report surveys assessing social anxiety and played the Prisoner’s Dilemma game designed to mimic social interactions. We examined whether peak-end ratings of personal distress and perceptions of one’s “co-player” during gameplay were associated with post-interaction recollections after the game and whether social anxiety served as a moderator for these associations. We hypothesized that socially anxious people would have higher peak-end and post-game ratings with a stronger correlation than less socially anxious people. Surprisingly,

what we found was just the opposite. Findings from this study have potential implications for understanding social anxiety, interactions, and behavior.

From Shame to Pride: A Journey Through the Stages of Ethnic Identity Development

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Yuliana Fernandez*[1], Marisol Brito [2], Lizette Ruiz[3], Dania Salgado[4], Dr. Lucía Alcalá [5]
[1]California State University, Fullerton, [2]California State University, Fullerton, [3]California State University, Fullerton, [4]California State University, Fullerton, [5]California State University, Fullerton

Abstract: Studying abroad has numerous benefits, but there is a wide gap between the demographics of students who have had the opportunity to do so. Consequently, research has primarily focused on White students' experiences. The present study investigated the impact a Study Abroad Program had on Latinx college students' development and how traveling for the first time to their parent's home country influenced their ethnic identity. Our sample included twelve students that participated in a semester long-program on "immigration and literacy," where they spent a week in Guadalajara, Mexico. Through their service learning, students actively learned about their culture and engaged with immigrants at two different migrant shelters. Participants were interviewed using semi-structured open-ended questions on topics related to their experiences in Guadalajara, expectations prior to the trip, and any changes in their views regarding their ethnic identity after the trip. Participants' responses were recorded, analyzed, and coded using thematic analysis. Preliminary findings suggest students' experiences clustered around three central themes: changes in ethnic identity, changes in parent-child relationship, and professional/academic development impact. All three themes included subcategories such as pride in their Latinx/Chicanx heritage, a positive benefit to their academic and personal development, and stronger connections with their parents. Academic retention of students of color continues to be a prevalent issue. The negative perceptions they have of their heritage may be another factor leading to more difficulties in academia and navigating educational institutions. Investing in service learning projects like this one could be a way to fight internalized racism.

Attitudes towards Psychological Online Interventions within a Hispanic Community

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Maria Peraltilla*[1], Dr. Page Anderson [2], Dr. Gabriel Kuperminc[3], Jennifer Perez[4], Donovan Ellis [5], Claudia A. Delbasso[6], Guillermo Sanchez[7], Yishai Yeremei Perez-Ponce[8]
[1]Georgia State University, [2]Georgia State University, [3]Georgia State University, [4]Georgia State University, [5]Georgia State University, [6]Georgia State University, [7]Georgia State University, [8]Georgia State University

Abstract: Psychological online interventions (POIs) have great potential to improve the accessibility of mental health resources, especially among underserved communities. Although there is research on Hispanics' usage of POIs few examine attitudes towards POIs. The aims of the present study are to (1) translate the Attitudes towards Psychological Online Interventions Questionnaire (APOI) from English to Spanish, (2) provide preliminary evidence for its utility in a Spanish-speaking population, and (3) assess the relationship between anxiety and depression severity and attitudes towards POIs among a sample of Hispanic adults. The forward-backward translation method was utilized. The study consisted of 71 Hispanic adult participants recruited from an undergraduate participant pool (n = 9, 13%) and the surrounding metropolitan community (n = 62, 87%). Participants completed a 10-15 minute survey through an undergraduate participant pool system or via QR code/link shared on social media networks and posted flyers. Results indicated that 35% (n = 25) of participants understood the majority of the Spanish APOI (SAPOI) and 35% (n = 25) of participants understood all SAPOI items. There was neither a statistically significant association between anxiety severity and attitudes towards POIs, r(65) =.056, p >.05), nor was there a significant association between depression severity and attitudes towards POIs, r(65) =.150, p > .05). Overall, this translated measure can improve the inclusion of Spanish speakers in research related to digital interventions and create a resource that may be used to mitigate the gap in unmet mental health needs among Hispanics through the use of POIs.

Bridging environmental enrichment with amantadine after controlled cortical impact injury in adult male rats

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Anna Carpio*[1], Dr. Anthony Kline [2], Jeffrey Cheng[3], Dr. Corina O. Bondi[4], Eleni H. Moschonas [5], Rachel Bittner[6], Vincent Vozzella[7], Connor Brennan[8], Rithik Eleti[9]

[1]University of Pittsburgh, [2]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research; Center for Neuroscience, University of Pittsburgh, Pittsburgh, PA, [3]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research, [4]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research; Neurobiology; Center for Neuroscience, University of Pittsburgh, Pittsburgh, PA, [5]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research; Neurobiology; Center for Neuroscience, University of Pittsburgh, Pittsburgh, PA, [6]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research, [7]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research, [8]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research, [9]Physical Medicine & Rehabilitation; Safar Center for Resuscitation Research

Abstract: Early environmental enrichment (EE) facilitates recovery after traumatic brain injury (TBI) but this approach is not clinically relevant as rehabilitation is not initiated early due to life saving measures taking priority. Yet, treating TBI early is vital for quicker recovery. Hence, we administered amantadine (AMT) as a bridge therapy before initiating delayed (7-days) and abbreviated (6h/day) EE, which mimics clinical rehabilitation. Bridging EE with AMT will result in better recovery than AMT or EE alone. Anesthetized male rats received a cortical impact or sham injury and then housed in standard (STD) conditions for one-week and administered either AMT (10 or 20 mg/kg) or saline (1-mL/kg) intraperitoneally for 7-days (bridge). EE began on day 8 for the AMT bridge and continuous EE groups. Motor and cognition were evaluated on days 7-11 and 21-25, respectively. The data showed that EE, whether alone or with AMT benefitted both behavioral outcomes (p<0.05) vs. STD. The 20 mg/kg AMT bridge + EE group acquired spatial learning in the water maze better than the EE alone group (p <0.05) but did not differ from EE alone or 10 mg/kg AMT bridge + EE in motor function (p >0.05). The 20 mg/kg AMT bridge group performed better than the EE alone group in the cognitive group, which supports the hypothesis. Also, despite not exhibiting an additive benefit in motor outcome, these data show that EE does not need to be immediately after TBI and does not have to be provided continuously to confer benefits.

Muscular ideal internalization and muscularity-oriented eating and behaviors: The role of negative affect

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Rebecca Mendoza*[1], Alexandra D. Convertino [2], Jamie-Lee Pennesi[3], Aaron J. Blashill[4]
[1]San Diego State University, [2]San Diego State University/University of California San Diego JDP, [3]University of Louisville, [4]San Diego State University

Abstract: Previous research has shown that the relationship between thin-ideal internalization and thinness-oriented eating disorder (ED) behaviors (e.g., restriction, purging) is moderated by negative affect, such that ED behaviors are highest when both internalization and negative affect are high. Recent research has identified muscular-ideal internalization and negative affect as important influences on muscularity-oriented ED behaviors (e.g., weight lifting, excessive exercise, increased food intake), but research has not yet been examined whether similar moderation effects as in thinness-oriented pathology exist for muscularity-oriented behaviors. The present study examined whether negative affect moderated the relationships between muscular-ideal internalization and muscularity-oriented ED behaviors. Data were collected from a sample of undergraduate students (N=1015) cross-sectionally. Three models were conducted, with muscular-ideal internalization as the independent variable, negative affect as the moderator, and muscularity-oriented eating, excessive exercise, and muscle building behavior as the dependent variables. The main effects of both internalization and negative affect were significant in all models, such that greater internalization and greater negative affect were both associated with greater muscularity-oriented outcomes. In the model with muscle building behavior as the outcome, there was a significant interaction (B = -.01, p = .005), such that at the highest levels of negative affect, internalization of the muscular ideal had no effect on muscle building behavior. Future longitudinal research is needed to explore other potential moderating factors of the association between internalizing the muscular body ideal and muscularity-oriented ED behaviors. Further understanding these outcomes may help improve the prevention and treatment of muscularity-oriented ED behaviors.

Does trait anxiety have an influence on depressive symptomatology depending on employment status in Spanish-speaking female university students in Puerto Rico?

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Jahleel Torres-Pérez*[1], Sebastián Bentz-Figueroa [2], Fátima B. Berríos-Cruz[3], Dariana Gil-Hernández[4], José A. Maldonado-Martínez [5], Giovanni Tirado-Santiago[6]
[1]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico, [2]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico, [3]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico, [4]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico, [5]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico, [6]Department of Psychology and Institute for Psychological Research, University of Puerto Rico, Río Piedras Campus, San Juan, Puerto Rico

Abstract: The COVID-19 pandemic has had a substantial impact on the mental health of college students. Recent studies reveal an increase in anxiety and depression symptoms in female college students. However, there is a literature gap regarding the joint effect of employment status and trait-anxiety on depressive symptomatology in Spanish-speaking female university students in Puerto Rico. We hypothesize that employment status and trait-anxiety exert a significant interaction effect on depressive symptomatology. We recruited 43 Spanish-speaking female university students (ages 18-25, M =20.7, SD =1.53) using an online survey consisting of the State-Trait Anxiety Inventory-Trait Subscale(STAI-T, Cronbach's α =0.83), the Patient Health Questionnaire-9(PHQ-9, Cronbach's α =0.77), and a demographic form. Then, we conducted a-two-way independent ANOVA and Tukey post hoc analysis. Although the interaction effect was non-significant, F (2,37)=2.47, p =0.099, it was of medium practical importance, η 2 g = 0.12. We found that employed participants with low anxiety (M =4.11, SD =2.20) had lower depression scores than their medium (M =11.50, SD =3.73) and high anxiety counterparts (M =10.6, SD =4.24), both p <.01. However, there were no between-subject differences in depression scores by anxiety level in the unemployed participants, all p >.05. These findings provide preliminary evidence that trait-anxiety may exert a different influence on depressive symptomatology in employed versus unemployed Spanish-speaking female university students. We recommend that future studies elaborate a more in-depth assessment of the joint effect of employment status and trait-anxiety through incorporating time spent working and performing extracurricular activities as covariates.

The Prevailing Role of Traditional Mexican American Cultural Values and Parenting Stress on Maternal Sensitivity

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Analise Segarra*[1]and Kimberly D'Anna Hernandez [2]
[1]Marquette University, [2]Marquette University

Abstract: Maternal stress is associated with disruptions to the mother-child bond and associated with changes in maternal behavior, including maternal sensitivity. Maternal sensitivity is defined as the level of responsiveness that a mother has toward her child during distress. However, some cultures, such as Mexican culture, revere motherhood child-rearing as fulfilling a traditional gender role and are supported by the value of familism, the centering of family relationships. However, whether the alignment with the traditional Mexican cultural values and others are related to parenting stress and maternal sensitivity is not clear. We hypothesized that mothers who align more with Mexican American cultural values and have lower pregnancy-related stress will display more maternal sensitivity during a stress task. At 6 months postpartum, mothers of Mexican descent (N=125) completed the Mexican American Cultural Values Scale (MACVS) and answered the Parenting Stress Index (PSI). Lastly, mother/child dyads underwent the Still Face paradigm, and maternal sensitivity to infant distress was measured. Preliminary results suggest there was no relationship between parental distress and maternal responsivity (R2 = -0.112, p = 0.212,). However, mothers that adhered to the traditional cultural value of familism were more responsive to their children (R2 = 0.195, p = 0.029). Additional analysis will determine if familism and other cultural values may be a moderator between parental distress and maternal sensitivity. Current results suggest that reverence of cultural values plays a large role in maternal behavior.

Intuitions and Health: Moral Foundations as Predictors of COVID-Related Health Behaviors

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Melànie Siems*[1]and Anna R. Harper, Ph.D. [2]
[1]Southern Nazarene University, [2]Southern Nazarene University

Abstract: COVID-19 has touched the lives of many in the United States. In an attempt to mitigate the virus, several strategies have been suggested, including mask wearing and social distancing. There is a perceived difference in how conservatives and liberals responded to these types of suggestions, with liberals responding more favorably; in Moral Foundations Theory (MFT) literature there is a similar divide. The five foundations posited by MFT are Care, Fairness, Loyalty, Authority, and Purity— liberals are associated with Care and Fairness while conservatives are associated with all five. Thus, it was hypothesized that mitigation behaviors would be associated with Care and Fairness. Participants responded to questionnaires regarding their typical priorities when engaging in moral decision-making and problem-solving, then reported their COVID-19 attitudes and behaviors, as well as demographic information. The results of bivariate correlations showed that the moral foundations of Care and Fairness were most notably associated with greater COVID-19 health behavior adherence, more favorable ratings of the effectiveness of COVID-19 mitigation strategies, and greater approval of the use of these strategies. A hierarchical multiple regression analysis with a nine predictor model of the five foundations and four demographic variables showed that Care was associated with greater observance of COVID-19 health behaviors, beyond the impact of these other variables, $\beta = 0.24$, 95% CI [0.03, 0.46], $t(112) = 2.30$, $p = .02$. The apparent importance of moral reasoning during the pandemic as being associated with mitigation strategies could have implications for other health behaviors as well.

Analyzing the Neural Processing Pathways and Clinical Symptoms of Co-morbid Misophonia and Tinnitus Amongst Undergraduate Students

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Saramarie Azzun*[1], Lauren E. Ethridge, Ph.D. [2], Jordan E. Norris[3]
[1]University of Oklahoma, Norman, [2]University of Oklahoma, Norman, [3]University of Oklahoma, Norman

Abstract: Misophonia is characterized as an auditory hypersensitivity to certain trigger sounds, resulting in a moderate or intense emotional response. Misophonia reportedly occurs at high prevalence rates among nonclinical populations and commonly presents with co-occurring conditions. Tinnitus, a complex phenomenon characterized as a sensory processing abnormality of variable pathogenesis, is a common co-occurring condition of interest. Overlap of misophonia and tinnitus potentially reflects shared neural mechanisms that we aimed to assess, in addition to general sensory hypersensitivities in a population of undergraduate students. Our study included 282 participants. Individuals with misophonia (Mean age: M = 19.35, SD = 3.54; Female: 33) and matched controls (Mean age: M = 19.28, SD = 2.93; Female: 170) completed self-report measures of misophonia and related symptoms, collected via Qualtrics™ and analyzed to evaluate symptom patterns. The Misophonia Questionnaire (MQ) was used to identify the presence of misophonia in participants and the Tinnitus Handicap Inventory (THI) appraised tinnitus symptom severity. An expected number of participants reported experiencing significant symptoms of misophonia (14.9%). Approximately 50% of participants with misophonia reported overlapping tinnitus whereas only 36.2% of controls reported experiencing tinnitus. The current results suggest elevated rates of co-occurring tinnitus in patients with misophonia compared to the normal population. Future efforts include assessing brain activity and sensory processing mechanisms using electroencephalography (EEG) with the same sample. Neural correlates of misophonia and tinnitus overlap will improve the mechanistic understanding of co-occurring conditions and aid in determining effective non-pharmaceutical-based therapies for individuals with misophonia.

The relationship among identity, executive functioning, and PTSD

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Stephanie Washburn*[1], Bailey Wagaman[2], Emalee Kurr[3], Dr. Steven Berman[4]
[1]University of Central Florida, [2]University of Central Florida, [3]University of Central Florida, [4]University of Central Florida

Abstract: Over 300 million adults worldwide suffer from post-traumatic stress disorder (PTSD; PTSD Statistics, 2021). With exposure to trauma, executive functioning can diminish (Aupperle et al., 2012) leading to a decrease in self-control and greater sensitivity (Bair & Steele, 2010). Trauma can also affect identity (Waterman, 2020) and lead to identity distress (Berman et al., 2020). Although it is known that trauma affects both executive functioning and identity, the possible direct link between identity and executive functioning has not been adequately explored. The current study examined the relationship between identity distress and executive functioning in order to investigate if identity variables better predict executive functioning than PTSD alone. Identity variables included identity distress, exploration, and commitment. Data was collected through an online anonymous survey with 107 young adults recruited from the large enrollment psychology courses at the University of Central Florida. Identity variables better-predicted executive functioning than PTSD alone. An independent samples t-test revealed that those who experienced trauma reported higher levels of identity distress and lower levels of executive functioning. Future studies might benefit from the use of longitudinal designs to determine a developmental order to these variables, which might aid intervention efforts in regard to which one(s) should be the focus of treatment in order to ameliorate the other(s).

Acceptability and Feasibility of Ecological Momentary Assessment Procedures to Measure Stress, Socialization, and Smoking in LGBTQ Young Adults

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Sara Rodrigue*[1], Jerel Calzo[2], Aaron Blashill[3], Hee-Jin Jun[4], Emma Burke[5], Pablo Cuellar[6], Lahiru Kodituwakku[7]
[1]San Diego State University, [2]San Diego State University, [3]San Diego State University, [4]San Diego State University, [5]San Diego State University, [6]San Diego State University, [7]San Diego State University

Abstract: This study aims to determine the acceptability and feasibility of using phone-based ecological momentary assessment (EMA) to measure how daily experiences of stress and socialization impact smoking (combustible cigarette use and vaping) among LGBTQ young adults. Participants completed a baseline survey and underwent training for the EMA protocol and study procedures. For the EMA, participants completed 4 daily scheduled EMA surveys and 1 end-of-day report measuring experiences with daily stressors, socialization, and smoking behaviors over 13 days. At the end of two weeks, participants completed an exit survey in which we assessed acceptability, feasibility, and appropriateness of the EMA protocol (i.e., data collection process, procedures) on a 5 point scale (1=Completely Disagree, to 5=Completely Agree). Participants also provide open-ended feedback. Across 3 weeks of recruitment, 20 participants completed the screening survey, with 18 deemed eligible; 12 participated in the study. All participants completed the full two week study, with n=8 completing >80%, and only 3 participants falling between the 40%-55% completion range, indicating moderate feasibility of the EMA method. Eleven participants completed the exit survey. Participants found the EMA survey items (M= 3.91) and procedures (M=3.89) to be acceptable. Mean feasibility was rated at 4.43. Participants described the EMA method as “convenient, quick, and intuitive to use” and that it “captured my real time experiences and provided glimpses of different contexts that cause me to vape more”. Future analyses will examine preliminary associations between socialization variables, stress, and smoking, and develop the pilot app for future research.

Sibling and Peer Attachments in Juvenile Prairie Voles

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Ennis Galaz*[1], Bruce S. Cushing [2], Adam Perry[3]
[1]University of Texas at El Paso, [2]University of Texas at El Paso, [3]University of Texas at El Paso

Abstract: Relationships play a critical role in social wellbeing, impacting both mental and physical health, with the disruption of social bonds associated with psychological disorders. The highly prosocial prairie vole is a translational rodent model that has been extensively used to understand the role of parent/offspring interactions as well as those associated with long-term bonds between adult males and females. However, social attachments, especially in human, also involves non-sexual attachments, “friendship”, between adult as well as juvenile peers. Therefore, the goal of this study was to use the prairie vole model to determine if juveniles prefer siblings over unrelated peers, if juveniles form peer attachments and the role of the neuropeptide oxytocin (OT), and vasopressin (VP) in the expression of juvenile preferences. Based upon the hypothesis that juvenile attachments is associated with familiarity we predicted that juvenile males and females would display a robust preference for their familiar sibling over a novel peer. We also predicted that OT neurotransmission conveys familiarity between pairs, while interactions amongst novel pairs would activate other neuropeptides such as vasopressin. To test this subjects were weaned on post-natal day (PD) 21, and were tested between PD 22 and PD 28. All subjects were first tested for their preference between a familiar sibling and an unfamiliar, same-sex peer. Half the subjects were then cohabitated with that novel peer for 24 hours, after which they were tested for the formation of a peer attachment. Sibling and peer preference data are currently being analyzed and will be presented.

Induced Sensory Processing Deficits in Larval Zebrafish by Bisphenol-A Exposure

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Daniela Hernandez*[1], Adam Roberts [2], Christopher Creighton[3], Fernando Licea[4], Luis Salazar [5], Courtney Sacramella[6], Gabriel Winter[7], Sam Mankatala[8]

[1]California State University, Fullerton, [2]California State University, Fullerton, [3]California State University Fullerton, [4]California State University, Fullerton, [5]California State University, Fullerton, [6]University of California, Riverside, [7]California State University, Fullerton, [8]California State University, Fullerton

Abstract: Autism Spectrum Disorder is a prominent developmental disability characterized by social deficits, restricted/repetitive behavior, and sensory processing difficulties. Contemporary research has linked epigenome modulators, Valproic Acid (VPA) and Bisphenol-A (BPA), to ASD development, indicating the need for further exploration. In order to understand the association between epigenetic changes and ASD development, larval zebrafish are used to explore the possible underlying molecular contributions. Zebrafish offer an array of benefits to this research, such as their translucency, relatively simple nervous system, and ability to absorb chemicals easily from their environment. To understand the progression of developmental disorders, zebrafish were exposed to Bisphenol-A (BPA) for 5 days post fertilization (dpf). Once exposed, the zebrafish were observed to determine if ASD-like behavior arises as a result of BPA exposure. We measured possible disruptions in sensory processing, as measured by prepulse inhibition (PPI), habitation, and locomotion. Prepulse inhibition measures an organism's ability to filter out unnecessary sensory information, while habituation describes an organism's ability to reduce reaction to repetitive stimuli. BPA-treated fish had a reduced ability to ignore irrelevant information as measured by the frequency of their c-start reflex. Additionally, BPA-exposed fish showed deficiencies in PPI. There was no difference in locomotor behavior in quality (repetitive circling) and quantity (distance traveled). Future studies will seek to determine the molecular mechanisms underlying the deficits in sensory processing.

Using Network Analysis to Study Relationships in Climate and Energy Legislation

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Spencer Paragas*[1], Andrew Scerri[2], Christian Lucero[3], Andrew Alexander[4]
[1]Virginia Tech, [2]Virginia Tech, [3]Virginia Tech, [4]Virginia Tech

Abstract: Political scientists have recently become interested in studying lobbying and donations to legislators by fossil fuel and related interest groups. While it is impossible to claim such activities cause legislators to pass ineffective climate and energy legislation, fine-grained analysis of a significant volume of such activities over time can support the less robust claim that these interest groups seek to influence legislators in the context of other interest groups who support effective climate and energy legislation. One way to conduct this kind of analysis is based on a version of network analysis. This poster demonstrates the results of such analysis of lobbying and donations to legislators in the US state of Virginia on 600+ climate and energy bills 2015-2022. We used R to analyze publicly available data on each bill, showing career donations to bill sponsors, lobbying disclosures, and where available public testimony. Admittedly impressionistic, the results appear to show a relationship between the volume of donations and lobbying directed at legislators and the outcomes of bills.

Systematic Investigation of the Quality of EEG Recording in Black Participants with Natural Curly Hair

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Katiasofia Gonzales*[1], Grit Herzmann[2], Noah Mitchell Pounds[3]
[1]The College of Wooster, [2]The College of Wooster, Psycology Departament, Neuroscience program Chair, [3]The College of Wooster

Abstract: Current EEG research has racial bias because common forms of electrodes lead to a poor connection for participants with thick or curly hair, excluding predominantly Black participants from EEG studies. Being interested in the other-race effect on facial recognition, we started to use Brain Vision's ActiCap flat electrodes to overcome this flaw in design. This systematic review analyzes the quality of the data recorded from 20 White and 20 Black participants on a forty-minutes face memory study. We analyzed the initial impedances of each electrode, the number of artifacts throughout the recording, the amount of data lost, the number of participants needed to be excluded, and the signal-to-noise ratio of the final event-related component. Our preliminary results indicate that the quality of the data obtained from both groups is comparable. A larger number of participants needed to be excluded from the Black than the White participant group. Data from Black participants also included slightly more unusable data. These small differences should not prevent researchers to make an effort of including all individuals in EEG recording. These results also show that ActiCap flat electrodes an effective tool for EEG studies including Black participants

The Effects of the Dopaminergic System on Functional Motor Recovery Following a Stroke

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Valerie Rojas*[1]and April Becker[2]
[1]University of North Texas, [2]Assistant Professor

Abstract: Strokes are a leading cause of disability in the United States. A promising avenue towards promoting functional recovery is to manipulate naturally occurring neuroplasticity mechanisms. Neuroplasticity, the brain's ability to reorganize synaptic connections following brain injury, underlies gains in behavioral rehabilitation and functional recovery from stroke. The mammalian dopaminergic system facilitates neuroplasticity through four main pathways, one being the Mesocorticolimbic pathway—originating from the Ventral Tegmental Area (VTA)—which promotes the facilitation of memory and learning processes. Neurological systems that influence neuroplasticity have heightened importance after neurological damage, when brain reorganization is vital. Understanding how the dopamine system aids in reorganizing neural circuits in the context of brain injury could enhance current treatments, such as dopamine agonists, and contribute to new therapies for neurological damage. This presentation will report efforts to investigating dopaminergic manipulation in the frame of stoke recovery as well as a proof of concept of alternative behavioral indicators of stroke. Our goals are to 1: evaluate the effects of VTA manipulation in diffrent stages of stroke recovery, and 2: validate an automatic assessment of hemiparesis (the paralysis of one side of the body) in a stroke model. The phasic dopaminergic signals are vital for skill cortical reorganization and behavior acquisition; thus, direct stimulation of dopaminergic cells in the VTA is a way to utilize phasic signaling in a therapeutic context. Direct stimulation of the dopaminergic cell population, we believe, will produce better recovery outcomes following stroke. This study will provide greater insights on how to better treat stroke.

A qualitative analysis of pathologist perceptions about breast cancer immunotherapy access

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

ekene onwubiko*[1], Jayda Grant[2], Taisha Gomez[3], Alexis Brown[4], Melissa Lopez[5], Adriana Espinosa[6], Francesca Gany[7], Devika Jutagir[8]
[1]City College of New York, [2]The City College of New York, [3]The City College of New York, [4]Memorial Sloan Kettering Cancer Center, [5]Memorial Sloan Kettering Cancer Center, [6]Memorial Sloan Kettering Cancer Center, [7]Memorial Sloan Kettering Cancer Center, [8]Memorial Sloan Kettering Cancer Center

Abstract: Triple-negative breast cancer (TNBC) grows and spreads faster than other breast cancers and treatment options are more limited. Black and Hispanic women are disproportionately likely to develop TNBC. Checkpoint inhibitors, a form of cancer immunotherapy, are recently approved for patients with PD-L1 positive metastatic TNBC or high-risk early-stage TNBC.   Problem: Immunotherapy is less likely to be administered to patients who are Black or of low socioeconomic status. This study assessed breast cancer immunotherapy access barriers/facilitators.   New York City metropolitan area pathologists who work with breast cancer tissue were interviewed about immunotherapy access. We conducted a preliminary analysis of the first 5 interviews collected. Interview questions probed themes we hypothesized were relevant to immunotherapy implementation. Seven coders independently analyzed data and reached consensus about emerging themes guided by the Consolidated Criteria for Reporting Qualitative Research. The emerging themes were: lack of specialized breast cancer pathologists; variability in PD-L1 test ordering criteria; financial barriers to having multiple types of PD-L1 tests available at a single institution; lack of autonomy to determine PD-L1 test selection; lack of in-house pathologists to interpret PD-L1 results; lack of formal training for PD-L1 testing analysis; lack of standardized PD-L1 test interpretation; challenges determining PD-L1 test outcomes. Pathologists reported a variety of barriers to PD-L1 testing, which could have downstream effects on breast cancer immunotherapy access. Future quantitative research is needed using electronic medical records to assess disparities in PD-L1 testing. Future qualitative research could study patient awareness and understanding of PD-L1 testing

Implementing a Needs Assessment for PRISM (Promoting Restorative and Integrative Mental Health OR Promotores de la Salud Mental Restauradora y Integrativa)

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Vanessa Salazar*[1]and Alicia Trotman, Ph.D.[2]
[1]Sul Ross State University, [2]Sul Ross State University

Abstract: Coupled with the need to promote good physical health at colleges for students, staff and faculty, there is an immense need to advocate for mental health awareness and suicide prevention. Recent studies have shown that there has been a bigger pool of college students feeling anxiety and depression in the past few years (Lipson et al., 2019; Reiff, et al., 2019). Approximately 58% of college students reported to have anxiety, 36% claimed depression, and 9.8 % experienced suicidal ideation (ACHA, 2016). With the advent of COVID-19, mental health is at risk due to the widespread disruption to instruction and student college life (Wang et al., 2020). Panayi (2020) emphasized universities should take a proactive stance in establishing mental health programs designed for a subsequent aftermath. Specifically, these programs should be crisis-oriented, and uniquely meet the psychological and psychosocial needs of those involved. Furthermore, these programs target context and trauma determinants shaping social and culturally informed support for students, staff, and faculty. This resembles a model of ”promotoras/es” or lay helpers used in many fields and culturally consistent with being a Hispanic Serving Institution (HSI) (CDC, 2019). Our objective is to create a multicultural and multi-layered mental health program for our university. Currently we are conducting focus groups and surveys to initiate the first step of data collection of the mental health needs of students, staff, and faculty. Our data analysis will be completed by the time of the convention.

A Survey of COVID-19 Pandemic Public-Health Data Tracking & Communication Practices for Racial and Ethnic Minorities in Southern California

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Adeline A. Rosales*[1]and Melawhy Garcia, MPH, Ph.D. [2]
[1]California State University, Long Beach, [2]California State University, Long Beach

Abstract: The COVID-19 pandemic has disproportionately impacted racial and ethnic minorities in California. The five counties in California experiencing the highest levels of COVID-19 deaths and infections are 1) Los Angeles 2) Orange 3) Riverside 4) San Bernardino and 5) San Diego. The purpose of this study is twofold: 1) discern which racial and ethnic group(s) have been affected by COVID-19 infections and deaths, and 2) assess the level of culturally tailored COVID-19 health information available at the county level. Part one of this retrospective observational study utilizes data from the UCLA Health Center’s COVID-19 Rates and Risk Factors by California County Dashboard to analyze the number of confirmed cases and deaths by race and ethnicity from April 2020 to May 2021 in five Southern California counties. Part two of the study is based on content analysis of five county public health department’s COVID-19 websites to understand the level of cultural tailoring for different racial and ethnic minority groups. Part one of the study demonstrates that, compared to Whites, Latinos experienced higher COVID-19 related cases in all five counties, and that Latinos experienced higher COVID-19 related deaths in four of the five counties. Preliminary analysis for part two of the study show that county COVID-19 websites vary in their availability and level of culturally tailored health information. Since racial and ethnic groups are experiencing higher rates of COVID-19 related cases and deaths, county COVID-19 related health information must be culturally tailored to promote health equity.

