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Summer Research Fellowship

Book of Proposals

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July 15, 2016

Dear UGA Faculty and Students,

We are delighted and honored to recognize this year’s CURO Summer Research Fellows, each of whom is featured here with a summary of his or her faculty-mentored research proposal. The goal of the CURO Summer Research Fellowship is to provide opportunities for intensive, immersive, faculty-mentored research experiences for academically talented undergraduates. The program advances the students’ knowledge and abilities to think critically, solve problems, and contribute to a greater understanding of the world.

We are proud of the accomplishments of present and past CURO Summer Fellows and with the mentorship provided by our exceptional faculty. The Summer Fellowship program has contributed to building a culture of undergraduate inquiry at the University of Georgia, and the CURO Summer Fellows serve as ambassadors, sharing their enthusiasm and expertise in a variety of professional forums on campus as well as at regional, national, and international meetings.

The 2016 CURO Summer Research Fellowship is funded through the Honors Program, the Office of the Senior Vice President for Academic Affairs and Provost, and the Alumni Association.

Please join us in congratulating these young scholars on the occasion of being awarded these prestigious fellowships. Please join us also in thanking the faculty research mentors whose support and guidance are crucial to the CURO Summer Fellows’ success.

Sincerely,

Dr. David S. Williams, ’79, ’82
Associate Provost and Director

Dr. Martin P. Rogers, ’01, ’11
Associate Director
Density-Dependent Selection Model for the Sociality of *Ceratina (Neoceratina) australensis*

Alison Adams; Mentor: Dr. David Hall, Genetics

Natural selection is acting every minute of every hour of every day. However, evolutionary responses to natural selection that are substantial enough to be measured can take long times, measured in tens to thousands of generations. For this reason, evolutionary ecologists often turn to mathematical models to test hypotheses. The proposed research will use a mathematical modeling approach to test a recent hypothesis concerning the evolution of sociality in a diminutive bee.

Dr. Sandra Rehan at the University of New Hampshire studies the social evolution and genetics of bees. Much of her recent work has focused on *Ceratina (Neoceratina) australensis*, the Australian small carpenter bee. This species is socially polymorphic with both solitary and social nests collected in the same populations. Nests can only be scored after they are collected in dead broken stems of giant fennel (*Ferula communis*) in southern Queensland, Australia. Stems are split lengthwise to reveal the nest and then the numbers of adult females present are counted. Solitary nests contain a single adult female bee and social nests contain two adult females. Interestingly, solitary nests tend to do better per female than social nests, but only when a parasitic wasp is absent. When the wasp is abundant, solitary nests suffer high levels of parasitism and loss of brood. Rehan’s research has led her to believe that cooperative brood care (“social nests”) is “more likely a product of latent genetic tendency for dispersal” and there is a “density-dependent selection maintaining the polymorphism of solitary dispersers and social non-dispersers.” The density dependence is hypothesized to be generated by the parasitic wasp: when solitary nests are dense, the wasp increases in numbers, which leads to an advantage for social nests and vice versa. Dr. Rehan initiated collaboration with Dr. Hall to address this hypothesis, since he has extensive experience using mathematical models to address evolutionary questions.

This summer, I will develop several mathematical models that capture the biology of this system. I will begin with density-dependent model for the interaction of the two types of female bees (social and solitary) and the wasp. The model will predict, using field data from Dr. Rehan for realistic parameter value estimates, the number of social and solitary nests in a population. Two important parameters that the model will incorporate are the rate of parasitism and the fitness cost of parasitism as they are expected to have important affects on the social-solitary nest balance. One prediction is that there will be parameter values where cyclic dynamics will occur because as the number of social nests increases, the rate of parasitism will decline, which will favor solitary nests. However, we also predict that a stable equilibrium will be possible for some parameter values as that is observed in nature. The model will be written to show the fluctuations in both the nests and parasitism, ultimately being used to find equilibrium.

After becoming familiar with modeling and analytical techniques on this first set of models, I will extend the models to include genetic variation in the bees for probability of being social versus solitary. I will then find the level of sociality favored at equilibrium for different parameter values. This work will allow us to test an evolutionary hypothesis in a mathematical framework.
Proposals

Structure from Motion and Ocean Color Analysis with Low-Earth Orbit Satellite Systems

Caleb Adams; Mentor: Dr. Deepak Mishra, Geography

The primary goals of the M.O.C.I Satellite mission are to provide 3D terrain modeling of the Earth’s surface using space based photogrammetry and to determine effective data compression and transmission techniques while training undergraduate students in STEM related fields. The secondary goals will investigate coastal phenology and land cover as well as off coast harmful algal blooms from river runoff. It will be used to monitor coastal water quality (phytoplankton, inorganic sediment, and colored dissolved organic matter) and the health and productivity of coastal wetlands. Monitoring these systems is important due to their ecological/economic productivity and vulnerability to human pressure and climate change. This proposal follows the University Nano-satellite Program’s objective to promote innovative partnerships among academia and industry in response to the White House STEM Education Plan by building and fostering learning through the development of curriculum and techniques to prepare students for the industrialized workforce.

The primary goal of the D.A.W.G. Satellite mission is to develop and operate the first moderate resolution coastal ecosystem and ocean color CubeSat with a focus on Earth science applications. The mission will generate multispectral moderate resolution imaging products to monitor coastal wetlands status, estuarine water quality, and near-coastal ocean productivity in compliance with National Aeronautics and Space Administration’s strategic objective of advance knowledge of Earth as a system to meet the challenges of environmental change and to improve life on our planet. The data will be used to monitor wetland biophysical characteristics and phytoplankton dynamics in estuarine and near shore waters. We will utilize a spectral imager to acquire image data between 400 and 800 nm. We will also use a Red, Green, and Blue light camera to perform experimental depth measurements and structure from motion from Low-Earth Orbit. The 3U CubeSat will contain all relevant flight systems such as Attitude Determination and Control System, 2.4 GHz radio band used for data transmission and radio bands used for commands/telemetry communications, a Micro-controller Unit, as well as power and thermal dispersion. We have partnered with NASA Ames for testing of the payload and communications. The proposed CubeSat will be delivered and subsequently deployed from the International Space Station via a Japanese H-II Transfer Vehicle, Russian Soyuz, or Commercial Cargo vessel under NASA CubeSat Launch Initiative.

We have begun the research and development of the hardware components necessary for both satellites and will begin development of our Attitude Determination and Control System, Electronic Power Supply, and Micro-controller Unit over the summer of 2016. During this research process we will develop many new capabilities for the University of Georgia such as space rated solar panel testing equipment, space-like environmental vacuum chambers, Helmholtz coils to test magnetic and gyroscopic control systems, orbital mechanics simulation software, and a potential UHF/VHF (ultra and very high frequency) ground station for Low-Earth Orbit communications. I will be actively involved in leading the research for all of the above capabilities. The research that
these missions provide will push UGA’s engineering program, and indeed the entire STEM program, forward as we push ourselves into space.
Senior Housing in Madison and Monroe, Georgia
Sarah Barrett; Mentor: Dr. Jerry Shannon, Geography

An increasingly important aspect of communities in the U.S is the availability of senior housing. The population of people 65 and over is growing twice as fast as the national average (1), meaning that communities need to consider how they are going to ensure adequate senior housing is available for the large aging population. I intend to look into this need by conducting research in conjunction with Georgia Initiative for Community Housing (GICH). Georgia Initiative for Community Housing is a program dedicated to helping communities meet their housing and neighborhood needs by creating an individualized local plan for each community that is accepted into their three year program. The results from my research can be implemented by GICH to enhance the plans for these communities. I plan to assess the current status of senior housing in Monroe and Madison, Georgia and the future needs of senior housing in these cities.

Assessing the current senior housing availability and future needs of these cities is not explicitly looked at by GICH but is a vital aspect in planning for the future of a city. Both Madison and Monroe, Georgia would benefit greatly from this research, as I would be providing useful information to these small cities that they might not otherwise be able to afford. Information regarding current senior housing stock and the projected future needs of senior housing in these two cities will allow Madison and Monroe, Georgia to make a more comprehensive and effective plan for their future senior housing needs.

I will be provided population data and projected population data independent of this research and use this data in conjunction with data I collect on senior housing facilities in these cities to assess the current senior housing condition and future senior housing needs based on the projected population. I plan to use an array of geospatial tools to collect and display this research. In addition to using quantitative data, I intend to conduct interviews with key stakeholders in these communities who may have expertise regarding senior housing. These interviews will provide me with information that data cannot, such as what members of the community see as important regarding the future needs of senior housing. Additionally, I intend to look at the accessibility of healthcare facilities in these two areas, as health care often becomes increasingly important with age. Using the two-step floating catchment area method (2) I would be able to measure the accessibility of healthcare in these two cities. Since I am implementing both quantitative and qualitative research, using an interactive program such as Esri’s story map to display my findings would be most effective. This program will provide me with a platform to display the maps I create with my data, including images of these cities and highlighting my interview findings.

Understanding current senior housing availability and the future needs of this type of housing in communities is imperative, especially with the currently large aging population. This research on Madison and Monroe will highlight to GICH and these two communities the future needs of senior housing, therefore allowing these cities to develop a better and more efficient plan for their future
References:

Effects of Fire in a Riparian Zone on Aquatic Fungal Production, Reproduction, and Biomass

Sarah Clement; Mentor: Dr. Amy Rosemond, Odum School of Ecology

Introduction:

Prescribed burns are a commonly used method of forest management. Many studies have been conducted on the effects of fire on biogeochemical functions, such as the cycling of organic and inorganic nitrogen (N). Though combustion results in a net loss of N from terrestrial systems, following the fire there is often a temporary increase in inorganic N that is biologically available. Studies conducted in streams where riparian zones have been effected by fire have shown that this N is loaded into the streams, causing N enrichment in the water.

Nutrient enrichment can have a large impact on stream ecosystems. One of the effects of artificial nutrient enrichment seen on aquatic fungi is an increase in the proportion of fungal productivity going to conidia production, rather than biomass. However, no studies have been conducted to test if the influx of nutrients following a burn would have a similar effect on instream fungi as artificial nutrient enrichment.

Fungi play an important role in stream ecosystem functions. Fungi colonize plant matter, increasing its nutrient quality and making it more palatable for leaf shredding macroinvertebrates. This allochthonous plant matter is a valuable food resource for nutrient poor-streams. After a fire in the riparian zone we may see a decrease in allochthonous resource inputs, as leaf litter that might have blown into the streams is burned.

Determining the effects of fire on aquatic fungi will deepen our understanding of the impacts of silviculture management tools and of natural forest fires on stream ecosystems. Given the limited data on aquatic fungal assemblages following a fire, it is hard to predict how the burn could affect fungal biomass, species richness, and species composition. The goal of this study is to elucidate the effects of fire on biomass and diversity of aquatic fungi. We aim to determine if bottom-up effects of altered riparian vegetation and allochthonous resources cause a change in fungal biomass and reproductive output. We will also investigate how the nutrient release of the fire impacts fungal biomass and reproductive output. We will use reproductive output in the form of conidia production as a means of determining fungal species richness and abundance. Finally, we are interested in the effect fire will have on fungal carbon allocation, particularly the ratio of carbon going to biomass versus reproduction.

