Eighth Annual

Spring Research Symposium

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St. Croix, U.S. Virgin Islands

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Central, cholinergic mediated effects on the pyloric central pattern generator of the Caribbean Spiny Lobster cannot overcome LP inhibition

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

The pyloric CPG produces rhythmic bursts of action potentials that control muscles of food sorting. When connectives from the CoG to the STG are cut, the pyloric CPG disappears. Thus, input from these higher centers are required to sustain the pyloric rhythm. Previous work demonstrated that direct superfusion of the STG with muscarinic agonists (such as pilocarpine and oxotremorine) transiently increased the frequency and duration of bursts by the pyloric dilators (PD) of the pyloric CPG while inhibiting activity of the ventricular dilator (VD) and lateral pyloric (LP) neurons. We hypothesize that the muscaranic stimulation of CoGs would produce identical effects on the pyloric CPG as 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 generally increases the frequency of the pyloric CPG up to 25% while increasing PD duty cycle and decreasing LP duty cycles. However, the absolute response depends on the initial frequency of the pyloric CPG. When the pyloric rhythm is fast (greater than 1.4 Hz) the duty cycle of PD increased from 0.3 ± 0.01 to 0.57 ± 0.15 while the duty cycle of LP decreases slightly from 0.30 ± 0.02 to 0.27 ± 0.06. In slower preparations 0.4 Hz, PD duty cycles increased only slightly from 0.153 ± 0.043 to 0.224 ± 0.007 while LP duty cycles were longer and virtually constant at 0.55 ± 0.03.
While these results agree with our general prediction that oxotremorine superfusion of the CoG will increase the frequency of the pyloric CPG, that response is totally dependent on the level of LP bursting. LP inhibition of PD is more powerful than PD inhibition of LP.

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Fractionation of sea anemone mucus to determine protective components

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Many have marveled at the way sea anemones are able to attack most creatures with their nematocysts (stinging cells), but some symbiotic animals are completely unaffected by the anemones stinging cells. The anemone's mucus is believed to protect these symbionts and the anemone itself from its stinging cells. To test this hypothesis we used the sea anemone *Condylactis gigantea* collected in Brewers Bay, St Thomas, VI. We coated 2% agar strips (with 5mM proline to activate nematocysts) with mucus from the anemone and brushed the coated strips against the tentacles of the anemone. The mucus gave nearly 100% protection to the coated agar strips. In an attempt to characterized the protective components within the mucus, we will fractionate the mucus using the Biotage SP1 purification system. Mucus will be collected from the *Condylactis* anemones and run through a fractionation column in either water or methanol solvent. Fractions of the mucus will then be tested on agar strips for protective agents using the anemone as a bioassay. If protective fractions are found, further fractionation will be done to isolate the protective components. We will then send our smallest working fraction to be further characterized by collaborators at the National Institutes of Health. We predict the protective compounds will be proteins or glycoproteins, however this is currently unknown.

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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. Studying the behavior of the initial axon development is the first approach to finding out the conditions necessary for axonal regeneration.

In the research experiment done, the behavior of initial axon development was studied. The differentiation of axon and neurite outgrowth was observed and analyzed using Image J under normal conditions. The behavior of the process growths was determined by inhibiting myosin. The axon and neurite extended faster when growing than retracting. Statistical analysis showed that the inhibition of myosin speeds up the extension process of axons and neurites faster than with the myosin. Myosin could be inhibited in regenerating axons to lower the retractions and increase the extension process. Future work would be to injure an axon and study its behavior at its injured site. Axon regeneration of an injured axon could then take place based on its site of injury.

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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 led 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 eelgrass 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 labeled 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 statistically 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 suggest very high numbers of mussel seeds might be a naturally occurring phenomenon. To test this further, more sites are needed.

