

Fourteenth Annual

# Fall Research Symposium



**September 23, 2012**  
**St. Thomas Campus**  
**College of Science & Mathematics**  
**University of the Virgin Islands**

# Fourteenth Annual Fall Research Symposium

September 23, 2012  
University of the Virgin Islands  
St. Thomas Campus, U.S. Virgin Islands

## **Sponsors:**

- ◇ National Institutes of Health, Minority Access to Research Careers (MARC) Program
- ◇ National Institutes of Health, Minority Biomedical Research Support Research Initiative for Scientific Enhancement (MBRS RISE) Program
- ◇ National Science Foundation, Historically Black Colleges and Universities Undergraduate Program (HBCU-UP)

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**How effective is Coral Reef Discovery Week? An assessment of the impact of an experiential learning opportunity in marine science for Virgin Islands high school students.**

**Sara Aubery, Elizabeth Clemens, Jane Conrad**, Alex Webb, Christine Settar  
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Coral Reef Discovery Week is a free camp for local high school students to learn about the natural marine resources and marine science career opportunities in their community of the US Virgin Islands (USVI). In 2012, the camp was held at the University of the Virgin Islands and was supported by the students and staff at the Center for Marine and Environmental Studies. The aim of the camp is to increase the diversity of marine science educational opportunities offered in the territory with the ultimate goal of increasing local participation in marine science. In past iterations of the camp, its effectiveness was assessed through a simple questionnaire given at the completion of the week's activities. Results from this questionnaire provided some input from the students but was not an effective mechanism to scientifically assess whether the attitudes, aspirations and knowledge of the students were being positively affected. In 2012, three forms of scientifically-based assessments were performed and analyzed to determine the impact of the experiential learning activities of Coral Reef Discovery Week on the students' knowledge of marine science, conservation and their attitudes towards pursuing a career in marine science. These assessments consisted of a pre- and post-test, observational studies during the camp and a focus group at the conclusion of camp activities. These assessments will ultimately be used to identify the strengths and weaknesses of experiential learning activities in marine science.

This research was funded by the Community Foundation of the Virgin Islands (CFVI), the Center for Marine and Environmental Studies, and the Sea Grant.

## **Mycobacteriophage Cluster Assignments by PCR Complicated by Genome Diversity**

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Mycobacteriophage are a group of bacteriophages or viruses that can infect Mycobacterial species. Mycobacteriophage were originally isolated from the *Mycobacterium smegmatis* and *Mycobacterium tuberculosis*. Presently over 2,500 have been isolated from environmental and clinical sources and nearly 400 phage genomes have been sequenced. Mycobacteriophage genomes are organized into clusters. Definitive assignment is by alignment of the entire genome with genomes of known phages. The 2011-2012 Phage Hunting class at Johns Hopkins University isolated 25 different phages. Attempts were made to place the different phages into clusters. Two different methods were used but produced conflicting results. High titer phage lysates used for PCR were developed by the students. A primer set developed by Victoria Hohenstein was used. The phages were amplified and selected reactions were treated and sequenced using a PCR primer. After conducting the series of tests, two lysates were successfully placed into sub clusters. Lysate 4 seemed to have been contaminated with Lysate 14. Lysates 2 and 7 came up with inconclusive results because of the presence of multiple bands for multiple primers. The remaining lysates remain of question. Because of this we are led to believe that the primers that were developed are not as specific as we would have hoped.

This research was conducted at Johns Hopkins University and was funded by NIH RISE grant 2R25GM061325 and the Genentech Foundation. This presentation is supported by NSF's HBCU-UP grant #HRD-0506096.

**Abundance and vertical distribution of *Squalus acanthias*, Spiny Dogfish, at Stellwagen Bank: daily and interannual patterns from 2008-2012**

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Jesús Pineda<sup>2</sup> and Victoria Starczak<sup>2</sup> (mentors)

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*Squalus acanthias*, commonly referred to as Spiny Dogfish, is a small coastal shark with a distribution ranging from Florida to Greenland in the Northwest Atlantic Ocean. It migrates north in the spring and returns to southern offshore waters in the fall. *S. acanthias* stocks are at risk to overfishing because sharks mature late in life (6 years male & 12 years female), and have a low fecundity rate. European and Northwestern Atlantic stocks have been severely depleted and overfished, respectively, within the past 10 years. To prevent stock collapse, it is important to understand the species' distributional patterns in relation to its environmental components. From 2008 - 2012, the relationship between internal waves and the distribution of *S. acanthias* was studied on southwestern flank of the Stellwagen Bank in Massachusetts Bay, MA. Current and temperature measurements of the water column were made from an anchored vessel (55 m water depth) with an Acoustic Doppler Current Profiler (ADCP), a temperature mooring, Conductivity Temperature Depth (CTD) casts, and echosounders (120 kHz and 200 kHz). The distribution of sharks in the water column was determined from echosounder records of their acoustical traces, and the identity of the traces assessed with an underwater video camera. Here we describe the temporal vertical distribution and abundance patterns (both daily and annually) of *S. acanthias* collected from 2008-2012 in relation to water temperature. We hypothesized that *S. acanthias* abundance would vary with water temperature because as migratory species, they move north and associate with cooler waters. Previous studies have shown that *S. acanthias* are most likely to be found in water temperatures below 15 °C, but studies have not detailed the local distribution with respect to temperatures at different water depths. Analysis of 1375 shark acoustic traces indicated large interannual variation in abundances of sharks below 25 m. Sharks were relatively abundant during 2008-2010 and rare in 2011-2012. In this study, the average measured abundance of sharks between 25 and 40 m water depth over the past 4 years was negatively correlated with the average measured water temperature at this depth range. Understanding the movement patterns of *S. acanthias* can be vital in fisheries studies and may be useful to fisheries management agencies to improve estimates of *S. acanthias* abundance.

This research was supported in part by NIH Grant # 5T34GM008422, by NOAA Sea Grant, WHOI's Interdisciplinary award (Mellon Joint Initiatives Fund), and WHOI's Marine Mammal Center.



## **The Role of LMNA in Human Longevity**

**Lavida Brooks**

Dr. Paola Sebastiani (mentor)  
Boston University

The LMNA gene produces lamin A and lamin C which are structural proteins that provide stability and strength to cells. These proteins are supporting components of the nuclear envelope that regulate the movement of molecules in and out of the nucleus. They also play a role in gene expression. Mutations in LMNA can cause serious health conditions, for example, dilated cardiomyopathy and the Hutchinson-Gilford Progeria syndrome, which causes premature aging. However, previous studies suggest that some of LMNA's protein products might have a role in normal aging and might also encourage human longevity. This study started by investigating the question "Do centenarians carry a different number of these mutations compared to people in the general population?" Genotype data of three single nucleotide polymorphisms (SNPs) rs915179, rs2485664 and rs2485668, in a set of 800 centenarians and 914 controls from the New England Centenarian Study was analyzed. Using association tests and a proportion tests of these SNPs showed that the control (people within the community) have a significantly larger number of these mutations than centenarians. From the above results the question "Is the survival of centenarians with this gene affected by their genotype?" was then investigated. A survival analysis with log rank tests was done in 1210 subjects from New England Centenarian Study for these SNPs rs915179, rs2485664 and rs2485668. The p-values were 0.386, 0.364 and 0.302 for each SNP. The analysis showed non-significantly different survival in centenarians carrying different genotypes. However, centenarian carriers of the heterozygous genotype for the SNPs rs2485664 and rs2485668 showed an extended survival compared to carriers of the homozygous genotypes. Investigation of the structure of the LMNA gene allowed for the discovery that the SNPs rs2485664 and rs2485668 are in a region of strong linkage with the coding variant, rs4641. Survival analysis of this SNP in another study of long-lived individuals showed that centenarians who are heterozygotes for rs4641 do significantly live longer than homozygotes. This mutation has been shown to cause an increase in body fat and metabolic syndrome, so that its effect is detrimental in younger people. However, in subjects who survive to extreme ages, this mutation becomes beneficial possibly because increased body fat may limit the problems of muscle wasting.