Methods:

The study will be carried out in three streams: one receiving a cut and burn treatment, one receiving a no-cut burn treatment, and one reference stream. We will compare pre-burn conditions (1 sampling date) to post-burn conditions (4 sampling dates) for all 5 elements of stream and fungal response measured in the study.

We will:

1. Analyze soil, water, and sediment samples for nutrient C:N:P.
(2) Collect and quantify leaf litter standing stocks. We will calculate leaves per area (mg/m²) to calculate benthic food resources available to the microbial fungi.

(3) Collect fungal spore (conidia) samples within the streams and identify and quantify them to analyze species richness and relative species abundance.

(4) Quantify fungal biomass via ergosterol extraction using leaves collected within the streams. Ergosterol will be calculated on a per gram leaf litter basis.

(5) Use additional ergosterol extracts to estimate production, via stable isotope analysis or radio labelled carbon uptake rates.

We will compare mean conidia concentrations and number of species identified (via conidia) in the streams before and after the treatment, using paired ANOVA. Regressions will be performed for conidia concentrations versus production rates and for biomass estimates versus production rates. Regressions will also be performed for nutrient concentrations versus biomass and nutrient concentrations versus reproductive output.
Proposals

Predicting Oyster Recruitment and Survival through Cheaply Obtained, Remotely Sensed Data

John Coffin; Mentor: Dr. Jeb Byers, Odum School of Ecology

Introduction:

The American Oyster, *Crassostrea virginica*, is an important ecosystem engineer in estuarine systems. Ecosystem engineers physically alter habitat for other species, stabilize banks and provide habitat for many estuarine species. Reefs worldwide have been reduced by 88% due to overharvesting and habitat degradation and loss. Resource managers need better data to implement optimal management practices and increase the efficacy of species management programs. Oyster recruitment and survival are thought to be influenced by current velocity and wave energy. Water body width exerts a nonlinear influence on current velocity, with currents being slow in both very wide and narrow bodies of water and faster in intermediate bodies. Water bodies with larger fetches have increased wave action. This study investigates the effects of current velocity and wave energy on oyster larval recruitment and survivorship. The study will also determine whether water body width and prevailing wind fetch can be used as proxies for current velocity and wave energy, respectively.

Hypotheses:

I predict that estuaries have four main zones—sounds, rivers, creeks, and creek heads—each with unique current and wave energy regimes. I expect an association between current velocity and oyster success, with recruitment highest in medium current velocities (sounds and creeks) and lower at high (rivers) and low (creek heads) velocities. A negative association is expected between wave energy and oyster survivorship. I also predict that water body width and wind fetch will be good proxies for current velocity and wave energy, respectively.

Methods:

- Fifteen sensor rigs will be constructed and rotated between sixty sites throughout the estuary surrounding St. Catherines Island, GA. Sites will represent a full spectrum of current and wave energy regimes and will log one month of data for each site.
- An inertial measurement unit, attached to a tethered float, will gather wave data and a flow meter will measure current velocity. Sensors will be read by an Arduino microcontroller powered by a solar panel. Measurements will be broadcast in real-time through a radio network. These rigs are based on units developed at the University of Georgia’s MakerSpace and presented at the Odum School of Ecology Graduate Student Symposium.
- Oyster recruitment and survivorship will be monitored at each site with two spat sticks. One stick will be monitored during rig placement at that site, and the other will be monitored for the duration of the study.
- GIS analysis of aerial photography will be used to predict the current and wave energy of each site using the water body width and prevailing wind fetch.
- Correlation between current and wave energy, and oyster recruitment and survival will be tested. Additionally, correlation between sensor data and GIS proxies will also be tested.
Proposals

Significance:

The low cost and open source nature of this project enables inexpensive replication, and provides a highly adaptable rig platform from which I and other researchers can develop and collaborate on future projects. To this end, I am publishing all rig schematics. If water body width and prevailing wind fetch are found to be effective proxies for current and wave energy, then analysis of aerial photography will provide an easy and cost-effective solution to predicting optimal oyster settlement.

A better understanding of relationships between abiotic drivers and oyster success will empower resource managers to make informed decisions regarding oyster management. This will profoundly affect the Georgia aquaculture industry, and will help identify ideal locations for oyster restoration projects and living shoreline designs, taking the guesswork out of management efforts and potentially saving resource managers and homeowners thousands of dollars.

References:


6 Coffin, J. L. “Can Oyster Larval Recruitment and Survivorship be Predicted through Cheaply Obtained, Remotely Sensed Data?”, Graduate Student Symposium, Athens, GA, Odum School of Ecology.

Proposals

Production of Ethanol using High Temperature Alcohol Dehydrogenase

Alexander Crowley; Mentor: Dr. Michael Adams, Biochemistry & Molecular Biology

The research I have been working on for two semesters by the time of this fellowship pertains to the production of biofuels using the hyperthermophilic Archaea *Pyrococcus furiosus*. This microorganism lives normally at temperatures of 95°C and naturally produces low levels of ethanol. The graduate student whose project I have been working on introduced an Alcohol Dehydrogenase (AdhA) into *Pyrococcus furiosus*, which created a pathway for ethanol production in conjunction with the native aldehyde ferredoxin oxidoreductase (AOR) enzyme and made far more ethanol than the native enzymes in *Pyrococcus furiosus*. The project from last semester was to create alternate pathways of ethanol production in *Pyrococcus furiosus*. I worked with the bifunctional acetaldehyde dehydrogenase (AdhE) enzyme from different thermophilic microorganisms in an attempt to create an efficient pathway for ethanol production. This enzyme can convert acetyl CoA into acetaldehyde and then also to ethanol. However, the native enzymes in the control strain used during growth experiments always produced more ethanol than the strains containing the inserted AdhE enzymes. The AdhE enzyme has to compete with the high affinity enzyme acetyl CoA synthetase for its substrate acetyl CoA, which hindered the production of ethanol in these strains.

Since that was not an efficient form of ethanol production, this semester the current project is to manipulate the native ethanol producing enzymes in *Pyrococcus furiosus* to increase ethanol production and to discover exactly how this pathway works. The pathway of native ethanol production in *Pyrococcus furiosus* involves the redox enzyme pyruvate ferredoxin oxidoreductase (POR) that decarboxylates pyruvate to acetaldehyde, and then the most likely next step is the native alcohol dehydrogenase (AdhC) turns acetaldehyde to ethanol. There are other alcohol dehydrogenases present in *Pyrococcus furiosus*, but AdhC is the most likely candidate. To test this theory, this semester three new strains have been made so far and have been used in a growth curve experiment at varying temperatures. The strains made contain *Pyrococcus furiosus* with both the AdhC and AOR enzymes deleted, the AdhC enzyme deleted, and the AdhC enzyme over expressed using a strong promoter added to the plasmid respectively. If the strain with the AdhC enzyme deleted produces ethanol in the same amounts as *Pyrococcus furiosus* wild type, then either AdhC is not involved in the native ethanol production pathway or another alcohol dehydrogenase took on the same role. The sample results taken from the growth experiment have not yet been analyzed in total, but an exciting discovery was made. The *Pyrococcus furiosus* strain grown at 95°C produced a significant amount of ethanol. This is the first example of significant ethanol production in *Pyrococcus furiosus* at temperatures this high as normally ethanol producing enzymes denature at such high temperatures. For this summer depending on results from this current semester, the proposed research would be to continue studying the native ethanol producing enzymes of *Pyrococcus furiosus* and possibly add other enzymes to increase the efficiency of a constructed pathway or to create a new pathway, specifically at higher temperatures of 90°C or greater.
An Examination of the Political Impact of Obama’s Appellate Court Appointments on Policy Issues

Bryson Culver; Mentor: Dr. Susan Haire, History

In the past fifty years, the appointment of judges to the lower federal courts has become a highly politicized and policy-driven activity. Beginning with the Nixon administration, Presidents have become increasingly inclined to appoint justices in order to further their policy goals. By installing judges who share an administration’s policy goals, the influence of these policy goals remain significant far beyond the life of the administration that spurred them. After Nixon, the successive Presidential administrations have installed appointment procedures and processes that aim to find the best candidates to fulfill this objective.

While the Nixon, Carter, and Reagan administrations enjoyed little opposition to their policy-based appointments, the later Clinton, Bush, and Obama administrations were forced to face Congressional reaction to partisan appointments. In the appointment process, the “Advice and Consent” of the Senate has historically been a formality. Before 1977, the confirmation rate was almost 100%; however, following a Senatorial reaction to the President’s politically motivated nominations, the actions of the opposition party reduced the confirmation rate to 65% under Clinton and almost 50% under Bush. Additionally, the confirmation process tripled in length with some nominations taking three years to be confirmed. These pressures combined with severe vacancy issues in the courts, forced the latter Presidents to find more moderate, confirmable candidates.

The changing political dynamics of the appointment process are shown in the actions of the judiciary. In looking at the voting records of judges, the conservative and liberal tendencies often follow the party of the judge’s appointing President. This trend especially manifests itself in the earlier nominations under Reagan and Carter as they had little political opposition. The trend varies more under Clinton, Bush, and Obama who were forced to compromise with a more politically aggressive Senate. Additionally, the emphasis on equal representation in the judiciary affected the political composition of the appointments.

The aim of this research is to determine the voting behaviors and trends of the Obama Appellate Court appointees who were named to the bench from 2009 and beyond. Keeping in perspective the various aspects of the appointment and confirmation procedure, I will be collecting data on the published U.S. Courts of Appeals’ decisions on their voting behavior from 2009-2012. In addition to gathering information on their confirmation and backgrounds from the Federal Judicial Center and other sources, I will be drawing on, and extending, the Multi-User Database on the U.S. Courts of Appeals. Comparing the decision making of Obama’s appointees to those named by previous presidents will give insight on the growing effect of this cohort on policy making in these courts.

I expect to see a growing presence of moderate appointments in the Appellate Courts. The conflict between the President and the Senate is the result of the polarization of appointees based on policy goals. Bench vacancies have grown under the Clinton and Bush Administrations leaving Obama little choice but to nominate moderate “confirmable candidates.” Additionally, Obama’s
commitment to diversifying the court might lead him to choose candidates that match racial, ethnic, or sexual qualifications with less regard to their political and policy motivations.

In an era of polarization, understanding the politics of the judiciary is essential. What is generally the least exposed branch of our government oftentimes has a large impact on the public policy of our country. By gaining insight to the effects of Presidential Appointments on the Appellate Courts, one can generate a better understanding of the ideological leaning of the judiciary and its possible sway in public policy.
Feminization of Amphibians in Developed Landscapes
Sara Diamond; Mentor: Dr. John Maerz, Warnell School of Forestry and Natural Resources

Land use creates many challenges for the conservation and management of wildlife. Increasing agricultural and suburbanizing landscapes result in a diverse cocktail of compounds running into and accumulating in fresh waters. Many of these compounds mimic natural hormones (e.g., estrogen), which can affect the sex ratios and result in the feminization of males or masculinization of females (Lambert et al., 2015). Altered sex ratios and feminization of males can lead to reproductive depression and declines in animal populations (Lambert et al., 2015).