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UVI Etelman Observatory Business Plan

Cassandra Benjamin & Odari Thomas
Professor Cynthia Gomez Martin (mentor)
University of the Virgin Islands

Have you ever wondered how stars are formed? Imagine having the opportunity to conduct research on this and other interesting topics right here at the University of the Virgin Islands. Unbeknownst to many students attending UVI, the university possesses an astronomical observatory which houses a 0.5 meter telescope. Once operational, it will be the eastern-most astronomical observational facility in the entire United States. Currently, it is being used by NASA researchers to conduct research on Gamma ray bursts although it holds the potential to be used for other research topics. Plans are also underway to transform the observatory into a “Green Estate” by making it entirely energy self-sufficient. The facility also possesses a botanical garden which houses native and non-native plant species which can be used to promote awareness of local plant ecology.

The plans for the Observatory will include getting it functional for the use of other astronomers to conduct research and to educate the community through outreach to inspire young people to pursue the sciences. We can also establish the University as a contender of locations for astronomical research. We have worked on not only gaining funding, and new software and equipment, but also to establish contacts with different astronomers who wish to use the Observatory.

This research is supported by NIH SEAGEP No. UF05034 Program and NSF HBCU-UP Grant # HRD – 0506096

Enhancing Academic Standards through Tutorials: Trends in STEM Tutoring Traffic at UVI St. Thomas

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Many universities and colleges provide tutoring services to enhance the academic performance of its student body. At the University of the Virgin Islands, the St. Thomas Campus Advising and Tutorial Services (CATS) Center offers tutoring services on weekdays from 9am to 7pm. To assess the quality and quantity of the STEM tutorials, all students receiving tutoring at the CATS Center are surveyed immediately following the conclusion of the tutorial. This research is dedicated to comparing tutoring traffic and knowledge gained from STEM tutorials offered at the St. Thomas CATS Center during academic years 2007-2008 and 2008-2009. UVI's science, technology, engineering, and mathematics (STEM) enrollment has increased by 3% between the academic years 2007-2008 and 2008-2009; this observation led to my hypotheses. Since STEM enrollment increased by 3% between academic years 2007-2008 and 2008-2009, the quantity of STEM tutorials should increase by approximately 3% during the same time period. The quality of the STEM tutorials should not decrease even though we're increasing the quantity of STEM tutorials. Therefore, at least 75% of the surveys should state that the STEM tutorial advanced the students' knowledge and understanding of the subject matter. Pursuing this research required analyzing data, developing queries, crafting pivot tables, and graphing the trends. The majority of research time was dedicated to reconciling and resolving data anomalies to ensure data integrity. The research concluded that during 2007-2008, 260 (89.7%) tutorials were dedicated to STEM courses; meanwhile in 2008-2009, 216 (38.8%) tutorials were dedicated to STEM courses. The hypothesis was disproved; although there was a 3% increase in STEM enrollment, the quantity of STEM tutorials decreased by 50.9% between the two academic years. However, the quality of the STEM tutorials increased from 97.7% in 2007-2008 to 99.5% in 2008-2009; these results exceeded my expectations. Succeeding this research, we have learned that further research is needed to investigate why STEM tutorials decreased. Recording the names of the students receiving tutoring would help us evaluate frequency and impact of individual tutorials. More efficient survey collection and storage methods should be implemented to ensure data accuracy, consistency, and privacy.

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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 use the organism *Drosophila melanogaster* as a model for human applications. 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's) 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. To accomplish this, we use transgenic flies with exogenously added nuclear receptors to determine cell types where they and their ligands are activated. Using florescent immune-staining, we identified 5 NRs present in *Drosophila* egg chambers. In addition, we observed that disruption of one particular NR, E78, caused a phenotype characterized by multi-layering and abnormal follicle cell arrangement in Stage 10 of egg chamber development. We believe that this lethal loss of function is caused by a dominant negative, where the excess of exogenously added NR has induced loss of function in the endogenous NR due to limited ligand. Our results strongly suggest E78 is required for oogenesis. Future tests, which are currently underway, will verify and better characterize this phenotype. Additionally, we plan to induce loss of function phenotypes with other nuclear receptors to help determine their function in egg chamber development. This brings us closer to learning the function of each NR, which can be used to gain a better understanding of the molecular mechanics of ovarian cell migration.

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

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Gamma-aminobutyric acid (GABA) is a neurotransmitter found in most invertebrates in vertebrates. GABA is generally inhibitory acting through receptors linked either to increase chloride currents or to G Protein cell inhibitor.