This research was funded by UVI NIH MARC Research Trainee Program Grant No. 5T34GM008422.

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

**Murchtricia Charles and Chantel Ible**

Dr. Justin Shorb (mentor)  
University of the Virgin Islands

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 Analyser). 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.

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

## Analysis of twenty species of the USVI fishery for overfishing

**Tasha Corneille**

Angela Dikou, PhD (mentor)  
The University of the Virgin Islands

Currently 44, 16, and 6 % of fish stocks are fully to heavily exploited, overexploited and depleted, respectively, worldwide. Overfishing is the depletion of fish from the population to such an extent that it can't be replenished naturally. Overfishing may occur as recruitment or/and growth overfishing. Recruitment overfishing is the removal of the fish from the population before it matures whereas growth overfishing is the depletion of larger size fish from the population such that fewer larger fish are represented in the catch. Fisheries management addresses overfishing for the sustainability of biological productivity through conservation of marine ecosystems. To determine whether or not overfishing is occurring at the USVI, data for 20 out of approximately 70 species of a port biosampling database [1980-2009] was analyzed and values of critical fish lengths ( $L_{mat}$ : length at maturity;  $L_{\infty}$ =infinite length) were obtained from FishBase. Specifically, trends in average fish size in the catch; differences in average fish size among gear types; and contrasts of critical fish size values of the catch with those reported at Fishbase for relevant populations were evaluated. Significant trends in average fish size were revealed through regression analysis; significant differences in average fish size among gear types were revealed through one-way Analysis Of Variance; contrasts between fish size critical values were evaluated graphically. During the thirty year period, mean fish size decreased for two species (mutton snapper,  $R^2_{adj.}=0.48$ ,  $p=0.0004$ ,  $Y=15529.84-7.57*X$ ; Spanish hogfish,  $R^2_{adj.}=0.99$ ,  $p=0.0331$ ,  $Y=7948.8-3.82*X$ ); increased for three species (longspine squirrelfish,  $R^2_{adj.}=0.23$ ,  $P=0.0023$ ,  $Y=-1103+0.65$ , spotted trunkfish,  $R^2_{adj.}=0.37$ ,  $P=0.0065$ ,  $Y=-3141.3+1.67*X$  and white grunt,  $R^2_{adj.}=0.48$ ,  $P=0.0281$ ,  $Y=-3128.16+1.72*X$ ); and remained unaltered for the rest of the fifteen species. However, contrast of critical values of  $L_{mat}$  and  $L_{\infty}$  from FishBase indicated that Spanish hogfish and spotted trunkfish may be subject to recruitment overfishing regardless of the negative and positive trends, respectively. Differences in mean fish size among different gear types were species-specific. In particular, there was significantly lower mean fish size for 6 out of 17 species caught with fish traps compared to the other fishing gear types. Mis-matches between the direction of trends in mean size of fish in the catch and contrasts of critical length values of fish with minimum, maximum and average values of fish length in the catch, indicate probable creeping overfishing. Examination of the whole suite of species in the future may assist in highlighting the magnitude of creeping overfishing in USVI fisheries and prompt appropriate adjustment of regulatory tools, such as protected areas, gear restrictions, and species-specific restrictions, by the Department of Planning and Natural Resources, if necessary.

Funding for this research was provided by the National Science Foundation (NSF) HBCU-UP grant #HRD-0506096.

## **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.

## **Optimization of Growth and Characterization of CVD**

**Jewel Cumberbatch**<sup>3</sup>, Maja Oblepias<sup>1</sup>, and Dr. Kevin Yager<sup>2</sup>

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The objective of this research project is to identify optimal growth and transfer conditions that minimize the number of atomic scale defects and grain boundaries in graphene sheets. Before fabricating high quality graphene-based electronic devices on a large scale, these questions must be addressed. Graphene is a two-dimensional one-atom thick material with sp<sup>2</sup>-bonded carbon atoms in a honeycomb shape lattice. This structure makes graphene the strongest and thinnest known material, about 200 times stronger than steel, with a high flexible mechanical structure, electron carrier mobility and thermal conductivity, making it a potential to use in nanoscale electronic devices. Our study involves the synthesis and characterization of the monolayer, bilayer and multilayer graphene. The samples are grown by chemical vapor deposition on copper substrates and characterized via Raman spectroscopy, scanning electron microscopy and scanning probe microscopy. Raman data of the quasi sp<sup>2</sup>-bonded carbon nanomaterial showed variations in the peak intensities for single layer, bilayer, and multilayer graphene. The ratio of the G and 2D peaks are used to distinguish the number of layers. Scanning electron microscope is used to characterize the growth and crystallinity of the graphene films. By employing these techniques, graphene structures and defects are found on monolayer, bilayer and multilayer fabricated. Our research will help researchers and developers to fabricate larger areas of graphene without relinquishing its intrinsic mechanical and electrical properties.

This Summer Undergraduate Laboratory Internship (SULI) and Visiting Faculty Program (VFP) was supported and funded by the US Department of Energy at the Brookhaven National Laboratory – Center for Functional Nanomaterials. This presentation was funded by NSF-HBCU-UP grant #HRD-0506096.

## **OSSEC Intrusion Detection System's Ability to Detect Denial-Of-Service Attack on the Linux Operating System**

**Sandra Daniel**

Dr. Marc Boumedine (mentor)

University of the Virgin Islands, St. Thomas Campus

Due to the growing number of cyber-attacks, Intrusion Detection System(s) (IDS) are becoming a vital part of any enterprises conducting business over the Internet. IDS monitor suspicious activities on a network and alert the system or network administrator of any abnormal activities. This idea of cyber-security emerged from a paper that introduced the notion of intrusion detection written by James Anderson in 1980. A common attack is the Denial of Service attack where computing or memory resources are stressed to serve legitimate traffic request. This study focuses on Host-based Intrusion Detection System, a software running on individual host machines that analyzes activities and maintains system file or integrity with a specific purpose of detecting DoS attacks. The main thrust of this research is the design and configuration of an IDS, such as the open source Office of State Security and Emergency Coordination (OSSEC). OSSEC performs log analysis, integrity checking, rootkit detection, time-based alerting and active response. Rules are defined in order to detect HIDS attacks such as DoS attacks, based on the analysis of the webserver (Apache) log files. To accomplish such a task, XML and regular expressions languages are used to identify patterns and respond by actions such as alerting the system administrator or stopping the attacks by killing processes. The next step is to test the IDS effectiveness by generating DoS attacks with the TevDos tool. This tool is used to simulate DoS attacks by sending multiple requests to the webserver (Apache). The effectiveness is discussed in terms of detection rate and false positive rate.