Food Expenditure Patterns of Mexican and Hispanic Consumers, A Cross-Country Comparison

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Tyson Ramirez*[1]and Dr. David. J Molina [2]
[1]University of North Texas, [2]University of North Texas

Abstract: This paper will examine food expenditure patterns of Mexican citizens and Hispanic-Americans in an attempt to construct a model that may predict future expenditure habits of culturally similar populations across borders. We concentrate on changes in food expenditure trends in Mexican consumers and the potential relationship to changes in food expenditure trends in Hispanic-American consumers. While absolute and relative income groups may affect expenditure levels, we anticipate that there will be a strong correlation between the food expenditure habits of the two populations. We obtained data on consumer expenditure levels from Mexico’s National Survey of Household Income and Expenditure produced by Mexico's INEGI and data for the US from the Consumer Expenditure Survey produced by the U.S.'s Bureau of Labor Statistics. There are some differences in the two food product coding indexes, so a matching process is needed to construct as close equivalent food expenditure categories as possible. Once the two survey data may be read and cross-examined in a common system, we obtain and analyze the data's descriptive statistics (using the statistical packages SAS and STATA). In the second step of the project we will develop an econometric model to test various hypotheses of the consumer behavior of these two populations filtered for ethnic origin. Further analysis will reveal the extent to which (if at all) the expenditure patterns of the two groups correlate with each other. Further analysis may also reveal what other factors may have a significant influence on food item expenditure amongst a population.

Exploring Income as a Moderator of the Relation between Parental Martial Status and Academic Achievement in African American Children

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Ahniah Charles*[1]and Dr. A. Nayena Blankson [2]
[1]Spelman College, [2]Professor

Abstract: The data used in this study are from pre-K and third grade years. Measures included mothers' reports of income and marital status when children were in pre-kindergarten and standardized measures of children’s reading ability when the children were in third grade.The aim of the current research was to examine income as a moderator of the association between parental marital status when children were in pre-K and their children’s reading academic achievement in third grade. The sample was comprised of 198 African American children who were seen in their pre-K year and kindergarten years and again in third grade. The present study builds on a previous study with the same participants, there was a significant relation between children's reading academic success and their family household structure, such as whether their parents are married, single, dating, or widowed. Results from that study showed that children of married parents scored higher on tests of reading achievement in kindergarten and third grade than children of cohabiting or single parents. The current study aims to expand upon these preliminary findings to examine income as a potential moderator. It was hypothesized that parents who report having higher levels of income available to them will have children with higher reading scores than parents who report having lower levels of income. However, among higher income participants, there should be no differences in child reading achievement across parental marital status groups. Among lower income participants, children of married parents are expected to score higher than children of non-married parents.

Science and Math Interest and Gender Stereotypes: The Role of Educator Gender in Informal Science Learning Sites

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Tina Monzavi*[1]and Kelly Lynn Mulvey [2]
[1]New York University, [2]North Carolina State University

Abstract: Interest in science and math plays an important role in encouraging STEM motivation and career aspirations. This interest decreases for girls between late childhood and adolescence. Relatedly, positive mentoring experiences with female teachers can protect girls against losing interest. The present study examines whether visitors to informal science learning sites (ISLS; science centers, zoos, and aquariums) differ in their expressed science and math interest, as well as their science and math stereotypes following an interaction with either a male or female educator. Participants (n = 364; early childhood, n = 151, M age = 6.73; late childhood, n = 136, M age = 10.01; adolescence, n = 59, M age = 13.92) were visitors to one of four ISLS in the United States and United Kingdom. Following an interaction with a male or female educator, they reported their math and science interest and responded to math and science gender stereotype measures. Female participants reported greater interest in math following an interaction with a female educator, compared to when they interacted with a male educator. In turn, female participants who interacted with a female educator were less likely to report male-biased math gender stereotypes. Self-reported science interest did not differ as a function of educator gender. Together these findings suggest that, when aiming to encourage STEM interest and challenge gender stereotypes in informal settings, we must consider the importance of the gender of educators and learners.

LOW ALCOHOL PREFERRING MICE SHOW CROSS-SENSTIZATION TO ETHANOL FOLLOWING REPEATED MORPHINE INJECTIONS

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Maribel Hernández*[1]and Stephen Boehm [2]
[1]Indiana University - Purdue University at Indianapolis, [2]Indiana University - Purdue University at Indianapolis

Abstract: Animal models show cross-sensitization to ethanol following intermittent administration of morphine, suggesting neuroadaptive changes caused by one drug can lead to sensitization of a secondary drug. Here we extended this question to high- and low-alcohol preferring replicate line 3 (HAP3/LAP3) mice. We assessed two doses of repeated intermittent morphine injections (10 and 20 mg/kg) using adult male and female HAP3 and LAP3 mice. Mice were habituated and administered an intraperitoneal injection of saline immediately prior to a locomotor assessment on days 1-2. On day 3, mice were assigned to either chronic morphine, acute morphine, or a saline control group, receiving intermittent injections and subsequent locomotor testing until day 11. Day 15, all mice received one injection of 2.0 g/kg ethanol to determine the degree of cross-sensitization. We hypothesized that only HAP3s would exhibit cross-sensitization to alcohol following repeated injections of morphine at both doses. We found that although HAP3s and LAP3s did not sensitize to 10 mg/kg morphine, LAP3s exhibited a modest cross-sensitization response to ethanol. At 20 mg/kg, we found that only LAP3s exhibited both sensitization to morphine injections as well as cross-sensitization to ethanol, suggesting LAP3s are more sensitive to the locomotor stimulatory effects of ethanol following repeated morphine injections. Contrary to our hypothesis, cross-sensitization between morphine and alcohol develops in mice genetically selected for low alcohol preference, and genetic selection for high alcohol preference blunts the development of morphine sensitization. Future work will focus on μ-opioid receptors in the VTA as a potential mediator of these responses.

A touchscreen-based Mnemonic Similarity Task to assess prelimbic to perirhinal cortex activation in young and aged rats

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Aleyna Ross*[1], Carly Logan [2], Terrence Gatton[3], Jennifer L. Bizon[4], Sara N. Burke [5], Sarah A. Johnson[6]
[1]Evelyn F. McKnight Brain Institute and Department of Neuroscience, University of Florida, Gainesville,Fl, [2]University of Florida, [3]University of Florida, [4]University of Florida, [5]University of Florida, [6]Rosalind Franklin University

Abstract: The mechanisms of cognitive aging and the factors that support brain resilience are currently unknown due to a limited understanding of the neural circuits responsible for cognitive decline. Previous work has demonstrated that older adults are impaired in their ability to distinguish between similar stimuli, as measured by the mnemonic similarity task (MST). To translate behavioral assessments used in clinical settings, we have adapted the human MST (e.g., Stark et al., 2013) for rodents. Using a variant of the object-cued spatial choice task developed by Ahn and Lee (2015), young (4 months) and adult (21 months) Fischer344 Hybrid x Brown Norway rats were tested on the rodent MST in a touchscreen operant chamber. This task requires rats to discriminate between stimuli that are morphed to have varying levels of feature overlap across trials. Aged rats were less accurate at performing this task than young animals. To further understand the neurobiology of this impairment, we are currently manipulating neural activity via the utilization of Designer Receptor Exclusively Activated by Designer Drugs (DREADDs). Adeno-associated viral vectors will be used to selectively express an inhibitory DREADD to inhibit neurons in the prelimbic cortex (PrL) that project to the perirhinal cortex (PER), which are two brain regions that are vulnerable in old age and critical for MST performance. These experiments are ongoing, but we hypothesize that manipulating PrL-PER activity will alter MST performance. Together these experiments may provide insight into how coordinated neural activity supports behavior and is disrupted in advanced age.

Coming Together for Something Good: Recommendations from a Scoping Review for Dissemination and Implementation Science to Improve Indigenous Addiction Treatment

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Meenakshi Richardson*[1], Katherine Hirchak [2], Oladunni Oluwoye[3], Melanie Nadeau[4], Kelsey Bajet [5], Jalene Herron[6], Alexandra Hernandez-Vallant[7], Angel Vasquez[8], Cuong Pham[9], Karen Oliver[10], Mariah Brigman [11]
[1]Washington State University, [2]Washington State University, [3]Washington State University, [4]University of North Dakota, [5]Washington State University, [6]The University of New Mexico, [7]The University of New Mexico, [8]The University of New Mexico, [9]University of Minnesota, [10]Kea Consulting,[11]Washington State University

Abstract: The following scoping review explores the current state of dissemination and implementation science for substance use disorders (SUD) among Indigenous communities and identifies best-practice SUD research paradigms and implementation strategies. Using the Preferred Reporting Items for Systematic Reviews and Meta Analyses (PRISMA) guidelines, PubMed and PsycInfo databases were searched to include articles written in English and published in the United States, Canada, Australia, and New Zealand using Indigenous population

terms and 35 content keywords. Emphasizing sustainability and equity, the adapted Reach, Effectiveness, Adoption, Implementation, and Maintenance (RE-AIM) framework was utilized, along with an assessment of rigor for each study with the Mixed Method Appraisal Tool. To date, 21 articles have been identified from the original unduplicated count of over 24,000 articles. The most frequently used approach in SUD research was community-based participatory research (CBPR). Western frameworks most recently adapted to Indigenous contexts included the Quality Implementation Framework and the Interactive Systems Framework due to the focus on addressing the complexity of tribal systems, the uptake of the intervention, and sustainability. Indigenous grounded models were also described. For example, two-eyed seeing, a framework that integrates both Indigenous and Western approaches, was highlighted to increase the success of the intervention implementation. Preliminary findings underscore the importance of meaningful community-engaged approaches. Strategies from CBPR included monitoring, assessment of adoption and fidelity. The integration of Indigenous grounded methods to re-center, re-align and culturally adapt Western frameworks to increase health equity and improve SUD treatment outcomes among Indigenous communities was also emphasized.

Understanding the Variations in Intervention Delivery for Behavioral Pediatric Weight Management

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Abby Bravo*[1]and Brian Saelens[2]
[1]Heritage University, [2]Seattle Children's Research Institute

Abstract: Title: Understanding the Variations in Intervention Delivery for Behavioral Pediatric Weight Management SHIFT is a family-based behavioral intervention study focused on helping children 7-11 years old with signs of obesity and their families make healthy behavior change to prevent health risks as they mature to young adults. In the study we had two different conditions. Families in both conditions got 20 weeks of individual family and child and parent group sessions. In one condition, families received care from a professional in health behavior modification. Peer-to-peer delivery was used in the other condition, where families received treatment from parents who had previously received the same intervention from professional interventionists. Results indicated that children who received the peer intervention were not as successful at changing their weight status as those who received professional intervention. However, there was no difference between conditions for the parent’s weight status change. We are interested in understanding why there was this difference. To understand what could have resulted in these findings, I will be creating a coding system to systematically examine potential differences in the delivery of the intervention by the professionals and peers. The outcomes may influence how families view responsibility, their relationship with interventionists, or other facets of how the intervention affects behavior change.

The Impact of Victim Blaming on the MMIWG Epidemic

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Samantha Cruz*[1]and Andy Pinedo[2]
[1]University of California, Berkeley, [2]Univeristy of Michigan

Abstract: Native American women and girls across the United States are disproportionately impacted by violence at rates higher than any other ethnic group. The movement known as Missing and Murdered Indigenous Women and Girls (MMIWG) advocates for the exposure, support, and need to address the issue from inhabitants of unceded Native land across the United States. We hypothesized that racism minimization of Native American women dictates the source of blame. After analysis of 4,000 survey responses on apathy towards the MMIWG epidemic, we found a relationship between racism minimization, dehumanization and place of blame. According to the predominantly non-Native perspective, racism minimization and dehumanization of Native American women is positively associated with victim blaming. Understanding if participants place blame for the abnormally high rates of violence on the system, victims, or an outside source provides a framework to improve the retention of supporters motivated to end violence against Native women and girls. Through the socio-historical contextualization of centuries of colonialism enacted against Native peoples suggests modern racism to be a large contributing factor towards the high rates of violence. Therefore, neglecting the lasting impacts of racism minimization towards Native American women enables a culture of victim blaming and ongoing complacency towards the high rates of MMIWG.

Regeneration response by myogenic stem cells in tissues of electric fish following serial tail amputations

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Daniel Montes*[1], Graciela Unguez [2], Oscar Velasquez[3]
[1]New Mexico State University, [2]New Mexico State University, [3]New Mexico State University

Abstract: Previous studies using electric fish, Sternopygus macrurus , revealed that myogenic stem cells (MSC) associated with muscle and the muscle-derived electric organ (EO) proliferated and contributed to the regeneration of new myogenic tissues. This study aims to increase our understanding of stem cell-based regeneration in vertebrates by characterizing the response of MSCs in teleost fish after repeated injuries. We hypothesize that an MSC-dependent mechanism of myogenic tissue regeneration, similar to mammals, is present in other electric fish species. Therefore, experiments are performed in which the distal-most segments of the tail in electric fish species, Brachyhypopomus Pinnicaudatus (aka, " Pinni "), are cut every 7 days for 10 amputation cycles (N=3). The 7-day blastema plus a proximal 2mm segment is collected for analysis using immunolabeled cryosections with an antibody against the MSC marker Pax7. To date, our data shows 1) blastema length over total body length per fish varied between 1.6 to 2.4% through 8 amputation cycles; 2) the number of MSCs increases in muscle tissue adjacent to the amputation site; and 3) MSCs associated with EO cells adjacent to amputation site don't change in number. The apparent increase in Pax7-positive MSCs in the proximal stump to replace lost myogenic cells in the regeneration blastema observed in these preliminary data suggest that Pax7-positive MSCs role in myogenic cell regeneration established in mammals is conserved in electric fish. Future studies will also focus on whether MSCs from muscle and EO contribute differently to the restoration of muscle and EO after injury.

Indigenous & Climate-Resilient Landscape Design

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Keanu Kaibetoney*[1], Tyrone Smith [2], Dominique M. David-Chavez[3]
[1]Colorado State University Fort Collins, [2]Director of Native American Cultural Center, [3]Assistant Professor of Indigenous Natural Resource Stewardship. Indigenous Land & Data Stewards Lab Director

Abstract: To address a longstanding need for Indigenous education, we are preparing a 70-acre field site and programming for community-based Indigenous science education, while serving CSU’s commitments as a land grant institution and needs identified by our local Native community. Which goes along with the method of identifying key components of Indigenous design applied in similar community-based Indigenous science program models. Project goals include engaging Indigenous and climate resilient design principles to develop a site that will support experiential learning and research opportunities for students, faculty, staff, and community members. Apply principles of climate-resilient landscape architecture and work in partnership with a natural resource survey intern to assess the natural elements of the site including the climate, soil, slope, drainage, sunlight, and vegetation. Undergo preliminary research based on Indigenous and climate-resilient models to inform a design plan for structures and outdoor areas that includes community-informed environmental, social, and cultural outcomes. Research, outreach, and activities at this field site will broadly focus on ecological restoration and cultural reconciliation efforts. These include an Indigenous garden, climate-monitoring station, traditional food harvesting, and a greenhouse for plant propagation. Results include identifying and compiling a portfolio of existing Indigenous and climate-resilient program models to inform architecture and design. Developing a stakeholder assessment plan for identifying needs and functionality the site could serve. Drafting a budget and proposal for site development and developing a presentation of research and proposal plan.

Observing Polyelectrolyte Surfactants and their Interaction with Pseudomonas Aeruginosa Biofilms in Relation to Cystic Fibrosis

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Angela Appiah-Kubi*[1], Charles Roth [2], Yadiel Varela Soler[3]
[1]Kean University, [2]Rutgers University, [3]Rutgers University

Abstract: Cystic fibrosis (CF) is a genetic disease characterized by chronic lung inflammation and recurrent lung infections caused by the bacteria Pseudomonas Aeruginosa. The bacteria utilize the lungs’ mucus layer to grow and multiply, enveloping themselves in a thick biofilm layer composed of an extracellular DNA and polysaccharide matrix. P.aeruginosa biofilm production is one of the factors that has led to the increase of drug resistance in CF patients and is now the primary cause of morbidity and mortality. This study investigated using negatively charged graft copolymers as surfactants to enhance the activity of standard antimicrobials tobramycin (TB) and polymyxin B (PB). To study the interaction of the biofilms with the polyelectrolytes, we employed “pre-treatment” minimum biofilm eradication concentration (MBEC) assays. The bacteria were allowed to form biofilms for 48 hours, exposed to different graft copolymers, and incubated for different exposure rates before the addition of varying concentrations of the antimicrobials. Our results revealed that the efficacy of TB and PB differed when the biofilms were pre-exposed to the polymers for different durations. Preliminary data indicated improvement in biofilm eradication with PB over TB. This suggests that the interaction of the polymers complements the mechanism of action of PB over TB, but that intrinsic differences among strains of P.aeruginosa isolated from individual patients can produce varying drug

responses. Further understanding of these interactions could allow us to develop more efficient polyelectrolyte surfactants that could enhance drug efficacy in biofilm eradication of P.aeruginosa and overcome biofilm-related drug resistance.

Identification of bacteriophage resistance mechanisms in the dental pathogen, Streptococcus mutans

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Fatima Herrera*[1]and Joshua Thomson[2]
[1]University of Detroit Mercy, [2]University of Detroit Mercy School of Dentistry

Abstract: Early Childhood Caries (ECC), in which primary teeth are affected by caries, is a significant public health problem. ECC is highly correlated with the presence of the cariogenic bacterium, Streptococcus mutans. Bacteriophage therapy to prevent or reduce disease associated with S. mutans has drawn recent interest. However, increasing evidence of widespread resistance to bacteriophage within S. mutans complicates its utilization. Therefore, we aimed to identify bacteriophage resistance mechanism(s) employed by S. mutans using bacterial strains isolated from saliva and the S. mutans bacteriophage, ΦAPCM01. Previous work showed that bacteriophage resistant strains had no defect in phage adsorption compared to sensitive strains and provided some evidence that they may gain resistance against exogenous phage infection from lysogenic phage infection. Here, we tested if ΦAPCM01-resistant S. mutans strains utilize abortive infection (Abi) systems to prevent bacteriophage replication. Early-log phase S. mutans were mixed with ΦAPCM01 at various multiplicities of infection and observed growth for 18 hours. If an Abi system was utilized in resistant strains, growth curves would abruptly plateau in the presence of phage. We observed that phage-resistant strains followed normal growth curves in the absence of phage, indicating these strains of S. mutans does not employ an Abi system. Multiple resistance mechanisms may play a role in S. mutans resistance to phage; however, elucidation of the mechanism may provide the key to successful bacteriophage therapy against the bacterium. Therefore, future experimentation will be designed to determine if the CRISPR-Cas systems in S. mutans are responsible for providing immunity from ΦAPCM01.

Assessment of Antimicrobial Effect of Essential Oils Against S.aureus and B.thailandensis

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Valerie Gee*[1]and Fernando Monroy[2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: In the United States more than 2.8 million antibiotic-resistant infections were reported. As a result, more than 35,000 deaths have occured. Essential oils (EO) are natural products derived from a single plant species, and recently have been studied due to their antimicrobial properties against varying bacteria. In this study, we used EOs against Burkholderia thailandensis (B. thailandensis), a gram-negative bacteria, and Staphylococcus aureus (S. aureus), a gram-positive bacteria, to test their antimicrobial properties. This study determines the MIC (minimum inhibitory concentration) of the EOs sage, tea tree, cassia, and chamomile on planktonic B. thailandensis and S. aureus . Dilutions ranging from 5%-0.01% concentration were taken with equal parts of a subculture ranging from 0.2-0.4 absorbance, as well as three controls, and left to incubate for 24 hours. Plates were read at an optical density (OD) of 630 nm and 490 nm. The antimicrobial property cut off was determined at an absorbance of 0.1. Eight samples were then spotted to prove the accuracy of antimicrobial susceptibility from the absorbances taken. The results demonstrated that cassia, chamomile, and tea tree were most effective against S. aureus , with an MIC of >5%. While tea tree and chamomile were most effective against B. thailandensis with an MIC of >0.5%. Sage was shown to be least effective against both, with an MIC of <5%. These findings may lead to alternative options to fighting and preventing bacterial infections with the use of EOs, due to the availability and affordability of EOs.

Combined temperature stress and trematode infection in the blue mussel, Mytilus edulis

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Alyssa Goncalves*[1], Helen C. Poynton [2], Kenneth Garrett Evensen[3]
[1]State University of New York at Maritime, [2]University of Massachusetts Boston, [3]University of Massachusetts Boston

Abstract: The blue mussel, Mytilus edulis is found throughout the North Atlantic, and blue mussel populations have been declining, particularly in the Gulf of Maine. In addition to declining populations, this species is experiencing a northward shift due to rising temperatures. These changes are most likely due to multiple stressors, such as climate change, diseases, and parasites. One such parasite is the trematode, Proctoeces maculatus. This trematode is found naturally on the US East coast and is also expanding its range northward. P. maculatus live a heteroxenous lifecycle, which consists of multiple hosts including, fish, birds, and mollusks. The infections caused by P. maculatus have negatively impacted the life of the blue mussel by causing castration, reduced growth, and, in extreme cases, death. To understand how trematodes and increased temperature affect blue mussels, we will collect mussels in June and July of 2022 during a marine heat wave of 90°F or greater. These collections will take place at three locations in Massachusetts: Folger Point (FP), Savin Hill (SH), and Nut Island (NI). Trematode infections will be determined using a qPCR assay from mantle tissue samples, and heat shock protein 90, 70, and 24 expression from gill samples will be measured using RT-qPCR to evaluate temperature stress in infected and uninfected mussels. The results from this research will draw connections between two active stressors in blue mussels, increased temperature and parasitic infections, and help us better understand population declines in the Gulf of Maine.

A Holistic Approach to Effective Autograding in an "A's For All" Learning Model

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Jesus Villalobos*[1], Dan Garcia [2], Jorge Nuñez[3], Destiny Luong[4], Jordan Schwartz [5], Harjot Multani[6], Sebastian Estrada[7], Jose Ochoa[8], Kamoni Fletcher[9]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]University of California, Berkeley, [4]University of California, Berkeley, [5]University of California, Berkeley, [6]University of

California, Berkeley, [7]University of California, Berkeley, [8]University of California, Berkeley, [9]University of California, Berkeley

Abstract: As learning models change, there is a departure from the “fixed time and variable learning” model to a “fixed learning and variable time” model known popularly as “A’s for All.” This model is characterized by consistent feedback and formative assessments instead of common summative exams with no feedback. By allowing variable pacing, students are able to learn until gaining proficiency without worrying about grades. They can expect to receive detailed feedback about their progress along with a pass to the next level, or supplementary materials and another opportunity to prove proficiency. At a small scale, this model requires minimal tooling but much energy and creativity. On the scale of large university courses, though, it is not sustainable to depend on staff readers to provide immediate feedback. In this investigation, we turn to a new software suite that dives into effective content creation, robust autograding, and the ability to provide immediate feedback. We begin with PrairieLearn (PL) – a platform that replaces single-instance questions with dynamic “variants” of a question. Along with a custom service that facilitates grading student work developed in the Snap! coding environment, we uphold the pillars of mastery learning: rich question availability and immediate feedback. Our developments are shaping a new way of assessing proficiency at scale. By reimagining what “grading” means while having autograded scores emulate historical trends, we will gauge our effectiveness. Our findings will serve as a roadmap to other large curriculums and courses, proving that “A’s for All” are both attainable and scalable.

Impacts of Speed, Direction, and Temperature of Lake Breezes on the Concentration of Ozone on the Shoreline of Lake Michigan

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Ardeshir Tabatabaei*[1], Gregory anderson [2], Kenneth Nicolson[3]
[1]Northeastern Illinois University, [2]Northeastern Illinois University, [3]Northeastern Illinois University

Abstract: Land-lake breeze circulation is an important meteorological phenomenon that is associated with ozone vertical structure. Lake breezes develop when the land becomes warmer than the water. As land warms up during the day, the air above it rises, and a low-pressure area is formed near the land. The density of the air over land becomes much less compared to the air over water, in turn, high-pressure cool air spreads across the water and proceeds over the land. Lake breezes have a major role in the production and transport of ground-level ozone on shorelines. Different aspects are to be evaluated in accordance with the production of ozone on the shoreline of Lake Michigan near the Chicago area, such as speed and direction of lake breezes, range of temperature, and gradient of water-air temperature that are related to high ozone concentration. Data from several sensors either in the lake water on buoys, or land stations along the shoreline will be sorted and analyzed in the R studio. Each meteorological aspect has a clear impact on the ozone concentration at ground level; there appears to be some synergism in this behavior. The result shows the presence of lake breeze is the main factor attributed to high ozone days. A large seasonal variation with peak ozone takes place in the summer and smaller values take place during the winter. June and July have the most days where the 8-hour ozone daily maximum exceeds 0.07 ppm.

Tetraspanin CD82 regulates hematopoietic stem and progenitor cell quiescence through modulation of TGFβ signaling

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Clara Bertoni*[1], Jennifer M. Gillette[2], Erica M. Pascetti[3], Muskan Floren[4], Chelsea A. Saito-Reis[5]
[1]Department of Pathology, University of New Mexico Health Sciences Center, University of New Mexico Comprehensive Cancer Center, Albuquerque, NM, [2]Department of Pathology, University of New Mexico Health Sciences Center, University of New Mexico Comprehensive Cancer Center, Albuquerque, NM, [3]Department of Pathology, University of New Mexico Health Sciences Center, [4]Department of Pathology, University of New Mexico Health Sciences Center, [5]Department of Pathology, University of New Mexico Health Sciences Center

Abstract: Hematopoietic stem and progenitor cells (HSPCs) are responsible for lifelong maintenance of the hematopoietic system. Upon hematopoietic stress, HSPCs are rapidly recruited into cell cycle, but ultimately must return to quiescence to prevent hematopoietic exhaustion. An ability to transiently modulate HSPC return to quiescence has the potential to extend the activation of HSPCs and improve patient outcomes from hematopoietic stresses and for transplantation therapies. Evidence from our laboratory demonstrates that the tetraspanin CD82 plays an important role in the regulation of HSPC quiescence and activation. Tetraspanins are membrane scaffold proteins with the ability to modulate signaling through the organization of membrane receptors and intracellular signaling molecules. Using a global CD82 knock-out (KO) mouse, our laboratory identified a reduction in long term-HSCs, resulting from increased HSPC activation and a decrease in quiescent HSPCs. Here, we test the hypothesis that CD82 promotes HSPC quiescence by augmenting TGFβ signaling. TGFβ, a multifunctioning cytokine, plays an essential role in supporting HSPC quiescence as a potent inhibitor of HSPC growth. Using a combination of confocal imaging and flow cytometry approaches, we quantified canonical and non-conical TGFβ signaling of HSPCs isolated from WT and CD82KO mice. Our results suggest that while CD82 does not impact non-canonical TGFβ signaling (ERK, p38, AKT), we find decreased SMAD2/3 activation in CD82KO HSPCs, consistent with reduced canonical TGFβ signaling. Together, these data suggest that CD82 regulates HSPC quiescence by augmenting canonical TGFβ signaling. Future directions will investigate how CD82 modulates TGFβ signaling and its potential therapeutic impact on hematopoietic stress.

Light/Dark bottle methodology for calculating primary production

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Alexa Torres*[1], Mónica Rodríguez Pabón[2], Pedro M Maldonado Rivera[3], Patricia N Vidal Geraldino[4]
[1]Universidad Ana G. Méndez, recinto Cupey / SEAS Island Alliance, [2]Universidad Ana G. Méndez, recinto Cupey / SEAS Island Alliance, [3]Universidad Interamericana de Puerto Rico, Recinto Metro / SEAS Island Alliance, [4]Universidad Interamericana de Puerto Rico, Recinto Metro / SEAS Islands Alliance

Abstract: Primary production is the reason for the beginning and the sustainability of all life, and the velocity of the quantity of energy captivated from sunlight that the organisms can use in the water. Fluctuations in the primary production capacity of the ecosystem occur because of the variation of species. This study is based on the ecosystem of the Laguna Grande located in Fajardo, Puerto Rico. This ecosystem is one of the three bioluminescent lagoons in Puerto Rico,

and it acts as a diverse resource for the local community, great for economic and recreational purposes. For this study, the purpose is to calculate the lagoon's net rate of primary production, which incorporates a formula that focuses on photosynthetic and respiration activity. The method used was the Light/Dark bottle methodology. The measurements were taken from February 2022 monthly, but the experiment will continue for the next three years. The measurements were taken with a YSI Pro DO meter, a water quality measurement instrument, that displays the temperature, dissolved oxygen, pressure, and salinity. The sampling was done by using eight BOD bottles, 4 clear ones, and 4 blacked-out ones. An initial measurement was taken with the help of a YSI and later put in the lagoon for 24 hours. After 24 hours, the bottles were taken out and each bottle was measured. The data is being analyzed to have a correlation between the dissolved oxygen and the seasons of the year between the clear and blacked-out bottles.

Dispersed Uranium Tailings and Their Influence on the Bacterial Community of Contiguous Navajo Nation Agricultural Soils

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Tionna Tapaha*[1], Irene Ane-Anyangwe [2], Palmer Netongo[3], David Willie[4], Zabari-Obyoni Bell [5]
[1]Navajo Technical University Biology Program, Crownpoint, New Mexico, [2]Navajo Technical University, [3]Navajo Technnical University, [4]Navajo Technical Univeristy, [5]Navajo Technical University

Abstract: Background: The Navajo nation has over 500 abandon uranium mines. The impact of the uranium spills from these mines on soil bacterial flora is unclear. We undertook a project to therefore assess the impact of uranium levels and soil bacterial population in five sites in Crownpoint. Method: For proper sampling, we collected four samples (15meters apart) from each of the following sites; Navajo Technical University (NTU) main campus, Dalton Pass, West mesa, Nahodishgish, and St. Paul. We used the Fluorat-02 5M analyzer to evaluate the uranium levels by phosphorescence, enhanced with sodium polysilicate. We also determined the pH levels, the physicochemical properties and cultured bacteria from these soil samples. Results: Soil was mostly Clay at NTU Main Campus and West Mesa with an average pH of 4 and 5.5 respectively. Mostly sandy soil was found in Dalton Pass (pH 7.4), Loamy soil in St. Paul Mission (pH 7.9) and Silt in Nahoodishgish (pH 8.3). The most acidic soils also recorded the highest levels of Sulphur (960mg/kg on average) and uranium i.e. 600 mg/Kg (range 2.5-2105mg/Kg) in West messa and 760mg/kg (range 126-917 mg/Kg) in NTU. Conclusion: This significant variability within sites was very concerning but reiterated the need for proper sampling in such studies.

