

Fifteenth Annual

Fall Student Research Symposium



September 29, 2013
St. Thomas Campus
College of Science & Mathematics
University of the Virgin Islands

15th Annual Fall Student Research Symposium

September 29, 2013
University of the Virgin Islands
St. Thomas Campus, U.S. Virgin Islands

Event Organized by

Emerging Caribbean Scientists Programs
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The **Emerging Caribbean Scientists Programs** increase research training and promote excellence for STEM (science, technology, engineering, and mathematics), psychology, and nursing students at the University of the Virgin Islands.



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**Ultraclean and Chloroform Yield High Quality DNA From
White Mangroves (*Laguncularia racemosa*)**

Abigail Rene and Joshua Hazel

Alice M. Stanford, Ph.D. (mentor)

College of Science and Mathematics, University of the Virgin Islands

Mangroves are an important part of our coastal ecosystem. They help protect coastal areas from tsunami and hurricane damage and serve as habitats for juvenile fish, insects, and small crustaceans. Knowledge of mangrove population diversity would help us determine what activities threaten the population and what conservation and restorative measures would be most effective. To determine the diversity of the mangrove population, DNA samples must be extracted and amplified. Mangroves are specially adapted to harsh environments such as marshy anoxic anaerobic soil and fluctuating salinity of the water bodies in which they grow; they synthesize high amounts of polysaccharides, polyphenols, and other secondary metabolites such as alkaloids and flavonoids which impede DNA extraction (Sunil Kumar Sahu et. al, 2012). This study investigated white mangroves (*Laguncularia racemosa*) from the U.S Virgin Islands and Jamaica using four protocols: a standard CTAB protocol, a modified CTAB (Xin and Chen, 2012), Master Pure™ Plant DNA purification kit, and UltraClean to determine which protocol would yield the purest DNA sample. Extracted samples were subjected to further cleanup using sodium acetate, proteinase K, and RNase H (ribonuclease H). The extracted DNA was analyzed using a UV spectrophotometer under dilution factors of either 50 or 20. In terms of quality RNase H and chloroform yielded the purest DNA with A260/A280 ratios of 1.86 and 1.77 respectively. Quantitatively, UltraClean and the modified CTAB and yielded DNA concentrations of 116.25 ng/uL and 79 ng/uL respectively. These results indicate that despite the chemicals that impede DNA extraction, high quality genomic DNA can be obtained and used for further genetic studies.

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HBCU-UP grant #1137472.

Design and Implementation of Autonomous Weather Monitoring Agents Using The Java Agent Development Environment

Andy Breton and Jamall Marsh

Dr. Marc Boumedine (mentor)

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

A software agent is an autonomous software that is able to observe its surroundings and do specific tasks depending on the environment to achieve its goals. Such features are well-suited in weather monitoring to detect changes (drastic or regular) and take action autonomously according to its given parameters. This study proposes a design and implementation of multi-agent architecture, which is capable of monitoring weather systems and alert users more effectively using reactive agents. These agents are able to react and take actions based on given parameters by fetching information from distributed servers and reacting to any changes or conditions specified by the users.

The agents were implemented with the Java Agent Development Framework JADE by monitoring the weather data server (Worldweatheronline.com). The agents are programmed with several parameters such as their behavior and set of actions to be taken upon changes in the weather patterns. In addition, by using the specified Internet Protocol (IP) addresses, locations of a specific geographical location can be monitored in almost real-time. Such agents will be beneficial to many stakeholders since multi-agent architecture is able to observe the most current weather status and alert users from multiple sites around the world about potential hazardous conditions.

This work is supported with the grant program NSF HBCU-UP #1137472 and the University of the Virgin Islands.

PINK1: A Mitochondrial Ribosome Associated Kinase

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In mammals, mitochondria are responsible for providing over 90% of energy in the form of ATP, which is generated by the process of oxidative phosphorylation (OXPHOS). Our recent studies revealed that the mitochondrial translation machinery responsible for the synthesis of OXPHOS components is regulated by the phosphorylation of mitochondrial ribosomal proteins (MRPs). In addition, PTEN-induced putative kinase 1 (PINK1) was identified as one of the kinases responsible for phosphorylation of MRPs in the proteomics analysis of various mitochondrial fractions. PINK1 is a Ser/Thr kinase involved in phosphorylation of Parkin (E3 ubiquitin ligase) in order to eliminate damaged mitochondria through mitophagy. Mutations in PINK1 and Parkin result in autosomal recessive Parkinson's disease (PD), associated with oxidative stress and neuronal cell death. We hypothesized that PINK1 is a ribosome-associated kinase responsible for phosphorylation of MRPs and regulation of mitochondrial translation in health and disease. In this study, we investigated the association of PINK1 with mitochondrial ribosomes prepared at different detergent concentrations by Western blot analysis using PINK1 and MRP-specific antibodies. Western blot analysis of mitochondrial ribosome fractions confirmed the association of PINK1 with the mitochondrial ribosomal subunits. Mass spectrometry analysis will be performed to further confirm PINK1 association with the subunits.

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Methods for Determining Among-Site Prevalence of Haemogregarine Parasites In Caribbean Damselfish Species

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Keywords: Caribbean, Habitat, Haemogregarine, Parasite, Pomacentridae

Changes in the composition of benthic habitats, especially the decrease in live coral cover, influences habitat availability for benthic stages of parasites and thus alters parasite-host dynamics. Haemogregarines are parasitic haemoprotozoans that parasitize on the erythrocytes (red blood cells), of vertebrates. Although parasitism of marine fish by haemogregarines is particularly common among marine fish, the mechanism of transmission to host fish and host-parasite dynamics are not fully understood. External fish parasites such as gnathiid isopods, may act as vectors of haemogregarines for reef fish. Gnathiids generally avoid live coral capable of ingesting them. This study aims to compare the prevalence of haemogregarine parasites in damselfish (Pomacentridae) based upon the premise that gnathiids inhabit locations with relatively low coral cover. Belt transect benthic surveys were conducted to determine the benthic habitat composition of two study sites. Preliminary field results indicate that Brewer's Bay has less live coral coverage at 9%, than does Fortuna Bay at 36%. Damselfish are caught at the study sites with modified cast nets and aquarium hand nets while snorkeling or SCUBA diving. Small samples of blood are collected with syringes from each fish to produce blood smear slides for parasite screening via 100x light microscopy. Multiple damselfish individuals have screened positive for haemogregarine-like structures within erythrocytes. Further screening is being conducted to compare haemogregarine prevalence among-site. This investigation will give insight into the importance of habitat quality on the health of reef fishes and increase understanding of the biocomplexity of marine reef ecosystems of the Caribbean.

This project was funded by the National Science Foundation (OCE-121615, P.C. Sikkell, PI) and UVI MBRS-RISE grant GM061325.