This research is funded by Emerging Caribbean Science (ECS) Program, the National Science Foundation (NSF) HBCU-UP grant #HRD-0506096 and the University of the Virgin Islands.

## **Designing an Effective Scheduling Algorithm**

**Lauritz A. David Jr**

Dr. Mark Boumedine (mentor)

University of the Virgin Islands, St. Thomas USVI

Many institutions, businesses, and organizations require scheduling to keep them on track with daily, weekly, monthly, and even yearly tasks. Scheduling is the action of sorting, organizing, and structuring required demands into available resources. In some cases there are constraints on the demands, which can only work for particular resources. There are two types of constraints; soft constraints and hard constraints. Hard constraints must be met for the demand to be scheduled, but the soft constraints are requests that are satisfied for convenience. For example a college schedule would have hard constraints such as the amount of seats in the class, but soft constraints such as the time the class was held. To implement this program, research was done on which algorithm (which is a step-by-step procedure for calculations) to use to get the best results in a reasonable amount of time. The *Tabu Search* algorithm was chosen because it was simple; it would check possible solutions and choose the one that satisfies all hard constraints and the most soft constraints producing a satisfying schedule. First a priority queue program organizes the demands from most constraints to least. Next, a blank schedule is created for the beginning of a binary tree. As the tree branches out the first row of branches adds one resource to a blank schedule, and creates leaves for each instance where the demand can fit in the schedule. This 'leaf' is called a node. Before the tree continues branching a cost function is added to determine which node satisfies most of the soft constraints without violating any hard constraints. The tree continues branching and adding demands into available resources and follows the branch with the best cost until there are no more demands to be placed creating a complete schedule. Learning that the University of the Virgin Islands also made its schedules by hand sparked an interest in seeing if it was possible to write a scheduling program and apply it to the UVI classes. Not only would the program schedule UVI classes but it will also find the best solution, satisfying as many constraints as possible.

Acknowledgements: The University of the Virgin Islands, ECS Program, SURE, The National Science Foundation, HBCU-UP. This research was funded by NSF HBCU-UP (Grant Number HRD – 0506096)

**Comparative Study to Determine the Water Quality Parameters of  
Bioluminescent Mangrove Lagoon and Salt River Bay, St. Croix, USVI**

**Anthonios Doliotis**, Lynisha Farrell, Anthonio Forbes, & Shelsa Marcel  
Dr. Bernard Castillo II and Kynoch Reale-Munroe (mentors)  
University of the Virgin Islands

Located on St. Croix, VI, Salt River Bay National Historical Park and Ecological Preserve contains both historic ruins and a diverse ecosystem. Salt River Bay is known for its mangrove forests and coral reefs. Bioluminescent dinoflagellates can be found throughout the bay. Dinoflagellates are small unicellular protists. Bioluminescence results from the conversion of chemical energy to light energy within the dinoflagellate. Bioluminescence appears to be most concentrated in Mangrove Lagoon. The main objective of this study was to determine and compare water quality parameters of Mangrove Lagoon and Salt River Bay. Water quality parameters, namely dissolved oxygen, salinity, temperature, pH, and turbidity were collected using YSI data loggers within the bioluminescent Mangrove and Salt River Bay. Salinity and temperature are the two water quality parameters that this research project focused on, and the results acquired were compared to known bioluminescent bays in literature. Results showed that salinity was 36.47 ppt in Salt River Bay and 37.98 ppt in Mangrove Lagoon, while temperature was 29.86C in Salt River Bay and 30.30C in Mangrove Lagoon.

This research was funded by UVI CS-Summer Undergraduate Research Experience Program, and NSF HBCUUP Grant Award No. HRD – 0506096.



## **Data Mining: Exploring the association between semantic categories and attributes in Large Databases.**

**Nichole Etienne**

Kostas Alexandridis (mentor)

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Data mining is an interdisciplinary field which refers to the process of extracting and analyzing the content and value of information from existing datasets and databases. From the existing information, associations are made through text mining (extracting or categorizing information within semantic categories) and identifying statistically important connections between attributes, among attribute states, and across states and attributes in the database. This results in the discovery of patterns of interconnectivity within and across data variables and their states. This research looks at (a) the emergence of significant patterns and associations among demographic, attitudinal and belief information in survey datasets collected across a range of participants of ecotourism activities (Kobriniski, 2012), and (b) how classified semantic categories extracted from open-ended text responses are linked across and within associative attributional databases. In addition, the research study examines the performance of a range of different data mining models and algorithms, to extract and explore patterns of associations. Such algorithms range from simple models (linear regression, cluster, and multidimensional factor analysis models) to complex tree algorithms (classification and regression trees, CHAID, Interactive Trees, Random Forest Trees), to probabilistic algorithms (such as Artificial Neural Network and Naïve Bayes Classifiers) . The importance of this research includes: benchmarking (i.e., finding the average model performance) in the development of a modeling platform for more advanced scientific inferences; facilitating the emergence and discovery of complex patterns of associations within existing data structures, and linking parametric (i.e., normally distributed) with non-parametric inference using machine learning and data mining tasks. Such analysis can aid the discovery and mining of complex patterns of relationships especially in large and seemingly unrelated relational database structures. After testing the prediction of the importance of ranking questions (3.1-3.7) with the decision tree, the mining model showed that questions were connected but 3.1 ( the importance of snorkeling trips) seemed most important, while 3.1(support of tourism), 3.4 (combining recreation and education, 3.5 (Scientific knowledge of corals ), 3.7(conditioning of corals ) and 3.3 ( snorkeling activities) followed in the linkage. In retrospect data mining allowed the numerical depiction of what was in the database allowing one the opportunity to notice connections as well as make predictions.

This research was funded by NSF HBCU-UP (Grant Number HRD – 0506096) and the MBRS-RISE Grant Award No. GM061325.

## **Preliminary Studies on Water Quality Parameters in Bioluminescent Mangrove Lagoon, St. Croix, USVI**

**Lynisha Farrell**, Anthonios Doliotis, Shelsa Marcel and Anthonio Forbes  
Dr. Bernard Castillo II and Kynoch Reale-Munroe (mentors)  
Mangrove Lagoon, St. Croix, USVI

Mangrove Lagoon is closely situated to the east side of Salt River Bay, south of Hemer's Peninsula, St. Croix, US Virgin Islands. This bay was part of a hotel/marina project produced by dredging an existing salt pond, which connected a previously enclosed pond to Salt River Bay in the 1960's. Currently, the bay has an oval shape, a depth of 4 meters, 250 meters in length, and 130 meters in width. Mangrove Lagoon is known for its bioluminescence. Bioluminescence results from the conversion of chemical energy to light energy. Small unicellular protists called dinoflagellates are responsible for the bioluminescence; however, the specific species has yet to be determined in Mangrove Lagoon. Each dinoflagellate emits greenish-blue light when it feels pressure against its cell wall, resulting in bioluminescence. The main objective of this study was to determine the water quality parameters of Mangrove Lagoon and compare two water parameters, salinity and temperature with known bioluminescent bays in existing literature. Water quality parameters were collected using a YSI data logger, which was deployed in the middle of Mangrove Lagoon. The YSI data logger collected water quality data every thirty minutes for 45 days within the lagoon. Our results showed that salinity is between 36.04-38.48 ppt and the temperature ranges from 29.07-32.01°C.