Developing vaccines to reduce triglyceride (TG) levels in American Indian/Alaskan Natives

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Feather Eagleman*[1]and Dr. Naomi Lee [2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: Cardiovascular disease (CVD) is one of the leading causes of death with a total of 659,000 people per year within the United States. Compared to Whites, American Indian/Alaskan Natives have a 30 to 40% greater mortality rate. There are numerous risk factors for CVD, including high triglyceride (TG) levels and low HDL cholesterol levels. Apolipoprotein C III (ApoC3) metabolizes TG and, as shown in preliminary studies, mice had been vaccinated with virus-like particles (VLPs) displaying human ApoC3 peptides to reduce TG levels. This research project seeks to assess the presentation of α-helical murine ApoC3 proteins conjugated to QBeta VLPs, as antigens. As the human ApoC3 protein is primarily α-helical, murine ApoC3 peptides are put into α-helical structures to present to the immune system. Biochemical interactions will be used to manipulate the helical structure of the antigens. The manipulated helical structure is an incredibly useful “bioactive structure” allowing attachment to the VLP to be displayed to the host immune system. QBeta VLP conjugation to murine ApoC3 wild type will be used as a control. A bifunctional cross-linker will be used to conjugate ApoC3 peptides via the surface exposed Lys and C-terminus Cys on the VLP and ApoC3 peptide. Synthesization of VLPs includes purification by use of size exclusion chromatography with a gravity column, gel electrophoresis, and PBS buffer exchange by dialysis. This research creates the groundwork for future vaccine projects involving animal models to evaluate the inhibition of ApoC3 and the reduction of TG levels to target CVD prevalence.

Adaptation of the Periodic Table to Kichwa: An Ecuadorian Native Language

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Mayra Miranda*[1], Jose Esteban Andino Enriquez [2], Manuel Alejandro Andino Enríquez[3], Paola Nathaly Martinez Arias[4], Sisa Pakary Chalán Gualán [5], Santiago Gualapuro Gualapuro[6]
[1]Cornell University, Ithaca., [2]YACHAY Tech University, Ecuador, [3]Yachay Tech University, [4]Yachay Tech University, [5]Yachay Tech University, [6]Ohio State University

Abstract: The lack of translation of chemical elements and their properties in minority languages can be a barrier in science education. This applies to the Ecuadorian native language: Kichwa. The adaptation of the periodic table to Kichwa can be a start to break the barriers of access to research and education. Kichwa is part of the Quechua language family, and has a rich linguistic diversity. To standardize chemical elements’ names, the Science for Kichwa research group has developed two proposals. The first proposal was based on four considerations: the etymology of the element, etymology of the element based on where elements were discovered, the scientist or national laboratory which discovered the element, and a direct translation from existing names of the elements in Kichwa language. The second proposal was the phonological adaptation of the elements’ name from Spanish to Kichwa. 146 people from different Kichwa pueblos were surveyed about the translations of names of the chemical elements based on the aforementioned considerations. It was found that Kichwa speakers preferred translations that were direct translations or Spanish-aligned phonology. This work is imperative for the advancement of Kichwa writing, and promoting science learning and research in Kichwa. By developing Kichwa chemistry vocabulary, bilingual science education could be made more accessible in Ecuador. Effective bilingual science education helps preserve Andean knowledge and the Kichwa language while empowering students.

The effects of a novel martial-arts based intervention: Hippocampal volume predicts reductions in posttraumatic stress symptoms in children with cancer

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Zazai Owens*[1]and Hilary Marusak [2]
[1]Washtenaw Community College, [2]Wayne State University

Abstract: Using a novel martial-arts based intervention to predict hippocampal volume and reductions in posttraumatic stress symptoms in children with cancer Youth with cancer experience an immeasurable amount of stress and trauma prior, during and after their cancer treatments. The treatment phase can take an emotional and physiological toll on youth and many pediatric cancer patients report posttraumatic stress symptoms (PTSS). Our prior research in pediatric cancer populations has demonstrated correlations between PTSS and variation in stress-sensitive brain regions, such as the hippocampus. The current study examines the impact of a novel martial-arts based intervention on hippocampal volume and PTSS in pediatric cancer patients, and whether baseline (i.e., pre-intervention) hippocampal volumes predict changes in PTSS over time. We predicted that PTSS symptoms would decrease over time. We also explored whether hippocampal volumes changed over time, and whether hippocampal volume at baseline predicted change in PTSS. Over a four-week period, 18 pediatric cancer patients or survivors (ages 5-17 years, eight female) participated in this prospective study. Before and after the four-week program, participants self-reported on cancer-related PTSS. Participants underwent structural magnetic resonance imaging (MRI) scans at baseline and then completed four weekly Kids Kicking Cancer classes. Differences in PTSS and hippocampal volumes from baseline (V1) to week 4 (V2) were tested using a paired-samples t -test. Results from this pilot study suggest that smaller hippocampal volumes may predict reductions in cancer-related PTSS following a martial arts-based intervention. Future studies explore whether clinical or demographic factors predict hippocampal size or change in PTSS.

Montana Models: Engaging Youth in Exploring How a Language Survives and Dies

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Cassandra Baker*[1], Dr. Mary Alice Carlson [2], Katherine McWalters[3]
[1]Montana State University, [2]Montana State University, [3]Montana State University

Abstract: Culturally responsive mathematics teaching not only improves student learning, it communicates to students that they are valued for who they are and not simply by what they can produce. With this in mind, we focused on the design features of mathematical tasks that reflect issues important to youth and their communities. We designed a task that supports youth in exploring how a language survives and dies. How a language survives depends on two things. First, on how many people speak the language. Second, on how many people the language holders pass on their language to. Most Native American tribes are experiencing near extinction of their languages. The United Nations Educational, Scientific and Cultural Organization declared 2022-2023 the International Decade of Indigenous Languages. They estimate 7,000 languages are spoken worldwide with approximately 40% endangered. Our research will focus on the students' cyclic modeling process. Students will begin with their authentic experience. They will then pose a mathematical question where they build a tool or model to address their question. They will interpret their answer and revise their solutions. Students will draw on their own cultural and community funds of knowledge as they engage in the modeling task. We will analyze their use of these tools to see how students utilize their resources to create meaningful solutions. Our research will bring awareness to this issue while also empowering students to create an actionable plan for their community.

An Interdisciplinary Approach to Developing a Virtual Microbiology Laboratory Using Game Development Skills

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Yaritza Parsons*[1], Soma Dotta[2], Prashanth Leela Gatreddi[3], Palak Hemantkumar Patel[4], Saisree Valluri[5], Bonaventure Louis Tuscano[6], Michael Geary LaMontagne[7]

[1]University of Houston-Clear Lake, [2]University of Houston-Clear Lake, [3]University of Houston-Clear Lake, [4]University of Houston-Clear Lake, [5]University of Houston-Clear Lake, [6]University of Houston-Clear Lake, [7]University of Houston-Clear Lake

Abstract: Laboratory experimentation is essential in learning about scientific study within various fields, but especially in STEM fields. During the COVID-19 pandemic, social distancing presented a unique challenge in performing physical laboratory protocols. Within STEM fields, the field of microbiology requires the use of specialized laboratories to carry out the proper protocols needed in studying microorganisms. With the loss of physical laboratory use during the COVID-19 pandemic, the microbiology department and the computer science department at the University of Houston-Clear Lake joined to create a virtual microbiology laboratory. The students participating in the development of this virtual lab include software engineering students and students in the microbiology department. Software engineering students work to develop the virtual microbiology laboratory using Unity’s real-time game development platform. The microbiology department serves as a “customer” to the software engineering students, as they learn to adequately engineer a software for their intended customer. With the development of this virtual microbiology laboratory, our goal is to perform the proper protocol steps of MALDI-TOF (matrix-assisted laser desorption/ionization-time of flight) processes and utilize laboratory equipment to complete the lab. This virtual laboratory will also aid the University of Houston-Clear Lake in developing MicroCURE, a Course-based Undergraduate Research Experience that includes a regional network of microbiology programs. The schools in this network collaborate in providing undergraduate research experiences. To better align the protocols between the institutions involved, virtual laboratories like this one are being developed for the purpose of teaching future undergraduate researchers proper protocols within the MicroCURE network.

Exploring Factors that Influence High-School Latinx Students to Choose STEM Majors Through an Experiential University Outreach Program

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Karla Paredes Aguilar*[1], Dr. Corey Knox[2], Dr. Sara P. Chavarria[3]

[1]University Of Arizona, [2]University of Arizona, [3]University of Arizona

Abstract: Although we are starting to see diversity increasing in STEM majors, students of color, including Latinx students, are still highly underrepresented in STEM majors and career fields. It is therefore critical to understand the reasons how and why Latinx students decide whether or not to seek higher education in STEM. As an undergraduate researcher for Linking Southwest Heritage Through Archeology (LSWHTA), an experiential university outreach program, I examine the factors that influence the decisions of Latinx high-school students to major in STEM. As a University of Arizona program partnered with the National Parks Service, LSWHTA engages high-school students in educational field trips throughout the Southwest that teach hands-on lessons about heritage, archaeology, environmental experiences, and STEM. Using a mixed-methods

research approach, I will collect data from pre-surveys, post-surveys, and short structured interviews about how the program and their prior opinions and attitudes influenced the participants' views on STEM majors and career options. By measuring the change in the responses, we attempt to better understand the benefits that experiential outreach programs and other factors have on the decisions made by high-school students, e.g., what major to pursue and whether or not to continue onto higher education. Educators and students may use this information as guidance to bring awareness to experiential outreach programs, to motivate majoring in STEM, and to increase the diversity of scholars in STEM fields.

Stimulating Participation in STEM

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Danielle Lindgren*[1], Geoffrey Morse[2], Susannah Stern[3], Laura Rivard[4], Jack Koster[5]
[1]Southwestern Community College, [2]University of San Diego, [3]University of San Diego, [4]University of San Diego, [5]University of San Diego

Abstract: As the demand for STEM professionals rapidly increases, the reality is an inadequate STEM workforce. This predicament is largely due to leakage of the STEM pipeline leading to the lack of STEM professionals despite early interest/enrollment of individuals in STEM programs. Factors related to participation in a STEM career include, but are not limited to, self-efficacy, engagement and performance. A problem within this deficit is the lack of women in STEM, which may be a result of prevailing gender stereotypes both inside and outside the classroom. In order to further study this, my team decided to implement various techniques aimed at increasing interest and self-efficacy in STEM in members of an elementary school all-female STEM program led by SciTech. We hoped to determine if our intervention would lead to increased self-efficacy and confidence. Our hypothesis was that self-efficacy would increase most in those who initially expressed low self-efficacy. Our intervention successfully increased self-efficacy, on average, but it did not reach the girls with low self-efficacy as effectively as it reached those with mid to high self-efficacy. Rather, the most dramatic increases were seen in those with mid to high-self-efficacy scores, who also performed better. Lack of self-efficacy is clearly an issue that may be linked to performance, which likely has a negative effect on future aspirations in STEM fields. The data is surprising and shows that action must be taken from a young age to show girls that gender should not be a factor in pursuing education and aspirations.

Segmenting pre- and post-treatment magnetic resonance images to determine the invasiveness of glioblastomas

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Tiara Crockett*[1]and Kristin Swanson[2]
[1]Arizona State University, [2]Arizona State University

Abstract: Eighty percent of all malignant brain tumors are glioma, originating in glial cells of the brain or spinal cord. The most prevalent glioma are glioblastomas. A challenge in the treatment of glioblastomas is assessing invasiveness. Brain segmentation separate and target abnormal cell tissue, with the goal of accurately depicting the tumor, helping medical providers establish accurate diagnoses and develop better treatment plans. We hypothesize that we will be able to create accurate models of glioblastoma invasiveness using segmentations. This is done by

selecting only the brightest signal on the magnetic resonance imaging (MRI) via the labs' workbench. Models are created to calculate tumor radius by approximating spherical volume. Gadolinium-enhanced T1-weighted MRI and radius are associated with different cell density thresholds of detection. Finally, the relative invasiveness is calculated. Pre-treatment segmentation is done to locate and develop a model of the invasiveness of the tumor. We are currently funded to collect image-localized biopsies in patients to validate our glioma invasion model predictions and help practically connect changes on MRI's and the extent of tumor invasion. We will soon begin post-treatment segmentations, conducted after the patient has received surgery (gross total or subtotal resection), chemotherapy, or radiation, which will allow us to determine the accuracy of our models. We will continue to collect data predicting patient-specific tumor growth, seek patient-specific markers of tumor progression, and identify predictors of response to therapy in individual patients. This work ultimately aims to improve treatment plans for patients with glioblastomas and will support further Neuro-Oncology studies.

Teaching Science and Culture on the Navajo Nation Using Traditional Foods

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Breanna Thompson*[1], Pia Sörensen[2], David A. Weitz[3], Vayu Maini Rekdal[4], Kathryn Hollar[5], Bill Yosses[6]
[1]Navajo Technical University, [2]Harvard University, [3]Harvard University, [4]Berkeley, [5]Harvard University, [6]Kitchen Garden Laboratory

Abstract: Food has always been a way to bring families together on the reservation. We can teach science in the context of Diné Philosophy and Navajo culture through workshops and lessons that include traditional foods that families make regularly. In this study, we implement this approach through experiments based on corn, which is culturally and nutritionally important for the Navajo people. In our first experiments, we use corn tortilla dough to teach the physics concept of elasticity. We first prepared corn tortilla doughs with varying amounts of water. By creating small cylinders of dough, then applying a weight on the top of the cylinders and documenting area and the change in length, we can calculate the Young's modulus, a measure of elasticity. In our experiments, we observe that the elastic modulus increased with the addition of water. In a separate set of experiments, we looked at the role of pH in preparing blue corn mush, a Navajo staple food. We measured the pH of boiled ash from branches of different juniper trees and observed differences in flavor when using these ashes to make the blue corn mush. These inexpensive experiments can be implemented in school, home, or afterschool settings. In visits to local high schools and on-campus events, demonstration of these experiments increased interest in science and engineering. Future work involves comparing the elasticity of corn flour vs. wheat flour, as well as developing experiments on the chemistry behind nixtamalization of corn.

Supporting First-Year Student Success through a Combination of High Impact Educational Practices

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Alexander Camarillo*[1], Dr. Philip A. Vieira[2], Maria De La Torre[3], Stacy Zamora[4]

[1]California State University, Dominguez Hills, [2]California State University, Dominguez Hills, [3]California State University, Dominguez Hills, [4]California State University, Dominguez Hills

Abstract: A disparity exists for first-generation minority students pursuing degrees and careers in STEM when compared to their white counterparts. Currently, there is a barrier between accomplishing goals in STEM due to the lack of availability of resources and opportunities such as: access to mentorship, quiet areas to study, financial support for exams and applications, amongst others. To address the need, a pedagogical study using transformative exploratory sequential mixed methods was utilized. This included designing a first-year seminar for the career development of entering undergraduate students at California State University Dominguez Hills. The seminar helped determine student interest in STEM careers and retention in STEM education. Titled Sex, Drugs, and Rock and Roll: The Neuroscience of Hedonism (UNV 101), the course-seminar included a variety of pedagogical strategies. One of pedagogical strategies utilized is Design Thinking (DT) training and Course-based Undergraduate Research Experiences (CUREs). Additionally, introductory EEG technology, Backyard Brains, was used for students to explore their research interests in the field of neuroscience. We examined whether students pursue extracurricular activities related to their career interests, made connections with a STEM mentor, joined STEM clubs, and applied to STEM jobs. The impact of this study includes providing a framework for which STEM departments can develop a survey course to recruit incoming students and encourage retention in STEM majors and careers. Lastly, this develops a pipeline for students to enter and graduate as a STEM major at this university and across the CSU-system to retain interest in STEM and join the STEM workforce.

Lived experiences of former STEM undergraduate mentors of an afterschool mentoring program

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Pamela Martínez Oquendo*[1], Kristin N. VanWyngaarden[2], Nikolaus Stevenson[3], Christine E. Cutucache[4]
[1]University of Nebraska-Lincoln, [2]University of Nebraska at Omaha, [3]University of Nebraska at Omaha, [4]University of Nebraska at Omaha

Abstract: Studies have identified gaps in science, technology, engineering, and mathematics (STEM) undergraduate students' skills, such as critical thinking and problem-solving, impeding employment opportunities post-graduation. It is essential to prepare students for employment in STEM fields, as these fields remain in high demand and offer competitive wages for economic stability. Research has revealed students gain critical thinking and problem-solving skills by engaging in mentoring experiences. Herein, we followed students for a decade after participation in our pre-professional training program, Nebraska STEM For You (NE STEM 4U). This phenomenological study used interviewing techniques to demonstrate how a mid-sized, metropolitan university STEM mentoring program supported fostered participants' transferrable skills post-involvement in the program. Key findings include the influence of the program on skills enhanced or learned during involvement. Importantly, 100% of students who took part in this mentoring program NE STEM 4U positively impacted a transferrable skill post involvement in the project, with the emergent themes of communication skills, perspectives, conflict resolution, professional development, and mentorship skills reported at the highest rates. Our results suggest undergraduate students' participation in an afterschool mentoring program promotes an overall understanding of mentorship and developed transferable skills post-

involvement in the program. Future studies should explore the perceptions of undergraduates from various mentorship programs.

On Life Satisfaction as a Predictor of Math Achievement

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Darryl Diptee*[1]and Dr. Frank Worrell [2]
[1]University of California, Berkeley, [2]University of California, Berkeley

Abstract: The United States historically lags other developed countries with regard to academic scores in Science, Technology, Engineering, and Mathematics (STEM) subjects. Increased student engagement in STEM is known to be associated with higher math achievement scores, but little is known about the relationship between student math achievement and their level of life satisfaction. Based on the premise that happier students learn better, I hypothesized that students with higher levels of life satisfaction produce higher math achievement scores. This study investigated the association between student math achievement and life satisfaction levels within a subset of the PISA 2018 dataset, focusing on US students only. Students from 174 public and private schools across 8 strata were included in the study (N = 4,838). The predictive power of students' perceived levels of life satisfaction (i.e., not satisfied, slightly satisfied, moderately satisfied, and very satisfied) on math achievement was examined, as well as potential moderating effects of gender on that relationship. Results reveal that there is a statistically significant increase in math achievement scores of students with higher levels of life satisfaction. Surprisingly, students with the highest level of life satisfaction (very satisfied) exhibited lower math achievement scores than those who were moderately satisfied, suggesting a "goldilocks zone" of life satisfaction – not too much, not too little - that correlates with optimal math achievement. Therefore, it stands to reason that maintaining moderate life satisfaction levels with goals that are always slightly out of reach may be a worthwhile consideration to maximize mathematical achievement.

Female Narratives of Belonging in Introductory Physics Courses

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Liliana Garcia*[1]and Laura Rios [2]
[1]University of California, Santa Barbara, [2]California Polytechnic State University, San Luis Obispo

Abstract: Introductory physics courses are designed to teach science, technology, engineering and math students foundational physics material. For STEM majors, a deep understanding of this material is essential for their continued success in STEM. To address the large achievement gaps in many introductory courses, instructors are employing significant active learning techniques, which often include peer-to-peer instruction. However, female-identifying students experience these beginning course activities differently than their male-identifying counterparts. In classrooms with a high degree of peer-to-peer interaction, negative or demoralizing social behaviors might negatively affect students' identity in the classroom. In this study, we analyze semi-structured interviews with female students studying in the Coast area of California with the aim of understanding female students' stories of struggle and how female students' self-identity is influenced by their experiences. Our results suggest that there is strong narrative that female students link their sense of "belonging" to how "well" they believed they were doing in class and when students believe they weren't "doing well," they avoid engaging out of dread of the judgments of other students or their professor. Understanding narratives of female students in this introductory course can help foster change to support all students in physics.

Supporting First-Year Student Success through a Combination of High Impact Educational Practices

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Alexander Camarillo*[1], Dr. Philip A. Vieira [2], Maria De La Torre[3], Stacy Zamora[4]
[1]California State University, Dominguez Hills, [2]California State University, Dominguez Hills, [3]California State University, Dominguez Hills, [4]California State University, Dominguez Hills

Abstract: A disparity exists for first-generation minority students pursuing degrees and careers in STEM when compared to their white counterparts. Currently, there is a barrier between accomplishing goals in STEM due to the lack of availability of resources and opportunities such as: access to mentorship, quiet areas to study, financial support for exams and applications, amongst others. To address the need, a pedagogical study using transformative exploratory sequential mixed methods was utilized. This included designing a first-year seminar for the career development of entering undergraduate students at California State University Dominguez Hills. The seminar helped determine student interest in STEM careers and retention in STEM education. Titled Sex, Drugs, and Rock and Roll: The Neuroscience of Hedonism (UNV 101), the course-seminar included a variety of pedagogical strategies. One of pedagogical strategies utilized is Design Thinking (DT) training and Course-based Undergraduate Research Experiences (CUREs). Additionally, introductory EEG technology, Backyard Brains, was used for students to explore their research interests in the field of neuroscience. We examined whether students pursue extracurricular activities related to their career interests, made connections with a STEM mentor, joined STEM clubs, and applied to STEM jobs. The impact of this study includes providing a framework for which STEM departments can develop a survey course to recruit incoming students and encourage retention in STEM majors and careers. Lastly, this develops a pipeline for students to enter and graduate as a STEM major at this university and across the CSU-system to retain interest in STEM and join the STEM workforce.

Health and Wellness in Marine Mammal Harvesting

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Hope Roberts*
University of Alaska, Fairbanks

Abstract: Title: Reconnection to Marine Mammal hunting and its positive effects on those tragically influenced by the American Boarding school era Vitamin D is a crucial part of native diets as the sun sets in some places for months at a time. In the past several decades, Vitamin D intake has been declining, causing rural natives to struggle with depression, substance abuse, and losing their children to the office of social services. In April 2022, Surreel Saltwaters conducted a pilot hunt for those who have been disengaged from their cultural practice of Seal and Sea Otter hunting. The reintroduction was successful, Seal oil and meat have the right amounts of Vitamin D to stabilize the Alaskan Natives who live in the dark winter months in Rural Alaska. We conclude that if we keep teaching those who have lost their cultural harvest through struggles of the boarding school era, the oil Pipeline, and the introduction of drugs and alcohol.

We can restart a resilience chain for those who need to learn to parent the 67% of Alaskan Native children in foster care traditionally while at the same time, teaching them to hunt for a lifetime. This study can reclaim indigenous ways of life from before colonization. We know that our ancestor's memory is built into our DNA as indigenous people. After all, if there is a generational trauma, there is generational power and resilience.

Analyzing and quantifying archaeological objects from culturally significant sites on the island of Kahoʻolawe to assess past ecosystem composition

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Lily Gavagan*[1], Dr. John HR Burns [2], Dean Tokishi[3]
[1]University of Hawaiʻi at Hilo, [2]University of Hawaiʻi at Hilo, [3]Kahoʻolawe Island Reserve Comission

Abstract: The island of Kahoʻolawe is one of the smallest main islands in the Hawaiian archipelago. It has withstood a duration of exploitation by humans and by natural factors influencing it's eroded condition. Nevertheless, Kahoʻolawe contains multiple historical materials, both organic and inorganic that could be a key part in assessing the composition of past ecological systems within the island. By using text analytics and quantitative statistics with one-way non-parametric tests, this pilot study's purpose is to attempt to quantify the commonly observed materials found amongst archeological sites on the island and determine if the abundance of the materials are different among the ʻIli (sections of the island). Despite this promising approach, using text analytics has proven to be difficult with confidently quantifying the appearance of materials among sites on the island. Thus, it is important to continue this investigation with quantitative surveys that could provide more confidence within the data. Nevertheless, the results from this pilot study has indicated a potential significant difference in the abundance of Cellana spp. and bedrock among the ʻIli indicating potential different compositions of different ecosystems on the island.

The Effects of E-liquids With Nicotine on Caenorhabditis elegans

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

MiLana Wiltshire*[1]and Stefanie Driggins [2]
[1]Claflin University, [2]Claflin University

Abstract: Among the youth in the U.S. e-cigarettes are a commonly used product. A recent survey reported that 84.7% of the youth in the study used flavored e-cigarettes. E-cigarettes do not contain tobacco but most of them contain nicotine. The current study used a chemotaxis assay to determine the effects of e-liquids with nicotine on wildtype (N2 Bristol) C. elegans . The C. elegans were exposed to various flavors of e-liquids, sterile water, propylene glycol (PG), and nicotine. The e-liquids were diluted to a 10:1 ratio with sterile water. Nicotine and propylene glycol were diluted to coincide with the amounts in the diluted e-liquids. The chemotaxis plates contained a diluted e-liquid, PG, or nicotine along with sterile water and the C. elegans . The plates were placed in an incubator at 25°C for 1 hour and then placed on ice. After 5 minutes, the first plate was removed and the C. elegans were counted and recorded using a chemotaxis index. The C. elegans on the remaining plates were then counted. Three experimental replicates were performed at different times for each e-liquid and the negative controls. The results of the pre-liminary data suggest that the C. elegans were strongly attracted to nicotine

(CI = 0.812), lava flow (CI = 0.394), and PG (CI = 0.374). This is in comparison to their attraction to strawberry pomegranate with a CI of 0.152 and Hawaiian POG with a CI of 0.0681. Future experiments will include the effects on a mutant strain (OSM-11).

Habitat effects on predation risk in the semiaquatic anole, Norops aquaticus

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Sattie Fisher*[1]and Chad Bishop [2]
[1]University of Montana, [2]Dean of Wildlife

Abstract: Quantifying how habitats vary in predation risk is important for understanding animals' habitat choices and differences in traits that could be driven by varying predation rates. On the macro-habitat level, human disturbance can create a shield of safety for prey as predators are more sensitive to humans. On the microhabitat level, areas farther away from the refuge and/or more visible to predators could experience higher risk. We used clay models of semiaquatic anoles, Norops aquaticus, to measure macro- and microhabitat effects on predation risk at the Las Cruces Biological Station, Costa Rica. Predators, such as birds, leave visible attack marks in the clay. We placed models along three different streams and measured various habitat characteristics: stream width, canopy cover, and the distance from the station. We also placed models in microhabitats that differed in height and distance to water (refuge). We found that the proportion of models attacked was highest at the stream closest to human activity. This stream was also the smallest stream. We found that overall height played a role in predation because the lower the lizard was to the ground the more likely it was to be attacked. Interestingly, our results contradicted our predictions that a lack of human presence and habitat openness would lead to higher predation rates. This suggests that predators are more active around smaller streams; alternatively, human activity could shield birds from their predators, creating higher predation risk for lower trophic animals like lizards.

Graduate Oral Presentations

STEM Education & Learning

BLACK BEYOND MEASURE: AN ANTI-DEFICIT EXPLORATION OF CULTURAL CAPITAL WITHIN A NATIONAL SOCIETY OF BLACK ENGINEERS (NSBE) CHAPTER AT A PREDOMINANTLY WHITE INSTITUTION (PWI)

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Rhonda Harley*
University of San Diego

Abstract: Due to this lack of inclusion, African American students' educational experiences often center on academic disparities, inequality of opportunity, and under-preparedness in career planning within the American education system. While there has been a fair amount of research on the lack of representation of Black students in the engineering disciplines, the heavy focus on quantitative data offers little insight into the unique ways students succeed and overcome institutional and systemic barriers in pursuit of their degree. Undergraduate experiences, for Black students, are not easily quantified solely through enrollment numbers, test scores, grade point averages, and graduation rates. An emerging approach to understanding the factors contributing to persistence and retention in engineering, particularly at a PWI, is to take an asset-based anti-deficit approach to study Black student success. This qualitative counter storytelling study utilized Yosso's (2005) Community Cultural Wealth (CCW) theoretical framework as a tool to illuminate the resource-rich experiences and community offerings of 12 Black students involved in the student-led National Society of Black Engineers (NSBE) chapter at the University of San Diego (USD). Study findings show that all six sources of capital outlined in the CCW theoretical framework were deployed, with multiple capitals interacting and influencing each other. Emergent themes highlight the multiple forms of CCW participants used to navigate unwelcoming environments, seek support from critical stakeholders, contribute to the collective community wealth of the NSBE chapter and advocate for themselves and others. Recommendations and suggestions for further research conclude this study.

Promoting Inclusive and Culturally Responsive Teaching Using Co-classes for General Chemistry

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Jessica Ortiz*[1] and Jesus M. Velázquez[2]
[1]University of California, Davis, [2]University of California, Davis

Abstract: The shift to remote teaching induced by the COVID-19 pandemic has increased pre-existing academic disparities in the student community, augmenting the disadvantages for students who already experience opportunity gaps. This work describes the implementation of an online chemistry co-class focused on providing educational and social support to first-generation, low-income underrepresented students enrolled in a General Chemistry course at the University of California Davis. The co-class offered concurrently with the General Chemistry course aimed to address the academic disparities induced by remote learning and the loss of classroom community during isolation. Students in the co-class were prepared academically in a smaller setup than their General Chemistry course (10–20 vs 500–600 students), which facilitated their engagement and participation in academic and community-building activities. Results from Fall 2020–Spring 2021 quarters show that students who participated in the CHE 98 co-class obtained higher grades in general, where 61% of the students received a C+ or higher in the General Chemistry course, compared to only 47% for the comparison group. Students also identified having a network of support as one of the class's strengths and had an interest in taking a similar course again. Our results highlight that providing an educational environment that is inclusive, culturally responsive, and supportive could promote equity among the student community and have a positive influence on underrepresented student retention in STEM. Therefore, the strategies discussed herein could be applied to develop analogous courses in remote and in-person teaching environments.

A critical approach to examine the racial and science identity formation of Latinx students

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Danielle Maxwell*[1], Kathryn N. Hosbein[2], Jeffrey L. Spencer[3], Ginger V. Shultz[4]
[1]University of Michigan, [2]University of Michigan, [3]University of Michigan, [4]University of Michigan

Abstract: The narrative that science is objective, value-free, acultural, and rooted within a system of meritocracy constrains the representation and advancement of non-majority groups in science. Although there are initiatives to improve the representation of non-majority groups in STEM, much of this effort focuses on achieving racial or ethnic diversity rather than recognizing students' diverse worldviews and identities in the classroom. To understand how students learn science, we need to understand how students engage with science and how this influences their personal and science identities. This study aims to understand how undergraduate Latinx students at Hispanic-Serving Institutions (HSIs) develop science identities and how racialized experiences may influence this development. In this study we use multiple theories of identity, a critical epistemological perspective, and qualitative research methods to build a conceptual framework and describe the salient experiences of our participants. We interviewed Latinx science majors at four HSIs in the southwestern United States. The interviews were transcribed verbatim and deductively coded and analyzed using two coding schemes developed for the theories of science/chemistry identity and racialized identity resources. Our preliminary analysis indicates that Latinx students use a variety of racialized identity resources to negotiate the formation of their science identities, and that positive or negative experiences with these resources can greatly influence their science identity formation. The results of this study will provide insights into how Latinx students engage with the culture of science, and advance our understanding of how to best support Latinx students throughout their undergraduate science education.

