

MONMOUTH
UNIVERSITY

SCHOOL *of* SCIENCE

13th ANNUAL
SUMMER RESEARCH PROGRAM
SYMPOSIUM

AUGUST 12, 2021

10:30 AM – 1:00 PM

ERLANGER GARDENS

Dear Friends,

I would like to take this opportunity to thank the supporters and university partners who contributed to the success of the 2021 Monmouth University School of Science Summer Research Program (SRP). Their contributions allow us to provide research opportunities for undergraduate students by funding their summer salaries as research assistants, acquire the supplies and equipment necessary to complete their research projects, and providing opportunities for students to travel to conferences and professional meetings to present their research. Without their collective philanthropy and support, the Summer Research Program would not be possible.

I would also like to acknowledge the faculty from the School of Science who dedicated their time and offered their expertise to mentor participating students.

Lastly, I offer congratulations to the student research assistants for their efforts and enthusiasm in completing their projects that are highlighted at today's Summer Research Program Symposium.

John A. Tiedemann, Assistant Dean
Monmouth University School of Science

2021 School of Science Summer Research Program

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2021 School of Science Summer Research Program

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Karly Nolan

Faculty Mentor: Dr. Jason E. Adolf

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Carrington Retzios

Faculty Mentor: Dr. Pedram Daneshgar

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Faculty Mentor: Dr. Davis Jose

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Faculty Mentor: Dr. Ilyong Jung

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Noah Rediker
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Faculty Mentor: Dr. Jiacun Wang

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Urban Coast Institute

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Faculty Mentor: Dr. Katerine Ramirez and Dr. Geoffrey Fouad

Department of Biology

BY-1

**GEOSPATIAL REPRESENTATION OF LOWER HUDSON RARITAN ESTUARY
WATER QUALITY**

**Nicholas Box
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Jason E. Adolf, Monmouth University Department of Biology**

**Funding Sources:
Monmouth University School of Science, Department of Biology, and Urban Coast Institute**

Abstract

The lower Hudson Raritan Estuary is a complex, urban, tidal water body that includes Raritan Bay, Sandy Hook Bay, the Navesink and Shrewsbury Rivers as well as influence by the Hudson River plume. The aim of this research was to collect spatially-explicit phytoplankton and water quality data from the lower Hudson Raritan Estuary to identify areas of disproportionate phytoplankton abundance or other parameters that might indicate poor ecosystem conditions. It was hypothesized that clear phytoplankton hotspots would arise and be sustained in near shore locations. Eight different water quality parameters were collected over ten weeks and all data were processed using R Studio. Implementation of underway data flow sampling was integral to the project as it allowed for the creation of maps that display real time, georeferenced water quality and phytoplankton data that do not exist elsewhere. Maps produced in this project suggest a system that is of predominantly good ecological status except for a few ‘hot spots’ that may be cause for concern.

BY-2

**DEVELOPING HARMFUL ALGAL BLOOM FORECAST MODELS
FOR MONMOUTH COUNTY, NJ COASTAL LAKES**

Karly Nolan

Monmouth University Department of Biology

Faculty Mentor:

Dr. Jason E. Adolf, Monmouth University Department of Biology

Funding Sources:

Monmouth University School of Science, Department of Biology, and Urban Coast Institute

Abstract

Coastal lakes in Monmouth County, New Jersey have previously demonstrated evidence of harmful algal blooms (HABs). HABs are an environmental threat in freshwater systems with the potential to produce potent neuro- and hepatotoxins that may ultimately limit access to and use of coastal lakes. HAB events can be highly irregular year-to-year and consequently difficult to predict as multiple variables may trigger HAB events. The purpose of this research was to begin development of a HAB forecasting model for Monmouth County coastal lakes. This research was conducted as part of the Coastal Lakes Observing Network (CLONet), using weekly time series of HAB abundance and environmental data from spring / summer 2019 to 2021. This research was a first step into creating a forecasting model for local HAB events by examining autocorrelation of HAB abundance as well as cross-correlations between HAB abundance and environmental parameters including temperature, rainfall and solar radiation. The ability to forecast HABs will become increasingly useful as HABs are predicted to intensify in the future with greater temperature and precipitation, in addition to expanding human development, all of which can influence the ecology of coastal lakes. Continuing to develop HAB forecasting techniques will allow environmental managers to better predict, prepare for, and respond to HAB events in the future.

BY-3

**COMPARATIVE SOIL ANALYSIS OF HEALTHY MARITIME FORESTS
AND GHOST FORESTS**

**Carrington Retzios
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Pedram Daneshgar, Monmouth University Department of Biology**

