

**MONMOUTH
UNIVERSITY**

SCHOOL OF SCIENCE

**MONMOUTH
UNIVERSITY**

STUDENT SCHOLARSHIP WEEK

**MONMOUTH UNIVERSITY
SCHOOL OF SCIENCE
17TH ANNUAL
STUDENT RESEARCH CONFERENCE**



April 20, 2018

2:00pm – 5:00pm

Edison Science Building

Multipurpose Room and Lobby

Poster Presentations of Student Research in

Biology

Chemistry and Physics

Computer Science and Software Engineering

Mathematics



**17th Annual
School of Science Student Research Conference**

**April 20, 2018
Edison Science Building
Multipurpose Room and Lobby**

AGENDA

- | | |
|--------------------------|---|
| 1:00 pm – 2:00 pm | Registration and Poster Set-up
Edison Science Building Multipurpose Room |
| 2:15 pm – 2:30 pm | Welcome and Opening Remarks
Assistant Dean John Tiedemann |
| 2:30 pm – 4:30 pm | Poster Session
Edison Science Building Multipurpose Room |
| 4:30 pm – 5:00 pm | Wrap-up and Closing Remarks |
| 5:00 pm – 5:15 pm | Break |
| 5:15 pm – 6:30 pm | Reception and Student Awards
Edison Science Building Lobby |
- Dean's Awards for Excellence in Research
School of Science Departmental Awards**



**17th ANNUAL STUDENT RESEARCH CONFERENCE
APRIL 20, 2018**

Department of Biology

- A-1 A DIATOMACEOUS DISCOVERY: PHYTOPLANKTON BIOMASS IN COASTAL BREAK ZONES EXCEEDS THAT OF OFFSHORE SURF ZONES
Gina Badlowski, Taylor Donovan, Rebecca Klee, and Kaitlyn Smith
Faculty Mentor: Dr. Jason Adolf
- A-2 USING FLOW CYTOMETRY TO MEASURE MIXOTROPHIC GRAZING IN *KARLODINIUM VENEFICUM*
Mia Collucci and Skyler Post
Faculty Mentor: Dr. Jason Adolf
- A-3 UNDERSTANDING HARMFUL ALGAL BLOOMS OF DEAL LAKE THROUGH NUTRIENT BIOASSAYS
Marissa DeTrre, Cidia Dominique, and Justine Violante
Faculty Mentor: Dr. Jason Adolf
- A-4 PHYTOPLANKTON AND SALINITY IN NEW JERSEY ESTUARIES: A COMPARISON OF TWO LOCAL SYSTEMS
Cassady Dougan, Brooke Redmond, and Connor Viducic
Faculty Mentor: Dr. Jason Adolf
- A-5 INVESTIGATING THE SURF ZONE FOR EVIDENCE OF PREVIOUSLY UNDESCRIBED SURF DIATOMS
Jeff Dudek, Karen Serrano, and Matthew Francis
Faculty Mentor: Dr. Jason Adolf
- A-6 TRENDS IN THE ABUNDANCE AND SPATIAL-TEMPORAL VARIATION OF SHARKS AND RAYS IN NEW JERSEY COASTAL WATERS
Gina Badlowski
Faculty Mentor: Dr. Keith J. Dunton

