Eleventh Annual

Fall Research Symposium

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Division of Science & Mathematics
University of the Virgin Islands

Eleventh Annual
Summer Research Symposium

September 20, 2009
St. Thomas, U.S. Virgin Islands

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The Effects of Oxotremorine on the Pyloric Central Pattern Generator of the Caribbean Spiny Lobster, *Panulirus argus*

Rifa Abdullah

Mentor: Richard Hall, PhD

In spiny lobsters, motor commands to muscles for eating are produced by small neural circuits known as the central pattern generators (CPG) that are located in four ganglia of the Stomatogastric Nervous System (STNS). The paired commissural ganglia (CoG) are part of the central nervous system (CNS) and send axonal projections to two peripheral ganglia: the esophageal ganglion (EoG) and ultimately through a solitary nerve to the distal stomatogastric ganglion (STG). We are investigating the ability of CNS neurons of the CoG to influence the activity of a peripheral CPG.

The pyloric CPG located in the STG produces rhythmic bursts of action potentials that power food sorting. When connectives from the CoG to the STG are cut, the pyloric CPG disappears; thus input from higher centers are required to produce a pyloric rhythm. Previous work demonstrated that superfusion of the STG with muscarinic agonists such as pilocarpine and oxotremorine transiently increase burst frequency and duration of bursts of the pyloric dilator (PD) of the pyloric CPG while inhibiting activity of the ventricular dilator (VD) and lateral pyloric (LP) neurons. We hypothesize that the CoG's utilize the same set muscarinic controls on the pyloric CPG as observed by direct superfusion of the STG. We predict that superfusion of the paired CoGs with oxotremorine will increase duty cycles of PD bursts while decreasing duty cycles of VD and LP bursts. To test this prediction, we superfused both CoGs with oxotremorine saline ranging from 10^{-5} to 10^{-4}M for five minutes and followed each treatment with a twenty-minute wash with lobster saline.

Oxotremorine superfusion of the CoG increases PD duty cycle up to concentrations of $2x10^{-5}$M oxotremorine but absolute changes depend on control burst frequency. At a pyloric rhythm of 1.4 Hz, the duty cycle of PD increased from 0.325 ± 0.007 to 0.569 ± 0.149. While preparations with rhythm frequencies of 0.4 Hz, PD duty cycles increased slightly from 0.153 ± 0.043 to 0.224 ± 0.007. The relationships between VD, LP, and PD duty cycles are complex and complicated by variations in VD and LP bursting. In general, as PD and VD duty cycles increase, LP duty cycles decrease. While oxotremorine superfusion of the CoG clearly increases PD duty cycle, it also increases variability in VD and LP bursting characteristics.

NIH MBRS-RISE Grant Number: GM061325

Explorations into the Properties of the Visceral Pericardium

Agene' Rogers and Frazly Alexander

Mentor: Paul Jobsis

The purpose of this study is to understand the function of the visceral pericardium (VP) and how it plays a role in recovering energy used during a cardiac cycle to return the heart to its initial relaxed state. The visceral pericardium is a thin sheet that covers the outer layer of the heart and consists of collagen and elastic fibers. Due to the orientation of the fibers, it was hypothesized that the VP could act as a spring that could affect the conditions at end systole and end diastole. The loading of the elastic "spring" on the VP would then increase the untwisting rate that allows the myocardium to expand in early diastole. To test this, the visceral pericardium of three pigs on separate occasions was disrupted with incisions and VP removal, and analysis of the heart's motion or behavior was conducted before and after the disruption. The images were digitally recorded with a high speed camera at both 200 and 400 fps. Measurements were then taken of gap widths at end systole and end diastole to note any changes and to test whether or not the VP really acts like a spring. It was predicted that gap size would increase at end systole. However, data analysis was inconclusive, with measurements not significantly changing. Further analysis of cardiac surface motions could aid in the testing of the hypothesis and show that the VP does play a certain role in the cardiac cycle.

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Risk factors for delayed transition from intake to approval for adoption in shelter puppies and kittens

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It is standard practice in many shelters for puppies and kittens to be isolated in foster care or returned to the relinquishing owner before they are transitioned to the adoption floor. This reduces the risk of infectious disease transmission and enables more animals to enter the sheltering system and eventually find lifetime homes. Factors that prolong the transition from intake to isolation and then to the adoption floor are costly and reduce the number of pets saved. In this study, we characterized a randomly selected group of puppies and kittens (≤26 weeks old) taken into PAWS Chicago in 2008 using shelter records. Statistical comparisons were made between two groups – those which took ≥20 days from intake to being approved for adoption by a veterinarian (Delayed group) with those that took ≤19 days (Not Delayed group). We hypothesized that puppies and kittens that were younger and/or lower bodyweight at intake would be more likely to be delayed. Reduced age, number of body systems identified as abnormal on the initial veterinarian exam and number of medications prescribed during the isolation period were all highly significant risk factors for delayed transition in both species (p<0.0001). Gender status and presence of a fever at intake were not statistically significant risk factors. Identification as a specific breed in puppies was not associated with delay, but DSH kittens were over-represented in the Delayed group (p<0.0001). We conclude that delays in transition from isolation to the adoption floor are less likely if older puppies and kittens, with fewer abnormalities detected at the initial veterinarian exam, are chosen by PAWS Chicago staff for intake into the shelter. This strategy should reduce costs and enable more lives to be saved.

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Cortical Axon and Neurite Differentiation Occurs Through Dynamic Myosin-Dependent Mechanisms

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Spinal cord injury (SCI) is one of the major medical conditions facing the world today. The spinal cord is part of the central nervous system (CNS), where signals are transmitted between the brain and various parts of the body. The CNS is made up of neurons which conduct electrical impulses away from the cell body via its axon and toward the cell body via its dendrites. SCI is where damage is done to the axon, and therefore signals are not able to travel on to the rest of the system. Many approaches have been made to regenerate axons, but none have been proven to be a complete success.

In the research experiment done, the differentiation of axon and neurite outgrowth was observed and analyzed using Image J under normal conditions. The differentiation of neurite and axon was studied by immunostaining, and the behavior of the process growths was determined by inhibiting myosin. Cells were also frozen in different substrates and then tested to see which protocol worked best. The axon and neurite extended faster when growing than retracting. The immunostaining analysis showed that the axon is not differentiable before 24 hours of plating, and the inhibition of myosin showed that the axon and neurite grew faster with fewer retractions than with the myosin. The frozen cells seemed to survive best in the highest concentration of glucose (30%). This would help in axon regeneration by knowing at what time to expect the axon development. Also myosin could be inhibited in regenerating axons to lower the retractions and increase the extension process. The freezing protocol can be used to freeze excess neurons to avoid sacrificing a rat each week.

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Bottom-Mussel Aquaculture does not Influence the Settlement of Mussel Seeds in Nearby Eelgrass Beds

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Eelgrass beds (*Zostera marina*) are considered one of the most important habitats in the Gulf of Maine. They provide homes for many marine organisms, in addition to serving as nurseries, refuges, and feeding grounds. They help protect the shoreline and help to clarify the water by acting as an intertidal riparian buffer. Many organisms such as shellfish, gastropods, polychaetes, fishes, and bivalves use eelgrass beds. In a species diversity study done at Hadley Point near the Mount Desert Island Biological Laboratory (MDIBL) in restored eelgrass beds and naturally grown eelgrass beds, blue mussels (*Mytilus edilus*) were the dominant species in summer of 2008. Mussels seeds, newly settled young mussels, accounted for more than 93% of the organisms found at each site. These beds, especially the restored beds, were located near a 47-acre bottom-mussel aquaculture site, which might explain the overwhelming number of mussels found. These findings lead us to a new question in summer 2009: are high numbers of mussel seeds a naturally occurring phenomenon in eelgrass beds or is this due to the mussel aquaculture site? Our hypothesis was that the aquacultured mussels lead to high seed levels. To test our hypothesis, we compared mussel seed density on eel grass at Hadley Point to that found near Bar Island where no mussel aquaculture is present. During low tide at Hadley Point, we randomly plucked six eelgrass blades. The blades were placed in separate ziploc bags labelled 1-6. Water parameters were measured, such as dissolved oxygen, salinity, and temperature. The same procedure was done at Bar Island for five consecutive weeks. Samples were taken back to the lab where they were all separately measured and then enumerated under the dissecting microscope. The numbers of mussel seeds found on each blade and the number of other organisms were recorded. A two-way ANOVA was done to test for statistically significant differences of mussel seeds found per cm blade as time changed at both sites. Dissolved oxygen, salinity, and temperature values were higher at Bar Island than at Hadley Point. There was a statiscally significant difference for the number of mussel seeds found per cm at both sites as time increased. However, there was no significant difference in the of mussel seeds found between the two sites. Therefore, we failed to reject our null hypothesis. Comparison of these two sites suggests very high numbers of mussel seeds might be a naturally occurring phenomenon. To test this idea further, more sites are needed.