Correlation Between Human Dimensions and Impaired Water Quality

Anthonios Doliotis and Kenisha Pascal

Dr. Avram Primack, Dr. Kala Fleming, and Dr. Wayne Archibald (mentors)
University of the Virgin Islands

Impaired marine near shore waters are associated with many terrestrial subwatersheds in the Virgin Islands. These impairments, including turbidity, fecal coliform, and enterococcus bacteria, are brought into the marine environment via runoff from the land. These impairments may be correlated with land development, improper drainage, and unpaved roads. In order to establish correlations between the human dimension of land development and poor water quality, a comparative study examining demographic data from the Virgin Islands 2010 Census and EPA STORET station data on water quality for 2009 to 2011 is being conducted. The location of each station was plotted using ArcGIS. By comparing variables such as age, race, income, place of birth, number of housing units, and other related variables within each estate to the location of impaired marine near shore waters, common variables among subwatersheds with impaired near shore marine waters will be determined.

This research was funded by the Water Resources Research Institute Fund # 205206.

Rainfall Patterns on St. Thomas

Ariane Ramsundar

Dr. David Morris and Dr. Avram Primack (mentors)
University of the Virgin Islands

The spatial variability of rainfall on St. Thomas was examined for the years around 1972-2013 using data from the National Climate Data Center (NCDC) and data that we gathered from new weather stations that we put out on different sites such as Botany Bay and Estate Mandahl. The distribution of rainfall showed some dependence on location. NCDC weather stations located in Charlotte Amalie Cyril E. King Airport and Fort Mylner showed ratios of 1.3:1 for monthly and annual accumulations. Data from our recent stations shows that windward sites tended to show higher rainfall at Botany Bay. Using these sites I was able to compare the precipitation data over the time periods. The data showed continuous change overtime between the areas of the island respectively to their precipitation patterns. With the historical data and future data from the weather stations being currently installed at different sites we were able to analyze how the weather has change and will be changing in the near future. This will be useful for future research into climate change. Further research and the new weather stations will provide tools for examining the effectiveness of environmental protection strategies.

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An assessment of salt pond ecological characteristics in high and low human impact areas on St. Thomas, USVI

Ayanna Hogan

Dr. Renata Platenberg (mentor)
University of the Virgin Islands

Salt ponds are coastal wetlands formed by the gradual closing of sheltered bays; they are surrounded by mangroves that provide habitat to nesting and foraging wetland birds. More importantly, salt ponds filter upland runoff, trapping sediment and contaminants thereby maintaining the water quality of the adjoining marine environment. Urbanization has led to an increase in runoff rich nutrients, sediment, and other non-point source contaminants entering salt ponds and the marine environment. Many ponds have been lost and altered through coastal development for resorts and condominiums, which could result in decreases in contaminants prevented from entering the marine environment by these coastal wetland filters. We are interested in examining the relationship between human development and ecological characteristics of salt ponds on St. Thomas, US Virgin Islands. Seven ponds were selected for sampling: three highly impacted ponds, one intermediately impacted pond and three ponds that receive little unnatural input. The water characteristics of each pond were recorded and water samples collected to measure the nutrient content within the ponds. In addition, pond characteristics were recorded, including shoreline vegetation, water color, depth and wildlife presence. Nutrients tested include nitrates, phosphates and sulfates and only show a difference in the ammonia levels of the various ponds. There were differences between impacted and non-impacted ponds in turbidity, total dissolve solids and dissolved oxygen levels but no difference in chlorophyll. Salinity and pH were highly correlated, and while the salinity of non-impacted ponds was lower than impacted ponds this may be more indicative of hydrology than water quality. Analysis of the collected water samples were expected to show higher nutrient levels in impacted ponds. The results of this study has determined a differences in high and low impact ponds the reason behind this difference will require further study of the ponds ecological properties.

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The Search of Extra-Solar Planets Using the Etelman VI Robotic Telescope

Bonnie President

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University Of The Virgin Islands

An extra-solar planet, or exo-planet, is a planet that orbits a star other than our Sun. The first extra-solar planets discovered were quite unlike those found in our own solar system, but recent studies are beginning to discover planets more similar to those nearby. Of particular interest, is the search for Earth-like planets in the so-called "habitable" zone, the orbital region around a star where liquid water may exist on the planet's surface. The first extra-solar planet was discovered by Polish astronomer Aleksander Wolszczan in 1990 using the Arecibo radio telescope and to date there are 911 confirmed extra-solar planets with many thousands more planet candidates. The 'transit' or 'eclipse' technique is favoured in the search for this class of exo-planets since it is least biased against their detection. The depth and shape of dips in the stellar light curve provide evidence for the presence of and, in some cases, details of the characteristics of a planet in orbit around the star. We present results of our Virgin Islands Robotic Telescope (VIRT) observing campaign on the known exo-planet system GJ1214b. Our results are presented as a test of the VIRT's ability to detect exo-planets using this technique.

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Utilizing Eye-Tracking to Determine Students' Comprehension of Chemistry While They Read

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Justin Shorb, PhD (mentor)
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Over the years, eye-tracking has proven to be an essential resource for Human-Computer Interaction Researchers around the globe. Eye-tracking is a technique where a subject's eye movement can be measured in order to locate of his or her point of interest at any given time. Additionally, it allows researchers to observe the sequence in which the subject is looking from one location to another. This in return can permit observers to determine whether or not the movement of one's eye can be used to indirectly study the cognitive responsiveness of a student. The basis of this study is to utilize eye-tracking to determine whether Chemistry students have the ability to make conceptual connections between different representations of the same Chemistry information. Making use of microscopic, macroscopic and symbolic representations, we would be able to observe the variations in attention which the student gave representations to determine their understanding of the relationship between them. There are a few ways to view the data of an eye-tracking experiment, however; we will be focusing on the saccade/ fixation mapping and heat mapping. After the experimental procedure and once the raw data was formatted, we then transformed that data using rotation matrices with Microsoft Excel and it was then imported to OGAMA (Open Gaze and Mouse Analyzer). With this software, we were able to view the both above mentioned mappings using the different module available in the OGAMA software. Initial results will be discussed regarding the analysis procedure and quality of the data.

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Investigating the effects of doping with transition metals on graphene substrates through computational methods

David Paulius

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Recent studies have been focused on the different uses and properties of graphene as electronic devices for its ideal properties of a semiconductor. This paper discusses the use of computational methods to study the effects of doping graphene with transition metals, such as the Fermi level shift as well as the class of semiconductor the material becomes (p-type or n-type). These structures are represented graphically through visualization software such as CrystalMaker and they allow us to extract the lattice coordinates of graphene (both in its pure and impure states); these coordinates along with other important pieces of data are then used to perform calculations using the Vienna Ab-Initio Simulation Package (VASP). VASP allows us to calculate the energies of the different structures of graphene and also it produces meaningful density of states and band structure diagrams. These band structure diagrams help us to identify the type of doping which has occurred by observing the Fermi level shift at the K-point (ultimately identifying the class of semiconductor), while the density of states diagrams show us the size of the band gap of graphene, ultimately giving clues to the mobility of the structure, as well as giving an idea behind the nature of semiconductor. The output from VASP was analyzed and compared with previously acquired results from external sources and with those gathered experimentally from previous studies.

