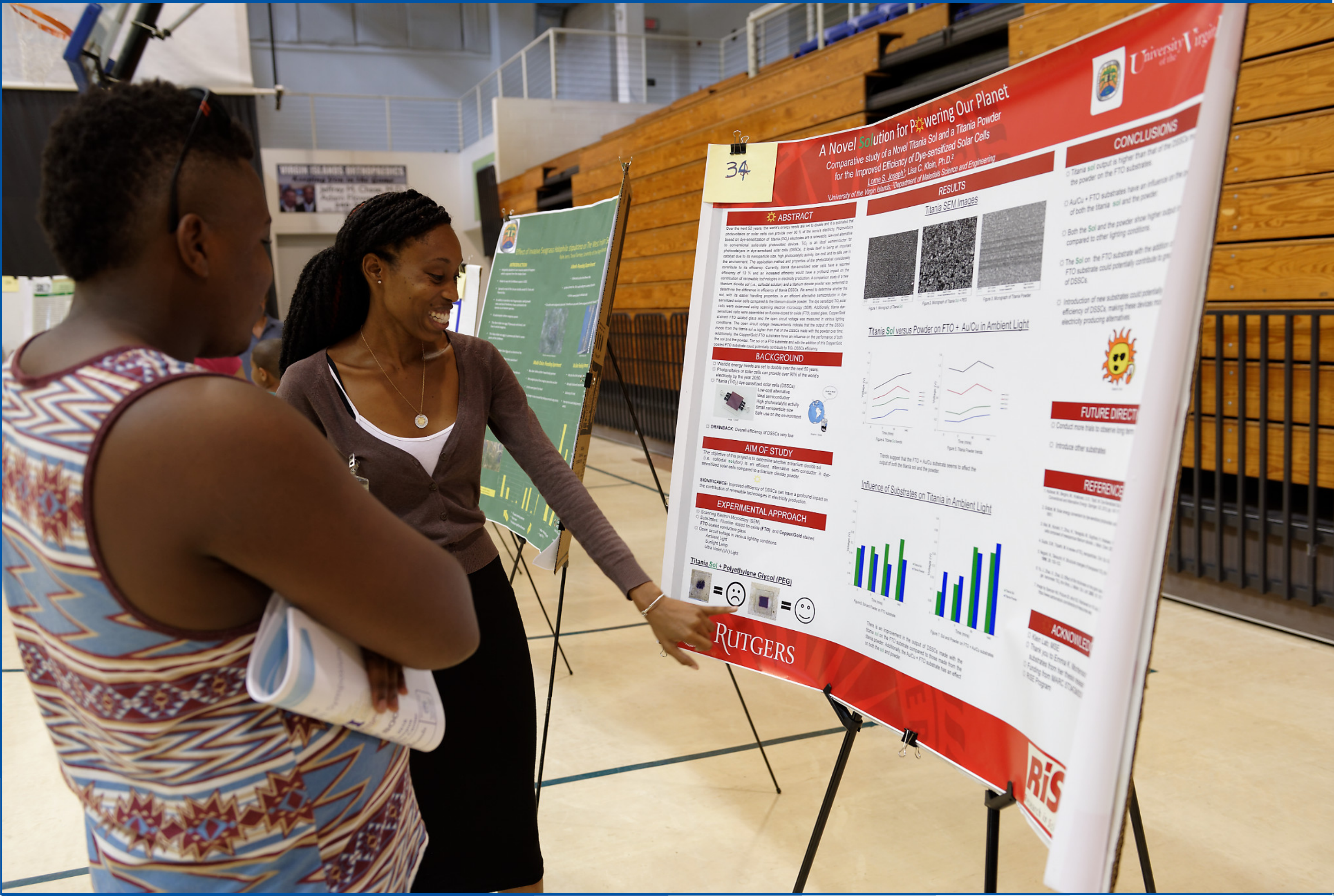
THE UNIVERSITY OF THE
VIRGIN ISLANDS PRESENTS...

THE 20TH ANNUAL STUDENT RESEARCH SYMPOSIUM

September 21st, 2019
1:00pm to 3:00pm
Sports & Fitness Center

ABSTRACT BOOK



Twentieth Annual Fall Student Research Symposium

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Saturday, September 21, 2019
University of the Virgin Islands
Sports & Fitness Center
St. Thomas Campus

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Event Organized by:
Emerging Caribbean Scientists (ECS) Program
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University of the Virgin Islands
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Emerging
Caribbean
Scientist

The Emerging Caribbean Scientists (ECS) 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.

Table of Contents
Fall 2019 Research Symposium Presenters

All presenters are UVI undergraduates. Graduate students are annotated with a star (*).

Metal-Related Sequestration Genes and Environmental Contaminants in Human Placentas

Shabree Anthony[1,2]
Mentor(s): Lauren Aleksunes[1]
Ranran Zhang[1], Ludwik Gorczyca[1], Cathleen Doherty[3], Brian Buckley[3]

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The placenta is a complex organ that is essential for fetal development by providing nutrients and protecting against exposure to chemicals and pathogens. One protective feature of the placenta is its ability to negate the toxicity of environmental contaminants by up-regulating sequestration proteins. Metallothioneins (MTs) are a class of nucleophilic proteins that bind and detoxify heavy metals such as cadmium (Cd), a chemical found in cigarettes, batteries, emissions, and food. This is important because cadmium has been shown to restrict fetal growth by limiting nutrient transfer from the mother, which increases the risk of low birth weight. In this study, we sought to assess relationships between the mRNA and protein expression of MTs and concentrations of Cd in healthy term placentas (N=28). We hypothesized that the expression of MT1A and/or MT2A would be directly proportional to Cd concentrations in placentas. Placentas were grouped according to those with <3 ng/g (N=14) or >3 ng/g (N=14) Cd concentrations (median [Cd] = 2.9 ng/g). Babies with placentas containing >3 ng/g Cd tended to have lower birth weights compared to placentas with <3 ng/g Cd (*p=0.058*). While no differences in MT1A or MT2A mRNA expression were observed when stratified by Cd concentration, levels of the two MT genes correlated with each other (R^2=0.63) as well as the heavy metal transporter ZIP14 (MT1A R^2=0.55; MT2A R^2=0.23). Further studies are needed to identify alternate metals beyond Cd that may be regulating placenta MT and ZIP14 mRNA levels. Establishing these relationships will provide insight into whether placentas exhibit variability in their responses to heavy metal exposures. This research was funded by NIH R01ES029275, R25ES020721, T34GM008422*,* and the Society of Toxicology Intern Program.

Key Words: Placenta, Cadmium, Metallothionein

Population Characteristics of the Velvety Free-Tailed Bat

Deslyn Bartlett, Creightanya Brewley, and Dijani Laplace
Mentor(s): Dr. Renata Platenberg

University of the Virgin Islands

There are 5 species of bats native to the Virgin Islands. *Molossus molossus* is a small insect eating bat and the main focus for this study. The Virgin Islands Bat Team has been monitoring populations of these local bats since 2008, and our aim was to analyse this data to evaluate population characteristics and to add to previous knowledge on a generally understudied fauna in the scientific community that are susceptible to modern ecological pressures. Using Microsoft Excel, we conducted a meta-analysis on *Molossus* capture data for the past 10 years to better identify any obvious trends/ relationships. We hypothesised that the mean *M. molossus* captures per survey would decrease across years (particularly before and after the hurricanes), the mean Body Condition Index (BCI) would show variation between years and would be lower in bats with higher ectoparasite load. Moreover, we expected that there would be significant differences in the population size and sex ratios between different survey sites. Population estimates were made using the Jolly-Seber CMR method, and tests of statistical significance were done using One Way-ANOVA, Chi-square and t-tests where appropriate. The results showed that there was no significant difference between mean *M. molossus* captures per survey two years before and after the hurricanes, while the BCI of *M. molossus* captures shows a slightly declining trend, and is significantly lower in 2019 than in 2009. Also, BCI in *M. molossus* was not negatively affected by ectoparasite presence. Furthermore, there is a significant difference in mean BCI, sex ratio, and age group ratio of *M. molossus* captures between Magen’s Bay and Stumpy Bay. *M. molossus’* insectivorous diet may have allowed it to suffer only minimal impacts due to the hurricanes, while differences in the resource availability and habitat use by gender may account for the difference seen between the sites. Ectoparasites and *M. molossus* also may have coevolved, explaining the lack of negative effect on general bat health.