This research was funded by NIH MBRS-RISE Grant Award No. GM061325, supported through UVI-Emerging Caribbean Scientists.

## **Mutation Detection in Familial Frontotemporal Dementia-Amyotrophic Lateral Sclerosis With Exome sequencing**

**Akima George<sup>1</sup>**

Dr. Joshua Sailsbery<sup>2</sup> and Dr. Kirk Wilhelmsen<sup>2,3</sup> (mentors)

1 University of the Virgin Islands

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Frontotemporal dementia with amyotrophic lateral sclerosis (FTD-ALS) is a disease that is often inherited in an autosomal dominant pattern. FTD is commonly associated with mild amyotrophy and two thirds of patients with ALS have brain pathology consistent with early FTD. Superoxide Dismutase 1 (SOD1) mutations are identified as a common cause of familial ALS on chromosome 21q22.11. The microtubule associated protein tau (MAPt) were the first mutations identified for FTD-ALS on chromosome 17q21.31. San Francisco Family B (SFB) was ascertained to have FTD-ALS, though SFB family members did not have a MAPt or SOD1 mutation. We began using massively parallel exome sequencing to map the mutation responsible for the disease in SFB. A recently identified common cause of familial and sporadic FTD and ALS is a hexanucleotide repeat in noncoding region of C9ORF72 gene on chromosome 9p21.2. The goal of this project is to use the exomic sequences from 10 individuals from SFB and 100 individuals without the disease to map the locus responsible for disease in SFB.

An REU Site Grant (DBI-1156840) to the University of North Carolina Chapel Hill supported this project. This presentation was supported by NIH MARC grant #5T34GM008422.

## Synthesis, Characterization and Preliminary In Vitro Studies of melanoma cells with mixed-metal Binuclear Ruthenium(II)-Vanadium(IV) complexes

**Michelle Gordon**

Javelyn Stubbs and Dr. Alvin Holder (mentors)  
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Photodynamic therapy (PDT) is a new non invasive procedure to inhibit the growth of many different kinds of cancer. PDT involves photosensitizers, which is a drug that once illuminated with light causes chemical reactions to kill the cancerous cells in that specific area that the light is being illuminated. Due to the drawback that PDT can only penetrate through one centimeter of cells, it is most popular in treating skin cancer. The National Cancer Institute reported that 76,250 new cases and 9,180 deaths have thus far been recorded in the United States for 2012. {**5**, 1,4-Bis(1,10-phenanthroline-5-ylsulfanyl)butane-2,3-diol, (phen<sub>2</sub>DTT)}, {**8**, [VO(sal-L-trypt)H<sub>2</sub>O]}, and {**7**, 1,6-Bis(1,10-phenanthroline-5-ylsulfanyl)hexane, (phen<sub>2</sub>S<sub>2</sub>C<sub>6</sub>)} were used as precursors to produce the new binuclear metal complexes {**3**, [Ru(pbt)<sub>2</sub>(tpphz)VO(sal-L-trypt)](PF<sub>6</sub>)<sub>2</sub>·4H<sub>2</sub>O}, {**4**, [Ru(pbt)<sub>2</sub>(phen<sub>2</sub>DTT)VO(sal-L-trypt)(PF<sub>6</sub>)<sub>2</sub>·3H<sub>2</sub>O} and {**6**, [Ru(bpy)<sub>2</sub>(phen<sub>2</sub>S<sub>2</sub>C<sub>6</sub>)] } by reaction with respective mononuclear transition metal compounds. The chemical and structural properties of these compounds were characterized by elemental analysis, ESI-MS, FTIR, UV/Vis, <sup>1</sup>H NMR spectroscopy. The photosensitizing properties of complexes **3** and **4** along with the control cobalt complex Na<sub>4</sub>[Co(tspc)OH<sub>2</sub>]<sub>2</sub> were examined with two cell lines; cancerous C32TG melanoma and normal, adult, noncancerous dermal fibroblast. Compounds **3** and **4** exhibited inhibition of cell growth of both cell line cultures, which indicates that these compounds are promising new photosensitizers that will be utilized in photodynamic therapy (PDT) in the near future.

This research was funded by MS INBRE and the presentation supported by NSF's HBCU-UP grant #HRD-0506096.

**Tris(triphenylphosphine)Rhodium(I) Chloride-Catalyzed Dehydrocoupling of Diphenylmethylsilane with Primary Aliphatic and Aromatic Amines**

**Renéscha V. Henderson**  
**University of the Virgin Islands**  
Colleen Scott, Ph.D. (mentor)  
Southern Illinois University

Catalytic investigations of a compatible tertiary diphenylmethylsilane with primary aliphatic and aromatic amines were employed to create silylamines. Tris (triphenylphosphine)Rhodium (I) chloride catalyst (Wilkinson's Catalyst), Palladium on Carbon were proven by  $^1\text{H-NMR}$  to successfully dehydrocouple diphenylmethylsilane with sec-butylamine, while Manganese Pentacarbonyl Bromide after 24 hours of reacting showed no sign of product, according to  $^1\text{H-NMR}$ . It was proven that Tris (triphenylphosphine)Rhodium (I) chloride, dehydrocouples at a faster rate than Palladium on carbon. Therefore, Wilkinson's catalyst effectively cross-dehydrocouples tertiary diphenylmethylsilane with aliphatic:  $n\text{-BuNH}_2$ ,  $\text{Sec-BuNH}_2$ ,  $\text{C}_6\text{H}_6\text{NH}_2$ ,  $\text{PhNH}_2$ , and  $\text{PhCH}_2\text{NH}_2$  to yield various silylamine compounds. The stability of the Si-N bonds were tested when contacted with deuterium oxide and revealed a highly favored Si-O bond. Primary aliphatic amines due to the strong nucleophilicity, rate of reaction was found to be greater than its anilines analogues. Since only tertiary diphenylmethylsilane was used, additional experiments are currently in practice to dehydrocouple secondary silanes with primary amines in the presence of Wilkinson's catalyst to study its stereoselectivity.

Financial support for this project was provided by the National Science Foundation under grant DMR-0552800, the Materials and Technology Center, the Department of Chemistry and Biochemistry, the Office of the Vice Chancellor for Research, the College of Science, and the College of Engineering at SIUC. This presentation is supported by NSF's HBCU-UP grant #HRD-0506096.

## **The Impact of Creative Problem Solving Training on Creative Thinking Skills**

**Davril Huggins and Tara Brim**

Dr. Kostas Alexandridis and Dr. Kimarie Engerman (mentors)  
Univeristy of the Virgin Islands, St. Thomas

Studies have shown that a relationship exist between creative problem solving (CPS) skills and retention. Therefore, the general purpose of this study was to examine the effects of CPS Training on the development of creative thinking skills for students at the University of the Virgin Islands. The participants (N=739) in the study consisted of 35% male and 65% female undergraduate students enrolled in Science 100 (SCI 100). The participants completed both pre and post assessments of the Torrance Test of Creativity (TTCT). The TTCT measures creativity based on age and grade. Participants in the experimental group received training in CPS. Also, throughout the semester, they received weekly assignments to foster their creative thinking skills. The control group received no training. The post TTCT scores of both the experimental and control groups were analyzed to compare means. Preliminary results show marginal significant differences in the post TTCT scores. Findings indicate that CPS is not innate. Students are to be trained in this area in order for them to be retained and persist through degree programs.