This project was supported by the National Science Foundation Research Initiation Award Grant # 1238839 - Investigation of Doping in Graphene.

Study and Analysis of Simplified Cellular Automata in the Context of Conway's Game of Life

Denny Smith

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Cellular automata have been used to design and create visual models and simulations of different phenomena in domains such as art, forest fires and social movement. One of the many applications of cellular automata is Conway's Game of Life. The game is represented by a collection of cells on a grid. An initial state shows where cells can be either dead or alive. A set of four rules allow the transition from state to state until all cells die or cells live forever. The objective of this research was to compare the behavior of cellular automata using simplified rules. For this study, a couple of Java implementations are used to analyze the behavior of various instances of the modified game and to establish baseline data for comparing the new simplified and the original game. Our main goal is to determine if specific states that are reachable in the Game of Life can also be reached with lesser number of rules. The first experiment uses three rules and collects data to characterize the behavior of the new automata. The data are then compared to the Game of Life's results. Preliminary results show that under specific conditions it is possible to simplify the behavior of the new automata producing lesser transitions to reach a given state from the initial state, hence showing a simplified behavior.

Funding provided by the National Science Foundation (NSF) HBCU-UP grant #1137472.

Vertical Chlorophyll Profiles in Salt River Bay and Bioluminescent Mangrove Lagoon, St. Croix, US Virgin Islands

**Gejae Jeffers,¹ Jamila Martin,¹ Michelle Zimmerlin,² and James Pinckney, Ph. D.²
Bernard Castillo II, Ph.D.¹ and Kynoch Reale-Munroe¹ (mentors)**

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Mangrove Lagoon is a shallow, semi-enclosed, man-made embayment created in the 1960's by a hotel project that is located within the Salt River Bay National Historic Park and Ecological Preserve. Mangrove Lagoon is notably bioluminescent year round and it is thought that *Pyrodinium bahamense var bahamense*, a phytoplanktonic dinoflagellate is the primary species responsible for the bioluminescent phenomenon. In order to investigate the vertical distribution of phytoplankton, chlorophyll A concentrations were obtained in both Mangrove Lagoon and in Salt River Bay for comparison at different depths during the day and at night. Chlorophyll A is bound within living cells of algae, phytoplankton, and other plant matter and plays an important role as an apparatus responsible for photosynthesis. Data were collected, compared and analyzed at four different sites, namely, in the middle of Mangrove Lagoon, the mouth of Mangrove Lagoon and two sites in Salt River Bay. Data were collected during the months of May, June and July in the morning between 9-11am and in the evening between 8-11pm. Chlorophyll a concentrations were measured at the water surface and every 0.5 m in depth. We observed that chlorophyll a concentrations were highest in Mangrove Lagoon (1.49 mg/L) compared to the other three sites. We also observed that during the day, chlorophyll a concentrations were highest near the bottom compared to the top meter. During the night, we have seen chlorophyll a concentration spread throughout the top and bottom meter.

This research was funded by NSF HBCU-UP Grant Award No. 1137472 and Department of Interior National Park Service.

Developing feeding preference methods: Starvation affects feeding preferences of long-spined black Sea Urchins *Diadema antillarum*

Jahnelle Rivera and Jarvon Stout

Dr. Teresa Turner (mentor)

University of the Virgin Islands, St. Thomas USVI

Sea urchins are important herbivores that eat macroalgae. In the 1980's there was a massive die off of sea urchin *Diadema antillarum* throughout the Caribbean. This die off led to an increase in macroalgae which led to a decrease in coral cover. This is because the algae overgrew the corals. To determine the effects of sea urchins and algae and how to increase urchin numbers, feeding preferences of urchins need to be known. Thus, we developed methods of testing feeding preferences in a sea water system. We conducted four cafeteria style experiments. For each experiment we collected approximately 20 urchins, and placed each in individual containers. We used algae abundant on the reef in Brewers Bay St. Thomas, U.S. Virgin Islands. We tested the red alga *Acanthophora spicifera* and the brown alga *Dictyota dichotoma* and found *Acanthophora* was preferred (t-test, $p < 0.01$). This may explain high *Dictyota* cover on Caribbean reefs. Our experiments also showed that starvation changes food preferences. In the experiment without starvation of urchins the red alga *Acanthophora* was eaten more than the brown alga *Sargassum polyceratum* (t-test, $p < 0.01$), but with 5 days starvation *Sargassum* was preferred. These results may have been influenced by many factors, such as stress on the urchins, loss of algae during the experiment, variation in algal chemistry, urchin size, and previous diet.

This research was funded by Grant Number: HBCU-1137472.

Comparative Study of Nutrient Content in Salt River Bay and Bioluminescent Mangrove Lagoon, St. Croix, US Virgin Islands

Jamila Martin, Lorne Joseph, Gejae Jeffers, and Khalin Nisbett
Bernard Castillo II, Ph.D. and Kynoch Reale-Munroe (mentors)
University of the Virgin Islands

In the 1960s, a hotel development located in Salt River Bay, US Virgin Islands created a man-made embayment, which today developed into the bioluminescent Mangrove Lagoon. Within Mangrove Lagoon, bioluminescent dinoflagellates emit light when the water is agitated, producing a vibrant glow. The primary factors influencing the abundance of these dinoflagellates are not yet fully understood. We observed that there was significant bioluminescence throughout Salt River Bay, however, the highest concentration was observed within Mangrove Lagoon. The main objective of this study was to examine the nutrient content in Salt River Bay and compare with Mangrove Lagoon to investigate if nutrient content influences the concentration of bioluminescent dinoflagellates. Four sample sites were selected for the collection of water samples for the analysis of nutrients. Water samples were obtained during the night between 9-11pm from the surface and bottom of the water column. The sample sites were located within Mangrove Lagoon, in the mouth of Mangrove Lagoon, and two in Salt River Bay, which is connected to open ocean. The nutrients tested for this study were Total Nitrogen (TN), Total Phosphorus (TP), Nitrates and Total Organic Carbon (TOC), all of which used EPA approved methodologies. The results of Pearson correlation analyses between Mangrove Lagoon and Salt River Bay did not reveal a significant difference (P -value < 0.05) for any of the nutrients tested.

This research was funded by NSF HBCU-UP Grant Award No. 1137472 and the Department of Interior National Park Service.

