

MONMOUTH
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SCHOOL *of* SCIENCE

12th ANNUAL
SUMMER RESEARCH PROGRAM
SYMPOSIUM

AUGUST 6, 2020

10:30 AM – 1:00 PM

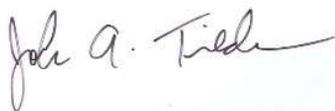
Virtual Zoom Sessions

Room 1 - <https://monmouth.zoom.us/j/91246468067>

Room 2 - <https://monmouth.zoom.us/j/95561377841>

Dear Friends and Colleagues,

I would like to take this opportunity to thank the supporters and university partners who contributed to the success of the 2020 Monmouth University School of Science Summer Research Program (SRP). Their contributions allow us to provide research opportunities for undergraduate and high school students by funding their summer salaries as research assistants, providing opportunities for students to travel to conferences and professional meetings to present their research, and acquire the supplies and equipment necessary to complete their research projects. Without their collective philanthropy, 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 the annual Summer Research Program Symposium.



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

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In addition to these corporate sponsors, Summer Research Program would also not be possible without the continued support of the School of Science Dean's Advisory Council along with a number of other University offices and programs, including Monmouth University's Office of the Provost and the Urban Coast Institute.

In addition, since its inception the program has benefited from contributions from faculty and staff from the Departments of Biology, Chemistry and Physics, Computer Science and Software Engineering, and Mathematics as well as alumni and friends of the School of Science.

12th ANNUAL SUMMER RESEARCH PROGRAM SYMPOSIUM

Thursday, August 6, 2020

Presentations by Department

Department of Biology

BY-01 Spatial And Environmental Variability Of HAB Abundance And Toxicity In Monmouth County Coastal Lakes

Karly Nolan

Faculty Mentor: Dr. Jason Adolf

BY-02 Comparing Phytoplankton Biomass And Species Composition Of Branchport Creek To Surrounding Shrewsbury Tributaries

Skyler Post

Faculty Mentor: Dr. Jason Adolf

BY-03 Post-Release Behavior And Survivorship Of Sharks In Land-Based Catch And Release Fisheries In New Jersey

Danielle Dyson and Breana DiRenzi

Faculty Mentor: Dr. Keith Dunton

BY-04 Determining The Migration Pattern Of Smooth Dogfish (*Mustelus canis*) Along The East Coast

Megan Malaty

Faculty Mentor: Dr. Keith Dunton

BY-05 Tracking Movements And Migrations Of Sandbar Sharks (*Carcharinus plumbius*) Along The East Coast Using Acoustic Telemetry Data For Management

Kerry L. McFeeters

Faculty Mentor: Dr. Keith Dunton

BY-06 Anti-Covid Microrna Therapy To Block The Expression Of The Spike, Envelope, Membrane, And Nucleocapsid Genes Of Sars-Cov-2

Flobater Gawargi

Faculty Mentor: Dr. Martin J. Hicks

BY-07 The Inhibiting Effects Of Essential Oils (Eos) On The Growth Of Multidrug Resistant *Acinetobacter baumannii*, *Enterobacter cloacae*, And *Pseudomonas aeruginosa*

Amanda Zappacosta, Gabriella Cleven, and Jackalyn Durante

Faculty Mentor: Dr. James P. Mack

BY-08 Differences In Behavior Among House Mice From Different Climates

Jesse Bragger

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-09 Using Environmental DNA (eDNA) to Track Black Sea Bass and Winter Flounder in a Controlled Tank Environment

Cameron Gaines

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-10 Using Microsatellite Genotyping To Characterize Migration Patterns In Striped Bass

Elizabeth Gill

Faculty Mentors: Dr. Megan Phifer-Rixey and Assistant Dean John Tiedemann

BY-11 Immune Function In Mice From Different Wild Derived Strains Subject To High Fat Diet

Jessy Khalil

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-12 The Relationship Between Maternal Body Size, Litter Size, And Body Size In Wild Derived Mouse Strains From The Americas

Julia Panebianco

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-13 Observing Differences In Maternal Care Among Different Strains Of Wild-Derived Mice

Caroline Reverendo

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-14 Turtles Of Lake Takanassee: How Does This Assemblage Persist?

Angelina K. Ireland and Sara R. Grouleff

Faculty Mentor: Dr. Sean Sterrett

Department of Chemistry and Physics

CE-1 Gravikinesis In Parmecium Cadatum And Its Effects On Motion Behavior

Jonah Resnick and Jacob Rappaport

Faculty Mentor: Dr. Ilyong Jung

CE-2 Coupling mechanism of ion gradient to torque generation and independent stator function of bacterial flagellar motor in Escherichia Coli (E. Coli)

Robert Zuback and Cassandra Fauber

Faculty Mentor: Dr. Ilyong Jung

CE-3 Thiazole-Based Peptoid With Methoxy Substituents As A Potential Anticancer Agent: A Computational Study

Olivia Enny

Faculty Mentor: Dr. Yana Kosenkov

CE-4 Oxazole-Based Peptoid With Methoxy Substituents As A Potential Anticancer Agent: A Computational Study

Roxy Nicoletti

Faculty Mentor: Dr. Yana Kosenkov

CE-5 Thiazole-Based Peptoid With Isopropyl Substituents As A Potential Anticancer Agent: A Computational Study

Amanda Prascsak

Faculty Mentor: Dr. Yana Kosenkov

CE-6 Thiazole-Based Peptoid With Isopropyl Substituents As A Potential Anticancer Agent: A Computational Study