Amphibians and fish are two common taxa that show hormone disruption and feminization in response to land use and development. For example, a number of studies show high rates of intersex male fish in urban landscapes, particularly downstream from wastewater discharge points (Tetreault et al., 2011). Other research shows that male frogs in agricultural landscapes show high rates of feminization including the development of oocytes (eggs) in their testes linked to the use of pesticides such as atrazine (Hayes et al., 2002, Hayes et al., 2006). Recent research suggests that frogs in a suburban landscape in Connecticut showed female biased sex ratios and are exposed to higher levels of estrogenic compounds (Lambert et al., 2016). It is hypothesized that estrogenic compounds that leak from septic tanks and run off from lawns and agricultural fields are responsible for the feminization of developing tadpoles, leading to higher numbers of females at metamorphosis (Lambert et al., 2016). Studies from other landscapes have not verified the generality of this phenomenon, and no study has examined whether adult male frogs in developed landscapes show feminization.

Recent research by Dr. Robert Bringolf, Associate Professor in the Warnell School of Forestry and Natural Resources, has shown high rates of intersex male fish in suburban and agricultural ponds in the Athens, Georgia region. The objectives of my study are to determine whether adult male Green frogs (Lithobates clamitans) and Bullfrogs (L. catesbeianus) show increased feminization among the same ponds compared to reference sites. Specifically, I will measure the secondary sexual characteristics of male frogs (size of ear and amount of yellow coloration on the throat), and I will examine the testes of male frogs to look for the presence of oocytes in the testes. In addition, I will determine the sex ratios of recently metamorphosed frogs at ponds with high intersex fish ratios compared to reference sites.

My study will be the first study to correlate patterns of feminization of fish and amphibians among the same ponds within the same landscape, and it will be the first study to look for evidence of feminization of male secondary sexual characteristics linked to feminization of gonads. My project has significant broader impacts. Endocrine disruption and the feminization of males can negatively impact reproduction and population growth, which may threaten species and impact conservation in developing landscapes. Amphibians populations are declining globally in large part due to habitat loss and degradation, and pollution and endocrine disruption is identified as a conservation threat (Hayes et al., 2006). My project will also be a collaboration between two labs, the Maerz Lab, which has a
focus on amphibian ecology and conservation, and the Bringolf Lab, which focuses on ecotoxicology and physiology of fish and wildlife.

References:


Glycomic Profiling of a Model Species (Medaka Fish) to Study the Physiological Response to Chronic, Low Level Ionizing Radiation in the Environment

Linda Egbosiuba; Mentor: Dr. Carl Bergmann, Complex Carbohydrate Research Center

Ionized radiation is any type of electromagnetic wave that carries enough energy to remove tightly bonded electrons from its orbit causing it to become charged or ionized. The higher energy and higher frequency portion of the electromagnetic spectrum from X rays and above are considered ionized. When ionized radiation passes through living tissue, elections are removed from neutral water molecules to produce H₂O⁺ which is a free radical. Free radicals are extremely reactive molecules and can lead to removed electrons and hydrogen atoms. This can cause progressive damage to the membrane, nucleus, chromosome, or DNA chain that leads to uncontrolled growth of cells and mutations. Exposure to high levels of radiation for an extended duration leads to detrimental effects such as cancer. Our atmosphere can absorb and filter radiation from outer space but still we receive low doses of gamma rays and heavily charged particles. This study investigates the physiological responses of the model vertebrae, Medaka fish (*Oryzias latipes*) to chronic low doses of IR via glycomic profiling.

Glycomics is the comprehensive study of all glycan structures of an organism. Mass spectrometry based technology developments provide a wonderful platform for studying quantitative changes in glycan distribution within the cell which is important for understanding the molecular function of each glycan structure. The specimen being used is Medaka fish (the Japanese Rice Fish). It is an ideal vertebrate model species due to available genome sequence databases (~800 Mb), which are vital to the successful interpretation of proteomics data (Kasahara et al., 2007). Before being used for sample preparation, the Medaka fishes were exposed to varying levels of low dose IR at the Savannah River Low Dose Irradiation Facility (LoDIF). The overarching goal is to quantify comparative proteomic and glycomic responses of Medaka across varying levels of chronic, low doses of IR, and identify proteins and glycans involved in organismal adaptation to environmentally relevant radiological exposure for development of targeted hypotheses aimed at elucidation of evolutionary pathways associated with IR exposure. This investigation will specifically focus on the glycomic responses of the Medaka fish to varying levels of chronic, low dose IR. A state-of-art glycomic methodology that pairs mass spectrometry with current bioinformatics tools will be used to provide a novel methodology to understanding the physiological effects of chronic, low dose IR on organisms.
As measured by roll call voting behavior, congressional polarization is up to the highest levels since the Civil War. As a result, congressional approval ratings are extremely low. A recent January Gallup poll pegged approval at 16%. While interest groups on both sides of the aisle have begun to research methods to fix the problem, there is comparably little scholarly research into Congressional institutions in recent decades. Moreover, the little work that exists focuses on existing data from roll call voting patterns of members. Often times, these votes are taken out of context and no additional details regarding lawmaking are provided.

My research proposal seeks to fill in some of these gaps. I would like to continue working with the University of Georgia Amending and Roll Call project, but expand my efforts beyond data collections. The University of Georgia Amending and Roll Call project is the first systematic effort to model the roll call generating process. Professors Madonna and Lynch have worked with undergraduate students to code data on all amendments to landmark enactments (as opposed to simply amendments that received roll call votes). They have reported a sharp increase in votes on “messaging” amendments. These are amendments offered solely for the purpose of putting partisan opponents on record, with little policy success. This, they argue, may serve to artificially increase polarization.

Through my own experiences on the project, I learned a great deal about congressional lawmaking. However, data alone is likely not helpful for members of the general public interested in congressional lawmaking. Most casual observers of politics are unlikely to download a dataset and skim through it. In order to better serve the public, I am proposing writing up and making publically available legislative bill histories on landmark bills passed during the most recent Congress. Working with Professors Madonna and Lynch, I will make these bills history available online for anyone to access.

The legislative histories will be based on information from the Congressional Record. It will include things like: What procedures were used in the House of Representatives? What procedures were used in the Senate? What did opponents of the bill argue? What did proponents argue? Was the bill part of the President’s agenda (i.e. was it mentioned in a State of the Union speech)? How many amendments were offered on the floor of both chambers? What was the vote split on key votes?

I believe this project will not only help further my education in congressional lawmaking, but help the broader public. Currently, the most thorough, publically available source for information on legislation is Wikipedia, which is extremely limited. Nothing exists that is comparable to Oyez for Supreme Court cases. This website also will aim to provide definitions and examples of contemporary legislative procedures, and dates regarding reauthorizations, government funding and the debt ceiling. This is all in an attempt to help the public to be more informed, and make the process more transparent.
Development and Construction of a Low-Earth Orbit ‘Structure from Motion’ Nanosatellite

Graham Grable; Mentor: Dr. Deepak Mishra, Geography

Structure from Motion (SfM) photogrammetry is an imaging technique capable of low-cost three-dimensional topographical models from Low-Earth Orbit (LEO). Typical three-dimensional terrain data requires complex camera setups including three-dimensional camera location definitions. However, SfM is able to eliminate complex setups through movement of the camera sensor and matching of overlapping images (Westoby, 2012). SfM has already proven to be a valuable instrument in monitoring the health and activity of various ecosystems on Earth. A group of researchers successfully studied calving of the Store Glacier in Greenland using an Unmanned Aerial Vehicle and SfM technology (Ryan, 2015). Despite the low-cost of SfM, its ability to produce useful terrain data anywhere on Earth is limited by the difficulty to setup in remote areas. A nanosatellite, a satellite typically in the shape of a cube and weighing less than one kilogram, equipped with SfM technology in LEO can cheaply gain valuable terrain data almost anywhere in the world.

Realizing this, Dr. Deepak Mishra and a team of undergraduates, including me, have been accepted into the United States Air Force University Nanosatellite Program (UNP) to develop a nanosatellite with SfM capabilities, the first of its kind, called MOCISat (Mapping and Ocean Color Imaging Satellite). MOCISat is only one of ten satellites chosen to become part of the UNP this year. The UNP helps to fund MOCISat and in return creates a rigorous system of reviews and requirements as a way to educate and prepare students for the workforce. MOCISat poses a unique set of mechanical-based challenges. These challenges are the focus of my research and include: 1) analyzing and developing power constraints, 2) developing attitude control, and 3) developing the test environment.

I will research and study each of the three challenges in order to contribute to the success of MOCISat and further develop SfM technology. While analyzing and developing power constraints (1), I will help research solar power generation, power distribution to subsystems (ex: SfM sensor, antenna, etc.), and Electromagnetic Interference (EMI). Researching solar power generation will require field experiments to confirm previously developed models, and simulation software will be used to analyze power distribution throughout MOCISat and to study EMI. The development of the attitude control (2) is closely related the SfM sensor as it will be responsible for pointing MOCISat towards Earth for successful collection of terrain data, and I will be working with other team members to research the constraints and requirements for attitude control. Developing the test environment (3) is very important as testing will simulate an LEO-like environment and determine which parts of MOCISat need to be replaced or re-designed. To simulate the test environment I will help setup Helmholtz coils, to produce a magnetic field similar to one in LEO; a vacuum and thermal chamber, to simulate the environment of LEO; and a shake bed, a table which vibrates to frequencies that would be found during launch conditions.

The research I will be performing with MOCISat will be valuable not only for the development of nanosatellites, but also for SfM technology in LEO. Additionally, my research will serve as a foundation for a new class to be offered yearly. Learning and researching the development
of a nanosatellite is personally important as a Mechanical Engineering student, and as the first stepping stone of my career in the aerospace industry.

References:

Local Effective Microorganisms: The Effect on Soil Carbon, Soil Nitrogen, and Plant Protein

Lori Hanna; Mentor: Dr. Dorcas Franklin, Crop & Soil Sciences

With the increase of the world population and the rising demand for agricultural products, innovation is necessary. Past innovations have led to dramatic increases in crop production, specifically chemical inputs of nitrogen and phosphorous which contributed to 50% of the increase in crop production up to 1989 (1). These chemical inputs, however, are environmentally unsustainable through nutrient runoff and economically unsustainable through the high cost of chemical fertilizers (2). In order to support the growing population and to adapt to changing agro-ecological conditions caused by rising global temperatures, sustainable innovations must be made (3). One such innovation that is being used widely in tropical and subtropical regions is Local Effective Microorganisms (LEM).