**Funding Sources:
Monmouth University School of Science, Department of Biology, and Urban Coast Institute**

Abstract

Maritime forests consist of numerous flora that support a large ecological diversity. A phenomenon that is becoming increasingly common is the appearance of ghost forests - former vibrant maritime forests that have been replaced by dead trees. The causation of ghost forests point towards climate change induced sea level rise leading to salt intrusion into forests which is detrimental for trees. Understanding the soil of maritime forests serves as an important tool for describing them, as soil properties can dictate the growth, development, and distribution of the vegetation. Additionally, soil analysis can potentially be an important tool in describing the puzzling ghost forest, and lead to conclusions about its existence. By comparing samples of soil from healthy maritime forests with ghost forests, variances between the samples were observed that point to specific impairments in ghost forests. Identifying the impairments that contribute to ghost forests is crucial in describing their origin, of which there is little published literature. 10 samples each of healthy soil and ghost forest soil were obtained from two sites -- Catus Island County Park and Sandy Hook National Recreation Area. Of the 40 total samples, nutrient testing, dissolved solids, salinity, respiration rates, pH, and moisture content were tested in 10 randomly selected healthy and ghost soils, with 5 samples coming from each site. The nutrients tested were nitrogen, phosphorus, and potassium, which in combination are indicative of soil fertility. Respiration was measured with a respirometer. The other parameters were measured with digital meters. The most significant disparities between the healthy and ghost samples were in salinity and moisture. The ghost soil samples were more saline, and more wet than the healthy soils. This information can be used to reaffirm the formation of ghost forests via saltwater intrusion.

BY-4

**DIFFERENCE IN WILDLIFE OBSERVATIONS BETWEEN COASTAL AND GHOST
FORESTS ACROSS NEW JERSEY**

**Emma Cusano
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Pedram Daneshgar, Monmouth University Department of Biology**

**Funding Sources:
Monmouth University School of Science, Department of Biology**

Abstract

Coastal forests are important ecosystems for hosting a variety of plant and animal species. These communities provide wildlife with the resources and habitat they need to survive and sustain their populations. Researchers have begun to witness emergence of ghost forests, coastal wetlands characterized by dead trees across New Jersey and the Atlantic coast due to climate change induced rising sea levels, bringing in saltwater that overtakes the existing freshwater coastal trees rely on for sustenance. This research focused on how wildlife species are impacted by the increasing presence of ghost forests that have stripped away areas for food and shelter, particularly through observation and identification. Recording evidence of wildlife sightings, acoustics, and activity, such as herbivory and nests, has provided extensive data on the existence of animal species within ghost forests compared to that of healthy coastal forests. Throughout the past few weeks, it has been noted that although detection of wildlife was similar between these two ecosystems, animal activity and their use of the environment around them was vastly different. While animals depend on coastal forests for ample food resources and various shelters, many wildlife species observed in ghost forests, which were mainly birds, only used the dead trees as spots to perch upon. Understanding the complexity of environmental changes and how entire communities of wildlife can be affected negatively may be useful for future studies that aim to protect wildlife species from displacement and vulnerability.

BY-5

CHARACTERIZING MARITIME FORESTS IN NEW JERSEY FOR OUTREACH

**Keilan Swanzey and Jagger Turano-Riley
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Pedram Daneshgar, Monmouth University Department of Biology

Funding Sources:

Monmouth University School of Science and Department of Biology

Abstract

Maritime forests are coastal forests that primarily form on sandy soils on barrier islands and spits where they are exposed to salt spray. These ecosystems are essential for coastal resilience and stabilizing the shoreline. They offer shelter to support a diversity of plants and animals, while protecting the mainland from strong weather patterns such as hurricanes and flooding. Along the coastline of New Jersey, these forests now only make up about 1% of the land and face challenges regarding conservation as they are not identified as an ecosystem worth conserving. Instead, the majority of the shoreline is home to beach-side residences and other land developments. In order for the remaining maritime forests to be conserved they need to be characterized and described to be shared to local coastal communities. In this study, maritime forests were examined in order to gain a better understanding of what lives within this environment and to share this information to communities across the state. By doing so, samples of various coastal species, both native and exotic, were collected in order to create a comprehensive herbarium collection to represent the diversity of maritime ecosystems. Within a year, we are hoping to have samples of every maritime species with the exception of threatened and endangered plants. While visiting the various sites across the state, video documentation was also recorded in order to create an outreach video that educates the public what maritime forests are, how they are impacted, and possible strategies for conservation in hopes to spread awareness of the significance of these forests.

BY-6

**EXPLORING SALT TOLERANCES OF LICHENS IN NEW JERSEY
COASTAL ECOSYSTEMS**

**Emily Vasquez
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Pedram Daneshgar, Monmouth University Department of Biology**

**Funding Source:
Urban Coast Institute**

Abstract

As climate change causes sea levels to rise and increased storm surge and intensity, coastal ecosystems may face changing environmental conditions of increased salinity. Lichen, whose range includes coastal ecosystems, are unique organisms comprised of algae and cyanobacteria living in a symbiotic relationship with fungus. They're able to attach to obscure surfaces such as trees and rocks and survive in harsh conditions such as drought, extreme heat and frost. Their unique abilities and their status as bioindicators make their presence or absence in a community valuable in providing information about ambient environmental conditions that may not be as easily ascertained by other species present. There is limited research on lichen distribution and salt tolerance, especially in New Jersey. Our objective was to determine how coastal lichens will respond to salt exposure that may come with climate change. To stimulate this, we set up a randomized block design testing 3 lichen species with six treatments of salt spray and salt water emergence. Functionality will be tested by weekly readings of chlorophyll content using a chlorophyll content meter (CCM 300), CO₂ emissions using a LI-6400XT Portable Photosynthesis System, and any changes in their appearance. This experiment will start at the beginning of the 2021 Fall Semester and continue until sufficient results are obtained. The goal of this experiment is to collect data on salt tolerances of coastal lichen for future habitat assessments and habitat restoration, and to add to the still small realm of lichen research data.