**Methods to Explore Mechanisms of Parasite Resistance by Invasive Lionfish,
Pterois volitans and *P. miles***

JoAnn Thomas-Lewis

Dr. Jennilee Robinson and Starlene Loerch (mentors)
University of the Virgin Islands

Natural predators for fish usually consist of other fishes as well as endo/ecto parasites. Invasive lionfish in the Caribbean, *Pterois volitans* and *Pterois miles* (Scorpaenidae), have no natural predators. Preliminary data from an experiment conducted at Coral World suggested lionfish are resistant to ectoparasites. Ectoparasite loads were compared between individual blue tangs, *Acanthurus coeruleus*, (Acanthuridae) and *P. volitans* placed in a *Monogenea* (Platyhelminthes) -infested aquarium. *A. coeruleus* was heavily populated with monogeneans vs. the lionfish which in a single case had one monogenean on its body. Another ongoing survey has suggested higher parasite numbers on native Pacific lionfish than Caribbean lionfish. This led to the research question: Why is the Caribbean lionfish resistant to these ectoparasites? We hypothesized that the basis of the lionfish resistance is their immune response to ectoparasite attachment. An overview of teleost immunity, as well as, potential methods for investigating *P. volitans*' responses to ectoparasites will be presented. For example, other studies have identified an increased production of the proinflammatory cytokine IL-1 in parasitized fish skin. Therefore, IL-1 expression levels could be detected in punch biopsies of fish tissue with an attached ectoparasite by indirect immunofluorescence assay (IFA) or via quantitative PCR for the IL-1 gene.

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**Association of the Novel Amyloid Protein, EF-hand1 and
its Homologous EF-hand2**

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EF-hand2 (EFhd2) is calcium binding protein prominent in the central nervous system (CNS) and overexpressed in Alzheimer's disease (AD). EFhd2 is associated with pathological forms of tau in terminally ill JNPL3 tauopathy mouse model and validated in AD brain. Although the physiological function of EFhd2 is unknown, it is known to self-oligomerize and form filamentous structures in vitro. In AD, EFhd2 oligomers may contribute to the aggregation of tau proteins to promote neuronal degeneration or survival. Also expressed in the CNS is mitoclaclin, EF-hand1. EFhd1 is a calcium binding protein involved in neuronal differentiation. A pathological hallmark of AD is mitochondria dysfunction. In the case of mitochondria dysfunction, EFhd1 may be released to the cytosol, forming a heterodimer with EFhd2. The research aimed to determine whether EFhd2 could interact with its homologous EFhd1. The recombinant proteins, His-EFhd2 wild type and His-EFhd2 Δ CC were expressed in E.coli bacteria. An in vitro protein-protein interaction assay using GST-EFhd1 as the bait protein and His-EFhd2 wild type and His-EFhd2 Δ CC as the prey were used to determine a possible interaction. The results demonstrated that EFhd2 does not associate with GST-EFhd1, indicating that EFhd2 and EFhd1 do not form a heterodimer under the conditions studied.

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Screening of Ciguatera Toxins Found in the Invasive Indo-Pacific Lionfish (*Pterois volitans*) in the United States and British Virgin Islands

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Bernard Castillo II, Ph. D. and Kynoch Reale-Munroe (mentors)
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In the early 1980s, the Indo-Pacific lionfish (*Pterois volitans/miles* complex) invasion began in the Atlantic Ocean. The non-native lionfish travelled up the eastern coast of the United States then further east to the Bahamas. By 2004, the lionfish began to travel south within the Caribbean and continue to travel toward South America. The lionfish population in the Caribbean have since expanded to alarming numbers, rapidly consuming native fish and have high reproductive rates. One strategy in controlling the increasing population of lionfish is to encourage human consumption of this fish. This poses a possible problem in the Caribbean as there is high prevalence of Ciguatera Fish Poisoning. In the Caribbean, there is the presence of a tropical dinoflagellate, *Gambierdiscus toxicus*. This dinoflagellate contains a gambiertoxin used for self-defence, which biomagnifies and biotransforms to ciguatoxin as it moves up the food chain. World-wide, over 400 species of fish have been found to accumulate the ciguatoxins in their tissues. Recently, the USFDA added the lionfish to their list of species that may contain ciguatoxins. These toxins affect humans neurologically and gastrointestinally. For this study, 33 lionfish samples were collected from the United States and British Virgin Islands and were processed for ciguatera toxin extraction using the United States Food and Drug Administration (USFDA) established protocol. The lionfish were collected at depths ranging from 6 to 32 m. The lionfish samples were 133-361 mm in total length and 40 –708 g in weight. The extracted ciguatoxins were sent to USFDA for toxicity analyses. Our results would allow our local government agencies and other organizations to make better informed decisions regarding the use of lionfish as a potential food source.

This research was funded by Department of Interior National Park Service, the NSF HBCU-UP Grant Award No. 1137472 and the ECS Honors Fund.

The Efficiency of an Error Correction Method in Reducing the Read Mapping Bias in Allele Specific Expression

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Dr. Titus Brown (mentor)
Michigan State University

Scientists have studied differentially expressed genes between samples to identify candidate genes that contribute to particular phenotypes. However, they have also wanted to know how gene expressions are regulated. Next-generation sequencing technology, allows scientists to obtain a count of mapped reads, bearing maternal and paternal alleles. Significant deviation of a 1:1 ratio of two alleles indicates allele specific expression (ASE), which suggests that the expression is regulated by *cis*-regulatory elements. However, measuring ASE is challenging because of the read mapping bias toward reference alleles caused by sequencing errors, polymorphisms and having to allow mismatches when reads are mapped to the genome. The aim of this study was to determine if an error correction method called Sequence Error Correction (SEECER), which corrects sequencing errors, could be used to reduce mapping bias and improve the accuracy of ASE in reads simulated from *Drosophila melanogaster*.

We used bioinformatics tools to perform the analysis, including the bowtie program, which was used to map reads to a reference genome, and the flux stimulator, which was used to produce reads and simulations of reads. Custom Python scripts were used to process sequencing data and analyze results.

A non-parametric Wilcoxon test indicated that SEECER significantly reduced mapping bias toward the reference allele ($p < 0.005$). There was a shift in the ratio of alleles closer to 1 (i.e., the frequency of allele ratios higher than one decreased after error correction). In the future, these results will be compared to an error correction method being developed within the lab.

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Alterations in Extracellular Redox States Affect Pancreatic β -Cell Insulin Secretion Levels

Lynisha Farrell

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Type 2 Diabetes Mellitus is a metabolic disease characterized by basal hypersecretion of insulin and insulin resistance, all features characteristic of a malfunction in the pancreatic beta-cell. Cellular redox states can be influenced by energy availability and reactive oxygen species (ROS). Recently, it has been suggested that an abnormal extracellular redox state could be linked to irregular cell function. The body regulates the redox state through a series of 'redox pairs', the primary extracellular pair being Cysteine (CyS) and Cystine (CySS). The effects of physiologically relevant alterations in redox potential on the function of the pancreatic beta-cell were thus investigated, with the hypothesis that there would be differences in insulin secretion with variations of the extracellular redox state.

Clonal rat beta-cells (INS-1 832/13) were cultured in 48-well plates to ~80% confluence. Acute incubations were performed in KREBS buffer under low (2mM) and high (8mM) glucose conditions using various concentrations of CyS and CySS. Insulin secretion (HTRF) and glycerol release (NADH luminescence) were measured.