Johanna Vonderhorst

Faculty Mentor: Dr. Yana Kosenkov

Department of Computer Science and Software Engineering

CSSE-1 NAO Robot Programming

James Cevalco and Aaron Nitzberg

Faculty Mentor: Dr. Jiacun Wang

CSSE-2 A Training Application For Time Management Skill

Bradley Xu and Youwei Huang

Faculty Mentor: Dr. Cui Yu

CSSE-3 Predicting ICU Length Of Stay For Heart Failure Patients Using Machine Learning Methods

Kevin Yuan

Faculty Mentor: Dr. Ling Zheng

Department of Mathematics

MA-1 Employing Thresholding And Wavelet Transformation To Remove Noise From An Audio Signal

Mackenzie Dalton

Faculty Mentor: Dr. Joseph Coyle

MA-2 Confdist: Development Of An R Package For Statistical Inference With Confidence Distributions

Odalys Barrientos, Samantha Cavalli, Matthew Lawson

Faculty Mentor: Dr. David Darmon

MA-3 Cubic Comparability Graphs

Olivia Verni

Faculty Mentor: Dr. David Marshall

MONMOUTH UNIVERSITY | BIOLOGY

**IAL AND ENVIRONMENTAL VARIABILITY OF HAB ABUNDANCE
AND TOXICITY IN MONMOUTH COUNTY COASTAL LAKES**

Karly Nolan

Monmouth University Department of Biology

Dr. Jason Adolf,

Monmouth University Department of Biology

Funding Sources:

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

Abstract

Harmful algal blooms (HABs) are a known and increasing environmental threat in freshwater systems such as coastal lakes. Researchers believe that climate change-driven increases in temperature and precipitation as well as increasing human development and populations drive increasing HABs. The presence of HABs can result in harm to the environment and lead to regulatory responses that limit community access to coastal lakes because the organisms that cause HABs, cyanobacteria, can make potent neuro- and hepatotoxins. The aim of this research was to gather data on HAB abundance in Monmouth County coastal lakes specifically by measuring cyanobacteria and toxin abundance in each lake and relating that to environmental and spatial variability. This research was an extension of the Coastal Lakes Community Observing Network (CLONet) that includes ten coastal lakes which have previously demonstrated evidence of HABs. It was hypothesized that spatial and environmental variability (e.g. rainfall) explain summer variability in coastal lake HAB and toxin abundance. Certain lakes, such as Deal Lake, presented a significant difference in HAB abundance and turbidity (ANOVA). A pattern evolved during the weeks of observation in which changes in rainfall were followed by correlated changes in HAB abundance. In addition, samples were taken for future measurement of chlorophyll and HAB species and toxin abundance by a qPCR assay. The information gleaned from this research could be used to predict freshwater HAB events in Monmouth County in the future. Understanding the origin of local environmental concerns can inform steps to preserve lakes so that they may continue to be a valued resource for the surrounding community.

**COMPARING PHYTOPLANKTON BIOMASS AND SPECIES COMPOSITION
OF BRANCHPORT CREEK TO SURROUNDING SHREWSBURY TRIBUTARIES**

Skyler Post

Monmouth University Department of Biology

Faculty Mentor:

Dr. Jason Adolf, Monmouth University Department of Biology

Funding Sources:

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

Abstract

Harmful algal blooms (HABs) negatively affect water quality in coastal estuaries both locally and globally. In previously conducted studies, Branchport Creek had 10-100 times higher chlorophyll levels than any other site along the Shrewsbury River, Navesink River, and Sandy Hook Bay, chlorophyll levels high enough to constitute a HAB. The dominant species in these Branchport Creek HABs was a potentially toxic dinoflagellate called *Akashiwo sanguinea*. This raised questions about the ecology of the surrounding tributaries in Shrewsbury. The goal of this study was to test the hypothesis that the biomass and species of phytoplankton in adjacent Shrewsbury tributaries is similar in composition to that of Branchport creek. After analyzing several stations in the upper Shrewsbury tributaries and comparing them to the stations in Branchport Creek, similarities in species composition were evident, with *Akashiwo sanguinea* remaining as the dominant species in both Branchport Creek and the Shrewsbury estuaries. While the species composition was similar amongst sites, there were some differences in the biomass, as chlorophyll levels tended to escalate more in the Shrewsbury tributaries than the Branchport creek stations. To further this study, annual sampling should be continued, as well as potentially expanding the analysis to other analogous sites.

**POST-RELEASE BEHAVIOR AND SURVIVORSHIP OF SHARKS
IN LAND-BASED CATCH AND RELEASE FISHERIES IN NEW JERSEY**

Danielle Dyson¹, Breana DiRenzi²

¹Monmouth University Department of Biology, ²Stockton University

Faculty Mentor:

Dr. Keith Dunton, Monmouth University Department of Biology

Funding Sources:

**NJ Sea Grant Consortium; Monmouth University School of Science
and Department of Biology**

Abstract

Worldwide, many shark species are drastically declining due to interactions with fishing sectors, both recreational and commercial. 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, uncertainties within recreational land-based shark fisheries such as capture stress, post release behavior, and survivorship need to be addressed. In this project, we used pop-off satellite tags (Wildlife Computers SPAT tags) attached behind dorsal fins to show post release response and behavior by tracking depth for up to 45 days. For longer term observations of survival and understanding movements and migrations, acoustic telemetry tags (Vemco V16-6H) were implanted in a sub-set of sharks. 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 34 sharks were captured: 24 sandbar sharks (*Carcharhinus plumbeus*), 5 sand tiger sharks (*Carcharias Taurus*), and 5 dusky sharks (*Carcharhinus obscurus*). All sharks ranged in size between 87 cm to 249 cm. Fight time showed that most sharks were landed on average within 4 minutes and remained landed for an average of 8 minutes before being released back into the ocean. 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.