BY-7

**EXPLORING GHOST FORESTS: ASSESSING THE IMPACT OF STORM SURGE
AND SEA-LEVEL RISE ON COASTAL FORESTS**

**Ashley Pastore
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Pedram Daneshgar, Monmouth University Department of Biology**

**Funding Sources:
Monmouth University School of Science, Department of Biology**

Abstract

Ghost forests, or areas of dead trees that were once a coastal forest, are becoming more and more common along the coastline of New Jersey. This is because an increase in storm surges, associated with sea level rise induced by climate change, has caused forests to be flooded with saltwater. Sea level rise has allowed for bordering salt marshes to encroach upon coastal forests as well. The ecology of ghost forests has not been described. Specifically, community composition and ecological function of ghost forests are not known. The purpose of this project was to compare the floral composition of a ghost forest to the coastal forests they once were and the salt marshes they may become, in order to better understand ghost forest ecological function. Cattus Island County Park in Toms River, NJ was the study site for this project. The park features several ecosystems including our four study treatments: healthy coastal forest, ghost forest, salt marsh, and transitional areas. Quadrats were established, and within each, species present and percent coverage were collected. With a full picture of the species found in each treatment and an understanding of their functional role, predictions can be made on the future of these ecosystems and their ecological significance. As climate change ultimately begins to leave its mark on New Jersey, this project can help ecologists and coastal engineers alike in planning for what is to be expected in coastal forests should the anticipated projections continue on their given course.

BY-8

**DEMOGRAPHICS OF THE LAND-BASED CATCH AND RELEASE SHARK FISHERY
IN NEW JERSEY**

**Trinity Caratenuto¹, Bre DiRenzi¹, Danielle Dyson², Emily Greenemeier¹,
and Kerry McFeeters¹
Monmouth University¹, Stockton University²**

Faculty Mentor:

Dr. Keith J. Dunton, Monmouth University Department of Biology

Funding Sources:

**New Jersey Sea Grant Consortium, Monmouth University School of Science,
Department of Biology**

Abstract

Worldwide, many shark species are drastically declining due to variety of factors such as habitat loss as well as interactions with both recreational and commercial fishing. However, despite common misconceptions, recreational fishing has surpassed the commercial industry in the total amount of sharks landed within many fisheries. With its growing popularity particularly in NJ, uncertainties within recreational land-based shark fisheries including demographics of the species captured as well as capture stress, post release behavior, and survivorship need to be addressed. Working with anglers, we evaluated the demographics of land-based shark fishery throughout its peak time. In addition, fight time, total time out of water, and release practices were recorded to see if these variables correlated to certain behavioral responses or increased physiological stress. A total of 63 sharks were captured; 47 sandbar sharks (*Carcharhinus plumbeus*), 13 sand tiger sharks (*Carcharias Taurus*), 2 Atlantic sharpnose sharks (*Rhizoprionodon terraenovae*), and 1 spinner shark (*Carcharhinus brevipinna*). All sharks ranged in size between 63 cm to 265 cm. Fight time showed that most sharks were landed on average within 7 minutes and remained landed for an average of 5 minutes before being released back into the ocean. A sub-set of sharks (n=18) were tagged with pop-off satellite tags (Wildlife Computers SPAT tags) attached behind dorsal fins to evaluate short-term post-release response and behavior for up to 45 days. For longer term observations of survival and understanding movements and migrations (n=19) were surgically implanted with acoustic telemetry tags (Vemco V16-6H). As more data comes back from satellite tags, we can evaluate the post release responses and mortality from these sharks and hopefully link it to certain practices observed. Overall, this data can provide information to make recommendations in New Jersey's land-based shark fisheries to aid in conservation and management of these species involved.

BY-9

**ANTI-COVID MICRORNA THERAPY BLOCKS THE EXPRESSION
OF THE SPIKE GENE OF SARS-COV2**

**Laura Sine, Victoria Demarco, Thomas Hintelmann, Flobater Gawargi
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Martin J. Hicks, Monmouth University Department of Biology

Funding Sources:

Bristol Myers Squibb, Monmouth University School of Science, Department of Biology

Abstract

Emerging viral diseases have increased in recent decades. In December 2019, an epidemic with low respiratory infections emerged in Wuhan, China. The disease, Covid-19 was found to be caused by a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). As of July 29, 2021, WHO has confirmed 195,886,929 global cases and 4,189,148 deaths worldwide, 606,686 in the USA. Fortunately, a vaccine has recently been approved, yet there are no therapeutics for infected individuals, and the threat of emerging vaccine-resistant strains remain. From advances in biotechnology, the genome and structure of SARS-CoV-2 is known. Three proteins are anchored in the viral envelope, Spike (S), Envelope (E), and Membrane (M), which is linked to the Nucleocapsid (N) protein connecting to the viral RNA genome. Our lab is developing an innovative therapy that delivers multiple therapeutic microRNAs to block the expression of distinct Covid viral proteins. The design of the anti-Covid microRNAs 1) mimics human microRNA cluster 17-92a structural stability, 2) forms guide-RNA substrates for the RNA induced silencing complex, and 3) are complementary to specific regions of the SARS-CoV-2 RNA genome without off-targets effects in the human genome. Twenty-one microRNA sequences were designed to target the S gene, six for N, two for M, and one for E. These were cloned into our microRNA-17-92 therapy vector which expresses six distinct anti-Covid RNA therapeutics simultaneously. We have transfected the S gene into our tissue culture model to measure the efficacy of the anti-Covid microRNA therapy to down-regulate the S gene expression. In our preliminary experiments we show a significant reduction in the Spike mRNA. Next steps are to examine the secondary structure of our RNA therapy using SHAPE-MAP to optimize RNA therapeutic stability in comparison to the stable structure of the original Mir-17-92a.