There were no differences in basal insulin secretion with respect to variations in different extracellular redox states. There were, however, changes in glucose/insulin secretion for the different redox states under a stimulatory glucose condition. Additionally, there was a trend towards an increase in glycerol release with increase in redox state.

It was hypothesized that differences in redox potential would be characterized by differences in function. Changes seen at different millivoltage (mV) potentials confirmed that different redox states produced different output levels of insulin secretion. In the basal conditions the highest insulin secretion was 11.83 (ng insulin/million cells/ 2 hours) for the -75 (mV) potential and the lowest insulin secretion level was 9.15 (ng insulin/million cells/ 2 hours) for the control (mV) potential. In the experimental conditions the highest insulin secretion was 67.59 (ng insulin/million cells/ 2 hours) for the -115 (mV) potential and the lowest insulin secretion level was 51.80 (ng insulin/million cells/ 2 hours) for the -75 (mV) potential. In relation to the different Cys/CySS ratios, insulin secretion levels were increased when the extracellular redox states were reduced.

A potential future study would be to determine the effects on redox states on ROS in the cell model, on HbA1c within Type 2 Diabetic patients, and to observe whether altering such redox states with pharmacological interventions provides a measurable benefit.

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Optimization of perfluorocarbon tracer data analysis using Visual Basic

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Harmless, odorless, perfluorocarbon gasses can be deployed and captured in order to model environmental airflow using an application called perfluorocarbon gas tracing (PFT). An understanding of numerous airflow related issues within complicated physical environments can be gained using Brookhaven National Laboratory's advancing PFT process. Applications of data from such understandings are directly beneficial towards homeland security, atmospheric research, and nuclear security issues. A demand for more efficient ways to translate, sort, and present PFT data has developed as this process evolves. My internship centered on creating a program that would interact with information from any one of three gas chromatographers' (GC) comma separated value (.csv) formatted data files, as well as .csv files output by machines used for capturing tracer gasses, and various additional external data files. This code is designed to distinguish between varying file states, and coordinate information amongst these data sources, providing the user with a number of calculations and graphical display options. Currently, I am creating a functional interface for graphical analysis in order to quickly and visually analyze data from thousands of samples in ways that have previously required time-consuming, manual efforts. This ongoing experience poses a creative and analytical challenge, while allowing me to provide a valuable contribution to an engineering department at a National Laboratory.

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Follow-up Observation of Gamma-Ray Bursts Detected by NASA Orbiting Observatories

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Today's technological advances have allowed for new discoveries that our ancestors would have never thought it existed. A perfect example of this is gamma-ray bursts. Gamma-ray bursts (GRBs) were first detected in the late 1960s by U.S. nuclear test detection satellites, which were designed to sense gamma radiation pulses emitted by nuclear weapons while in space. These bursts are one of the most distant and brightest objects that can be detected within our universe and are also believed to be one of our few insights into understanding more about the structure and evolution of our universe. NASA operates several satellites built to detect the activity of GRBs; the importance of this study is to use the Etelman telescope to make follow-up observations of these GRBs after they have been identified by NASA satellites. We began by examining the capabilities of the telescope to determine the precision of the telescope and to further understand the telescope's capabilities and by preparing the telescope's automated response software, which allows it to respond to any automated triggers. In addition, we worked on getting the computers at Etelman to communicate with the computers at the Goddard Space Flight Center. We plan to test and verify this communication system and to examine some already well-known GRBs to determine how well we are able to identify these objects and to catch some new GRBs as they take place.

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**Mathematical modeling and control of co-transmitting soil-transmitted
helminthes**

Nichole Etienne

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Soil Transmitted Helminths (STH) refer to a group of nematode worms causing human infection through the contact of parasite eggs or larvae which usually thrive in tropical or subtropical regions of the world. These worms usually enter the human body via direct or indirect transmission, sometimes even via skin penetration. Infection by such worms may result in impairment in physical, intellectual or cognitive development. Over the past few years the numbers for individuals being infected by such parasite has greatly increased, raising concerns worldwide. Definitely there is a need for a good understanding of the STH transmission dynamics that may help control the number of infection in order to reduce morbidity in the affected areas of the world.

Mathematical modeling of infectious diseases has proven significantly beneficial in increasing our understanding of the population biology of pathogens and the effects of interventions via the exploration of different infection- or disease related-parameters for their likely outcomes. The use of mathematical modeling for getting insights into STH infection dynamics and control therefore could be highly advantageous. The STH model used in this research is based on a basic model derived from the work of Anderson and Medley. In this, the age-structure of host population is taken into consideration as well as worm population and the different parameters of transmission and contact. All of which are modeled by a set of partial differential equations.

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Near Earth Objects (NEOs)

Odelmo Joseph

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The objective of this study was to search for known and unknown NEOs. History proves that foreign space objects collided with earth before causing great disaster. According to the George E. Brown NEO survey Act, NASA is to detect 90 percent of NEOs with diameter of 140 meters or greater by 202. NEOs are any objects outside the earth's atmosphere that orbit within our galaxy. NEO's generally consist of comets and asteroids. On each night of observing "darks" and "flats" would be first taken with the telescope. Darks and flats are needed to clean up the pictures taken and make the data more interpretable. For any known asteroids an ephemeris was made to keep track of the asteroid. Frames were taken of the known area with hope that the asteroid was there. Once an object is detected through the blinking of frames, the brightness and light flux is measured to fully confirm that it is an asteroid. Theories have been thought of and formulated about riding asteroids to mars or other neighboring planets. The search for NEO's may prove to be beneficial and lifesaving. While only known asteroids were examined during the summer, future work is in progress to continue analyzing the night's sky in search of unknown asteroids.

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Updating the Analytical Chemistry Curriculum II

Recaldo Rogers and Sena Hussein
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Rainwater is free from impurities except for those that are picked by rain from the atmosphere and from physical contact with materials. Wind-blown dust (Here in the VI, "Sahara Dust" is a known problem), decomposing organic matter, fecal droppings from birds and animals on the catchment areas can be sources of contaminations of rainwater, leading to health risks from the consumption of contaminated water from storage tanks. Clean catchments and storage tanks supported by good hygiene can offer drinking-water with low health risk, whereas a poorly designed catchment and storage system can affect the human population greatly by having high health risks. Pathogens such as *Cryptosporidium*, *Giardia*, *Campylobacter*, *Vibrio*, *Salmonella*, *Shigella*, *E. Coli* and *Pseudomonas* have been detected in rainwater. These bacteria are representative of different pathogens that can be found in rainwater, however, rainwater usually carries a lower rate of these pathogens than can be found in other water sources. Due to atmospheric CO_2 rainwater is slightly more acidic than stream water. Acidic rainwater can dissolve heavy metal salts (e.g. those containing Zn, Cu, Al, and Pb) and other impurities from materials of the catchment and storage tank. In most cases, chemical concentrations in rainwater are within acceptable limits; however, elevated levels of zinc and lead have been reported.