Analytical Chemistry

Geographical Sourcing of Marijuana: An Untargeted HS-SPME-GC-MS Approach

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Janet Crespo Cajigas*[1], Lauryn E. DeGreeff[2], Kenneth G. Furton[3], Howard Holness[4]
[1]Florida International University, [2]Florida International University, [3]Florida International University, [4]Florida International University

Abstract: There have been many uncertainties related to the canine detection of marijuana due to the widespread, ongoing legalization of Cannabis sativa (i.e. marijuana) throughout the United States of America (USA). This sociolegal issue has resulted in an increasing interest regarding the generalization and specification within canine detection of marijuana. More specifically, canine trainers have expressed concerns on whether canines can generalize on the odor of marijuana regardless of the origin of their training materials. This study aims to differentiate multiple marijuana samples from a variety of regions in the USA based on the volatile organic compounds (VOCs) found in their odor profile. In this research, a heated headspace (HS) solid phase micro-extraction (SPME) technique is implemented for the collection of both terpenes and cannabinoids from marijuana. The headspace samples were analyzed using two full-scan, optimized methods on a gas chromatograph coupled to a mass spectrometer (GC-MS), and a variety of chemometric

tools were applied to the data to enable differentiation and potential classification between sample populations. Principal component analysis employed in this study has demonstrated a disparity between marijuana varieties using the VOCs extracted from their odor profile. With this information, it is possible to also determine specific biomarkers that are common between samples and if necessary, adjust canine training to improve generalization of their target. Moreover, this work expands on the foundation already established in SPME-GC-MS research regarding the differentiation of similar-like substances of forensic and agricultural interest such as hemp and marijuana or distinct varieties of foodstuffs.

Investigation of the degradation, concentration, and detection of Contaminants of Emerging Concern in snow made reclaimed water

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Marquis Yazzie*[1], Jani C. Ingram[2], Edgar R. Civitello[3], Catherine R. Propper[4], Anita J. Antoninka[5]
[1]Northern Arizona University, [2]Regents' Professor in Department of Chemistry and Biochemistry, [3]Associate Professor in Department of Chemistry and Biochemistry, [4]Professor in Department of Biological Sciences, [5]Assistant Research Professor in School of Forestry

Abstract: Reclaimed water, treated wastewater that may originate from domestic, industrial, and agricultural sources, is used for crop irrigation, groundwater recharge and snowmaking in locations that experience water scarcity. Contaminants of emerging concern (CEC) are organic molecule pollutants that represent an environmental health threat and are often found in reclaimed water. CECs include pharmaceuticals, personal care products and other compounds that can act as endocrine disruptors and are released into the environment. CECs are unregulated and may persist in the environment. This study will evaluate CECs found in wastewater such as DEET, iohexol, acetaminophen, carbamazepine, caffeine, acesulfame-K and sucralose. The selected CECs will be evaluated for degraded products, detection, and concentration. We hypothesize that the number and concentration of CECs in snow made from reclaimed water is different than that found in the source of reclaimed water because of exposure to environmental conditions. Our study will investigate the degradation chemistry and concentration of selected analytes in snow made reclaimed water and reclaimed water. Samples will be collected at a local water treatment facility and on the slopes of a local ski area that uses reclaimed water to make snow. Organics in the samples will be concentrated using solid phase extraction followed by organic analysis using liquid chromatography mass spectrometry. Reclaimed water snow, natural snowfall and reclaimed water samples will be compared for their analytes of interest and concentration. Reclaimed water usage will increase with increasing water scarcity therefore this research is important to evaluate health risks for biological and environmental communities.

Quantifying the accumulation of metals and metalloids in plant tissue and soils near abandoned uranium mine sites on the Navajo Nation

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Mialynn Jim*[1], Marissa Mares[2], Jani C. Ingram, PhD[3]

[1]Northern Arizona University, [2]Northern Arizona University, [3]Northern Arizona University

Abstract: Mining on the Navajo Nation took place from the 1940s to the 1980s to assist with US defense purposes. At the end of the mining period there were no remediation efforts to clean-up the mine sites. Currently, there are over 500 unremediated abandoned uranium mines sites on the Navajo Nation. In these areas, mining-related contaminants can spread into the environment by leaching into the groundwater as most contaminants are water soluble. In this study, two communities on the Navajo Nation, located in Cove and Red Valley, Arizona, requested to have their livestock tracked and chemically analyzed to determine exposure to contaminants. The purpose of this study is to quantify the accumulation of metals and metalloids in plants and soils grown in the Cove, AZ grazing areas and compare it to a reference site in Red Valley, AZ where uranium mining did not occur. The methods include digesting the soils and plants using EPA method 3051A on a CEM MARS microwave digestion system and analyzing with both an atomic absorption spectrometer and an inductively coupled plasma mass spectrometer. Preliminary studies of soil and plants in Cove, AZ found uranium, vanadium, arsenic, and manganese were at background levels. In this study, we collected and analyzed additional soil and plant samples to verify any contaminant issues that may expose the livestock to elevated levels of uranium, arsenic, vanadium, and manganese. The results of this work and previous studies will be discussed with respect to the exposure of the livestock grazing in these areas.

Design and Fabrication of a Planar Calibration-Free Ion Selective Electrode Platform

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Eliza Herrero*[1]and Philippe Buhlmann[2]
[1]University of Minnesota, [2]University of Minnesota

Abstract: The quantification of electrolytes in bodily fluids is a critical step in both the diagnosis and management of many diseases and is traditionally performed using potentiometric ion-selective electrodes in clinical blood analyzers. These instruments, however, are expensive to own and operate, thereby limiting access to health care for patients in resource-limited areas. To overcome these inequities, paper has been proposed as a substrate for portable and miniaturized potentiometric sensors due to its low cost and high availability, but its use presents performance limitations. Due to these problems, as well as potential applications in wearable devices, I developed potentiometric sensors fully integrated into a knitted polyester fabric for application in both aqueous and biological samples. These textile-based devices require only 30 μL sample volume and respond in a theoretically predicted manner over four orders of magnitude—an order of magnitude improvement from analogous paper-based devices. Working towards selective devices, polyvinylchloride-based sensor membrane material was deposited on textiles to form highly hydrophobic ion-sensing and reference membranes fully embedded within the polyester fabric. This is the first example of a potentiometric sensor that both embeds membranes into a fabric and uses the fabric to wick samples into contact with both the sensing and reference membrane. To characterize the novel devices, and understand potential substrate-sample interactions, I used potentiometric data, scanning electron microscopy, and elemental analysis of devices and materials. This work will drastically improve the design and performance

of electroanalytical sensors, eventually increasing access to medical testing for patients in resource-limited areas.

Chemistry, Physical Chemistry, & Materials Research

Exposure of functional coatings to smoke volatile phenol compounds and affect of coating to grape ripening

Discipline: Chemistry
Subdiscipline: Other

Lindsay Garcia*[1], Trung Tran[2], Darrell Cole Cerrato[3], Michael Penner[4], Yanyun Zhao[5], Elizabeth Tomasino[6]
[1]Oregon State University, [2]Oregon State University, [3]Oregon State University, [4]Oregon State University, [5]Oregon State University, [6]Oregon State University

Abstract: The grape and wine industry has been severely impacted by wildfires. Persistent exposure to smoke compromises the quality of grapes and adversely produces undesirable sensory characters in wine. No current methodologies are effective at mitigating smoke taint in wine. Innovative films coatings were developed to prevent smoke compounds from entering grapes. Coatings were made using cellulose nanofiber (CNF) as a coating forming matrix. Other functional ingredients were incorporated into CNF to develop four different film types. In this study, both the film's impact on grape physiology and efficacy in reducing smoke taint in wine were investigated. Pinot noir grapes from the Southern Oregon Research and Extension Center vineyard were spray-coated on the vine at three grape growth stages. After harvest, the grapes' size, weight, Brix, pH, and titratable acidity were analyzed. Pinot noir grapes, harvested from Woodhall III Vineyards in Monroe, Oregon, were coated and smoked in specially designed cages covered in low density polyethylene greenhouse film. After grapes were smoked for 6 hours, half were washed to determine whether smoke compounds bind or are blocked by the coatings. Smoke compounds in grape juice and wine were analyzed using GCMS. Results from the Southern Oregon experiment did not have a significant effect on grape physiochemistry, nor did it hinder grape ripening. Post-harvest coating and smoking showed various results for mitigation of smoke volatile phenols. The collective results of this study show that some of the film coatings are promising in mitigating smoke taint and ensuring healthy grape ripening.

Elucidation of the Mechanism of Endoperoxide Formation in the Anti-Malarial Drug, Artemisinin using Deuterated Isotopologues

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Kaitlyn Varela*[1]and Francis Yoshimoto[2]
[1]University of Texas at San Antonio, [2]University of Texas at San Antonio

Abstract: Artemisinin, an endoperoxide-containing plant natural product, is used to treat malaria. Commercialization of artemisinin is difficult due to the small amount produced by the plant source, Artemisia annua . By understanding the mechanism of endoperoxide formation of artemisinin, its biosynthetic pathway can be exploited for mass production. Dihydroartemisinic acid (DHAA) is the precursor of artemisinin that undergoes a spontaneous autoxidation process

to form the endoperoxide bridge. This transformation involves four steps: 1. an ene reaction at the C6-position of DHAA and molecular oxygen to yield an allylic hydroperoxide, 2. Hock cleavage of the hydroperoxide to cleave the C4-C5 bond, 3. addition of a second oxygen molecule to form a peroxide, and 4. subsequent polycyclization to yield artemisnin. To further elucidate the mechanism of endoperoxide formation from DHAA, regioselectively deuterated DHAA isotopologues were synthesized. It was hypothesized that these deuterated DHAA derivatives could yield new mechanistic insight in the endoperoxide forming process. Indeed, these deuterated DHAA isotopologues at C3 and C15 converted to artemisinin at a slower rate compared to their nondeuterated DHAA counterpart, revealing kinetic isotope effect values between 2-3. These results suggest multiple ene reactions occurring at the C3-, C6-, and C15-positions of DHAA and molecular oxygen to initiate the endoperoxide forming cascade reaction. Light was also discovered to initially promote the conversion of DHAA to artemimsinin. However, over time light rearranged artemisinin to a different product that lacks the endoperoxide functional group. These studies show how artemisinin is formed through multiple pathways from DHAA in nature.

Potential energy surfaces are generated to calculate vibrational properties of isotopomers of formaldehyde from second-order perturbation theory

Discipline: Chemistry

Subdiscipline: Physical Chemistry

Ahyssa Cruz*[1]and Dr. Walter Ermler[2]

[1]The University of Texas at San Antonio, [2]The University of Texas at San Antonio

Abstract: Potential energy surfaces (PESs) can be explained as the relationship between the geometry and energy of a molecule. A PES is defined in terms of the Born-Oppenheimer approximation which states nuclei within a molecule are stationary compared to electrons, specifying its geometry. The PES is mapped out by changing the molecules nuclear coordinates. There are various possible applications of PESs including the exploration of property structures. This may include finding the optimum energy shape of a molecule, calculating rates of chemical reactions, and in this case calculating vibrational-rotational spectra and related properties. An algorithm-based software package was used to develop a code, MolecGeom, that calculates bond lengths, bond angles and dihedral angles for any polyatomic molecule for any desired incremental geometric changes. This symbolic code provides data to curate accurate PESs for the calculation of molecular vibration-rotational spectra and properties. Results of calculations of line frequencies, spectral intensities and property expectation values are reported for formaldehyde (H 2 CO): 2830, 1749, 1502, 2819, 1168, and 1246 cm -1 , with errors of 0.71%, 0.17%, 0.13%, 0.85%, 0.08% and 0.24%, respectively. Calculations of these properties for deuterium and tritium isotopomers of formaldehyde are also reported. This study shows how errors can be reduced to less than 1% using accurate analytical representations of PESs and property surfaces in the context of a Rayleigh-Schrodinger perturbation theory method that scales linearly with molecule size. The results demonstrate how spectral data can be calculated from first-principles for molecules, including those that are short-lived and toxic.

Development of Copper-Modified Functionalized Mesoporous Silica Nanomaterials and Investigation of Antimicrobial Properties for Wound Healing Applications

Discipline: Materials Research
Subdiscipline: Materials Research

Maricely Ramirez*[1]and Tewodros Asefa[2]
[1]Rutgers University-New Brunswick, [2]Rutgers University-New Brunswick

Abstract: Chronic wounds are a significant and growing problem affecting patients worldwide, especially in developing countries. An important risk factor is the formation of biofilms: persistent organisms that grow on the skin and other surfaces. It is estimated that 74% of chronic or hard-to-heal wounds contain some biofilm formations - and they have a high tolerance to antibiotics, antiseptics, and inflammatory processes of wound healing. Mesoporous silica nanoparticles (MSNs) have been researched over the years as promising drug delivery systems because of their biocompatibility, high loading capacity, and ease of surface modifications. The pores in these nanomaterials can be decorated by a gatekeeper which can be used for additional functionalization and the improvement of pharmacodynamical characteristics. Meanwhile, copper at the nanoscale has been shown to have antibacterial and fungicidal effects for several years. It is 99% less costly than silver, another antimicrobial metal, and it has the added advantage of promoting angiogenesis (development of new blood vessels). By incorporating copper within the pores of MSNs, the systems we are developing will have the ability to provide a "one-two punch" approach to mitigating bacterial biofilm on chronic wound surfaces. More specifically, we propose using copper-loaded silica nanoparticles coupled with other active agents and explore their synergistic effects on bacteria common to biofilms, S. aureus, and E. coli .

Determination of salivary sialic acid through nanotechnology: a useful biomarker for cervical cancer screening

Discipline: Materials Research
Subdiscipline: Materials Research

Alondra Hernandez Cedillo*[1]and Miguel Jose Yacaman[2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: Cervical cancer (CC) is a global public health problem. In 2020, despite being preventable, CC is the fourth type of cancer that causes the most female deaths. Human papillomavirus (HPV) infection is the main cause of cervical cancer. Precancerous lesions are characterized by abnormal cellular in the areas surrounding the uterine cervix. Papanicolaou (Pap) smear cytology has remained an important tool for CC screening however has shown low sensitivity for detection. Saliva has been proposed as an alternative medium in the monitoring of biomarkers that can be useful for the screening of various human diseases. Sialic acid (SA) is present in all human fluids; the highest amounts are found in human saliva. Metastatic cancer cells often express a high density of sialic acid-rich glycoproteins. Recently, we have shown that small amounts of SA in an aqueous solution may be easily detected by the alternative method of Surface-Enhanced Raman Spectroscopy (SERS) produced by citrate-reduced silver nanoparticles (cit-AgNPs) with simplified processing of saliva samples. A primary aim of this study is to determine SA levels in the saliva of patients who have been diagnosed with precancerous lesions and cervical cancer by applying SERS to measure levels of SA in human saliva using a colloidal suspension of cit-AgNPs. Our results showed a sensitivity/specificity of 65%/93% with a cutoff to distinguish between precancerous lesions/cancer cases of SA 22 mg/dL, as established from a ROC analysis. Our results suggest that SA may be a more useful biomarker than a Pap smear to detect CC.

Computer & Information Sciences, Statistics & Engineering

Using Multi-view 3D Reconstruction for Understanding Descriptions of 2D Images

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

Rodolfo Corona*[1], Shizhan Zhu[2], Dan Klein[3], Trevor Darrell[4]
[1]University of California, Berkeley, [2]University of California, Berkeley, [3]University of California, Berkeley, [4]University of California, Berkeley

Abstract: Language provides a natural interface for humans to interact with robotic systems. Because robots are embodied in the world, they must be able to understand the links between language and their visual perception for this communication to work. Additionally, although visual signal from cameras may be 2-dimensional, they capture views of a fundamentally 3-dimensional world. We hypothesize that explicitly reasoning about 3D structure is beneficial for this type of language learning. This presentation will describe the Voxel-informed Language Grounder (VLG), a machine learning system that uses a multi-view reconstruction model to derive explicit 3D voxel representations of objects, which it leverages to reason about the language used to describe to them. VLG employs a multimodal neural network used to extract joint features from images and text, which it supplements with features from a transformer used to correlate the text with the predicted voxel map. We use the ShapeNet Annotated with Referring Expressions (SNARE) benchmark as a testbed. SNARE tasks agents with selecting a target object against a confounder given images of both objects and a text caption describing the target. VLG attains state-of-the-art reference game accuracy (2.0% improvement over the closest baseline) on SNARE, improving over systems which do not employ explicit 3D representations in their structure. Further, we show that the largest improvements are gained on a split of captions focusing on describing the geometry of objects, highlighting the contribution of using explicit 3D representations when learning language in the context of 2D images.

Development and validation of a continuous representation of human sex physiology

Discipline: Computer & Information Science
Subdiscipline: Computer & Information Sciences

sergio gonzales*[1]and Sherri Rose[2]
[1]Stanford University School of Medicine, [2]Stanford University

Abstract: The use of assigned sex at birth (ASAB) to represent an individual’s sex physiology in electronic health records (EHR) erases the existence of sex minorities: people with difference in sexual development or modified sex physiology through exposures. It ignores intrinsic and extrinsic sources of variation in human sex physiology for sexual majorities and minorities alike. All genes variants including those invovled in sex physiology, have variable expression and activity. Moreover, expression and activity are modified by diseases and exposures. As part of a broader project to identify sexual minorities in EHR, I propose a method to compute a real-valued representation of human sex physiology using variational autoencoders (VAEs) in a multitask setting. I leverage well studied sex specific variation in routine laboratory studies as inputs and health conditions—that have well documented differences in prevalence and evidence for sex specific etiology—as outputs. This allows the VAE to learn a single real-valued variable that is based only on physiologic biomarkers and is predictive sex specific health outcomes. I hypothesize that this variable can replace ASAB in existing models of human health and disease without loss of performance for sexual majorities while improving performance for sexual minorities. I use the All of Us Project dataset, which is unique in its size and representation of sex not as ASAB. Preliminary results show meaningful input space separation by sex and gender identity of patients. Embedding methods and VAE architectures to handle multiple or missing lab values are ongoing.

Optimizing optical crossing in Silicon Photonics applications

Discipline: Engineering
Subdiscipline: Other Engineering

Juan Villegas*[1]and Mahmoud Rasras[2]
[1]New York Univeristy Abu Dhabi, [2]New York University Abu Dhabi

Abstract: Integrated Electronic-Photonic chips are every day more relevant, specially in the fields of bioengineering for high precision sensors and telecommunications, for high speed links. The responding increase in density of integrated optical systems on chips means a larger need to create complex interconnecting buses. In contrast to metal interconnects of traditional CMOS technologies, it's harder to fabricate multiple layers of silicon waveguides to interconnect photonic devices on a chip, however, two waveguides can cross each other and maintain to a limited extent the directionality of their inputs. In modern electro-optic chips, as the number of crossings that a waveguide may experience increases, so does the need to minimize their losses and the amount of energy coupled to any of the crossed lines. We analytically study mechanisms to maximize the crossing efficiency and demonstrate the use of a combination of mode mismatch analysis, mode imaging, and topological optimization to generate different configurations of waveguide crossings. Resulting arrangements exhibit very low losses and cross-coupling. We obtain insertion losses as small as 0.040 dB and -54.6 dB crosstalk for 2-way (cross shaped) crossings, as well as 0.236 dB insertion loss and -44.3 dB cross-talk for 4-way (octogram asterisk shaped) crossings. These are, to our knowledge, the best reported for the C-Band communication bandwidth (centered at 1550 nm) for the quasi transverse electric (TE) polarization state. Most importantly, the results presented demonstrate different strategies that can be applied in the design of similar structures to maximize their efficiency in other bandwidths or polarization states.

Nutrient Intake Patterns and its Association to CVD Risk Factors for US Hispanics/Latinos

Discipline: Mathematics
Subdiscipline: Statistics

Jeanette Varela*[1], Dr. Briana Stephenson[2], Dr. Josiemer Mattei[3], Dr. Daniela Sotres-Alvarez[4], Yasmin Mossavar-Rahmani[5], Luis Enrique Maldonado[6], Amanda Mcclain[7], Martha Daviglus[8]
[1]Harvard University, Graduate School of Arts and Sciences, [2]Harvard University, [3]Harvard University, [4]University of North Carolina, Chapel Hill, [5]Albert Einstein College of Medicine, [6]University of Southern California, [7]San Diego State University, [8]University of Illinois at Chicago
Abstract: Poor diet is a major risk factor for cardiovascular disease (CVD) in US Hispanic/Latino adults. However, the role diet plays in shaping different CVD outcomes by Hispanic heritage groups is not fully understood. Despite various differences in characteristics among Hispanic groups, nationally-representative surveys continue to aggregate this population into one group or as seen in the National Health and Nutrition Examination Survey (NHANES), two large groups (e.g. Mexican-Americans versus other Hispanics/Latinos) in an effort to preserve model stability of smaller-sized groups during analysis. This limitation can impact our understanding of the inter-relationship of diet and disease. The Hispanic Community Health Study/Study of Latinos (HCHS/SOL) has targeted data collection to capture detailed information on the heterogeneity of six Hispanic/Latino backgrounds. In this study, we examined the generalizability of nutritional and cardiometabolic health of Mexican-Americans and other Hispanics/Latinos by comparing nutrient intake patterns derived using factor analysis separately in NHANES and HCHS/SOL. Five nutrient intake patterns were identified for both surveys, which accounted for 66.9% and 67.0% of the variance explained, respectively. Furthermore, each derived factor was categorized into quintiles and evaluated for its associations to major CVD risk factors using logistic regression analysis. This talk will discuss the results of this analysis and its implications for future research examining diet-disease relationships in this population.

Bioengineering/Biomedical Engineering & Engineering (general)

A Tale of Two Mice: Sustainable Electronics Design and Prototyping

Discipline: Engineering
Subdiscipline: Engineering (general)

Vicente Arroyos*[1], Maris Viitaniemi[2], Nicholas Keehn[3], Vaidehi Oruganti[4], Winston Saunders[5], Karin Strauss[6], Vikram Iyer[7], Bichlien Nguyen[8]
[1]University of Washington, Seattle, [2]Microsoft, [3]Microsoft, [4]Microsoft, [5]Microsoft, [6]Microsoft Research, [7]University of Washington Paul G. Allen School of Computer Science and Engineering, [8]Microsoft Research
Abstract: Electronics have become integral to all aspects of life and form the physical foundation of computing; however electronic waste (e-waste) is among the fastest growing global waste streams and poses significant health and climate implications. We present a design guideline for sustainable electronics and use it to build a functional computer mouse with a biodegradable printed circuit board and case. We develop an end-to-end digital fabrication process using accessible maker tools to build circuits on biodegradable substrates that reduce embodied carbon and toxic waste. Our biodegradable circuit board sends data over USB at 800 kbps and generates 12 MHz signals without distortion. Our circuit board dissolves in water (in 5.5 min at 100 ◦C, 5 hrs at 20 ◦C) and we successfully recover and reuse two types of chips after dissolving. We also present an environmental assessment showing our design reduces the environmental carbon impact (kg CO2e) by 60.2% compared to a traditional mouse.

Hold On Tight: How Friction Influences Climbing in Cicada Nymphs and Adults

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Joshua Pulliam*[1], Jake Socha[2], Mary Salcedo[3]
[1]Virginia Polytechnic Institute and State University, [2]Virginia Polytechnic Institute and State University, [3]Virginia Polytechnic Institute and State University

Abstract: Insects exhibit many adaptations for overcoming complex terrain, enabling behaviors such as climbing, digging, and skimming the surface of water. Nymphs of the periodical cicada (genus: Magicicada) burrow below ground and climb vertical surfaces such as trees, grass, and stone, searching for areas to emerge as adults. Although the body of the nymph and adult cicada are drastically different, climbing remains an imperative part of their survival. Cicadas must overcome difficulties with climbing unknown surfaces at the cost of emergence or mating. Here, we investigated how adults and nymphs of M. septendecim interact with areas of low friction, using PVC pipes as models for vertical perches. We recorded 220 trials of cicadas climbing 15.9 mm diameter pipes using a synchronized camera array (Hero 4 Black, GoPro, D850, Nikon). The pipes were wrapped in green matting to provide a surface for climbing. A single gap in the matting (6–36 mm) served as a low-friction slip challenge. We also varied frictional characteristics, wrapping the pipes in sandpaper (60, 150, and 220 grit) to examine the influence of friction variation on climbing performance. From these trials, success rates decreased as grits became finer, from 77% (60 grit) to 58% (150 grit) in adults and 92% to 58% in nymphs. Neither were capable of griping the smoothest sandpaper surface. Combined with previous knowledge of their hook-like tarsal claws, these data demonstrate that cicadas require frictional gripping for climbing, and more broadly contribute to our understanding of mechanical limitations of arboreal locomotion in insects.

Using a Bioengineered Immune-enhanced Tumor-on-a-chip (iTOC) Platform to Improve T Cell-Killing Capabilities

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Marco Antonio Rodriguez*[1], Aleksander Skardal[2], Joal Beane[3], Mahsa Kheradmandi[4], Hemamylammal Sivakumar[5]
[1]The Ohio State University, [2]1) Department of Biomedical Engineering, The Ohio State University, 2) The James Comprehensive Cancer Center, The Ohio State University, [3]The James Comprehensive Cancer Center, The Ohio State University, [4]The James Comprehensive Cancer Center, The Ohio State University, [5]Department of Biomedical Engineering, The Ohio State University

Abstract: T-lymphocytes (T cells), can detect and kill cancer cells via tumor associated antigens. Leveraging effector function in adoptive cell therapies (ACT) has allowed for success against certain cancers; however, heterogenous tumor antigen expression on tumor cell reserve limits the effectiveness of single antigen targeting therapies. Therefore, there exists a need for the development of ACT treatments capable of targeting heterogeneous cancer cell populations. We have developed a bioengineered tumor-on-a-chip platform with the aim of enhancing the tumor antigen recognition repertoire of tumor infiltrating (TIL) or peripheral blood lymphocytes (PBL).

This approach was optimized using a C57BL/6 mouse model with B16 melanoma tumors. Harvested lymph node and tumor cells suspended in hyaluronic acid and gelatin hydrogels, forming tumor organoids, were embedded into a custom polydimethylsiloxane (PDMS) microfluidic device. TIL or PBL were then perfused through our device, to interact with tumor and immune cells, enhancing their tumor antigen recognition. Fresh tumor organoids were then fabricated on a 48 well plate, and perfused lymphocytes were transferred to these naive tumor organoids to test effector function. ATP and calcein release assays, along with LIVE/DEAD staining and imaging of target organoids, were carried out to analyze cytotoxic effects of lymphocytes. Furthermore, interferon gamma (IFNγ) levels were quantified to assess lymphocyte activation. Preliminary results indicate that lymph node-integrated hydrogel tumor organoids combined with flow conditions from our device produce a more effective lymphocyte population. With parameters derived using this mouse analog, we will transition to human patient samples to further evaluate this personalized immunotherapy approach.

Electrophoresis-Mediated Characterization of Full and Empty Adeno-Associated Virus Capsids

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Adriana Coll De Peña*[1]and Anubhav Triptahi[2]
[1]Brown University, [2]Brown University

Abstract: Adeno-Associated Virus (AAV) has shown great potential in gene therapy, being one of the leading platforms for viral gene delivery, due to its low immunogenicity, lack of pathogenicity in humans and ability to provide long-term gene expression in vivo . However, the large-scale manufacturing of high-quality Adeno-associated virus (AAV) has been severely limited by the lack of rapid, high-throughput characterization platforms that require low volumes. Here we propose a methodology that integrates electrophoresis-based microfluidic analysis of AAV samples with a mathematical model for the rapid and reliable analysis of purity of AAV samples in terms of full and empty capsids. The current gold standard, Analytical Ultracentrifugation, requires close to 400 µL of sample, is not scalable and has a turnaround time of 6 h per sample. In contrast, the proposed approach requires less than 10 µL of sample at concentrations of 5 x 10 11 -1 x 10 12 VP/mL, with a turnaround time of 6-15 min per sample, and an average error in the predictions of 5%. Overall, this method offers a way to rapidly iterate through AAV samples to evaluate the purity of the sample, which we believe addresses a critical need as addressed by the gene and molecular therapy community.

Optimization of phospholipid chemistry for improved lipid nanoparticle (LNP) delivery of messenger RNA (mRNA)

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ester Alvarez Benedicto*[1], Daniel J Siegwart[2], Lukas Farbiak[3]
[1]UT Southwestern Medical Center, [2]UT Southwestern, [3]UT Southwestern.edu

Abstract: Lipid nanoparticles (LNPs) have been established as an essential platform for nucleic acid delivery. Efforts have led to the development of vaccines that protect against SARS-CoV-2 infection using LNPs to deliver messenger RNA (mRNA) coding for the viral spike protein. Out of the four essential components that comprise LNPs, phospholipids represent an underappreciated opportunity for fundamental and translational study. We investigated this avenue by systematically modulating the identity of the phospholipid in LNPs with the goal of identifying specific moieties that directly enhance or hinder delivery efficacy. Results indicate that phospholipid chemistry can enhance mRNA delivery by increasing membrane fusion and enhancing endosomal escape. Phospholipids containing phosphoethanolamine (PE) head groups likely increase endosomal escape due to their fusogenic properties. Additionally, it was found that zwitterionic phospholipids mainly aided liver delivery, whereas negatively charged phospholipids changed the tropism of the LNPs from liver to spleen. These results demonstrate that the choice of phospholipid plays a role intracellularly by enhancing endosomal escape, while also driving organ tropism in vivo . These findings were then applied to Selective Organ Targeting (SORT) LNPs to manipulate and control spleen-specific delivery. Overall, selection of the phospholipid in LNPs provides an important handle to design and optimize LNPs for improved mRNA delivery and more effective therapeutics.