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). We are mapping GABAergic projections to see where GABA is being created and transported.

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 crabs, GABA was found in defuse regions in the commersural ganglion (COG's) and projected through the inferior esophageal nerve(ion's) to GABA containing cells in the esophageal ganglion (EOG)where we see distinct cells, and axonal projections to the stomatogastric nerve (stn). These axonal projections continued in the stn bu was terminated at the STG. As in crabs, no GABA containing cell bodies were observed in the STG and no GABAergic axons projected beyond the STG. What was surprising was the greater thickness of the neural sheaths in the lobsters compared to those of the blue crab. More accurate localizations of GABAergic cell endings will require additional experiments where the 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 are able to better understand the path that GABA takes and how it affects certain cells like those in the STG. Studies will include the manipulation of neural signaling with GABA agonist and antagonists in temperature acclimated lobsters.

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

Adrianne Crooke
Frank Naya, Ph.D (mentor)
SURF Award

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 if there are any cofactors that interact with the c-terminus of the MEF2C gene and second determine the DNA-binding specificity of MEF2C. 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.*

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Improved Classification of Segments of *E. coli* DNA into Promoter and Non-Promoter Categories

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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 uses three methods, in the following sequence: 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. Another research group has 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 segments known to not be promoters served as control segments. The features previously 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. *The goal of the present study is to test the hypothesis that by using the same methods, but replacing the neural network with other classification algorithms, one could obtain a greater percentage of correctly classified DNA segments.* In our research, using either the inductive machine learning C4.5 decision tree algorithm or naïve Bayes algorithm implemented in WEKA, led to a result of correct classification rates of 82% or 84%, respectively. These results are slight improvements over previous classification rates and suggest inductive machine learning could effectively assist biologists to more rapidly identify previously unknown promoters in the future. Future studies will compare use of different classification algorithms provided by WEKA and examine other DNA data sets.

This work was partially funded by NSF HBCU-UP Grant # HRD – 0506096 awarded to the University of the Virgin Islands.

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 retinoic 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 an 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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Determination of the advantages (or disadvantages) of multi-component ethnomedical preparations over single drug therapies

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Ethnomedicine comprises medical knowledge that developed over generations within various societies before the era of modern medicine. These health practices combine herbal, animal, and/or mineral-based materials together to create therapies that help to diagnose, treat, or prevent illnesses and promote well-being. Here in the Caribbean, there are numerous indigenous plant species that many herbalists use to prepare such therapies. However, since most of this knowledge is transmitted orally through the community, there is a lack of documentation on the methodologies used in these preparations so the knowledge can eventually become lost over time. Additionally, there has not been much research on these combination therapies to show how they actually work and if they may in fact be better than single-drug therapies (Western medicine). Our group's research objective was to develop a protocol by which we can test the effectiveness of multi-component ethnomedical preparations over single drug therapies. *We hypothesized that ethnomedical preparations which contain numerous compounds, act together synergistically to provide a more enhanced effect in terms of treatment than the single-drug therapies*. Six plant species were collected (*Leonotis nepetifolia, Tillandsia recurvata, Tecoma stans, Melicoccus bijugatus, Pluchea symphitifolia, Cuscuta americana L.*) based on their potential medical value, type of preparation, traditional uses, and availability. Selected plants were then utilized to prepare decoctions, infusions, and tonics. The cytotoxicity of the selected plant extracts was evaluated using a brine shrimp lethality test. Shrimp were grown and were pipetted onto petri dishes along with 4.5 ml of the plant extract. Number of dead vs. live shrimp was counted over a time frame of 24 hours. To determine the anti-microbial activity of the selected plants, a bacterial assay was used. *Serratia marcescens* were inoculated onto petri dishes and allowed to grow. Approximately 10 µL of each extract was placed onto a disk and bacterial growth inhibition was measured via the disc diffusion method. Completion of this study should lead to a better understanding of the advantages or disadvantages of multi-component ethnomedical preparations over single drug therapies.