**DETERMINING THE MIGRATION PATTERN OF SMOOTH DOGFISH
(*Mustelus canis*) ALONG THE EAST COAST**

**Megan Malaty
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Keith Dunton, Monmouth University Department of Biology**

**Funding Sources:
NJ Sea Grant Consortium; Monmouth University School of Science
and Urban Coast Institute**

Abstract

The smooth dogfish, *Mustelus canis*, is a relatively small demersal species of shark found along the East Coast that often inhabits the coastal bays and shallow inshore waters. Although this species is a commercially and recreationally targeted as well as caught as bycatch, relatively little is known about its migratory movements. To understand movement patterns along the New Jersey Coast, smooth dogfish (n=20) were surgically implanted with Vemco V9 acoustic transmitters. Thirteen female and seven male smooth dogfish (75.5 - 116 cm FL; 1.45 to 3.84 kgs) were tagged in Rockaway, New York using bottom trawl and long line. Collaborators within the Atlantic Cooperative Telemetry Network provided acoustic telemetry data throughout the east coast. Detection data was imported into Google Earth Pro to create individual tracks of each shark's movements and seasonal patterns. Smooth dogfish primarily migrate north in the summer months, going as far north as Massachusetts and migrate south in the winter months, going as far south as Florida. Gender does not seem to have a major role on the migration of these sharks and some sharks seemed to have high residency near their tagging locations. This study provides the first insight into the direct movement patterns of this species, which is important to help determine conservation and management strategies as populations of smooth dogfish have the potential to be heavily impacted due to their low fecundity and slow growth rates.

**TRACKING MOVEMENTS AND MIGRATIONS OF SANDBAR SHARKS
(*Carcharinus plumbius*) ALONG THE EAST COAST
USING ACOUSTIC TELEMETRY DATA FOR MANAGEMENT**

**Kerry L. McFeeters
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Keith Dunton, Department of Biology**

**Funding Sources:
New Jersey Sea Grant Consortium
Provost Summer Scholars**

Abstract

The sandbar shark (*Carcharinus plumbius*) is a large coastal shark that is widely distributed along the East Coast and is federally listed as prohibited from landing and harvest. While their movements are well documented within nursery grounds, there is limited knowledge about their coastal movements beyond traditional tag-recapture data. In 2016-2020, to examine the coastal movements, migrations, and residency patterns; Sandbar sharks (n=50; 40 females/10 males 114.3-226 cm total length) were surgically implanted Vemco V-16 acoustic transmitters. Collaborators within the Atlantic Cooperative Telemetry Network provided acoustic telemetry data throughout the east coast. Detection data was filtered and imported into R-Program and Google Earth to individually track shark movements. Sandbar sharks tended to remain local in NJ post tagging during the summer months (June-August). From November-April, individuals migrated south mainly to North Carolina, but going as far as Florida. A total of, 96% of the tagged individuals were detected in or around Delaware Bay, which is a major nursing ground and is near where they were tagged. This information provides information on coastal movements and residency of sandbar sharks which had important management and conservation implications since this population undergoes fishing pressure through the recreational community which could be impacting their populations.

**ANTI-COVID MICRORNA THERAPY TO BLOCK THE EXPRESSION
OF THE SPIKE, ENVELOPE, MEMBRANE
AND NUCLEOCAPSID GENES OF SARS-COV-2**

Flobater Gawargi
Monmouth University Department of Biology

Faculty Mentor:
Dr. Martin J Hicks, Department of Biology

Funding Sources:
Bristol Myers Squibb; Monmouth University School of Science and 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 27, 2020, WHO has confirmed 16,296,635 global cases and 649,662 deaths worldwide, 146,968 in the USA. There are no vaccines nor specific therapeutic drugs against SARS-CoV-2. 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 simultaneously block the expression of these distinct viral proteins. In the current work, we propose an anti-Covid microRNA therapy designed to degrade each of the mRNA transcripts of these critical genes, stopping viral assembly, and reducing the severity of infection. The design of the anti-Covid microRNAs 1) mimics microRNA cluster 17-92 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. In the first phase, six microRNA sequences are being cloned into microRNA-17-92 therapy vector, while the S gene is being cloned into our mammalian expression vector p3x-FLAG-tag. The S gene will be expressed in our tissue culture model to measure the efficacy of the anti-Covid microRNA therapy to down-regulate S-protein expression. Subsequently, we will be testing the efficacy of each anti-Covid microRNA to knockdown the expression of the viral proteins, E, M and N.

**THE INHIBITING EFFECTS OF ESSENTIAL OILS (EOs) ON THE GROWTH OF
MULTIDRUG RESISTANT *Acinetobacter baumannii*, *Enterobacter cloacae*,
and *Pseudomonas aeruginosa***

**Amanda Zappacosta, Gabriella Cleven, and Jackalyn Durante
Monmouth University Biology Department**

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

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

Abstract

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

Initially, 83 essential oils (EOs) were previously tested in our lab at 100% concentration on Muller Hinton II agar using the Kirby-Bauer Disk Diffusion Test to determine which essential oils had inhibiting effects on the growth of multidrug resistant *A. baumannii*, *E. cloacae* and *P. aeruginosa*. Of the 83 EOs tested, arborvitae, cassia, cinnamon bark, clove, cumin, oregano and thyme were very effective in inhibiting the growth of these bacteria. To determine the minimum inhibitory concentration (MIC) of these select essential oils, various dilutions were prepared using jojoba oil. The zones of inhibition were measured for all plates after 24 hours of incubation at 37°C.

