MONMOUTH UNIVERSITY
SCHOOL OF SCIENCE

MONMOUTH UNIVERSITY
STUDENT SCHOLARSHIP WEEK

21ST ANNUAL

SCHOOL OF SCIENCE STUDENT RESEARCH CONFERENCE

APRIL 14, 2023

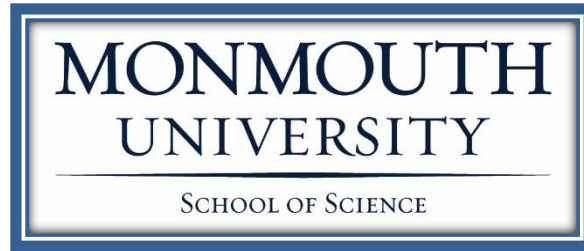## Featuring Poster Presentations of Student Research

Department of Biology
Department of Chemistry and Physics
Department of Computer Science & Software Engineering
Department of Mathematics
Marine and Environmental Biology & Policy Program

ANNUAL STUDENT RESEARCH CONFERENCE

APRIL 14, 2023

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Department of Computer Science and Software Engineering

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Ava Taylor

Faculty Mentors: Dr. Raman Lakshmanan, Department of Computer Science and Software Engineering

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Abby Eck and Julia Kalynchuk
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Marine and Environmental Biology and Policy Program

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MEBP-5   SPATIAL AND TEMPORAL PATTERS OF THE PROHIBITED ATLANTIC
ANGEL SHARK, *Squatina dumeril,* WITHIN THE MID-ATLANTIC BIGHT
>   *Jessica B. Maguire*
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>   *Program*

MEBP-6   ARE STRIPED BASS (*Morone saxatilis*) OVERWINTERING IN THE
MANASQUAN RIVER ESTUARY?
>   *Emily Olynyk, Erin Oscar, Gildon Smith, Julia Panebianco, Kennedy*
>   *Fruit, and Nico Landino*
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>   *Assistant Dean John Tiedemann*

MEBP-7 ANALYZING THE ABUNDANCE AND TYPES OF MICROPLASTIC FOUND ON HATHAWAY BEACCH IN DEAL, NEW JERSEY
Nicole Cappolina
Faculty Mentor: Assistant Dean John Tiedemann

BIOLOGY DEPARTMENT

BY-1

TRANSCRIPTOMICS OF ORAL TISSUES IN SUBJECTS WITH PERIODONTITIS

Maxwell Rosen
Department of Biology

Faculty Mentor: Dr. Aina Ananda, Department of Biology

ABSTRACT

Periodontal disease is a chronic inflammatory condition that affects 2 in 5 American adults. The disease is caused by a microbial infection of soft tissue within the mouth, which leads to gum recession, bone damage, and tooth loss if left untreated. Advanced periodontal disease can also contribute to systemic inflammatory diseases such as heart disease, diabetes, arthritis, and stroke. Although it is widely established that microbial community dysbiosis is linked with periodontal disease severity, the microbiota's structure and the causal microbes in periodontitis are not yet fully understood. Our study hypothesizes that an imbalance in a core set or oral microbes occurs in diseased tissues, which results into the alteration of the transcriptome in these tissues. We will first identify differentially-expressed genes in afflicted oral cavity tissues from publicly-available RNA-sequencing data from the National Center for Biotechnology Information (NCBI). Using Gene Set Enrichment Analysis (GSEA), we will identify biological pathways that are differentially regulated in the host tissue. Metagenomic analysis, using molecular data from databases such as Human Oral Microbiome Database (HOMD) and the NIH Human Microbiome Project, will also help to characterize the ecology of the human oral microbiome in healthy and diseased oral tissues. Our study aims to uncover the relationship between oral microbiome ecology, oral microbiome gene expression, and host tissue gene expression. Machine learning will be employed to build prediction models for the health status of patients. Our catalog of the molecular pathways involved in periodontal disease development and progression will be informative for the development of novel diagnostic and therapeutic strategies, thereby improving the overall health of affected individuals.

MANUKA ESSENTIAL OIL DECREASES PROLIFERATION AND CAUSES APOPTOSIS IN HT-1080 FIBROSARCOMA CELLS

Noa I. Bass
Department of Biology

Faculty Mentor: Dr. Dottie Lobo, Department of Biology

ABSTRACT

Since research on the effects of essential oils on human cell lines is limited, the goal of this project was to treat cancer cells lines with manuka essential oil at different concentrations and ascertain the effects on cell proliferation on a variety of cell lines, including normal fibroblast (CUA-4) and fibrosarcoma (HT-1080) cells. Manuka oil is popular in many skincare products because of its antibacterial and anti-inflammatory properties that treat several skin conditions. However, manuka oil also contains an active ingredient that is commonly found in herbicides and is potentially toxic to human cells at certain concentrations. To study the effects of this essential oil on cultured cells, cell lines were grown on 24-well plates, and subconfluent cultures were treated with varying concentrations of manuka oil for 24 hrs. The effect of the oil on proliferation and viability was measured through direct cell counting using trypan blue dye exclusion and through the use of an MTT assay. As the concentration of oil increased, viability of all cell lines tested decreased. MTT assay results also reflected this trend, with a significant decrease in MTT activity seen in cells treated with 500 µg/ml manuka oil. To determine if the decreased cell numbers observed from manuka oil treatment is the result of apoptosis, PARP cleavage assays were performed in HT-1080 cells. HT-1080 cells were found to have significant levels of PARP cleavage after 4 hours of treatment with manuka essential oil, indicating that the cells were undergoing apoptosis.

CREATION OF A HYPOXIC STATE DECREASES THE PROLIFERATION OF HT-1080 FIBROSARCOMA CELLS

Michael Catalfumo
Department of Biology

Faculty Mentor: Dr. Dottie Lobo, Department of Biology

ABSTRACT

Hypoxia is characterized as a state in which tissues become oxygen deprived. Under hypoxic conditions, proteins called Hypoxia-Inducible Factors (HIFs) become activated to turn on the expression of important genes (Kaelin, 2019). HIFs, particularly HIF-1α, serve as markers in studying hypoxia.