BY-10

**GENE THERAPY FOR BRAIN TUMORS: IDENTIFICATION OF NEW
THERAPEUTIC TARGETS BASED ON RNA STRUCTURE**

**Thomas Hintelmann, Laura Sine, Victoria Demarco, Flobater Gawargi
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Martin J. Hicks, Monmouth University Department of Biology

Funding Sources:

Bristol Meyers Squibb, Monmouth University School of Science, Department of Biology

Abstract

Individuals diagnosed with glioblastoma multiforme (GBM) have a short life expectancy of 12-15 months. This project is to develop therapies for effective and continuous drug delivery to the brain, targeting cancer-driving genes. Tumor cell proliferation in GBM is often stimulated by epidermal growth factor receptor (EGFR) and is important for tumor cell survival. In our lab, we are developing RNA therapies to alter the splicing mechanism of EGFR to block its activation, thus stop tumor cell growth. Our approach uses an adeno-associated virus gene transfer vector encoding RNA therapeutics targeting critical elements of the EGFR pre-mRNA transcript. We have examined the 'pre-mRNA structurome' of EGFR to evaluate the accessibility of targetable regions. To advance our therapeutic strategy, we have analyzed the secondary structure of the EGFR transcript using selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). SHAPE-MaP reactivity profiles were generated revealing the structure of splicing and cryptic polyadenylation signal (PAS) elements within the targeted region. We identified enhancer binding motifs surrounding the 5' splice site and hidden elements of a cryptic polyadenylation signal. Based on these structural profiles, we generated RNA therapies that interact with structural elements to unravel the hidden polyadenylation signal with the potential to activate expression of the short therapeutic isoform. In this project, we cloned these therapies into our therapeutic delivery platform and tested their efficacy to alter EGFR gene expression in tissue culture cells. Currently, we are evaluating *in vitro*, the therapeutic RNA interaction with the target sequence of the EGFR pre-mRNA transcript.

BY-11

**THE SYNERGISTIC EFFECTS OF ESSENTIAL OILS (EOs) ON THE GROWTH OF
MULTIDRUG RESISTANT *Enterobacter cloacae* and *Pseudomonas aeruginosa***

**Gabriella Cleven and Jackalyn Durante
Monmouth University Biology Department**

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

**Funding Sources:
Kevin Young '89, Monmouth University School of Science, Department of Biology**

Abstract

In recent years, the overuse of antibiotics has resulted in bacteria evolving to become resistant, rendering many of these drugs ineffective in modern medical treatment of bacterial infections. Two specific bacteria highlighted in the 2019 antibiotic resistance report from the CDC include: *Enterobacter cloacae* (*E. cloacae*) and *Pseudomonas aeruginosa* (*P. aeruginosa*). These bacteria primarily infect immunocompromised people in nosocomial settings such as the intensive care unit (ICU).

Initially, 102 essential oils (EOs) were tested against *E. cloacae* and *P. aeruginosa* at 100% concentration on Muller Hinton II agar. This testing was done using the Kirby-Bauer Disk Diffusion Test. Of the 102 EOs tested, arborvitae, cassia, cinnamon bark, oregano, and thyme proved to be very effective in inhibiting the growth of *E. cloacae* while cassia, cinnamon bark, cumin, cypress, and siberian fir were effective against *P. aeruginosa*. The minimum inhibitory concentration (MIC) of these select EOs were determined by preparing dilutions using jojoba oil. The zones of inhibition were measured for all plates after 24 hours of incubation at 37°C.

To determine the synergistic effects between these select EOs, various dilutions were prepared using jojoba oil and the MIC was determined for each pair. Then the fractional inhibitory concentration (FIC) index was calculated to estimate the interaction between two essential oils. The results showed that the effectiveness of the pairs made from arborvitae, cassia, cinnamon bark, oregano, and thyme against *E. cloacae* were additive. The pairs made from cassia, cinnamon bark, cumin, cypress, and siberian fir against *P. aeruginosa* showed that cassia with siberian fir, and cinnamon bark with siberian fir had an indifferent effect, while cassia with cypress, cumin with cypress, and cumin with siberian fir were synergistic. The remaining combinations were additive. Future research will include synergistic testing of the EOs with the leading antibiotics.