Ligands are ionic or neutral Lewis bases (electron pair donors) that can bind to a central metal atom or ion (Lewis Acid). Ligands act as Lewis bases (electron pair donor), and the central atom acts as a Lewis acid (electron pair acceptor). Ligands have at least one donor atom with an electron pair used to form covalent bonds with the central atom. In this case the ligand we used is 1,10-phenanthroline.

In this study, we will be developing an experiment for use in the analytical curriculum in which we will be able to simultaneously determine the binding constants for a series of M-L complexes and determine the metal ion concentration for a series of metal ions unknown water samples. We then will use the developed method to test cistern water for the presence of Fe and Cu. For our initial studies, the two metal ions that were used for this experiment Cu^{2+} and Fe^{2+} . The Fe complex is octahedral and has a maximum absorbance at 550nm. The Cu complex is distorted tetrahedral and has a maximum absorbance at 725nm and this can be seen using a UV-Vis spectrometer. The concentration of the metal-ligand complexes can be determined spectrophotometrically by measuring the absorbance spectra of a series of standards. The absorbance of is directly proportional to concentration and is modeled using Beers Law ($A = abC$, where a is the absorptivity constant, b is the cell path length, and C is the concentration). The program HYPSPPEC was used to determine the binding constants, K_D for each complex. Each spectra was saved to an EXCEL .txt file, formatted, and then loaded into HYPSPPEC. After data analysis, K_D values were determined based on a preset degree of convergence (typically 0.10 %). No more than 100 analysis cycles were required for convergence of the data.

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Updating the Analytical Chemistry Curriculum I

Sena Hussein and Recaldo Rogers
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Determination of the composition of Soda Ash using acid-base titrimetric analysis
The main goal of this project was to update the analytical chemistry curriculum and develop new experiments that could be used in the analytical chemistry curriculum. Various experiments were done to test the instrument that was used. The first experiment involved the analysis of a mixture of sodium bicarbonate and sodium carbonate or Soda Ash, Na_2CO_3 and NaHCO_3 . Soda Ash has significant economic importance because of its applications in manufacturing glass, chemicals, papers, detergents, and many other resources. This chemical has been used since ancient times. For instance, the ancient Egyptians made glass containers from soda ash (borosilicate glass) and the early Romans expanded its use as an ingredient in medicine and bread. Soda ash comes from Trona ore which is a dry mined to recover the ore (mineral) from seams below the surface. One of the largest known Trona deposits is found in Green River Basin which is located in southwestern Wyoming. The Green River facility converts Trona ore to soda ash this is done in a multistep purification process. This is done by crushing Trona which is then heated to remove unwanted materials. This process converts the ore to commercial grade soda ash. Water is finally added and the solution is filtered to remove all impurities. Lastly, this is then boiled to form crystals. The goal of this experiment was, by using the Microlab data acquisition system, was to validate the ability to accurately determine the percent composition of soda ash using titrimetry.

Using standardized 0.1160M HCl a measured sample of soda ash was titrated and monitored using a calibrated pH electrode. The titration curve demonstrated the expected results, with the pH of the soda ash solution at ~ 12.5 , which decreased as acid was added. The two inflection points appeared as expected and at the expected pH. The first equivalence point indicates the protonation of carbonate ion represented by $\text{CO}_3^{2-} + \text{H}^+ \rightarrow \text{HCO}_3^-$ and the second equivalence point indicates the second protonation of bicarbonate, $\text{HCO}_3^- + \text{H}^+ \rightarrow \text{H}_2\text{CO}_3$.

Determination of K_a values for monoprotic and diprotic molecules

The purpose of this experiment was to determine the K_a values for a monoprotic and diprotic product. The K_a is equilibrium constant for the partial ionization of "weak acids" in water. In this case, the weak acid is p-Amino Benzoic Acid. The K_a value roughly looked about 10^{-6} . For a monoprotic acid, the acid dissociation constant, K_a , is equal to the pH at the half-neutralization point. Titration of a known amount of weak acid using standardized base allows one to determine the volume required to completely titrate the acid. The pH at one-half this volume is equivalent to the $\text{p}K_a$. The same process was used to titrate a diprotic acid (tartaric acid), and using the same process, both $\text{p}K_{a1}$ and $\text{p}K_{a2}$ values were determined. Comparison of our results with literature values showed close agreement (± 0.5 pK units) for both experiments.

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Identification of Monogeneans on Caribbean fish using 18S-5.8S rDNA

Shakaro Richardson

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Monogeneans are ectoparasitic flatworms that attach to the gills or skin of freshwater and marine fish. The two families of fish that were the focus of this study were the Ostraciidae and the Acanthuridae, which may be parasitized by Monogenea of the genus *Neobenedinia* in the Caribbean. Fish were caught off the western coast of St. Thomas in a local fisherman's traps and placed on ice. Monogeneans were removed from these fish by soaking in freshwater (the result of the thawed ice). Fish were then returned to the fisherman. The water from acanthuriids and ostraciids was separately filtered through a plankton mesh to collect any ectoparasites. Ectoparasites were placed in a petri dish by washing the filter mesh with fresh water. Next, the parasites were identified by stereomicroscope, separated into individual tubes, and submerged in 95% ethanol for preservation. DNA extraction was performed on triturated monogeneans using the Qiagen DNeasy Blood and Tissue kits. Universal PCR primers targeting the 18S and 5.8s of eukaryotic rDNA was used to copy this genomic region. Agarose gel electrophoresis was used to confirm copies of DNA were amplified from the monogenean DNA extracts in the PCR assay. PCR amplified DNA will be cloned on a plasmid in *Escherichia coli*. DNA sequence data will be useful to determine if *Neobenedenia* spp. are *N. mellini* or a separate species (Candidatus *N. paraguensis*).

Detection of Ehrlichia in Ticks of *Odocoileus virginianus* (White-tailed deer) from the Virgin Islands National Park

Shanan Emmanuel and Tasha Corneille
Jennilee Robinson, PhD (mentor)
University of the Virgin Islands

Ticks are among the notorious hematophagous vectors known to carry deadly zoonoses. Research has shown that the deer in the US are host to two prominent species of ticks, *Ixodes scapularis* and *Amblyomma americanum*. These ticks are vectors of bacteria including Ehrlichia, Rickettsia, Anaplasma, and Lyme disease. These bacterial diseases threaten both wild and domestic animals, and are capable of being spread to humans.

The goal of this study was to identify what species of ticks are on the invasive *Odocoileus virginianus* (white-tailed deer) found in the Virgin Islands National Park (VINP) and whether these ticks are infected with potentially pathogenic Ehrlichia. We hypothesized that *Ixodes scapularis* and *Amblyomma americanum* were present on the deer of the VINP and host Ehrlichia.