- A-7 SEASONAL DIET AND PREY SELECTIVITY OF ATLANTIC STURGEON IN A COASTAL MARINE AGGREGATION
Marissa C. DeTorre
Faculty Mentor: Dr. Keith J. Dunton
- A-8 DESIGN OF AN IMMUNOGENIC AND ANTI-EGFR RNA THERAPEUTIC TO ALTER RNA AND PROTEIN EXPRESSION IN GLIOBLASTOMA MULTIFORME
Sara Falotico, Nicole Sivetz, and Peter Nekrasov
Faculty Mentor: Dr. Martin J. Hicks
- A-9 DESIGN AND DELIVERY OF DNA ENCODING RNA THERAPEUTICS TO ALTER THE EXPRESSION OF ONCOGENIC TRANSCRIPTS IN GLIOBLASTOMA
Kevin Gallagher, Sarah Falotico, Nicole Sivetz, and Peter Nekrasov
Faculty Mentor: Dr. Martin J. Hicks
- A-10 SYNTHESIS OF A MINI-REPORTER CONSTRUCT TO TEST GENE TRANSFER OF RNA THERAPEUTICS
Koushik Muralidharan, Arbaz M. Khan, Kerianne Fuoco, and Hemangi Patel
Faculty Mentor: Dr. Martin J. Hicks
- A-11 DELIVERY OF THERAPEUTIC RNA MOLECULES TO ALTER EPIDERMAL GROWTH FACTOR RECEPTOR EXPRESSION IN GLIOBLASTOMA MULTIFORME
Nicole Sivetz, Sanjana Akula, Anjali Chakradhar, Ester Teper, Lucy Zou, Sarah Falotico, and Peter Nekrasov
Faculty Mentor: Dr. Martin J. Hicks
- A-12 EXAMINING THE ROLE OF FASCIN IN PRIMARY BRAIN CANCERS
Mehdi Husaini and Esra Celik
Faculty Mentor: Dr. Cathryn Kubera
- A-13 DEVELOPMENT OF A CRISPR-CAS9 PLASMID TARGETING THE *GALLUS GALLUS* GABRA2
Charlotte Kelly
Faculty Mentor: Dr. Cathryn Kubera
- A-14 CHARACTERIZING THE EXPRESSION OF GABA_A RECEPTOR SUBUNITS IN DEVELOPING *GALLUS GALLUS* CHICK
Nadine Khalil and Victoria Reggio
Faculty Mentor: Dr. Cathryn Kubera
- A-15 THE USE OF ESSENTIAL OILS TO COMBAT *STREPTOCOCCUS PNEUMONIAE*
Eric Bryan
Faculty Mentor: Dr. James Mack

- A-16 NEW APPROACHES TO STUDYING GENE EXPRESSION IN HOUSE MICE
Bradley Kraft
Faculty Mentor: Dr. Megan Phifer-Rixey
- A-17 VARIATION IN REPRODUCTIVE TRAITS AMONG HOUSE MICE ADAPTED TO DIFFERENT CLIMATES IN THE AMERICAS
Tiffany Longo
Faculty Mentor: Dr. Megan Phifer-Rixey
- A-18 DNA EXTRACTION FROM ATLANTIC STURGEON SPINE AND FIN TISSUE
Brian Reiss
Faculty Mentor: Dr. Megan Phifer-Rixey
- A-19 IDENTIFYING PATHWAYS WITH SIGNALS OF GLOBAL REGULATION LINKED TO ENVIRONMENTAL ADAPTATION IN HOUSE MICE
Sebastian Vera
Faculty Mentor: Dr. Megan Phifer-Rixey
- A-20 LIPID RAFT DYNAMICS DURING CO-USE OF ALCOHOL AND STIMULANTS
Marta Telatin, Pooja M. Shah, and Natalie C. Negroni
Faculty Mentor: Dr. Dennis Rhoads
- A-21 SOURCES OF STRIPED BASS (*MORONE SAXATILIS*) IN THE MIXED-STOCK RECREATIONAL FISHERY IN NORTHERN OCEAN COUNTY, NEW JERSEY
Nikole Andre, Anjali Tampy, and Cassady Dougan
Faculty Mentor: Assistant Dean John Tiedemann and Dr. Megan Phifer-Rixey

Department of Chemistry and Physics

- A-22 UNRAVELING THE B TO A CONFORMATIONAL TRANSITION IN DUPLEX DNA CONSTRUCTS AT SINGLE BASE PAIR RESOLUTION
Kirsten P. Lawson
Faculty Mentor: Dr. Davis Jose
- A-23 A SPECTROSCOPIC APPROACH TO UNDERSTAND THE STRUCTURAL INTRICACIES OF NON-CANONICAL NUCLEIC ACID CONFORMATIONS
Brandon C. Rosenblum and Jacqueline R. Evans
Faculty Mentor: Dr. Davis Jose
- A-24 EXPLORING OXALZOLE-BASED MACROCYCLE BINDING TO DNA
Omar Shah
Faculty Mentors: Dr. Yana Kholod and Dr. Dmytro Kosenkov