Cobalt chloride ($CoCl_2$) has been used in many cell types to stimulate the activation of HIF-1α and thus chemically mimic creation of a hypoxic environment (Sanchez and Cardenas, 2019). The purpose of this study was to determine if $CoCl_2$ could create a hypoxic environment in HT-1080 fibrosarcoma cells, and how this would affect proliferation. Confluent cultures of HT-1080 cells were treated with either 100 µM or 250 µM of $CoCl_2$ for 1 hour, 4 hours, or 24 hours. Using western blot analysis, it was determined that HIF-1α expression could be detected at 1 hour with 250 µM of $CoCl_2$ and at 4 hours with 100 µM of $CoCl_2$. Maximal expression of HIF-1α occurred after 24 hours. To study the effect pf $CoCl_2$ treatment on proliferation, HT-1080 cells were plated onto 24-well plates and were treated with 100 µM or 250 µM of $CoCl_2$ for 24 hours. Untreated cells served as the control. All cells were counted using trypan blue dye exclusion. 100 µM $CoCl_2$ treatment decreased proliferation by 9%, while cells treated with 250 µM $CoCl_2$ resulted in a 40% decrease of proliferation. Therefore, $CoCl_2$ creates a hypoxic environment for HT-1080 cells, and decreased proliferation of these cells.

Hypoxia may influence the expression of cancer stem cell markers, including Oct4 and Sox2, which may be regulated by nitrogen-activated protein (MAPK) signaling. Through western blot analysis, JNK protein was shown to be expressed in control and hypoxic cultures. Hypoxia treatment alone did not appear to activate JNK. The expression of Oct4, Sox2, and other MAPK signaling proteins will be tested.

CYPRESS ESSENTIAL OIL LIMITS PROLIFERATION OF FIBROSARCOMA CELLS

Dianelys Garcia
Department of Biology

Faculty Mentor: Dr. Dottie Lobo, Department of Biology

ABSTRACT

Cypress oil is an essential oil derived from evergreen coniferous trees native to Southern Europe and Western Asia. Cypress oil exerts anticancer properties due to their natural terpenes which induce apoptosis and cell cycle arrest, in turn limiting tumor growth and metastasis. The components of cypress essential oil include a total of 20 constituents which represent 98.1% of the oil. These include: α-pinene (48.6%), δ-3-carene (22.1%), limonene (4.6%) and α-terpinolene (4.5%) which are the main components comprising 79.8% of the oil. A cell line of HT-1080 (fibrosarcoma) cells were treated with cypress essential oil at different concentrations and the effects were determined. Proliferation was measured by direct cell counting using trypan blue dye exclusion and MTT assay. Proliferation of HT-1080 fibrosarcoma cells demonstrated a significant decrease with increased concentration of cypress essential oil. In addition, high concentrations of cypress essential oil also decreased MTT activity which therefore confirmed a decrease in viability due to essential oil treatment. Western blot analysis will be used to ascertain if the decreased viability is a result of apoptosis by detection of PARP cleavage. The effects of cypress essential oil will also be tested on normal fibroblast cells to compare differences in signaling. The signaling of normal-contact inhibited cells treated with cypress will be compared to the cancerous cell line.

BY-5

THE EFFECTS OF ESSENTIAL OILS (EOS) ON THE GROWTH OF MULTIDRUG RESISTANT BACTERIUM *Klebsiella pneumoniae*

Chiara Zambon, Ileana Plummer, and Nico Santorelli
Department of Biology

Faculty Mentor: Dr. James P. Mack, **Department of Biology**

ABSTRACT

Due to the overuse and misuse of antibiotics, multidrug-resistant bacteria have become a growing global healthcare issue. Health professionals are unable to treat many multidrugresistant bacterial infections with traditional medicinal practices. These bacteria are forming at a higher rate than present antibiotics can treat. Natural medicinal products such as essential oils (EO's) are being studied to test the effectiveness of treating multidrug bacterial infections compared to antibiotics. Natural EO's are presently being used in healthcare settings to help combat these multidrug drug-resistant bacteria. Antibiotic-resistant bacterial infections are an increasing threat within healthcare settings due to the high rate of antibiotics being used to treat patients, which could be unnecessary and cause the patient to develop a resistance to antibiotics. In our study, the essential oils arborvitae, cassia, cinnamon bark, melaleuca, and thyme were tested against the multidrug-resistant bacteria of our choice, Klebsiella pneumoniae. The carrier oil jojoba was used to dilute the EO's concentration and to determine the EO's effectiveness in inhibiting the growth of Klebsiella pneumonia. The EO's listed showed the greatest success upon testing and were chosen after demonstrating high success rates during the initial testing of 119 total EOs at 100% concentration. Antibiotics were also used to see how the oil zones of inhibition compared to those of the EO's. The current antibiotics healthcare workers use to treat Klebsiella pneumoniae include Amikacin, Ceftriaxone, Colistin, Imipenem, Meropenem, and Tigecycline. The antibiotics in our study were tested to compare the zones of inhibition to those of the EO's. Once completed, research was continued to determine the Minimum Inhibitory Concentration (MIC) for each essential oil. The MIC for each essential oil was determined using the Kirby-Bauer Disk Diffusion Susceptibility Method. We found that out of the essential oils we used that arborvitae, cassia, and cinnamon bark were more effective in inhibiting growth of Klebsiella pneumonia than the antibiotics.