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Lack of alarm responses in the long spined sea urchin *Diadema antillarum* and the reef urchin *Echinometra viridis*

Jan-Alexis Barry and Teresa Turner

The ability to detect a predator before being consumed is a very advantageous trait. Alarm responses are a survival tactic initiated by the chemical detection of a predator or injured heterospecifics and conspecifics (Snyder and Snyder 1970). Many species of sea urchins (e.g. *D. antillarum* and *E. viridis*) demonstrate an alarm response to injured conspecifics, but their responses to predator's presence have been poorly documented (Snyder and Snyder 1970). My question was whether or not the presence of a predator, *Cassis tuberossa* (King helmet shell), can trigger an alarm response in both species. My null hypothesis stated: the predator's presence would not render an alarm response, so they would not move away from the predator. My hypothesis stated: the presence would trigger an alarm response, and I predict that the urchins would move away from the predator. I tested these hypotheses with a field experiment at Brewers Bay St. Thomas. I collected *D. antillarum* and placed them a sandy bottom. For the control group, I squirted fresh sea cucumber body fluids into the current towards the urchins because it was proven that these urchins aren't affected by these fluids (Snyder and Snyder 1970). I put the Helmet shell under a crate directly in the path of the current, and let the scent flow over the urchins, then I observed their behavior for 5 min. I replicated this experiment three times with *D. antillarum*, and then repeated with *E. viridis.* In both species, there was no movement observed at all. We conclude that the presence of the predator did not trigger an alarm response in the urchins.

This work was supported by NSF HBCU-UP grant number HRD – 0506096

Acceleration of Logarithmic Convergence

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Our summer research was dedicated to the acceleration of the convergence of infinite series, $\sum_{n=1}^{\infty} a_n$, where $\lim_{n\to\infty} \frac{a_{n+1}}{a_n} = 1.$ Such series are generally referred to as logarithmic series.

If $\{a_n\}_{n=1}^{\infty}$ and $\{b_n\}_{n=1}^{\infty}$ are sequences converging to A and B respectively and if $\lim_{n\to\infty} \left| \frac{a_n - A}{b_n - B} \right| = 0,$ then we say that $\{a_n\}_{n=1}^{\infty}$ converges more rapidly than $\{b_n\}_{n=1}^{\infty}$.

Throughout this paper, $\varphi(n)$ will denote a differentiable function on $[1,\infty)$ that satisfies $\varphi(n) > n$. Furthermore, we shall use ($S(\varphi(n))$) to denote the $\varphi(n)$-th partial sum of the series $\sum_{n=1}^{\infty} a_n$.

First, we define T as a transformation on the partial sums of $\sum_{n=1}^{\infty} a_n$ that satisfies:

a. $T(S(\varphi(n))) \to S,$ and

b. $T(S(\varphi(n)) = S(\varphi(n)) + D(\varphi(n))$, where $D(\varphi(n)) = \frac{S(n) - S(\varphi(n))}{1 - \frac{1}{\rho}}$.

We then show that if $\lim_{n\to\infty} \frac{D(\varphi(n))}{S - S(\varphi(n))} = 0$, then $\lim_{n\to\infty} \left| \frac{T(S(\varphi(n))) - S}{S(\varphi(n)) - S} \right| = 0.$

This result leads naturally to the class of series accelerators $T_{\varphi,\rho}(S(n)) = \frac{S(n) - (1/\rho) S(\varphi(n))}{1 - (1/\rho)}$,
which are extensions of the T_m accelerators by Clark and Gray (see [3]).
It turns out that the quantity ρ in the formula for $D(\varphi(n))$ is not an arbitrary positive number, but rather one that is closely associated with the convergent series $\sum f(n)$ via:
$\varphi'(x) f(\varphi(x)) = \rho f(x).$

We conclude our research by showing how our accelerators can be used to accelerate the convergence of the series $\sum_{n=1}^{\infty} \frac{1}{n^2}$.

This research is funded by NSF HBCU-UP - Grant Number HRD 0506096

Confirmation of high definition comparative genomic hybridization (CGH) results with PCR

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Dr. Peter Nagy, University of Iowa

This research aims at detecting copy number changes in a patient that displays mild mental retardation, attention deficit hyperactivity disorder, oppositional defiant disorder, and other symptoms. We hypothesize that the patient has a copy number variation in the form of a deletion or duplication. If there is a deletion then it will lead to the loss of genes that are important to neural development. If there is a duplication then it will lead to duplicate copies of genes that are important to neural development.

Comparative Genomic Hybridization (CGH) was performed with a 385K low resolution CGH array. A 1.2Mb deletion on chromosome five of the patient's DNA was identified. A 2.1M high resolution CGH array was performed to have a more accurate determination of the deletion's breakpoints. According to the Marie Baekvad-Hansen et al. paper, a 2.2Mb deletion on chromosome five lead to the deletion of 15 genes that contributed to a patient having congenital heart disease and mental retardation. Six of these genes were similarly lost in this current study's patient. However, congenital heart disease is not present in this study's patient. This leads to the conclusion that the six genes lost in this study's patient account for the presence of mental retardation. Currently the breakpoints of the 1.2Mb deletion identified by this study are in the process of being confirmed by PCR.

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Bacterial Flora in the Reproductive Tract and Mammary Gland of the St. Croix White Hair Sheep

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Hair sheep farms in the Caribbean are exclusively for meat production. Between all sheep breeds in this region, the St. Croix White hair sheep is the most common, due to their superior adaptation to tropical conditions and other traits such as good proliferation and resistance to parasites. The reproductive performance of livestock is negatively affected by uterine infections, which translates to a decline in profit potential for local farmers. In addition to uterine infections, mastitis is one of the more common health problems affecting sheep and goats. Moreover, reduced milk yield caused by mastitis leads to decreased growth of the lambs (Fthenakis and Jones, 1990). To date, studies using local ewes have been conducted to evaluate the effect of the type of feed on growth and carcass traits in lambs (Dodson et al., 2005; Godfrey and Weis, 2005), the effects of ram exposure on uterine involution and luteal function during the postpartum period (Godfrey et al., 1998), behavioral and endocrine responses of ewes exposed to different mating stimuli around estrus Godfrey et al., 2001), etc. However, there is no information about intramammary bacterial pathogens and normal flora of the reproductive tract of local hair sheep (e.g., St. Croix White hair sheep). This information will be of great significance to sheep producers confronting cases of mastitis or uterine infections. The uterine tract from cull ewes (n=4) were used to collect bacterial samples for classification and bacterial count. In previous pilot experiments, the method of collecting bacterial samples from the reproductive tract using the laparoscope was unsuccessful. A slightly different approach was used which was very time consuming and caused a delay in collection of data. Data collection is still ongoing.

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Alpheid Shrimp Reduce Burial Time of Corkscrew Anemone

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The corkscrew anemone *Bartholomea annulata* resides at the sand-hard substrate interface and provides a home for many organisms including species of cleaner shrimp, which aid in coral health. This bottom-dwelling anemone is subject to sand burial by burrowing lugworm's mound, as well as by natural sand inundation. Snapping shrimp, *Alpheus* spp., which reside at the base of *B. annulata,* have been observed using its pleopods to remove sand from buried anemones. Does this behavior significantly improve the ability and time of an anemone to be unburied? In field experiments, anemones were buried with and without alpheids. A day later observations were made of whether the anemones were buried or not. Lab experiments were conducted in shallow pools where anemones were subjected to the same treatments (with and without alpheids), and checked at fifteen minute intervals. Tests show that there is no difference for an alpheid to significantly improve the ability of an anemone to become unburied, in the field (p-value = 0.4924, T-test) and in the lab (p-value = .9058, T-test), although the alpheids did reduce the amount of time anemones were buried (p = 0.0439, T-test). The digging behavior of the alpheid shrimp may be used more to maintain an anemone's burrow than to rescue the anemone from burial.