Acknowledgements: ECS Honors Fund, NSF HBCU- UP ACE grant award #1623126 and the Virgin Islands Bat Team

Computational Predictions of Protein Structure in Response to Single Amino Acid Mutations

Hairol Breton
Mentor(s): Corey O'Hern

Yale University

Point mutations can induce conformational fluctuations of backbones and side-chains in protein structures. Understanding and predicting the new conformation presents a challenge in computational molecular biology. Therefore, “Backrub” was employed to model the change in a protein’s backbone conformation due to a point mutation. It functions by rotating segments of the protein backbone as a rigid body about an axis defined by the starting and ending alpha carbon atoms of the segment. Root-mean-square-deviation (RMSD) depicts how different the conformations between two proteins are in angstroms(Å). Therefore, the goal is to optimize Backrub’s span (range of amino acid residues that undergo Backrub motion) and temperature to obtain a backbone RMSD (between Protein Data Bank mutant and its computational version) of 0Å. That would indicate the backbone conformations of the PDB mutant and its computer-generated version are the same. Our protocol consisted of a wildtype protein structure (1hel) that underwent varying point mutation depending on the PDB mutant whose backbone conformation was to be replicated. Furthermore, Backrub was ran with varying temperature and span. Three computer-generated mutants were obtained due to three simulations. Finally, three backbone RMSDs were calculated and the average was taken. For our first PDB mutant (1heo), the control (backbone RMSD between PDB mutant and wildtype) was 0.091Å. Therefore, the span and temperature were optimized to get an average backbone RMSD that was below 0.091Å. If successful, this would indicate the protocol assisted me to get closer to an average backbone RMSD of 0Å. Thus, Backrub was applied to 61 residues at a temperature of 0.6kT. As a result, the average backbone RMSD between the 1heo computer-generated mutant and PDB mutant was 0.326Å. However, if the span was kept constant at 61 residues and the temperature dropped to 0.3kT, the average backbone RMSD dropped to 0.300Å. Finally, if the temperature was kept constant at 0.6kT and the span was dropped to 11 residues, the average backbone RMSD was reduced to 0.121Å. Therefore, the span and temperature are directly proportional to the average backbone RMSD. We can conclude that the best setting (due to the lack of time) at which one can convert the backbone conformation of the wildtype (1hel) into their respective mutants (1heo, 1her, and 1hem) is the following: temperature=0.6kT and span=11 residues. Overall, Backrub’s temperature and span play a huge role in predicting the conformation of a wildtype that has underwent point mutation. In the future, this protocol will be continued by further reducing the span and temperature until an average backbone RMSD of 0Å is reached. If this protocol is perfected, it will help scientists predict which molecules can bind to a novel mutant and how they will bind. It will also reduce the amount of time spent on the experimental determination of mutant proteins.

Funding acknowledgement: This research was supported by the University of the Virgin Islands (UVI) MARC Grant GM008422 of the National Institutes of Health (NIH).

Cliff Swallow Landings: Comparing Flight Trajectories of Cliff Swallows to the Relative Retinal Expansion Velocity Model

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Landing is a critical task for any flying animal, in that the animal must slow to a speed that results in minimal load on the limbs while also maintaining sufficient speed to reach their target. However, while landing trajectories have been investigated in laboratory experiments, quantitative field recordings of landing behavior have not been widely studied nor incorporated into mathematical models for how visual perception can guide landing tasks. The model of interest in this study was the Relative Retinal Expansion Velocity (RREV) model. RREV is a mathematical model used to quantify the rate of which an object increases in size as it is being approached, independent of how fast the organism is moving. We recorded the landing trajectories of Cliff Swallows approaching their nests in the field using high-speed 3D videography. By doing this we were able to quantify the speed, deceleration, and calcite their RREV. We hypothesized that the RREV model would provide a more consistent measure of approach trajectory than speed, kinetic energy, or deceleration. The results of this experiment can help us understand how animals control motion through visual inputs in complex natural environments.

Funding: SOLAR, NSF, ONR, UNC

Exploring the Marine World: An Introduction into STEM-based Careers for Virgin Islands Youth

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Mentor(s): Dr. Kristin Grimes & Howard Forbes Jr.

University of the Virgin Islands - Center for Marine and Environmental Studies

Many students in the Virgin Islands have not had access to marine science education. Although it is only offered in public highschool, students in private schools or homeschooling programs,do not have access to this. The Youth Ocean Explorers, allows students from grades 7th through 12th to be exposed to authentic marine science-based research and career opportunities within this field. This four-week program uses a combination of classroom presentations and interactive outdoor activities to highlight to students the connection between each component of STEM (Science Technology Engineering and Mathematics) with marine science. Students' knowledge, attitudes and commitment to Marine and environmental concepts and actions are assessed using a pre and post survey modified from the CHEAKS (Children's Environmental Attitudes and Knowledge Survey). We compared 2017 data to 2018 pre and post test data and found that the number of students that would see themselves in a science or research career, as well as showed interest in a science career, increased between 2017 and 2018. The Youth Ocean Explorers increased participation in Marine science enrichment during the summer months, where students would experience "brain drain".

Funding: National Science Foundation (Award #1649300) and the Community Foundation of the Virgin Islands

A Literature Review: In silico Molecular Docking Analysis of Natural Marine Products as Anti-cancer and Anti-inflammatory Agents

Alanica Canonier and Juchara Margetson
Mentor(s): Dr. Neelam Buxani

University of the Virgin Islands

Protein-ligand docking infers the position of the main binding sites of a ligand when it binds to a protein receptor. Docking studies have been proven to be a crucial tool that aids in the structural diversity of natural products to be utilized in an organized manner for drug discovery. Several software programs have been developed to perform molecular docking such as Schrodinger Glide, AutoDock Vina, Chimera, SwissDock, GalaxyPepDock, and MOLS 2.0. In our research, we are focusing on assessing anti-cancer and anti-inflammatory potential of marine natural products obtained from online chemical databases or research articles, by using Schrodinger's Drug Discovery Software package and results will also be counter confirmed with Chimera. In our study, based on Schrodinger Glide's energy score, the compounds showing strong interactions with target protein in terms of hydrogen bond and hydrophobic interactions would be selected for further laboratory studies.

Acknowledgements: Summer Undergraduate Research Experience Summer Sophomore Research Institute NSF HBCU- UP ACE grant award #1623126

Comparison of Four Leafy Green Vegetables with Two Nutrients Strength Solution in NFT Systems

Makayla Carino
Mentor(s): Donald Bailey

University of the Virgin Islands

Nutrient Film Technique (NFT) hydroponics is a vegetable production system that uses inorganic nutrients dissolved in water instead of soil. Initial nitrogen levels in these systems are 200 mg/L. Aquaponic systems is an integrated fish and vegetable production system uses low nitrogen of 50 mg/L. This research compares high and low nitrogen levels in the production of leafy green vegetable (Muir and Tropicana lettuce, Genovese basil, Mei Qing Choi pak choi) in NFT systems. We had six identical NFT systems that consist of ten 6.1 meters long channels, a reservoir tank filled up to 400 L of water. Three systems containing 200 mg/L of nitrogen in the control systems and three systems containing 50 mg/L in treatments systems. Our goal is to determine if low nutrients reduced growth and production. Here we report that we saw no significant difference in plants heights for all varieties. Chlorophyll was significantly low for Muir and Tropicana lettuce in the 3rd week (Muir control: 14.54 treatment: 9.11, Tropicana control: 22.16 treatment: 13.12, $P = < 0.05$). The average plant weight of Tropicana and Muir treatment performed better than the control (Tropicana control: 52 treatment: 83, Muir control: 69 treatment: 87), the Genovese basil and Mei Qing Choi pak choi were not significantly different between control and treatment. We show that for the lettuce crops yield better in the treatment with low nitrogen 50 mg/L.

Funding: NSF HBCU-UP ACE grant award #1623126

Bullying, Sexual Orientation, and Suicidal Ideation in High School Students in the U.S. Virgin Islands

Alexanne Carr
Mentor(s): Dr. Noreen Michael
Dr. Aletha Baumann and Dr. Deborah Brown
University of the Virgin Islands

Suicidal ideation among teenagers is a special concern because of the social and personal dynamics of that age group. In particular, experiences related to being bullied and sexual orientation may contribute to suicidality. A literature review found that being bullied on school property is associated with deteriorated mental health, suicidal behaviors, and suicidal ideation. A recent review of 16 studies of cybervictimization and suicidal ideation found that persons under the age of 25 who have been cyberbullied are twice as likely to experience suicidal ideation than those who have not been cyberbullied. For youth who do not report being heterosexuals, a relationship between sexual orientation and suicidal ideation show that they are more likely to report suicidal ideation than those of other sexual orientation. The current study examined the relationships between being bullied in school, being cyberbullied, sexual orientation and suicidal ideation among public high school students in the U.S. Virgin Islands (USVI). The Youth Risk Behavior Survey conducted in the USVI, in 2017, provided the secondary data used to answer the research question: “Are there relationships between being bullied on school property, being bullied electronically, and sexual identity and suicidal ideation among public high school students in the USVI?” Of the 1,782 USVI high school participants, 1,678 (94.2%) of respondents completed the four survey questions related to this study. Three chi-square tests for independence showed that each independent variable has a significant relationship to suicidal ideation ($p < .001$). Suicidal ideation was significantly and strongly correlated with being bullied electronically and on school property. Students who identified as bisexual were three times more likely to report suicidal ideation than their heterosexual counterparts. Gay, lesbian, and youth who reported not sure about their sexuality were two times more likely to report suicidal ideation than their heterosexual counterparts. It is important to note that the sample represented the public high school population only. This research supported the alternative hypothesis that being bullied on school property, being cyberbullied, and not identifying as a heterosexual are linked to suicidal ideation. Because the USVI has strong religious roots and homophobic attitudes, we need to understand how to help bisexual, gay, lesbian youth deal with discrimination and avoid suicidal ideation. Future research should explore the benefits of creating a protective climate that would provide an inclusive school environment for all students.