XEROPHILIC AND XEROTOLERANT FUNGI AS A SOURCE OF NOVEL ANTIBACTERIAL COMPOUNDS

Alex Kalina and Dante Kiett
Department of Biology

Faculty Mentor: Jon Polishook, Department of Biology

ABSTRACT

Xerophilic and xerotolerant microfungi, those fungi that can grow at or tolerate a low-water availability and typically cause food spoilage, were isolated from several dried herbaceous plants purchased as spices, dried seeds and honey in local grocery stores as a model for natural product discovery. The spices, seeds and diluted honey were placed on DG18 agar to select for fungal species able to grow in a low-water availability environment for up to 21 days. Any emerging fungal growth from the seeds, spices or honey were subcultured onto malt extract agar slants and incubated at room temperature (20-22C) until significant hyphal growth was observed. From 8 types of plant parts and honey, 48 fungal isolates were recovered representing 20 morphotypes, based on macroscopic features. Some of the fungal genera isolated include *Penicillium*, *Alternaria* and several non-sporulating strains. These fungal morphotypes were then regrown on cornmeal, malt-extract and potato dextrose agar petri plates for 14 days at room temperature. The antibiotic potential of these morphotypes was assessed by placing agar discs of each morphotype / production agar on top of a gram-positive and gram-negative bacterial strain embedded in Tripticase Soy agar. Antibiotic evaluation was assessed by the size of any zone of inhibition after overnight incubation. The zones of inhibition will be compared to commercially available antibacterial compounds to determine novelty.

ABSENCE OF RECEPTOR DYSREGULATION ACCOUNTS FOR RESISTANCE TO ALCOHOL WITHDRAWAL SYMPTOMS IN A MODEL FOR ADHD

Ilona J. Maczka and Emily M. Ferris
Department of Biology

Faculty Mentor: Dr. Dennis E. Rhoads, Department of Biology

ABSTRACT

The purpose of this research was to determine the biochemical basis for alcohol withdrawal symptom resistance in adolescents of the Spontaneous Hypertensive Rat (SHR) strain. SHR is of interest as a model for attention deficit hyperactivity disorder (ADHD). Previous work in our laboratory modeled off-prescription use of amphetamine-based ADHD medications (e.g., Adderall) in combination with alcohol for adolescent Long Evans (LE) rats and Wistar-Kyoto (WKY) rats. Co-administration reduced alcohol withdrawal symptoms in these strains, suggesting severity of withdrawal symptoms was modulated by alcohol-amphetamine interactions. Thus, we were interested in how the ADHD model SHR would respond to alcohol alone and in combination with amphetamine. In contrast to the other rat strains, SHR displayed none of the more severe alcohol withdrawal symptoms characteristic of adolescents. This led to our hypothesis that SHR have neither alcohol-induced upregulation of excitatory glutamate receptors (NMDA and AMPA) nor downregulation of modulatory adenosine receptors, a combination we believe is responsible for severe alcohol withdrawal symptoms in adolescents. Samples of homogenized brain frontal lobe were obtained from SHR following consumption of control or ethanol-containing liquid diets. Proteins were separated by polyacrylamide gel electrophoresis (SDS-PAGE). Western blotting with chemiluminescent detection was used to determine levels of NMDA receptor, AMPA receptor, adenosine 1 receptor (A1), and the enzyme GAPDH as an internal control. Quantitative measurements showed no significant differences in receptor protein densities between brain preparations from control and ethanol-consuming SHR rats. The results of this research suggest SHR are resistant to alcohol withdrawal symptoms based on the absence of the expected brain receptor dysregulation during alcohol consumption. The resistance to biochemical and behavioral changes in SHRs raises the possibility that individuals with an ADHD diagnosis may also be resistant to developing alcohol withdrawal symptoms following prolonged alcohol consumption.

CHEMISTRY AND PHYSICS DEPARTMENT

EXPLORING THE LOCAL CONFORMATION OF INDIVIDUAL G4 LAYERS IN HUMAN TELOMERIC G-QUADRUPLEXES

Dayana Khalil, Riya Ajmera, Gioanna Curci
Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose, Department of Chemistry and Physics

ABSTRACT

The formation of G-quadruplex (GQ), a non-canonical nucleic acid secondary structure, can inhibit the elevated telomerase activity that is common in most cancers. The global structure and stability of the GQs are usually evaluated by spectroscopic methods and thermal denaturation properties. Most of the biochemical processes involving GQs involve local conformational changes of GQs at the guanine tetrad (G4) level. These local conformational changes are difficult to follow as it is impossible to isolate spectroscopic signals of individual layers of a GQ structure. To overcome this problem, using a synthetic GQ-forming DNA strand, we developed a method in which individual G4 layers in GQs are composed of site-specifically incorporated 6-methylisoxanthopterine (6MI), a Circular Dichroism (CD)-active fluorescent base analogue of guanine. In this study, experiments were performed with human telomeric 22AG sequence (5′-AGGGTTAGGGTTAGGGTTAGGG-3′) where 6MI monomers site-specifically replaced guanines at the positions 3,9,15 and 21. The CD and fluorescence properties of the GQ structures with and without the ligands were characterized under various conditions. Further, thermal denaturation studies showed that the stability of the GQ-ligand complex varies depending on the position of incorporated 6MI probes. The results also showed that the local conformation of individual G4 layers in a GQ due to binding the binding of specific ligand varies with the position of the G4 layer in the GQ structure as well as the chemical charecterstics of the ligands used. This method can be used to understand the details of GQ-protein and GQ-drug interactions at the individual G4 layer that will help design new drugs for treating GQ-related diseases.

SINGLE-PROTON TORQUE GENERATION OF THE BACTERIAL FLAGELLAR MOTOR OF *Escherichia coli*

Vincent Manning, Maddison Beahm and Julia Kalynchuk
Department of Chemistry and Physics

Faculty Mentor: Dr. Ilyong Jung, Department of Chemistry and Physics

ABSTRACT

Escherichia coli (*E. coli*) has been studied meticulously since their discovery to distinguish their role in the indication of water quality. The anaerobic bacterium is typically found in the intestinal tract of humans and animals as a normal flora. However, in studies focused on water quality, *E.coli* has evidently been found to propagate in untreated water due to sewage or animal waste contamination. In order to understand the bacterium's motility towards favorable environments contingent on the changing chemical gradient and composition of water, we investigate the torque generating components of *E.coli* known collectively as the bacterial flagellar motors (BFM). In particular, the torque generating protein complex inside the BFM, consisting of several stators and a rotor, that propels *E. coli* employs proton motive force to generate an electrostatic interaction for cell locomotion. By analyzing the minimum torque that is generated by a single stator, we can then approximate the total number of protons that flow through each torque generating unit. Our results indicate that a single-proton is capable of generating enough torque required for flagellar rotation. Through the understanding of how the bacterial flagellar motor functions, we may be able to understand how to inhibit their motion in order to prevent the spread of *E. coli* contamination.