A-25 ANALYSIS OF EXCITATION ENERGY TRANSFER IN PIGMENT-PROTEIN COMPLEXES WITH PyFREC SOFTWARE ANALYSIS OF EXCITATION ENERGY

Julia Farnan and Grant Gillan

Faculty Mentors: Dr. Yana Kholod and Dr. Dmytro Kosenkov

A-26 MICROWAVE ASSISTED SYNTHESIS OF QUINAZOLINES

Nicole Sivetz, Erik Smith, and Tyler Soobryan

Faculty Mentor: Dr. Massimiliano Lamberto

A-27 CLONING OF T7 RNA POLYMERASE

Karla Clavelo

Faculty Mentor: Dr. Jonathan Ouellet

A-28 SELECTION OF AN APTAMER THAT BINDS GLUCOSE

Emma Stowell

Faculty Mentor: Dr. Jonathan Ouellet

Department of Computer Science and Software Engineering

A-29 MONMOUTH MEDICAL CENTER SURGEON RESIDENCY PROGRAM EVALUATIONS MOBILE APP

Kalyna Reda

Faculty Mentor: Dr. Raman Lakshmanan

A-30 IT LAB ASSISTANT APPLICANT WEBSITE AND DATABASE

Paul Miceli

Faculty Mentor: Professor Jan Rohn

A-31 INTERACTIVE CAMPUS MAP FOR MONMOUTH UNIVERSITY

Paul Bundac, KerryAnn DeMeester, Daniel Kelly, and Megan Rapach

Faculty Mentor: Dr. Daniela Rosca

A-32 MYXR

Craig Holbrook, Peter Natoli, Agbai Iroha, and Matt Drew

Faculty Mentor: Dr. Daniela Rosca

A-33 TRUFISHING MOBILE APPLICATION

Robert Thompson, Liam Grover, Joseph Gudzak, and Jack Olszewski

Faculty Mentor: Dr. Daniela Rosca

- A-34 AMERICAN SIGN LANGUAGE RECOGNITION AND SPEECH
Zainy M. Aljawy
Faculty Mentor: Dr. William Tepfenhart
- A-35 MONMOUTH UNIVERSITY'S SCHEDULING ENVIRONMENT (MUSE)
Joey Baldasari, Michael Hunt, Stephen Kresevic, Evan Scarpino,
and Roberto Tanenbaum
Faculty Mentor: Dr. Cui Yu
- A-36 XANADU: A CONVENIENT WEB-BASED OCR TOOL
Matthew Fullerton, Anthony Hamill, William Jones, Thomas Reilly,
and Luke Tomkus
Faculty Mentor: Dr. Cui Yu

Department of Mathematics

- A-37 ANALYSIS OF IRREGULAR PATTERNS IN TIDAL ELEVATION
Dillon Henrichsen
Faculty Mentor: Dr. Joseph Coyle
- A-38 ANALYZING THE EFFECTIVENESS OF THE 2010 NEW JERSEY EMERGENCY
OPERATION PLAN MANDATE
Taylor Donovan and Dillon Henrichsen
Faculty Mentor: Dr. Richard Bastian
- A-39 STATISTICAL ANALYSIS: DOG-OWNER BEHAVIOR IN PLAY PARKS
Melissa Culmone and Davie DiMasi
Faculty Mentors: Dr. Richard Bastian and Dr. Lindsay Mehrkam
- A-40 STATISTICAL ANALYSIS OF SPORT LEADERSHIP BEHAVIOR, ATHLETE
SATISFACTION AND GROUP COHESION AMONG DIVISION 1 FEMALE
COLLEGIATE SOCCER PLAYERS IN THE U.S.
Rebecca Klee, Alyssa Parker, and Larissa Russo
Faculty Mentors: Dr. Richard Bastian and Coach Kristine Turner
- A-41 STATISTICAL ANALYSIS ON THE EFFECTS OF ESSENTIAL OILS ON
BACTERIA
Justine Kukowski and Eric Bryan
Faculty Mentors: Dr. Richard Bastian and Dr. James Mack