LEM is a solution of locally derived microbes produced using leaf litter from nearby forest and carbohydrate rich substances. The purpose of these microbes is to improve crop yield by increasing photosynthesis, producing hormones and enzymes, controlling soil diseases, and accelerating decomposition in the soil (4). Anecdotally, this method is working, but there is little scientific evidence on the impacts of LEM to the soil community, nutrient cycling and availability, and the overall nutrient density of plants. If this innovation is a sustainable solution and could reduce the use of chemical inputs or alter the carbon footprint of agriculture, it must be recommended with a clear understanding of the mechanisms behind it.

For my research, I will be collaborating with Dr. Franklin and her team of graduate students to research the mechanisms and impacts of LEM. My research focus is how application of LEM affects 1) ratios of total carbon and total nitrogen in the soil 2) plant available nitrogen 3) carbon dioxide (CO₂) respiration of the plants and 4) protein density. Graduate student Laura Ney is already researching the yield of crops. To expand on this, I will measure the protein content of two types of legumes to determine if increased quantity correlates to increased quality.

My research will be a parallel study conducted in conjunction with Ney’s research with two study sites: Watkinsville, Georgia and Monteverde, Costa Rica (UGACR). At the UGACR campus, LEM is used in the composting of waste as a nutrient source for the organic gardens. Costa Rica is an excellent study site because the warm weather and humidity are ideal for rapid completion of the composting process, for crop production, and for more rapid LEM culturing. Black beans are a staple for those that live throughout the region and it is also important to study this technique in the climate and microbial ecosystem where it is currently being used. I will have 18 plots of edamame (soybeans; Glycine max) in Watkinsville, Georgia and 18 plots of black beans (Phaseolus vulgaris L.) in Costa Rica. The plots will be divided into LEM, false-LEM, and controls. I will collect soil and plant samples and analyze them for carbon, nitrogen, and protein. I will also collect CO₂ respiration measurements. I will assist Dr. Franklin’s team in keeping the fields well managed for more consistent and accurate results.

This fellowship would make it possible to travel to Costa Rica to research in the environment of existing application. I must stress that this is not an innovation that is being proposed for future
use. It is being used on crops, compost, and animal waste throughout the tropics and subtropics right now. The outcome of my project could lead to changes in fertilizer use, changes in how we analyze and reduce the carbon footprint of agriculture, and changes in the nutrition of the plants themselves. It is urgent and imperative that we understand the impact of this innovation.

References:


Cas Protein Complexes in Adaptation of Streptococcus Thermophilus Type II-A CRISPR-Cas System

Erin Hollander; Mentor: Dr. Michael Terns, Biochemistry & Molecular Biology

For bacteria and archaea, adapting to a changing environment enables the evolution of novel defense systems. One such adaptation is the recently discovered CRISPR-Cas system, which resides in approximately 50% of bacteria and 90% of archaea.1 This system efficiently defends the microorganisms from nucleic acid invaders through versatile loci that serve as a heritable “memory” of past invasions.

The CRISPR-Cas system uses a three-stage process to mediate phage resistance: (1) adaptation, (2) expression, and (3) interference. During adaptation, the CRISPR-Cas system recognizes a PAM sequence (Protospacer Adjacent Motif) on an invading foreign nucleic acid and incorporates the protospacer sequence into the CRISPR array. These segments, known as “spacers,” are interspersed between short, identical DNA sequences called “repeats.” Transcription of the array and cleavage of the resultant transcript in the expression stage leads to small CRISPR RNAs (crRNAs). Finally, during interference, crRNAs recognize and bind to invading nucleic acids. Cleavage of the crRNA – phage DNA complex by Cas proteins, guided by crRNAs, enables the microorganism to successfully defend itself from the viral invader.1

This research project focuses on the Type II-A CRISPR1 (CR1) system of S. thermophilus, a key bacterium used in the dairy industry during fermentation.2 With only four proteins, this system is the simplest and most widespread CRISPR system in S. thermophilus.1 The invader silencing protein of Type II systems, Cas9, is a powerful tool for genome editing, allowing targeted modification of sequences involved in the immune mechanism. This project utilizes the Type II-A CR1 system of S. thermophilus. The universal proteins Cas1 and Cas2 are present along with Csn2 and Cas9. Cas9 is the signature protein of Type II systems.1

In my third year at the Terns lab, I am now focusing on the possibility of the Cas proteins forming complexes during the process of adaptation. Cas1 and Cas2 have previously been shown to form a complex in the CRISPR-Cas system of E. coli.4 As these two proteins are ubiquitous among CRISPR-Cas systems with highly similar functions, it was hypothesized that these two proteins would complex together along with Csn2. His-tagged Cas1 had previously been shown to pull down in a complex with Cas2 and Csn2 in an affinity assay when Cas2 and Csn2 were overexpressed on a plasmid. My work will focus on better understanding the complex formed by the Cas proteins and how it functions in vitro in spacer generation and integration into a CRISPR locus.

As one of the simplest systems in S. thermophilus, the Type II-A system is an excellent model with which to derive the mechanisms of the Cas proteins and the CRISPR-Cas system as a whole. With only four proteins, the system has a broad range of applications, including novel gene therapy techniques, preventing the transference of antibiotic resistance genes, and protecting beneficial microbes such as S. thermophilus from phage attack.1,3,5
References:


Evaluation of Cas4 Function in CRISPR-Cas Adaptation

Jesse Hu; Mentor: Dr. Michael Terns, Biochemistry & Molecular Biology

Given that viruses are the most abundant biological entities on the planet, bacteria and archaea have evolved extensive protective systems to defend against genetic invaders (Suttle, 2007). One component of this defense is CRISPR-Cas (clustered regularly interspaced short palindromic repeats–CRISPR-associated), an adaptive prokaryotic immune system found in nearly all archaea and half of prokaryotes (van der Oost et al, 2014). This system is composed of a CRISPR array and associated Cas proteins, which vary by specific CRISPR system type. The CRISPR array affords memory of past infections and contains identical repeats separated by variable sequences known as spacers, which are derived from a foreign nucleic acid. In brief, CRISPR functions in three stages: adaptation, CRISPR RNA (crRNA) biogenesis, and crRNA guided interference. During adaptation, new spacers are captured from the invader and incorporated into the CRISPR array through a process called integration. The CRISPR array is then transcribed during crRNA biogenesis, and the transcript is processed to generate small crRNAs complementary to invader DNA. Finally, during interference, the crRNA guides Cas proteins to the invader, allowing for catalytic cleavage of foreign genetic materials (Heler et al, 2014).

For the last semester, I have worked with Julie Grainy, a PhD student in the Terns lab studying the mechanism of adaptation for CRISPR-Cas systems of Pyrococcus furiosus (Pfu) and Thermococcus kodakarenensis (Tko). Pfu, is a hyperthermophilic archaeon that contains 7 CRISPR loci, each sharing the same proteins for adaptation, Cas1 and Cas2, which are conserved across all CRISPR systems (Majumdar et al., 2015). Tko is a highly related hyperthermophilic archaeon with 3 CRISPR loci, which also share Cas1 and Cas2 to achieve adaptation (Elmore et al., 2013).

Though the result of adaptation has been characterized and both Cas1 and Cas2 have been demonstrated as necessary for integration, the biochemical mechanisms of adaptation are not fully understood (Makarova et al., 2011; Nuñez et al., 2014). Furthermore, recent unpublished work in the Terns lab has uncovered a requirement for a third Cas protein, Cas4, in mediating adaptation. In vivo data acquired by the Terns lab suggests that Pfu Cas4-1 has an inhibitory effect on adaptation, but that Pfu Cas4-2 is required. This is an intriguing result that I want to test in vitro, in order to better understand the mechanism of Pfu Cas1, Cas2, Cas4-1, and Cas4-2 and their role in spacer selection, processing, and integration. Although Tko adaptation has not been studied in vivo, I am interested in testing Tko Cas1, Cas2, Cas4-1 and Cas4-2 in vitro as they are highly conserved with Pfu. Tko also contains a third Cas4-3 protein that I am interested in characterizing.

Therefore, this summer, my proposed research will focus on better understanding the process of adaptation by evaluating the functions of Pfu and Tko Cas4 proteins in vitro. I predict that some Cas4 proteins may inhibit integration, but others may also be essential for integration to occur. Spacer integration by Pfu and Tko Cas1 and Cas2 will be simulated using a radiolabeled spacer that can be integrated into an artificial CRISPR locus. This locus will then be visualized through autoradiography to assess integration. The effect of different Cas4 proteins will be measured by these assays. Determination of integration site within the CRISPR loci will be determined through sequencing. Proteins for these reactions have already been cloned, expressed, and purified. Moreover, I will work
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with Julie to design and test methods evaluating the preceding steps of adaptation, such as spacer selection, cleavage, and processing. Using these approaches, I hope to gain a better understanding of how CRISPR-Cas acquire new spacers, and hence gain immunity to new invaders.

References:


The Effect of Saharan Dust Events on the Distribution of Pathogenic Vibrio Species in Tropical Waters

Kylie Isaack; Research Mentor: Dr. Erin Lipp, Environmental Health Science

Vibrio is a genus of marine bacteria that has species that are harmful to both human health and economics. Studies done through CDC show that there has been an increase in Vibrio infection in the past twenty years (Newton, 2012). Some of the human diseases include the severe diarrheal disease cholera (V. cholerae), shellfish associated gastroenteritis (V. parahaemolyticus), and seawater associated wound infections (V. vulnificus). The economic effects include infection in both fish and shrimp harvested for seafood production. Previous studies in our lab have determined that Vibrio have a tendency to bloom in response to iron addition, something that is bountiful in the tropical Caribbean waters after dust from the African Saharan Desert is deposited during seasonal dust storms (Westrich et al., 2016). The iron-rich dust is blown from desert source regions by easterly trade winds and deposited thousands of miles away in downwind ocean water. Our lab has taken samples of ocean water before, during, and after these dust storms have deposited nutrients in tropical waters. We hypothesize that there will be higher counts of pathogenic Vibrio species within the samples that were obtained after the arrival of dust storms, compared to pre-dust conditions.

Finding the link between pathogenic Vibrio blooms and the arrival of Saharan dust clouds proves to be an important topic in public health. Using satellite tracking, the dust storms can be observed and predictions can be made as to where they will deposit once they travel across the Atlantic. This means that we would have the potential to warn residents of these affected areas that the dangerous bacterial blooms were present. Typically, phytoplankton are the organisms that are studied in response to Saharan dust, but bacterial blooms are also a significant part of their ecosystems and deserve further study.

We have samples that were collected from surface waters in the Florida Keys during Saharan dust events during the summers of 2014-2015. I will be using Vibrio specific TCSB agar to further isolate these unknown Vibrio species followed by DNA extraction. We will then examine the presence of pathogenic genes within the sample using specific pathogenic PCR targets. These procedures will be done to both the pre-dust and post-dust samples so we can compare the results at the end of the experiment. By doing this we hope to further understand the connection between the growth of these harmful Vibrio populations and their link to the Saharan dust events.