Data from several published sources were researched to further analyze the antibiotic resistance of *A. baumannii*, *E. cloacae* and *P. aeruginosa*. EOs that had inhibitory effects against *E. cloacae* were cinnamon bark, clove, oregano, tea tree oil, thyme, and pepper fruit (*Dennettia tripetala*). Mainly EOs containing carvacrol, cinnamaldehyde, eugenol, paracymene, and thymol were most effective against *E. cloacae*. EOs that showed activity against *P. aeruginosa* included; basil, *C. osmophloeum*, eucalyptus, mint, oregano, rosemary, sage, thyme. Eucalyptus and coriander oils stood out as strong inhibitors of *A. baumannii* in recent published studies. In addition, synergistic testing of antibiotics and EOs together have yielded promising results in lowering the dosage needed to treat bacterial infections.

BY-08

**DIFFERENCES IN BEHAVIOR AMONG HOUSE MICE
FROM DIFFERENT CLIMATES**

Jesse Bragger

Monmouth University Department of Biology

Faculty Mentor:

Dr. Megan Phifer-Rixey, Department of Biology

Funding Sources:

Bristol Myers Squibb; Monmouth University School of Science and Department of Biology

Abstract

There are now many examples of environmental adaptation in widely observed species. House mice, *Mus musculus domesticus*, have adapted to their new environments in the Americas after their arrival ~500 years ago from Western Europe. Behaviors are a class of phenotypes that can have a great impact on fitness of an individual including mating success, food search, or predator avoidance. It is known that nesting behavior varies over a climatic gradient on the East Coast of the United States and that those differences have a genetic basis. Little is known about variation in other behaviors in these mice, like exploratory behavior, activity levels, and risk aversion all of which may contribute to fitness. In this experiment, mice from wild-derived house strains derived from five locations (Saratoga Springs, New York (NY); Edmonton, Alberta, Canada (EDM); Gainesville, Florida (FL); Tucson, Arizona (AZ); and Manaus, Amazonas, Brazil (BR)) were tested using two classic rodent behavior assays, a light and dark test and an open field test spaced one week apart. This study will ask if there are there differences in the use of refuges and exploratory behavior between both male and female mice of strains derived from different locations. Preliminary data suggests a difference in ambulatory activity between males and females and that New York mice are more active.

BY-09

USING ENVIRONMENTAL DNA (EDNA) TO TRACK BLACK SEA BASS AND WINTER FLOUNDER IN A CONTROLLED TANK ENVIRONMENT

Cameron Gaines

Monmouth University Department of Biology

Faculty Mentor:

Dr. Megan Phifer-Rixey, Department of Biology

Funding Source:

Monmouth University Urban Coast Institute

Abstract

Sampling environmental DNA (eDNA) from ocean water is an affordable, effective, and quick method used to identify and determine the presence and absence of marine and aquatic communities without the potentially negative impacts of traditional methods like electrofishing or trawling. However, its potential is limited without controlled studies that test the sensitivity of different eDNA detection methods and that establish key parameters like shedding and decay rate. The purpose of this project is to investigate shedding and decay of Black Sea Bass, *Centropristis striata*, and Winter Flounder, *Pseudopleuronectes americanus* under controlled conditions and to compare detection methods: qPCR and metabarcoding. Water samples were obtained at regular intervals prior to, during, and after the residence of the fish in the tank and were filtered by collaborators. We then extracted DNA from the filters following protocols to limit contamination. Now, we are building amplicon based libraries using metabarcoded eDNA that will be sequenced so that we can qualitatively and quantitatively track DNA from the fish through the course of the experiment. Once complete, metabarcoding results will be combined with qPCR results from collaborators to compare sensitivity and estimate shedding and decay rates.

**USING MICROSATELLITE GENOTYPING
TO CHARACTERIZE MIGRATION PATTERNS IN STRIPED BASS**

Elizabeth Gill

Monmouth University Department of Biology

Faculty Mentors:

**Dr. Megan Phifer-Rixey, Department of Biology
Assistant Dean John Tiedemann, School of Science**

Funding Sources:

**Bristol Myers Squibb; Berkeley Striper Club; Monmouth University School of Science,
Department of Biology and Urban Coast Institute**

Abstract

Striped bass support an economically valuable sport fishery. Striped bass are anadromous with the three major spawning grounds on the Atlantic Coast: the Hudson River, the Chesapeake Bay, and the Delaware River. Anglers along the New Jersey coast may be harvesting fish from any of the geographically distinct spawning grounds. In this study, we use microsatellite genotyping and population genetic analyses to identify the stock-specific origin of striped bass in the recreational fishery in northern Ocean County, New Jersey and to estimate the relative contribution of individual stocks to the fishery. Citizen anglers provided fin clips and size data from striped bass angled throughout the region. Samples were analyzed for the first year of the program. Results suggest that most of the stock fished in NJ waters comes from spawning grounds in the Chesapeake Bay and the Delaware River. However, there was also support for some genetic differentiation between fish from offshore sites compared to fish from Sandy Hook and Barnegat Bay. In order to further explore these results, we will be doing genetic analysis on an additional season of fin clips. This will help to increase statistical power and help determine if trends are consistent from year to year. Together, these data can be used to better understand the dynamics of migration in this fishery and to inform conservation and management strategies.

**IMMUNE FUNCTION IN MICE FROM DIFFERENT WILD DERIVED
STRAINS SUBJECT TO HIGH FAT DIET**

Jessy Khalil

Monmouth University Department of Biology

Faculty Mentors:

Dr. Megan Phifer-Rixey and Dr. Jeffrey Weisburg, Department of Biology

Funding Sources:

**Bristol Meyers Squibb; Monmouth University School of Science
and Department of Biology**

Abstract

Wild house mice have shown evidence of adaptation to variation in their environment across latitudinal clines. One aspect of their biotic environment that varies and can impact survivorship is exposure to pathogens and parasites. In this study, we plan to compare aspects of immune function between mice from wild-derived strains from the Americas that are kept on both a standard rodent diet and a high fat chow. At the morphological level, we will compare spleen size relative to body length as the spleen has a critical role in the immune system. At the cellular level, we will be comparing T and B cell composition using immunofluorescence assays. With the data from this experiment, we hope to determine if there is variation among strains in aspects of immune function and in the context of different diets.