Chemical Engineering

Exploring high-dimensional energy landscapes in systems with complex, avalanche-like motion

Discipline: Engineering
Subdiscipline: Chemical Engineering

Clary Rodriguez Cruz*[1]and John Crocker[2]
[1]University of Pennsylvania, [2]University of Pennsylvania

Abstract: Many soft, squishy multi-component materials (soap foams, emulsions, pastes, granular systems and living cells) are known to exhibit similar viscoelastic properties and complex, intermittent dynamics. Recent simulations have related their phenomena to the geometrical properties of their energy landscape, which provide an abstract high-dimensional description of the systems' total energy function. We demonstrate the ability to experimentally explore the geometry of these energy landscapes, using a mayonnaise-like jammed emulsion that consists of transparent droplets amenable to confocal microscopy. We observe super-diffusive particle motion and large cooperative particle rearrangements, or avalanches, which correspond to high-dimensional trajectories having a self-similar fractal structure. Our experimental results agree with simulation data as well as with bulk rheology measurements of the formulated emulsion. Similarly, we explore high-dimensional trajectories of stock market returns, which have been shown to display non-random intermittent dynamics at the single-component level. We learn that the statistics of this system are comparable to those of our emulsion in high-dimensional space, displaying analogous displacement distributions and avalanche dynamics. Our goal is to introduce this simple statistical framework in high-dimensional space as a method to directly compare the dynamics of many seemingly different systems with similar complex, avalanche-like behaviors.

Short chain fatty acid influence on normal and estrogen deficient bone remodeling

Discipline: Engineering
Subdiscipline: Chemical Engineering

Carley Cook*[1], Ashlee Ford Versypt[2], Brenda J. Smith[3]
[1]University at Buffalo, [2]University at Buffalo, [3]Indiana University School of Medicine

Abstract: Osteoporosis is a debilitating disease in which bone resorption chronically exceeds bone formation. Estrogen deficiency, a major contributor to osteoporosis, influences the cytokines involved in bone health through T cell populations. A promising area of research to treat osteoporosis involves the use of dietary interventions to increase the production of short chain fatty acids (SCFAs) by gut metabolites. These SCFAs have been shown to increase Tregs. These Tregs modulate osteoblast production (bone forming cells) via Wnt signaling. However, a previous model pointed to other SCFAs influences on bone health. We hypothesize that dietary induced increases of SCFAs could treat bone loss caused by estrogen deficiency. In this work, we will utilize new data to inform and expand our multicompartment ordinary differential equations model of SCFA influence on bone. We will consider the possibility of SCFAs having a direct action on bone health as well as other indirect actions caused by the increase in Tregs. We will then alter the bone compartment of the model to include Th17 cells. Then we will simulate an estrogen deficient case by altering parameters related to estrogen in bone health. Lastly, we will artificially dose this case with SCFAs to explore the action of SCFAs on estrogen deficient bone loss. Using the model, we will identify other potential actions of SCFAs on bone health and we will be able to predict if increased SCFAs could counteract estrogen deficient bone loss. These insights on bone health could lead to improved treatment and prevention protocols for osteoporosis.

Lanthanide Binding Tag Peptides for the Foam Fractionation of Rare Earth Elements

Discipline: Engineering
Subdiscipline: Chemical Engineering

Luis Ortuno Macias*[1], Charles Maldarelli[2], Pan Sun[3], Stephen Crane[4], Kathleen Stebe[5], Wei Bu[6], Binhua Lin[7], Mark Schlossman[8], Raymond Tu[9]
[1]The City College of New York, [2]The City College of New York, [3]NSF's ChemMatCRAS, University of Chicago, [4]University of Pennsylvania, [5]University of Pennsylvania, [6]NSF's ChemMatCARS, University of Chicago, [7]NSF's ChemMatCARS, University of Chicago, [8]University of Illinois at Chicago, [9]The City College of New York

Abstract: Solvent extraction is widely used for separation of rare earth elements trivalent cations (REEs) from an aqueous phase into an organic solvent. This process is energy intensive and environmentally unfriendly. Here, we exploit the high affinity of a surface-active Lanthanide Binding Tag (LBT) peptide (LBT1, YIDTNNDGWYEGDELLA), that coordinates selectively with Ln3+ ions for its use in a bio-inspired extraction processes in which the complexed peptide adsorbs to the air/aqueous interfaces of bubbles for foam recovery. To understand the surface activity and identify the bound cationic species at the air-water interface, we characterized the surface molecular adsorption and arrangement of LBT1 and the more surface active LBT1-LLA. For this, we measured the relaxation dynamic tension of the each LBT in the absence and presence of Terbium. X-ray reflectivity (XRR) and X-ray fluorescence near total reflection (XFNTR) measurements on the adsorbed layer were used to compute the surface concentration of the peptide and the Ln +3 cation. The addition of three hydrophobic residues to LBT1 increased the surface density of the peptide by three-fold. Additionally, the LBT1-LLA improved the adsorption of Tb3+ ions to the air-water interface up to approximately 30% over LBT1 peptides. The interfacial density of Tb-bound LBT1-LLA increased between 50% and 100% compared with the Tb-free, unbound LBT1-LLA. The enhancement in the surface activity of LBTs peptides is improved by the addition of hydrophobic residues appended to the C-terminus of the peptide. This improvement in the hydrophobicity of these biomolecules could be advantageous for a eco-friendly separation method.

Astronomy & Astrophysics

Searching for Planets and Brown Dwarfs around Young Accelerating Stars

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Kyle Franson*[1]and Brendan Bowler[2]
[1]The University of Texas at Austin, [2]The University of Texas at Austin

Abstract: Directly imaged planets and brown dwarfs are key tools in studying the formation, evolution, and atmospheric physics of wide-separation substellar objects. However, imaging campaigns have been challenged by the low occurrence rate of the long-period planets and brown dwarfs capable of detection with current facilities. As a result, only about a dozen exoplanets with separations between 10 and 100 AU have been imaged. We aim to overcome these low occurrence rates by targeting stars exhibiting small proper motion differences (accelerations) between Hipparcos and Gaia EDR3 that indicate the presence of unseen substellar companions. Over the past two years, we have launched a multi-facility, systematic high-contrast imaging survey of the accelerating stars most likely to harbor long-period giant planets and brown dwarfs with the goal of imaging new substellar companions. In this talk, I will present an overview of our program, our novel approach to efficient target selection, and early results including the first brown dwarf companion discovered through this survey. New substellar companions found through this program will be excellent targets for follow-up orbital and spectroscopic characterization with future facilities including JWST.

Probing the Physics of Circum-Galactic Medium using Fast Radio Bursts: Insights from CAMELS simulations

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Isabel Medlock*[1]and Daisuke Nagai[2]
[1]Yale University, [2]Yale University

Abstract: T he circumgalactic medium (CGM) is the region of diffuse gas surrounding a galaxy. Its physics, though complex and not well understood, is the new frontier for astrophysics as it is essential to our understanding of the formation and evolution of galaxies. In the era of multi-wavelength astronomical surveys, one promising probe of the CGM are fast radio bursts (FRBs), millisecond-long luminous extragalactic pulses of radio waves. The dispersion measure (DM) of FRBs, a measure of all the matter the pulse interacts with on its way to Earth, is useful for quantifying and locating baryons in the CGM. In this work, we analyze the Cosmology and

Astrophysics with Machine Learning Simulations (CAMELS) simulations, comprising over 4000 state-of-the art cosmological, computational simulations, and spanning a wide range of astrophysical and cosmological parameters. Using the CAMELS we explore how varied implementation of the physics of the CGM as well as varied parameters and redshift (an analog for distance and age) impact the distribution of the DM. We find a strong dependence of the DM on two parameters: Ω m (the density needed for the universe to re-collapse) and ASN1 (stellar feedback, specifically energy per unit star formation rate). Looking at the distribution of DM for various redshift snapshots we find an increase in mean DM with increasing redshift. Lastly, we model expected DM distributions for mock FRBs. Our results indicate the feasibility of using FRBs as probes of the physics of the circumgalactic medium .

Investigating the Empirical Relationship between the CaII Triplet and Metallicity

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Sebastian Monzon*[1]and Marla Geha[2]
[1]Yale University, [2]Yale University

Abstract: Our MilkyWay (MW) hosts a population of dwarf galaxies and globular clusters which, due to their proximity, can be resolved into individual stars. These satellites are prime targets for investigations into galaxy formation, dark matter and cosmology but are often contaminated by foreground MW stars. The globular clusters (GC) satellites have well defined metallicity distributions such that accurate measurements of metallicity (or [Fe/H]) can be powerful membership distinguishers. Using Keck/DEIMOS archival data processed by an updated data reduction pipeline (PypeIt), we investigate the Ca II triplet lines at 8498, 8542 and 8662Å whose strength empirically changes as a function of metallicity. We developed a metallicity measurement routine using a sample of GC systems with known [Fe/H] distributions. Initial measurements suggest we might be able to extend the empirical relationship past the traditional absolute magnitude limit of the main sequence turnoff. By exploring the success rate of our routine at the lowest signal-to-noise regime using artificially degraded data, we plan to define a new relationship for main sequence stars in our sample. Our ultimate goal is to compare measurements of [Fe/H] for satellites around Andromeda (M31) to satellites orbiting the MW which has typically only been done using spectra of integrated light.

The Galactic Scale Effect of Supermassive Black Hole Activity in the Galaxy NGC 1068 from Southern African Large Telescope Fabry-Pérot Spectroscopy

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Raphael Hviding*[1], Dr. Kevin Hainline[2], Dr. Ryan Hickox[3], Dr. Petri Väisänen[4]
[1]University of Arizona, [2]University of Arizona, [3]Dartmouth College, [4]South African Astronomical Observatories

Abstract: When supermassive black holes (SMBHs) at the centers of galaxies accrete surrounding material they produce an inordinate amount of energy and light, becoming Active Galactic Nuclei (AGNs) and potentially outshining the very galaxy in which they live. Observations and theory alike suggest that AGN activity plays a vital role in how galaxies, like our own Milky Way, change and grow. NGC 1068, as one of the closest and brightest AGNs in the night sky, is the optimal testbed for directly observing the interaction between the feeding SMBH and the rest of the galaxy. While the central few lightyears of NGC 1068 have been intensely studied for the past few decades, the remainder of the galaxy remains relatively unexplored. In this work, we strive to obtain observations of NGC1068 across tens of thousands of lightyears using Fabry-Pérot (FP) spectroscopy, a technique ideally suited for discerning the effect of an AGN, with one of the world's largest observatories: the Southern African Large Telescope (SALT). Our observations are the largest resolved spectroscopic maps of NGC 1068 and confirm the existence of pockets of gas ionized by the AGN that are roughly thousands of lightyears across. We postulate that these regions may be due to enhanced SMBH accretion in the past, providing constraints on the life cycles of AGN in all galaxies. We have already proposed to obtain follow-up observations of NGC 1068 which will conclusively determine the ionization mechanism, providing insight into the coevolution of AGN and their host galaxies through cosmic time.

The Epoch of Giant Planet Migration: A Near-Infrared PRV Survey for Giant Planets Around Young Sun-like Stars

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Nhat Quang Tran*[1], Brendan P. Bowler[2], William D. Cochran[3], Mike Endl[4], Suvrath Mahadevan[5], Joe Ninan[6], Guðmundur K. Stefánsson[7], Chad F. Bender[8], Samuel Halverson[9], Arpita Roy[10], Ryan C. Terrien[11]
[1]University of Texas, Austin, [2]University of Texas, Austin, [3]The University of Texas, Austin, [4]McDonald Observatory, [5]Pennsylvania State University, [6]Pennsylvania State University, [7]Princeton University, [8]Steward Observatory, [9]Jet Propulsion Laboratory, [10]The Space Telescope Science Institute, [11]Carleton College

Abstract: The presence of giant planets interior to the water ice lines of Sun-like stars indicates that inward orbital migration is a common phenomenon. However, the processes by which these gas giants arrived at their present-day locations are poorly constrained because previous radial velocity surveys have largely avoided young stars. Young stars have intrinsic astrophysical RV "jitter", or noise, that overwhelms planetary signals at visible wavelengths. Moving into the near-infrared wavelength range (NIR) has been shown to reduce this variability, opening the possibility of finding giant planets around young stars. I am carrying out a large precision RV survey of intermediate-age (20-200 Myr) GK dwarfs in young moving groups with the Habitable Zone Planet Finder (HPF), a stabilized high resolution NIR spectrograph located at the Hobby-Eberly Telescope. The goals of this program are to determine the timescale and dominant physical mechanism of giant planet migration by measuring their occurrence rates at young ages and comparing them to established frequencies at older ages. In this talk I will present the survey design and initial results, including the first measurements of stellar jitter in the NIR for a large sample of young Sun-like stars and an overview of the first candidate planets to emerge from this program.

Physics

A Practical Source of Coherent Light from a High-Performance On-Chip Microresonator Optical Parametric Oscillator

Discipline: Physics & Astronomy
Subdiscipline: Physics

Edgar Perez*[1], Gregory Moille[2], Xiyuan Lu[3], Jordan Stone[4], Feng Zhou[5], Kartik Srinivasan[6]
[1]Joint Quantum Institute, NIST/University of Maryland, [2]Joint Quantum Institute, NIST/University of Maryland, [3]Joint Quantum Institute, NIST/University of Maryland, [4]Joint Quantum Institute, NIST/University of Maryland, [5]Joint Quantum Institute, NIST/University of Maryland, [6]Joint Quantum Institute, NIST/University of Maryland

Abstract: As research in fields like quantum information science, metrology, and sensing advance towards field-deployable technologies, the need for a compact laser with access to various (and sometimes hard to access) wavelengths becomes increasingly important. Microresonator optical parametric oscillators (μOPOs) can provide the path for accessing the relevant wavelengths, because of their ability to redistribute energy from pump photons of frequency ω p to signal and idler photons with frequencies ω s and ω i , respectively. In particular, the output frequencies can be significantly different from the pump frequency, potentially reaching otherwise hard-to-reach wavelengths. However, in addition to wavelength access, conversion efficiency and output power are critical, and to date, no χ(3) μOPO device has been able to simultaneously realize high-performance with respect to all three metrics due to challenges in coupling engineering and in the suppression of competitive processes. By addressing these issues through coupling design and hybrid mode family phase-matching, our work demonstrates a silicon photonics OPO device with unprecedented performance, approaching that of more conventional fiber-based and table-top technologies. Our silicon nitride microresonator produces output signal and idler fields with over 150 THz of frequency separation from a 980 nm pump, and shows a pump-to-idler conversion efficiency exceeding 25% with an output power exceeding 10 mW, enough for use in a downstream application. This work shows how an optical parametric oscillator on a chip can simultaneously satisfy the efficiency, scalability, and power requirements needed for future applications of compact chip-integrated laser technologies without compromising on wavelength access.

Engineering Light-Activated Microswimmers for Controllable Motion

Discipline: Physics & Astronomy
Subdiscipline: Physics

John Castaneda*[1], John G Gibbs[2], Jennifer S Martinez[3]
[1]Northern Arizona University, [2]Northern Arizona University, [3]Northern Arizona University

Abstract: The dynamic movements of flocks of birds and schools of fish ensue due to the individual moving organisms altering their velocities based upon the behavior of their nearest neighbors. These collective "active matter" behaviors also exist at the micron and nanometer scale. For example, "microswimmers" convert chemical energy into motion on a length-scale comparable to biological prokaryotic cells. An example of our artificial, nonbiological microswimmers is a catalytic Janus particle that has surface-asymmetry with specific physico-chemical properties at different locations upon the particle. Controlling this asymmetry may allow one to engineer these kinds of dynamics exhibited. In this talk, I will focus upon light-activated, self-propelled microswimmers with controlled morphology and catalytic behavior. My goal is to investigate the solid/liquid interface of light activated microswimmers in order to engineer collective motion and responsive assembly as a function of aqueous, external fields, and morphology of microswimmers. I propose that it is possible to engineer photoactive microswimmers for desired motion directly from a metal oxide photocatalyst, magnetic materials and combing these microscale swimmers with other nanoscale structures through: Physical Vapor Deposition (PVD) and Glancing Angle Deposition (GLAD) with electron beam and thermal evaporating systems; Constructing microswimmers from photoactive materials such as TiO_2 that gives a more effective level of control in comparison to traditional catalysts since the activity, intensity of propulsion can be turned on-and-off using UV light; Designing microswimmers with a coating of precise nanostructures. Combined, these ideas allow for the creation of active microswimmers that exhibit controllable collective motion and behavior.

Quantum neurons: towards scalable, quantum neuromorphic computing

Discipline: Physics & Astronomy
Subdiscipline: Physics

Rodrigo Araiza Bravo*[1], Susanne Yelin[2], Khadijeh Najafi[3], Xun Gao[4]
[1]Harvard University, [2]Harvard University, [3]IBM, [4]Harvard University

Abstract: Quantum computation promises to speed up machine learning algorithms. However, most current quantum machine learning architectures rely on a digital implementation of a variational circuit, which in turn is hard to train, and obscures the source of potential quantum advantage. Another approach that is gaining speed is that of neuromorphic quantum computation, where a neurological model for brain-dynamics or artificial intelligence is quantized to be compatible with quantum hardware. This approach brings new architectures to quantum machine learning which have been designed to solve problems useful to a variety of scientific communities such as computational neuroscience and machine learning. In this presentation, we introduce a quantized version of a perceptron, a very simple model for single-neuron behavior, based on the unitary dynamics of already available quantum computers. Moreover, we show that this quantization extends the computational capabilities of a single quantum perceptron as it may indeed be able to perform universal computation, while a classical perceptron is unable to perform universal classical computations. We discuss an experimental proposal for our perceptron in a currently-available quantum computer, and show the success of our architecture at solving quantum computation, as well as real-world problems.

Electrical and Thermal Quality Control tests for the ATLAS ITk Barrel Strip Tracker

Discipline: Physics & Astronomy
Subdiscipline: Physics

Arianna Garcia Caffaro*[1]and Paul L. Tipton[2]
[1]Yale University, [2]Yale University

Abstract: ATLAS is one of the four main experiments at the Large Hadron Collider (LHC), the world’s largest particle accelerator. The ATLAS detector is designed to record high energy particle collisions, allowing us to probe the Standard Model of particle physics. This experiment is currently running with proton-proton collisions at 13TeV and is scheduled to undergo a High Luminosity (HL) upgrade which aims to increase the number of collisions per second by a factor

of ~7. This increase in data will allow us to study rarer particle interactions. However, in order to prepare for the HL upgrade, ATLAS must replace its current Inner Detector with an all-silicon Inner Tracker (ITk) capable of detecting, reading out, and storing the increased collision data, as well as withstanding the increased radiation. The ITk is made up of a pixel detector surrounded by a silicon microstrip detector. In this talk, I will discuss the electrical and thermal quality control tests performed on the barrel strip components to ensure they meet the specifications required to make the ITk upgrade a success.

Geoscience & Environmental Science

Did insect herbivore assemblages track Eucalyptus across the globe for 50 million years?

Discipline: Geoscience
Subdiscipline: Other Geoscience

Luis Giraldo Ceron*[1], Peter Wilf[2], Michael P. Donovan[3], Maria A. Gandolfo[4]
[1]The Pennsylvania State University, [2]The Pennsylvania State University, [3]Cleveland Museum of Natural History, [4]Cornell University

Abstract: The Laguna del Hunco (LH; 52.2 Ma) locality, in Argentinean Patagonia, has yielded diverse floras with multiple plant lineages that today survive in rainforests of the West Pacific, highlighting former Gondwanan connections between South America, Antarctica, and Australia. However, whether the ancient insect herbivore assemblages tracked survivor plant taxa through time — a major question in biogeography — has only been tested in Agathis (Araucariaceae) fossils. Here, we describe the abundant and diverse insect herbivore damage found in ~220 Eucalyptus leaves from LH and compare it with modern Eucalyptus herbarium specimens to test for the persistence of insect herbivore assemblages. Twenty-eight rainforest-associated and 11 possibly rainforest-associated living Eucalyptus species were selected for comparison, given that LH is interpreted as a vegetational mosaic wherein Eucalyptus dominated volcanically disturbed areas alongside rainforests. An additional 66 Eucalyptus species that occur in seasonally wet environments were included. So far, we have reviewed ~3500 herbarium specimens, pertaining to 12 living Australian Eucalyptus species. In the fossils, we found 27 damage types, 17 corresponding to external feeding, three to galling, and seven to mining. Seventeen damage types seen in the fossils have been recognized in extant Eucalyptus specimens, 11 corresponding to external feeding, three to galling, and three to mining. The nearly identical suites of insect herbivore damage found in fossil and modern Eucalyptus suggest that insect herbivore assemblages have tracked Eucalyptus through time and space, although some of the similarity could result from convergence in damage type morphology, particularly for external feeding.

Heavy Metal(loid) Contamination of Medicinal Plants: Implications for Public Health of Indigenous People.

Discipline: Life Sciences
Subdiscipline: Environmental Science

Richelle Thomas*[1], Jean McLain[2], Robert Root[3], Gilberto Curlango-Rivera[4]

[1]The University of Arizona, [2]The University of Arizona, [3]The University of Arizona, [4]CICESE, Center for Scientific Research and Higher Education of Ensenada

Abstract: Medicinal plants are critical to the continuation of Native American and Indigenous communities' identity and culture. Unfortunately, heavy metal uptake by medicinal plants poses a potential health risk, as levels of metal uptake by plants and subsequent exposure to humans are unknown. Heavy metal contamination to soils can result from anthropogenic activities; this has occurred within many indigenous communities because of colonial mineral and energy mining development on Native lands. This research project will measure uptake of heavy metals from soils (including arsenic and uranium) by traditional medicinal plants using analytical chemistry (i.e. ICP-MS, X-ray fluorescence) and biological techniques (i.e. plant root border cell activity assessment; analysis of soil microbial communities). Data will be used to conduct an exposure assessment to predict any resulting human health risk. Findings will be shared with the Diné (Navajo) community for use in developing medicinal plant usage guidelines that are protective of community health. It is expected that the developed environmental justice guidelines will be transferable across other indigenous peoples and communities, as they share medicinal plants and similar histories of legacy mining.

On Fragmentation: Lakota Values of Unity and Relationality for a Sustainable Future

Discipline: Life Sciences
Subdiscipline: Environmental Science

Joseph Gazing Wolf*
Standing Rock Sioux Tribe & Arizona State University

Abstract: We live in an age of fragmentation: land, ecological, social, economic, governmental, religious, etc. Colonial power works by convincing those it wishes to rule that they are fundamentally different from everyone else around them, even within their own communities. Today, people in the United States and elsewhere actively seek out tribes to join based on race, gender, class, livelihood, neighborhood, religion, etc. Once a group is formed, the 'other' outsiders are identified and often villainized. This fragmentation has made it virtually impossible to unite as a species to face the multiple crises that threaten our population: the rise of autocracy, climate change, pandemics, economic inequities, etc. This presentation utilizes a case model looking at the Lakota people and their value systems based in unity and relationality with all living beings and with Grandmother Earth. This model is used an exemplar of how human populations may live in tightly-knit tribal communities while embodying interconnectivity with every other tribe and nation across the world. General values of the Lakota people are shared along with specific examples in narrative form from the experiences of the presenter who is an enrolled member of the Standing Rock Sioux Tribe.

Uncovering novel targets of toxicity induced by embryonic exposure to environmental pollutant 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD)

Discipline: Life Sciences
Subdiscipline: Environmental Science

Layra Cintron-Rivera*[1]and Jessica Plavicki[2]

[1]Brown University, [2]Brown University

Abstract: Dioxins are a widespread class of highly persistent and toxic pollutants. Epidemiological and laboratory studies have found that organisms undergoing development are most sensitive to dioxin exposure; however, the molecular mechanisms mediating developmental toxicity remain poorly understood. In this study, we utilized the zebrafish model to investigate potential targets of embryonic dioxin toxicity and to identify novel phenotypes following exposure. Zebrafish are a great model for developmental toxicology research because they are initially transparent during development, allowing researchers to visualize the effects of toxicity in vivo . 2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD) is the most potent dioxin compound and has been found to activate the ligand activated aryl hydrocarbon receptor (AHR). Activation of AHR leads to craniofacial malformations by downregulating sox9b , a member of the SoxE gene family. We hypothesized that TCDD induced AHR activation additionally targets sox10 , another member of the SoxE family, and that organ systems which require sox10 expression during development such as the ear and peripheral nervous system (PNS) would also be affected. We exposed zebrafish embryos at 4 hours post fertilization (hpf) to TCDD and used both immunohistochemistry staining and in vivo confocal imaging of transgenic zebrafish to determine the effects of TCDD exposure on the development Sox10+ and adjacent structures. We found that TCDD exposure leads to changes in the expression of Sox10 in the jaw, pharyngeal arches, and ear at 72 hpf and adversely affects early development of the PNS. Together, these findings reveal novel target systems and mechanisms of action for TCDD-induced toxicity.

Cell/Molecular Biology I

Identification of pesticides that alter autophagy: Implications for Parkinson’s disease risk

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Marisol Arellano*[1], Jeff M. Bronstein[2], Lisa M. Barnhill[3], Shash Khemka[4]
[1]University of California, Los Angeles, [2]David Geffen School of Medicine, University of California Los Angeles, [3]David Geffen School of Medicine, University of California Los Angeles, [4]David Geffen School of Medicine, University of California Los Angeles

Abstract: Parkinson’s disease (PD) is an increasingly prevalent neurological disorder that is partly characterized by aggregation of alpha-synuclein and progressive loss of dopaminergic neurons. Autophagy is a lysosomal degradative pathway to clear aggregated proteins; dysfunctional autophagy has been implicated in the pathogenesis of PD. Further, increased risk of PD has been associated with exposure to pesticides commonly used in the Central Valley of California (CVC). Thus, we hypothesize that pesticides commonly used in the CVC impair autophagic flux conferring increased risk of developing PD. We developed a two-phase cell-based screen to identify pesticides that alter autophagy. In phase one, we utilized fluorescent, pH-selective dyes and confocal microscopy to determine the effects of pesticides on autophagosomes and lysosomes in human neuroblastoma cells (SK-N-MCs). We identified twenty-one pesticides that altered autophagosome and/or lysosome counts greater than 30% compared to vehicle-treated cells for further study. We detected pesticides with a known association to PD (e.g., rotenone) but importantly, we identified several pesticides that had not been previously implicated to alter PD

risk (e.g., diuron). In the second phase, we determined alterations in the autophagosome cargo protein SQSTM1 /p62 and the lysosome-associated membrane protein 2a (LAMP2a) using immunocytochemistry. We found that exposure to most of the pesticides positively identified in phase one also resulted in changes to p62 and/or LAMP2a detection (e.g., ziram). Studies are underway to determine how these pesticides alter autophagic flux in vivo using zebrafish . These studies will identify pesticides that potentially alter risk of developing PD and warrant clinical evaluation.

Dual Mitophagy Effector and Cell Death Mediator BNIP3 Degradation via Vesicular Transport to Evade Cell Death

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jose Delgado*[1], Logan Wallace Shepard[2], Sarah W. Lamson[3], Christopher J. Shoemaker[4]
[1]Dartmouth College, [2]Dartmouth College, [3]Dartmouth College, [4]Dartmouth College

Abstract: Autophagy is a lysosome-mediated process wherein dysfunctional or unwanted components of the cell are degraded and recycled. When there is insufficient oxygen (hypoxia), cells use autophagy to degrade mitochondria, an oxygen-demanding organelle, to match oxygen consumption and availability. Autophagic degradation of mitochondria, termed mitophagy, in response to hypoxia has protective roles in various disease pathologies, including cancer and cardiomyopathy. Mitophagy is facilitated by proteins that mark mitochondria for degradation. One of these proteins is BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 (BNIP3), a dual functioning membrane protein that mediates mitophagy and induces cell death. The molecular mechanisms that modulate BNIP3-mediated mitophagy are still largely unknown. To identify molecular factors involved in BNIP3-mediated mitophagy, we performed a genome-wide CRISPR-Cas9 screen in MDA-MB-231 breast cancer cells, a model for metastatic cancer cells that form dense hypoxic tumors. Contrary to current models, our screen revealed that the BNIP3 protein is not predominately degraded in a mitophagy pathway. Instead, the accumulation of BNIP3 in a hypoxic environment leads to a dual localization to mitochondria and the endoplasmic reticulum (ER), where it follows an autophagy-independent route from the ER to the lysosome. BNIP3 accumulation at the ER has been shown to induce cell death. We hypothesize BNIP3 may mediate cell death at the ER in hypoxia and this uncharacterized alternative pathway serves as a quality control mechanism to evade cell death. Ultimately, studying the properties of BNIP3 is uncovering how the cell decides to utilize mitophagy for hypoxic adaptation or to initiate cell death.

Developmental Regulation of CD8+ T cell Exhaustion

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Viviana Maymi*[1]and Brian Rudd[2]
[1]Cornell University, [2]Cornell University

Abstract: While advances in CD8+ T cell biology have facilitated revolutionary immunotherapies for cancer and chronic viruses, T cell exhaustion remains a barrier to patient health. CD8+ T cell exhaustion is the hierarchical loss in proliferation, cytokine production, and effector function of

CD8+ T cells after chronic antigen exposure. However, an important unanswered question is why some CD8+ T cells become more exhausted than others. Our lab showed that a previously-overlooked source of CD8+ T cell heterogeneity—developmental origin—determines T cell fate after acute infection. Adult T cells (derived from bone marrow stem cells) become memory precursors, while neonatal T cells (derived from fetal liver stem cells) become short-lived effectors. Based on these data, I hypothesized that the degree of exhaustion observed in CD8+ T cells is linked to their developmental origin. To test this, I transferred neonatal and adult CD8+ T cells into recipient mice and compared their responses to a chronic virus (LCMV clone 13) via high-parameter flow cytometry. Neonatal CD8+ T cells preferrentially became highly functional effectors, whereas adult cells became exhausted. Interestingly, neonatal cells' effector skew corresponded with enhanced proliferation and migration into tissues early in infection. Late in infection, neonatal cells maintained a distinct phenotype, and may be more responsive to PD-1 blockade than their adult counterparts. To understand the functional consequences of these differences, we are currently comparing their transcriptome and behavior in tumors. Collectively, our data suggest that the developmental origin of CD8+ T cells plays a deterministic role in their fates during chronic infection.