References:

Investigation of a Fast, Tunable Microwave Photonic Phase Shifter
Aneek James; Mentor: Dr. Mable Fok, College of Engineering

Importance of Microwave Phase Shifters:
Microwave Phase Shifters are a vital component to communication systems today for signal processing and microwave beam directing. For example, phase shifters are the main components that make up phased array radars, devices that can send electromagnetic signals in one particular direction. This functionality has many uses in broadcasting, optical communications, and many more fields. Recently, for example, the MESSENGER spacecraft sent on a NASA mission to Mercury was the first deep-space mission to use a phased-array antenna for communications, proving it’s potential use in future missions [1]. Phased array antennae are also used in weather research, as evidenced by the National Severe Storms Laboratory’s project using a US Navy phased array antenna to gather information on thunderstorms and tornadoes [2].

Operational Theory of Phase Shifter:
The mathematical description of a phase shifter is relatively simple. If given a radio frequency (RF) sinusoidal signal, i.e. \( \cos(2\pi ft) \), a phase shifter will ideally alter the signal by adding a phase shift \( \phi(f) \) inside the term:

\[
\cos(2\pi ft + \phi(f)) \tag{1}
\]

where \( \phi(f) \) should be a constant value for all frequencies (as shown in Figure 1). The frequency range for which the phase shifter can achieve this behavior without unevenly altering the amplitude of the signal defines its operational bandwidth. Though many electrical phase shifters exist in the market, the nature of electrical circuits reduces the possibilities for increasing the operational bandwidth of a phase shifter and ensuring full 360° phase shift capabilities.

Microwave Photonics:
Microwave photonics (MWP) has grown in popularity in the past couple of years due to the number of advantages it possess over traditional microwave engineering systems. Incorporation of photonic components into microwave systems allows MWP to be inherently immune to electromagnetic interference, to exhibit low signal attenuation over large distances, and to be tunable at fast speeds [3-5]. These benefits contribute to MWP phase shifters as having a far larger operational bandwidth. As of now, there are a number of realized of
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microwave photonic phase shifters, but none that prove to be a fast, tunable alternative. For viability in dynamic systems where requirements for signal processing can change rapidly, the need for a fast alternative is growing every year.

Goals and Objectives for Research Project:

I propose investigating several promising schemes to design a microwave photonic phase shifter that is fast and widely tunable. Two possible schemes that will be investigated the most thoroughly are: 1.) coherent population oscillations using an electroabsorber (EA) and 2.) modifying a true time delay scheme into a pure phase shifter. Both schemes are of interest due the optical effects which they are based on being phenomena with fast response times (i.e GHz range). If these phenomena can be used to control the tuning of the phase shifter, it is possible to see an extraordinary improvement to the versatility of current schemes.

References:


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Finding the Epitope of VAC69 to Allow for Early Detection of Multiple Myeloma

Manasa Kadiyala; Mentor: Dr. J. M. Pierce, Biochemistry & Molecular Biology

Human Multiple Myeloma (MM), a cancer of the plasma cells, is one of the most common hematologic cancers in the United States and is currently without a cure or reliable method of early diagnosis. In collaboration with Cohava Gelber, a mouse monoclonal IgG antibody (VAC69) has been identified that specifically recognizes a glycoepitope on MM cells over chronic myelogenic leukemia (CML) cells even with their similar lineage and characteristics. VAC69 is, therefore, a prime candidate for a useful MM early detection biomarker; it binds with a glycoprotein membrane molecule solely located on MM cells, not cells of prostate, breast, cervical, or other cancer types. This project will focus on determining the chemical structure of the glycomarker in the monoclonal IgG antibody and how it is regulated during cancer progression.

Early detection of cancers is critical for their successful treatment. Since abnormal glycosylation of cell surfaces is an indication of oncogenesis, identification of cell surface glycans that represent these alterations is essential to find new cancer markers. Over the years, development of monoclonal antibodies as diagnostic tools for identification of several cancer-associated glycans has been used with varying degrees of success. Almost all antigens that recognize and bind to mAbs can also bind to regular non-cancerous cells, potentially decreasing the effective functionality of the antigenic targets. The focus of this research is to define the epitope of monoclonal antibody VAC69, which shows specificity for multiple myeloma (MM), as well as ovarian carcinoma, and does not bind to non-cancerous cells and tissues when tested using differential immunization. In five MM cell lines, the epitope is expressed on what appears to be a single glycoprotein with molecular weight of about 80KDa. The identification of this glycoprotein remains undefined and is a component of this research. VAC69 was produced by the C. Gelber laboratory and has been provided to us in collaboration between the Pierce and Gelber laboratories. Preliminary results show that treatment of MM cell lysates with PNGaseF (N-glycanase) results in the loss of VAC69 binding to Western blots of MM cell lysates, demonstrating that the epitope is most likely part of an N-glycan or N-glycopeptide. We aim to further characterize the sequence, structure and cell type-specificity of this epitope, which will allow VAC69 to be evaluated as a potential diagnostic and therapeutic tool for cancers such as multiple myeloma.
Environmental Consequences, Tic Symptom Severity, and Psychological Comorbidities in Children with Tourette Syndrome  
Colleen Keeler; Mentor: Dr. Ronald Blount, Psychology  

This summer, I will continue my work with the Pediatric Psychology Lab under the direction of Ronald Blount, Ph.D. I will collect data from campers at Camp Twitch & Shout, a weeklong summer camp for children with Tourette syndrome (TS), and their caregivers. With this data, I aim to clarify how environmental consequences (e.g., environmental reactions to displaying tic symptoms, family socioeconomic status [SES]) influence tic symptom severity and psychiatric comorbidities in children with TS. TS is a neurological disorder that typically develops between the ages of 3 and 9 years (National Institute of Neurological Disorders and Stroke [NINDS], 2014). TS symptoms include repetitive, involuntary vocalizations and/or movements, known as tics (NINDS, 2014; e.g., eye blinking, head jerking). An estimated 200,000 Americans suffer from the most severe form of TS (NINDS, 2014). More than 80% suffer from psychiatric comorbidities, with Attention Deficit Hyperactivity Disorder (ADHD) and Obsessive Compulsive Disorder (OCD) being the most common (Centers for Disease Control and Prevention, 2015.)  

Researchers have examined how factors within the family environment, such as SES and environmental consequences of the display of tics, are related to the likelihood of developing TS and severity of tic symptoms. Capriotti et al. (2014) recently found that the majority of youth suffering from chronic tic disorders report experiencing consequences of tic behavior (e.g., attention, getting out of performing unpleasant tasks) that are correlated with greater tic severity. Another study determined that an unstable family environment, which is often a consequence of TS, might contribute to the worsening of tic symptoms (Hong et al., 2013). SES has been identified as a risk factor for developing TS and chronic tics (Miller et al., 2013). Family accommodation to the child’s symptoms is another factor of interest, as it has been linked to higher functional impairment in children with OCD (Storch et al., 2007). Because TS and OCD are both characterized by repetitive behaviors, the same relationship may exist in children with TS.  

I will expand upon this pioneering research. Utilizing standardized measures, I will look at factors such as environmental consequences to children’s TS symptoms and how much parents accommodate their child’s TS symptoms, as well as demographic factors, such as SES, education level, and racial background. I will then examine how these factors relate to child’s tic severity and internalizing and externalizing disorder symptoms. I hope to identify environmental consequences that relate to children’s tic severity and their experience of comorbid disorders. My findings have the potential to inform the development of family-focused behavioral interventions that will help children with TS cope with tic and comorbidity symptoms.  

All study procedures have been approved by the University of Georgia’s Institutional Review Board. Families of Camp Twitch & Shout attendees will receive an email from the camp asking them to complete measures six weeks prior to camp. Informed consent or assent will be obtained from all participants before completing any measures. The following measures will be completed by children: (a) Multidimensional Anxiety Scale for Children-2nd Edition, (b) Tic Symptom Self-Report (c) Behavior Assessment Scale for Children-2nd Edition, d) Child Demographic Questionnaire (Wei, et
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al., 2013; Leckman & Cohen, 1999). Caregivers will complete the following proxy-report measures: (a) Multidimensional Anxiety Scale for Children, (b) Behavior Assessment Scale for Children-2nd Edition, Parent Rating Scales, (c) Tic Symptom Parent Report, d) Tic Accommodations and Reactions Scale. (Capriotti et al, 2014.) I hypothesize that lower SES (e.g. lower income, lower parent education) will be associated with greater severity of tic symptoms and higher prevalence of comorbid disorders. Additionally, I hypothesize that as environmental consequences of the child’s TS symptoms increases, severity of tic symptoms and prevalence of comorbid disorders will increase.

References:
Mapping and Ocean Color Imaging (MOCI) Satellite
Adam King; Mentor: Dr. Deepak Mishra, Geography

Overview:
This satellite, the Mapping and Ocean Color Imaging (MOCI) Satellite, will be built to provide proof-of-concept for photogrammetry using Structure from Motion (SfM) technology from space. It will also be used to provide imaging data to allow the principal investigator, Dr. Deepak Mishra, to study coastal and wetland statuses. This satellite is classified as a Nanosatellite (NanoSat), meaning that its form factor and size fits within smaller-scale design restraints. The MOCI Satellite will be designed for maximum flexibility of transportation in order to complete its mission. Ideally, the NanoSat will be deployed from a module on the International Space Station (ISS) deemed the “Kibo” module. Upon release, the satellite will use a combination of Reaction Control System (RCS) wheels and magnetorquers to stabilize its orbit. The mission duration is expected to be 18 months.

Research – End Goal:
The primary mission goals is to use space-based photogrammetry to provide 3D terrain modeling of the Earth’s surface. This will be accomplished using the NanoCam C1U (NC1U), a moderate resolution, visible light camera. This will provide proof-of-concept for Structure from Motion (SfM) photogrammetry measurement from Low-Earth Orbit (LEO). This data will allow monitoring of wetland biophysical characteristics. The 3D SfM data will be the first of its kind from a NanoSat platform. The results of this can be applied to various fields, since the computation applied to moderate images could also be applied to higher-resolution imaging missions. The secondary goals of this mission will be to investigate coastal land cover and phenology as well as river runoff that causes harmful off-coast algal blooms. This data will then be used to monitor the quality of coastal water, such as phytoplankton dynamics, color-dissolved organic matter, and inorganic sediment in estuarine and near-shore waters.

Initial Research and Early Contributions:
My initial contributions to this project will include, but are not limited to:

- Integration of the Attitude Determination and Control System (ADCS) and development of control software to stabilize movement during image capture
- Research of orbital mechanics, aerodynamic drag, and physical modeling simulations
- Research into use and modification of the National Aeronautics and Space Administration (NASA) Core Flight Software (CFS) for use on the NanoSat

Currently, our undergraduate team is in the beginning phases of this project. I will assist in development of software for use in obtaining data from the ADCS to correct for attitude variations. These simulations will begin with the creation of a virtual environment to test our detumbling sequence code to ensure that we are obtaining our desired results before physical testing.
Using NASA's General Mission Analysis Tool (GMAT) software, I will also aid in the virtualization\(^6\) and understanding of how the NanoSat would behave in space during the mission. This program takes into account orbital mechanics and aerodynamic drag as well as mission duration specifications.