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ISSR-PCR Protocols for Zanthoxylum monophyllum

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The plant that I studied was the Zanthoxylum monophyllum, also known as the yellow prickle. Zanthoxylum monophyllum is a member of the citrus family, which is native to subtropical areas. Z. monophyllum is 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 was trying to answer during this research project was “What is the best ISSR protocol for Z. monophyllum?” I did ISSR experiments on this plant to find out more information about its DNA fingerprint and what ISSR- PCR protocol would work to show the fingerprint. I studied ten different primers; three of those primers were anchored. I tested each primer with Z. monophyllum to see which one would produce the best bands. Because I was looking for a protocol that best worked for the understudied plant, the hypothesis was that one of the protocols that used anchored primers would be the best protocol. I predicted the ISSR recipe that contained anchored primers would be effective and that 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 procedures performed by the authors of the papers when they set up their experiments and I formed the experiment in the same way, following the guidance of my mentor.

As mentioned, ten different primers were used in this experiment and part of creating a protocol process was to discover which of the primers worked best with the plant. During the course of the research, none of the primers worked for Z. monophyllum. Changing the temperatures of the thermocycling stage and trying out increased quantities of taq DNA polymerase did not improve my plant’s amplification.

This work was funded by the NSF HBCU-UP grant # HRD-0506096.

A novel Method on how to Populate a Euclidean Distance Matrix in R2 using Statistical Data and Probability

Leeanna Hyacinth & **Alfonso Rodriguez, Jr.**
Robert Stolz, PhD (mentor)
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Location Proteomics attempts to accurately define and model the location of proteins within a cell. Protein location in a cell gives information that helps to determine protein functionality in the cell. Previously, the relative position and number of objects in a protein image were laid out using a simulated distance matrix and multidimensional scaling techniques in MATLAB. A randomly generated distance matrix is recreated based on the probabilities of the different range of distances. Because the distance matrix was essential for outlining the distribution of objects in a generative model of a protein image, two properties of this matrix were investigated: the rank and resulting number values. The result of the former states that the rank of a Euclidean Distance Matrix in a two-dimensional plane (R2) is at most 4. When creating the distance matrix, the first four rows are populated using random selection based on probability. Then, the entries of the remaining rows are restricted to specific numerical values that are based on the entries of the previous four rows. From this restriction, it was concluded that the distance matrix is rank deficient. With the latter, we attempt to prove that with the proposed method for populating the distance matrix, it is guaranteed always to return real number values.

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Trace Metal Analysis of Cistern Water Samples in the USVI

Stella Jarvis, Jonathon Donnell
Stanley Latesky, PhD (mentor)
University of the Virgin Islands

Water quality in cisterns is a major concern in the Territory of the US Virgin Islands. As part of an endeavor to do a detailed survey of the water quality in the territory, a number of cistern water samples were collected for analysis. The instruments used were a Varian 820 Inductively Coupled Plasma- Mass Spectrometer (ICP-MS) and a Metrohm 850 Professional Ion Chromatographic System, which were used to perform detailed analyses of cationic impurities and anionic inorganic species respectively. This work involved metal analysis and was performed using the Inductively Coupled Plasma-Mass Spectrometer (ICP-MS). The instrument was first tuned using a standard containing 5ppb of Ba, Be, Ce, Co, In, Pb, Mg, Tl, and Th. Then the water samples were run simultaneously with a 20ppb internal standard solution that contained Bi, Sc, In, Tb, and Y. 10 replicates of 20 reads each were averaged for each sample, with concentrations determined by fitting to a standard curve. A minimum of three standards for each determination were used. The blanks used consisted of 2% nitric acid in water. The range of the standards was from 10 to 500 ppb, depending on the analysis being done. Some samples had to be digested because they contained solid impurities that needed to be dissolved or removed. A Varian sample digestion system was used at a temperature of 370K. The samples were digested with a mixture of nitric acid and hydrochloric acid (concentrated nitric; 6 M hydrochloric) (aqua regia) overnight. The resulting solid materials were dissolved and diluted with 2% nitric acid and filtered using 0.2 μm syringe filter, and these samples were ran again. To date, we have done a detailed analysis of over forty water samples. In all cases, no significant trace contaminations were found.