This research is funded by UVI RISE grant # GM061325.

A Prospective Format to Incorporate Astronomy on Different Academic Settings in the US Virgin Islands

Yudis Castillo Rodriguez
Mentor(s): Dr. Antonio Cucchiara
Dr. David Morris
University of the Virgin Islands

It is now demonstrated that the 21st century population of STEM students requires an innovative approach to engage them in the classroom and for them to retain complex scientific concepts. Particularly important is the development of this new framework in areas where science teachers are less exposed to effective educational developments, training and curriculum updates.

In the past two years, the University of the Virgin Islands Physics program has developed new curricula to teach astronomy courses at the undergraduate level (to both physics majors and non-majors) and at the Kindergarten-12th grade level. The content is integrated specifically with the usage of a *Starlab* inflatable planetarium and small (8-inch) commercial optical telescopes. The planetarium and the telescopes are made accessible to all educators in the Territory.

In this poster we will highlight the results of the first iterations of the new curriculum for undergraduate students at UVI, and the curriculum material resources (lesson plans, planetarium material, assessment instruments) available to educators within and outside the Territory.

The author gratefully acknowledges support for this work through NASA grant NNX16AL44A and NSF HBCU-UP Target Infusion Project Grant #1719265.

Evaluating differences in microbial communities between white plague diseased and healthy Caribbean coral species

Kathryn Cobleigh
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Nicholas McKnight, Laura Mydlarz and Monica Medina
University of the Virgin Islands; University of Texas at Arlington; Pennsylvania State University

The Caribbean is highly prone to disease outbreaks and is therefore considered a "hotspot" for disease. White plague disease (WPD) is one of the most destructive diseases in the Caribbean, targeting major reef building species. Once infected, corals display white lesions on their tissue which is accompanied by distinct shifts in their microbiome. 16s rRNA sequencing data was analyzed following a disease transmission experiment in order to disentangle the microbial shift of prominent Caribbean coral species. Samples were collected from heathy tissue, disease exposed tissue, and from the white plague band of *Orbicella annularis*, *Orbicella faveolata*, and *Colpophyllia natans* to identify bacteria that play a significant role as the coral hosts' health declines. There was an increase of *Rhodobacteracaea* bacterial species as the corals were exposed to WPD. Conversely, was a sharp decline in *Microcococcacea* in the white plague banding indicating the gradient within the microbiome as the coral becomes infected.

Funding: National Science Foundation EAGER Grant

Magnetohydrodynamics Post-Processing Pipeline

Gerlinder Difo-Cheri
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University of Virginia, University of Virgin Islands

Protostellar outflows are a crucial component for early star formation due to their role in the efficient removal of angular momentum as well as helping determine a star's accretion rate and final mass. Protostellar outflows are currently understood to be magnetic in nature but data produced through direct observations of these jets are limited in detail. Therefore, numerical models such as the magnetohydrodynamical (MHD) time dependent code, ZEUS-MP(Hayes, J.C. et al 2006), simulates the distribution of density and temperature throughout the evolution of a magnetically driven outflow. This specific project involves the construction of a pipeline for the automatic processing of MHD simulation results in order to include chemistry as well as dust and gas radiative transfer. The pipeline would further simulate line emission for comparison with real observations. Progress on this pipeline has arrived at the stage where MHD simulation results are used as input for the chemical abundance code, KROME(Grassi, T. et al 2014).

Funding: NASA Grant

Marine Water Chemistry & Suspended Sediment Concentration in the Salt River Bay National Historical Park and Ecological Preserve, St. Croix, USVI

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USVI Department of Planning and Natural Resources[3]

Salt River Bay National Historical Park and Ecological Preserve was created in 1992 with the intent to preserve, protect, and nationally interpret the natural, historical, and cultural resources in the area. The area includes a mangrove forest, a submarine canyon, coral reefs, seagrass beds, coastal forests, and is rich in indigenous and modern cultural history. Salt River Bay falls into Class B waters and was listed on the U.S. Environmental Protection Agency (EPA) approved U.S. Virgin Islands' 2016 list of impaired waters. Listed impairments included Dissolved Oxygen (DO), Turbidity, Fecal Coliform and Enterococci. The main objectives of this study were to assess the quality of the water and determine if parameters tested met current regulations. Over a three-month period, water samples were collected at six sites within Salt River Bay. Samples were tested for suspended sediment concentration (SSC), nutrients, water temperature, salinity, and DO. Results showed that SSC ranged from 4.10 mg/L– 9.07 mg/L, with a mean of 6.39 mg/L. Combined mean water temperature, salinity and DO were 30.1°C, 38.5 ppt, and 5.0 mg/L, respectively. Nutrient results were still in process. Results from this study suggested that temperature, salinity, and SSC were within normal limits; however, DO fell below the current minimum regulations of 5.5 mg/L.

Funding provided by UVI NSF HBCU-UP ACE grant award #1623126 and NOAA's Coral Reef Conservation Program (CRCP), project # 31213.

HPV and Innate Immunity: Defining the Role of the ATR DNA Damage Response Pathway on the Immunogenicity of HPV Infected Cells

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The Human Papilloma Virus (HPV) is the most common sexually transmitted virus with a lifetime risk of infection of greater than 80%. Persistent infection with high-risk types of HPV (e.g. HPV16, HPV18, HPV31) is associated with the development of cancers, most notably cervical cancer and an increasing number of head and neck cancers. Infection occurs at the basal layer of the epithelium, where the virus replicates in undifferentiated epithelial cells at very low copy numbers. Differentiation of the epithelial cells triggers the productive phase of the viral life cycle, which is marked by viral genome amplification to 1000s of copies per cell and the production of mature virions. Previous studies from our lab demonstrated that activation of the ATR-dependent DNA damage response pathway is required for viral episomal maintenance in undifferentiated cells as well as productive viral replication upon differentiation. Even with viral replication, HPV infected cells exhibit a reduced anti-viral type I interferon (IFN- α/ β/K) response and can persist within the host. However, little is known about ATR and the activation of the type 1 interferon response during HPV infection. In this work, we investigated the role of ATR in the antiviral interferon response in HPV infected cells. We hypothesized that ATR activity prevents activation of type 1 interferon expression by promoting DNA repair, thus allowing immune evasion. To test this hypothesis, we inhibited ATR in HPV-infected cells then utilized Western blot analysis to analyze the expression of interferon-stimulated genes (ISGs), qPCR to measure type I IFN expression and Southern blots to examine HPV viral DNA. Our preliminary data indicated that ATR activation suppresses IFN-β expression, but not the expression of IFN- α, and IFN-K. Our long-term goal is to further understand how HPVs persist within the body, ultimately allowing us to identify therapeutic targets to treat HPV-associated diseases.

This research was funded by the University of North Carolina at Chapel Hill Summer of Learning and Research program and the University of the Virgin Islands MARC program NIH grant # #5R25GM061325-13

Command -Line Tool to Manipulate Model-Specific Registers

Angie Estien
Mentor(s): Barry Rountree
Cassie Tucker and Tre' Jeter
Lawrence Livermore National Laboratory

Efficiency as it relates to supercomputing has become an important factor. Researchers are investigating possible solutions in areas such as energy consumption, retired instructions and cache misses. Model-Specific Registers (MSR’s), also referred to as registers, provide access to telemetry and control to computer processors. However, the process to read a register or write to a register requires kernel-level access, in addition to the rdmsr and wrmsr instructions provided by Intel, and even then the registers can only be accessed one at a time. This becomes a very tedious task considering the number of registers within a central processing unit (CPU), especially when conducting performance profiling . The objective of this project was to create a tool that could access the required registers and decrease the setup time for performance profiling. We also used FIRESTARTER which is an open source program processor stress test utility that measures power consumption by stressing the cpu, gpu and/or main memory. FIRESTARTER allowed us to change our power limit consumption and measure instructions retired per cycle. For this project we intended to combine the rdmsr and wrmsr functionality in one program, then create functions that would provide access to batch operations, and finally allow us to toggle specific bits within the registers. We were able to create a prototype program that would allow users to use the command-line to access specific MSRs. The functionality included reading the MSRs, writing to the MSRs and resetting the MSRs. In the future we would like to increase the number of MSRs that the program can be accessed, both listed and unlisted by Intel.