Role of Nicotinamide Nucleotide Adenylyltransferase-1 (NMNAT1) in Chromatin Remodeling and Gene Regulation

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Yessenia Cedeno Cedeno*[1]and Robert A. Coleman[2]
[1]Albert Einstein College of Medicine, [2]Albert Einstein College of Medicine

Abstract: NMNAT1 is a metabolic enzyme responsible for local NAD+ production in the nucleus. Nuclear metabolic enzymes are thought to provide local metabolites for chromatin remodeler enzymes (e.g., SIRT1). However, the dynamic function of these metabolic enzymes in potentially regulating chromatin remodeling and transcriptional dynamics remains poorly understood. Our goal is to define the role of NMNAT1 in regulating chromatin remodeling enzyme activity, chromatin structure, and gene expression. We hypothesize that the cycling of NMNAT1 on the genome produces local NAD+ gradients that regulate chromatin-modifying enzyme activity, influencing rapid changes in chromatin structure and gene expression of target genes. We will employ a powerful combination of structure/function studies, genomic approaches, and live-cell single-molecule tracking microscopy to determine how NMNAT1 and metabolite levels regulate chromatin and transcription. Preliminary data show that NMNAT1 and SIRT1 chromatin remodeling enzymes display similar binding kinetics on the genome, suggesting that metabolic enzymes potentially serve as "power plants" to fuel and regulate the action of chromatin remodeling enzymes. In addition, deletion of NMNAT1 in U-2OS cells results in a significant reduction of NAD+ levels. Analysis of cell morphology revealed an enlarged nucleus and decondensed chromatin compared to parental cells. This suggests that low NAD+ levels may limit the histone deacetylase activity of SIRT1, leading to hyperacetylation of chromatin. Together, these preliminary results indicate the importance of NMNAT1 and NAD+ levels to the overall chromatin structure and metabolic homeostasis in the cells. Therefore, this study will define new paradigms regarding gene expression and regulation.

Exploring distinct coupling mechanisms for FGFR signaling

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Claudia Rodriguez*[1], Claire de la Cova[2], Melissa Garcia Montes de Oca[3], Michael Stern[4], Cindy Voisine[5], Te-Wen Lo[6]

[1]University of Wisconsin-Milwaukee, [2]University of Wisconsin-Milwaukee, [3]Northeastern Illinois University, [4]Northeastern Illinois University, [5]Northeastern Illinois University, [6]Ithaca College

Abstract: Fibroblast Growth Factor Receptors (FGFRs) are highly conserved Receptor Tyrosine Kinases that have been implicated in human diseases and cancers. Upon ligand binding, FGFR signaling activates RAS and the RAF-MEK-ERK kinase cascade. C. elegans has a sole FGFR, EGL-15, that is expressed in the hypodermis and controls fluid balance. Genetic screens in C. elegans have been exceptionally useful for discovery of negative and positive regulators of EGL-15. For example, EGL-15 signaling is inhibited by CLR-1, a receptor tyrosine phosphatase. On the other hand, EGL-15 signaling requires coupling to the adaptor SEM-5, a C. elegans ortholog of human GRB2. The EGL-15-SEM-5 interaction may be mediated by two mechanisms: direct coupling via the EGL-15 C-terminal domain, and indirect coupling through a second factor termed SOC-3. We hypothesize that CLR-1 and EGL-15-SEM-5 interactions each impact the level of EGL-15 signal transduction and ERK activation. In this work, we quantified ERK activity in egl-15, soc-3, and clr-1 mutants. We utilized an in vivo biosensor termed the ERK Kinase Translocation Reporter (ERK-KTR) and demonstrated that it is a faithful reporter of ERK activity in C. elegans. Our results showed that loss of CLR-1 resulted in significantly increased ERK activation. In clr- 1 mutants, loss of either the EGL-15 C-terminus or SOC-3 did not reduce ERK activation. However, animals lacking both coupling mechanisms had significantly reduced ERK activation. Our quantitative data indicates that ERK activation by EGL-15 is inhibited by CLR-1 and is mediated by two redundant EGL-15-SEM-5 coupling mechanisms.

The effects of depleted uranium on mitochondrial function in zebrafish

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Phillip Kalaniopio*[1], Matthew Salanga[2], Ronald Allen[3], Abby Rambo[4]

[1]Northern Arizona University, [2]Northern Arizona University, [3]Northern Arizona University, [4]Northern Arizona University

Abstract: A consequence of modern combat for people living or working near war zones is exposure to depleted uranium (DU). DU is released from armor-piercing projectiles, which release shrapnel and produce uranium oxide particles (e.g., U_3O_8 , UO_2) upon striking a hard target. Humans near the impact are exposed to DU through inhalation of airborne particles, shrapnel injuries, or wound contamination. Research in uranium chemical toxicology has raised uncertainty as to the risks of DU exposure and mechanisms of action. The central question is whether internalized DU causes persistent cellular and genetic damage. We address this question using a novel microimplantation method in zebrafish larvae to emulate DU shrapnel injuries and waterborne exposures to model inhalation and ingestion. Preliminary data show that mitochondria near internalized DU particles are more likely to contain disorganized cristae than contralateral or sham mitochondria, suggesting proximity-dependent toxicity. Waterborne DU exposures at concentrations below federal safe limits result in impaired cellular metabolism, possibly due to disrupted mitochondria like those observed in the implant study. Others have proposed that DU adduction to DNA’s phosphate backbone activates DNA repair mechanisms and leaves a potential for unresolved DNA lesions or incorporation of mutations following the repair process. Here, we test the hypothesis that the observed mitopathies are results of uranium-induced mitochondrial genome damage. We are testing our hypothesis using a highly sensitive method for quantifying DNA lesions, semi-long run (SLR) qPCR, where an increase in lesion frequency for uranium-exposed subjects would support our hypothesis.

Cell/Molecular Biology II

Impairment of hematopoiesis by deletion of the von-Hippel Lindau (Vhl) gene in bone cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Betsabel Chicana Romero*[1], Hanna Taglinao[2], Jennifer O. Manilay[3]
[1]University of California Merced, [2]University of California Merced, [3]University of California Merced

Abstract: Hematopoiesis is the continuous production of red blood cells, white blood cells, and platelets in the bone marrow (BM). The production of the red blood cells that carry oxygen through your body is also known as erythropoiesis. White blood cells are important against infections, for example B cells produce antibodies against foreign pathogens. Osteoblasts (OBs) and osteocytes (OCYs) are bone cells that have been shown to support hematopoiesis in the BM. The von-Hippel Lindau protein (VHL) regulates oxygen sensing in the body and is crucial for proper control of oxygen changes. When this gene is deleted in OCys and mature OBs, it leads to a higher bone density and improper bone formation. We hypothesized that proper bone formation is essential for B cell development and erythropoiesis. Therefore, we utilized Dmp1 -Cre; Vhl conditional knockout mice (cKO), in which the Vhl gene is deleted in OBs and OCYs. This cKO mice display higher bone growth, smaller bone marrow (BM), and an overall decrease in BM cellularity compared to wild-type (WT) mice. B cell development was significantly decreased in frequency, while erythropoiesis was increased in the cKO BM. We observed that cKO B cells had increased apoptosis and decreased proliferation. We found reduced CXCL12, a key cytokine for early B cell development, and increased EPO, a key cytokine for erythropoiesis in the cKO BM serum. These studies reveal details of the molecular mechanisms by which Vhl in Dmp1 expressing bone cells indirectly supports B cell development and erythropoiesis in the BM.

Characterization of a G Protein-Coupled Receptor Implicated in Intestinal Lipid Homeostasis of Drosophila melanogaster.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Daniela Barraza*[1], Paula I. Watnick[2], Bat-Erdene Jugder[3], Rita Wang[4]
[1]Harvard Medical School, [2]Boston Children's Hospital/Harvard Medical School, [3]Boston Children's Hospital, [4]Harvard Medical School

Abstract: The enteroendocrine cell (EEC) senses stimuli in the intestinal lumen through various receptors, including G Protein-Coupled Receptors (GPCRs). Upon activation, EEC GPCRs regulate expression and secretion of enteroendocrine peptides (EEPs) that control important physiological processes including satiety, intestinal contractions, and systemic metabolism. Recent evidence suggests that EECs also play a role in regulating intestinal innate immunity through EEPs. However, the mechanisms underlying this regulation are not well understood. Our lab found that, in addition to regulating intestinal lipid homeostasis, the Drosophila melanogaster EEP Tachykinin (Tk) acts as a cytokine to regulate the intestinal innate immune response. We recently discovered that mutation of the EEC-specific GPCR GPRx yields the phenotype of a Tk mutant: Lipid accumulation in the intestine. Based on this observation, we hypothesized that GPRx regulates expression and release of Tk from EECs, and therefore, intestinal innate immunity. To test this hypothesis, we specifically knocked down GPRx in Tk-expressing EECs (Tk> GPRx RNAi) and measured transcription of Tk using qRT-PCR analysis. We also assessed survival and colonization phenotypes of GPRx mutant and knockdown flies upon infection with Vibrio cholerae. Surprisingly, we not only observed decreased transcription of Tk, but also of other EEPs found in Tk-expressing EECs like Neuropeptide F (NPF) and Diuretic Hormone 31 (DH31). In addition, we observed altered survival and higher bacterial burdens in both GPRx mutant and GPRx knockdown flies. We conclude that GPRx 1) regulates transcription of EEPs and 2) plays a role in the response to intestinal infection.

Itaconate as a regulator of hematopoietic stem and progenitor cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Katia Nino*[1], Taylor S. Mills[2], Zhonghe Ke[3], Rachel Culp-Hill[4], Angelo D'Alessandro[5], Craig Forester[6], Eric Pietras[7]

[1]University of Colorado Denver - Anschutz Medical Campus, [2]Division of Hematology, Department of Medicine, University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA, [3]University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA, [4]Department of Biochemistry and Molecular genetics, University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA, [5]Division of Hematology, Department of Medicine and Department of Biochemistry and Molecular genetics, University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA, [6]Division of Pediatric Hematology/Oncology/Bone Marrow Transplant, University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA, [7]1Division of Hematology, Department of Medicine and Department of Microbiology and Immunology, University of Colorado Denver Anschutz Medical Campus, Aurora, CO, USA

Abstract: Acute myeloid leukemia (AML) is the most common leukemia in adults, constituting approximately 20,000 cases this year alone. As a disease of aberrant myeloid cell expansion, AML oftentimes arises in patients with pre-existing mutations in hematopoietic stem and progenitor cells (HSPC) known as clonal hematopoiesis of indeterminate potential (CHIP). Loss of function mutations in the TET2 dioxygenase are common in individuals with CHIP leading to DNA hypermethylation, aberrant HSPC self-renewal and overproduction of inflammatory cytokines. However, mechanism(s) linking inflammation and aberrant self-renewal in TET2 -deficient HSPC, and their contribution(s) to CHIP pathogenesis are not well characterized. We hypothesize that inflammation may collaborate with TET2 loss of function to promote an altered metabolic program that promotes HSPC self-renewal. We found that treatment of WT and Tet2 -/- HSPC with the inflammatory cytokine, interleukin (IL)-1b significantly increased the metabolite itaconate. As a metabolic regulator, itaconate limits energy production via inhibition of mitochondrial metabolism. Using a loss-of-function approach, we found that Acod1 -/- mice have increased proportions of committed progenitors at the expense of immature progenitors vs WT. Gain-of-function assays using 4-octyl itaconate, a cell permeable itaconate derivative, demonstrated that itaconate limits IL-1b-mediated HSC differentiation. These findings support a model whereby itaconate promotes self-renewal. We are now assessing whether inflammation-driven itaconate production is necessary and sufficient to promote aberrant metabolism, DNA hypermethylation and CHIP/AML pathogenesis. Collectively, these studies may identify a therapeutically targetable metabolic program that forms a pathogenic bridge between inflammation and the epigenome.

The role of Spenito and m6A in establishing sexually dimorphic metabolism

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Arely Diaz*[1]and Tânia Reis[2]
[1]University of Colorado Denver/Anschutz Medical Campus, [2]University of Colorado Denver/Anschutz Medical Campus

Abstract: Genetic studies of obesity have revealed major hereditary contributions to variation in body weight, but the vast majority of these remain unidentified. Additionally, it is well established across species that males and females are fundamentally different with regards to metabolism, but these underlying molecular mechanisms are incompletely understood. To fill this gap in knowledge, I exploit the robust genetic, cellular and molecular tools of Drosophila melanogaster paired with metabolomic and transcriptomic analysis. My project focuses on the role of the conserved RNA-binding protein Spenito (a.k.a. Nito) and RNA modification by methylation (m 6 A) in establishing sexually dimorphic metabolism. Preliminary data suggest that Nito is required in fat cells to establish sex differences in fat storage. At the molecular level, I found that Nito is also required in the same fat cells for the canonical sex-specific pattern of gene expression that regulates dimorphisms in other processes. In the absence of Nito, female fat cells express a mix of male and female transcripts and at the organismal level, males and females no longer show differences in fat levels. We next aim to determine to what extent m 6 A modification is involved and identify the downstream effectors that control dimorphic fat storage. Ultimately, my work will elucidate the molecular mechanisms underlying differences in male and female metabolism.

Defining CLS-2 and SPD-1 Function in Central Spindle Assembly in C. elegans Sperm Meiosis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sebastian Gomez*[1], Diana Chu[2], Chu Huynh[3]
[1]San Francisco State University, [2]San Francisco State University, [3]SFSU

Abstract: Male infertility is a serious concern for many Americans. To elucidate how infertility arises, researchers are using the Caenorhabditis elegans nematode to study chromosome

segregation. To ensure proper chromosome segregation during mitosis and oocyte meiosis, a central spindle structure is initiated by the kinetochore protein, CLS-2, at the midzone region of the segregating chromosomes. CLS-2 then recruits SPD-1, a microtubule bundler protein, to elongate the spindle. Interestingly, sperm meiosis lacks this pattern thus questioning whether sperm meiosis has a distinctive mechanism of chromosome segregation. In the case of C. elegans sperm meiosis, few microtubules are present in the midzone except those tied to the lagging unpaired X chromosome. We hypothesize that CLS-2 and SPD-1 do not play a significant role in central spindle assembly in sperm meiosis. Instead, sperm meiosis relies on the pulling forces of the kinetochore-connected microtubules rather than the central spindle. We will deplete CLS-2 and SPD-1 in young adult C. elegans males using auxin-inducible degradation and apply immunostaining techniques to observe our proteins of interest. We will also use live imaging to observe any differences in chromosome segregation patterns before and after treatment with auxin. In both experiments, CLS-2 and SPD-1 fail to localize to the midzone except to the location of the lagging unpaired X chromosome. In males depleted of CLS-2 or SPD-1, we expect the spatial and temporal characteristics of segregating chromosomes to be similar to wild-type. Understanding SPD-1 and CLS-2 function can elucidate the molecular mechanisms required for forming healthy sperm.

Cancer Biology I

Distinct Wnt Signaling Thresholds Required for Polyposis in the Proximal and Distal Stomach

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Elizabeth Delgado*[1], Linda C Samuelson[2], Theresa M. Keeley[3], Elise S. Hibdon[4], Kevin P. McGowan[5], Merritt G. Gillilland[6], Justin A. Colacino[7], Elena Stoffel[8]
[1]University of Michigan, Ann Arbor, [2]University of Michigan, Ann Arbor, [3]University of Michigan, Ann Arbor, [4]University of Michigan, Ann Arbor, [5]University of Michigan, Ann Arbor, [6]University of Michigan, Ann Arbor, [7]University of Michigan, Ann Arbor, [8]University of Michigan, Ann Arbor

Abstract: Familial adenomatous polyposis (FAP) is a genetic disorder characterized by the formation of precancerous polyps throughout the gastrointestinal tract. Polyps form in response to increased Wnt signaling caused by mutations in the adenomatous polyposis coli (APC) gene. The vast majority of FAP patient gastric polyps are benign growths located in the proximal corpus, with less frequent distal antral polyps more closely associated with gastric cancer. Given these stark differences in polyp localization and severity, we hypothesized that there is a regional sensitivity to Wnt signaling along the gastric proximal-distal axis, and that a 'just-right' level of Wnt signaling is required for gastric polyposis. To model gastric polyp formation in FAP patients, we used mice with an inducible APC loss-of-function mutation and studied gastric tissue responses one month after Wnt activation. We found that, where submaximal levels of Wnt signaling are sufficient to initiate growth in the corpus, maximal levels are required for antral hyperproliferation. Notably, 'high-Wnt' stem cells are retained in the antrum and lost from the corpus, suggesting maximal Wnt activation is unfavorable for polyposis in the proximal stomach. To gain insight into regional differences in Wnt response, we performed RNA sequencing on corpus and antral organoids following Wnt inhibition. Transcriptomic analysis revealed that many

Wnt target genes have unique expression patterns in the corpus and antrum, which may be driving the differences observed in pathological settings. This work will help inform clinicians on FAP gastric disease by defining how APC mutations differentially drive polyp formation in the stomach.

Characterizing an IL-6 Induced PIM1 Expression Pathway in Renal Cell Carcinoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Kimberly Meza*[1]and Sheldon Holder[2]
[1]Brown University, [2]Brown University

Abstract: Renal cell carcinoma (RCC) is the most common kidney neoplasm, accounting for over 430,000 new cases worldwide and 179,000 deaths annually. PIM1 overexpression is associated with poor clinical outcomes in patients with RCC. PIM1 is a constitutively active effector serine/threonine kinase with roles in tumor progression including cell proliferation, apoptosis, invasion, and migration. Yet, the mechanisms underlying PIM1 expression and its function in RCC are not fully understood. Here, we explore the expression of PIM1 in RCC and identify potential signaling pathways influencing PIM1 expression. The pro-inflammatory cytokine IL-6 signals through the JAK/STAT pathway to stimulate PIM1 expression in pancreatic cancer. Our results show that four RCC cell lines, 769-P, 786-O, ACHN, CAKI-1 but not RCC-4 cells overexpress PIM1 relative to normal renal proximal tubule epithelial cells. ELISA results show that in RCC cell lines, IL-6 secretion correlates with PIM1 protein levels. Treatment with ruxolitinib, a JAK1/2 inhibitor, leads to a dose and concentration dependent decrease in PIM1 levels. Interestingly, 769-P cells demonstrate increased PIM1 levels but do not secrete IL-6. Notably, ruxolitinib treatment did not affect PIM1 levels in 769-O cells. Our initial studies suggest that differential expression of PIM1 among RCC cell lines may be linked to autocrine IL-6 signaling. Moreover an IL-6/JAK-independent pathway resulting in increased PIM1 protein levels likely exists in 769-P cells. Further investigation is required to elucidate the contexts of PIM1 regulatory pathways in order to develop novel targeted anti-cancer strategies in RCC.

Targeting GCN2 Regulation of Amino Acid Homeostasis in Prostate Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ricardo Cordova*[1], Jagannath Misra[2], Angela J Klunk[3], Marcus J. Miller[4], Tracy G. Anthony[5], Roberto Pili[6], Ronald C Wek[7], Kirk A Staschke[8]
[1]Indiana University, [2]Indiana University, [3]Indiana University, [4]Indiana University, [5]Rutgers, [6]University at Buffalo, [7]Indiana University, [8]Indiana University

Abstract: A stress adaptation pathway termed the integrated stress response (ISR) has been suggested to be active in many cancers including prostate cancer (PCa). Here, we demonstrate that the ISR kinase GCN2 is required for sustained growth in androgen-sensitive and castration resistant models of PCa both in vitro and in vivo. GCN2 is activated in wide range of PCa cell lines and PCa patient samples due to limitations of essential amino acids and accumulation of cognate tRNAs that are reported to be activators of GCN2. Using CRISPR-based phenotypic screens and genome-wide gene expression analyses of control and GCN2-depleted PCa cells, we demonstrate that GCN2 is critical for expression of multiple SLC transporter genes, including amino acid transporters, and we confirmed the importance of transporter genes in PCa fitness. We identified one transporter, SLC3A2 (4F2), as a key SLC gene induced by GCN2 and is essential for PCa proliferation. Of importance, expression of SLC3A2 partially restored amino acid levels and growth due to loss of GCN2. Our results indicate that select amino acid limitations activate GCN2 in PCa, resulting in the upregulation of key amino acid transporters, including 4F2 (SLC3A2), which provide for nutrient import to facilitate protein synthesis and metabolism required for PCa progression. We conclude that GCN2 and the ISR are promising therapeutic targets for both androgen-sensitive and castration-resistant prostate cancer.

Harnessing metabolic dependencies in pancreatic cancers

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Joel Encarnacion-Rosado*[1]and Alec Kimmelman[2]
[1]NYU Grossman School of Medicine, [2]NYU Grossman School of Medicine

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest types of cancer. A factor that contributes to the poor prognosis of the disease is the tumor microenvironment (TME).The PDAC TME is mainly composed of excessive fibrosis and desmoplasia, which creates a harsh environment resulting in hypoxia and altered nutrient availability.To promote survival and proliferation in this environment, PDAC cells reprogram glutamine (Gln) metabolism.Previous studies have demonstrated that PDAC cells use Gln to support proliferation and redox balance.Previous attempts to inhibit Gln metabolism using glutaminase inhibitors resulted in rapid metabolic reprogramming and therapeutic resistance.We hypothesized that using a glutamine analogue, such as 6-Diazo-5-oxo-L-norleucine (DON), could broadly target glutamine metabolism in PDAC and prevent rapid adaptation. Indeed, DON treatment led to a significant decrease in proliferation and various metabolites involved in central carbon, lipids and nucleotide metabolism, suggesting that DON creates a metabolic crisis . Additionally,we observed a significant decrease in tumor growth in various in vivo models (syngeneic,immunodeficient) using DRP-104 (sirpiglenastat), a novel pro-drug version of DON that was designed to circumvent DON associated GI toxicity and allow the therapeutic exploration of broad glutamine antagonism.Mechanistically, we found that ERK signaling is increased as a compensatory mechanism through receptor tyrosine kinase activity.Combinatorial treatment of DRP-104 and Trametinib(MEK1/2) inhibitor led to a significant increase in survival in a syngeneic model PDAC.These pre-clinical results suggest that broadly targeting glutamine metabolism could provide a new therapeutic avenue for PDAC and that the combination with an ERK signaling inhibitor could potentially further improve the therapeutic outcome.

Targeting inositol-requiring enzyme-1 (IRE1) affects triple-negative breast cancer chemotherapy sensitivity and prevents chemotherapy-related cardiotoxicity

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Yismelin Feliz Mosquea*[1], Kenysha Clear[2], Adam Wilson[3], Brian Westwood[4], David Soto-Pantoja[5], Katherine Cook[6]

[1]Wake Forest University School of Medicine, [2]Wake Forest University School of Medicine, [3]Wake Forest University School of Medicine, [4]Wake Forest University School of Medicine, [5]Wake Forest University School of Medicine, [6]Wake Forest University School of Medicine

Abstract: Triple-negative breast cancer (TNBC) is one of the most highly aggressive breast cancer types that predominately affect young and minority women. TNBC patients are more likely to receive cytotoxic chemotherapy regimens since they have limited targeted options. This results in severe side effects resulting in chronic cardiac dysfunction. Another issue compounded in the risk of developing cancer and chemotherapy-related toxicities is obesity. Obesity is associated with worse overall survival in women with TNBC. Inositol-requiring enzyme-1 (IRE1) is an arm of the unfolded protein response (UPR) pathway that plays a crucial role in tumor development. It has been shown that IRE1/XBP1 protein levels are upregulated in TNBC. To determine the role of obesity and IRE1 targeting on chemotherapy response and the development of therapy-related cardiac toxicity, female BALB/c mice were placed on control (low fat) and Western (high fat) diets and injected mammary gland tissue with 4T1-luciferase murine TNBC cells. Mice were treated with doxorubicin (DOX) with or without IRE1 blockade. Cardiac function was measured. Tumor and cardiac tissue was collected. We found that Western diet stimulates primary tumor growth, decreases DOX responsiveness, and potentiates cardiac dysfunction. Furthermore, we found that the combination of targeting IRE1 with DOX enhanced chemotherapy responsiveness in TNBC preclinical models. Moreover, DOX alone reduces cardiac function, but this effect was prevented by targeting IRE1. Also, IRE1 blockade reduces fibrosis in combination with DOX. Overall results suggested that systemic suppression of IRE1 protected cardiac tissue in mice treated with doxorubicin while enhancing anthracycline-mediated tumor killing.

Cancer Biology II

Regulation of the G2/M Cell Cycle Checkpoint by BRCA1

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Yanira Gonzalez-Rodriguez*[1]and Samuel F. Bunting[2]
[1]Rutgers University, [2]Rutgers University

Abstract: The onset of cancer is caused by mutations arising from unrepaired DNA damage. The G2/M cell cycle checkpoint reduces the risk of chromosome mutations by preventing cells with unrepaired DNA damage from entering mitosis. The tumor suppressor protein, BRCA1, is required for normal induction of the G2/M checkpoint, but it is not clear how BRCA1 activates the checkpoint. Based on the hypothesis that BRCA1 regulates the activity of specific signal transduction proteins that regulate the transition from G2 to M phase of the cell cycle, we measured the activity of checkpoint regulators after induction of DNA damage. B-lymphocytes derived from wild-type and BRCA1-mutant mouse spleens were treated with ionizing radiation to induce DNA double-strand breaks. The proportion of cells entering mitosis was quantified by flow cytometry, and the activation of DNA damage responses was analyzed by Western blotting of key signal transduction components. Our results show that Aurora-A kinase, a key protein that promotes the transition into mitosis, remains active after DNA damage in BRCA1-mutant cells. Measurement of mitotic cell populations revealed that Aurora-A hyperactivity in BRCA1-mutant cells correlated with a failure of the G2/M cell cycle checkpoint, allowing cells to enter mitosis even after DNA damage. We find that treating BRCA1-mutant cells with an Aurora-A inhibitor can rescue the G2/M checkpoint. Overall, our results demonstrate a novel mechanism for the regulation of cell division by BRCA1 and offer a potential opportunity for future clinical interventions to reduce cancer susceptibility in patients with BRCA1 mutations.

The role of chemotherapy-induced fibrosis in the maintenance of tumor initiating cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Omar Lujano Olazaba*[1], Emily Kogan[2], Mikella Robinson[3], Samuel F. Gilbert[4], Carrie D. House[5]
[1]San Diego State, [2]SDSU, [3]SDSU, [4]SDSU, [5]SDSU

Abstract: Ovarian cancer patients initially respond to cytotoxic chemotherapy but most relapse with chemoresistant disease. Research over the years supports the notion that tumor-initiating cells (TICs), a subpopulation of drug resistant stem-like tumor cells, are responsible for facilitating relapse and therapies targeting these elusive cells may prolong remission. Alterations of the extracellular matrix that facilitate adhesion of TICs is poorly understood in ovarian cancer, particularly following chemotherapy. Our preliminary data shows that fibroblast activation in response to cytotoxic chemotherapy leads to changes in ECM composition. Using ex-vivo decellularized peritoneum tissues from mice exposed to chemotherapy or vehicle treatment, we observed a 2-fold increase in growth in peritoneums pre-exposed to chemotherapy. We further show that TICs have activation of NF-kB signaling that regulates expression of integrins known to preferentially bind to these ECM proteins. NF-kB is a family of transcription factors that respond to signals in the tumor microenvironment to promote proliferation, chemoresistance, and survival. Therefore, we hypothesize that alterations in ECM proteins following chemotherapy permits TIC adhesion and growth through NF-kB mediated integrin expression. To investigate this hypothesis, we will explore the ECM proteins that are critical for adhesion and growth of ovarian TICs, identify if chemotherapy enhances production of these proteins, and test the role of NF-kB in mediating integrin-ECM adhesion of TICs to different substrates. These studies will uncover interactions between TICs and ECM through their unique expression of integrins and clarify the role of different NF-kB transcription factors in regulating TIC survival via integrin signaling.

Investigating "Taste Bud" Cells in the progression of Pancreatic Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Daniel Salas*[1]and Howard C. Crawford, PhD[2]
[1]University of Michigan and Henry Ford Pancreatic Cancer Center, Henry Ford Health System, [2]Henry Ford Pancreatic Cancer Center, Henry Ford Health System

Abstract: Pancreatic ductal adenocarcinoma (PDA) is a deadly disease with a 5-year survival rate of only 11%. Progression of the PDA is marked by the transdifferentiation of acinar cells into metaplastic ducts. Metaplastic tuft cells (MTCs) are a specialized subset of the metaplastic epithelium that is more commonly known in taste buds that allow the sensing of bitter, sweet, and umami substances. Studies have determined that MTCs have different roles depending on

where they reside. Interestingly MTCs are not present in the normal pancreas and are only present during PDA progression in both humans and mice. Furthermore, the population of MTCs in the pancreas disappears as PDA progresses into invasive carcinoma. We know little about the role of MTCs in the pancreas, but prior studies have suggested their role as a progenitor cell during PDA. We have generated a unique mouse model to drive lineage tracing of MTCs during PDA, and I have preliminary data to suggest that MTCs are not disappearing as PDA progresses but can transdifferentiate into Neuroendocrine Cells (NECs). Our collaborations with Dr. Rosalie Sears have led to a publication that investigates NECs, which are a highly aggressive cell type in PDA. The paper by Dr. Sears shows that Myc drives NE development in PDA. Our central hypothesis is that Myc is a driving factor in MTCs transdifferentiating into NECs and through our unique lineage trace mouse model we can trace MTCs into PDA development when we overexpress or knockdown Myc in MTCs specifically.

SIRT5 Inhibition Causes Increased Oxidative Stress and Impairs Tumor Growth and Metastasis

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Irma Fernandez*[1], Robert S. Weiss[2], Yashira Negron Abril[3], Jun Young Hong[4]
[1]Cornell University, [2]Cornell University, [3]Cornell University, [4]Cornell University

Abstract: Cancer cells undergo metabolic reprogramming to support the increased energy demand needed for their exponential growth. Consequently, targeting key metabolic enzymes has emerged as a potential avenue to selectively inhibit tumor growth. The mitochondrial sirtuin SIRT5 regulates protein post-translational modifications on metabolic enzymes by catalyzing the removal of succinyl, malonyl, and glutaryl moieties. SIRT5 is over-expressed in human breast cancers and other malignancies. We hypothesized that SIRT5 promotes breast cancer progression by facilitating metabolic reprogramming. SIRT5 knockdown in human cancer cells inhibited anchorage independent growth but had little effect on non-transformed cells. To examine how SIRT5 loss impacts tumorigenesis in vivo , we utilized MMTV-PyMT transgenic mice, which are prone to mammary adenocarcinoma and lung metastasis. Sirt5 KO MMTV-PyMT mice had increased survival, decreased tumor size, and reduced lung metastases, compared to Sirt5 WT MMTV-PyMT controls. SIRT5 KO cancer cells had higher levels of reactive oxygen species and displayed lower levels of important antioxidants such as NADPH and GSH. My results show that genetic SIRT5 disruption in breast cancer cell lines and mouse models caused increased succinylation of IDH2 and other metabolic enzymes, increased oxidative stress, and impaired transformation and tumorigenesis. Therefore, we developed potent selective and cell-permeable small-molecule SIRT5 inhibitors. Pharmacological inhibition of SIRT5 impaired mammary tumor growth in both transgenic and human breast cancer xenograft mouse models, with no apparent toxicity. Considering that Sirt5 KO mice are generally normal, with only mild phenotypes observed, these data establish SIRT5 as a promising therapeutic target for treating aggressive breast cancer.