- A-42 STATISTICAL ANALYSIS ON EDUCATING STUDENTS WITH AUTISM SPECTRUM DISORDER
Justine Kukowski and Nicole Cimaglia
Faculty Mentors: Dr. Richard Bastian and Dr. Stacy Lauderdale
- A-43 β -HYDROXY- β -METHYLBUTYRATE EFFECT OF PHYSICAL PERFORMANCE ON ATHLETIC POPULATIONS
Shannon McAleer and Anthony Hamill
Faculty Mentor: Dr. Richard Bastian
- A-44 STATISTICAL ANALYSIS OF OCEAN WAVE HEIGHTS IN THE EAST COAST
Jennifer Minor and Kimberly Bianchi
Faculty Mentors: Dr. Richard Bastian and Dr. Thomas Herrington
- A-45 STATISTICAL ANALYSIS OF SYNOVIAL FLUID IN CANINES WITH CCL TEARS
Jennifer Minor and Tiffany Longo
Faculty Mentor: Dr. Richard Bastian
- A-46 STATISTICAL ANALYSIS OF THE RELATIONSHIP BETWEEN DYADIC-PLAY STRUCTURE IN DOGS AND OWNER BEHAVIOR
Larissa Russo and Kelsey Gripp
Faculty Mentors: Dr. Richard Bastian and Dr. Lindsay Mehrkam
- A-47 VARIATION IN VIOLENT CRIME
Peri Trembley and Elizabeth Roderick
Faculty Mentors: Dr. Richard Bastian and Dr. Marie Mele
- A-48 MANGROVE ECOSYSTEMS AND FRAGMENTATION IN THE BAHAMAS
Michael Welch and Kyle Frankenbush
Faculty Mentors: Dr. Richard Bastian and Dr. Pedram Daneshgar



Department of Biology
Abstracts

**A DIATOMACEOUS DISCOVERY: PHYTOPLANKTON BIOMASS IN COASTAL
BREAK ZONES EXCEEDS THAT OF OFFSHORE SURF ZONES**

**Gina Badlowski, Taylor Donovan, Rebecca Klee, and Kaitlyn Smith
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Jason Adolf, Department of Biology

Surf diatoms refer to diatoms that accumulate to high cell concentrations in break zones of sandy shores. These diatoms form brown patches in the surf on a semi-permanent basis. Approximately eight different diatoms have been identified specific to break zones, although none have been described along the United States' Atlantic East Coast. The presence, or lack thereof, of surf diatoms along the East Coast has not been investigated thoroughly. In this study, we explored the site-specific differences that exist in phytoplankton composition and productivity among three locations along the New Jersey Coast. Within Monmouth County, New Jersey, beaches along Belmar Beach, Long Branch, and Sandy Hook National Park were sampled. Water samples were collected from both the off-shore surf zone and on-shore break zone of each of the three sites and used for extracted chlorophyll *a* analysis. Additionally, diatom community diversity was assessed with the use of microscopy. It was hypothesized that the break zone would have a greater chlorophyll *a* content as well as abundance of diatoms at all sites sampled. A two-way analysis of variance (ANOVA) supported that there was a significant difference in chlorophyll *a* content between the surf and break zone (P-Value= 0.007) as well as between sites (P-Value= 0.015). No species exclusively described from break zones were discovered, but a common surf zone diatom was identified. It is possible the use of anthropogenic structures, such as groins in break zones, may increase particle retention of diatoms and alter local food webs.