Funding for this research is provided by NSF/HRD ERP award no. 1036183.

## Molecular Diagnostics can Detect and Identify Prokaryotic and Eukaryotic Pathogens in Terrestrial and Marine Organisms

**Abrar Husein**

Jennilee Beth Robinson, PhD (mentor)

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Molecular diagnostics, PCR and DNA analyses, can differentiate between prokaryotic or eukaryotic pathogens' unique DNA sequences. The proteobacterial order, Rickettsiales contains numerous pathogens including medically important *Rickettsia* and *Ehrlichia* spp. transmitted by ticks. *Babesia*, blood-borne protozoan parasites, are also transmitted by ticks. *Rhipicephalus sanguineus*, the brown dog tick, is ubiquitous and distributed worldwide. *R. sanguineus* transmits numerous pathogens, including disease-causing *Rickettsia*, *Ehrlichia* and *Babesia* to humans and animals.

*R. sanguineus* was recently implicated in transmission of fatal Rocky Mountain spotted fever (*Rickettsia*) infections to humans. Previously, a *Rickettsia*-specific PCR assay amplified DNA fragments of various sizes from total genomic DNA extracted from *R. sanguineus* of V.I. canines. When visualized by gel electrophoresis, amplified DNA matches the expected length, 381 bp, of the *Rickettsia* *gltA* gene region targeted by this assay. To test my hypothesis that *R. sanguineus* in the V.I. are infected with *Rickettsia*, I gel-purified the PCR amplified ~381 bp DNA fragments. The purified DNA was submitted for direct DNA sequencing and cloned on a plasmid in *Escherichia coli* for future analyses. Sequence results obtained from either gel-purified or cloned DNA will reveal if the amplified ~381 bp DNA is from *Rickettsia* or from non-specific PCR-amplification.

PCR-RFLP assays can quickly detect and differentiate between species that cause canine babesiosis. Species of *Babesia* are known to cause diseases in select hosts including dogs, cattle and humans. *B. canis* and *B. gibsoni* are the cause of severe disease and fatality in V.I. canines. Infections require different, high-risk treatments. Unfortunately, rapid diagnostics required to determine appropriate treatment are not available here. Therefore, I developed an assay that will rapidly detect and differentiate between agents of canine babesiosis. The assay (RFLP) uses restriction endonucleases to cut PCR-amplified DNA into different length fragments based on nucleotide sequence differences. Conserved PCR primers were selected to amplify 18S rDNA from all canine *Babesia* pathogens. Selected enzymes will generate unique fragment lengths for each pathogen, allowing species differentiation. An attempt was made to include a related hematozoan parasite of fish, *Haemogregarina*.

This research was funded by NSF HBCU-UP (Grant Number HRD – 0506096).

## Protein HbpA and Deformin Activity in Erythrocytes

**Gemel Joseph**

Laura Hendrix, Ph.D. (mentor)

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*Bartonella bacilliformis*, a species of the pathogenic genus *Bartonella*, enters human red blood cells and this parasitic relationship leads to Carrion's disease, which is characterized by severe acute anemia. Although *Bartonella bacilliformis* is contained within the specific geographic area of Peru, Ecuador, and Colombia and can be monitored with antibiotics and insecticides, it remains an organism of great interest because its parasitic capabilities and the disease states in which it induces makes it unique among human pathogens. The protein deformin, which can be found in culture supernatants of *B. bacilliformis*, produces indentations on red blood cell membranes that allow the bacterium to enter the cell. The *Bartonella* protein HbpA (hemin-binding protein A) contains a repeated region of approximately 1,400 Daltons in *B. bacilliformis* strain KC583 that is missing in strain KC584. Strain KC584 is unable to produce deformin in culture supernatants. Researchers discovered that the region required for producing deformations has a molecular weight of 1,400 Daltons, but they have been unable to sequence the region. We hypothesized that *Bartonella bacilliformis* KC583 hemin-binding protein A (HbpA) is required for the appearance of indentations on human red blood cell membranes known as deformations and thought to be required for entrance of the bacterium into erythrocytes. Our methods were as follows:

1. Grow bacteria on blood agar plates in PBS overlays and transfer PBS overlays with bacteria onto BCYE Legionella plates
2. Perform protein assays of culture supernatants and cell pellets of strains KC584 & KC583 from BCYE plates
3. Perform deformin assays with strains KC584 & KC583
4. Indirect Fluorescent Antibody Stain of deformed red blood cells
5. Purify antibodies using protein A agarose
6. Analysis of IgG Fractions by Electrophoresis
7. Inhibit deformin activity using antibody and deformin sera

Our results show that the additions of the  $\alpha$ com1,  $\alpha$ HbpA,  $\alpha$ Bb antibodies and normal rabbit serum have no significant effect on deformin activity of *Bartonella bacilliformis*. These results do not indicate a relationship between these proteins and the deformin activity of *Bartonella bacilliformis*.

This research was funded by Texas A&M Health Science Center College of Medicine, Office of the Dean and Texas A&M Health Science Center Office of the Vice President for Research and Graduate Studies; Scott and White Hospital Research Foundation.

This presentation is supported by NSF's HBCU-UP grant #HRD-0506096.



## Development of Water Quality Labs for General Chemistry at UVI

**Clyde Joseph** and Micadel Hazell

Dr. Justin M. Shorb (mentor)

University of the Virgin Islands

There are different styles of chemistry laboratories: some have been proven to be more effective at helping students to master the material. The four types of labs, as defined by Domin<sup>1</sup>, are expository, inquiry, discovery and problem-based. Up until this past year at UVI, all of the laboratories were expository or discovery styles. These use given procedures which students follow like a cookbook recipe. The inquiry and problem-based styles of lab make use of student generated procedures. Research has shown that having students generate their own procedures improves the ability for students to think creatively and retain information longer. In this work, a set of water quality tests were used as a foundation to design new laboratory exercises for general chemistry. The choice to incorporate water quality testing was decided based on the ubiquitous appeal water quality measurements have within our island territory. Laboratory exercises and their pedagogical design are discussed for measuring pH, turbidity, and salinity/Total Dissolved Solids.