Assessing the Role of Extracellular Matrix-Integrins in Metastatic Squamous Cell Carcinoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

John Aleman*
University of Colorado, Anschutz Medical Campus

Abstract: Patients with metastatic squamous cell carcinoma (SCC) have a dismal survival rate. Cancer stem cells (CSCs), and the extracellular matrix (ECM) associated with the tumor can increase metastasis. The role of the ECM protein laminin and its integrin receptors in affecting ECM rigidity, CSCs, and SCC metastasis are not completely understood. Our laboratory has generated mouse SCC driven by keratin15+ stem cells with Smad4 loss and Kras G12D mutation. Cells lines derived from these mice, despite arising from the same genetic background, have different metastatic abilities when transplanting back to recipients Using RNA-sequencing, I found that metastatic SCC cells have increased levels of laminin-binding integrins compared to their non-metastatic counterparts. Laminin-binding integrins, including integrins α4 and β6, and several laminins were higher at the protein level in metastatic HNSCC. Metastatic SCC cells were enriched in transforming growth factor-beta (TGFβ) signaling components and TGFβ inhibition significantly reduced the invasion of metastatic HNSCC cells in vitro . Additionally, while SCC cells cultured on a stiff ECM demonstrated increased invasion, those cultured on a soft ECM displayed increased CSC characteristics. My data suggest that metastatic SCCs increase laminin-binding integrin expression and deposit high levels of laminin to enhance metastasis, alter ECM rigidity, and increase CSC characteristics. I am currently investigating the functional role of these molecules and ECM rigidity in regulating metastasis, CSCs, and immune cell infiltration in vivo . Ultimately, these results will guide mechanistic and prognostic regulators of HNSCC metastasis and lead to superior treatment options.

Microbiology

Fungal communities experience rapid secondary succession during the first year following a wildfire in California chaparral

Discipline: Life Sciences
Subdiscipline: Microbiology

M. Pulido-Chavez*[1], Sydney I. Glassman[2], James W. J. Randolph[3], Cassandra Zalman[4], Loralee Larios[5], Peter M. Homyak[6]
[1]University of California, Riverside, [2]University of California, Riverside, [3]University of California, Riverside, [4]Chapman University, [5]University of California, Riverside, [6]University of California, Riverside

Abstract: The rise in wildfire frequency and severity across the globe has increased interest in secondary succession, how a community changes over time. However, despite the role of soil fungal communities in the regeneration of post-fire vegetation and biogeochemical cycling, the lack of measurements immediately post-fire and at high temporal resolution has resulted in a limited understanding of fungal secondary succession. However, there is evidence from pine forests that pyrophilous "fire-loving" fungi exist and dominate the post-fire environment. We hypothesize that these pyrophilous fungi drive fungal secondary succession. Thus, to investigate wildfire's immediate and temporal effects on fungal successional dynamics, we sampled soils at 17, 25, 34, 67, 95, 131, 187, 286, and 376 days after a Southern California wildfire in fire-adapted

chaparral shrublands, where wildfire is recognized as the initiator of plant secondary succession. We used qPCR of the 18S rRNA to assess fungal biomass and Illumina MiSeq sequencing of the ITS2 region to assess fungal richness and composition. Wildfire reduced fungal biomass by 86% and richness by 68%. Moreover, the burned fungal communities experienced rapid succession, with five compositional turnover periods. Analogous to plants, pyrophilous fungi increased post-fire and drove successional dynamics. Succession was initiated by the Basidiomycete yeast Geminibasidium, which traded off with the filamentous Ascomycetes Pyronema, Aspergillus, and Penicillium . Our unprecedented high-resolution temporal sampling captured post-fire fungal secondary successional dynamics and showed that putative tradeoffs in thermotolerance, colonization, and competition, among dominant pyrophilous fungi control fungal secondary succession with possible implications for ecosystem function.

Pseudomonas aeruginosa type IV pili-mediated directional motility enhances microbial competition

Discipline: Life Sciences
Subdiscipline: Microbiology

Andrea Sánchez Peña*[1]and Dominique H. Limoli[2]
[1]University of Iowa, [2]University of Iowa

Abstract: The bacteria Pseudomonas aeruginosa (Pa) and Staphylococcus aureus (Sa) coinfect the lungs of patients with cystic fibrosis. Given that their coisolation is associated with poor patient outcomes, understanding how interspecies interactions influence infections is important to increase treatment opportunities. Previously, we demonstrated that Pa moves towards Sa through type IV pili (TFP)-mediated motility. Here we studied the consequences of this attraction. Live single-cell confocal imaging was performed to visualize and measure Sa survival in coculture with Pa in a spatially structured environment. In the presence of wild type Pa , Sa multiplied and formed microcolonies, but as Pa approached, it invaded and dispersed the edges of Sa colonies, reducing colony size. We hypothesized that invasion of Sa colonies provides Pa a competitive advantage during coculture. Accordingly, a TFP-deficient Pa mutant (D pilA), was unable to invade and was significantly less competitive. Surprisingly, Sa colonies exhibited higher cell packing and colony edge thickness during coculture with D pilA than in monoculture. To determine if Pa uses a combination of motility and secreted antimicrobials for effective competition against Sa , we imaged Pa mutants unable to produce HQNO, pyoverdine, pyochelin, LasA, or combinations thereof. While loss of Pa antimicrobials improved Sa survival, Pa remained proficient at invasion and colony dispersal. We propose that Pa attraction towards, invasion, and dispersal of Sa colonies allows Pa to concentrate antimicrobials to maximize competition. These data reinforce accumulating observations that spatial structuring is a determinant of microbial community resilience during intection.

Spatial organization of phenotypically diverse bacteria during collective migration

Discipline: Life Sciences
Subdiscipline: Microbiology

Lam Vo*[1], Henry Mattingly[2], Thierry Emonet[3]
[1]Yale University, [2]Yale University, [3]Yale University

Abstract: Cell-cell variability in cell populations complicates treatments of cancer, infections, and diseases. Thus, it is crucial to understand how cell-cell variability modulates a population's behaviors. The project will address this problem by studying how a group of gut bacteria, Escherichia coli , coordinates collective migration despite having diverse swimming behaviors, or tumble biases. Our lab recently found that an isogenic, migrating group of E. coli cells spatially organize themselves based on their chemotactic abilities, allowing them to travel at the same speed. We hypothesized that this spatial organization enables communities of bacteria to adapt their migrations across different environments, but how physical properties of the environments affect this phenomenon is not yet determined. Here, we will report our efforts to determine how pore size affects the chemotactic abilities and spatial organization of swimming phenotypes during collective migration. Based on our mathematical equations of cell diffusion and chemotactic abilities, we predicted that cells with low tumble biases will lead in liquid environment, but cells with intermediate tumble biases will lead in porous environment. To experimentally test this prediction, we engineered fluorescent E. coli strains with titration systems of a tumble regulator, CheZ, and designed a novel microfluidic device to observe how groups of migrating cells with different tumble biases are spatially organized in two environments, agarose and liquid environments, under the microscope. Using these technologies, the goal is to combine our quantitative measurements and mathematical models to understand what enables communities of bacteria to effectively expand into and colonize new environments.

Interleukin-2 regulates the balance of Th1 and Tfh lineage commitment during acute viral infection

Discipline: Life Sciences
Subdiscipline: Microbiology

Krystal Charley*[1]and Matthew Williams[2]
[1]University of Utah, [2]University of Utah

Abstract: During acute viral infection, activated CD4 + T cells differentiate and expand to generate effector cells that help eliminate the pathogen. Upon resolution of infection, a small proportion survive and form long-lived memory T cells. Interleukin-2 (IL-2) drives T cell expansion by signaling through the high-affinity IL-2 receptor. Effector T cells expressing the high-affinity IL-2 receptor (IL-2Ra) are biased towards terminal Th1 differentiation, whereas T cells with low IL-2R expression give rise to T follicular helper T cells and memory T cells. We tested the hypothesis that continued IL-2 signaling to CD4 + T cells during the later stages of the response drives effector versus memory fate decisions via down-regulation of a transcription factor, TCF-1. We found that disruption of IL-2 signals to effector T cells prevented their terminal differentiation and promoted the formation of memory T cells, suggesting that IL-2 is a critical signal for T cell differentiation when T cells vary in their expression of IL-2Ra. Furthermore, sustained IL-2 signaling throughout the effector response was required for the emergence of effector cells that have lowered expression of TCF-1, a key transcription factor implicated in the differentiation of memory T cells. Disruption of IL-2 signaling also resulted in increased memory T cell formation. Inducible deletion of TCF-1 in effector T cells revealed both TCF-1-dependent and independent roles for IL-2 in suppressing the formation of Tfh cells. Overall, our results show that IL-2 plays a central role in specifying T cell survival, function and memory formation following viral infection.

Elucidating impacts of phosphate-driven root phenotypes during bacterial colonization of plants

Discipline: Life Sciences
Subdiscipline: Microbiology

Kevin Santiago Morales*[1]and Sarah Lebeis[2]
[1]Michigan State University, [2]Michigan State University

Abstract: Plants have evolved an extensive range of adaptations to allow successful proliferation as they are very susceptible to their immediate environment. The ability of plants to selectively choose bacteria to form part of its microbiota is one of such adaptations. Plant-associated microbes can affect plant development under stressful conditions, such as phosphorus (P) deficiency. P moieties inaccessible to plants are ubiquitous in soils and providing adequate amounts of P is a recurring concern in agriculture. We hypothesize that plant-associated microbes that can solubilize P will provide a benefit to plants grown under P deficiency, and that this behavior can be modulated within a bacterial synthetic community (SynCom). In this study, epiphytic (plant surface) and endophytic (within plant) bacteria from wild Medicago sativa (alfalfa) tissues were isolated and used to design a SynCom. Isolates were screened for activity of interest such as auxin hormone production, ability to use plant metabolites as carbon sources, and P solubilization. The model plant Arabidopsis thaliana (Arabidopsis) will be used to identify isolates that positively affect plant phenotype under P stress, which will be incorporated into the SynCom. Preliminary results have shown that a high number of alfalfa isolates are capable of solubilizing P, while a small number are capable of producing auxin. Using this approach, we aim to elucidate the mechanisms that mediate plant-microbe interactions when plants are grown under P deficiency and apply these into effective management of other crop plants.

Exploring The Functional Role Of A TetR Transcriptional Regulator In A Drug-Resistant, Non-Tuberculosis Mycobacterial Pathogen

Discipline: Life Sciences
Subdiscipline: Microbiology

Ronald Rodriguez*[1]and Sarah Stanley[2]
[1]University of California, Berkeley, [2]University of California, Berkeley

Abstract: Mycobacterium abscessus (Mabs) is an emerging, non-tuberculosis mycobacterial pathogen responsible for a wide variety of pulmonary and skin infections that are difficult to treat with standard antimicrobial chemotherapy. A better understanding of the cellular and molecular mechanisms associated with antibiotic resistance in Mabs is necessary for achieving better therapeutic success in the future. Mabs is highly resistant to nearly all anti-mycobacterial agents, a class of drugs with specific activity against mycobacterial species. Among these is Ethionamide (ETH), which is currently utilized as a second-line agent to treat drug-resistant tuberculosis infections. ETH inhibits mycolic acid biosynthesis, which are long chain fatty acids found on the outer membrane of mycobacteria. Mechanisms of ETH resistance remains unexplored in Mabs . Through whole genome sequencing of spontaneous ETH resistant mutants and screening a

library of transposon (Tn) mutants in the presence of ETH, we identified marR as a genetic determinant of ETH resistance. Deletion of marR (Δ marR) confers resistance to ETH. marR encodes for a member of the TetR family of transcriptional regulators, many of which have been implicated in anti-mycobacterial resistance in Mabs . Abrogating TetR activity in Mabs lead to upregulation of mmpS and mmpL genes, which encode for membrane proteins required for growth in the presence of anti-mycobacterial agents. We found that mmpS5 and mmpL5 were upregulated in Δ marR bacteria, suggesting these genes may play a role in ETH resistance. Future studies will focus on identifying mechanisms downstream of MarR that are associated with ETH resistance.

Animal Sciences/Zoology, Marine Sciences, & Plant Sciences/Botany

Description of seven new Exoprosopa (Diptera: Bombyliidae) species from Madagascar

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Alan Mata*[1]and Michelle Trautwein[2]
[1]Cornell University, [2]California Academy of Sciences

Abstract: Madagascar is an African island that is known for its biodiversity and for its many endemic species, which includes members of the Dipteran family Bombyliidae. Many Bombyliids mimic bees and wasps in appearance and behavior. They are also ectoparasitoids of various insects such as butterflies, beetles, grasshoppers, and even spiders. Bombyliids have a cosmopolitan distribution, with the exception of oceanic islands and Antarctica. The diversity within Bombyliidae is extensive, with over 5,000 species described worldwide. In the Afro-tropical region, there are 1,416 species described. In Madagascar alone, there are 18 species described which are distributed among 9 different genera. The majority of the Bombyliid diversity in Madagascar comes from the genus Exoprosopa , with 7 species described. Here, we describe an additional seven new Exoprosopa species from Madagascar that were found in the Type Collection at the Natural History Museum in London but were never described. Describing new species in Madagascar is essential because we are losing a lot of the diversity on the island due to heavy deforestation efforts. These massive deforestation efforts will prevent us from discovering new species, thus not understanding how diverse Bombyliids are in Madagascar.

Biodiversity catalogs reveal understudied organisms and geographic bias: a case study with the World Spider Catalog

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Jacob Gorneau*[1], Lauren A. Esposito[2], Franklyn Cala-Riquelme[3], Siddharth Kulkarni[4]
[1]California Academy of Sciences, [2]California Academy of Sciences, [3]California Academy of Sciences, [4]University of Wisconsin-Madison

Abstract: Biodiversity catalogs record the history of taxonomic work and are a guide for taxonomic and systematic works. Their digitization in recent decades has allowed for accessibility. Among invertebrates, spiders are one of the most diverse groups, with about 50,000 described extant species. The World Spider Catalog, started in 2000 by Norman I. Platnick, currently represents the largest taxonomic database of any animal group. These biodiversity data, paired with insights from genomic studies regarding higher-level classifications of spiders, provide a hotbed for species description, resulting in a best-case scenario for addressing the biodiversity crisis. Despite this, taxonomic bias may neglect groups that could benefit from further study, and result in an overabundance of taxonomic effort on others. We develop a taxonomic ratio relating new species descriptions to other taxonomic changes. We hypothesize families with a higher number of species descriptions relative to other taxonomic changes indicate more taxonomic effort may produce additional species, whereas if less species are being described relative to other taxonomic changes, it may suggest not as many species remain. Our results highlight spider families that warrant priority in species discovery, and trends over time and zoogeographic region assist in understanding the effects of new technologies and highlight disparities in more species-diverse areas, particularly in the Global South. This research serves to inform arachnologists in identifying high-priority groups for species discovery and more broadly, highlights the benefits of maintaining a taxonomic database for scientists studying biodiversity.

First Genomic Evidence of Viral Disease in the Scombrid Fish Family

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Savanah Leidholt*[1], Rebecca Vega Thurber[2], Emily Miller[3], Andre Boustany[4], Kyle Van Houtan[5], Tatiana Galvin[6], Alexander Norton[7], Mark Dasenko[8]
[1]Oregon State University, [2]Oregon State University, [3]Monterey Bay Aquarium Research Institute, [4]Monterey Bay Aquarium, [5]Monterey Bay Aquarium, [6]Oregon State University, [7]Monterey Bay Aquarium, [8]Oregon State University

Abstract: Aquaria and aquaculture facilities are powerful tools for conservation and sustainability for some of the world's most heavily harvested fish species. However, high densities among conspecifics lead to animal disease outbreaks in these settings. One long standing disease, Puffy Snout Syndrome (PSS), causes localized, collagenous tissue growths on the head and face in numerous fish taxa (tuna, mackerel, sardines, anchovies, trout) PSS is an intriguing disease that has thus far only been seen in captive held fish populations with extraordinarily high mortality rates when present. Despite this, little is known about the causative agent(s) of PSS and the immune response they elicit. Therefore, we leveraged metatranscriptomic data of symptomatic-captive, asymptomatic-captive and asymptomatic-wild Pacific Mackerel (Scomber japonicus) to evaluate PSS infections. Our aims were to 1) analyze genes and gene pathways active in the immune response to PSS and 2) annotate and characterize viral transcripts in order to identify potential causal agents. Host transcripts showed distinct differences between differentially expressed genes in wild and captive-held mackerel. Our analysis also revealed viral transcripts encoding for RNA-dependent RNA-polymerases within the samples, with higher abundance in symptomatic mackerel than asymptomatic mackerel. Our results provide the first genomic evidence for a viral disease agent responsible for PSS and offer insight into disease mitigation for aquaria and aquaculture facilities holding these fish taxa.

Intra-canopy leaf variation in deciduous oaks (genus Quercus): from leaf construction to energy return

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Claudia Juliana Garnica Diaz*[1], Siddarth Machado[2], Raiza Castillo-Argaez[3], Nicholas Smith[4], Daniel J. Johnson[5], Grace P. John[6]
[1]University of Florida - Gainesville, Florida, [2]University of Florida. School of Forest, Fisheries and Geomatics Sciences, [3]University of Florida. Department of Biology, [4]University of Florida. Department of Biology, [5]University of Florida. School of Forest, Fisheries and Geomatics Sciences, [6]University of Florida. Department of Biology

Abstract: The leaf economic spectrum (LES) is a framework used to explain coordination of leaf structure and metabolism. Yet, most studies employing the LES follow a sampling protocol that focuses on outer canopy leaves while ignoring variation through canopy positions (CP). Here, we characterized the impacts of the light on leaf structure across canopy positions and evaluated their functional implications on photosynthetic light responses and water relations. We sampled branches from sun-exposed and shaded parts of 30 canopy trees across five deciduous oak species at Lilly-Dickey Woods, Indiana. As oaks have expressed large variation in their leaf morphometrics in previous studies, we predicted that sun-exposed leaves would have more complex morphology and thicker lamina demanding construction costs. However, contrary to expectations from the LES, sun-exposed leaves would also have faster maximum rates of energy return due to greater investment in photosynthetic machinery. Our results suggest that structural and compositional traits varied significantly across species and CP, while traits associated with an investment in photosynthetic area change more based on species, than CP. Structural changes did not induce a significant difference in maximum photosynthetic assimilation. In terms of water movement, sun-exposed leaves maintained lower turgor loss points [tlp] (p-value<0.001), such that its shifts are likely a mechanism to maintain open stomata for evaporative cooling and gas exchange. Coordination of investment in photosynthetic machinery, structural support, and high osmotic potentials allow trees to maximize carbon assimilation and water status across light environments within the canopy outside of the constraints of LES tradeoffs.

Historical Multi-Environmental Trials Reveal Elite Grain Sorghum Hybrid Trends from 1970-2021

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Fabian Leon*[1], Lorin Harvey[2], William Rooney[3]
[1]Department of Soil and Crop Sciences, Texas A&M University, [2]North Mississippi Research and Extension Center - Pontotoc Branch Experiment Station, Mississippi State University, [3]Department of Soil and Crop Sciences, Texas A&M University

Abstract: Sorghum (Sorghum bicolor [L. Moench]) is among the most important cereal crops worldwide and is widely grown throughout diverse geographies and production schemes in Texas. Public and private breeding programs seek to maintain adaptation to these environments while increasing grain yield, which is the ultimate arbiter of hybrid performance. The objective of this work was to identify patterns in the breeding and testing of elite grain sorghum hybrids that

could be exploited to achieve genetic improvement. To assess these patterns retrospectively, Texas A&M AgriLife Research's Crop Testing program's data of multi-environment trials from 1970 to 2021 were analyzed. The trends depict a sinusoidal pattern of yield improvements since 2000 and outline a strong positive correlation between grain yield and plant height indicating a need for the adoption of taller hybrids. Plant height, days to flowering, exsertion, and testweight were all positively correlated to grain yield with greater correlations arising from rainfed trials. Additionally, a principal component analysis of Texas county-level environments was conducted to delineate ecoregions in Texas with similar environmental effects on hybrid performance. This approach clustered the Blacklands and Upper Coast regions together as the highest yielding environments and the Lower Valley and Panhandle regions as the poorest environments. The results suggest that the current delineation of distinct production regions is caused by available moisture and rainfall. Our results suggest that sorghum improvement priorities should include the adoption of taller hybrids and targeted breeding for specific drought scenarios which are the preeminent environmental factors affecting hybrid performance.

A Receptor-Like Proteins PAN2 is required for ABA and dark-mediated grass stomatal closure

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Le Liu*[1]and Michelle Facette[2]
[1]University of Massachusetts Amherst, [2]University of Massachusetts Amherst

Abstract: Stomata are small pores on the leaf surface of land plants that facilitate gas exchange. Grass stomata have fast stomatal responses, which may be associated with the dumbbell-shaped guard cells and lateral subsidiary cells. The fast movement of grass stomata might be part of the reasons why we see grass everywhere. Subsidiary cells are thought to reciprocally exchange water and ions with guard cells. However, the relative contribution of subsidiary cells and the mechanisms of how they contribute is unclear. To untangle the role of subsidiary cells in stomatal closure, we measured stomatal function in pan1 , pan2 , and pan1pan2, mutants. PAN2 and PAN1 are receptor-like proteins important for correct subsidiary cell formation.   To determine if the stomatal function of individual stomatal complexes is dependent on correct subsidiary cells' morphology, we measured stomatal aperture in different genotypes of plants treated with ABA. In all genotypes, stomata with abnormal subsidiary cells show closure defects in response to ABA. This is direct evidence that correct subsidiary cells are essential for closing the stomatal pore. We also found that PAN2 has a role in stomatal function other than PAN1. We will further do drought experiments to uncover the drought tolerance of the plants to dissect if subsidiary cells are contributing to the plant's drought tolerance. This work will provide insights into corn breeding.

Biochemistry & Genetics

Defining Pericytes as a Novel HIV Reservoir of the CNS

Discipline: Life Sciences
Subdiscipline: Biochemistry

Oandy Naranjo*[1], Silvia Torices[2], Olivia Osborne[3], Paul Clifford[4], Michael Stangis[5], Michal Toborek[6]
[1]University of Miami Miller School of Medicine, [2]University of Miami Miller School of Medicine, [3]University of Miami Miller School of Medicine, [4]University of Miami, [5]University of Miami Miller School of Medicine, [6]University of Miami Miller School of Medicine

Abstract: Successful antiretroviral therapy (ART) has significantly decreased the mortality and morbidity of individuals infected with HIV. Still, low levels of HIV replication persist in viral reservoirs and lead to immune activation and chronic inflammation. The CNS was thought to be protected from HIV infection. However, experiments on microglia and astrocytes indicated that these cells are all capable of active and latent viral infection. BBB pericytes have been shown to regulate brain paracellular and transendothelial fluid transport at the BBB, maintain homeostasis of the CNS microenvironment, and maintain BBB integrity. Additionally, a significant portion of BBB pericytes are derived from a myeloid origin which are cells known to be key players in HIV infection. We use a novel HIV reporter, named HIVGKO, that allows for purification of latently infected cells in absence of reactivation. Fluorescence-activated cell sorting was performed to isolate active, latent, and uninfected populations of BBB pericytes. Here we use ddPCR and RNAscope analysis to confirm that these cell populations are indeed capable of active and latent HIV infection. Transcriptome analysis indicates key differences in angiogenesis and cell cycle arrest pathways. Our data will help to understand the modulation of CNS viral reservoirs and provide key molecular targets in developing novel protective therapeutics for those suffering from HIV associated neurocognitive disorders.

The Lipid Bilayer's Role in Membrane Protein Folding and Function

Discipline: Life Sciences
Subdiscipline: Biochemistry

Citlayi Villaseñor*[1], Neha Kamat[2], Valentina Dimitrova[3], Alexandra Karagiaridi[4], Kristen Rivera[5], Heather Pinkett[6]
[1]Northwestern University, [2]Northwestern University, [3]Northwestern University, [4]Northwestern University, [5]Northwestern University, [6]Northwestern University

Abstract: Within cells, alpha helical membrane proteins are co-translationally folded from the ribosome into the lipid bilayer with assistance from translocons and insertases. To regulate proper folding, cells initiate stress response pathways. This homeostatic process results in an increase in chaperones, a reduction in RNA transcription, and enhanced transcript degradation. While mechanisms of this regulatory signaling are still under investigation, we understand even less about the role of the lipid bilayer in membrane protein folding and misfolding. To isolate the impact of the lipid bilayer’s biophysical properties on membrane protein folding, we use cell free protein expression which lacks translocons, insertases, and chaperones. The membrane protein we are studying is the nontypeable H. influenzae (NTHi) ABC transporter, SapABCDF. The SapABCDF transporter hydrolyzes ATP to deliver heme and antimicrobial peptides into the cytoplasm of NTHi. We use a vesicle flotation assay to measure protein incorporation into the membrane after cell free expression. Our results suggest that the membrane proteins of this complex incorporate into the membrane as confirmed by western blot analysis and lipid Rhodamine B fluorescence. These results are the first demonstration that a cell free system can be employed to express an ABC transporter. Future goals of this project are to measure the

biophysical properties of the vesicles added to these cell free reactions to determine how changing specific membrane properties affects expression, insertion, folding, and functionality of the SapABCDF complex. Understanding these relationships will help us uncover potential mechanisms of membrane protein folding and misfolding.

Alteration of NKX2.5-DNA Binding in Response to Non-Coding Genomic Variants

Discipline: Life Sciences
Subdiscipline: Biochemistry

Edwin Peña-Martínez*[1]and José A. Rodríguez-Martínez[2]
[1]University of Puerto Rico- Río Piedras, [2]University of Puerto Rico- Río Piedras

Abstract: Transcription factors (TFs) are sequence-specific DNA-binding proteins that can bind to regulatory regions of the genome. Mutations in TFs have been proven to alter how these proteins recognize and interact with our DNA, leading to many diseases. For example, variants of NKX2-5, a cardiac TF essential for heart development, have been associated with congenital heart diseases (CHDs). However, mutations within the non-coding genome and their associations with diseases like CHDs, have remained unexplored. Non-coding genomic variations affect how TFs recognize DNA and may disrupt TF-DNA binding. Using a position weight matrix (PWM) specificity predictive model, I can identify mutations predicted to impact NKX2-5 recognition. Using the ~84 million Single Nucleotide Polymorphisms (SNPs) reported in the 1000 Genomes Project, I identified 8,475 predicted to affect NKX2-5 binding. I found 901 SNPs localized in cardiac enhancers and 30 disease-associated SNPs from the GWAS catalog predicted to affect NKX2-5 binding sites. Finally, TF-DNA binding can be scored with the predictive model by comparing it with a reference genome. Variants rs7350789 and rs7719885 were predicted to have the most significant impact on TF-DNA binding affinity with ΔPWM scores of 258 and -212, respectively. These variants were prioritized for in vitro validation through Electrophoretic Mobility Shift Assay (EMSA) using full-length NKX2-5. After performing an EMSA, both variants resulted in differential TF-DNA binding. After successful in vitro validation, we will determine the impact of these variants on gene expression using a Luciferase reporter assay.

Signficance of Mitochondrial Fusion Proteins, MFN1 and MFN2, to form Unique Mitochondrial Structure in Retinal Photoreceptor Cells

Discipline: Life Sciences
Subdiscipline: Genetics

Angel Banuelos*[1], Akihiro Ikeda[2], Sakae Ikeda[3], Michael Landowski[4], Sam Grindel[5]
[1]University of Wisconsin-Madison, [2]University of Wisconsin-Madison, [3]University of Wisconsin-Madison, [4]University of Wisconsin-Madison, [5]Unviersity of Wisconsin-Madison

Abstract: Mitochondria, the energy generating organelles, dynamically undergo fusion and fission to take various forms in different cells. Mitochondrial dynamics have been linked to complex cellular processes such as metabolism, immune response, and cell death, but the exact relations between form and function are still unknown. Retinal photoreceptor cells, the energy intensive neurons that process light in the eye, are an excellent model for investigating the significance of mitochondrial form because they have a uniquely uniform arrangement of elongated mitochondria in the inner segments and one large mitochondrion in each of the presynaptic terminals. I hypothesize that the development and maintenance of mitochondrial form through mitochondrial dynamics is vital for sustaining photoreceptor health and function. In this project, I test this hypothesis using mice with photoreceptor cell-specific knockout of genes related to mitochondrial fusion and fission. I examine affected retinal phenotypes using immunohistochemistry, histological stains, high resolution microscopy, and a variety of analyses of specific mitochondrial functions. Preliminary results from rod photoreceptor cell specific knockout of the mitochondrial fusion proteins, MFN1 & MFN2, show fragmentation of mitochondria in rod cells is followed by extensive photoreceptor degeneration by adult age. This work provides novel insights into the regulation of mitochondrial form, the downstream influences of form change, and the link between dysfunctional mitochondrial dynamics and neurodegeneration.

Decoding the Epitranscriptome of Thermococcus

Discipline: Life Sciences
Subdiscipline: Biochemistry

Clayton Speed*[1]and Thomas Santangelo[2]
[1]Colorado State University, [2]Colorado State University

Abstract: From Microbes to man all organisms modify their RNA to change its chemical complexity and cellular functionality. 5-methylcytosine is a modification that alters the structure and half-life of ribosomal RNAs and tRNAs, but recent evidence has found that this modification is widespread across the transcriptomes of plants and humans. Our efforts focus on a new model organism Thermococcus kodakarensis which is a hyperthermophilic microbe, that extensively modifies its RNAs with 5-methylcytosine through a mechanism which is largely identical to that of humans. Using classic genetic manipulation and contemporary biochemical techniques we have mapped all sites of 5-methylcytosine in RNAs from cells which lack the conserved enzymes which encode the RNA methyltransferase writer proteins which install 5-methylcytosine on RNA. In this work we biochemically show that the NSUN family methyltransferase enzyme, TK2304, is a bona fide mRNA modifying enzyme. Through both Top-Down and Bottom-Up approaches we demonstrate that Tk2304 has expanded substrate specificity and selectively targets mRNA for 5-methylcytosine modification via in vitro methylation assays which rescued endogenous methylation capacity. This work lays the foundation to identify the necessary and sufficient sequence elements required to install 5-methylcytosine on mRNA, and thus decode the rules that Life uses to determine when, where, and how an RNA will be modified.