**USING FLOW CYTOMETRY TO MEASURE MIXOTROPHIC GRAZING
IN *KARLODINIUM VENEFICUM***

**Mia Collucci and Skyler Post
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Jason Adolf, Department of Biology

Karlodinium veneficum is a mixotrophic protist (photosynthetic and phagotrophic) that has been linked to harmful algal blooms (HABs) and fish kills in coastal ecosystems worldwide. Their mixotrophic nature is aided by a toxin, karlotoxin (KmTx), that immobilizes prey and deters grazers that might predate on *K. veneficum*. Previous studies of *K. veneficum* growth and mixotrophic grazing have used laborious microscope techniques to count cells, limiting the amount of experiments that can be done in a reasonable amount of time. The goal of this study was to develop a simple flow cytometry-based method to measure mixotrophic grazing of *K. veneficum* on prey species. A flow cytometer can distinguish cells in mixed-cultures based on optical properties and can count cells far quicker than a person at the microscope. Experiments were set up in 24-well plates by establishing different triplicated treatments (*K. veneficum* alone, prey alone, *K. veneficum* and prey together). Different strains of *K. veneficum* and different prey species were tested. Cells were counted on a BD Accuri C6 flow cytometer and distinguished on biplots of forward angle scatter and red fluorescence. Mixotrophic feeding experiments analyzed by flow cytometry showed patterns of grazing and feeding in *K. veneficum*, as well as toxic activity associated with this dinoflagellate. Our findings provide a critical understanding of prey interactions with *K. veneficum* and will lead to further study of its impact on fish kills in coastal waters.

**UNDERSTANDING HARMFUL ALGAL BLOOMS OF DEAL LAKE
THROUGH NUTRIENT BIOASSAYS**

**Marissa DeTorre, Cidia Dominique, and Justine Violante
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Jason Adolf, Department of Biology

Harmful algal blooms (HAB) of cyanobacteria have become a growing threat to freshwater systems such as coastal lakes. As the blooming events become more frequent and more intense it becomes more important to understand what is causing such blooms. Anthropogenic influence including both climate change and nutrient loading are potential forces influencing the HABs. To understand the cyanobacterial harmful algal blooms that have been effecting Deal Lake, a nutrient addition bioassay was conducted. Nitrogen, Phosphorus, or both nutrients were added to Deal Lake water samples from three different locations around the lake to determine which nutrients limit phytoplankton growth. The study sites selected were coastal, central and the southwest tributary of the lake and the samples were incubated within the lake itself to retain natural conditions. *In vivo* Fluorescence and Flow cytometry were used to determine the presence of Chlorophyll a and phycocyanin within each of the samples. The southwest arm of Deal Lake had the lowest levels of chlorophyll a most likely due to lack of light from loose muddy sediments. The coastal location was determined to be limited by phosphorus and have the greatest amount of phycocyanin present across all samples. This may be an indicator that this location is most at risk for a bloom when the conditions become ideal. The nutrients traveling that source from the southwest arm that is heavily influence by anthropogenic nutrient loading could be the cause of harmful algal blooms in other locations throughout the lake.

**PHYTOPLANKTON AND SALINITY IN NEW JERSEY ESTUARIES:
A COMPARISON OF TWO LOCAL SYSTEMS**

**Cassady Dougan, Brooke Redmond, and Connor Viducic
Monmouth University Department of Biology**

Faculty Member:

Dr. Jason Adolf Department of Biology

Although phytoplankton are the foundation of the aquatic food web, they have the potential to cause algal blooms that are harmful to other species. This study is being conducted to examine the difference in phytoplankton composition and abundance between the Shrewsbury and Navesink River Estuaries. These two estuaries differ in freshwater inputs because of the Swimming River leading into the Navesink River from its western end. However, they have similar watersheds and are related in shape, size, climate, and location. These similarities allow for the observed salinity levels to be the determining factor in phytoplankton composition. Starting at the northern tip of Sandy Hook Bay and ending at the entrance of the Navesink River Estuary, water samples and YSI measurements will be taken at seventeen different locations. In the lab, the water samples will be analyzed for phytoplankton species composition and abundance using several techniques. It is hypothesized that the Shrewsbury and Navesink will differ in phytoplankton composition due to the difference in salinity of the waterbodies and that the Navesink River will have a higher abundance of phytoplankton due to its freshwater inputs that are often associated with nutrient loading. Since high abundances of toxic phytoplankton degrade water quality and often cause fish kills, the results of this experiment may be helpful to fishery managers and water quality monitors.