Ticks were collected from two deer found dead from the VINP and preserved in ethanol. Ticks (n=40) were chosen randomly and observed according to their distinguishing features to identify their species. All 40 ticks were triturated then heated overnight at 55°C. DNA was extracted from the lysates using the Qiagen DNeasy Blood and Tissue Kit, then stored at -20°C. Universal oligonucleotide primers that targeted ixodid 12S mitochondrial rDNA confirmed the recovery of PCR amplifiable DNA. Tick DNA extracts (n=18) were chosen at random, then screened for Ehrlichia with two rounds of PCR, a primary and nested round of amplification. DNA agarose gels (1.5%) were used for viewing PCR results.

The ticks ranged from larvae, nymph and adults (partially and fully engorged ticks). The 12S mitochondrial rDNA amplicons confirmed the recovery of amplifiable DNA for 40 (100%) of DNA extracts. Ticks were morphologically identified as either *Rhipicephalus microplus* (cattle tick) or *Anocentor nitens* (tropical horse tick). *Ixodes scapularis* or *Amblyomma americanum* were not present on the two deer in the study. DNA agarose gels did not reveal amplified DNA following primary PCR for Ehrlichia. Nested PCR resulted in a band of the expected size, which indicated the presence of Ehrlichia canis in at least one sample.

This research will expand the awareness of the citizens of the USVI on what species of ticks are present in the territory and the pathogens they may possess. It will also enable persons in authority to take action where the importation of the *Odocoileus virginianus* is concerned, as the deer species may pose as a potentially fatal threat to native wildlife.

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***MyTrail*: Trail Tracking and Map Creation without GPS Usage**

Shelsa Marcel

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University of South Florida

This research focuses on an approach to track trails and create maps solely through the use of inertial sensors and distance measuring tools. GPS positioning and navigation is limited in its availability, coverage and security. This fact can have significant repercussions for our military, emergency response, business and private sectors. As a result, our approach works to contribute to solving the issue of GPS tracking limitations with specific application to the problem of bike trail tracking/mapping. Our method uses ubiquitous sensing by employing a mobile phone application and sensors (accelerometer, speed/distance measurement, gyroscope, and compass) attached to a bicycle, a novelty in approaching this problem. This setup equips the user with the ability to track/map a trail by gathering data while riding the bicycle. The trail is later mapped by sending data to a computer which produces a map of the trail with the only potential GPS use being that of the provision of starting and ending coordinates. The sensors gather data on distance, direction and inclination. The result will be a precise map created without the limitations of the need for pre-marked routes and GPS navigation present in earlier approaches at solving this problem.

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The study of proteins indicated in the pathogenesis of amyotrophic lateral sclerosis using a *C. elegans* model

Shenee' Martin and Ilana Pena-Gonzalez

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Amyotrophic lateral sclerosis (ALS) is an adult onset neurodegenerative disease that affects nerve cells and motor neurons, resulting in paralysis and eventually death. ALS pathogenesis can be due to mutations in TAR DNA binding protein (TDP-43) and fused with sarcoma or translocated in liposarcoma (FUS/TLS). However, the functions and pathogenic mechanisms of these proteins are not well understood. This project uses *Caenorhabditis elegans* (*C. elegans*) as a model organism to study TDP-1, the ortholog of TDP-43, and FUST-1, the ortholog of FUS/TLS, in *C. elegans*. These DNA/RNA binding proteins are similar in structure and shape but it remains unclear what the potential relationship is or the mechanistic pathways involved in producing the ALS phenotype. We have developed a worm overexpressing transgenic TDP-1 and a worm deleted for *fust-1*; both have been proven to be toxic in *C. elegans* in response to a heat stressor. Preliminary results show that TDP-1 over expression worms were able to return to a more wild type state after RNAi of TDP-1 overexpression and heat shock treatment. Additionally, TDP-1 over expression worms undergoing induced thermotolerance had a higher survival rate than *tdp-1* deletion worms-. Based on these results, we expect that when we cross TDP-1 overexpression worms with *fust-1* deletion worms the survival rate of the worms will increase compared to either mutation on its own. These results will further our understanding of TDP-43 and FUS/TLS in people who suffer from ALS.

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Investigation in the Use of Optical Spectroscopy to Determine Metal-Ligand Binding Constants

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Metal ligand binding constants (K_f) values are important for a number of reasons in relation to biochemical and chemical processes. In biochemistry, they are important in the understanding of the mechanism of binding metal ions to proteins and enzymes. For example, such complexes aid in the transport of essential metal ions across cellular membranes and the removal of metal ions from the body. In nuclear chemistry, these studies are important to the understanding of the separation of radionuclides during the manufacturing and waste processing of nuclear materials. In the past, the customary approach used in determining binding constants consisted of titration and gravimetric methods. This study, using iron, chromium, and copper (metals found in high concentrations in the preparation of radionuclides), sought to determine the validity of using infrared and ultraviolet-visible spectrophotometry to determine binding constants for a variety of metal-ligand complexes. First, we had to learn how to use two analytical instruments- the Varian Fourier-Transform Infrared Spectrometer (FTIR) and the Varian Ultraviolet-Visible Spectrometer (UV-Vis). We then constructed a library of FTIR spectra of common chemicals using three different sampling techniques- Attenuated Total Reflectance (ATR) of solids, liquid sampling, and ATR sampling of liquid mixtures. We at first tried using FTIR spectrometry to determine the binding constants but found that the ATR cell did not have enough energy throughputs to allow such determinations. Subsequently, we used UV-Vis spectrometry to obtain our spectral data and we then used commercially available HYPSPPEC software that allowed us to perform spectral subtraction followed by spectral analysis to determine the binding constants. We used two different ligands, ethylenediaminetetraacetic acid (EDTA) and ethyleneglycoltetraacetic (EGTA) acid, both known to form 1:1 ML complexes, in order to test the efficacy of the spectral determination of the M-L binding constants. Our studies showed that our constants agreed well with literature constants.

Funding for this research was provided by NSF-HBCU grant #HRD-0506096 and VI-EPSCoR.

Recovery of high quality DNA from ixodid ticks collected off *Odocoileus virginianus* (White-tailed deer) in the Virgin Islands National Park

Tasha Corneille and Shanan Emmanuel
Jennilee Beth Robinson, PhD (mentor)
University of the Virgin Islands

In recent years, there have been numerous tick-borne diseases reported in the continental U.S. In hearing this, one cannot help but to wonder whether or not the United States Virgin Islands are at risk in the spread of tick-borne diseases. The Virgin Islands National Park (VINP), is a popular site for tourist attraction and a home to White-tail deer (*Odocoileus virginianus*). They were once brought to the Virgin Islands for recreational purposes and are currently under investigation to see if they host ectoparasites that may carry pathogens. Considering how these deer can potentially lead to deadly diseases such as *Rickettsia*, *Anaplasma* and *Babesia*, deer that reside in the VINP national park are vehicles of these tick-borne diseases that could ultimately land on a passer-by.