Funding: CECOR

Phylogenetic Distribution of Exogenous Fatty Acid Acquisition and Membrane Incorporation Proteins in Gram Negative Bacteria

Kwame Forbes
Mentor(s): Dr. David Giles

University of Tennessee at Chattanooga

Bacteria are constantly assessing their environment for cues that determine their behavior and livelihood. Fatty acids represent niche-specific molecules that can serve as nutrient sources, membrane-modifiers, and signaling molecules. The protein machinery that recognizes, uptakes, and assimilates fatty acids into membrane phospholipids is differentially possessed by bacteria. The purpose of this study was to identify homologs of *Vibrio cholerae* fadL, fadD and membrane acyltransferases among bacteria for phylogenetic analyses. Using the Integrated Microbial Genomes database (IMG/JGI), homologs to the fatty acid uptake and assimilation machinery were identified in completely sequenced genomes. Representatives from genera (>90%) possessing fadL (long chain fatty acid transporter) were selected as the organisms targeted for subsequent homolog searches, thus limiting the survey to bacteria possessing the full pathway. The software Geneious was utilized for nucleotide sequence alignment and subsequent phylogenetic analysis using MrBayes for construction of Bayesian inference and model choice. The distribution of fatty acid uptake and assimilation pathway revealed distinct clades, primarily consisting of *Vibrionales*, *Alteromonadales*, *Aeromonadales*, *Pastuerellales* and *Enterobacterales*. The clades *Vibrionales*, *Alteromonadales* and *Aeromonadales* clearly exhibited a larger repertoire of genes dedicated to fatty acid acquisition and membrane incorporation.

Funding: National Science Foundation

Family Reunification: Clustering Malware Variants

Rhonda Forbes
Mentor(s): Marc Boumedine

College of Science and Mathematics, University of the Virgin Islands

Every couple of seconds, a new malware program is created. Traditional anti-malware software relies on malware signatures to recognize malware. To avoid it being detected, authors use different techniques to change the malware signature, though retaining the same functionality. Researchers are looking into various ways to combat this by combining several features of malware to identify malware variants faster. In this research, we will be focusing on the features represented as strings extracted from the portable executable (PE). Strings were chosen because they can give a hint to the programs' behavior. We want to see if it's possible to use string features to discern if programs that have similar behavior can be grouped together in the same family. This research seeks to determine: if strings can be clustered into their respective groups based on the Jaccard distance. If they can be clustered, then the malware comes from the same family. We applied the following methodology: feature extraction, strings were collected from 16 malware and 16 benign in the same families. We then preprocessed the PE to clean the data. Next, the Jaccard distance was used to create a dissimilarity matrix between all the programs. Hierarchical clustering was used to cluster based on the average distances between them. We experimented with a different number of clusters. The results with the two clusters show the program accurately clustered the malware and benign groups. As we increased the number of clusters, the benign programs remained in the same group, while the malware were reassigned to different clusters. These results suggest that malware reassigned to the same group are derived from the same family.

This research was supported by the Emerging Caribbean Scientists Program, the NSF HBCU-UP ACE award #1623126 and a grant from the Department of Energy National Nuclear Security Administration (#DE NA0002686) Minority Serving Partnership Initiative.

Total Phenolic Content and Synergistic Properties of Plant Mixtures

Alaysia George and Nafeesa King
Mentor(s): Dr. Bernard Castillo II

University of the Virgin Islands

Phenolic compounds are phytochemicals that are found in various plants species, as well as in fruits and vegetables. Phenols are aromatic organic compounds with the molecular formula C□H□OH. These compounds can be found in many different classes, including antioxidants, lignin, carotenoids, and flavonoids. Consuming plants that contain large amounts of phenols can be very beneficial to human health by reducing the chances of developing diseases like cancer, diabetes, and multiple cardiovascular diseases. People either consume individual plant products or in mixtures, like in tea, soups, etc. This is especially true in the Caribbean, where fruits and herbs are often combined to make drinks and teas. For this study, we collected three different plants in the Virgin Islands, namely: Lemongrass (*Cymbopogon citratus*), Cuban Oregano (*Plectranthus amboinicus*), and Spinach (*Spinacia oleracea*). The main objective of this study was to determine the synergistic effect by combining multiple plant extract and determine its total phenolic content (TPC). We also wanted to determine any differences between the calculated and experimental TPC values between mixed plant extract. The Folin-Ciocalteu method was used to determine the TPC (mg GAE/g DW) of plant extracts, while the absorbance was measured in a UV-Vis spectrophotometer at 765 nm. Our results showed that Spinach had the highest mean TPC (4.475 ± 0.410 mg/g GAE/g DW) while Lemongrass had the lowest value (4.073 ± 0.044 mg/g GAE/g DW). A one-way ANOVA test showed that there was no significant difference between the TPC values of each plant tested ($p= 0.4288$). The mixture with the highest experimental TPC was Lemongrass and Spinach (5.698 ± 0.224 mg/g GAE/g DW), while the mixture of Oregano and Lemongrass had the lowest value (2.873 ± 0.000 mg/g GAE/g DW). One-way ANOVA analysis showed a significant difference between all the experimental values for the plant mixtures ($p = 7.0 \times 10^{-5}$). Comparison between calculated and experimental TPC values of Lemongrass and Spinach ($p= 0.00239$), Oregano and Lemongrass ($p=0.00482$), and Oregano and Spinach ($p= 0.00414$) all showed significant differences. When comparing calculated and experimental TPC values for the mixture of all the plants, one-way ANOVA analysis did not show any significant difference ($p= 0.75022$). Throughout our study there was no clear pattern showing that the paired mixtures of different plants were significantly different for each combination. However, it was not definitive that the calculated values were higher when compared to the experimental values. We can conclude that there is a positive synergistic effect if all the plant extracts were combined rather than a mixture of two samples. These results showed that it would be more beneficial to consume these plants separately rather than consuming them as mixtures.

This research was funded by NSF HBCU-UP ACE Grant Award No. 1623126.

A Purification Method for Nickel from Seawater for Isotope Analysis

Tione Grant
Mentor(s): Tim M.Conway, Matthias Sieber, Brent A. Summers

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Nickel (Ni) is an important micronutrient in oceanic environments, typically with low surface concentrations that increase with depth. Ni isotope analyses offer the potential to provide insight into the cycling of Ni throughout the oceans. However, accurate and precise isotopic analysis requires the separation of Ni from the complex sea salt matrix. At USF, we have previously used a two-stage method involving batch extraction by Nobias PA-1 chelating resin and AGMP-1 anion resin to separate Fe, Zn, and Cd from major salts in seawater, but we found that this method is not effective for separating Ni from Na. Therefore, in order to comprehensively investigate Ni isotope distributions, a different method for separating the trace metal from the large concentrations of major cations present in seawater was needed. Here, we present a new chemical purification method that separates the typical trace amounts of Ni from the high concentrations of major salts (Na and Mg) in seawater, allowing isotopic analysis. Our method builds upon our existing published methods using Nobias PA-1 and AGMP-1 resins by incorporating a second Nobias PA-1 resin microcolumn. This extra column allows us to fully separate Ni from Na, Mg and other interfering elements, before analysis of Ni by double spike mass spectrometry via Thermo Neptune MC-ICPMS. We also present new Ni isotope data from isotope standards, reference materials and Atlantic seawater samples.

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Mailman Scanner Web Interface Update

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Mailman is an out-of-band email collection web application to analyze suspicious emails. It is used to collect emails, extract attachments, and record the information in a searchable database. John Donaldson, at the Lawrence Livermore National Laboratory, was once an intern developed Mailman approximately 10 years ago. However, mailman is outdated and is harder to maintain with no API (Application Programming Interface) that supports integration from tools used by the lab. For this project, we created a python virtual environment and developed a web application using Python-Django and a REST API project. The updated web application includes new functionalities such as JSON-centric, a searchable function that looks through the list of emails on the web application or REST API, and accessibility of REST API application from the web application. A foundation of mailman is set in place along with JSON-centric REST API application running that developers can continue to develop Mailman and include new functionalities.

This work was performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under Contract DE-AC52-07NA27344.

Astroglial CD38 is involved in Opioid-Mediated Anti-nociception in a Neuropathic Pain Model

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Understanding chronic pain mechanisms would allow for better pain treatment. Calcium is a very important signaling molecule and CD38, a transmembrane protein, is involved in the regulation of calcium homeostasis. Using the spared nerve injury model of chronic neuropathic pain in 6-12-month-old wild type (WT) and CD38-deficient (CD38KO) mice, we found that both mice developed similar magnitudes and significant mechanical hypersensitivity. Next, we found that a centrally (15 mg/kg) but not a peripherally (1.5 mg/kg) acting dose of the mu-opioid receptor agonist, loperamide, completely normalized mechanical hypersensitivity in the WT mice but had no effect in the CD38KO mice. Together, these results suggest that CD38 is not involved in the development and maintenance of neuropathic pain, but its presence in the central nervous system is required for the pain-relieving action of mu-opioid receptor agonists. To further understand how CD38 might mediate opioid-induced anti-nociception, we performed in-situ hybridization and immunohistochemistry in spinal cord and dorsal root ganglion (DRG) tissue from WT mice and found that CD38 is localized in astrocytes in spinal cord and satellite glial cells in DRG. Altogether, our results suggest that CD38-expressing astrocytes are required for effective opioid therapy of neuropathic pain.