To enable our satellite to record images and transmit data, we will be utilizing NASA's CFS. I will aid in researching the documentation for the software, gaining an understanding of it's general uses and how it would tie into the mission as a whole. The CFS is expected to act as a bridge between sensors to the software we will build and also as a bridge between the software output and actuators\(^7\).

Definitions:
1. **photogrammetry** – the science of making measurements from photographs, including 3D rendering using several 2D images
2. **nanosatellite** – an artificial satellite with a mass between 1 and 10 kilograms
3. **magnetorquer** – a satellite system for attitude control, detumbling, and stabilization build from electromagnetic coils; creates a magnetic field that interfaces with an ambient magnetic field, usually Earth's, so that the counter-forces produced provide useful torque
4. **phenology** – the study of cyclic and seasonal natural phenomena, especially in relation to climate and plant and animal life
5. **attitude** – the orientation of an aircraft or spacecraft, relative to the direction of travel
6. **virtualization** – the conversion of something to a computer-generated simulation of reality
7. **actuator** – a device that converts electrical input to mechanical output
Effect of Invasive Macroalgae *Gracilaria vermiculophylla* on Feeding Behavior of *Dasyatis Americana*

Katie Maddox; Mentor: Dr. Jeb Byers, Odum School of Ecology

**Introduction:**

Seaweeds are rare on the Georgia coast because of high turbidity in the water column, which reduces light to insufficient levels, and a paucity of hard substrata for attachment. However, a non-native ecosystem engineer has recently invaded, the seaweed *Gracilaria vermiculophylla*, which survives due to a mutualistic interaction with native tubeworms. This invader could have a major impact on the physical characteristics and trophic relationships of Georgia’s estuarine communities. *G. vermiculophylla* forms a layer of substrate that, before its introduction, was not present on Georgia’s mudflats. This addition of *G. vermiculophylla* has dramatically boosted primary productivity and native invertebrate populations.

However, it is possible that higher-level predators may also benefit from *G. vermiculophylla*’s presence. *Dasyatis americana*, or the southern stingray, is readily found on the mudflats along the southeastern United States. The southern stingray feeds on a wide range of invertebrates such as shrimp and clams, which are some of the species that proliferate within the mats formed by *G. vermiculophylla*. My study will focus on the effect the emergence of this landscape-altering seaweed has on the feeding behavior of *D. americana*.

**Methods:**

I will quantify the effects of *G. vermiculophylla* on the southern stingray and its prey base using both a field and a lab experiment. I will initiate a study on the mudflats in Wassaw Sound, Savannah, Georgia where *D. americana* are found. On mudflats where *G. vermiculophylla* is present, two plot treatments will be manipulated: a treatment that excludes stingrays and a treatment in which they are not excluded. Treatments will each have three replicates. Stingrays will be excluded using evenly spaced stakes that will not interfere with the passage of water or medium to small-sized organisms. After running for three tidal cycles, I will quantify the magnitude of their feeding effect by comparing the abundance of invertebrates within the *G. vermiculophylla* plots that have been exposed and not been exposed to stingrays.

Next I will conduct a lab-based behavioral study to investigate the effect the density of *Gracilaria vermiculophylla* has on the foraging behavior of the southern stingray. My study will be conducted in the UGA Marine Extension Service aquarium on Skidaway Island, Georgia. Within a 5000 gallon tank, I will anchor *Gracilaria vermiculophylla* to the substrate at the bottom of the tank using one of four density treatments: 0g/m², 50g/m², 100g/m², and 1000g/m². One density treatment will be tested at a time in a sequential random block design. These reflect actual densities of *G. vermiculophylla* recorded in Wassaw Sound. Each treatment will be replicated five times, replacing the stingray for each replicate. Twenty juvenile clams, *Mercenaria mercenaria*, will be placed in the tank one hour prior to the addition of the stingray. I will run each trial for three hours and record prey survival in order to index which *G. vermiculophylla* density most interferes with ray foraging. The trials will be videotaped to enable me to quantify complementary behavioral metrics, including exploratory time,
excavation rates, and foraging behaviors. Collectively my project will give insight into how *Gracilaria vermiculophylla* affects the foraging of *Dasyatis americana*.

**Conclusion:**

It is known that more invertebrates are found in areas with greater *Gracilaria vermiculophylla* density, however it is unclear whether *G. vermiculophylla* physically interferes with stingray foraging. There may be a threshold in *G. vermiculophylla* density at which point it becomes difficult for *Dasyatis americana* to forage. Due to the potential for a threshold effect, I would expect to see higher stingray foraging rates in the 100g/m² treatment.

**References:**


Investigations of Histone Chaperone Protein (NAP1) as it pertains to the CAAX Protein Shunt Pathway

Michael Morgan; Mentor: Dr. Walter K. Schmidt, Biochemistry & Molecular Biology

CAAX proteins play vital roles in cellular process such as cellular differentiation, proliferation, and apoptosis. Because of this, CAAX proteins are commonly involved in carcinogenesis and many are targets of therapeutic strategies. A subset of CAAX proteins are Ras GTPase proteins. Roughly a third of all human cancers involve mutated forms of Ras, including 95% of pancreatic cancers and 60% of solid tumors overall. Years of cancer research have sought to block the oncogenic properties of these Ras proteins with little success, but major efforts continue at both the federal, academic, and industry levels.

To better understand the signal transduction pathways that involve CAAX proteins, Dr. Schmidt’s lab investigates the post-translational modifications (PTMs) that regulate the activities of CAAX proteins. There are three distinct modifications that occur to RAS, and these have been presumed to generally occur to all CAAX proteins (Figure 1). The first PTM is farnesylation of the CAAX motif. Subsequent PTMs involve proteolysis and carboxylmethylation. Using the yeast model, the Schmidt lab has recently discovered a novel branch to the standard PTM pathway herein referred to as the shunt pathway. In this pathway, CAAX proteins complete farnesylation but are not subsequently modified. These proteins are “shunt pathway” candidates.

My research project this summer will investigate NAP1, a histone chaperone protein. Elevated expression of NAP1 occurs in malignant appendicial carcinoids and goblet cell adenocarcinoids. Based on Dr. Schmidt’s past research, the hypothesis being tested is that NAP1 is a shunt pathway protein. Objectives of my research include the creation of NAP1 expression plasmids and NAP1 mutants as tools to investigate the importance of the shunt pathway to NAP1 biology. The lab is very proficient at making yeast expression plasmids, and this work can be easily completed over the summer timeframe of the proposal. Both shunted and standard model mutants will be created to assess the impact of PTMs on NAP1-dependent phenotypes. Green fluorescent protein (GFP) tagged versions of NAP1 will also be created to investigate effects on subcellular localization. The effects on NAP1 function will be followed using assays that focus on cell death and anaerobic
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I will also confirm that the NAP1 CAAX motif directs proteins to the shunt pathway by transferring the motif onto other reporters used to study both the shunt and standard PTM pathways. These investigations are expected to support NAP1 as a shunt pathway protein, giving us greater insight into the pathways used by CAAX proteins. These findings will in turn help guide the development of therapeutic agents aimed at disrupting the PTMs associated with CAAX proteins. NAP1-dependent cancer therapy may benefit from strategies that interrupt farnesylation (i.e. the first PTM) rather than subsequent PTM steps. By contrast, Ras-dependent cancer therapy could target each PTM step but might be improved to reduce off-target effects by focusing on just the subsequent steps to avoid disrupting the function of shunt pathway CAAX proteins.

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Satellite Development and Photogrammetry using Structure from Motion
Nicholas Neel; Mentor: Dr. Deepak Mishra, Geography

During the summer of 2016, I will be conducting satellite research with Dr. Deepak Mishra. A team of undergraduate students has been selected by the Air Force Research Laboratory to create a Cube Satellite which uses images taken from Low-Earth Orbit to compile into a 3D model in which we can analyze the results and determine structures from the images. This concept is called structure from motion.

As soon as the term begins, we will work on creating a complete virtual model of our satellite in order to test it in NASA’s GMAT software which is a program NASA released for simulations. When we have our model completed, we will ensure that the mission we have chosen is feasible.

Initially, we need to be able to test communications so that we are able to transmit data from large distances. This will be done by the development of drones to carry a transceiver to various altitudes to test the success of a transmission. This will be where we will be required to develop encryption algorithms to securely transfer our data. We will also be testing various image compression algorithms to attempt a lower file size to be transmitted.

Next, we shall work with the college of engineering to construct testing environment for our satellite’s components. This will include the manufacturing of a Helmholtz coil to try and replicate the magnetic field that the satellite will deal with while it is in orbit. We also will be ensuring that our system reaches a safe equilibrium temperature. This is so it will operate within each components operational temperature range.

For our actual payload, we will attempt to compile images into a single 3D object file using the SIFT algorithm. We will start by scaling the problem down to determining object’s size by taking photographs in the lab. We will first try to implement a custom program to analyze the data. If this succeeds we will do the same procedure using drones.

If we are able to achieve all that is above over the summer then we will be ahead of what the Air Force requires. Now, I will explain why this research matters.

The reason we care about structure from motion is to be able to identify flood plains as well as flow patterns. We will also be able to use this data as a measure of environmental health. We will work closely with the center for geospatial research to apply our received data to its full potential.
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Ideological Republican Factions in State Legislatures
Robert Oldham; Mentor: Dr. Charles S. Bullock, Political Science

Since the 2010 midterm elections, the Republican Party has been split between “establishment” and “extremist” ideological factions. This division was exemplified in the House of Representatives when the ultra-conservative Freedom Caucus revolted against Speaker John Boehner. In the U.S. Senate it is seen in the obstructionism of Ted Cruz, and in the 2016 presidential primary it is shown when anti-Washington candidates like Donald Trump pit themselves against “insiders” like Jeb Bush. From there, Republican factions only get more complex. Many younger conservatives identify as libertarians, evangelical Christians as social conservatives, and the wealthy as pro-business progressives. To accommodate these diverging interests, the Party must pitch a big tent.

Previous research has noted Republican divisions. Deutchman and Lucas found the major divide among House Republicans to be between social liberals and social conservatives.¹ Bond and Evans saw it as between establishment types and the 2010 Tea Party freshmen. Their research shows that representatives elected in 2010 were less likely to support “functional” legislation such as government funding bills than members who were elected before then.²³ Others have studied factions’ effect on gridlock. Muirhead thought that the popular notion of gridlock being caused by the growing ideological divide between the parties obscures the real culprit: the extremist wing of the Republican Party which disempowers moderates who want to work with Democrats on issues of general agreement. ⁴ By refusing to allow centrists to bring bipartisan legislation to a vote (the Hastert Rule requires a majority of Republicans to agree to advance legislation), extremist Republicans have crippled Congress’s ability to legislate.