Funding for this research was provided by SEAGEP (SouthEast Alliance for Graduate Education and Professoriate). The ICP-MS was purchased using funds provided by the US Department of Education Title III HBCU program. Further funding for the instrument was obtained from the USGS and the UVI College of Science and Mathematics.

An Experimental Comparison of the Relative Accuracy of Bayes Net and J48 Algorithms as Implemented in the Weka Data Mining Software

Mary Mootoo
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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 the Bayes Net algorithm and the J48 algorithm implemented in the *Weka 3.7.0* data mining software package. Different data sets are used to see which algorithm correctly classifies the data more accurately. The current results show that the Bayes Net algorithm is correctly classifying the data sets more accurately than the J48 algorithm.

Thanks to NSF HBCU-UP grant number HRD – 0506096 for supporting and funding this research.

Generative Models Using Random Walks with Intensities

Mohammad Mustafa & **Zina Dore**
Robert Stolz, PhD (mentor)

Scientists have utilized fluorescence microscope images which show protein shape, as well as capture protein motion in order to better understand the cell. Various means have been used to describe protein shape and location to enhance understanding of protein function. For this project, we will utilize gray-level co-occurrence matrices and random walks. Through this, we hope to be able to build a generative model of a cell.

Gray-level co-occurrence matrix is a numerical representation of the distribution of intensity over an image. Creating an image using gray-level co-occurrence matrices involves collecting information on gray-level co-occurrence matrix, modeling the gray-level co-occurrence matrix, and using that information to generate an image that has similar properties of the original image. A random walk will be utilized in the image generation. The two dimensional random walk will follow a path, that also varies with intensity, based on probabilistic information from the gray-level co-occurrence matrix.

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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 that 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. We investigated the effect of changing tidal patterns on the interaction between these two species as one way to gain further insight into 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. The snails seek shelter during hot low tides. In fact, on average only 9.6 % of snails were outside of shelters at low tide. This did not vary with treatment. Also, predation is significantly greater at shorter distances to a shelter, (ANOVA, $p = 0.018$). This field experiment conducted from mid July to August contrasted with observations made in March during which thousands of snails remain out of crevices in open air during low tide, 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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Mate Selection in Young People

Indira Turney

L. Michael Lovaglia, PhD (mentor)

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 part of the first hypothesis, 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 were to be willing to marry someone who is five years or 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?

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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 yeasts 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 constants via isothermal titration calorimetry

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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 manufacturer'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, University of the Virgin Islands, U.S. Virgin Islands.
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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 solutions from various algorithms and mathematical models. This research is a continuation of my initial research during the Summer Undergraduate Research Experience (S.U.R.E.) Program in the summer of 2009 and proposes a solution based on the popular Tabu Search Algorithm. It has been implemented in both C++ and Java using the Cyril E. King Airport, U.S. Virgin Islands as a model with three specific constraints. Each flight must be assigned to: 1) its general boarding gate, 2) the first available gate or, if none are available, the gate with the least waiting time, and 3) a gate large enough to accommodate it. Presently, ten experiments have been conducted using summer and fall 2009 and spring 2010 scheduled flight data. The flight data includes 135 scenarios (the amount of hours of commercially-scheduled aircraft activity at the airport) and 404 flights (arriving and departing). Also, only 380 scheduled-commercial flights and 24 random, unscheduled flights were used in these experiments. Cargo flights, on the other hand, were not included because they are assigned to gates at the airport's terminal; however, "cargo" gates are being added to accommodate these flights in the future. In each experiment, it took [the program] an average of 18 milliseconds to assign the optimal gate to each flight with minimal to no delay. The results show that with the increase of the amount of flights, there will also be an increase in the program's running time by *n*, or linearly; however, the program's running time also depends on the amount constraints and gates included and each constraint's growth rate. As a result, I will be using the big O notation to analyze and measure each new constraint's growth rate as I expand and test the program with more traffic and gates. This will also assist me in calculating and predicting 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. The major specifications of the testing system include an Intel Atom N280 (1.66GHz) C.P.U., a 2GB memory module (RAM) operating at 667MHz, a 160GB Hard Drive Disk, and Windows XP SP3.

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