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PI’s: Dr. Thomas Molitor & Dr. Sabita Roy

Apicomplexan Parasites in Damselfishes

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Apicomplexa are a diverse Phylum composed of intracellular protozoans including parasites like *Plasmodium spp.*, the causal agent of Malaria. Malaria is a life-threatening disease vectored by the *Anopheles* mosquitoes. Apicomplexa infect the red blood cells of coral reef fishes including *Stegastes adustus,* the dusky damselfish in the Caribbean. The life cycle, mode(s) of transmission and host effects are unknown. For example, while intracellular protozoa are found in the blood of damselfishes, it is not known whether they infect the other tissues of these hosts. Many Apicomplexa, such as *Toxoplasma gondi*, cause distributed infections throughout their host's tissues. We hypothesize that fish with parasites in their blood are also infected in their organs, and that the quantity of intracellular blood parasites negatively affects the fish's condition. In this study, twenty *S. adustus*, which are known to harbor blood infections, and three sympatric fish, which are not known to harbor blood infections (one parrotfish *Halichoeres bivittatus,* and two French grunts, *Haemulon flavolineatum*), were collected from near-shore reefs in Brewer's Bay St. Thomas, USVI and anesthetized in a clove oil solution. Blood was collected from the sinus venosus, thin smears were prepared for microscopy and remaining blood was placed in a citrate-anticoagulant buffer. The fish were housed in storage tanks and were later either dissected to collect the organs (liver, heart, brain and gut) or released back to the reef. Several methods of analysis were employed to identify, isolate, and quantify the protozoa. Microscopic analysis of Giemsa-stained thin blood smears enabled detection of intraerythrocytic infections. PCR analysis employed three apicomplexan specific primer sets for the 18S rRNA and one fish-specific primer to screen DNA extracts. Percoll density gradients were useful in separating blood cells, and we also successfully cultured infected blood samples. Giemsa-stain analysis indicated (12 out of 20) 60% infection in damselfish blood whilst the sympatric French grunts were uninfected. However, PCR identified infection in all twenty damselfish and the French grunts. PCR analysis of the damselfish organs indicated Apicomplexa infection in the liver, heart, brain, and gut of all fish tested, even those without visible blood infection. Apicomplexa DNA was also detected in the organs of sympatric fish (the French grunts' liver, heart, and brain and the parrotfish's liver and gut). Apicomplexan parasites can cause either catastrophic damage or relatively little impact to their hosts. However not enough is understood about the parasite- host interaction. Future studies to identify parasite proteins and histology of parasite infected cells will help us gain a better understanding of the parasite-fish interaction and characterization of this novel apicomplexan.

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The Role C/O Ratio Plays in the Abundances of Specific Molecules in a Disk Midplane

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Protoplanetary disks are circumstellar disks of matter, including gas and dust, from which planets eventually form. The disk midplane is the coldest region of the disk, which is caused from the stellar radiation not being able to get through it. Within the disk midplane, there is a “great deal” of chemistry involved, playing a role in the material over time. Also, due to the planets being formed in the midplanes of the disks, the composition and evolution of the material here is important. With this project, we aim to explore and understand how and why the chemical changes occur in planet-forming material before these planets start forming. We also looked at three different sets of C/O Ratios, so we can understand the influence of these ratios on the abundances of specific molecules. This would lead to an understanding on how chemistry alters the C/O ratios of the gas and ice in the time of the planet formation, as well as an understanding of the presence of specific molecules in the atmospheres of planets and exoplanets, across host stars of different metallicity.

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Tough and Biologically Stable Hydrogel Adhesives

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Tough adhesion between hydrogels and wet materials is important to many applications such as tissue adhesives, bio electrics, drug delivery and wound closure. However, current methods to achieve tough adhesion require the wet materials to have functional groups, involving toxic chemicals or unstable adhesion. Topological adhesion presents a way to bond any hydrogel to any wet material, without requiring any functional groups from the wet materials themselves. In our approach, we use biocompatible polymer chains to achieve strong adhesion and retain softness. When triggered, the polymer chains form a network, in topological entanglement with the two polymer networks of the hydrogel and the other wet material, stitching them together like a suture at the molecular scale.

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The Role of Cancer Associated Fibroblasts in Maintaining Cancer Stem Cells

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Breast cancer is one of the leading causes of cancer related deaths in females. Current treatment options for breast cancer ultimately fail, resulting in cancer relapse. One explanation for recurrence after treatment is the presence of cancer stem cells (CSCs). CSCs have high proliferative potential and are able to initiate tumor growth. In order to target CSCs, it is important to understand how CSCs are maintained. Recent studies have shown that cancer-associated fibroblasts (CAFs) aid in the maintenance of CSCs. CAFs are an abundant cell type in the tumor microenvironment and have been found to promote tumor growth and confer resistance to anti-cancer drugs by supporting cancer stem cells. We hypothesized that CAFs promote and maintain the growth of cancer stem cells in a novel tumor model (MCaP). Mammary carcinoma cells (MCaP) were propagated in culture from a tumor that developed spontaneously in an aged mouse. Cancer cells, along with CAFs were expanded from the isolated tumor. Cancer cells were grown as a mixed culture with CAFs or alone after enrichment. A colony growth assay was used to assess the formation of CSCs, which grow as colonies. Cultures were fixed and stained with cytokeratin and colonies were counted manually. Colony size was quantified using ImageJ. Flow cytometry was performed to detect and quantify surface expression of CSC markers CD44 and CD24 in mixed cultures and isolated cancer cells. To investigate whether CAFs enable cancer cell resistance to chemotherapy, we measured the dose response to cyclophosphamide or paclitaxel. Immunofluorescence was performed on tissue sections of metastatic lymph node and primary tumor. Tissues were stained with cytokeratin, aldehyde dehydrogenase (ALDH), and alpha-sma (SMA). From the colony growth assay we noticed that colony formation and the size of colonies were both increased when MCaP cells were cultured with CAFs. Flow cytometry showed that MCaP cancer cells grown with CAFs resulted in the appearance of a CD44 high/CD24low population. This CSC population was not seen in cancer cells grown alone. After treating cells with paclitaxel or cyclophosphamide, we saw no notable difference in the viability of cancer cells in the presence or absence of CAFs. Immunofluorescence staining showed ALDH was expressed in SMA-positive CAFs, but not in cytokeratin-positive cancer cells. Although we did not find that CAFs protected cancer cells from chemotherapy, CAFs appear to have a positive effect on the size and quantity of CSC colonies. In addition, we detected a CD44 high, CD24 low CSC population in mixed cultures. CAFs were found to express the CSC marker ALDH, with expression increasing as the size of the tumor increased. This finding suggests that CAFs may provide a niche for CSCs. In conclusion, these results suggest that CAFs play an important role in maintaining CSCs in the MCaP mouse model.

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Assessing Decontamination and Sterility Protocols for 2019 Rocksat Astrogenomics Program

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Mentor(s): Dr. Ashley Matchett
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University of the Virgin Islands

Life, on earth, is said to be ubiquitous. That applies, specifically to microscopic life that have evolved to survive and grow in some of the most extreme environments. In truth its very hard to encounter an environment on earth that is not colonized by some tenacious microscopic life or another. In addition, removal of life, specific of the vestiges of any life, is also very difficult. It as been hypothesized that some microorganisms can in fact, can survive for long periods in time in space like environments, in a putatively quiescent state or dormant phase. Various studies have sought to address the possibility of extraterrestrial life, particularly in the form of detailed biochemical examination of earthbound or surface recovered meteorites, which underpins a theory postulated by Berzelius (1834) called Panspermia. The UPR NASA 'RockSat' team aims to collect and analyze micrometeorites sampled from beyond the Karmen Line, the technical definition of outer space. To do so, the team built a payload designed to be launched on a Sounding Rocket (fig 2) in Early August. This payload has various components controlled by electronics and computer system to collect, record and safeguard the samples. This payload (fig 3) is divided on three main subsystems: video, collection and decontamination.

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GRB 190202A: A Study of the Most Energetic Cosmic Explosions from the U.S. Virgin Islands

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University of the Virgin Islands

Gamma Ray Bursts (GRB) are the most powerful events that takes place in the Universe. They result from either the explosion of a star at the end of its lifetime or the collision of two neutron stars. These devastating events last just a few milliseconds to a couple of minutes. My goal was focusing on GRB 190202A and creating a light curve that shows both its optical and X-ray light activity over a time period. Data were acquired by the Las Cumbres Observatory telescope network (LCO), from this data I was able to measure the amount of energy emitted by the GRB through time (Magnitude).

I created a Python code to easily import publicly available optical and X-Ray data (taken from satellites) to build a multiwavelength light curve. I used a linear curve fit with both optical and X-ray data and compared it with the GRB theoretical models. The fit presents a visible break in all the data around 10^5 seconds after the explosion. This behavior is rare among GRB's, and with this we could potentially determine the opening angle of the jet through which the GRB energy was emitted. If this behavior is confirmed, we will conduct a more detailed study to collect more data and compare our results with larger samples of GRBs.

UVI students and faculty have access to LCO and the V.I. Robotic Telescope (in St. Thomas) and are building their own Gamma-ray satellite (UVI-GREAT) in order to discover more GRBs in the incoming years.