**THE RELATIONSHIP BETWEEN MATERNAL BODY SIZE, LITTER SIZE,
AND BODY SIZE IN WILD DERIVED MOUSE STRAINS FROM THE AMERICAS**

**Julia Panebianco
Monmouth University Department of Biology**

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

**Funding Sources:
Bristol Myers Squibb; Monmouth University School of Science and Department of Biology**

Abstract

Wild house mice present an opportunity to understand natural phenomena using the power of a genetic model system. Recently, it has been shown that house mice have adapted to environmental variation in the Americas. For example, mice in northern locations are bigger than mice in southern locations. In addition, differences in litter size and pup size have been observed among wild derived mouse strains from different locations. In general, strains from colder, northern locations have more pups and larger pups than strains from warmer, southern locations.

One hypothesis is that such differences result from selection on body size. As body size increases, so will pup size and litter size. However, another hypothesis is that litter size and pup size may be selected on directly by seasonality of resources. Mice from very seasonal locations may have larger litters and larger pups because there are more limited opportunities to breed. Here, we plan to use a cross between a strain from New York and a strain from Brazil to learn more about the relationship between the traits. An F₂ mapping population will be created to measure maternal size. We will then intercross the F₂s to measure pup size and litter size. The data will help determine the range of variation in all of the traits and determine if QTL mapping for these traits will be informative.

**OBSERVING DIFFERENCES IN MATERNAL CARE AMONG DIFFERENT STRAINS
OF WILD-DERIVED MICE**

**Caroline Reverendo
Monmouth University Department of Biology**

**Faculty Mentor:
Dr. Phifer-Rixey, Department of Biology**

**Funding Sources:
Bristol Meyers Squibb; Monmouth University School of Science
and Department of Biology**

Abstract

Mus musculus, house mice, are important model systems because of their genetic, physiological, and anatomic similarities to humans. Past research has shown that wild mice from colder regions tend to be larger in size. The purpose of this experiment is to investigate another potential difference among mice from different climates, specifically maternal care. Maternal care includes, but is not limited to huddling, licking, retrieval of pups, and nest-building. We will be observing maternal care behaviors in mouse strains derived from Brazil, Florida, New York, and Canada. To observe these mice, we plan to use a video monitoring system of the home-cage. We are building a monitoring system for our experiment using low-cost Raspberry Pi computers and camera modules based on open source plans and software with a web interface that allows for live-streaming and accessibility to the camera module's settings and footage. Many traditional behavioral assays require expensive and disruptive apparatus. This flexible solution will allow us to observe behaviors in the home cage with less disturbance and for longer periods of time. Once deployed, we will use video analysis to assess variation in maternal care investment.

TURTLES OF LAKE TAKANASSEE: HOW DOES THIS ASSEMBLAGE PERSIST?

Angelina K. Ireland¹ and Sara R. Grouleff^{1,2}

Monmouth University Department of Biology¹, Marine and Environmental Biology and Policy Program²

Faculty Mentor:

Dr. Sean C. Sterrett: Monmouth University Biology Department

Funding Sources:

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

Abstract

Highly urbanized, coastal areas represent a challenge for organisms that must move across landscapes to complete their lifecycle. Freshwater turtles are an ectothermic vertebrate group that requires movement to disperse to other habitats, find suitable nesting areas, and seek refugia during extreme climatic events (e.g. extreme heat, drought, floods). For long-lived vertebrates, a sustainable and functional population may be indicated by a normally distributed size class or an estimate of $\lambda \geq 1$ (i.e. population growth rate). However, large population estimates without evidence of recruitment may result in a population that is unable to persist over time. We surveyed a freshwater turtle assemblage using baited hoop traps in a spatial capture recapture framework in four different sections of Lake Takanassee, Long Branch, NJ, from 2019-2020. Each individual captured was identified, measured, weighed, uniquely marked and released at its point of capture. Over two seasons, we made 251 total captures of 159 individuals of four species; eastern painted turtle, snapping turtle, red-eared slider (non-native) and eastern musk turtle; all common suburban inhabitants. Snapping turtle made up 27% of our individual capture but 81% of the total turtle mass (632 lbs. total). It is clear that habitat partitioning is occurring with non-native red-eared sliders being found primarily in the eastern most section of the lake. Additionally, we found 11 individuals moved between different sections of the lake connected by box culverts, indicating that movement is possible and relatively common. Using data from our first recapture event, and leveraging a 57% recapture rate in 2020, we compare estimates of density for 3 species of turtles using several commonly used abundance estimators. The goal of this study is to understand if this turtle community can functionally persist in a highly human-dominated landscape with threats such as roads, pollutants, fragmentation, human interference and watershed modifications.