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Nuclear Receptors Identified in Migratory Cells of Drosophila Egg Chambers

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Ovarian cancer is the 5th leading cause of cancer death for American women. This is primarily because it is not diagnosed until it has metastasized and affected other areas of the body. To bring scientists closer to developing cancer treatment for this invasive disease, we look to Drosophila melanogaster. It has been shown that the process by which cancerous epithelial cells in human ovaries metastasize is genetically and morphologically similar to the process by which follicle cells in the egg chambers of Drosophila migrate. Both of these processes are controlled by signaling pathways, and one of these pathways is controlled by nuclear receptors, particularly steroid hormone receptors. Nuclear receptors (NR) are ligand-regulated transcription factors that are essential for normal growth and development. We specifically studied NRs in Drosophila egg chambers because they have strong human homologues and Drosophila provides a simplified system to uncover their roles, and possibly their unknown ligands. Our aim is to identify which of the 18 known NRs are activated during oogenesis. Our results identified 5 NRs present in Drosophila egg chambers. In addition, we observed that disruption of 1 NR, E78, via dominant negative caused a phenotype characterized by multi-layering and abnormal follicle cell arrangement. Our results suggest E78 is required for oogenesis. Future tests, which are currently underway, will verify and better characterize this phenotype. The results of our research can be used to gain a better understanding of the molecular mechanics of ovarian cell migration.

This research was funded by NIH MARC Grant # GM008422 and the Leadership Alliance

Tracking GABA-ergic Neurons in the nervous system of the Caribbean Spiny Lobster

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Gamma-aminobutric acid (GABA) is a neurotransmitter found in most invertebrates in vertebrates. GABA is generally inhibitory acting through receptors to increase chloride currents or to activate G protein cell inhibitos.

In this study, we are looking at the location and projections of GABA containing neurons found in the *Panulirus argus* stomatogastric nervous system (STNS). With this information we can then study how GABA influences small neural circuits such as those used for food sorting or chewing. Based on earlier studies with blue crabs we expect GABAergic neurons to be found primarily in the anterior STNS but not to project beyond motor circuits in the stomatogastric ganglion (STG).

GABA containing cells were located using rabbit anti-GABA and visualized with anti-rabbit antibodies labeled with Alexa 488. Alexa 488 epifluorescence was measured using Leica FLIII macroscope equipped with a sooled digital camera and analyzed in Photoshop™.

Unlike the blue crab, GABA was found in diffuse regions in the paired commissural ganglia (COG) and project through the inferior esophageal nerves (ion) to GABA-containing cells in the esophageal ganglion (EOG) where we see distinct cells, and axonal projections passing through the stomatogastric nerve (stn) to the STG. As in crab, no GABA-containing cell bodies were observed in the STG and no GABAergic axons projected beyond the STG. The neural sheaths in lobsters were of surprising thickness compared to those of the blue crab which made identification of axonal terminals difficult. More accurate localizations of GABAergic cell endings will require additional experiments where these sheaths are removed or rendered porous.

We now know where GABA is being created and stored and will next identify GABAergic targets. By doing this, we will better understand the path that GABA takes and how it affects certain small motor circuits like those in the STG. Studies will include the manipulation of neural signaling with GABA agonists and antagonists in temperature acclimated lobsters.

This project was sponsored by NIH MBRS-RISE Grant Award No. GM061325 and NSF HBCU-UP grant number HRD – 0506096

Differences in aggression may explain differences in numbers of *Periclimenes yucatanicus* and *P. pedersoni* inhabiting corkscrew anemones

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Several species of crustaceans reside on the corkscrew anemone, *Bartholomea annulata*, including the Spotted Cleaner Shrimp (*P. yucatanicus*) and the Pederson Cleaner Shrimp (*P. pedersoni*). Field surveys indicate that *P. yucatanicus* (Py) is often found solitarily while *P. pedersoni* (Pp) is found in groups. We wondered if this difference in sociality can be explained by a difference in aggression of the two species. We placed pairs of shrimp in a small container for 15 minutes and recorded various aggressive or non-aggressive actions. Three treatments were conducted (Pp vs. Py, Pp vs. Pp, and Py vs. Py) to test for differences in inter- and intraspecific aggression. We found a significant difference in the number of aggressive acts among the three trials ($p = 0.011$, ANOVA) where the aggression was significantly less in the Pp vs. Pp experiment in comparison to the Pp vs. Py and Py vs. Py trials. While there was no significant difference in aggression level between the two species in Pp vs. Py trials ($p = 0.430$, t-test), there is a higher level of aggression in the experiments containing the *P. yucatanicus*. These results may explain why the *P. yucatanicus* are more like to be found alone while the *P. pedersoni* are found in groups.

Funding for this work was provided by MBRS-RISE 5R25GMO61325

Was the orange cup coral introduced to the Caribbean?

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The orange cup coral, *Tubastraea coccinea*, is an azooxanthellate stony coral that is indigenous to the Pacific. Besides *T. coccinea*, there are no other known coral species that are found in both the Pacific and Atlantic oceans. Its first documented reports on the coasts of Curacao and Puerto Rico were in 1943. *T. coccinea* is not reef building, but will grow on coral reefs and so may pose a threat to native coral species that do in fact build reefs. Corals are important in the protection of our coastlines and an asset to the economy. Although distributional studies have hypothesized that *T. coccinea* was introduced to the Caribbean from the Pacific, there are no genetic data to test this hypothesis. We are investigating whether there is genetic variation between Western Atlantic and Indo-Pacific *T. coccinea*. Pacific samples were previously extracted using a CTAB protocol. DNA was extracted from Caribbean samples using the DNeasy protocol. We then used the samples in PCR reactions with mitochondrial and nuclear primers. The primers we used targeted gene regions that have variation in other coral species. Once DNA sequences are obtained from these PCR products, comparison with each other and other sequences from Genbank will determine the amount of genetic variation between Caribbean and Pacific samples. If there is no variation, then this supports the hypothesis that the species was introduced and we fail to reject our null hypothesis that there is no difference between the genetic sequences of *T. coccinea* from both oceans. We can further this research by using a larger sample size with samples from more Caribbean localities.

This work was supported by NSF HBCU-UP grant number HRD - 0506096, NSF Grant EF-0531735 to SLR and the ECS Honors Fund.

The Effect of Seascape Structure on the Spatial Distribution of Juvenile Fish Within Benner Bay Mangrove Lagoon, St. Thomas, United States Virgin Islands (USVI)

Christina Colletti

Mentor: Dr. Simon Pittman, NOAA

Back-reef systems have generally been accepted as providing a nursery function for fish. Mangroves have been highlighted as the main habitat component contributing to prime fish nursery habitat. The appeal of mangrove habitat to many juvenile fish species is due primarily to both the shelter their roots offer from predators and the prey sources they provide. Although mangroves are an important and characteristic component of fish nursery habitat, recent research suggests that the nursery function of an area may be dependent on the connectivity between many different habitat types. Examining the nursery function of an area from the perspective of its habitat mosaic is important because many Caribbean fish species utilize several biotopes throughout their daily home ranges. This study explores the effect of seascape structure on the spatial distribution of juvenile fish by relating the composition of biotopes within seascapes to the density and diversity of fish caught within Benner Bay Mangrove Lagoon on St. Thomas, USVI. Fish were surveyed using traps placed about one meter from the mangrove edge, eight times per month during July 2008 till December 2008. Spatial information pertaining to seascape structure was obtained by visual census of the area and transcribed to digital format using GIS (Geographic Information Technology). Information about the seascape preference of juvenile fish obtained from this study is valuable for conservation and management applications, especially for the formation of marine protected areas.