McCarty found polarization in state legislatures to be similar to polarization in Congress but did not study whether factions cause similar trouble for party leadership.⁵ If Muirhead is correct and congressional gridlock is the result of intraparty splits between “centrists” and “extremists” rather than rising polarization between the parties, then it is important to know if state legislative factions exist and if they behave similarly to congressional factions.⁶ Focusing on state legislatures can reveal the effect of ideological factions in a variety of legislative settings. Some states have institutional rules such as filibusters and variations of the Hastert Rule that could impede party leadership from advancing an agenda when extremists object. Studying the differences in faction strength between states that have these rules and those that do not can show whether or not party factions are responsible for creating state-level gridlock or at least hindering Republican leadership goals.

To examine state legislative factions, I will analyze a sample of roll call votes across state legislatures in time periods with varying degrees of polarization. I want to know if certain Republicans vote against party leadership in consistent groupings and on consistent issues. Roll call votes will reveal if factions persist over time, if they consistently stick together, and if the issues that they form around are changing. Particularly important are the differences between factions that formed before and after the 2010 midterms because it is likely that the ideological Tea Party movement has increased Republican factionalization. I will also look into several other questions including: Do factions tend to form in the lower or upper chambers of state legislatures? Do moderate and liberal states develop the same factions as conservative states? Does a legislator’s district ideology or leadership status affect
faction membership? There is plenty to learn from state legislative factions, but my primary focuses will be seeing if the national Republican divide is mirrored in state legislatures, if the existence of ideological factions correlates with increased polarization and gridlock, and if institutional rules increase a faction’s ability to obstruct party leadership.

References:
Emerging Ivermectin Resistance of *Dirofilaria immitis* Prompts Need for Improved Heartworm Medication for Dogs

Connor O'Neill; Mentor: Dr. Adrian Wolstenholme, Infectious Diseases

Macrocyclic lactones (ML) are currently the only available preventative for *Dirofilaria immitis* (heartworm) infections in dogs (Vatta, *et al.*, 2014). In the absence of an alternative treatment, lack of efficacy (LOE), or resistance, towards ML’s has been increasingly reported among *D. immitis* strains since 2005 (Pulaski, *et al.*, 2014). Although most of these LOE strains have been reported in the Mississippi Delta region of the United States, their true prevalence and impact on overall animal health remain unknown (Wolstenholme, *et al.*, 2015). Furthermore, while many different anti-heartworm medications exist on the market, they are all categorized as ML’s (Wolstenholme, *et al.*, 2015). Therefore, if *D. immitis* strains develop LOE towards one brand of ML medication, then they can just as easily develop LOE towards the rest of the medications on the market (Wolstenholme, *et al.*, 2015).

In response to this threat to animal health, the ultimate objective of this proposed research is to discover an improved treatment for *D. immitis* infections before their developing LOE defeats current ML preventatives. To accomplish this, it is important to understand the mechanism by which ML medications such as ivermectin interact with both the *D. immitis* pathogen and the host’s immune system. Peripheral blood mononuclear cells (PBMC’s) from the immune system of an uninfected dog will recognize and bind to *D. immitis* parasites while they are in the larval stages of their life cycle (Wolstenholme, *et al.*, 2015). When ivermectin is added to an infected blood sample at a low concentration, it enhances the ability of the PBMC’s to recognize and bind to parasites (Vatta, *et al.*, 2014). However, because there is no direct interaction between the parasite and the drug, ivermectin should only increase recognition and binding to parasites without LOE (Vatta, *et al.*, 2014). Therefore, it is anticipated that if ivermectin suppresses the ability of *D. immitis* pathogens to bypass the host’s immune system, then it should only make a noticeable impact on non-LOE parasites.

To test this hypothesis, larval *D. immitis* parasites will be extracted from blood samples from infected dogs. These parasites will then be mixed with immune cells, which will be extracted from blood samples from uninfected dogs. Ivermectin will then be added to some samples while other samples will remain completely free of ivermectin. The ability of the PBMC’s to bind to and kill parasites in each blood sample will be observed. These data will be recorded to electronic records and analyzed to compare the ability of PBMC’s to kill *D. immitis* parasites in the presence or absence of ivermectin. If the PBMC’s in samples with ivermectin bind to and kill a significantly greater quantity of *D. immitis* parasites, then the original hypothesis is supported. Likewise, if no significant difference is found in this ability between the presence and absence of ivermectin, then the original hypothesis is not supported. Should this hypothesis fail to gain sufficient support in this research, alternative mechanisms among the host’s immune system and ML’s like ivermectin will be further investigated.
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1259.
Increased Levels of Tissue-Nonspecific Alkaline Phosphatase in Hypophosphatasia

Trey Powell; Mentor: Dr. Luke Mortensen, Animal & Dairy Science

Hypophosphatasia (HPP) is a rare genetic disease that prohibits the process of bone mineralization due to severely low levels of tissue-nonspecific alkaline phosphatase (TNAP)\(^1\). Infantile HPP manifests with complications including hypercalcemia, vitamin B\(_6\)-dependent seizures, and craniosynostosis. These patients die from respiratory failure. Other forms of HPP include perinatal, childhood, adult, and odonto-HPP with symptoms ranging from still birth to loss of teeth\(^2\). As there is no current cure for Hypophosphatasia, any combination of these genetic abnormalities leads to the death of over 50% of people diagnosed or suffering from HPP within nine months of birth\(^3\).

Current investigations into HPP therapy include bone chip transplants, mesenchymal stem cell therapy (MSC), and enzyme replacement therapy\(^4\)\(^5\)\(^6\). Enzyme replacement therapy was recently approved for human use. This therapy hinders the livelihood of HPP patients, as it requires daily intravenous treatment, and symptoms quickly reappear if treatment is stopped\(^1\). This therapy does not provide a high quality of life for the patients, thus creating a need for a new therapy. Mesenchymal stem cells derived from bone tissue have shown promise to treat HPP with a low allogenic transplantation rejection rate and by increasing bone mineralization and regaining muscle mass in patients receiving MSC therapy\(^7\)\(^5\). Therefore, MSC therapy should be explored as a curative treatment for HPP.

The research of The Mortensen Lab of the University of Georgia’s Regenerative Bioscience Center involves improving upon MSC therapy as a treatment for HPP. As a CURO Summer Fellow, I will further the work on MSC therapy by transfecting MSCs with viral vectors to deliver elevated levels of TNAP to the bone. I aim to express soluble TNAP within the cells and allow cells to secrete the TNAP into their environment. Modification to the expression of TNAP will be monitored with in vitro studies using an enzyme activity assay. My work this summer will lead to in vivo studies where administration of MSCs expressing high levels of TNAP into the cellular space could rescue bone mineralization, thus providing a more effective treatment for HPP.

My work will have larger implications in biomedical research. I aim to use MSCs as a means to deliver therapy to diseased tissue. My work will model this technique for treatment of other diseases.
References:


A Study of the Prevalence, Community Awareness, and Environmental Levels of *M. leprae* – A Baseline Survey in Ayappakkam, Tamil Nadu, India

Vineet Raman; Mentor: Dr. Corrie Brown, Pathology

Leprosy is an infectious disease caused by the bacteria *Mycobacterium leprae*. Though it has largely been eradicated in industrialized countries, leprosy is still found in developing areas, with South America and Southeast Asia currently accounting for 81% of all new cases. Furthermore, leprosy’s five-year incubation period and ability to remain dormant for up to twenty years make early detection difficult. As a result, typical cases present with severe symptoms characteristic of late-stage leprosy such as visible deformities and visual impairment, leading to what the World Health Organization (WHO) terms Grade 2 Disability (G2D) cases. These G2D cases indicate a lack of health infrastructure capable of detecting the early stages of leprosy. Southeast Asia has documented an increase in numbers of Grade 2 Disability (G2D) cases; the number of G2D cases in India alone reached 500,000 in 2015.

In 2005, the National Leprosy Eradication Program (NLEP)—an initiative of the Indian Ministry of Health—declared that leprosy had been “eliminated as a public health problem” as the prevalence rate of 0.95 cases per 10,000-member population had declined below the threshold of 1.00 case per 10,000-member population. However, recent community surveys conducted by the National Institute of Epidemiology (NIE), a WHO Collaborating Center for Leprosy Research, in the state of Tamil Nadu have indicated that the actual prevalence of leprosy may be higher than previously reported. Despite these findings, no long-term cohort studies currently exist in Tamil Nadu that examine the epidemiology of leprosy.

The objective of this project is to conduct a cross-sectional study of the prevalence of leprosy in Ayappakkam, a sub-urban district 40 kilometers west of Chennai, the capital of Tamil Nadu. By means of our study, we also hope to measure the level of awareness of leprosy in the community, describe and evaluate the experiences of leprosy patients and their family members as they seek help and progress through the existing health systems, examine the presence of *M. leprae* in the patient specimens by characterizing the pathogenic bacteria as multibacillary or paucibacillary, and to determine any additional risk factors that contribute to likeliness of infection.

Consequently, we will randomly sample from the 50,000-member Ayapakkam community that has been characterized demographically by the NIE. We will stratify our sample to ensure adequate representation of different socioeconomic and demographic backgrounds. We will use standardized NELP definitions for the diagnosis of leprosy in the cohort and external experts from the Central Leprosy Training and Research Institute (CLTRI) to validate the diagnoses. Trained field workers will use standardized questionnaires to gather data on socio-economic, demographic, and clinical characteristics of leprosy patients. A semi-structured questionnaire will be utilized to collect information regarding the informal and formal treatment experiences of leprosy patients and the general level of awareness of the disease. Environmental *M. leprae* specimens will be collected using standard scientific protocol to ensure the bacteria remain out of human contact and are not contaminated.
My role as research assistant would be to become well-versed in literature regarding leprosy, manage the default inputs for data collection devices (tablet computers), and to conduct field visits to ensure methodical and accurate collection of data. After data collection is complete, I will analyze the data and write a final report.

We will share the data gathered with managers from the NELP for use in their plans for possible interventions. Our findings will also help us to educate the Ayappakkam community on important aspects of leprosy, in addition to providing a much needed baseline for the establishment of further long-term cohort studies to analyze the disease trends, transmission dynamics and the efficacy of leprosy treatment services.