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Microbial Diversity Analysis of Marine Samples in St. Thomas, USVI Using Metagenomic DNA Sequencing

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A wide diversity of microorganisms, including bacteria, archaea, and fungi are found in marine habitats. Marine habitats contribute to 71% of the Earth surface, for this reason, the microbiome in the ocean was explored. The study aims to determine the biological marine water quality and to investigate the impact of anthropogenic disturbances on the composition and diversity of microbial communities. Variations in these microbial communities serve as ideal indicators for determining whether anthropogenic activities have significant effects. The methodology included high throughput sampling, DNA extraction, differentiation, RT-PCR and metagenomic sequencing techniques. DNA sequence-based metagenomics was used to analyze DNA acquired from the various seawater samples in St. Thomas. Sequence analysis of a large amount of data generated from the microbial communities was made feasible using a bioinformatics tool known as Metagenomic Rapid Annotation using Subsystem Technology server (MG-RAST). Further studies are currently underway, in which the marine microbial diversity will be explored on the island of St. Kitts. The findings of this study will be used to provide an in-depth comparison.

Keywords: microbial diversity, marine water, metagenomics, St. Thomas, St. Kitts

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The Effects of Different Antibiotics on Pseudo-nitzschia Diatoms and their Microbial Communities

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Pseudo-nitzschia diatoms are photosynthetic unicellular algae found in marine habits. This genus produces a toxin known as Domoic Acid (DA) which can cause amnesic shellfish poisoning. While only produced by the diatoms, DA toxins have been found in zooplankton, shellfish, crustaceans, echinoderms, worms, and marine animals. Numerous and diverse bacteria surround Pseudo-nitzschia diatoms, potentially representing a symbiotic relationship. For this project, we tested whether antibiotics could remove bacteria from cultures of three species of Pseudi-nitzschia without impairing diatom growth. We observed Pseudo-nitzschia growth with antibiotics by measuring chlorophyll A fluorescence (a proxy for cell number). We also plated cultures on marine agar plates to determine whether bacteria continued to grow after antibiotic treatment. We found that most antibiotic treatments resulted in breakthrough bacterial growth several days of treatment. One antibiotic treatment eliminated bacteria but also inhibited (either directly or indirectly) diatom growth.

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Testing for differences in susceptibility, lesion progression rate, and transmissibility among coral species for stony coral tissue loss disease (SCTLD) in the US Virgin Islands

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A disease with characteristics matching those described for stony coral tissue loss disease (SCTLD) was identified affecting reefs to the southwest of St. Thomas, US Virgin Islands (USVI) in January 2019. SCTLD was first described as affecting corals in the Florida Keys Reef Tract near Miami in 2014 and has caused significant declines in reef-building coral populations throughout the Keys. The case description of Florida SCTLD identifies twenty-two different species of reef-building corals as being affected, and data on disease prevalence suggest that certain species are more affected than others. This project used laboratory-based transmission experiments and the monitoring of individual corals in the field through time to test a hierarchy of species susceptibility to USVI SCTLD. Laboratory results indicated that the USVI SCTLD is able to be transported by seawater and that there is no statistical difference between incidence rates of six important reef-building species. This suggests that under equal pathogen exposure, all six of the species will exhibit signs of SCTLD which has significant implications for Caribbean coral community structure.

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Visualizing the Hidden World: Utilizing CARD-FISH to Detect Microbes Exposed to Oil

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The Deepwater Horizon Oil Spill of 2010 released more than four million barrels of oil into the Gulf of Mexico, causing significant damage to marine life in the water column and surrounding shorelines. Several methods, including application of chemical dispersants, were used to remediate the oil spill. Dispersants break oil into smaller droplets, enhancing degradation by abiotic processes as well as by marine microbes. This study takes a microscopic look at how two hydrocarbon-degrading genera of microbes, Alteromonas and Alcanivorax, aggregate in the presence of oil and oil plus dispersant. We used Catalyzed Reporter Deposition-Fluorescent in Situ Hybridization (CARD-FISH) to analyze microbial aggregation in three mesocosm treatments with natural surface seawater from coastal Texas: surface seawater (Control), water accommodated fraction of oil (WAF), and diluted chemically enhanced water accommodated fraction of oil (DCEWAF). We hypothesized that there will be higher amounts of micro-aggregates (<0.20 mm) compared to single cells in oil treatments vs untreated seawater, and that both genera would be more abundant in micro-aggregates than the free-living population. The utilized probe specific to Alcanivorax was designed and optimized for high intensity fluorescence, which we found was greatest at 55% formamide. Preliminary analysis of total community and CARD-FISH counts indicate that there is a higher number of micro-aggregates in WAF and DCEWAF compared to the control treatments, and that Alteromonas and Alcanivorax were proportionally more abundant in aggregates in oiled treatments. This study may lead to implications for further research in understanding the role micro-aggregates play in hydrocarbon degradation and the role known hydrocarbon degraders play in those micro-aggregates.

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Classifying Malware: What Machine Learning Techniques are Most Effective?

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Machine Learning is one of the most important underpinnings in modern research and technology. It is the field of Computers Science that uses mathematical techniques to enable computers to do specific actions without the need for explicit instruction from a programmer. Malware is a computer program designed with the intent to damage computers. Cyber-attacks from malware are one of the most imperative issues facing law enforcement agencies as well as the general populace, and the need for innovative solutions to address these attacks is exigent. The advent of Machine Learning means that it can be used to develop software solutions that effectively classify malware. But what Machine Learning algorithms are most effective at classifying malware samples? This is the main focus of this research. I hypothesize that Decision Tree algorithms are more effective at classifying malware than Random Forest algorithms. In order to test this, a training dataset with vectorized malware samples was obtained. Next, utilizing the data analysis tool Weka, the malware data was mined. By using the number of samples and features as parameters, experiments were performed to determine which of the two algorithms had a higher classification rate. Based on the preliminary results obtained from the experiments, Decision Trees were more effective at classification than Random Forests. However, further investigation is required since there is a distinct possibility that the type or combination of features being investigated may have an effect on the effectiveness of an algorithm. In addition, research has shown that including more features will yield a higher classification rate for both algorithms.

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Analysis of Public Network Exposures with GRC ShieldsUp and UPA

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The technological world as we know it is advancing at a steady rate. While this may hold great promise for the future, there are also various drawbacks as technology is used everywhere. The need for defences against hackers has become critical, making the study of network exposures to identify and prevent cyber-attacks a leading research interest. This effort investigates what exposures can be readily discovered on a network, if common patterns emerge for a given location, and whether certain measures can be adapted and developed for use by broader sections of the population. A popular, web-based network analysis tool, GRC *ShieldsUP!*, was used to examine exposed network ports and record data using various clients and networks at selected intervals. Unfiltered Port Analysis (UPA) was utilized to extend the GRC analysis for additional data used to correlate network exposures with known exploits. Results over time and between devices were analysed and compared. Given the consistency and utility of results, GRC *ShieldsUP* and UPA can be recommended to organizations to prevent hacker attacks and promptly mitigate network breaches.

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UVI GREAT CubeSat Satellite: Gamechanger for Astrophysical Studies

Jordina Pierre
Mentor(s): Dr. David Morris and Dr. Antonino Cucchiara

University of the Virgin Islands

The CubeSat project was originally developed to provide university science communities the opportunity to create a space program and have affordable access to space. In this project, I worked on The University of the Virgin Islands Gamma Ray Experiment for Astrophysical Transits (UVI-GREAT), which is a 3 Unit (3U) CubeSat that will enable us to study Gamma-Ray Bursts (GRBs) in space. The purpose of UVI-GREAT is to detect, localize, and characterize GRBs which help scientists understand more about the beginning of the universe as well as learn more about the creation of chemical components. A key element of UVI GREAT is a scintillator crystal. When the GRBs occur, the light interacts with the crystal which then produces UV light that is converted into a digital signal. During the summer, we tested different configurations with the light tight box, scintillator crystals, and the Charged Coupled Device (CCD) Camera. The light-tight box was used to simulate the dark space environment which allowed us to test the scintillators to guarantee their effectiveness. In order to do this, we used the CCD camera to take pictures of the scintillators and the radiation source to determine whether light was actually being produced. Because we are in the lab, we used radioactive sources such as Cesium-137 and Sodium-22 which produce Gamma-Rays and play the role of the GRBs in space. We also used a CCD Camera in the lab instead of a Silicon Photomultiplier (SiPM) which will be used to convert the GRB signal onboard UVI-GREAT.

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Post-Hurricane Analysis of the Invasive Seagrass Halophila stipulacea

Quiannah Potter
Mentor(s): Dr. Alice Stanford
Jeraun Dolphin
University of the Virgin Islands

Halophila stipulacea is an invasive seagrass species that is currently present in the local waters of the United States Virgin Islands. Its native ranges include the Indian Ocean and the east coast of Africa, and it was first reported in the USVI in 2012. This seagrass is capable of rapid expansion, which displaces our native seagrasses and affects the diversity of our fish communities. The purpose of this study was to continue an ongoing study of *Halophila stipulacea* by conducting a post-hurricane assessment of the seagrass at Brewers Bay in St. Thomas. We hypothesized that there would be multiple genotypes of *H.stipulacea* found in Brewers Bay. We also hypothesized that there would be a difference in the proportion of the genotypes at Brewers Bay when compared to pre-hurricane data. We performed PCR on our DNA samples which was followed by gel electrophoresis. Lastly, the concentration of the DNA libraries created were quantified. Due to the fact that we are awaiting the sequencing results, DNA library concentrations from last year were analyzed and compared to sample sets from previous years using a one-way ANOVA and Tukey HSD test. The ANOVA test showed that one or more of the sample sets were significantly different. The post hoc Tukey HSD test revealed that each sample set was significantly different from each other. The results indicate an increase in the mean concentration of DNA over the years. This may imply an improvement in our lab techniques over time. Another analysis will be conducted when the sequencing results are retrieved in order to test our hypotheses.