Funding Source: Virgin Islands Division of Fish and Wildlife, Department of Planning and Natural Resources

Identifying cofactors and determining DNA-binding specificity for the transcription factor MEF2C

Adrianne Crooke
Mentor: Dr. Paul Jobsis

Myocyte enhancer factor 2 family of transcription factors are ubiquitously expressed in most tissues but are primarily active in striated muscle (cardiac and skeletal) and the brain. There are four transcription factors in this family (MEF2 A-D) that help to regulate the function of muscle cells. It is not known how the different MEF2 genes are able to bind particular promoters to start the transcription of a certain gene. However, all MEF2 transcription factors bind the same consensus sequence in target gene promoters and *in vitro* they have been shown to act similarly. However MEF2 factors likely activate different target genes *in vivo* based on mouse knock out phenotypes. MEF2C knockout mice have shown that MEF2C is critical in embryonic heart development. Knockout MEF2C ventricles fail to form (embryonic day 7.5) making the knockout phenotype embryonic lethal. Two experiments were conducted to first determine to determine if there are any cofactors that interact with the c-terminus of the MEF2C gene and second determine the DNA-binding specificity of MEF2C. To determine if there are any cofactors that interact with the c-terminus of the MEF2C gene, the c-terminus of the MEF2C gene was cloned into the vector pGEX-2T which contains GST in order to make a GST construct so that it can be used in a GST pull down assay to determine if there are any cofactors that interact with the c-terminus of MEF2C. To determine DNA-binding specificity of MEF2C, a chimera of MEF2C and MEF2A, which has one amino acid difference between the two, was constructed by inducing a point mutation in the MADS and MEF2 domain of the MEF2C gene. The construct will be used in transfections in muscle cells to determine whether the target genes activated by MEF2C chimera are more similar to those activated by MEF2A or MEF2C. The importance of this research is that it will enable us to better understand the *in vivo* roles of MEF2C in striated muscle development because it is currently unknown how individual MEF2 factors activate specific target genes. These studies will help us to better understand how individual MEF2 factors regulate unique transcriptional programs *in vivo.*

This project was sponsored by NIH MARC Grant # GM008422

Effective Classification of Segments of *E. coli* DNA into Promoter and Non-Promoter Categories using Decision Tree Algorithm c4.5

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Promoters are the sections of DNA to which RNA polymerase first binds before starting transcription of each gene. Promoters are critically important, because they vary from gene to gene and influence the regulation of genes, that is, influence which genes will be turned on and which will be turned off at any given time. The most accurate method of identifying promoters is via biological experiments, but biological experiments can be prolonged and expensive. As a result, researchers would like to find a more efficient method to recognize promoters, for example, inductive machine learning classification. In general, this process follows three steps: feature extraction from a "training set" of data, classifier building using one of many possible algorithms, and classifier testing using a "testing set" of data. Rani et al. (2007) applied this approach to the classification of segments of *E. coli* DNA, previously known to be either promoters or not promoters, into promoter and non-promoter categories. The features they used for classification were the frequencies of occurrence of the 16 types of dinucleotides in each DNA segment. Using a neural network classification algorithm, 78% of the sequences were classified correctly. Our research improves on the results of Rani et al. (2007) by using the inductive machine learning C4.5 decision tree algorithm implemented in WEKA, instead of a neural network algorithm. Using this algorithm led to correct classification of 82% of the DNA segments. The preliminary results of this experiment slightly improve previous results and suggest inductive machine learning could effectively assist biologists to more rapidly identify previously unknown promoters in the future.

Rani, TS, SD Bhavani and RS Bapi. 2007. Analysis of E. coli promoter recognition problem in dinucleotide feature space. *Bioinformatics* 23: 582-588.

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Primitive Weird Numbers of the Form $2^k pq$

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A weird number is a natural number n that is abundant but not pseudoperfect. In our research we worked on finding primitive weird numbers of the form $2^k pq$. Our focus was finding primitive weird numbers when k is exceptionally large. There are infinitely many weird numbers, because the product of a weird and a prime number, greater than the weird number, will produce another weird number. So from the few weird numbers known infinitely many weird numbers can be produced. A primitive weird number is not the product of another weird number. We employed the use of the computer programming software Mathematica and UBasic. Our research was successful as we have found the largest weird numbers known.

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The effects of 9-cis retinoic acid on 1,25-dihydroxyvitamin D3-mediated transcriptional activation in Atlantic bottlenose dolphin (Tursiops truncatus) skin cells

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The vitamin D pathway, mediated by the bioactive form of vitamin D3, has been well characterized in terrestrial animals. Vitamin D intake via diet or exposure to UVB- radiation triggers the synthesis of 1,25-dihydroxyvitamin D3 (1,25D3), the biologically active metabolite of vitamin D3, within the skin. 1,25D3 binds to the nuclear vitamin D receptor (VDR), which is a ligand-activated transcription factor regulating a large suite of genes. VDR's activation requires heterodimerization with another nuclear receptor: the retinoid X receptor (RXR). The RXR/VDR formation identifies and binds to vitamin D response elements (VDREs) within the promoters of certain genes to induce their expression. We are interested in whether 9-cis retinoic acid (9-cis RA), RXR's ligand, acts negatively or synergistically with 1,25D3 in regard to the vitamin D pathway. The effect that 9-cis RA has on the vitamin D pathway is controversial. We are using dolphin skin cells as our model because neither vitamin A nor vitamin D pathways have been well-studied in marine mammals, and each may serve as a potential innate immune mechanism within dolphin skin. Luciferase assay results show that 9-cis RA moderately activates transcription of a vitamin D sensitive promoter, albeit not nearly as strongly as that by 1,25D3. Combined exposure to 1,25D3 and 9-cis RA produces similar transactivity of this promoter as 1,25D3 alone, suggesting that 9-cis RA, if anything, exerts a positive effect on 1,25D3-mediated transcription. Through Western blot analysis and real-time PCR, results show that 9-cis RA had no influence on neither RXR nor VDR protein levels; however 9-cis RA did have an effect on vitamin D-inducible expression of specific genes. Because dolphins may be appropriate models for humans, elucidating the effects that 9-cis RA has on the vitamin D pathway in dolphin skin cells provides information for crosstalk between the two pathways and for the appropriate vitamin A supplementary intake with respect to vitamin D in humans.

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The application of dielectrical relaxation spectroscopy to determine the water content of various acetaminophen powders

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A powder is a dry, bulky solid composed of a large number of very fine particles that exhibit the properties of both a solid and a liquid. This makes it hard to characterize their behaviors under certain conditions. One of these conditions of interest is moisture absorption, which negatively impacts the physical and chemical stability of the powder. This is an important factor for drug manufacturers to consider because moisture absorption leads to the accelerated hydrolysis/decomposition of the drug. However, there is a lack of non-destructive methods that these companies can employ to measure the moisture content of their powdered formulated drugs during manufacturing or storage. Our objective was, thus, to determine if Dielectrical Relaxation Spectroscopy (DRS) could be used to evaluate the water content of various grades of acetaminophen. This study investigated the potential application of Dielectrical Relaxation Spectroscopy (DRS) as a nondestructive method to measure the moisture absorption of three grades of acetaminophen. Acetaminophen samples were exposed to nine humidities ranging from 7-100 % RH for approximately five hours. Relative permittivity was measured thereafter over a frequency range from 1kHz to 9MHz. Water content was shown to be dependent on particle size and humidity. As humidity increased, water activity increased. Micronized and Semi-Fine grades of acetaminophen were not as significantly influenced by moisture absorption as Powder grade.

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Finding Weird Numbers of the Form $2^k pq$

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Weird Numbers: what are they and why are they important? These numbers are defined as any number *n* whose sum of proper divisors are greater than *n* but no subset of which can be rearranged as a sum that exactly equals *n*. In more complex terms, a weird number is an integer that is abundant but not pseudoperfect. For example, the smallest weird number 70 has a set of proper divisors {1,2,5,7,10,14,35} that add up to greater than 70 itself, but if you were to add up any or all of its divisors, you would not obtain the sum of 70, the original number. The smallest such number 70 is not so closely followed by the second smallest weird number, 836. With their increasing complexity and rarity as they approach infinity, you can imagine why the mathematical world has not fulfilled the quest for finding them. However, the research completed by my mentors, my colleagues, and I, aimed to find weird numbers not yet found, focusing on those of the form $2^k pq$. We seek an algorithm where you would choose a *k* and input it into the algorithm to find a pair of primes, *p* and *q*. From there, you would run a test on the *p* and *q* to determine if $2^k pq$ actually is a weird number. Two group members worked on finding numbers with very large values of *k*, but my group member and I focused on finding numbers with all the smallest values of k=1, 2, 3, etc., that we could handle. By hand, five numbers were found through tedious and time consuming equations, but using *Mathematica 3.0,* we were able to design a program that would find weird numbers for us. Weird numbers can be used for encryptography; the study of encryption codes that are used to protect information passed over the internet. With the positive results discovered in our research, we plan to have these numbers published in some form so that they can be observed by the mathematical community.