To conduct this research project, ixodid ticks were identified to the genus-level based on their morphological type, life stage, and gender. DNA extraction was done on a series of 40 deer ticks using the Qiagen DNAeasy Blood and Tissue Kit. The efficiency of the Qiagen DNAeasy ticks were analyzed based on the concentration and purity of the tick DNA extractions using UV spectroscopy. Data from the spectroscope was measured from six ixodid deer ticks (1, 15, 25, 27, 30, 34). For ticks 1 and 25, the 230 wavelength expressed high contaminant levels. Also ticks 1, 25, 27, and 34 at the 325 wavelength reported values that indicated high particulate levels present in the sample. Furthermore, three ticks, (27, 30, and 34) had low DNA yield whereas ticks (1, 15 and 25) yielded concentrated DNA extractions. Overall, tick 15 showed no sign of large particles or other contaminates. Moreover this sample had high levels of tick DNA with a concentration of 203g/ml. To further acknowledge the quality of these tick DNA extractions, gel products were compared. As expected, tick 15 had conversely high quality DNA, as visualized by clean, bright bands on the gel electrophoresis results.

To understand the levels of low yield DNA present in DNA extractions, the Qiagen kit troubleshooting section stated that lower yields could be attributed to poor storage prior to DNA extraction and that DNA yields are dependent on the type, size, age and the storage of material. Despite the flaws present in the DNA extraction, the Qiagen DNeasy Blood and Tissue kit was effective at yielding high quality tick DNA.

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**What is Brewing in Brewers Bay?
Detection of Coliform and Enterococcus in Brewer's Bay**

Tiffany-To'Quoya Smith

Christine Udycz, Halimah Blanc, Melinda Bryan, Sha'Quan Clarke, Sabrina Katwaru, Jerice Lake, Kiana Lee, Kishelle Parsons, Nneka Powell, Krystle Ruan-Callwood, Inzinga Smith, Tamika Turnbull, Melissa Van Drieson, and Jennifer Xavier-Callwood

Dr. Jennilee Robinson (mentor)
University of the Virgin Islands

Factors that may influence the number of pathogens in marine water include temperature, rainfall, animals and human waste, as well as run-off from the roads and hills. When these agents are present in beach waters they pose a risk to human health. Water quality can be measured via indicator organisms, such as the coliforms and enterococcus bacteria. These species are from human or animal origin. They also survive as long as, or longer than other pathogens in marine water. Their increased density can indicate the severity of fecal contamination, a source of various human pathogens including bacteria, eukaryotic parasites and viruses. The University of the Virgin Islands (UVI) Microbiology for the Health Sciences (BIO301) summer session class of 2013, measured the concentration of fecal indicator bacteria from three areas on Brewers Bay Beach. We hypothesized these bacteria can be washed downhill into the bay by heavy rainfall. We measured the concentration of enterococci, total coliform, and fecal coliform for three consecutive Mondays in July. Additional samples were collected at UVI's Center for Marine and Environmental Science building grounds near the bay, and two sites east the bay along the roadside gut that flows into Brewer's Bay when rainfall is heavy. Marine samples (10 ml) were collected using sterile 15ml tubes and diluted to 100 ml using distilled water in sterile bottles. Enterolert or Colilert reagents were mixed samples and incubated overnight in Quanti-Tray 2000 plates. We were able to detect enterococcus, total and fecal coliform in Brewer's Bay water, as well as in the gut leading to the bay. Indicator bacterial concentrations were also compared to daily rainfall amounts.

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Variation in Fish Assemblages Among Sites at Cockspur Island and Tybee Island, Savannah, GA

Zola Roper

Dr. Carla Curran and Jennifer Gut (mentors)
Savannah State University

Estuaries and surf zones are important habitats for fish. Determining what fish assemblages inhabit estuaries and surf zones of sandy beaches can help government organizations make better management and conservation decisions. The purpose of the present study was to determine the fish assemblages among sites at Cockspur Island and Tybee Island in Savannah, GA. Six sites, including two estuarine sites at Cockspur Island and four surf zone sites at Tybee Island, were sampled once a month from March to June 2013 using a seine net during an ebbing spring tide. A total of 61 fishes at “Cockspur Bay” and 13 fishes at “Cockspur Northeast” were collected. A total of 19 fishes were collected at “Tybee Jetty,” 20 fishes at “Tybee 3rd Street,” 61 fishes at “Tybee Pier,” and only 10 fishes at “Tybee Creek.” Tybee Pier was the most diverse site based on the Shannon-Weiner Diversity Index (0.84) with a high number of gulf kingfish *Menticirrhus littoralis* (n=24) followed by Cockspur Bay (0.82) with a high number of spot *Leiostomus xanthurus* (n=20). The diversity in sites were lower for: Cockspur NE (0.47) with a high number of spot (n=8), Tybee 3rd Street (0.37) with a high number of gulf kingfish (n=24) and Florida pompano *Trachinotus carolinus* (n=14); Tybee Creek (0.35) with a high number of spot (n=7); and Tybee Jetty (0.32) with a high number of Florida pompano (n=15). The major finding of this study was that there was a difference in fish assemblages at Cockspur Island and among sites at Tybee Island, GA, thus rejecting the null hypothesis. For example, there was a higher diversity of fish species at Cockspur Bay (13 species) and Tybee Pier (10 species) compared to Tybee Jetty (n=4), Tybee 3rd St. (n=3), and Tybee Creek (n=3). One reason for the high diversity at Tybee Pier might be the fact that the area contains a pier with barnacles, which may provide food for fishes.

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Judges

NAME	INSTITUTION	TITLE
Marc Boumedine	University of the Virgin Islands	Associate Professor of Computer Science
Lorraine Buckley	University of the Virgin Islands	Visiting Associate Professor
Gloria Callwood	University of the Virgin Islands	Professor of Nursing
Kimarie Engerman	University of the Virgin Islands	Assistant Professor of Psychology
Richard Hall	University of the Virgin Islands	Professor of Biology
Paul Jobsis	University of the Virgin Islands	Associate Professor of Biology
Stan Latesky	University of the Virgin Islands	Professor of Chemistry
Karissa Poszywak	Virgin Islands Department of Education	State STEM Director
Stephen Ratchford	University of the Virgin Islands	Associate Professor
Jennilee Robinson	University of the Virgin Islands	Assistant Professor of Biology
Ludence Romney	Virgin Islands Department of Education	Mathematics Coordinator (STT/STJ)
John Shapley	University of Illinois Urbana-Champaign	Emeritus Professor of Chemistry
Pat Shapley	University of Illinois Urbana-Champaign	Emeritus Professor of Chemistry
Justin Shorb	University of the Virgin Islands	Assistant Professor of Chemistry
David Smith	University of the Virgin Islands	Professor of Physics
Alice Stanford	University of the Virgin Islands	Professor of Biology
Robert Stolz	University of the Virgin Islands	Professor of Mathematics
And UVI Masters of Marine and Environmental Science Graduate Students		

Notes

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