Ecology/Evolutionary Biology

Genomic traits of microbiomes from streams in the National Ecological Observatory Network

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Saeed Kariunga*[1]and Jane C. Marks[2]
[1]Northern Arizona University, [2]Northern Arizona University

Abstract: Genomic traits, genome size (GS) and GC content, provide insight into bacterial evolution and the selective mechanisms that shape microbial community composition. The structure and size of the genome affects rates of metabolism, growth and reproduction, which drive nutrient cycling. Nutrient limitation has been demonstrated to reduce the size of bacterial genomes and affect nucleotide composition. Although marine and soil microbiomes are well studied less research has been done on inland freshwaters. We processed 70 metagenomes from the National Ecological Observation Network (NEON) taken from 21 wadeable streams across the United States, to test how genomic traits vary across environmental gradients. The sequences were processed using a metagenomic bioinformatics workflow. We found a mean Genome Size of 5.5 Mbp and 53 % GC. Genome size was negatively correlated with both carbon and nitrogen concentrations, which we suggest is related to carbon use efficiency and nutrient limitation. Both genome size and GC content were positively correlated with temperature. These relationships indicate that both water chemistry and temperature induce selective changes in stream benthic microbiome characteristics.

Insecticide resistance reduces tolerance to multiple stressors in the Colorado potato beetle, Leptinotarsa decemlienata

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Erika Bueno*[1]and Dr. Yolanda Chen[2]
[1]University of Vermont, [2]University of Vermont

Abstract: In agroecosystems, insect pests are constantly under pressure from multiple sources of natural and anthropogenic stress. Exposure to multiple stressors has been demonstrated to improve insect performance, through a process known as cross-tolerance, where protective mechanisms in response to one stressor also provide protection against another form of stress. To address whether insecticide resistance primes insects to become cross-tolerant of other stressors, we examined phenotypic responses to single and combined stress exposure among resistant and susceptible Colorado potato beetles (CPB). Specifically, we conducted a full-factorial experiment with two temperature treatments (25 C and 40 C) crossed with two insecticide treatments (water-control and sublethal dose of imidacloprid). To get a comprehensive assessment of phenotypic impacts, we examined changes in mobility, herbivory, development, female fecundity, and mortality. Contrary to our expectations, resistant beetles were more sensitive to both single and combined stress than susceptible beetles, as demonstrated by reduced mobility and herbivory following stress exposure. Interestingly, developmental time and female fecundity were not significantly impacted by exposure to single and combined stress in both susceptible and resistant beetles. Overall, our findings demonstrate that selection towards insecticide resistance does not result in cross-tolerance between elevated temperature and sublethal insecticides. We speculate that physiological trade-offs associated with resistance may negatively impact the ability of insects to tolerate multiple stressors. Taken together, our results highlight the importance of understanding the interactive effects of multiple stressors on insect performance while revealing the impacts of insecticide resistance on stress tolerance in an economically important pest.

Evaluating and integrating genetics, GPS telemetry, and cameras to count cougars and bobcats in a temperate rainforest

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cameron Macias*[1], Kim Sager-Fradkin[2], Mark Elbroch[3], Jennifer Adams[4], Sara Cendejas-Zarelli[5], Lisette Waits[6]
[1]University of Idaho, [2]Lower Elwha Klallam Tribe, [3]Panthera, [4]University of Idaho, [5]Lower Elwha Klallam Tribe, [6]University of Idaho

Abstract: The Lower Elwha Klallam Tribe (LEKT) sets annual harvest regulations that differ from those of Washington State. Until now, however, no data had been collected on predator populations in the tribe's historic use area and we lacked information for setting sustainable harvest regulations and addressing long-term conservation concerns. To address this data gap, we are using a combination of noninvasive genetic sampling, GPS collars, and a camera grid to estimate cougar (Puma concolor) and bobcat (Lynx rufus) abundance on the Olympic Peninsula. First, we used scat-detection dogs to locate and collect felid scat samples across our 606 km 2 study area. Of the 665 scat samples collected during 2018-2020, we identified 168 cougar scats and 424 bobcat scats. We identified a minimum count of 27 individual cougars using 11 microsatellite loci. Genetic individual identification of bobcat samples is ongoing. Second, we equipped 14 cougars and 6 bobcats with GPS collars between 2018-2022 to estimate minimum counts using home range overlap estimation. Third, we deployed a 74-camera grid each summer during 2019-2021 to estimate cougar and bobcat abundance using space-to-event modeling. Next, we will build models that integrate data from each method to provide more precise abundance estimates, as well as evaluate the relative precision of estimates across individual methods. Moving forward, cameras can provide the LEKT with a noninvasive and cost-effective approach to long-term wildlife monitoring if we can demonstrate that cameras produce abundance estimates that are comparable to established enumeration methods.

Brassica tournefortii, an invasive plant species, tolerates more stressful climates in its invaded than in its native range

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Clarissa Rodriguez*[1], Loralee Larios[2], Janet Franklin[3]
[1]University of California, Riverside, [2]University of California, Riverside, [3]University of California, Riverside

Abstract: Biological invasions are one of the main drivers of global environmental change. Successful invasive species management is contingent on identifying areas that are vulnerable to invasion. Species distribution modeling can be used to create spatial prediction maps of suitable habitat for an invasive species, using occurrence records. However, for invasive species colonizing new territory and climate, the climatic niche (i.e. climate suitable for establishment) of the invader may not be stable, leading to inaccurate maps. We used Brassica tournefortii, a plant native to the Middle East and Northern Africa, that has been invading the Southwestern United States and Northern Mexico, as our model species. To quantify and model the species' niche in its home and introduced range, we used global occurrence records, climate, and soils data. We assessed the stability of its realized climatic niche and identified environmental factors that are most important in shaping the distribution of the species in its introduced range. Our models detected that Brassica tournefortii’s realized climatic niche is different between its native and introduced ranges, as only 79% of the niche was shared. Within the introduced range, Brassica tournefortii is experiencing a 29% niche expansion into a more resource-limited, arid climate compared to its native range, and 20% of climatically suitable habitat has not yet been occupied. Our results indicate that we may be underestimating areas at risk for invasion, and should include both native and introduced occurrence records to improve the accuracy of predictions used for invasive species management.

High-dimensional characterization of phototroph-heterotroph interactions

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Chandana Gopalakrishnappa*[1], Zeqian Li[2], Seppe Kuehn[3]
[1]University of Illinois at Urbana-Champaign, [2]University of Illinois at Urbana-Champaign and University of Chicago, [3]University of Chicago

Abstract: Interactions between phototrophic and heterotrophic microbes lie at the heart of global biogeochemistry, ecosystem productivity, and biofuel generation. These microbes are known to interact with each other via resource exchange and competition - Phototrophs provide organic carbon to heterotrophs and heterotrophs provide essential micronutrients to phototrophs while they compete with each other for inorganic nutrients such as phosphorus and nitrogen. However, we lack a quantitative understanding of how the chemical nature of the environment affects interactions between phototrophs and heterotrophs. To address this, we conducted experimental studies to assay interactions between the phototroph, Chlamydomonas reinhardtii , and the heterotroph, Escherichia coli as a function of five environmental parameters - pH, buffering capacity, and availability of three non-substitutable resources - carbon, nitrogen, and phosphorus. To aid this high-dimensional study, a high throughput droplet-based microfluidic platform that offers a way to rapidly construct thousands of environmental conditions was implemented. Using this platform, we have screened for interactions in our model phototroph-heterotroph system in ~500 environmental conditions, amounting to ~200000 microcosms on the microfluidic platform. Our results show that the parameters pH and buffering capacity control the interaction structure in phototroph-heterotroph communities. Further, the nature of the carbon source - glycolytic or gluconeogenic is also shown to alter the interaction structure via effects on environmental pH. These results are in contrast to the prevailing view that phototroph-heterotroph interactions are governed primarily by the exchange of and competition for resources. Our work presents a new view of how the chemical environment impacts phototroph-heterotroph interactions.

Effects of simulated soundscapes on calling in Cope’s Gray Treefrog

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

James Erdmann*[1]and Michael Reichert[2]
[1]Oklahoma State University, [2]Oklahoma State University

Abstract: Soundscapes, or the acoustic makeup of an environment, can play an important role in driving and constraining acoustic signaling across species. Animals can alter their signaling behavior to maintain effective communication in the presence of different acoustic backgrounds, but little is known about how these responses vary across the wide range of soundscapes present in nature. We explore this question in a population of Cope’s Gray Treefrogs (Hyla chrysoscelis) by performing a field playback experiment of simulated background noise derived from a variety of habitats the species could potentially be exposed to. These stimuli consist of spectrally averaged noises from a combination of natural, urban, forested, and grassland habitats. Preliminary results suggest that there are stimulus-specific responses, with frogs having lower calling efforts when exposed to stimuli incorporating more anthropogenic noise sources. Frogs show individual variation in the type of behavioral response, with some increasing calling effort while others cease calling, two distinct strategies to handle signal masking. These findings shed light on the level to which behavioral plasticity may play a role in explaining the geographical variation of mating signals, and highlight challenges of studying the acoustic adaptation hypothesis.

Ecology/Evolutionary Biology & Other Life Sciences

Evolutionary Responses to Contaminants

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Yeraldi Loera*[1]and Dr. Shane C. Campbell-Staton[2]
[1]Princeton University, [2]Princeton University

Abstract: In an increasingly polluted world, contaminants have become a significant threat to biological homeostasis and may be eliciting rapid evolutionary responses in exposed wildlife populations. In 1980, Lake Apopka, Florida, experienced a chemical spill releasing thousands of gallons of pesticide mixtures resulting in its classification as a superfund site. Many of these pesticides function as endocrine-disrupting chemicals (EDCs), which affect steroid hormone levels and signaling. The exposed native population of American alligators (Alligator mississippiensis) at Lake Apopka has consequently displayed widespread aberrant sexual development and a drastic decrease in population density following exposure. Surprisingly, the population rebounded a decade later despite the chronic multigenerational persistence of these pesticides in the environment. Despite extensive physiological studies describing the acute and long-standing effects of exposure, the potential role of natural selection in aiding population recovery at this site remains unknown. Using transcriptomic analyses, we aimed to fill this gap by describing changes in gene expression within the ovaries of exposed and unexposed alligators. We used ovarian samples from 14 juvenile alligators from the contaminated lake and 14 from a nearby control late for RNA sequencing. We then used a multitude of bioinformatic methods for analyzing the transcriptome at the specific gene level, and the modular level of genes to analyze changes in the genomic regulatory structure. We predict these studies will help inform our understanding of responses to contamination at the transcriptomic level and highlight signatures of natural selection that could have aided in the adaptation of population-level resilience to contaminants.

Laying the groundwork: Drivers of post-fire early-seral plant community trajectories in western Cascadia

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Liliana Rangel-Parra*[1], Madison M. Laughlin[2], Jenna E. Morris[3], Daniel C. Donato[4], Joshua S. Halofsky[5], Brian J. Harvey[6]

[1]University of Washington, [2]University of Washington, [3]University of Washington, [4]Washington Department of Natural Resources, [5]Washington Department of Natural Resources, [6]University of Washington

Abstract: As climate warms and fire potential increases, understanding the dynamics of early-seral forest communities— post-disturbance plants that dominate prior to canopy closure— is of increasing importance . Early-seral forest communities are often high in biodiversity and ecosystem service provisioning, and they lay the groundwork for long-term forest trajectories. Western Cascadia (west of the Cascade Crest in Washington and northern Oregon) is characterized by infrequent, large, and severe wildfires, and recent fire events provide a key window to study early-seral forest community dynamics. In this study, we ask: How do post-fire early-seral plant communities 1) compare to pre-fire plant communities, and 2) vary across levels of pre-fire stand age, fire severity, and topoclimate conditions? We used a network of 86 long-term monitoring plots within recent fires (2015-2018) where we recorded general plot characteristics and percent cover of all herbaceous and woody plants to calculate community indices (e.g. , richness, diversity) and composition. Overall, we documented approximately 250 species across all study fires in the region. Preliminary results highlight that pre-fire stand age is a strong driver of community richness and diversity. Burn severity alone may be less important than pre-fire stand age, but may interact with pre-fire stand age to shape post-fire plant communities. Pre-fire stand age at time of fire may provide a template for species composition prior to burning, structural refuge or exposure after burning, or range in mechanisms of post-fire population recovery. These ongoing analyses provide key insights into early-seral dynamics and forest community trajectories after wildfire.

Population genomics and demographic history of Golden Dorado (Salminus brasiliensis) across their geographic range

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Nadia Fernandez*[1], Andy J. Danylchuk[2], Lisa M. Komoroske[3]

[1]University of Massachusetts Amherst, [2]University of Massachusetts Amherst, [3]University of Massachusetts Amherst

Abstract: The Neotropical region of South America contains the highest biodiversity on the planet, yet we have limited knowledge of the biology, ecology, and evolutionary history of many of the species inhibiting this area. Given that this region of the planet is facing immense anthropogenic pressures, basic fundamental knowledge of these species is critical for understanding how they will respond to disturbances and how we can mitigate such effects. Golden dorado (Salminus Brasiliensis) and its sister clade is a Neotopical fish species with a wide geographic distribution, making it a good candidate species for understanding how populations are connected and their populations dynamics through space and time. Therefore, we aim to understand their contemporary population structure and their historical populations' demography (over the past thousands of years). We utilize citizen science and genomic approaches which include assembling a high-quality reference genome and conducting population-level genomic sequencing throughout the wide distribution of Golden Dorado. Our preliminary results indicate relatively average levels of heterozygosity, and we expect to find a) genetic differences of populations across their distribution, especially at large hydroelectric dams and b) fluctuations of population sizes and connectivity relative to major geological events that influenced the hydrological regimes of South America. Examining how fish populations respond to major events both in deep time and on contemporary timescales will give us a greater understanding of a) the evolutionary drivers in Neotropical fish species, and b) how freshwater fish populations may respond to increasing human-mediated pressures.

Using diving performance to explain changes in foraging ecology over ontogeny in the Lake Chapala Garter Snake (Thamnophis eques obscurus)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Elsie Cecilia Carrillo*[1]and Dr. Rita S. Mehta[2]
[1]University of California, Santa Cruz, [2]University of California, Santa Cruz

Abstract: Ontogenetic shifts, or changes from birth to adulthood, play an important role in snake foraging ecology. Some snakes experience ontogenetic shifts in diet, reflecting their ability to capture and consume prey, including some garter snakes that switch from feeding on terrestrial prey as a juvenile to more aquatic prey as an adult. We question whether there are physiological or behavioral changes over ontogeny that facilitate dietary shifts in two closely related juvenile semi-aquatic garter snakes, which are excellent models for studying diving performance. For our comparison, we selected the Lake Chapala garter snake (Thamnophis eques obscurus) which is more aquatic, and the checkered garter snake (Thamnophis marcianus marcianus) which is more terrestrial. As a proxy for foraging behavior, we will quantitatively compare three diving performance metrics over the first year and half of life including: 1) breath-hold duration via submersion in a PVC tube, 2) decreased heart rate percentage upon submersion via a fetal doppler and conducting gel placed over the heart, and 3) burst swimming speed across a small wading pool. We hypothesize that foraging behavior changes over ontogeny as snakes gain competency in prey acquisition due to changes in diving performance. Specifically, we predict that each diving performance metric will increase over ontogeny, with the more aquatic Lake Chapala garter snake experiencing the greatest performance increase across each measure. This study will allow us to determine whether dive metrics change over ontogeny, and ultimately help explain ontogenetic changes in diet in semi-aquatic garter snakes.

Understanding ecological patterns among wolf-like canids of the Southern Great Plains through isotopic methods

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Celine Cortes*[1], Kent Smith, Ph.D.[2], Nicholas Czaplewski, Ph.D.[3], Leland Bement, Ph.D.[4]

[1]Oklahoma State University-Center for Health Sciences, [2]Oklahoma State University-Center for Health Sciences, [3]Sam Noble Museum of Natural History, [4]Oklahoma Archaeological Survey

Abstract: Human persecution of North American wolf-like canids (subfamily Caninae, genus Canis) has severely reduced their range and diversity. This is notably evident in the Southern Great Plains of the U.S., spanning Oklahoma, Texas, and New Mexico. Prior to roughly 1950, this region supported the now extinct Great Plains wolf, in addition to the locally extinct gray wolf and red wolf. The Mexican wolf is restricted to sparse releases and recovery program area in New Mexico, and current diversity is largely comprised of the coyote and domestic dog. As interspecific antagonism and competitive exclusion are known to affect behavior and resource access, diversity fluctuation poses important ecological questions. Were niche partitioning or dietary shifts employed to reduce competition during historical overlap? Following wolf eradication, have coyotes overtaken the “wolf niche?” To address these questions, we isotopically analyzed adult skeletal elements from institutional collections. Specimens were grouped by taxon, subregion, and collection date. Analyses included radiocarbon dating for chronological age of historical specimens, and stable carbon (13 C) and nitrogen (15 N) isotopes for dietary composition and relative trophic position, respectively. Radiocarbon dating revealed ages 385 to 125 +/- 15 years before present. Preliminary stable isotope data demonstrated no significant differences in pre-1950 and post-1950 coyote values. Unchanged dietary composition and trophic position could be due to insufficient temporal coverage or human influences. Additional specimens are currently being analyzed and will bolster temporal, geographic, and taxonomic coverage. These data will contribute to conservation evaluations surrounding threatened North American canids.

Neurosciences, Genetics, & Other Life Sciences

Alpha-tubulin mec-12 and TRPV channel osm-9 are required for amphid sheaths’ response to nose touch in Caenorhabditis elegans

Discipline: Life Sciences

Subdiscipline: Neurosciences

Tope Awe*[1], Andres Vidal-Gadea[2], Jessica Adams[3], Dayton Oblinger-Hammond[4]
[1]Illinois State University, Normal, IL, [2]Illinois State University, [3]Illinois State University, [4]Illinois State University

Abstract: Neuroglia (Glia) are typically considered to be supporting cells for development of neurons and synaptic transmission. These supportive roles in sensory and synaptic transmission have been thought to occur through the maintenance of neuronal morphology. However, recent studies are showing that glia can respond to sensory stimuli in a cell-autonomous manner. This suggests that glia play a more active role in the modulation and integration of sensory stimuli. In Caenorhabditis elegans (C. elegans), the amphid sheath glia (AMsh) has been shown to respond to hard touch and aversive odorants independent of the ASH neuron known to detect these stimuli. However, the mechanoreceptor responsible for the detection of the hard touch stimulus in AMsh remains unidentified. Here, I used RNA interference and calcium ratiometric imaging techniques to screen for genes required for the response of AMsh glia to nose touch in C. elegans . Global RNAi knockdown of mec-12 and osm-9 genes one at a time resulted in attenuated

response of AMsh to touch stimulus on the nose of C. elegans . It remains unclear how the two genes interact to mediate touch response of the amphid sheath glia in C. elegans .

Prefrontal parvalbumin interneurons support neural encoding during behavioral adaptation in mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

Carlos Johnson-Cruz*[1]and Vikaas Sohal[2]
[1]University of California, San Francisco, [2]University of California, San Francisco

Abstract: Rodents, primates, and humans use their medial prefrontal cortex (mPFC) to adapt behavior to changing environments. Inhibitory cells in the mPFC expressing parvalbumin, or parvalbumin-positive interneuron (PVIs), are important when adopting new behavioral strategies in cognitive tasks. Their specific role in shaping the activity of mPFC neurons during cognitive flexibility is little understood.To study this, we used a transgenic mouse line with impaired cognitive flexibility due to disrupted PVI development. Using one-photon micro-endoscopic calcium imaging, we record single-cell neural activity in the mPFC of these mice before and after they receive a drug improving their performance on a task requiring cognitive flexibility. We observe that this behavioral rescue coincides with changes in the single-cell and population-level neural activity. Post-treatment, individual neurons increase the strength of their response to different phases of the cognitive task. Neural representations of different task features increased their distinctiveness in mutant mice after treatment. Understanding the neural correlates of cognitive impairments associated with interneuron deficits could help better target treatments for psychiatric disorders like schizophrenia that affect parvalbumin-positive interneurons.

Clinical and Molecular Consequence of Respiratory Syncytial Virus (RSV) Genetic Diversity in Chicago, Illinois

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Estefany Rios Guzman*[1], Lacy M. Simons[2], Taylor J. Dean[3], Ramon Lorenzo Redondo[4], Egon A. Ozer[5], Michael G. Ison[6], Judd F. Hultquist[7]
[1]Northwestern University, Feinberg School of Medicine, [2]Division of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA., [3]Division of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA., [4]Division of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA., [5]Division of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA., [6]Division of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA., [7]Division of Infectious Diseases,

Northwestern University Feinberg School of Medicine, Chicago, IL 60611, USA. 2 Center for Pathogen Genomics and Microbial Evolution, Northwestern University Institute for Global Health, Chicago, IL 60611, USA.

Abstract: Respiratory Syncytial Virus (RSV) is a single-stranded, negative-sense RNA virus that is a major cause of global acute respiratory tract infections (ARTIs). Among infants, RSV results in nearly 34 million severe ARTIs annually and it is similarly responsible for large disease burdens in vulnerable adult and immunocompromised populations. While some studies have associated RSV serotype with disease severity in children, it is unclear if the same holds in adult populations and what the mechanism underlying this association might be. Here, we hypothesize that differences in RSV genotype are associated with differences in disease severity and presentation in adults. To test this hypothesis, we will assess the viral load and genetic diversity across a cohort of adult patients diagnosed with RSV and test for association with clinical and demographic data extracted from electronic health records. Of the 402 residual clinical RSV+ specimens (i.e. nasopharyngeal swabs) collected, 127 RSV genomes have been sequenced using an optimized amplicon-based strategy for Illumina next-generation sequencing. Phylogenetic analysis illustrates a temporal selective pressure on RSV genetic diversity. In addition, the 2021-2022 RSV season is RSV-B predominant, which differs from the 2019-2020 RSV season. These data will be integrated with our extracted clinical and demographic data to assess genotype-specific correlations. Future studies will focus on mechanistic interrogation of RSV genetic differences associated with higher disease severity or worse patient outcome, including viral entry and immune evasion assays. Ultimately, this work will expand mechanistic and epidemiologic understanding of RSV pathogenesis with clinical applications to hospitalized adult populations.

Analysis of conditional colocalization relationships and hierarchies in three-color microscopy images

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Jesus Vega*[1], Bruno da Rocha-Azevedo[2], Aparajita Dasgupta[3], Khuloud Jaqaman[4]
[1]University of Texas Southwestern Medical Center, [2]University of Texas Southwestern Medical Center, [3]University of Texas Southwestern Medical Center, [4]University of Texas Southwestern Medical Center

Abstract: Colocalization analysis of multicolor microscopy images is a cornerstone approach in cell biology . It provides information on the localization of molecules within various subcellular compartments and allows the interrogation of known molecular interactions in their cellular context. However, almost all colocalization analyses are designed for two-color images . This limits their applicability and the type of information that they reveal, leading to underutilization of multicolor microscopy images . Here we describe an approach , termed “conditional colocalization analysis,” for analyzing the colocalization relationships between three molecular entities in three-color microscopy images . Going beyond the question of whether colocalization is present or not, it addresses the question of whether the colocalization between two entities is influenced, positively or negatively, by their colocalization with a third entity. We benchmark this novel approach and showcase its application to investigate receptor-dowstream effector colocalization relationships in the context of functionally relevant plasma membrane locations.

Vibrio parahaemolyticus O3:K6 ecotype displays increased cold sensitivity due to chromosomal recombinations

Discipline: Life Sciences
Subdiscipline: Microbiology

David Silva*[1], Dr. Jeffrey Turner[2], Hailey R. Wallgren[3], Jordan Wolfkill[4], Boris Ermolinsky[5], Daniele Provenzano[6]
[1]Texas A&M University Corpus Christi, [2]Texas A&M University Corpus Christi, [3]Texas A&M University Corpus Christi, [4]University of Texas Rio Grande Valley, [5]University of Texas Rio Grande Valley, [6]University of Texas Rio Grande Valley

Abstract: Vibrio parahaemolyticus is the leading cause of gastroenteritis worldwide, partly as a result of clonal expansion of the highly pathogenic O3:K6 serotype. Genomic analysis of environmental V. parahaemolyticus O3:K6 strains isolated from the Pacific Northwest (PNW) led to the discovery of a novel ecotype harboring a deletion of seven genes (VP1884 through VP1890), all of which have been found previously to be upregulated upon bacterial culture at cold temperatures. This is noteworthy because, in the PNW, the virulent O3:K6 has been displaced by the O4:K12 serotype as the principal cause of V. parahaemolyticus gastroenteritis, perhaps as a result of its inability to survive on ice upon seafood harvest. Allelic exchange with the lacZ reporter gene from V. cholerae and the tetR selection marker from pBR332 was employed to generate VP1884-VP1890 null clones in clinical V. parahaemolyticus RIMD 2210633 and BAA-238 strains to test the hypothesis that this set of genes affects bacterial viability at cold temperatures. The VP1884-VP1890 mutants grown at 10°C displayed impaired growth kinetics compared to their WT counterparts. Similarly, survival of the mutant strains at 4°C was severely affected compared to WT counterparts. The rationale for undertaking these experiments is to uncover the molecular underpinnings that reveal the comparative lack of gastroenteritis caused by O3:K6 serotype in the PNW compared to other locations worldwide. The significance of the project is global because selection temperature sensitivity in Vibrios is likely caused by environmental conditions but also by public health measures and seafood handling practices characteristic of the PNW.

Examining perspectives of researchers regarding genetic research on the Navajo Nation

Discipline: Life Sciences
Subdiscipline: Genetics

Carissa Sherman*[1], Katrina Claw[2], Nanibaa' Garrison[3]
[1]University of Colorado, Anschutz Medical Campus, [2]University of Colorado, Anschutz Medical Campus, [3]University of California, Los Angeles

Abstract: The Navajo Nation is reevaluating a moratorium on genetic research that was put in place in 2002. While the moratorium was instituted because of cultural concerns and a lack of genetic research policies, there is still limited empirical work assessing the perspectives of Navajo people and other stakeholders regarding genetic research. To address this gap, this project aims to examine the perspectives of principal investigators (PIs) with Navajo Nation Human Research Review Board (NNHRRB)-approved projects on hypothetical genetic research. An online survey with both qualitative and quantitative questions was designed to characterize current NNHRRB-approved projects and to investigate if and how a genetic component might be added if the

moratorium was lifted. Researchers with a biological aspect to their project were invited to participate (n=70) in the survey. Survey respondents (n=29) included 31% Navajo PIs and 69% non-Navajo PIs. 54% of respondents (n=20) collected human samples (e.g., blood, etc.) as a part of their projects. Our results show that if the moratorium on genetic research ended, 44% of respondents (n=16) were unsure about adding a genetic component to their projects, while 28% (n=10) of respondents were interested in adding a genetic component. We characterized a hypothetical genetic research dimension to NNHRRB-approved projects to offer perspectives from the scientific workforce for tribal leaders to consider regarding the moratorium and a possible future genetic research policy. However, further study is needed to understand the potential barriers, benefits, and ethical and cultural considerations from the Navajo people.

Traditional Knowledge

Therapeutic Efficacy of Alpha 7 Nicotinic Acetylcholine Receptor Positive Allosteric Modulator in an Ischemic Stroke Model

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Katherine Hernandez*[1], Sterling Ortega[2], Kaitlyn Bambino[3]
[1]University of North Texas Health Science Center, [2]Associate Professor, [3]Research Technician

Abstract: Stroke is a leading cause of disability and the fifth leading cause of death. The risk of stroke increases with age and females exhibit more severe stroke outcomes than men. Women have unique risk factors which drastically increases their risk of a stroke during pregnancy, menopause, and in advanced age making stroke a health disparity. Currently, alteplase is the only FDA approved drug used to dissolve the clot. However, it has a short window for treatment efficacy, thus making the discovery of new drugs for stroke treatment important. Alpha7 nicotinic acetylcholine receptors (a7-nAChRs) are found ubiquitously in neuronal and immune cells. Studies have shown that PNU12059 (PNU), a positive allosteric modulator (PAM) of a7-nAChRs, promotes cognitive function and modulates the immune system to be anti-inflammatory in young animals. Using the middle cerebral artery occlusion (MCAO) stroke model, we hypothesize that PNU will reverse neurological function in MCAO aged mice. In addition, PNU will promote neuroprotection by inhibiting stroke-induced inflammatory neuropathological immune cells. This presentation will show data in both male and female mice at 8-12 weeks old and 18-20 months of age after treatment with 3 doses of PNU. Results will be shown on the changes in motor function using rotarod and cognition using Y-maze. Infarct volume will be evaluated using coronal brain sections stained with 2,3,5-triphenyl tetrazolium and Fluoro-Jade. Immunological data of the different inflammatory cytokines (IL-6, TNF-alpha, IL-1) will be shown, alongside with evaluations of IL-17 infiltration of the ipsilesional brain parenchyma.

Indigenous Community Needs at the Forefront: The Tao People of Lanyu

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Maricela Arce*[1]and Eric Hadley-Ives, Ph.D.[2]
[1]University of Illinois Springfield, [2]University of Illinois Springfield

Abstract: Taiwan is home to many Asia-Pacific Indigenous tribes including the Tao people who live on Lanyu (Orchid Island), which is located southeast of the main island. Currently, the Tao people are facing health, infrastructure and cultural dangers. Due to a nuclear waste site located on Lanyu, island residents are developing health issues; given the proximity of Lanyu to the nearest main land, the Tao people lack of reliable transportation and medical services; as a result of tourism influx, Indigenous cultural practices routinely are disregarded, disturbed and disrespected. Using information gathered from interviews and personal interactions, this project aims to provide awareness of the depth of the challenges Tao people face and present the proposed potential solutions which will lead to their better quality of life.

About SACNAS & The National Diversity in STEM Conference

The largest multidisciplinary and multicultural STEM diversity event in the country, 2022 SACNAS – The National Diversity in STEM Conference serves to equip, empower, and energize participants for their academic and professional paths in STEM. From October 27 to 29, 2022, college-level through professional attendees are immersed in cutting-edge scientific research and professional development sessions, motivational keynote speakers, a Graduate School & Career Expo Hall, multicultural celebrations, and an inclusive and welcoming community of peers, mentors, and role models. The conference is a training ground for the next generation of diverse STEM professionals, aiming to level the playing field for first-generation college students of color through mentorship, professional development, and networking opportunities. For more information, visit www.sacnas.org/conference. The conference is hosted annually by SACNAS (Society for the Advancement of Chicanos/Hispanics & Native Americans in Science). For over 49 years, SACNAS has served as an inclusive organization dedicated to fostering the success of Chicano/Hispanics & Native Americans, from college students to professionals, in attaining advanced degrees, careers, and positions of leadership in STEM.