CE-3

CREATING A COST EFFICENT METHOD TO DETERMINE THEOPHYLLINE RIBOSWITCH ACTIVATION

Thomas Hintelmann, Olivia Enny, Mika Schievelbein, and James Tilton
Department of Chemistry and Physics

Faculty Mentor Dr. Johnathan Ouellet, Department of Chemistry and Physics

ABSTRACT

A riboswitch is a small piece of RNA in structure that binds a molecule to itself to turn on or turn off a gene. As a result, riboswitch regulation provides an opportunity to develop targeted therapies for various diseases. Currently one of the only ways to determine activation of a riboswitch in an organism is to perform Fluorescent Activated Cell Sorting (FACS). This machine requires a large amount of upkeep and a trained technician to use. Most smaller research universities do not have the resources to be able to use this type of machine which greatly limits the amount of research that can be performed on riboswitches. This project is built based on 3 different cloning methods; Gibson assembly, golden gate assembly, and PCR assembly. To test this, the lab is currently taking plasmids and performing these assemblies using fluorescent genes, GFP-UV and mCherry, as well as the sequence for the theophylline riboswitch. Once these genes are cloned, the hope is to view under UV light which of the fluorescent genes are expressing. The amount of expression will be quantified using ratio-metric fluorescence. If GFP-UV and mCherry express this will tell that the theophylline riboswitch is active. If only mCherry is active this will tell theophylline is riboswitch is inactive. These measurements can be used to measure activation of other riboswitches as well

CE-4

BIOGEOCHEMISTRY OF MICROPLASTICS WITHIN AQUATIC ENVIRONMENTS IN REGARDS TO SMALL AND LARGE-SCALE EXTRACTION, PHYSICAL TRANSPORT, AND CHEMICAL SPECIATION

Luke M. Collier
Department of Chemistry and Physics

Faculty Mentor: Dr. Tsanangurayi Tongesayi, Department of Chemistry and Physics

ABSTRACT

Each year, over 380 million tons of plastic are produced and added to our planet. Yet over 50% of these produced plastics are strictly for single use, leading to high rates of improper disposal. Microplastics, defined as plastic fragments less than five millimeters in diameter, contribute to significant pollution in various environments mainly due to plastic degradation (i.e., plastic waste against sand, tires against pavement, washing of clothes). Microplastics have proven to present significant health issues towards humans and aquatic life. Due to their size, the ability to extract microplastics from commercial and environmental samples has proven difficult. Comprehensive research and its results on how microplastics are extracted, transported, and interact within their ecosystems has led to increased awareness and interest in microplastics and their effects. In this study, density separation using different salt solutions (i.e., NaCl, NaBr) and digestion methods (i.e., H_2O_2) were carefully analyzed and examined for highest extraction yield. The results of this project will include the most effective methods, chemicals, and procedures for extracting microplastics found in consumer and commercial soap products. In addition, the interactions between how microplastics interact with heavy metals such as lead (Pb) and chromium (Cr) based on Ph are discussed. Although multiple methods of small-scale separation and their limitations are discussed in this study, large-scale implementation of these methods are exhibited at a local wastewater treatment plant (WWTP). This study will allow for further investigation to occur regarding the biogeochemistry of microplastics, as well as provide separation methods that can be applied to additional large-scale operations, such as mobile water remediation systems and industrial WWTPs.

COMPUTER SCIENCE
AND
SOFTWARE ENGINEERING DEPARTMENT

CSSE-1

CONNECT 4 IN JAVA

Zaccery Tarver
Department of Computer Science and Software Engineering

Faculty Mentor: Gil Eckert, Department of Computer Science and Software Engineering

ABSTRACT

Connect 4 is a classic Hasbro board game for two players. Each player is assigned red or yellow as their color, and the one that makes the first move is determined by a 50:50 roll. Each player takes turns placing their pieces in a vertical game board until one of them gets four in a row – this person is then the winner. If no more moves are available, and if neither player has won, then the game is declared a draw. Connect 4 has been recreated digitally in the Java programming language as a fun experiment to gain a deeper understanding of the Java API (Application Programming Interface). This was made possible by using GUI (Graphical User Interface) tools that the API provides.

Extensive research was done in the API to create a visually interesting experience that this game demands. Game pieces were created as JComponents and rendered using Ellipse2D.Double, a class that allows graphics to be drawn in a circular shape. The Game class is the main driving force behind the program, which not only sets up the board with these pieces, but it also listens for mouse click inputs on each of the in-game buttons, which are then received as the player's chosen move.

Connect 4: Java Edition allows the user to play against a friend. Both users use the same device but alternate who is using it in agreement with the turn order. But the user can also play against a computer, who can be set to a weak or tough difficulty setting. The computer always chooses the best move, but plays it based on a random factor. With a weak CPU, it is less likely to pick the best move. However, with a tough CPU, it plays the best move more often.

NFC (NEAR-FIELD COMMUNICATION) CHAT APP
DECLUTTERING BULLETIN BOARDS
WITH ANONYMOUS MESSAGING USING NFC TECHNOLOGIES

Arielle Sinicin and Zoë Klapman
Department of Computer and Software Engineering

Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering

ABSTRACT

Bulletin boards are an integral aspect of college campuses to distribute information on upcoming events, clubs, local organizations, and more. However, these boards can quickly become cluttered as more and more organizations create posters and cover up the other posters already on the board. The goal of our application, NFC Chat, is to provide a creative solution to bulletin board clutter that involves physical user interaction through use of NFC Tags. In addition to solving bulletin board clutter, the app also creates a new, innovative way to have an anonymous communication on posted information.