MONMOUTH UNIVERSITY | CHEMISTRY *and* PHYSICS

**GRAVIKINESIS IN PARMECIUM CADATUM AND ITS EFFECTS
ON MOTION BEHAVIOR**

**Jonah Resnick and Jacob Rappaport
Monmouth University Department of Chemistry and Physics**

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

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

Abstract

The premise of the study is to understand how paramecium can sense the force of gravity, and account for it. Paramecia are small, microscopic creatures, and they have a property of heading towards negative charges known as galvanotaxis. We are using this property to learn more about them and track their motion. This motion is dependent on two factors: physical properties of the cell and physiological response of the cell, which occurs on the interior of the cell wall. Gravitikinesis is dependent on the polarization of mechanoreceptors within the cell membrane of these paramecium. Fundamentally, when a specimen of paramecium encounters a gravitational field, depending on the location of the force on the paramecium on the cell membrane, it will move to produce a forward locomotion, or decrease its velocity to slow down or move in reverse. In this experiment, to better understand this motion of paramecium, it is examined through a microscope with a camera to record how it reacts when encountered with varying charges. As the paramecium move through the chamber based on the location of the charges, their motion is recorded, and with MatLab coding, the exact swimming parameters are studied.

**COUPLING MECHANISM OF ION GRADIENT TO TORQUE
GENERATION AND INDEPENDENT STATOR FUNCTION OF
BACTERIAL FLAGELLAR MOTOR IN ESCHERICHIA COLI (E. COLI)**

**Cassandra Fauber and Robert Zuback
Monmouth University Department of Chemistry and Physics**

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

Abstract

The bacterial flagellar motor in Escherichia Coli (E. Coli) is a mechano-chemical energy converter that couples a transmembrane proton gradient to motor rotation. It is responsible for cell motility, biofilm formation, and pathogenicity. Motors roughly 40nm in diameter are rooted in the cell membrane and contain proteins that function as rotors and stators. A stator protein binds a cation that generates a power-stroke on a rotor protein that is turned at a discrete angle. This induces rotation of an extracellular flagellar filament which exerts a force on the cell surface at roughly 1000pN. These motors operate in response to an environmental chemical gradient. The structure and macroscopic mechanisms of the motor are understood, but the coupling mechanism that converts torque to speed is still under scrutiny. Another area of study is determining stators function independently in motor rotation. This research examines these aspects of motor function. The resurrection of E. Coli from zero-load explores stator independence or co-labor in motor rotation from 0 to ~300hz. Resultant torque-speed relationships at varying loads and speeds show that stators operate independently from one another. Too, that electrostatic forces position the stator and rotor in place while, a steric push causes rotation of the motor. Future research will be conducted on these preliminary results.

**THIAZOLE-BASED PEPTOID WITH METHOXY SUBSTITUENTS
AS A POTENTIAL ANTICANCER AGENT: A COMPUTATIONAL STUDY**

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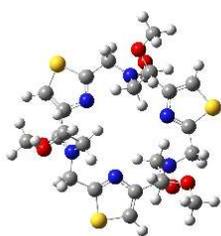
Funding Sources:

American Chemical Society Petroleum Research Fund;

Monmouth University School of Science and Department of Chemistry and Physics

Abstract

The problem of cytotoxicity of cancer treatments is an issue that has been investigated in the field of chemistry and medicine. The cytotoxicity of these treatments can cause many problems in patients undergoing cancer treatment such as: cognitive impairment, osteoporosis, and cardiotoxicity. The goal of this project is to contribute to design of potential anti-cancer drugs that will have a much lower cytotoxicity to healthy cells and may reduce the side effects that patients undergoing cancer treatment will experience. To accomplish this, we survey thiazole based peptoids that may selectively bond to the telomeres of tumor cell DNA. We also aim to investigate the effect that ions present in cell environment have on the stability of these ligands. The molecules and ion-molecular complexes that are being studied in this research project were built in GaussView and then computed using the Density Functional Theory methods in Gaussian. In this research, the molecule has been put into model solvent environment (water and ions), in order to replicate the conditions that the molecules would be in when they are used as medications. The solutions under study have molecule to sodium chloride ratios of 1:0, 1:1 or 1:2, as pictured. It was found that the molecules with a ratio of 1:2 were the most stable.



It was discovered that sodium has a stabilizing effect on the molecules that were studied. It was also found that water also has a stabilizing effect on the molecules. The next stage of this project is to use molecular docking software to simulate how the molecules being investigated would attach to DNA. The most stable molecules of each ratio are shown.

**OXAZOLE-BASED PEPTOID WITH METHOXY SUBSTITUENTS AS
A POTENTIAL ANTICANCER AGENT: A COMPUTATIONAL STUDY**

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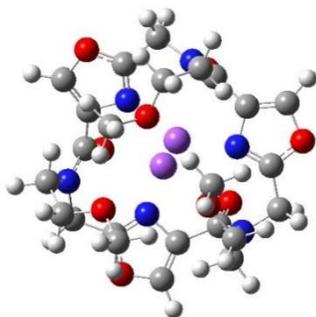
Dr. Yana Kosenkov, Department of Chemistry and Physics

Funding Sources:

American Chemical Society Petroleum Research Fund;

Monmouth University School of Science and Department of Chemistry and Physics

Abstract



Various small organic ligands have been designed and evaluated using *in silico* strategies for their potential use as anticancer drugs with low toxicity. These ligands bind to macromolecules in telomeric DNA, interfering with the reverse transcription function of the ribonucleoprotein complex telomerase. Many human cancer cells use telomerase to lengthen the 3' end of their telomeres, allowing for cellular immortalization. By interfering with the function of telomerase, tumor growth could be inhibited. Oxazole macrocycles with methoxy substituents are a potential candidate for targeted telomerase inhibition, as they are thought to bind selectively to certain secondary structures found in telomeric DNA, such as the G-quadruplex.

These peptoid macrocycles were studied using computational chemistry methods to determine their most likely conformations in solution. Simulations were performed both in chloroform and in water, and with different levels of sodium ion concentration. Simulations using 1:1 and 1:2 ratios of peptoids to sodium chloride were conducted, as well as simulations where sodium chloride was not included. The addition of sodium chloride provides a source of monovalent cations, which significantly improve the stability of peptoid macrocycles. These sodium ions may also play an important role in promoting binding affinity for DNA, which is negatively charged. Determining the lowest energy conformation of these molecules allows for ligand binding to be simulated through molecular docking.