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This research was funded by NSF HBCU-UP (Grant Number HRD – 0506096)

**Age-related changes in glial cell line-derived neurotrophic factor (GDNF) protein expression and neuromuscular junction morphology in the rat**

**Annesha King**

Dr. John Spitsbergen, Ph.D and Monica McCullough (mentors)  
Western Michigan University, Biological Sciences, Kalamazoo, MI

Aging is a process that affects and decreases the performance of the body, the mobility, productivity and health. Aging of the neuromuscular system decreases the movement of the body. The gradual loss of spinal nerves which send motor impulses from the brain to the muscles is said to be age-related. One possible explanation for the loss of motor neurons with age could be due to loss of neurotrophic factor support. One of the most potent neurotrophic factors for peripheral motor neurons is glial cell line-derived neurotrophic factor (GDNF). GDNF is critical for proper motor neuron development and alterations in GDNF levels can have effects on early motor neuron survival. GDNF is an excellent candidate for controlling motor neuron plasticity in adult organisms. In the current study, extensor digitorum longus (EDL) and extensor hallucis longus (EHL) are considered to be fast-twitch muscles and soleus (SOL) a slow-twitch muscle. The purpose of this current study was to examine GDNF protein content in skeletal muscles at different ages, as well as to study the structure of the neuromuscular junction (NMJ) and examine GDNF co-localization at the NMJ. The SOL, EDL, and EHL muscles of the left sides from ages 3, 5, and 8 weeks, and 6 and 24 months were analyzed for GDNF protein content measured using enzyme-linked immunosorbent assay. Distribution of GDNF and the structure of the neuromuscular junction were visualized by immunohistochemistry in muscles from the right side. The results show that GDNF protein content peaks in all muscles between 5 and 8 weeks of age and declines thereafter. The EHL had the highest level of GDNF protein content of the three muscles examined. The images generated for immunohistochemistry showed that the structure of the NMJ and the distribution of GDNF may be altered with age. The results showed how GDNF protein content declines in the muscles and also how the structure of the NMJ and GDNF co-localization changes with age. Keywords: GDNF, Skeletal Muscle, Aging, Sarcopenia, Neuromuscular Junction, Motor Neurons

Funding by NSF award number DBI-1062883 and UVI NIH MARC Research Trainee Program Grant No. 5T34GM008422

## **Experiential Social Learning for Coral Reef Resilience**

**Elena Kobrinski**

Kostas Alexandridis (mentor)

UVI Masters of Marine and Environmental Studies; UVI Center for Marine and Environmental Studies (CMES); UVI College of Science and Mathematics/  
Computational Sciences

The goal of this research is to determine if there are any differences in attitudes, beliefs and behaviors from experiential social learning after visiting a coral reef, and how that learning experience relates to coral reef conservation efforts, increasing coral reef resilience. This study is expanding upon a similar project that is taking place at the University of the Virgin Islands (Alexandridis et al. 2010). While the study at the University involves the experiential participation of undergraduate students, this study expands the same dimensions of the research into the local community, similarly evaluating participants that are visiting coral reefs through ecotourism business establishments in the U.S. and British Virgin Islands. A number of participants in ecotourism activities in the U.S. Virgin Islands (St. Thomas, St. John and St. Croix), as well as the British Virgin Islands (Tortola, Virgin Gorda) were surveyed and ecotourism business establishment managers and staff members were interviewed. Our results show that experiential learning in marine and environmental ecotourism activities enhances participation conservation attitudes and dispositions at varying degrees. We found that socioeconomic and demographic factors influence the level of conservation-based attitudes, and that increasing opportunities for local participation in such activities promotes and fosters attitudinal and dispositional changes with respect to environmental conservation. We argue that social-ecological sustainability and resilience depends on the level of stewardship between conservation-based ecotourism activities and local and/or regional perspectives in sustainable development.

Funding for this research is provided by NSF VI-EPSCoR Award No. 0814417.

## **Developing a PCR protocol for the Greater Bulldog Bat (*Noctilio leporinus*) in the Northern US Virgin Islands**

**Thalia Lake** and Shanelle Farrington

Dr. Alice Stanford (mentor)

University of the Virgin Islands

Bats are a vital link in the food chain system. Some species control the mosquito population and others serve as pollinators. *Noctilio leporinus* (order Chiroptera), is commonly called the greater bulldog bat because of its features. *Noctilio leporinus* is the largest species of bats found in the Virgin Islands. It is suspected that the populations are declining due to natural and anthropogenic causes. This may lead to decreased biodiversity within the bat populations of the Virgin Islands. Population genetics data are needed in conservation planning to identify means of protecting our species and their habitats. Before we can assess genetic diversity, we must develop a Polymerase Chain Reaction (PCR) protocol for *N. leporinus* that can be used to generate population genetics data. We extracted nuclear DNA (deoxyribonucleic acid) from tissue that was excised from the bat's wing. We hypothesized that 55 degrees would be the optimal annealing temperature. For each primer, we tested a range of annealing temperatures of 55-63 degree Celsius to determine the best PCR protocol. The results were then visualized using gel electrophoresis. Conclusively, each primer has one particular temperature at which it works best. The protocol that was developed was successful using the primers at annealing temperatures between 55 degrees Celsius and 59 degrees Celsius.

This research was funded by Vento Foundation and the National Science Foundation's HBCU-UP program-(grant # HRD-0506096).

## Applying Digital Normalization to Transcriptome Sequencing: Effects of Varying Coverage

**Danny Lynch<sup>1</sup>**

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Advances in next generation sequencing (NGS) have led to a wealth of data being produced by the scientific community. These large data sets require new software pipelines to lower the cost of transcriptome assembly. Digital normalization, a single pass algorithm that reduces the size of shotgun sequence data sets, is one such tool. The purpose of this study was to determine if digital normalization could be effectively used to reduce RNA-Seq data sets while retaining sufficient information for accurate *de novo* assembly. We hypothesized that digital normalization at varying coverage values would produce assemblies similar to those obtained from processing non-normalized data. Using a yeast reference transcriptome and a known RNA-Seq read set, we digitally normalized the raw reads at varying coverage levels. We then assembled the original and normalized read sets and compared the resulting transcriptome assemblies with the reference. We found that at varying coverage values, the digital normalized assembly contained fewer errors than the non-normalized data for the yeast dataset's *de novo* transcriptome assembly. Furthermore, when the raw reads were aligned against each of the assemblies, it was discovered that the digitalized assemblies returned a 20% more accurate mapping than the non-digitalized assemblies. By more efficiently processing RNA-Seq data using digital normalization, it will be possible to assemble complete transcriptomes in a fraction of the current time. This increased knowledge will facilitate greater understanding of gene expression and function. Eventually, this could help improve direct patient care and future biomedical research endeavors.

This research was funded by National Science Foundation Grant #0939454. This presentation is supported by NIH's MBRS-RISE Research Program - GM061325.

## **Threats to Our Reefs: Lionfish Invasion in St. Croix, USVI and GIS Mapping of Distribution**

**Shelsa S. Marcel**

Dr. Bernard Castillo II and Prof. Kynoch Reale-Munroe (mentors)  
University of the Virgin Islands

The incursion of the invasive species of lionfish, *Pterois volitans*, in the Western Atlantic and Caribbean has been an issue of great scientific concern since their first detection in the Atlantic in 1992. November 28<sup>th</sup>, 2008 marked the first confirmed sighting of lionfish in the waters around our United States Virgin Islands territory, specifically St. Croix. Only four years later, St. Croix waters are being ravaged by proliferating populations of these indigenously Indo-Pacific lionfish. *Pterois volitans*' presence in the ecological system of our waters could have detrimental effects on native populations of fish, the local fishing industry, and the ecology of our coral habitats. In reaction to this invasion, there have been early dive attempts at search and recovery efforts of lionfish around the island of St. Croix, USVI. Our study aimed to create a GIS map of the spatial distribution and abundance of lionfish using the data from these dives, in response to the threat of the lionfish. The island was divided into six sectors, each sector serving as a dive spot for the collection of data on lionfish GPS location and abundance. GIS, Geographic Information System, was then used as a tool to plot the data onto a satellite map of the territory. The resulting map is a powerful tool useful for identifying spatial distribution and determining regions of abundance of lionfish around St. Croix, enabling analysis and solution development concerning this current threat to our reef.