Each club or organization that would normally post a plain poster to the bulletin board also attaches an NFC Tag. When people who pass by the board put their phone up to the poster, (as they would do with other NFC technologies, such as ApplePay) they will be able to join the conversation about information and the organization from NFC Chat app. Once in a conversation, the user will be able to converse with other users by typing a message, tapping the tag before posting the message. The app features also include tracking locations of tags, show them on a map, and an Augmented Reality feature to show the poster.

NFC Chat is an iPhone application built using iOS Frameworks, including but not limited to: CoreNFC, MessageKit, MapKit, and ARSceneKit. The app is designed using the Model, View, Controller software design pattern, developed using Swift programming language construct as protocols, delegates, observers, notifications, and more. The backend of our application utilizes Google's Firebase services, specifically Firestore noSQL Document database, and Firebase Cloud Storage.

CSSE-3

**USING ULTRA-WIDEBAND (UWB) TECHNOLOGY
TO TRACK OCCUPANCY IN ROOMS**

Meghan Granit, Kiran Ramjisingh, and Jordan Strobing
Department of Computer Science and Software Engineering

Sponsor: Mr. Guy McIlroy, Koliada Embedded Systems

**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering**

ABSTRACT

On school, college, corporate and hospital campuses, it remains imperative to prepare for emergency evacuation. By leveraging ultra-wideband technology, we are able collect occupancy data at various rooms and locations in real-time to assist in the evacuation process. Our system utilizes UWB broadcast sensors to ping occupant's mobile devices in range, computes distance from sensor to place them in a room. Gathered distance and identified location data is sent to a cloud-based database service to visualize occupancy in each room on a dashboard, and prepare for efficient evacuation in an emergency. The theory behind the evacuation has been developed over the past two years. Meghan Granit, Jordan Strobing, and Dr. Jiacun Wang (Department of Computer Science and Software Engineering) have published two papers proving that this is an effective way to start an evacuation process. Having real-time information is necessary to notify occupants on fast and safe evacuation routes.

The ultra-wideband broadcast sensors are based on Qorvo chip with Koliada Embedded Systems mesh network platform. The sensors communicate with an iOS application to gather distance data anonymously. The data is sent as UDP packets to server, which uses a REST API service to forward to noSQL MongoDB database. A React web application visualizes the available data on an easy to understand dashboard.

CSSE-4

STATMOSPHERE: A UNIQUE VIDEO GAME

Adriel Juarez and Anthony Cross
Department of Computer Science and Software Engineering

**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering**

ABSTRACT

When it comes to video games, it is essential to stand out and be unique. *Statmosphere* is a two-dimensional puzzle platformer video game, where the goal is to reach from the start of the level to the end, all while navigating platforms and avoiding traps. Before you start the level, however, you are able to apply a limited set of modifications to the attributes of your character, like speed, jump height, and health. Each level has multiple unique combinations of attribute modifications that can be used to beat the level.

This video game is designed to be played on computers running Windows. It is coded in C# language and uses the Unity game engine. Progress and save data are stored and manipulated using JSON files. Users can opt to play with either a keyboard or an Xbox controller.

MU-SOS AND MUPD-SOS

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**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering**

ABSTRACT

MU-SOS and MUPD-SOS are mobile apps that provide a new-age approach to on-campus safety.

Through MU-SOS - an iPhone app - students and staff will have an outlet to report emergency incidents and view all high priority notifications posted by Monmouth University Police Department (MUPD). MUPD can then respond quicker to incidents, be more informed about concerning situations, and provide a higher level of care to the reporter. The functionality of this application includes instant messaging with officers in-route of the emergency, tracking of exact location reported incident and reporter on app's maps. MU-SOS aims to improve the security and safety on Monmouth University's campus.

There is also a companion MUPD-SOS iPhone/iPad app that directly interacts with the MU-SOS application. This app will be utilized by anyone within the Monmouth University Police Department that will be involved with responding to emergencies on campus. This application provides MUPD with certain functionality, such as location tracking of those who report an emergency on MU-SOS, direct messaging with the reporter of the emergency, and the ability to post a report to the MU-SOS feed of reports for students/staff to stay more informed as to problems that could be happening on campus.

Both MU-SOS and MUPD-SOS apps are developed using iOS Frameworks, Swift programming language, Model-View-Controller software methodology, and Google Cloud Firebase authentication and noSQL Firestore Database services.

CSSE-6

MID-ATLANTIC OCEAN RESOURCES DATA PORTAL APP

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Sponsor: Mr. Karl Vilacoba, Monmouth University Urban Coast Institute

**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering**

ABSTRACT

The Marco consortium gathers and distributes ocean resources data along five Mid-Atlantic states. The data is available from GIS-based repositories. The mobile app we have developed allows users to visualize and analyze ocean resources using ArcGIS mapping services in an interactive manner. Users have access to over 5,000 map layers which include information about fishing, marine life, habitat areas, and more. With the Marco Portal app, users will be able to easily search and filter through data layers, to see map visualizations, data summaries, and have set their favorite and active map layers.

The application is built natively for iPhone mobile platform and developed in Swift programming language. It uses a REST API provided by MARCO service for access to data categories/themes, theme layers and sublayers.

CSSE-7

FOOD AND FITNESS

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Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering

ABSTRACT

Food and Fitness is an all-expansive web application to fit the users' personal needs of their fitness journey to help them obtain their health goals in an efficient manner. The Food and Fitness web application does the heavy lifting in logging the user's daily food and exercise to help them better understand how to better themselves. After registration the user will answer one-time questions about their goals and personal health. These questions will be used to help guide the user in the right direction on their journey to better health. A user can view their goals and progress on the progress page which is updated manually by the user to see how much they are progressing in their Food and Fitness journey.

The full stack web application is developed using web development programming languages - HTML, CSS, and PHP-, Codeigniter - a web application framework, mySQL - relational database, and two APIs - NutritionIX and WGER API's. The APIs are used for general information about different foods and workouts. The app is meant for anyone to use and make it easier for people to take control of their health with a simple but helpful webapp.