BY-12

**THE IMPACT OF DIET AND GENETIC BACKGROUND ON PATTERNS OF GENE
EXPRESSION IN HOUSE MICE FROM AMERICAS**

Nico Landino

Monmouth University Department of Biology

Faculty Mentor:

Dr. Megan V. Phifer-Rixey, Monmouth University Department of Biology

Funding Sources:

Bristol Myers Squibb, Monmouth University School of Science, Department of Biology

Abstract

Body size in house mice (*Mus musculus domesticus*) follows Bergmann's Rule, the observation that size tends to be correlated with latitude, with larger animals at higher and typically colder locations. New wild-derived strains of house mice from New York, Brazil, Arizona, Florida, and Canada, are prime examples of this rule. Nevertheless, the underlying mechanism driving Bergmann's Rule is not yet fully understood. Previous results pointed to specific genes that may contribute to variation in body size in house mice. In particular, there is strong evidence that changes in regulatory regions are important. However, it is not yet known how changes in the environment might affect body size and which genes may be involved in that response. In this study, male and female mice from different locations have been fed a typical breeder diet or a high fat diet in order to both evaluate the impact on size and on patterns of gene expression. Extracting RNA from the liver, an organ with high metabolic activity, will help identify genes involved in response to a change in diet. After extraction, RNA will be used to generate RNA-seq libraries for further bioinformatic analysis. When complete, this work will help identify genes that contribute to Bergmann's Rule in house mice.

BY-13

eDNA AS A TOOL FOR MONITORING TURTLE SPECIES IN COASTAL LAKES

**Delaney Mestey-Jones
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Megan V. Phifer-Rixey, Monmouth University Department of Biology**

**Funding Source:
Urban Coast Institute**

Abstract

Environmental DNA (eDNA) is DNA that is shed by organisms into the environment. eDNA can be used as a genetic tool, helping scientists determine if specific wildlife species are present without disrupting habitat. In our study, the goal was to develop a protocol for using eDNA to detect the presence of turtle species in coastal lakes around Monmouth County. The coastal lakes provide important habitat for many taxa, but surveying turtles with traditional methods is time intensive. We sampled water from Monmouth County coastal lakes and filtered the samples to collect eDNA. We then extracted DNA from the filters and quantified it. Samples from areas known to have turtles of interest were also collected as positive controls. Species specific primers will be used amplify the DNA via polymerase chain reaction to determine the presence or absence of different turtle species in the lakes. In addition, we are refining this approach into a teaching protocol to bring eDNA into high school and undergraduate courses. Overall, this research will both help evaluate eDNA as a tool for monitoring ecologically important species and as a tool for education and outreach.

BY-14

**VARIATION IN TRAITS RELATED TO REPRODUCTION IN NEW STRAINS OF
WILD-DERIVED MICE FROM THE AMERICAS**

**Julia Panebianco and Caroline Reverendo
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Megan V. Phifer-Rixey, Monmouth University Department of Biology

Funding Sources:

Bristol Myers Squibb, Monmouth University School of Science, Department of Biology

Abstract

Populations of wild house mice (*Mus musculus domesticus*) from the Americas show evidence of environmental adaptation. For example, mice from different climates differ in body size and nesting behavior. Preliminary results also indicate differences among populations in traits related to reproduction. Such traits are fundamental to fitness but are often hard to study in wild populations and their role in environmental adaptation is not yet known in this system. Here, we report the results of a preliminary, observational study of maternal care behaviors in new wild derived strains from the Americas. Maternal care includes, but is not limited to, huddling, retrieval of pups, and nest-building. We used video monitoring of the home-cage to observe natural behaviors of mothers 3-5 days post-birth with minimal disruption. Behavioral events were recorded, and time spent engaged in classes of events was quantified for over forty mice. Preliminary results suggest variation in maternal care behaviors among the different populations and data collection is ongoing. In addition, we propose a new study of a different aspect of maternal care, ultrasonic vocalization among mothers and pups. Overall, this research will help us better understand the role of reproductive traits and life history strategies in adapting to different climates.

BY-15

**EVALUATION OF COASTAL LAKES AS TURTLE HABITAT IN
MONMOUTH COUNTY, NEW JERSEY**

**Megan Malaty and Christopher Meehan
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Sean C. Sterrett, Monmouth University Department of Biology

Funding Sources:

Urban Coast Institute, Monmouth University School of Science, Department of Biology

Abstract

Suburban areas represent fragmented landscapes with high human density. Suburban coastal lakes in New Jersey were originally estuaries that were built for freshwater resources, recreation, and aesthetics but also represent most of the remaining freshwater habitats for wildlife on the coast. Many turtle species live in coastal lakes and require specific habitat characteristics to meet their needs, including nesting and basking habitats, connectivity for movement around lakes, and riparian habitats that protect from human disturbance. Additionally, the non-native red-eared slider (*Trachemys scripta elegans*) has been introduced to most coastal lakes due to their long-term link to the pet trade. Coastal lakes have potential to be suitable wildlife habitat; however, there are few examples of explicit wildlife management in coastal lakes. We evaluated eight coastal lakes for necessary habitat requirements of freshwater turtles. First, we used basking surveys (3 visits) and hoop trapping (10 traps per lake, 1 night) to detect turtle species at each lake. Then we evaluated each lake based on nesting habitat, basking substrate, riparian buffers and potential for road mortality. Across lakes, we detected four common species but not all species were represented at each lake; many lakes were dominated by *T.s. elegans* (84% of captures during trapping). Some lake perimeters were made almost entirely out of constructed seawall which did not allow for nesting turtles to exit the lake. However, there was evidence of recruitment for native and non-native species. In situations where turtles could exit, they were immediately met by busy roads. Natural and constructed basking substrate were limited in most lakes, but turtles were found to use constructed substrate as diverse as concrete, boat ramps and islands. The dominance of red-eared sliders is concerning for the persistence of the Eastern painted turtle (*Chrysemys picta*) due to competition for basking substrate and food resources.