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Exact Confidence Intervals for the Youden Index and Corresponding Optimal Cut -Point using Normally Distributed Pooled Data

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When it comes to cutting costs in epidemiological studies, pooling specimens into smaller samples is a common and effective practice. Through the Youden Index, the data obtained from these pooled samples measures the diagnostic effectiveness of biomarkers and helps choose the optimal cut-point. The Youden Index (or Youden Statistic), a function of sensitivity and specificity, is the maximum vertical distance between the Receiver Operating Characteristic (ROC) curve and the 45 degree chance line. The objective of this study is to make use of the generalized approach to estimate and test the Youden Index using normally distributed pooled data. To accomplish this, the classical and generalized procedures for the Youden Index will be compared using the normally distributed pooled biomarker data for the low-risk and high-risk patients. The biomarker data is then analyzed using confidence intervals, power of the test, and size of the test. The simulation study showed the effectiveness of the generalized approach compared with the classical approach, even when large samples are utilized. A descriptive example to demonstrate the advantages of the proposed generalized procedures over its classical counterpart is discussed using the Duchenne Muscular Dystrophy (DMD) data available from Vanderbilt University at http://biostat.mc.vanderbilt.edu/wiki/Main/DataSets.

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Calculating Uncertainties in VIRT

Silene Prentice
Mentor(s): Dr. David Morris

University of the Virgin Islands

Etelman Observatory is home to the Virgin Island Robotic Telescope (VIRT). Donated to UVI in the 1970s, VIRT is a 0.5m Cassegrain Telescope and is primarily operated by UVI professors and students. This research facility focuses primarily on astrophysical investigations, but how precise are the data VIRT gives us? The focus of my research is to make observations of known variable stars, stars with irregular brightness, and a Gamma-ray Bursts (GRBs), beams of extremely energic explosions. These observations will help us to better characterize the capabilities and systematic uncertainties of the VIRT.

To begin, I created a list of Delta Scuti variable stars, a particular class of high-amplitude, short-period variable stars. I didn’t need to make a list of GRBs because they happen at random but frequently. After following the VIRT instrumental procedures to begin observing and collecting calibration images, I entered the coordinates into VIRT and collected a series of over 250 and 800 images on the Delta Scuti and GRB, respectively. Next, I ran my series of images through astrophotometry software, AstroImageJ and SAOImageDS9. Astrophotometry software are used by astronomers to make brightness measurement of their target and to make graphs of how it changes over time, known as light curves. For the known variable star, I used the light curves from my data and compared it to established catalogs. My observations verified the brightness of the Delta Scuti star to be 12.76 magnitudes, the amplitude variation to be .024 and the period to be 0.057 days with an uncertainty of +/- 0.005. In addition, we made measurements of the newly discovered GRB 190627A, a star that exploded approximately 10.31 billion years ago, with a brightness of 18.38 magnitudes, recorded by VIRT at 13h 11m 19s after the initial GRB detection by the Swift satellite.

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Self-Sufficient Solutions for Island Communities

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Mentor(s): Dr. Greg Guannel and Megan Grant

Carribean Green Tech Center, Ethelman Observatory, University of the Virgin Islands

Sunlight and water are two of the most abundant renewable resources in the world, especially in the Caribbean. When properly used they are among the most efficient ways to produce energy and additional resources for anyone who implements them. One example of this is through a solar water heater. With the use of solar energy and some carpentry, we were able to construct a working solar water heater and test, at different weather types (overcast, sunny, cloudy, etc.) and with different collector hose types (rubber and steel), how this affects the heating and efficiency of the heater.

A second example is through rainwater collection. We constructed shed-like structures with three different roofing materials to look at which one collects the most rainwater using pressure sensors and data loggers. We also considered having the roofs at different angles to see whether too much or too little of an angle would lead to less water in the catchment system.

Funding: NSF

Supporting Emerging Aquatic Scientists (SEAS) Your Tomorrow: Bridge to Ph.D. Program

Kaliegh Schlender
Mentor(s): Kristin Wilson Grimes, Marilyn Brandt, Mónica Medina, Carrie Jo Bucklin, and Nastassia Jones

University of the Virgin Islands, Pennsylvania State University, Southern University and A&M College

Supporting Emerging Aquatic Scientists (SEAS) Your Tomorrow program is composed of three programs designed to increase diversity and inclusion of underrepresented minorities (URM) and those from other underserved groups in the marine sciences. The first program offers U.S. Virgin Island middle/high school students' field and lab experiences through the 4-week summer program, Youth Ocean Explorers. The second program provides research and professional internships for UVI freshman and sophomore students with territorial partners like the Virgin Islands Department of Planning & Natural Resources. Finally, the "Bridge to the Ph.D. Program" allows Master of Marine & Environmental Science students from the University of the Virgin Islands to explore Ph.D. options in partnership with Pennsylvania State University (PSU). Students participate in an 8-week summer program: 1-week orientation, followed by three 2-week rotations in different labs with coral reef expertise (Drs. Mónica Medina, Iliana Baums, and Roberto Iglesias-Prieto), ending with a 1-week program close-out. During the summer students gain professional development skills (e.g., resume, cover letter, and writing and advice through the PSU Writing Center). In addition, students are mentored weekly by UVI and PSU faculty, plus URM professionals and faculty from other institutions to discuss topics like imposter syndrome, work-life balance, and potential alternate career paths. Funding for Supporting Emerging Aquatic Scientists (SEAS) Your Tomorrow at the University of the Virgin Islands (UVI) is supported through the National Science Foundation's INCLUDES Program.

Keywords: career development, marine science, Bridge to Ph.D., U.S. Virgin Islands

Computational Molecular Orbital Analysis for 1,4-diazabicyclo[2.2.2]octane

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1,4- Diazabicyclo[2.2.2]octane (DABCO), or triethylenediamine, has the chemical formula, N□(C□H□)□. This organic reagent is used as a catalyst in numerous industrial processes. The reagent is known to easily form a free radical and because of this can be used as an antioxidant free radical scavenger in several different chemical processes. Numerous groups have found that the radical cation, generated in-situ using a variety of chemical, spectroscopic or electrochemical methods, demonstrates delocalization of the free-radical electron through the sigma () carbon-nitrogen framework (ESR or UV-Vis spectroscopy). Using computational computer programs (in our case, Gaussian), we have performed computational Molecular Orbital (MO) calculations, determining the orbital energies for the complete set of molecular orbitals, and comparing the energies of the Highest Occupied Molecular Orbital (HOMO) and the Lowest Unoccupied Molecular Orbital (LUMO), using a variety of computational methods (Hartree-Fock Self Consistent Fields (H-F SCF) or Density Functional Theory (DFT), using a variety of different basis sets) to experimental results. Our computational results are consistent with what has been seen spectroscopically using ESR or UV-Vis spectroscopy.

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Assessment of Water Quality in UVI –Albert A. Sheen Campus Drinking Water Fountains

Deon St. Jules
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In 1974, the Safe Drinking Water Act was passed to protect the quality of the drinking water by providing a basis level of consumption of most contaminants. The Environmental Protection Agency (EPA) has set parameters for the quality of water towards the highest level of consumption of it. These parameters are most likely drawn from specific contaminants, which can be classified as any physical, chemical, biological, or radiological substances found in the water. Maximum Contaminant Levels (MCLs) are the highest level of contamination that is allowed in drinking water and has set standards that give permissible limits to all water systems. In the University of the Virgin Islands-Albert A. Sheen campus, students are skeptical of the water quality especially from the drinking fountains. In an informal survey to students on campus, not all students drink water from the water fountains. The purpose of this research was to test the water quality parameters in all the UVI-Albert A. Sheen campus working drinking water fountains using HACH kits. We also wanted to compare the water quality of the fountains to a commercial drinking water. We hypothesized that Albert A. Sheen fountains' water quality will have a significant difference in levels of metal and non-metal contaminants compared to commercial drinking water. Parameters tested were metals (Arsenic, Copper and Lead) and non-metals (Phosphate, Chloride and Nitrate). Samples were taken from 6 of 9 drinking fountains found from Residence Hall (RHC), Evan's Center (EVC) and the Northwest Wing (NWW) Trellis. Our results have shown that Arsenic is not present in all samples. Copper was highest (0.5 ± 0.28 mg/L) at RHC and lowest (0.14 ± 0 mg/L) at EVC. Lead was highest (2.67 ± 2.3 ⍰g/L) at EVC and the lowest (1.0 ± 0.5 ⍰g/L) at NWW and from the commercial drinking water. One-way ANOVA showed that there was no statistically significant difference between all the drinking water fountain samples and the commercial water for Lead ($p = 0.474$) and Copper ($p = 0.541$). Nitrate was the highest (5.1 ± 2.0 mg/L) in RHC and lowest at EVC (3.8 ± 6.0 mg/L). Phosphates highest was (0.23 ± 0 mg/L) at EVC and the lowest (0.223 ± 0.001 mg/L) at NWW. There was a statistical significant difference for Free Chlorine determined by one-way ANOVA ($p = 0.0351$) between all water samples. A Tukey *post hoc* analysis revealed that commercial water sample and RHC samples were significantly different ($p= 0.0241$). There was also no statistical difference between all samples for Total Chlorine ($p = 0.5855$). In all samples, Lead levels were above the EPA standard. Copper, Arsenic and all non-metal contaminants were below EPA standards. The water quality of the commercial drinking water was similar to the drinking fountains found at UVI based from the EPA Standards.