FLUDZ – A CROWDSOURCED FLOOD DATA COLLECTION, DISTRIBUTION, AND ANALYSIS SERVICE

Ava Taylor
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**Faculty Mentors: Dr. Raman Lakshmanan, Department of Computer Science
and Software Engineering**

Dr. Geoffrey Fouad, Geographic Information System Program

ABSTRACT

Fludz is a mobile app and GIS-based data service that utilizes crowdsourced data for users can report flood data from their local area and analyze other reported real-time data. Users can drop pins to report data or view specific areas and streets that are flooded, where flooding may be increasing or decreasing, if there are hazards in the roads, and the depth of the flooded areas all based on the reports of other app users. It provides a map of all data points reported by other users, allowing anyone to access the information. An advanced search feature allows users to query the system for historical flood data based on location, date ranges, specific storms, and other criteria.

This service demonstrates application of multiple technologies – Crowdsourcing, GIS (Geographic Information System) data collection and modeling, easy to use mobile app, cloud-based repository for large volume data collection and distribution - to help our communities in so many ways.

A service like this has the potential to reduce mortality and injury during flood events as it can guide evacuation to safe areas by avoiding flooded streets. There are many apps that report weather or use real-time data collection to present information (e.g., traffic conditions) to users. However, currently there is no widely used application for the purpose of collecting and presenting local flood data to users in this way. This app is an effective way for information reach the public in the event of a flood.

MATHEMATICS DEPARTMENT

DETERMINING OFFSHORE WIND DEVELOPMENT IMPACT ON MARINE RESOURCES USING NONPARAMETRIC TESTS

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Faculty Mentor: Dr. Richard Bastian, Department of Mathematics

Client: Dr. Jason Adolf, Department of Biology

ABSTRACT

An alternative to fossil fuel-based energy is the development of offshore wind energy. This is rapidly occurring on the continental shelf off the coasts of New Jersey and New York. However, there are concerns on how installing the wind farms might affect marine ecosystems. This study focuses on the statistical analysis of environmental data collected at the Orsted Ocean Wind 1 'control' and 'impact' sites. The 'impact' site is where the construction of the wind turbines would take place, and the 'control' site is where no modification takes place. A Before-After-Control-Impact (BACI) experimental design is done to complete an environmental assessment of marine resources prior to and after the construction process. Our research question is: how similar or different are the 'control' and 'impact' sites before the wind farm construction takes place? Also, does season impact any of the given parameters (which includes salt, temperature, turbidity, pH, and dissolved oxygen)? To move towards answering our research question, we looked at the descriptives of each parameter between the impact and control sites. Parameters were grouped into seasons (Summer, Winter, Spring, and Fall). Interaction plots were constructed for parameters according to location and season. The Shapiro Test was utilized to determine the normality of each parameter according to location. Most parameters came back non-normal. This elicited the use of the Wilcoxon Test which compares groups when normality is violated. The current state of our project involves the testing of the bootstrapped ANOVA and other methods that support non-normal parameters for a dataset which utilizes replication.

STATISTICAL ANALYSIS OF OBESITY IN DACHSHUNDS WITH INTERVERTEBRAL DISC DISEASE

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Faculty Mentor: Dr. Richard Bastian, Department of Mathematics

Client: Martha Cline, DVM, ACVN,
Red Bank Veterinary Hospital, Department of Clinical Nutrition

ABSTRACT

Evidence linking obesity as a risk factor for intervertebral disc disease (IVDD) in dogs is lacking. This study focused on the Dachshund breed, as they are at an increased risk for developing IVDD. A sample of 133 dachshunds from Red Bank Veterinary Hospital were included in this study. Body condition score (BCS) was recorded for 91 dogs presenting to the general practice service for a routine exam with no evidence or history of IVDD. BCS and modified Frankel score (MFS) were recorded for 43 dogs that presented to the neurology service with a confirmed diagnosis of IVDD by MRI. It was hypothesized that dachshunds diagnosed with IVDD are more likely to have a higher BCS than dachshunds without IVDD, and that BCS and MFS are inversely related in dachshunds diagnosed with IVDD. Logistic regression was used to analyze the relationship between the binary response IVDD and the ordinal predictor BCS. Model selection was performed using deviances and Akaike information criterion (AIC). Body weight was considered as a potential predictor for inclusion in the model, but excluded due to selection criteria. In the logistic regression model, the BCS predictor was significantly associated with IVDD; for every one unit increase in BCS, the odds of IVDD increased by a factor of 1.63. A two sample bootstrapped t-test was used to analyze the difference in mean weight between dogs with and without IVDD, which resulted in no statistically significant difference in mean weight. For the group of 43 subjects affected by IVDD, the strength of association between BCS and MFS was measured using Spearman's Rho correlation. A weakly positive, yet statistically significant, correlation of 0.33 was observed between BCS and MFS.

STATISTICAL ANALYSIS ON THE SCALING
OF RED MANGROVE SERVICES IN THE BAHAMAS

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Faculty Mentor: Dr. Richard Bastian, Department of Mathematics

Client: Dr. Pedram Daneshgar, Department of Biology

ABSTRACT

Red Mangroves provide vital services to various ecosystems that reside mutually within their coastal vegetation. Mangroves are coastal, tropical plants that are adapted to loose, wet soils, salt water and being periodically submerged by tides. Their natural infrastructure protects a wide range of species and provides shelter. Services provided by the mangroves correlate to the number of species present within the environment. To determine whether the services of Red Mangroves proportionally scale along with their size/ density, fifteen mangroves were identified based on observation and measured according to their abundance of stilts/branches, leaf count, length, diameter and the number of species. The Mangroves, as a whole, were viewed as cylinders in order to compute their volume, as well as their carbon, biomass, and diversity. It is hypothesized that as the size of the Red Mangrove increases(Volume mm^3, Biomass, and Carbon), the services will increase(Diversity of species). We will use a robust linear model to test if the services of Red Mangroves scale. We want to show that the model has a positive slope, as stated by our hypothesis. Since our data is scarce, a robust linear model will be used because we do not meet the assumptions of a general linear model. Power analysis will also be examined to predict how many Red Mangroves are required to produce high power.