**THIAZOLE-BASED PEPTOID WITH ISOPROPYL SUBSTITUENTS AS
A POTENTIAL ANTICANCER AGENT: A COMPUTATIONAL STUDY**

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Funding Sources:

**American Chemical Society Petroleum Research Fund;
Monmouth University School of Science and Department of Chemistry and Physics**

Abstract

Although surgical, radiative, and chemotherapeutic cancer treatments have improved over recent years, the toxicity of anti-cancer drugs is still an urgent problem in the field of cancer research. Ligands, which are small organic molecules, have been proposed as anti-cancer drugs, since they bind to DNA macromolecules in telomeres to inhibit tumor growth. The cytotoxicity of these potential drugs is estimated based on the selectivity of their binding to specific DNA conformations. This research focuses on theoretically modeling ligands that have shown promise as anti-cancer drugs with low toxicity. Specifically, these ligands are oxazole peptoid macrocycles. Different molecules belonging to this unique class, depending on their structure and substituents, bind in a highly selective fashion to certain DNA forms, such as the double-helix, parallel, anti-parallel, G-quadruplex, and mixed-type hybrid structures. Such oxazole based peptoid macrocycles can be chosen for optimal binding to these specific DNA conformations in order to execute the targeted inhibition of telomerase in cancer cells. Computational chemistry had been employed to study conformational equilibrium in these designated sets of oxazole peptoid macrocycles and the effect sodium cations have on this conformational equilibrium. Therefore, low energy conformations have been located for neutral oxazole peptoid macrocycles, as well as complexes with one and two sodium ions. The simulations have been conducted in solution of chloroform and water. It has been determined that sodium ions stabilize certain conformations significantly, since the optimized geometries of these systems have shown to have lower relative energies.

**THIAZOLE-BASED PEPTOID WITH ISOPROPYL SUBSTITUENTS AS
A POTENTIAL ANTICANCER AGENT: A COMPUTATIONAL STUDY**

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**Funding Sources:
American Chemical Society Petroleum Research Fund;
Monmouth University School of Science and Department of Chemistry and Physics**

Abstract

Each year, thousands of lives are saved as a result of the wide variety of effective and innovative treatments available to those fighting cancer. However, along with their undeniable benefits, these treatments also come with their share of risks. In particular, chemotherapy, a method of treating cancer that uses drugs to kill cancer cells, puts a patient at risk of experiencing the harmful side effects of cytotoxicity. These effects result from the lack of selectivity in the binding of the drugs, which bind not only to DNA conformations common in cancer cells but also to DNA of healthy somatic cells in the body, resulting in damage and death to rapidly growing cells such as those in the bone marrow, hair follicles, and the lining of the stomach and intestines. Neurological and reproductive damages have also occurred.

Current research into the topic of improving anticancer drugs to reduce cytotoxic effects has identified certain oxazole-based macrocycles as promising candidates. These molecules have been found to exhibit more selective binding behaviors than in chemotherapy drugs currently on the market, making them less likely to target healthy cells and more likely to target the G-quadruplex and other forms of DNA found in cancer cells. Computational chemistry provides an inexpensive, time-saving method of testing the binding capabilities of these molecules with DNA without having to conduct large numbers of experiments in a wet lab setting. This project was focused around the use of computational chemistry methods to determine which conformations of these macrocycles exhibit the highest binding affinity for the DNA molecules in cancer cells. The stabilizing and energy-reducing effects of the addition of one or two sodium ions to the macrocycles was also studied.

MONMOUTH
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COMPUTER SCIENCE *and*
SOFTWARE ENGINEERING

NAO ROBOT PROGRAMMING

James Cevasco¹ and Aaron Nitzberg²

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Funding Sources:

**Bristol Myers Squibb; Monmouth University School of Science
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Abstract

The purpose of this research project is to explore dialogue and facial recognition features of the NAO robot. Several coding projects have been designed by the students, which together allow for them to have interactive conversations with the robot, and test the robot's ability to detect, learn, track, and remember the names of human faces. 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 Choreograph desktop application. The NAO robot can connect to the internet and gain its own IP address, at which point a computer can locate NAO and communicate with it wirelessly. Once computer programs are written by a user, Choreograph can send those programs to be run on NAO via this wireless connection. The findings of this study have demonstrated several ways in which the robot can converse with humans, and how the robot can adapt its conversations based on a face it recognizes. By giving students a better understanding of how these robot functions work, this project sets up a strong base for students to build off of in future projects to explore more complex problems with the NAO robot.

Sources

NAO. (2018, May 18). Retrieved July 27, 2020, from <https://robots.ieee.org/robots/nao/>

A TRAINING APPLICATION FOR TIME MANAGEMENT SKILL

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**Bristol Myers Squibb; Monmouth University School of Science
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Abstract

Time management is one of the most important soft skills that students should learn, practice, and reinforce; however it is often difficult, especially for those who do not sort out what needs to be done and make plans of their time in the first place. In fact, the higher the grade one is in, the more likely that one gets stressed on time management. Reason 1: course work gets harder and requires more time; Reason 2: older students rely more on themselves. This project is to design a new tool that helps to train students making plans of their time and developing good study habits.