This research was funded by NIH MBRS-RISE Grant Award No. GM061325, supported through UVI-ECS (Emerging Caribbean Scientists) program.

**Generation of an EFhd2 null mutant for the study of self-oligomerization and its association with the microtubule-associated protein tau**

**Shenee' Martin**, Eva N. Cruz, and Jaime Vaquer-Alicea III  
Irving E. Vega, Ph.D. (mentor)

University of Puerto Rico, Rio Piedras Campus, Department of Biology, San Juan, PR

The hyperphosphorylated microtubule-associated protein tau is implicated in the pathobiology of neurodegenerative diseases known as tauopathies. The identification of proteins associated with tau may provide insights that contribute to the understanding of tauopathies. Previous research work contributed to the identification of the novel protein EFhd2 as a tau-associated protein linked to tau-mediated neurodegeneration in tauopathy mouse models and Alzheimer's disease. However, the molecular requirements that mediate the interaction between these two proteins are unknown. EFhd2 is a calcium binding protein of unknown physiological function. Biochemical analysis on this novel protein indicated that EFhd2 is phosphorylated by the protein kinase complex Cdk5/p25. Thus, the aim of this project was to develop an EFhd2 null mutant that allowed us to evaluate whether or not the association between EFhd2 and tau protein and also the putative oligomerization of EFhd2 depends on calcium binding and phosphorylation state of EFhd2. A conserved aspartate residue known to be required for EFhd2 calcium binding activity was mutated to alanine. Additionally, another missense mutation was incorporated to exchange the identified serine residue, where EFhd2 is phosphorylated, to alanine. The mutant EFhd2 generated was defective in calcium binding activity and not phosphorylated by Cdk5/p25. A modified direct-ELISA was used to determine the interaction between the generated EFhd2 null mutant, wild type EFhd2 and recombinant tau. The results showed that mutating the phosphorylation site and calcium binding domain do not affect the self-oligomerization of EFhd2. The generation of the EFhd2 null mutant allows us to obtain insights into the molecular properties of the novel protein EFhd2 and its association with tau.

This research was funded by UVI NIH MARC Research Trainee Program Grant No. 5T34GM008422.

## What lion fish eat

**Charles Martin**, Nalinie Raminaraine, Nikita Thompson

Richard S. Nemeth (mentor)

McLean Marine Science Center. University of the Virgin Islands

The invasive Pacific lionfish (*Pterois volitans*) was introduced to the Caribbean in the early 1990's and has been rapidly expanding its range. It was first found in the US Virgin Islands in 2008 and is now becoming a common sight on most coral reefs. This study will examine the potential impact of lionfish on Virgin Islands reef fishes. The main focus of my research was the relationship between predator and prey size. By measuring the mouth gape height and length of the lion fish will help us understand what kind of prey can be eaten by lion fish. Lionfish collected from local fisherman were used to collect information on size, weight, sex and gut contents. Once stomachs were removed from lionfish the contents were weighed, measured and identified to the lowest taxonomic level. By identifying the different food items, we are able to pinpoint what kind of species lion fish are targeting. Prey were separated into three body types: elongated (e.g. wrasses), heavy bodied (e.g. groupers), disk shaped (e.g. surgeonfishes). My hypothesis is that small lion fish can only eat skinny or thin prey while larger lionfish will begin to eat disk-shaped prey. If my hypothesis proves to be correct, then this suggests that bigger lion fish eat different species of prey than small lionfish which can help us identify the fish species that are mostly targeted by lion fish of different sizes. This information is helping us with the evaluation of lion fish impacts on local fish populations.

This research was funded by NSF VI-EPSCoR Grant. This presentation is supported by NSF's HBCU-UP grant #HRD-0506096.



## Major Selection: No Minor Decision

**Darrell Mercer**

Dr. Kostas Alexandridis (mentor)  
University of the Virgin Islands

Selecting a major is one of the most important decisions a college student has to make during their undergraduate career. Some people are committed to a decision regarding their major right from the beginning of their college careers, while others may be indecisive and try a couple of different majors before they settle into one they prefer. Our research examines self-motivation and the role of the family as decisive forces in the involvement of choosing a major. From the Fall 2011 semester – Spring 2012 semester, 37 group peer student interviews with a total of 135 participants were completed and transcribed. The interviews were then entered into the NVivo qualitative analysis software and coded into nodes and further more into themes, using a Grounded Theory qualitative social science methodological analysis. The purpose of this study is to understand the reasoning for why and how students chose their college majors. Our qualitative cluster analysis results based on narrative similarities indicate that a number of important clusters can be identified as drivers of college students' selection of major. Specifically we identified clusters based on two thematic groups namely: Clusters based on College majors; and clusters based on factors influencing selection. *Important college major clusters* include: (a) Social Science and Business majors; (b) Environment, Nursing, Math majors, and; (c) Criminal Justice, Computer Science, Chemistry and Engineering majors. *Important selection factor clusters* include: (a) Achievement and life goals; (b) Family and peer influences; (c) potential for financial returns; (d) Helping others and the community, and; (e) College Experience. Understanding how the clusters relate to each other will help us see what motivates college students' selection of a major.

Partial funding for this work is provided by NSF/HRD ERP award no. 1036183, from NSF HBCU-UP(Grant Number HRD – 0506096) and the MBRS-RISE Grant Award No. GM061325.

## Investigation of Filtering Metagenomic Sequencing Data on Assembly

**Tobias Ortega-Knight**<sup>1, 2, 3</sup>

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Environmental genomicists are often overwhelmed by the sheer amount of metagenomic sequencing data produced in a single experiment. One computational tool to process this data is digital normalization, a new heuristic approach that reduces sequencing data to a minimum while preserving maximum information content. Smaller data volume facilitates faster, more accurate, and more memory efficient assembly. In this study, we hypothesize metagenomic data filtered by digital normalization successfully reduces the data volume without losing information. First, we mapped reads to reference genomes from the Human Microbiome Project (HMP) mock data set. We then performed metagenomic assembly on raw, normalized, and normalized partitioned reads. Next, we mapped the raw reads to the *de novo* assemblies and compared them to the reference to determine if information from the normalized reads was lost and/or if there was an advantage in the normalized assemblies. Our results from the mapping analysis show the digitally normalized assembly had 1.33% increase in reads mapping compared to the raw read assembly and retained information that would have been lost. The normalized and partitioned assembly only lost 2.49% of reads that mapped when compared to the nonnormalized assembly results. The nonnormalized assembly took 57 minutes to complete and used approximately 16.1 gigabytes of memory. The digitally normalized assembly took 8 minutes to run, 7.125x faster than the nonnormalized assembly, and used 34 megabytes of memory, a 485% reduction in memory capacity. The digitally normalized and partitioned assembly finished in 11minutes (5.18x faster) and used 48 megabytes of memory, a 344% decrease in memory compared to the nonnormalized assembly. This investigation shows that digital normalization can reduce redundant reads and their associated errors in metagenomic sequencing data, thereby significantly decreasing the time and computational resources required to perform *de novo* assembly without sacrificing sensitivity. This tool will enable researchers to filter and assemble metagenomic sequencing data sets that are currently too large to assemble using conventional methods.