BY-16

**ASSESSING THE STATE AND DYNAMICS OF A TURTLE ASSEMBLAGE IN
LAKE TAKANASSEE, NEW JERSEY**

**Christopher Meehan and Megan Malaty
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Faculty Mentor:

Dr. Sean C. Sterrett, Monmouth University Department of Biology

Funding Sources:

Urban Coast Institute, Monmouth University School of Science, Department of Biology

Abstract

Highly suburbanized, coastal areas represent a challenge for all wildlife, but especially reptiles that require certain habitat characteristics, including connectivity to adjacent habitats, suitable nesting areas, basking substrate and refuge during extreme climatic events (e.g. extreme heat, drought, floods). Turtles are long-lived reptiles that inhabit suburban NJ coastal lakes and some species are robust to human modification, but are not immune to these impacts over longer temporal scales (i.e. effects on populations take time to realize). To understand the state and dynamics of turtles in a highly suburbanized landscape, we intensively surveyed a freshwater turtle assemblage using baited hoop traps in sections of Lake Takanassee, Long Branch, NJ, during summers from 2019-2021. Each captured individual was identified, measured, weighed, uniquely marked and released at its point of capture. Over 3 seasons, we made 326 total captures of 177 individuals across four species; Eastern painted turtle, snapping turtle, Eastern musk turtle and the non-native red-eared slider. Snapping turtles and painted turtles made up 29% and 44% of our individual capture but 91.1% and 8.4% of the total sampled turtle biomass, respectively. Non-native red-eared sliders made up 21% of individual capture. Further, we found partial partitioning of lake sections by painted turtles and red-eared sliders, which compete for limited resources. 18 turtles (10%) moved between sections of the lake separated by box culverts, suggesting that movement in response to temperature, direct human disturbance or resources is possible. We found a female bias for our most common species, snapping turtle (M:F; 0.73:1) and Eastern painted turtle (0.65:1), suggesting that road mortality is not influencing this population. Using single year, Schnabel closed capture-mark-recapture models, we also provide the first density estimates for commonly encountered species in Lake Takanassee.

BY-17

**MONMOUTH COUNTY BEACH NESTING BIRD
MONITORING AND STEWARDSHIP PROGRAM**

**Kerry McFeeters and Elizabeth Gill
Monmouth University Department of Biology**

Mentors:

Assistant Dean John Tiedemann, Monmouth University School of Science

**Christina Davis, Emily Heisler, Taleen Demirdjian, and Michael Heine
New Jersey Division of Fish and Wildlife**

Funding Sources:

**New Jersey Division of Fish and Wildlife Endangered and Nongame Species Program
Monmouth University School of Science**

Abstract

New Jersey beaches are popular tourist destinations, attracting thousands of visitors every summer. They are also a very important ecosystem for many species including beach nesting birds. The Piping plover (*Charadrius melodus*), American oystercatcher (*Haematopus palliatus*), Least tern (*Sterna antillarum*), Common tern (*Sterna hirundo*), and Black skimmer (*Rynchops niger*) are all beach nesting birds that are prominent in New Jersey's coastal zone. The Piping plover is federally listed as threatened and state listed as endangered, the Least tern and Black skimmer are both state listed as endangered, and the American oystercatcher and Common tern are both listed as state species of special concern. The Piping plover and American oystercatcher are territorial nesters, while the Least tern, Common tern, and Black skimmer are colonial nesters. These birds share nesting habitats and are facing threats including development, recreational beach use, and predation from foxes, crows, falcons, gulls, and even household pets.

The New Jersey Division of Fish and Wildlife (NJDFW) manages and monitors sites where these birds nest. During this internship, we worked with the NJDFW to maintain populations of these bird species throughout Monmouth and Ocean Counties. Surveys of the sites and populations were conducted daily, fences were maintained to delineate restricted areas to eliminate human disturbance to allow proper nesting to occur, and outreach was conducted to help educate beachgoers about conservation of these species. Although results of this year's nesting season have not been completely determined yet as some birds are still nesting and not all chicks have fledged, chick yields have been low this year mainly due to fox predation and flooding of many sites during storms.

Department of Chemistry and Physics

CE-1

Understanding the Conformational Polymorphism of DNA Using Fluorescent Base Analogues

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Faculty Mentor:

Dr. Davis Jose, Monmouth University Department of Chemistry and Physics

Funding Sources:

Monmouth University School of Science, Department of Chemistry and Physics

Abstract

The deoxyribonucleic acid (DNA), the genetic information carrier of living organisms, is highly malleable and exhibits conformational polymorphism. Apart from the classic Watson-Crick B-form double helix, it can adopt other structures such as A-form, Z-form, G-quadruplexes (GQs), i-motif, etc. This polymorphism exhibited by DNA is crucial in the execution of many important biological processes. It is known that the A-form DNA is involved in DNA packaging and the GQ structures found at the guanine-rich regions of DNA and RNA plays important role in cancer and aging. In this project, the structural intricacies of GQs were explored using three complementary spectroscopic methods, UV-Vis absorbance, Circular Dichroism (CD), and fluorescence spectroscopy. To understand the dependence of GQ stability on salt concentration, GQ thermal melting experiments were performed and the results showed that as the salt concentration increases the thermal stability of the GQs increases. To investigate the local conformation of guanine tetrads, the basic structural component of GQs, a synthetic DNA strand where the fluorescent analogue of guanine, 6MI, is incorporated site-specifically and the fluorescence changes are followed. The results showed that even with the incorporation of 6MI, stable GQs are formed and the local conformation can be tracked by following the fluorescence intensity changes of the probe. In the future, we aim to introduce therapeutically relevant small organic molecules to probe the effect of binding on the structure and stability of GQ structures

CE-2

**INVESTIGATION OF SWIMMING *PARAMECIA* UNDER VARYING
ELECTRIC FIELD**

**Nimra Nadeem and Shalom Saffer
Monmouth University Department of Chemistry and Physics**

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

**Funding Sources:
Bristol Myers Squibb, Monmouth University School of Science,
Department of Chemistry and Physics**

Abstract

Paramecia are unicellular organisms that are predominately studied in biology due to their abundant population in nature. Interestingly, they exert a stronger propulsive swimming force when swimming upward (against gravity) than when swimming downward (along gravity). This behavior, so called gravikinesis, is very surprising because it shows that *Paramecia* can sense their apparent weight, only $\sim 80\text{pN}$. In order to understand the underlying mechanism, we investigate how electric field and viscosity of the swimming medium influence on their gravikinetic response. In particular, we employ galvanotaxis technique that aligns a trajectory of swimming *Paramecia* with electric fields. The technique will allow us to analyze *Paramecia*'s swimming parameters describing their helical trajectories and the beating of their cilia. In this study, we will show our new experimental set-up and preliminary data about *Paramecia*'s trajectory changes as a function of electric field as well as a *Paramecium* culturing method using bacteria to multiply a single *Paramecium*.

**Department of
Computer Science and Software Engineering**

CSSE-1

NEURAL NETWORK-ENABLED IMAGE RECOGNITION WITH FPGAs

**Noah Rediker
High Technology High School**

**Faculty Mentor:
Dr. Joseph Chung, Monmouth University Department of Computer Science & Software
Engineering**

**Funding Sources:
Monmouth University School of Science
Department of Computer Science & Software Engineering**

Abstract

This research explored the topic of neural network-enabled image recognition using Field Programmable Gate Arrays (FPGAs). For real-time image recognition in the field using neural networks, FPGAs are an attractive option because of their low latency, portability and power efficiency. FPGAs are re-programmable integrated circuit devices whose logic can be changed as needed. Like Graphics Processing Units (GPUs), FPGAs excel at performing many simultaneous computations, making them suitable for parallelizable tasks such as neural network analysis. The learning curve of hardware design that is required to program FPGAs can be less of a hurdle with “high-level synthesis” (HLS) toolkits like LeFlow, which can be used to deploy Python/TensorFlow neural networks to FPGAs. The aims of this project were to assess the performance of FPGAs for machine learning applications and their accessibility for novice hardware designers. We trained various neural networks using Python and Tensorflow. Using LeFlow HLS, the networks were then deployed on low-cost FPGA hardware and tested to obtain metrics including image recognition performance, accuracy and power consumption. These metrics enabled comparisons to similar neural networks that were deployed using on-premise computers and cloud-based machine learning platforms with GPUs. Our intro-level FPGAs produced acceptable image recognition performance and accuracy, while using a fraction of the power required by CPUs/GPUs. We concluded that, while tools like LeFlow eliminate the need to manually program FPGAs with neural net code, hardware design training and expertise are still needed to develop real-world machine learning applications using FPGA hardware.

CSSE-2

ANALYZE A UNIVERSITY'S ASSESSMENT SYSTEM FOR ALIGNMENT WITH CURRICULUM

Isabella Chiaravalloti, Anna Nardelli

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Faculty Mentor:

**Professor Gil Eckert, Monmouth University Department of Computer Science
and Software Engineering**

Funding Sources:

**Monmouth University School of Science
Department of Computer Science and Software Engineering**

Abstract

Programs that receive ABET accreditation meet certain quality standards that assure the program's graduates are prepared for employment in computer science careers as they enter the workforce. Part of the accreditation process seeks to affirm that the courses taught reflect the advertised curriculum and embody the ABET accreditation outcomes. This project sought to develop a metric to gauge the level of alignment between course syllabi from the computer science (CS) curriculum at Monmouth University (MU) to descriptions found in the MU course catalog and to ABET computer science accreditation outcomes. A method called Natural Language Processing was used to analyze these documents for each course in the program. Documents were separated into lists of individual words, commonly called 'a bag of words'. Various Python libraries such as NLTK, pandas, and matplotlib were used along with Jupyter Notebook to produce the data used for comparison. From this, the frequency of each word was calculated, and compared to the other documents for each course. A formula was developed to calculate 'a measure of similarity' between the syllabus, the course catalog description, and the ABET outcomes. From the results, the research suggests that courses with a higher composite similarity measure are more closely aligned with the computer science curriculum at Monmouth University and with ABET computer science accreditation outcomes.