MA-4

STATISTICAL ANALYSIS ON MA 050

Matt Wolyn and Kyle Broesler
Department of Mathematics

Faculty Mentor: Dr. Richard Bastian, Department of Mathematics

Client: Dr. David Marshall, Department of Mathematics

ABSTRACT

Most students upon enrollment at Monmouth University undergo a math placement test in order to be properly placed according to their skill level. Scores range from 1 to 4, with 1 meaning the student did not demonstrate proficiency in pre-algebra skills and 4 meaning the student was proficient in pre-calculus math. Those students who score a 1 on the math placement test are placed into a remedial, non-credit bearing course, MA050: Pre-Algebra Mathematics. Our goal of this research is to analyze whether MA050 successfully prepares students for their next math course. We will dive into analysis that focuses on logistic regression and multinomial regression in order to try to predict future class scores of the students who scored a 1 on the math placement exam based on their performance in MA050.

MARINE AND ENVIRONMENTAL BIOLOGY AND POLICY PROGRAM

EFFECTS OF THE DEAL LAKE OUTFLOW ON A NEARBY SWIMMING BEACH

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Faculty Mentor: Dr. Jason Adolf, Department of Biology, MEBP Program
and Urban Coast Institute

ABSTRACT

Deal Lake is a polluted coastal lake located in Monmouth County, NJ. Deal Lake directly drains into a nearby swimming beach. *Enterococcus,* bacteria found in the intestinal tract of mammals, has been previously identified in Deal Lake indicating the presence of fecal material which could have many other pathogens within it. Deal Lake has been observed to harbor cyanobacteria that create potentially toxic harmful algal blooms (HABs). The goal of this research was to gather samples from different sites of Deal Lake and Loch Arbour Beach in the outflow location to test if there is a presence of *Enterococcus* and / or HABs in the swimming areas. It was hypothesized that water quality conditions at the beach outflow would reflect conditions in the lake. Four sites were sampled: the shoreline, ocean area parallel from the outflow, ocean past the groin end, and the outflow spot at the groin. Water quality measurements were conducted at each site and samples of each site were collected. FIB testing was conducted in the four ocean sites and in a Deal Lake site closest to the ocean. qPCR assays were taken to measure toxin gene abundance.

Results to date indicate that the water conditions of Deal Lake have an influence on the water conditions of Loch Arbour Beach. Deal Lake drains right into Loch Arbour Village Beach Club potentially affecting water quality conditions, which is why testing in the outflow areas of a polluted lake to a swimming beach is important for the community.

FECAL INDICATOR BACTERIA (FIBs) IN DEAL AND SUNSET LAKE NJ

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Faculty Mentor: Dr. Jason Adolf, Department of Biology, MEBP Program
and Urban Coast Institute

ABSTRACT

Fecal indicator bacteria known as FIBs, are bacteria that originate from the guts of warm-blooded animals and birds. FIBs can commonly make their way into bodies of water due to runoff after a major precipitation event. FIB presence is considered to be a potential public health hazard to swimmers if their levels are above a regulatory threshold (104 CFU per 100 mL). Certain coastal lakes in New Jersey, such as Deal and Sunset Lake, are known to have high levels of FIBs. Knowing and understanding what specific events trigger high FIB levels is important to then identify the next steps to be taken to decrease the potential public health threat. In the Fall of 2022, an independent study was conducted over 7 weeks to gather information regarding how FIB levels in Deal and Sunset Lake fluctuate depending on rainfall events. A specific FIB, known as *Enterococcus*, was the primary bacteria that was analyzed during this experiment. Weekly water samples from several locations within each lake were collected and analyzed to determine mpn per 100 mL. It was hypothesized that elevated FIB levels would occur as a direct result from heavy rainfall. The results of this study suggested otherwise, in which there was neither a positive or negative relationship between rainfall and elevated FIB levels. This suggests the possibility that other factors were responsible for high or low FIBs. The results provided evidence for a separate explanation, displaying a possible relationship between FIBs and site location.

ASSESSING THE IMPACTS OF SEA-LEVEL RISE ON BIRD AND MAMMAL POPULATIONS IN MONMOUTH AND OCEAN COUNTY COASTAL FORESTS

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Faculty Mentors: Dr. Pedram Daneshgar and Dr. Sean Sterrett, Department of Biology, MEBP Program

ABSTRACT

Coastal forests are ecosystems that serve as crucial habitats for countless plant and animal species. These areas provide wildlife with the resources they need to survive and sustain their populations. Researchers are witnessing the death of coastal woodlands across New Jersey and the rest of the northeast. As saltwater encroaches upon a healthy freshwater forest, the salt intake by trees results in their death, and ultimately the functions of the ecosystem change.

The goal of this project is to assess the differences in wildlife composition and ecosystem services between healthy coastal forests and dead ghost forests in Toms River and Sandy Hook, New Jersey. Evidence of wildlife sightings, acoustics, and activity, such as scat and nests, were recorded to provide data on wildlife populations within each ecosystem. This research hypothesized that there is a significant decline in wildlife biodiversity and mammal abundance in ghost forests compared to healthy forests because of climate change-induced sea level rise. Although detection methods were similar between these two ecosystems, wildlife presence and their use of the environment were vastly different. Bird species, such as the osprey, *Pandion haliaetus*, were observed within ghost forests where they mainly utilized dead trees as spots to perch, but no mammals were seen in this ecosystem. The absence of mammals within ghost forests is an alarming consequence of climate change and its effect on wildlife populations in coastal areas. The information gathered from this research could be applied to wildlife population studies and further research regarding ecosystem transitions and subsequent habitat alterations. Understanding the complexity of environmental changes and how entire wildlife communities can be negatively affected may be valuable for future studies that aim to protect wildlife species from displacement and vulnerability.