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Use of Magnetic Resonance Imaging to Detect Iron Levels in Alzheimer's Disease

Shawn Garcia

Faculty Mentor **(s):** Dr. John Florida, University of Florida Biomedical Engineering
Affiliations: University of Florida Neuroscience Department, SEAGEP Program

Magnetic Resonance Imaging (MRI) was used in this study to detect iron levels in hippocampus tissues taken from patients suffering from Alzheimer's Disease or control patients (patients without Alzheimer's disease) from the University of Florida Human Brain Tissue Bank. The region of hippocampus was extensively studied because it is one of the regions of the brain that is affected in Alzheimer's disease. It is a component of the brain that belongs to the limbic system and plays important roles in spatial navigation and long-term memory. Findings from this research and other research projects that are very similar is important because Alzheimer's disease is incurable, degenerative, and terminal.

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ISSR-PCR Protocols for *Zanthoxylum monophyllum*

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The plant that I am studying is the *Zanthoxylum monophyllum*, or the yellow prickle. *Zanthoxylum monophyllum,* is a member of the citrus family, which are native to subtropical areas. *Z. monophyllum* is also one of the many understudied plants in the Virgin Islands. Experimenting with the *Z. monophyllum* will help us learn more about this plant in our ecosystem. The question that I am trying to answer is "What is the best ISSR protocol for *Z. monophyllum*?" I am doing ISSR experiments on this plant to find out more information about its DNA fingerprint and what ISSR- PCR protocol works to show the fingerprint. I am studying ten different primers, three of which are anchored. I am testing each primer with *Z. monophyllum* to see which one produces the best bands. Because I am looking for a protocol that works best for the understudied plant, the hypothesis is that the protocol that uses anchored primers would be the best protocol. I predict the ISSR recipe that contains anchored primers would be effective and there will be distinct bands when viewed. The method that I used to develop an ISSR-PCR protocol was influenced by papers of similar experiments that I have read. I looked at the way the authors of the papers set up their experiments and I formed the experiment in the same way. As mentioned, ten different primers were used in this experiment and part of creating a protocol was to discover which of the primers worked best with the plant. So far, none of the primers have worked for *Z. monophyllum*. I also tried changing the temperatures of the thermocycling stage and trying out more taq DNA polymerase. None of those changes improved my plant's amplification.

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Horizontal Gene Transfer Analysis in Cyanobacteria

Kelvin Harry

Fenglou Mao, Ying Xu

This research focuses on the analysis of potential Horizontal Gene Transfer (HGT) events within the cyanobacteria species. Using 14 genomes collected from various cyanobacteria that live in diverse habitats including some from saltwater, freshwater and hot spring environments, embedded quartet analysis was done to determine possible HGT events. This information will then be displayed in a histogram-like image to show probable HGT events. Analysing this data concludes that there are large possibilities that HGT events may have occurred in previous generations of cyanobacteria. The data also shows that as more genomes are added, the possibilities of HGT increase substantially.

I would like to thank, The Ying XU lab, and the University of Georgia for providing facilities for this research. Special thanks to Dr Maria Poptova and Dr Fenglou Mao for guidance in completing this project.

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Red Blood Cell Bioreactor

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Erythropoiesis is the process by which red blood cells (RBCs) are made. In normal adult humans, the process occurs in the bone marrow, but in mice, it takes place in the spleen and the liver. Although the body can produce billions of RBCs every day, currently in culture, RBCs are not generated easily or in nearly sufficient numbers that could be used for transfusion purposes. By creating an environment that may more closely resemble that present in the bone marrow than what has been achieved previously in culture, we hope to generate fully mature, transfusable RBCs. The Palis lab, at the Medical Center of the University of Rochester, has discovered that cells derived from mouse embryo continue to divide until introduced to a medium that lacks dexamethasone. In the absence of dexamethasone they will proceed to differentiate into mature RBCs. The availability of this starting material makes the prospect of making RBCs closer to realization, however, the goal of bringing the cells to full maturity is yet to be reached. We hypothesize that past efforts to culture RBCs have failed because of the transient mechanical instability of the membrane during late-stage erythropoiesis. To overcome this instability we are implementing a bioreactor that will allow the cells to be compacted and mechanically stabilized while they differentiate. Precursor cells obtained from the Palis lab were used. The bioreactor, made of an ultrathin porous nanocrystalline silicon (pnc-Si) membrane and polydimethysiloxane (PDMS), allows for flow to enter and leave the device while compacting cells against the porous membrane. Ideally, the cells generated from this procedure will have a stable enough membrane to complete the process of erythropoiesis in culture. There are many clinical applications that will benefit from in vitro RBC production. Currently, there are not enough donors to accommodate the need for transfusion in many parts of the world, therefore, this availability of viable blood cells produced at high purity will avoid many complications, some life-threatening, which can arise due to transfusions.

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ISSR amplification of *Laguncularia racemosa* unsuccessful

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The molecular diversity of many common, albeit understudied, plants in the Virgin Islands is unknown. Knowledge of molecular diversity may help protect many recognized products and services used by Virgin Islanders via the upkeep of their respective genetic diversities. One such plant, the white mangrove, *Laguncularia racemosa*, whose particular services include conservation of the shoreline and a nursery for juvenile fish, algae, and other aquatic organisms, was studied. It was the effort of our lab to determine a sound protocol, involving ISSRs (a molecular marker system that requires little information on the desired DNA fragment, but rather the short tandem repeats that encase them) as primers that would prove efficient and have visibly distinct and reproducible bands. We applied various published techniques to finding a suitable protocol for *L. racemosa.* Thus, I hypothesized that a procedure very similar to the ones that I read in four published papers would prove effective with *L. racemosa*, because of the similarity between the procedures and the wide range of plants that were studied. I also hypothesized that anchored primers (primers with an arbitrary nucleotide attached to the tandem repeat) would have greater reproducibility of bands. A total of ten randomly picked ISSR primers were used. None of the primers produced bands even when the quantity of taq DNA polymerase and DNA were altered positively and the annealing temperature was set to 50^{o}C versus the initial 52^{o}C. Thus, there was no difference between anchored and non anchored primers, as neither of them has produced bands thus far. This may mean that the ten ISSR primers are non complementary to any given loci on the genome of *L. racemosa* or that further alterations to the protocol must be made. It may also mean that the DNA was either not quantified correctly or that it was contaminated. The case may also be that ingredients used in the protocol, such as taq DNA polymerase are not fully functioning, as deviations from their ideal holding temperatures may cause them to degrade and hinder the reproducibility of bands.

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Fluorescence Microscopy Images of Varying Numbers and Lengths of Microtubules

Blanche Letang

Mentors: Dr. Robert Murphy and Aabid Shariff

Microtubules, in addition to actin filaments and intermediate filaments, are found in the cytoskeleton of the eukaryotic cell and aid in maintaining cell structure. These vital cell organelles and their structures are quite important in cancer research studies, as they are key components in a cancer cell's ability to grow. As part of developing automated methods for High Throughput Image Analysis, we attempted to obtain images of microtubules of varying lengths and sizes. A single microtubule is simply a polymer of α and β tubulin dimers which is ultimately polymerized into a bundle of 13 protofilaments. In each 25 nm long bundle, the positively charged β tubulin dimers are exposed at one end, while the negatively charged α tubulin dimers are exposed at the other. This results in a significant amount of polarity in the molecular structure of the microtubule and, in some part, contributes to the dynamic instability of the microtubule. During polymerization, both the α and β dimers are attached to two GTP molecules. As long as they are in this state, the dimers can grow freely. This continues until one of the GTP molecules is hydrolyzed and broken down into a GDP molecule. While dimers attached to GTP are fairly stable and can continue to polymerize, GDP dimers disassemble and depolymerize. There is a fair amount of existing work which demonstrates that this depolymerization of microtubules occurs naturally within a temperature range of 37 degrees C to 4 degrees C or in the presence of a prominent cancer treatment drug, Nocodazole. With this information in mind, we first attempted to obtain fluorescence microscopy images of varying numbers and lengths of microtubules by subjecting live 3T3 animal cells to a drop in temperature. The cells were placed under the microscope in a heating chamber set to 37 degrees C and a fluorescence microscopy image was immediately acquired. The heating chamber was then shut off and images of the cell were acquired at approximately 30 min intervals, as the temperature slowly decreased. Using this method, we saw no significant change in the number and lengths of the microtubules. We also attempted to obtain fluorescence microscopy images of varying numbers and lengths of microtubules by adding a 20 μM solution of Nocodazole to the cells, while under the microscope. Before adding the drug, an image of the cells was acquired. Immediately after this, Nocodazole was added and fluorescence microscopy images were again acquired at approximately 30 min intervals. The addition of the Nocodazole caused depolymerization and much shorter microtubules than we began with, thus allowing us to obtain significant images of varying numbers and lengths of microtubules.