This research was funded by; Michigan State University and the National Science Foundation Grant# 0939454. This presentation is supported by NIH's MBRS-RISE Research Program - GM061325.

## **Biometric analysis of the invasive Pacific lionfish (*Pterois volitans*) in the Virgin Islands**

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Indo-Pacific lionfish (*Pterois volitans*) are precipitously invading the waters of the Caribbean and tropical Atlantic. Due to their population explosion and aggressive behavior, lionfish have the potential to become the most devastating marine invasion in history by significantly reducing the abundance of coral reef fishes and leaving behind a devastated ecosystem. It was first found in the US Virgin Islands in 2008 and is now becoming a common sight on most coral reefs. In order to understand its potential impact on native fishes, we need to learn more about its biology and basic life history characteristics. The analysis of weight length data is usually directed toward two objectives; (1) Mathematically relating the relationship between weight and length; (2) Measuring the variation from the expected weight for length of individual fish as indications of corpulence, well-being, or gonad development. Several different ratios have been developed to describe these relations between fish length and weight. These ratios are universally used as measures of fish well-being (condition). Length and weight of sample lionfishes (**N= ~50**) were obtained. The Fulton's Condition Factor was done to determine the ratio between the observed weight and an expected weight dependent on the fish's length. According to the ANOVA Analysis that was obtained (**N=48**) the **average female length = 23.855 cm** and **average male length = 26.746 cm**; (**F = 3.9715, P< 0.05**). Weight analysis indicated (**N=48**) the **average female weight = 228.586 g**; **average male weight = 357.658 g**; (**F = 12.883, P< 0.001**).

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This Research was funded by NSF VI-EPSCoR Grant number 0814417. This presentation is supported by NSF's HBCU-UP grant #HRD-0506096.

## **Nationality and Ethnicity and Zimbardo's Time Perspective Inventory**

**Latisha Ramsey and Curlis Joseph**

Dr. Kimarie Engerman and Dr. Kostas Alexandridis (mentors)  
University of the Virgin Islands

The Virgin Islands has become a culturally diverse community as many citizens with different nationalities make the USVI their home. Therefore, each citizen's perception of time could positively or negatively impact operations within the USVI community. This is the case because time perspectives are influenced by socio-cultural values, religious beliefs, and ideas. Zimbardo and colleagues (Zimbardo & Boyd, 2008) noted that there are six common time perspectives in the western hemisphere. These perspectives are: (1) the past negative; (2) past positive; (3) present hedonistic; (4) present fatalistic; (5) future; and (6) transcendental-future time perspective. The research presented here aims to identify, quantify, and evaluate the time perspective distribution among undergraduate students at the University of the Virgin Islands. Experimental sample data were collected from students enrolled in Science 100 (SCI 100) on the St. Thomas Campus for the period 2010-2012. The Zimbardo Time Perspective Inventory (ZTPI), and the Transcendental-Future Time Perspective Inventory (TFTPI) were administered to measure the study participants' construct of time. Student's nationality and ethnicity were collected through self-reported questionnaires. Results demonstrate that cultural, social, economic, educational and ethnic background interacts in statistically significant ways with student's time perspectives. For this reason, students should be made knowledgeable about their time perspective since it impacts future career and personal paths.

Funding for this research is provided by NSF/HRD ERP award no. 1036183.

## **Evaluating the abundance and size distribution of Indo-Pacific lionfish (*Pterois* spp.) in the US Virgin Islands**

**Nikita Thompson**, Charles Martin, and Nalinie Ramnaraine  
Richard S. Nemeth (mentor)  
University of the Virgin Islands

Over the last decade, the invasion of the Indo-Pacific lionfish have captured the attention of many scientists and researchers, due to the poorly understood ecological impacts the invaded species can have on the marine ecosystems and native organisms. Because of its voracious appetite and lack of predators, the lionfish population is rapidly increasing; therefore, this may be challenging for managers when trying to control the population and reduce the potential negative impacts.

In the U.S. Virgin Islands, the lionfish sighting have become more frequent over the last few years. To aid USVI managers in the efforts to control the population and reduce the number of lionfish, this study will focus on evaluating the abundance and distribution patterns and size structure of the lionfish population in specific habitat types. My goal is to identify habitats with the highest abundance of adult and juvenile lionfish and determine if they are selecting specific habitat types. We used stratified random sampling to select ten replicate sites per habitat which included mangroves, seagrass beds, and coral reefs. Fish surveys were carried out in each habitat type along 25 x 4m (large fish) and 25 x 2m (small fish) transects. We also recorded fish diversity at each site using one 30 min roving diver survey. Survey data was added to a database compiled of information from past and current lionfish sightings within the USVI. The database and habitat-specific surveys will allow me to examine the effects of habitat on lionfish demographics.

Funding for this study was provided by VI-EPSCoR Incubator Grant and S-Stem.

## **The SERV-ILEK Project: Social-Ecologically Resilient Visions using Integrated Local Environmental Knowledge**

**Alex Webb**

Kostas Alexandridis (mentor)  
University of the Virgin Islands

One of the primary difficulties in understanding and managing for environmental sustainability within a systems context is the concept of uncertainty or surprise. However; uncertainty is an inherent component in all complex adaptive systems, such as a social-ecological system, and therefore should be embraced and anticipated. Managing for environmental sustainability then, includes not only an understanding of the normative values contextualizing it but also the ability to identify and promote resilient solutions in the face of an ever changing and dynamic world. The SERV-ILEK project seeks to add to the rapidly growing discipline of sustainability science by examining the multidimensionality of collective community visions for the future. It will also investigate the mechanisms and processes that inform those visions. The project employs a two phase methodological approach: a) Participatory scenario planning group exercises aimed to uncover the perceived drivers impacting not only the future but study the emergent dimensions or narratives as a knowledge structure. b) Game theoretic Role Playing Games (RPG) in which participants will engage in strategic collaborative decision making in exercises using scenarios identified during the scenario planning stage. The benefits and broader impacts of this project are the exploration of collective alternative futures as well as the provision of an evidence based decision support mechanism to resource managers related to the resilience and value laden goals of a diverse range of community groups.

Funding for this research is provided by NSF VI-EPSCoR award no. 0814417. Additional partial funding was supported by the initiative-based project EO-5 "Creation and Sustainable Governance of New Commons through Formation of Integrated Local Environmental Knowledge", Research Institute for Humanity and Nature (RIHN), Japan.

## **Judges**

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Dr. Marilyn Brandt  
Dr. Angela Dikou  
Ms. Kathleen Dudemaine  
Dr. Kimarie Engerman  
Ms. Joanna Gyory  
Dr. Nasseer Idrisi  
Dr. Paul Jobsis  
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### **VI Department of Education**

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Mr. Gerald Walters

### **University of North Carolina**

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Ms. Samira Brooks  
Mr. Joel Durand

The event organizers thanks the mentors and judges who have volunteered their time and energy to critique these student presentations. You have made a huge contribution to the success of our students, symposia, and community. Your dedication to the advancement of young Caribbean scientists is greatly appreciated.  
Thank you!

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