Theories and common practices related to time-management techniques are explored for this research. The types of work considered for planning are those that need to be completed by students in their own time. They are classified into 4 groups: (1) time-fixed tasks; (2) assignments with deadline; (3) events that require preparation; and (4) long-run targets. They are handled differently in practice, so the algorithm should be adaptive to the logic accordingly. In addition, prioritization, execution and persistence are also highly valued in the design. As the proof-of-concept, this tool is currently implemented as a web-based system. Based on the available time provided, the immediate time plan is automatically generated to suggest the allocation of time slots to meet the work need of a student. Upon that, adjustment is easily doable. This computer application will help students develop time management skill in order to accomplish their study goals in the face of various distractions in the real-world environment. Further work of this project will bring more possibilities.

**PREDICTING ICU LENGTH OF STAY FOR HEART FAILURE PATIENTS USING
MACHINE LEARNING METHODS**

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Faculty Mentor:

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Funding Sources:

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

Abstract

The intensive care unit (ICU), providing intensive treatment for critically ill patients, is the unit with the highest mortality in a hospital. In addition, the cost in ICU is expensive. The common goal for hospitals and patients is to minimize the length of stay (LOS) in ICU to reduce the cost and to improve the quality of health care. Predicting ICU LOS for patients at admission can facilitate the hospital resource management and is beneficial for patients' health outcome. However, it is not an easy task. ICU physicians can only accurately predict LOS for about half of the admissions. Machine learning has been successfully applied in various fields including health care, which can automatically learn from large and complex datasets. This project is to study the performance of different machine learning algorithms, including linear regression, logistic regression, gradient boosting machine, random forest, and neural network, on the prediction of ICU LOS using historical electronic health record (EHR) data. The data utilized in this study is MIMIC-III, an openly available critical care dataset developed by the MIT Lab for Computational Physiology, comprising deidentified health data associated with about 60,000 ICU admissions at Boston Beth Israel Medical Center between 2001 and 2012. This dataset includes patients' comprehensive health records, e.g., demographics, vital signs, lab tests, chart events and discharge notes. Diagnosis is an important factor of ICU LOS and heart failure is one of the ten diseases with the largest number of patients in MIMIC-III. Hence, this preliminary project focuses on the predication of length of stay in ICU for heart failure patients. The pipeline established in this project can be easily extended to the whole MIMIC-III dataset.

MONMOUTH UNIVERSITY | MATHEMATICS

MA-01

**EMPLOYING THRESHOLDING AND WAVELET TRANSFORMATION
TO REMOVE NOISE FROM AN AUDIO SIGNAL**

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Saint Michael's College**

**Dr. Joseph Coyle
Monmouth University Department of Mathematics**

**Funding Sources:
Monmouth University School of Science and Department of Mathematics**

Abstract

We explore the use of thresholding on noisy audio signals to produce a signal that best replicates the original without the additional background noise. The thresholding is used in conjunction with two different types of wavelet transformations, the Haar wavelets and the Daubechies 4 wavelets. The original audio signal considered is combined with multiple different types of background noises: monotone, increasing, and decreasing. Results related to simulated data are compared to those when real audio and noise are used. In particular, the results related to artificial simulations are used to predict optimal thresholding values that minimize background noise in the reconstructions.

**CONFDIST: DEVELOPMENT OF AN R PACKAGE FOR STATISTICAL INFERENCE
WITH CONFIDENCE DISTRIBUTIONS**

**Odalys Barrientos, Samantha Cavalli, Matthew Lawson
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**Faculty Mentor:
Dr. David Darmon, Department of Mathematics**

**Funding Sources:
Bristol Myers Squibb; Monmouth University School of Science
and Department of Mathematics**

Abstract

Despite the frequent misuses of P -values, they continue to appear in scientific publications as a foundation of scientific evidence. P -values are often misinterpreted and fail to provide information about the size of an effect, since even the smallest effects can produce statistically significant P -values if the sample size is large enough. Confidence distributions provide a better alternative to extract statistical information from any given data set.

We created a package for constructing confidence distributions from data using R, a programming language for statistical computing. We implemented software to compute confidence functions for various parameters of different distributions, including but not limited to means via one-sample, two-sample, and paired t -tests, variances of Gaussian distributions, rates of exponential distributions, and proportions for binomial distributions. For each parameter we compute the confidence distribution, density, and quantile function, as well as a confidence curve. We also implemented confidence functions via nonparametric tests, including the Wilcoxon Signed-Rank Test and the Wilcoxon Rank-Sum Test.

Since P -values are readily provided by statistical software, they have become the norm and scientists regularly report them in studies. By creating this package, we have made confidence distributions available for scientists to use as a better alternative for statistical inference. The confidence distribution package provides an easy and principled way to estimate and make inferences about parameters.

CUBIC COMPARABILITY GRAPHS

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Faculty Mentor:

Dr. David Marshall, Department of Mathematics

Funding Sources:

Monmouth University School of Science and Department of Mathematics

Abstract

A graph G is a comparability graph, or a divisor graph, if its vertices can be labeled with distinct positive integers so that vertex v is adjacent to vertex w if and only if either v divides w or w divides v . This project concerns the problem of determining whether or not a given graph is or is not a comparability graph. The problem has been resolved for several families of graphs, including complete graphs, bipartite graphs, trees, path, and cycle graphs. Cycle graphs are the regular graphs of degree 2, with even length cycles being comparability graphs and odd length (greater than 3) cycles not. In an effort to generalize this example, we turned our attention to the family of cubic graphs, or regular graphs of degree 3. While the problem of classifying all cubic graphs as either comparability or non-comparability graphs is hard and far from complete, we were able to accomplish several goals. These include proving a sufficient criterion for a cubic graph to not be a comparability graph and constructing several infinite families of cubic comparability graphs and several infinite families of cubic non-comparability graphs. Our constructions are based on a detailed analysis of potential triangle configurations in cubic graphs, as well as known forbidden subgraphs in comparability graphs.