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Bayesian Networks for Mining Census Data in Order to Develop Effective Marketing Strategies

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Mentor: Marc Boumedine, University of the Virgin Islands, St. Thomas Campus

Millions of dollars are spent each year in order to develop cost-effective marketing strategies based on one or few key segments such as income, geographic or demographic segmentation. This research proposes Bayesian networks techniques in order to automatically determine the population income based on census data. Census data provide valuable information such as hours-per-week, race, age and can be exploited effectively through machine learning algorithms and decision support systems. Bayesian Networks can be viewed as graphical models that code probabilistic relationships among variables of interest. It can be used to learn causal relationships and also gain understanding about a problem domain and predict consequences of intervention. This research experiments with Bayesian algorithms implemented in Weka 3.7.0 data mining software package. The model is trained with 32,561 training data sets obtain from census data sets (Ronny Kohavi and Barry Becker). The current results thus far show that 83.8% of the census training data have been correctly classified into two segments: greater than 50K and less than 50K. In the future, we would like to improve this percentage by looking at different algorithms and comparing them to see which algorithm is more efficient.

Reference: Ronny and Kohavi, Census data http://archive.ics.uci.edu/ml/datasets/Census+Income.

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Primers that work for a Caribbean Plant

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*Coccoloba uvifera (*sea grape) is a Caribbean plant that is grown on the coastal regions. *Coccoloba uvifera* is vital because it is used for medicinal purpose such as diarrhea, and it has high content of vitamin A and vitamin C. This plant is also used as hedges around the costal areas. Before genetic diversity can be studied, molecular analysis techniques must be developed. One of the molecular anlaysis techniques is the ISSR technique, it is an inter simple sequence repeat. This technique functions by a marker system or better known as microsatelites that amplifies the section between the repeats, in addition it mostly targets the di- and trinucleotide repeats. The primary purpose is to find the proper protocol for *Coccoloba uvifera "*Sea grape" and also to test which primers work best. I used ten different primers and out of ten; some were anchored and some non anchored primers. I created and used a protocal derived from different papers. So far there are five primers that work with the *Coccoloba uvifera*, which makes future studies of genetic diversity possible to learn and possible discoveries of different functions of this plant. The primers that worked for *Coccoloba uvifera* were AGAGAGAGAGAGAGAGC (anchored), GCCGCCGCCGCCGCC (non-anchored), ACCACCACCACCACCACC (non – anchored), CACACACACACACACAT *(anchored*), and AGAGAGAGAGAGAGAGT (anchored).Since these primers work, scientist can use this technique to learn more about the plant's population genetics.

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Do Pigeons Know What They Know and Behave Accordingly?

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Metacognition is said to be the ability to perceive one's own mental states. It is objectively defined as the ability to judge one's chances of success or failure at a task before actually performing it. Metacognition has recently been reported in several different animals including monkeys, orangutans, dolphins, and rats. In birds, however, no conclusive evidence has yet been found. To investigate metacognition, we presented four pigeons with a same-different discrimination with arrays containing either few (2, 3, 4) or many (8, 9, 10) items. From prior studies, we know that pigeons' performance is good with many items, but poor with few items. In this experiment, we included an "increase" button that the pigeons could use to increase the number of items in the array. When the number of items is small, if the birds know that they do not know the correct answer, then they should peck at the "increase" button in order to obtain more information. Once the number of items is large enough for the birds to know the answer, they will have to hit a "decision" button and then choose either Same or Different displays. Our study consisted of four phases: a Baseline Phase and Phases 1, 2, and 3. Results from the Baseline Phase supported previous findings which suggest that pigeons' performance is good when the arrays contain a large number of items, but poor when the arrays contain only few items. In Phase 1, pigeons learned to peck at a decision key before making the same-different choice. All of the pigeons learned this task and their accuracy was similar to accuracy during the Baseline Phase. In Phase 1 we also measured reaction times: 1) the time from presentation of the display to the decision key peck and 2) the time from the peck at the decision key to peck at the display. In the first case, pigeons were faster when the arrays contained fewer items; in the second case, pigeons were faster when the arrays contained more items. In Phase 2, pigeons learned to use the "increase" button; they were required to peck at this button so that they could learn that they had the possibility to increase the number of items. All of the birds learned this task. This was a necessary step before Phase 3, the critical phase in which the birds can choose whether to increase the number of items in the display or choose the "decision" key to make their final response. At the moment, the birds seem to be choosing the "decision" key regardless of the number of items in the arrays. More training will be needed to be certain that they are not choosing to increase the number of displayed items. If this preliminary observation is confirmed, then we too will not be able to conclude that pigeons exhibit metacognition. Before giving up the effort, we will make modifications in our experimental design to encourage pigeons' use of the "increase" button.

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Waiting for the Tide to Come In: Foraging Activity of *Nucella ostrina*

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It is increasingly important to understand the potential effects changing temperature can have on behavior and species interactions, which affect ecological community structure. The rocky intertidal predator prey relationship between the whelk, *Nucella ostrina* and the barnacle, *Balanus glandula*, similarly to other species interactions, can be modified by changing abiotic factors. An investigation on the effect of changing tides on the interaction between these two species is one way to gain further insight on potential effects of climate change. At Friday Harbor, Washington, a quasi-field experiment was conducted in which barnacle mortality and snail positions were quantified and compared to temporal and tidal height emergence time (n=3 replicates per treatment; treatments were areas; 62cm, 32 cm, 13 cm above artificial shelters). Data loggers were used to measure temperature both inside and outside the artificial shelter. We found that greater predation occurs significantly at shorter distances to a shelter, (ANOVA, $p = 0.018$). Also, the snails seek shelter during hot low tides. This field experiment conducted from mid July to August contrasted with observations made in March, suggesting that behavior was more strongly influenced by abiotic factors in the summer such as higher temperatures and daytime low tides. This information can be used for building models that show trends of foraging activity with changing climate to aid in management strategies as changing conditions shift community structure in rocky intertidal communities such as this one.

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Snapping shrimp, *Alpheus* spp., instantaneously acclimate to the Caribbean corkscrew anemone *Bartholomea annulata*

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The Caribbean corkscrew anemone *Bartholomea annulata* houses many shrimp symbionts, which live on and near the anemone's tentacles, including snapping shrimps, *Alpheus* spp., which reside by the anemone's column. The ability of the shrimp to maintain this commensalism with the anemone without being stung or consumed is poorly understood. Studies have shown that some anemonefishes and some shrimp of the genus *Periclimenes* acquire protection from the stinging tentacles of other species of sea anemones after a lengthy acclimation period, wherein individuals display specific behaviors after initial contact with an anemone until they no longer trigger a detectable stinging response. The purpose of this investigation was to determine the acclimation behavior and time of *Alpheus* spp. to *B. annulata.* Shrimp were collected and isolated from sea anemones for 4 plus days. Shrimp were then randomly selected and placed haphazardly near a sea anemone. The time and the behavior of both shrimp and sea anemones were monitored and recorded until the shrimp was settled underneath the anemone. After one hour, the acclimated shrimp was removed and immediately placed near a second sea anemone, where behavior and time was again monitored. No statistically significant difference in acclimation time between isolated and previously acclimated shrimp was present ($p = 0.589$, T-test). Shrimp were consistently observed moving immediately into the anemone without triggering any detectable stinging response. This instantaneous acclimation is considerably less then that seen by other researchers for anemonefishes and *Periclimenes* spp., which took at least 2 h and 40 min to become acclimated. *Alpheus* spp. may have an innate protection from corkscrew anemone stings.