CSSE-3

AI SCHEDULING: CREATING A SYSTEM TO OPTIMIZED MATCHING SYSTEM

**Joshua Kim, Katherine Liu
Tufts University, Rutgers University**

Faculty Mentor:

**Professor Katie Gatto, Monmouth University Department of Computer Science
and Software Engineering**

Funding Sources:

**ICFNJ/Pfizer, Monmouth University School of Science, Department of Computer Science
and Software Engineering**

Abstract

Researchers engaged in the creation of a machine learning platform, designed to build and test a smart scheduling system. The system is optimized for matching between availability and needs students and available resources.

CSSE-4

DESIGN A MONMOUTH UNIVERSITY ENQUIRY CHATBOT WITH A NAO ROBOT

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Faculty Mentor:

**Dr. Jiacun Wang, Monmouth University Department of Computer Science
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Funding Sources:

**Bristol Myers Squibb, Monmouth University School of Science, Department of Computer
Science and Software Engineering**

Abstract

NAO is an autonomous and programmable robot with a long list of possible functions that involve topics such as human interaction, object sensing, and humanoid movements. NAO can be programmed by a user using the Python programming language, and the Choregraphe desktop application. In this project, we have programmed NAO to be a chatbot that can converse with humans and answer questions about Monmouth University, its department of computer science and software engineering, and the professors and programs within the department. The robot listens to the user and understands the key words of what he or she is saying in order to determine how it will respond. This project sets up a strong base for students to build on to explore more complex problems with NAO.

Department of Mathematics

MA-1

IS EVERY HERONIAN QUADRILATERAL A LATTICE QUADRILATERAL?

**Jacqueline Aquino, Alicia Caravella, Thomas Gresco, Emily Malool,
Brooke Tortorelli, and Antonio Vinagre,
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Faculty Mentor:

Dr. Susan H. Marshall, Monmouth University Department of Mathematics

Funding Sources:

ICFNIJ/Pfizer, Monmouth University School of Science, Department of Mathematics

Abstract

Heronian triangles are a specific type of triangle where each side length is an integer and the area is an integer. Researchers have proven that all Heronian triangles are lattice triangles, meaning they have integer placements on the coordinate plane. The aim of this research is to generalize this result to all Heronian quadrilaterals. To prove that the Heronian quadrilaterals are lattice, this research focuses on gathering data from special cases, such as Brahmagupta quadrilaterals, Newton quadrilaterals, and parallelograms. Brahmagupta quadrilaterals are cyclic Heronian quadrilaterals with integer diagonals. Newton quadrilaterals are Brahmagupta quadrilaterals where one side of the quadrilateral is the diameter of the circle. A Heronian parallelogram is a Heronian quadrilateral with two pairs of parallel sides. In order to determine whether these quadrilaterals are lattice, they must first be plotted on the coordinate plane. If the coordinates are integers, then the quadrilateral is lattice; however, if the coordinates are rational there is more work to be done. The next step would be to use Fricke's method, which finds a single rotation of the quadrilateral, moving each vertex to integer coordinates. The utilization of Fricke's method allowed for these quadrilaterals to be classified as lattice. By proving theorems centered around side lengths and diagonal triangles, it was proven that all Newton quadrilaterals and Brahmagupta isosceles trapezoids are lattice. We conjecture that all Brahmagupta quadrilaterals are lattice. The situation for Heronian parallelograms is more complicated, but we conjecture that certain Heronian parallelograms are lattice.

Urban Coast Institute

UCI-1

**FEMALE LABOR FORCE PARTICIPATION RATES VERSUS CHILDCARE
AVAILABILITY IN NEW JERSEY**

James Allan

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Dr. Geoffrey Fouad, Monmouth University Geographic Information Systems Program

Funding Source:

Urban Coast Institute Heidi Lynn Sculthorpe Summer Research Grant

Abstract

The labor force of a community is an important driver of its economy. Labor force participation reflects companies' access to workers, as well as people's access to job opportunities. However, as previous research and census data reveals, there are gender disparities of participation in the labor force in New Jersey. These disparities can be attributed to "traditional" household responsibilities, physical distribution of childcare amenities in New Jersey, and the financial and time costs of raising children. The present study examines the relationship between labor force participation by gender and licensed childcare facilities, focusing on their spatial distributions. We use employment and population data from the United States Census Bureau, and childcare facilities data collected from the State of New Jersey. We aggregate data at the census tract level, akin to an urban neighborhood. We use maps, hot-spot analyses of geographic clusters, and regressions to compare labor force participation rates to available childcare facilities. Results indicate that female labor force participation rates are generally larger in areas where childcare facilities are more available. The hot-spot analyses reveal geographic clusters of female labor force participation rates that are relative to clusters of childcare facilities, specifically in rural parts of central and south New Jersey where female labor force participation and the number of childcare facilities are both significantly low. In a regression controlling for age, income, and population, one additional childcare facility relates to an increase of 0.2 to 0.5 percentage points in labor force participation, and the increase is larger for females. Future work includes an analysis at smaller scales within the state to examine where the relation between female labor force participation and childcare availability is stronger (possibly in suburban communities) and weaker (possibly in communities where childcare does not happen at licensed childcare facilities).