References:


Obesity is the condition of having excess body fat (adipose tissue), and a Body Mass Index greater than 30. Obesity has reached epidemic proportions with 35% of adult Americans being obese (Ogden 2016). It is also the leading cause of preventable death in the USA, making it one of the top research priorities. Obesity results from the increased production and size of adipocytes, fat cells, in adipose tissue. This results from imbalance between food intake and energy expenditure, leading to an excessive accumulation of adipose tissue. While genetics plays a role in obesity, the health related risks of obesity and the difficulty individuals have losing weight, may be better explained by epigenetic factors. One such epigenetic factor, Coactivator-Associated Arginine Methyltransferase 1 (CARM1) catalyzes modification of proteins such as histones at adipogenic genes and appears essential to the transformation of preadipocytes into mature adipocytes and perhaps the proliferation of adipocytes (Therrien, 2009). The cellular memory of CARM1-catalyzed asymmetric arginine modifications in visceral and subcutaneous adipose tissue (VAT and SAT) adipocytes may impact the ability to gain and lose weight (Yadav, 2008). Our main goal this summer is to identify the optimal compound that inhibits proliferation of adipocytes, the process of adipogenesis, and the maintenance of mature adipocytes on site. CARM1 is essential to the preceding processes and, if inhibited, could lead to the blockage of the development of harmful, mature fat cells. However, adipocyte cell-type-specific epigenetic analysis within adipose tissues has been difficult, because mature adipocytes are exceptionally large fragile cells that tend to lyse during isolation and manipulation. Nonetheless, Dr. Meagher’s laboratory recently developed innovative tools to enable adipocyte-specific epigenetic analysis of chromatin structures including fluorescence activated nuclear sorting of adipose tissue nuclei and a preadipocyte cell line that fluoresces when cells started to differentiate into mature adipocytes (ADNp::RFP (Ambati, Submitted). This allows us to quantify the data and determine if the inhibition of the compound is actually taking place. I will begin by inhibiting adipocyte development of this cell line using the natural compound CARM1 inhibitor Ellagic Acid and then move on to pharmaceuticals newly designed to inhibit CARM1 (Kang, 2014). The fluorescence activated nuclear sorting will be used to determine when a cell has started to differentiate, and if the drug compounds being used are inhibiting the preadipocytes from differentiating into mature fat cells. If inhibition occurs, we will further determine the effectiveness of the drug in discontinuing adipogenesis and its effect on the proliferation of adipocytes on site. Our translational medicinal goal is to reduce obesity and its harmful comorbidities including cardiovascular disease, some cancers, type II diabetes, inflammation, and dementia by testing this next in mouse models.
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Evaluation of the Effectiveness of Georgia Department of Natural Resources Hunt and Learn Program

Shelby Telfer; Mentor: Dr. James Martin, Warnell School of Forestry & Natural Resources

Introduction:

Experiential learning is a model that describes how individuals learn. Specifically, this model describes learning as "the process whereby knowledge is created through the transformation of experience" (Kolb 1984). Environmental education often employs this process of learning to allow children and adults to gain new experiences while simultaneously developing skills and understanding of nature and the outdoors (Kolb 1984). This approach is commonly implemented to alleviate the Nature Deficit Disorder crisis (Louv 2005).

The Georgia Department of Natural Resources Wildlife Resources Division (WRD) employs the experiential learning model when it comes to training young hunters. Since the 1980’s, the WRD has collected data that reflect a general decline in the number of Georgia licensed hunters. It is a concern that this decline may be attributed to a lack of participation by young hunters. Wildlife professionals suggest this decline has been caused by increased urbanization, competition with other recreational activities, and an overall issue with the ease of access to wildlife populations and acceptable hunting areas (Killmaster 2014). In an attempt to reverse this decline, WRD has implemented the Hunt and Learn Program.

The Hunt and Learn Program is a series of Advanced Hunter Education workshops offered at the Charlie Elliott Wildlife Center (CEWC) in Mansfield, Georgia. The first workshop was offered in May 2010. These workshops focus on the development of hunting basics, wildlife management, and firearm safety. Children between the ages of 10-17 are invited, along with a parent or guardian, to a weekend of experiential learning opportunities that focus on various game pursuits including squirrel, rabbit, white-tailed deer, northern bobwhite, wild turkey, and the sport of falconry. Participants are given the opportunity to earn their Hunter Education certificate, receive instruction from experts in the field, learn firearm safety, participate in multiple hunts, and learn culinary skills to prepare their game.

Objective:

The objective of this study is to evaluate changes in participant’s knowledge, attitude, and behavior as a result of participating in the Hunt and Learn Program.

Methods:

A retrospective survey will be designed and administered electronically using the UGA Qualtrics platform. The target audience for this survey are past participants of the Hunt and Learning Program (N = 320). The administration of the electronic survey will include a pre-notification email, initial survey distribution, two reminder emails, and final email asking participants to respond (Dillman, 2007). Analysis of the survey data will be conducted using SPSS. Cronbach’s alpha for each construct will be determined as a test of reliability (Cronbach, 1951).
Outcomes:

This project will provide CEWC and the WRD Hunter Education program with information critical to evaluate the effectiveness of the Hunt and Learn Program. Georgia is one of only a few states in the US that has developed an educational program of this kind. The stakeholders will use the results of this evaluation to improve their program model, and share it with other states to assist them in building new programs, or improving existing programs. Results of this evaluation will ultimately benefit the conservation and management of Georgia’s wildlife.

References:


Adapting a CRISPR-Cas System into a Novel Gene Expression Knockdown Platform

Nikita Vantsev; Mentor: Dr. Michael Terns, Biochemistry & Molecular Biology

What started off as a strange repeating sequence of nucleotides found in the genomes of various types of prokaryotes, 50% of bacteria and 90% of archaea (Doudna et al. 2016), was later found to be the prokaryotic adaptive immune system, changing the notion that only vertebrate animals can possess an adaptive immune system. The CRISPR-Cas system consists of the CRISPR (clustered regularly interspaced short palindromic repeat) locus on a prokaryote genome: invader sequences (spacers) separated by a short repeat sequences, and Cas (CRISPR associated) proteins. CRISPR-Cas systems protect prokaryotes from viruses and other invader nucleic acids.

A CRISPR-Cas system utilizes a three step process: Adaptation, in which a prokaryote integrates a short sequence of invader nucleic acid into its own CRISPR locus to become a spacer; CRISPR-RNA (crRNA) biogenesis, in which the spacers are transcribed and processed to become crRNA molecules; and invader silencing, during which Cas proteins use the guiding crRNA, to interfere with and silence future invaders (Terns et al. 2014). There are six distinct types of CRISPR-Cas systems in prokaryotes that differ primarily in the proteins responsible for invader silencing. The diverse types of CRISPR-Cas systems each execute the same three basic steps but use different RNA and protein components (Terns et al. 2014).

What makes CRISPR-Cas systems a highly relevant topic today is its new found role in genetic engineering. The Type-II CRISPR-Cas system uses a single DNA nuclease protein, Cas9, guided by base-paired tracrRNA and crRNA, to introduce nicks into the invader DNA sequence. By artificially designing a sgRNA, combining both tracrRNA and crRNA, Cas9 can be programmed to target and nick specific genes in a wide range of organisms (Jinek et al. 2012).

The purpose of this research project is to adapt the Csm invader silencing complex in Type-III CRISPR-Cas of Lactococcus lactis, as an efficient mRNA knockdown research tool. Our previous research on the Csm system has shown that it can efficiently target RNAs that are complementary to the guide-crRNA (Terns lab unpublished). I will be using genetic and biochemical methods to first, introduce mutations in the active sites of Csm proteins responsible for RNA cleavage, second, transform and express the plasmid containing the complex and the guide-crRNA sequence in E. coli, and third, let the Csm-crRNA complex, programmed by the guide-crRNA sequence, target a specific gene transcript of E. coli genome (we would be primarily targeting the mRNA of a lipoprotein (lpp), lacZ, and other highly expressed non-essential cellular proteins). Next, I will use the Northern blotting (RNA analysis technique) to probe for the mRNA produced by the targeted gene (lpp of lacZ). Based on the size of the target mRNA produced by the different variations of Csm mutants, I will be able to tell if the Csm-crRNA complex successfully cleaved the mRNA message. Additionally, I will assay for expected reduction of the protein products. By conducting a series of experiments on the Csm-crRNA complex activity and analyzing mRNA and protein data, I hope to figure out the role of each protein in mRNA targeting, which will help to determine the pathway by which CRISPR-Cas Type-III invader silencing works. Conducting these experiments would also allow me to optimize for the most efficient and accurate mRNA silencing tool in E. coli. In the long run, I hope that this novel
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gene expression knockdown platform that we develop, will be effective for genetic engineering and gene discovery applications in a broad range of bacteria such as those that we depend upon for production of our food, pharmaceuticals, and new biofuels.

References:


Dementia is a major threat to public health. Due to the world’s aging population the prevalence of dementia is expected to triple by 2050. Studies show almost all aging adults will experience dementia symptoms as a result of decreased cerebral blood flow and white matter damage leading to a newly recognized form of dementia known as vascular cognitive impairment (VCI). Previously, clinicians attributed most cognitive decline to Alzheimer’s disease, however with the recognition of pronounced vascular changes exhibited by dementia patients this view is now being challenged. In 2012, the National Institute of Neurological Disorders and Stroke (NINDS) Stroke Progress Review Group cited “prevention of vascular cognitive impairment” as a major research priority as vascular dementia currently contributes to approximately 20% of all dementia cases.

There currently is no Food and Drug Administration approved treatment for VCI. In response to the demand for a viable VCI treatment, we have developed a safe, inexpensive treatment method known as remote ischemic conditioning (RIC). For this particular treatment, a blood pressure cuff is applied to the arm and repeatedly inflated and deflated promoting the brain to protect itself. In a recent publication by our group, we demonstrated in a murine VCI model that RIC effectively prevents white matter damage and cognitive impairment by increasing cerebral blood flow (CBF), and reducing the accumulation of amyloid-beta 42 protein.

Numerous therapies for dementia have failed in human clinical trials due to the use of animal models not truly representative of the human condition. The current absence of an effective, translatable dementia treatment indicates a clear need for a more human-like animal model for the development of a successful treatment. As a result, we are developing a novel VCI pig model in order to test RIC prior to clinical trials. The pig brain has comparable size and structure to the human brain. Most importantly, the pig brain has a similar composition of white and gray matter to ours and is at a similar stage of myelination, a characteristic vital to the successful development of a translatable treatment. We hypothesize that after sustaining a VCI injury, pigs will demonstrate cognitive deficits both the short and long-term, but RIC treatment will result in significant improvements in overall cognition.

One of the major assessment tools used to determine if a VCI treatment is effective is observing changes in cognitive function, specifically learning, memory and behavior. This May, I will evaluate the ability of 6 month-old male pigs to perform two cognitive tests: object recognition and open field. The animals tested in this phase of the study will be used as a baseline for normal pig cognition, memory, and behavior. I will play a primary role in the experimental design, data collection, analysis and interpretation of these object recognition and open field tests with this test group of pigs. In addition, I will continue to aid in animal habituation, VCI surgeries, pre- and post-operative care and RIC treatments. These pigs’ performance will be compared to RIC treated and non-treated VCI pigs in the next phase of this study. Development and characterization of key changes in the VCI piglet model from RCI treatment utilizing analyzed data from this summer's
uninjured pig model will enable a more robust and predictive assessment of novel treatments that will likely lead to more success in human clinical trials.

References:


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