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Applications of the Hough Transform in Image Analysis

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Image processing and analysis has become a widely growing field with many applications, from biology to medicine. A popular method that has been explored and practiced is the implementation of the Hough Transformation (Hough 1962) to detect lines. We present an analytical explanation of the Radon and Hough transform. Hough, as noted by Deans (1983), is a special case of the Radon Transform. The Radon Transform is the basis for the creation of images in CAT (Computed Axial Tomography) scans. Additionally, image processing techniques, like edge detection, are applied to the resulting image. From here, the Hough Transform can be used to extract lines, curves, or objects in an image. We will further present a practical application of the Hough Transform and our work in image edge detection using Matlab.

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ISSR-Protocol Established for Local Plant Killer

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A well known plant introduced to the United States Virgin Islands (USVI) is killing local plants. In the USVI, *Melicoccus bijugatus* better known as "Genip" is a naturalized plant that is very invasive. As a result, *M. bijugatus* is presently changing the structure of the USVI's forests and is endangering local plants. To gain more understanding and knowledge of *M. bijugatus*, the inter-simple sequence repeat (ISSR) technique will eventually be used to study the population genetics of the plant species. My research asks, what is the most effective ISSR-protocol specific to *M. bijugatus*? Based on similar research, I predict that anchored primers (primers with a base pair not part of the repeat sequence that forces the primer to anneal/stick at the end of the DNA repeat) will work best in procuring an effective protocol. In order to develop a protocol, a DNA extraction from *M. bijugatus* leaves was taken. That was followed by creating a Polymerase Chain Reaction (PCR) master mix and thermo cycling the mix with DNA and primer to amplify the DNA. Lastly an electrophoresis gel containing the mix was run and the results were recorded. Out of the ten primers used, two anchored primers as well as two non-anchored primers showed positive results for creating an ISSR-protocol for *M. bijugatus*. As a result, it can be concluded that both anchored and non-anchored primers work for *M. bijugatus*. Future studies can focus on which *M. bijugatus* population has the highest diversity and require more studies as well as how to eradicate those populations to preserve local plants.

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Cleaner shrimp *Stenopus hispidus* affects the mean size but not load of the flatworm parasite *Neobenedenia mellini* on a Caribbean reef fish

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Monogenean trematodes are harmful to reef fish because they damage the fishes' skin and make them more susceptible to disease (Thoney and Hargis 1991). Fish may be cleaned of parasites and other debris by cleaner fishes or shrimps at cleaning stations. The effectiveness of cleaner fish is well documented, but the role of different cleaner shrimp species is not well studied (Becker and Grutter 2004). The ability of cleaner shrimps to remove parasites should have a positive impact on fish health by reducing damage to the host's skin. In addition, reduced parasite size could reduce overall parasite populations on the reef by removing the parasites with the greatest reproductive output. The number and mean length of parasites from fish that did or did not have access to cleaning shrimp was quantified *to test the hypothesis that the banded coral shrimp (Stenopus hispidus) affect the monogenean loads and the average size of monogenean parasites on the blue tang fish (Acanthurus coeruleus)*. Blue tang were housed in a semi-natural aquarium where they were constantly exposed to the infective stages of the parasite. The control treatment contained 14 blue tang and the experimental treatment contained 14 blue tang and 25 banded coral shrimps. Observations were made to see if there were any interactions between fish and shrimps. After two weeks, each of the fish were given freshwater baths for three minutes to remove their parasites. The parasites were preserved in ethanol and counted. The banded coral shrimp did not affect the parasite loads between the two treatment groups ($p=0.696$, t-test). This is in contrast to our results from last year's experiment with the Pederson cleaner shrimp (*Periclimenes pedersoni*), where the Pederson shrimp was found to reduce the monogenean loads on the blue tang. The parasites were photographed under a microscope and their lengths measured using computer software NIH Image J. The average parasite length was significantly smaller on fish that had access to the banded coral shrimp ($p=0.0005$, t-test). During our observations, no cleaning behavior was witnessed which makes us question whether the banded coral shrimps actually clean. Our results conclude that the banded coral shrimp is not an effective cleaner of the monogenean trematode and more research on what exactly it cleans needs to be done.

References:
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ISSR protocol has been established to aid in conservation of endangered native plant, *Erythrina eggersii*

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Erythrina eggersii (Cock's-spur) is a native plant of Puerto Rico and the Virgin Islands that is currently classified as threatened and endangered. Habitat destruction such as quarrying has significantly contributed to the plant's future extinction. No research was reported on this plant species. As a result, there is only a small amount of information about the potential uses of the plant. In order to prevent local extinction, the main goal is to obtain knowledge about *E. eggersi.* Therefore, I conducted a study to determine an effective inter-simple sequence repeat (ISSR) protocol specific to *E. eggersii* that will yield visible DNA bands. After reading four similar studies, a temporary protocol was created using the protocols obtained from the studies. Ten randomly selected primers (anchored and non-anchored primers engaged in the Polymerase Chain Reaction (PCR) process. I placed the amplified DNA in an electrophoresis gel and then observed and recorded the results. The results from six PCR reactions showed that two primers, one anchored (CA8T1) and the other non-anchored (GCC5), showed visible bands for the various ISSR protocols that were performed for *E. eggersii*. However, the inconsistency of the results led to the manipulation of the created protocol; such as lowering the annealing temperature and increasing the concentration of taq polymerase. Yet, these results illustrate primary knowledge of *E. eggersii* that may be useful in the future for its conservation. Further studies can be conducted to determine whether this species is diverse. Diversity is crucial for survival and in this situation survival is the major issue for *E. eggersii*. In addition, other studies can be conducted to determine whether medicinal properties exist within this species or whether there is any biological use for this native plant.

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Preliminary Analysis of Chloroplast DNA Spacer Regions (cpDNA) in Oca (Oxalis tuberosa) Reveals Two Potential Maternal Genome Contributors

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Oca (*Oxalis tuberosa*) is a domesticated tuber crop of the South American Highland and is clonally propogated as subsistence produce by the Andean natives. Molecular phylogenetic research has been done on oca to examine extent that domestication has affected its cytologica and genetic makeup and to assess oca's rate of evolution. Oca is found to be polyploid with eight sets of chromosomes (8n) and a base chromosome number of eight (x=8). A number of taxa in *Oxalis* share this base chromosome number of x=8, classifying oca into a clade referred to as the *O. tuberosa* alliance. Within the alliance are several tuber-bearing, wild *Oxalis* that are found to be among the most closely related of oca and are suspected to be putative progenitors of the domesticate species. *O. tuberosa, O. picchensis, O. chicligastensis,* an unnamed wild tuber-bearing taxon from Bolivia (Bol. W/T), and an unnamed wild tuber bearing taxon from Lima (Lima W/T) have been identified as possible recent ancestors of oca which scientists have made an attempt to explore. Because research involving nuclear DNA has reached inconclusive results in the identification of a single maternal and paternal genome contributor, we have observed sequence data of chloroplast DNA spacer regions (CpDNA). CpDNA is known to be found in the chloroplast which has been donated by the maternal or egg cell. Spacer regions in the chloroplast are utilized to observe divergent characters between closely related taxa. We observed four differerent CpDNA spacers: *trnT*-trnL, *psbA-trnH, trnS-trnT*, *trnS-trnG* (Hamilton). The sampling was from previously extracted and fresh DNA extracts of *O. tuberosa, O. picchensis, O. cicligastensis,* Bol. W/T, Lima W/T and 13 other non tuber-bearing taxa. We aligned sequence data using Sequencher 4.9 (Gene Codes Corp., 2009) and used WINCLADA (Nixon, 1999) and PAUP 4.0 (Sinauer Associates Inc., 2009) softwares to analyze the sequences and generate evolutionary trees. Preliminary results on the *trnT-trnL* spacer reveals *O. picchensis* and Bol. W/T. as having equal proximal relation to oca and the most similar CpDNA sequencesto oca. Both trees resulting form the analysis softwares resulted in identical trees, supporting one another in the inferred relationships. This preliminary data suggests that the DNA has at least two genome contributors, abnormal for chloroplasts and that the two taxa (*O. picchensis* and Bol. W/T) are both putative maternal progenitors of oca. In future research, we intend to analyze remaining cpDNA spacer regions : *psbA-trnH, trnS-trnT*, *trnS-trnG* (Hamilton) and compare the generated trees to observe any supporting or dissimilar relationships. Implications for this research extend to plant breeding, where knowledge about favorable traits in wild relatives (i.e., resistance to pests and disease, robust fruit development, minimal nutrient requirements) may apply to addressing the forseen world food shortage and preventing species extinction.