EXPLORING RESTORATION STRATEGIES
FOR SALT FLOODED MARITIME FORESTS

Emma Gould
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Faculty Mentor: Dr. Pedram Daneshgar, Department of Biology, MEBP Program

ABSTRACT

The frequency of storm surges, sea-level rise, and saltwater intrusion events that threaten native maritime forest species are projected to increase due to climate change. It is vital to have restoration strategies in place for when such events occur to reestablish ecologically productive ecosystems before invasive species begin to dominate the area. This study investigated which salt-tolerant species would be best to introduce to an affected ecosystem after a salt-flooding event and after how much rainfall they should be planted to optimize plant health. To accomplish this, a greenhouse experiment was conducted, testing six native species planted at three different times after an initial salt-flooding event. A watering regime that mimics monthly precipitation in the region was used to maintain the plants. Plant health was quantified via a health index, with scores recorded weekly throughout the experiment. Findings suggest species such as *Iva frutescens*, *Spartina alterniflora*, and *Panicum virgutum* tolerate higher soil salinities than species like *Liquidambar styraciflua* or *Juniperus virginiana*. This implies that creating a salt marsh ecosystem may better support plant health and biodiversity than creating a maritime forest ecosystem after a salt-flooding event occurs. Identifying which native species can withstand the effects of salt-flooding and thereby restore salt-affected areas most effectively will help to safeguard our shores against the impacts of climate change.

SPATIAL AND TEMPORAL PATTERS OF THE PROHIBITED
ATLANTIC ANGEL SHARK, *Squatina dumeril,* WITHIN THE MID-ATLANTIC BIGHT

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ABSTRACT

Globally, Angel sharks (*Squatina* spp.), are one of the most threatened species of sharks with more than half of the 22 extant species currently classified as Threatened on the IUCN red list. Atlantic angel sharks (*Squatina dumeril),* are a "data deficient" species that ranges along the east coast of the US and is currently federally prohibited from being harvested. Distribution of this species along the east coast has been found to vary with depth and season. The objective of this study was to evaluate the spatial and temporal distribution of Atlantic angel sharks in the Mid-Atlantic Bight, through analysis of long-term coast wide offshore bottom trawl surveys conducted by the NJDEP, SEAMAP, and NMPS. Surveys were conducted seasonally and ranged from the Gulf of Maine to Cape Canaveral, FL which covers the Atlantic angel shark's entire geographic range. The highest number of angel shark captures on the Northeastern coast occurred the summer season, and the highest number of captures on the Southeastern coast occurred in the winter season. A small subset of sharks (n=5) was surgically implanted with Vemco acoustic transmitters to evaluate long-term movements within this region. Sharks were detected at 22 different sites (n=1,388 unique detections) along the coast with most of the detections occurring off MD and NC. This information shows strong northerly summer and southerly winter migrations. Data also showed that Atlantic angel sharks migrated away from nearshore habitat in the winter months and were almost exclusively found offshore until early spring. Since Atlantic angel shark populations with the US are "data deficient", this information can is important in the understanding and conservation of this species.

ARE STRIPED BASS (*Morone saxatilis*) OVERWINTERING
IN THE MANASQUAN RIVER ESTUARY?

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and Nico Landino[1]**

Department of Biology[1,2], Marine and Environmental Biology and Policy Program[2]

**Faculty Mentor: Dr. Jason Adolf, Dr. Maddie Balman and Assistant Dean John Tiedemann
Department of Biology, MEBP Program**

ABSTRACT

Striped bass (*Morone saxatilis*) begin to move into overwintering habitats as water temperatures cool in late November or early December. Some stripers winter in nearshore ocean waters; other coastal migrants overwinter where spawning occurs including the Hudson River, the Delaware River, and the Chesapeake Bay and its tributaries while others overwinter in non-natal rivers and bays along the coast from New Jersey to North Carolina. Information on the overwintering habitats of striped bass within estuaries and coastal rivers is limited and poorly understood. The location and extent of optimal inshore overwintering habitats likely vary among years. Typical inshore overwintering locations that have been identified include sheltered harbors and embayments, tidal creeks, sluggish river pools, and adjacent freshwater areas. Inland winter aggregations in northern waters occur primarily in sheltered habitats where the threat of displacement by tidal action or runoff driven currents is minimal. The objective of this project is to do a preliminary study using environmental DNA (eDNA) techniques to determine whether the Manasquan River is an overwintering habitat for striped bass. Analysis of eDNA from water samples has become an established method for determining species presence in a particular location. For the purpose of this preliminary study, the Manasquan River Estuary was divided into two zones, the lower and the upper estuary. Four locations in each zone were sampled once monthly November – March. Water temperature and salinity was measured at each sampling site and surface water samples were collected for eDNA analysis. In the lab, DNA was extracted from each sample using a Qiagen DNeasy PowerWater extraction kit following the manufacturers protocol. Final analysis will be accomplished using a species-specific real-time qPCR TaqMan assay that uses 102-bp fragment from the cytochrome c. oxidase subunit I (COI) mitochondrial marker to detect striped bass.

ANALYZING THE ABUNDANCE AND TYPES OF MICROPLASTICS FOUND ON HATHAWAY BEACH IN DEAL, NEW JERSEY

Nicole Cappolina

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Faculty Mentor: Assistant Dean John Tiedemann

ABSTRACT

The rise in global plastic production in recent decades has caused an influx of plastic debris in the natural environment and continues to cause harm to many organisms. Microplastics (MP's) are fragmented from larger plastics and are defined as 5mm or less in size on average. MP's can enter the environment through a variety of sources and can be found in different colors, shapes, or sizes. The abundance of microplastics present on beaches pollutes the marine environment and can be detrimental to the health of both wildlife and humans. Wildlife can ingest plastics or become entangled by them. Additionally, bivalves can filter feed microplastic particles and develop diseases that affect the aquaculture industry. Plastics are also found in many everyday products that humans ingest. This study examined types, quantities, and distribution of microplastics found on Hathaway Beach in Deal, NJ and compared the results to baseline data found for this beach in the spring of 2022. The data showed that 42 plastic items were collected in the current study, compared to 89 plastics found in the preliminary data. The most common type found was fragments, while preliminary data from the baseline survey found that the most common type was films. It is important to analyze the abundance of plastics in the natural environment in order to pinpoint sources and develop mitigation strategies or improve management programs to help reduce plastics in the environment and prevent further harm from wildlife and humans.