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Dimensionality Reduction in single cell RNA-seq analysis: Independent Component Analysis as an Alternate Matrix Factorization Technique to Principal Component Analysis

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Principal Component Analysis, PCA, is a commonly used dimensionality reduction technique in single cell RNA-seq (scRNA-seq) analysis. PCA projects high-dimensional data onto a lower dimensional space while maintaining maximum variance between the components. However, there is a restraint where each principal component must be orthogonal to the other. Independent Component Analysis, ICA, projects high-dimensional data onto a low dimensional space such that the components are as mutually independent as possible. This is achieved by maximizing non-gaussian combinations of the observed data. As a result, there is no orthogonality restraint as with PCA. This study was based on the hypothesis that ICA does not have the orthogonality restraint of PCA and may be a suitable alternative to PCA in the dimensionality reduction step of scRNA-seq analysis. The motivation is that ICA could possibly provide more insight to the biological structure of single cell data. To ensure that the results between ICA, and PCA were comparable, both methods were incorporated and run separately in Seurat which is an R package for scRNA -seq data analysis. Furthermore, both ICA and PCA methods, were given scaled normalized matrices, and tested across different clustering resolutions. Through the analysis of the top marker genes from each method, as well as cluster classification by cell type, the investigation revealed that ICA is a viable alternative to PCA in scRNA-seq analysis.

Reef Restoration: Tracking Coral Growth on Different Nursery Structures

Brianna Swanston
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University of the Virgin Islands and The Nature Conservancy

Coral reefs are important coastal habitats for fisheries, tourism, and shoreline protection, but have been decreasing at an alarming rate for many decades. Because of this rapid decline, organizations like The Nature Conservancy (TNC) are working to apply different methods to actively restore coral. For the past eight years in St. Croix, TNC has been propagating endangered coral species in an effort to restore their populations. One approach TNC is using involves fragmenting corals into smaller pieces and growing them in underwater coral nurseries for 9-12 months until they are large enough to be outplanted back onto coral reefs. This has typically been done using a structure called a Tree but this year, TNC established a new coral nursery and is testing a new type of easier-to-build nursery structure, called an A-frame. The main goal of this project was to determine the difference in growth rate of the coral species Acropora cervicornis between the two different nursery structures within three different nursery sites. We hypothesized that there will be no difference in the growth rate of the coral on the two structure types. To determine this information, I analyzed photos of corals in their nurseries at different time periods following fragmentation. Coral size measurements were calculated using the system Image J. The data was then processed in an excel spreadsheet and pivot table to calculate average growth rates. It was found that over the first month after fragmentation, coral fragments at the Cane Bay West nursery site showed the highest average growth rate overall. After three months of monitoring, the Tree structures showed to produce a higher growth rate than the A-frame structures. Continued monitoring is needed to determine if these outcomes are consistent and to understand the reasons for differences in growth.

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The Variation of Total Phosphorus in Mangrove Sediments with Increase in Grey Infrastructure

D'Shaunique Walters
Mentor(s): Dr. Tiffany Troxler and Marbelys Garriga
Florida International University

Phosphorus is a significant nutrient that has a key role in biogeochemical cycles, but excessive phosphorus contributes to the eutrophication of coastal waters. Eutrophication can potentially lead to toxic algal blooms that are a threat to public health and the environment. Therefore, there is a need for the management of the number of phosphates entering the water to prevent phosphorus enrichment. Fortunately, coastal sediments can be used to monitor phosphorus concentrations in coastal waters. Mangrove ecosystems are wetlands located in tropical coasts worldwide. Many coastal wetlands including mangrove forests have a significant role in the removal of phosphorus and nitrogen from the environment. Globally, mangrove ecosystems are rapidly declining due to anthropogenic and natural stressors. These anthropogenic stressors include deforestation, aquaculture, marina development, and runoff from urban and agricultural areas containing chemicals. Grey infrastructure refers to man-made concrete structures such as buildings. **We hypothesized that there will be a significant increase in total phosphorus in mangrove sediments as grey infrastructure increases from the natural, less-developed areas to dense, urban areas.** This study focused on mangrove forests located in one natural (Shark River) and two urban (Cocoplum and Matheson Hammock) sites located within Miami, Florida. Cocoplum and Matheson Hammock mangrove forests were selected because they are influenced by anthropogenic factors such as marine transport, sewage, and dense urban grey infrastructure. Shark River mangrove forest was selected because it is in Florida's Everglades and has limited influence from anthropogenic stressors. To test our hypothesis, we collected three cores from the edge and center of the forest. These cores were replicated and divided into five segments. Next, each of the segments was homogenized with the corresponding segment of another core to produce one sample. The samples were then analyzed for bulk density and phosphorus content. Preliminary results revealed that there is a significance ($P = .003$) in the phosphorus concentration between the Cocoplum and Matheson Hammocks. This indicates that there is a phosphorus variation between urban sites with different amounts of grey infrastructure. These techniques can be used for future experiments to monitor phosphorus concentrations in coastal waters via coastal sediments. The positive impact of our research will be beneficial, as our findings will facilitate the application of monitoring phosphorus using mangrove sediments to prevent phosphorus enrichment.

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CubeSat Instrument for Gamma Ray Detection

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This project was to build an instrument for gamma ray detection to be equipped on the University of the Virgin Islands' Gamma Ray Experiment for Astrophysical Transients (UVI-GREAT). The objective is to detect gamma ray bursts that correspond to collapsing neutron stars and black holes. Gamma ray bursts are energetic electromagnetic events produced by merging neutron stars and black holes. These gamma ray bursts are hypothesized to be the counterparts of gravitational waves. With the limited sky coverage of the Laser Interferometer Gravitational Wave Observatory and BurstCube, UVI-GREAT will increase the coverage area for gamma ray burst detection to near full-sky coverage. To detect the gamma burst from extragalactic sources, the instrument will be built using cesium iodide scintillators, silicon photo-multipliers and a DRS4 evaluation board on a 3U CubeSat. The device is functional and produces results within range of NASA GSFC results, with the exception of low energy sources not being measurable by this device. UVI-GREAT will hopefully be launched in 2022-2023.

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Recursive theory-of-mind in the Design of Deception: Rational Model of Lying and Lie Detection in Children

Azriel A. Williams
Mentor(s): Lauren Oey and Adena Schachner, PhD

University of California at San Diego

It is widely known that keeping the goals of other people in our minds helps us decide what action to take. The purpose of the experiment was to develop and test a two-person “Truth or Lie” test to be used with youth to see how they reason socially. Can people successfully lie and successfully detect lies by taking into consideration another person’s goals and the statistics of the world and do children develop this skill? We modified a single-player web-based deception game called “Truth or Lie” to allow two players to compete against each other in person over multiple rounds. The goal of the game is to gain more points than your opponent. The Marble-Picker randomly samples six marbles from a container and then decides whether to lie about how many red marbles were sampled and, if so, how extreme a lie to tell. If the Marble-Picker reasons about the Decider’s behavior and goals, he/she should craft believable lies. The Marble-Picker gains points if s/he told the truth or successfully lied. The Decider then chooses to accept or reject the Marble-Picker’s statement. The Decider gains points for successful detection of lies and loses points for false accusations. Players switch roles every round. When detecting lies, the Decider should take into account the Marble-Picker’s goals; e.g., liars are probably not going to generate lies that are extreme. We recruited and tested 2 dyads from the UCSD student population. Although we do not have enough data to draw conclusions, preliminary data show that when the Marble-Pickers randomly drew 1-3 red marbles, they would add at least 1 more to their reported marble drawings to give to the Decider. But when Marble-Pickers randomly drew 4-5 red marbles, they started reporting the true number of marbles drawn. At least 75% of the time, the Deciders claimed the Marble-Pickers lied when “no marbles” was reported. The Deciders were less likely to report a lie when the Marble-Picker said 2-5 marbles. We predict that when playing this game, that the Marble-Pickers would be weighing the risk of having a lower lie being rejected but telling the truth about a higher number of marbles drawn because they are thinking about how a higher number may seem to the Decider. We also predict that the Deciders will think about the way the Marble Pickers are framing their lies (meaning that when people are generating lies, they are trying to make their lies believable).We plan on running more adult participants in order to have a sufficient sample size to determine the utility of the two-person “Truth or Lie” test before testing young children (age four to eight years). We predict that over the course of development, children will learn to control for the extremeness of their lies, and thus show a development in their ability to reason about other people’s minds.

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