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Mathematical Models of Digital Sounds to reproduce Human voices?

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Suppose that someone that you cared for deeply lost his or her voice to a severe bout of laryngitis. Suffering from this debilitating complication of the disease can cause severe emotional and psychological problems and can even lead to chronic depression. Fortunately, mathematical modeling has the capacity to recreate and mimic various natural and unnatural sounds. In our fieldwork, various raw sound data were recorded from different people using sound processing software. Once stored on the computer it was placed into "fully integrated technical computing software" (Wolfram Research) where we fragmented the samples in order to seek out specific cycles in the characteristics of the waves. Once broken down, we had the software apply a Fourier analysis in order to determine an accurate mathematical model for the raw sound data. A Fourier series is an expansion of any periodic function $f(x)$ in terms of an infinite sum of sines and cosines. Since vibrations that create waves in air molecules produce sound and since waves are cyclical, Fourier analysis is ideal for examining their respective characteristics. After the models were generated we searched for numerical patterns in the coefficients of the sines and cosines and compared the coefficients generated by male and female voices to one another. We expect further research in the application of Fourier analysis to sound data to lead to improvements in sound processing and the synthesis of musical instruments.

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Mate Selection in Young People

Indira Turney

Mentor: Michael Lovaglia, Ph.D.

With more women than men obtaining doctorate degrees today, this will result in an increase in the discrepancy between the salary, education level, and social status of men and women. This phenomenon will bring about a change in mate selection. Previous research has shown that inconsistency in spouses' income is a significant predictor of marital dissatisfaction. With the current economic condition, a person of higher social and economic status may be a more desirable mate. This study examined what factors influence college men and women's choice of mate and how willing these students are to marry a person of another race. Research questions included: what are the lowest levels of income potential, career potential, and educational attainment that university students will accept in a potential mate. Using the convenience sampling method, 34 students (aged 19 through 24) from the Summer Research Opportunity Program (SROP) volunteered to participate in this study by completing the Relationship Choice Survey, designed by this researcher. The first hypothesis, based on previous studies, was that women would be more likely to desire high-income potential in an ideal mate, high education level and greater career potential. I also hypothesized that men would primarily look for physical attractiveness in an ideal mate. My third hypothesis was that women are less likely to marry a person of a different race than men are. Independent sample t-tests were conducted comparing men and women's mate preferences. Results supported the first hypothesis in that women are more likely to select a mate with great income potential ($p = .044$), whereas there was no significant preference for men. Contradicting the first hypothesis, men were more likely to prefer an ideal marriage partner who had a high level of education ($p = .044$). There was no significant preference for career potential in either men or women. Supporting the second hypothesis, results suggested that men were more likely than women to be willing to marry someone who is five years or more younger than they are ($p < .001$). Also supporting the third hypothesis, women reported that they were less likely than men to participate in interracial marriage ($p = .019$).

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Can a Conserved Regulator for Fungal Morphology Propagate as a Prion?

Cherissre Tyrell-Boateng, University of the Virgin Islands
2009 University of California San Francisco Summer Research Training Program

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Prions are misfolded, aggregated forms of proteins that act as infectious agents. A class of diseases such as scrapie in sheep and bovine spongiform encephalopathy in cattle are caused by the prion protein called PrP. A prion disease can spread from one organism to another if the second organism eats the tissue containing the protein aggregate. The budding yeast *Saccharomyces cerevisiae* is a model organism that has been used to better understand how prions function because yeast have been shown to have prions. Yel007w is a transcriptional regulator in *S. cerevisiae* required for haploid invasive growth and diploid pseudohyphal growth. It is a conserved regulator required for morphogenesis in distantly related fungi. Intriguingly, a computational study identified Yel007w as a likely prion candidate. The goal of this research project is to determine whether this regulator of fungal morphology (Yel007w) can propagate as a prion. Sup35 prion domain fused to green fluorescent protein GFP is known to form prions when overexpressed. We designed a system to overexpress a candidate prion domain from Yel007w which had been fused to GFP. Identification of aggregation from this GFP fusion would suggest prion behavior. In addition, we designed assays to further test whether this regulator of fungal morphology can propagate as a prion. We were unsuccessful in cloning in the Yel007w gene, but we were able to clone in the non candidate prion domain (non cPrD). We believe the non cPrD localizes to the nucleus like the full length protein (Yel007w), and does not aggregate like Sup35 prion domain. Future work will be done to clone in the Yel007w gene to identify whether this prion candidate can propagate as a prion. These studies will contribute to the identification of novel prion forms and their function in *S. cerevisiae*.

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Determination of Metal-Ligand Binding Constant via Isothermal Titration Calorimetry

Ophelia Wadsworth

Mentor: Dr. Gregg Lumetta, Pacific Northwest National Laboratory,
Department of Energy,
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The role of nuclear energy in today's global economy is a pivotal one; however, there is a cost to such technology. Currently, the major concern is the storage of radiotoxic waste from spent nuclear fuel. Separation of actinides from lanthanides in nuclear waste reduces its toxicity and enables proper long-term storage. Trivalent actinide-lanthanide separation via phosphorus-reagent extraction from aqueous komplexes is a method currently used to accomplish such separation. Buffers, as well as carboxylic and aminopolycarboxylic acids, complex the actinides in solution, allowing the lanthanides to be extracted. Metal-ligand binding via isothermal titration calorimetry (ITC) was studied to determine the binding constants of such reactions. This would determine if ITC is a viable method for actinide-lanthanide separation. ITC was accomplished with the utilization of a microcalorimetry system (MCS). MCS was first calibrated according to manufacture's specifications. Nd(OTF)3 was titrated with Na-L-lactate (and vice versa); a wide variety of concentrations was used to ascertain the reaction with the best heat generation, optimizing the binding constant. Each reaction failed to generate enough heat for MCS to calculate the binding constant. Further experimentation is necessary in order to determine the correct experimental design that will produce results. Future work entails adjusting the concentrations of each reagent until enough heat is generated with each titration to determine the binding constants.

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Using Tabu Search to Solve the Gate Assignment Problem

Troi Williams, and Marc Boumedine (mentor)

University of the Virgin Islands, U.S. Virgin Islands

From the year 2000 through the year 2008, there has been an approximate 10.2% growth in the number of passengers flying around the world (733,850,823 in 2000 and 808,536,596 in 2008). As a result, airport administrators are continually searching for faster and more efficient ways to assign gates to incoming aircraft using search algorithms and mathematical models. This research proposes a solution based on the popular Tabu Search Algorithm. It has been implemented in C++ using the Cyril E. King Airport, U.S. Virgin Islands as a case study. These two specific constraints are considered: 1) the aircraft must be assigned to its general boarding gate and, 2) the aircraft must be assigned to the first available gate or, if none are available, to the gate with the least waiting time. Presently, five experiments have been conducted using summer 2009 scheduled flight data. The flight data included 75 scenarios (the amount of hours of commercially-scheduled aircraft activity at the airport) and 225 flights (arriving and departing). Also, only 210 scheduled-commercial flights and 15 random, unscheduled flights were used in these experiments. In each experiment, the algorithm found the optimal schedule assignment. Additional experiments show that the execution time increases linearly with the number of flights. Currently, I am expanding and testing this algorithm with more traffic, gates, and complex constraints. In the future, I will analyze its efficiency against other algorithms and calculate the amount of time it will take to assign s aircraft to k gates, with c constraints, where all three variables are any finite number.

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