**INVESTIGATING THE SURF ZONE FOR EVIDENCE
OF PREVIOUSLY UNDESCRIBED SURF DIATOMS**

**Jeff Dudek, Karen Serrano, and Matthew Francis
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Jason Adolf, Department of Biology

Phytoplankton are important primary producers in the marine energy web. Phytoplankton can be found in virtually every marine environment in the photic zone where enough light penetrates for photosynthesis. The surf zone is defined as the area where the ocean meets the landmass, and is characterized by nearly constant wave action, resulting in a high energy and highly volatile and dynamic environment. One form of phytoplankton- diatoms- contains species that are only found within surf zones, so-called surf diatoms. Surf diatoms have not been studied or described on the eastern coast of the United States, including New Jersey. We aim to investigate the surf zone in three locations along the local New Jersey coastline. We will determine if surf diatom species that have been previously described in other geographic locations of the world are present here, and determine the species and abundance. We will collect water samples and conduct uniform tests to determine abundance, species composition, and chlorophyll *a* concentrations. We will compare sites and determine statistical differences by performing ANOVAs. Data so far have shown a statistically significant difference in chlorophyll *a* concentration, or phytoplankton biomass, between the three different sites. This study will determine the presence of surf diatoms in New Jersey and give insight to the species composition of phytoplankton in the surf zone.

**TRENDS IN THE ABUNDANCE AND SPATIAL-TEMPORAL VARIATION
OF SHARKS AND RAYS IN NEW JERSEY COASTAL WATERS**

Gina A. Badlowski
Monmouth University Department of Biology

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

Worldwide, numerous coastal shark and ray species have shown drastic declines in populations. Many of these species are of great conservation need because of their currently low population levels as well as k-selected life history traits making the understanding of their abundance and distribution patterns essential for both conservation and management issues. The coast of New Jersey has been shown to have abundance of shark and ray species, but patterns and distributions of species are relatively unstudied. In 1988, the New Jersey Department of Environmental Protection (NJDEP) initiated an Ocean Trawl Survey to evaluate the states fishery resources. This survey, is conducted 5 times throughout the year encompassing the entire coast of NJ inshore of 30 m, representing one of the longest running and comprehensive fishery surveys conducted along the east coast allowing long-term patterns of species to be identified. Utilizing the NJDEP survey from (1988-2016) we identified spatial and temporal patterns of abundance (CPUE) and habitat of 4 species of commonly captured sharks; Atlantic Angel Shark, Sand Tiger Shark, Dusky Shark, Thresher Shark, and 3 species of rays; Roughtail Stingray, Southern Stingray, and Spiny Butterfly Ray. All of these species showed strong patterns in spatial and temporal variation with all species being most abundant from June-October and within the southernmost portion of the survey. This identification of spatial and temporal patterns of these species allows for better insight of their populations, distributions, and migratory habits, which is necessary for conservation and appropriate management actions for these species.

**SEASONAL DIET AND PREY SELECTIVITY OF ATLANTIC STURGEON
IN A COASTAL MARINE AGGREGATION**

Marissa C. DeTorre
Monmouth University Department of Biology

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

Atlantic Sturgeon, *Acipenser oxyrinchus oxyrinchus*, is a federally protected species that undergoes large coastal migrations. Aggregations of Atlantic Sturgeon are known to occur in several coastal locations, including large seasonal aggregations in the spring and fall off the coast of New York. This New York aggregation is known to consist of sub-adults largely from the Hudson River. To understand potential reasons why sturgeon aggregate, temporal changes in diet were examined from sub-adult fish within these coastal aggregations. The prey of the Atlantic Sturgeon was determined through stomach contents, collected through non-lethal gastric lavage in both the Spring (n=28) and Fall (n=39) of 2013. Thirteen unique prey taxa were identified with Atlantic Sturgeon ingesting large numbers of Gammarid amphipod spp. in both seasons. In addition to gammarids, the sturgeon diet included considerable numbers of *Glycera dibranchiata*, *Leitoscoloplos fragilis*, *Squilla empusa* and other various polychaete, oligochaete and crustacean species. Concurrent studies indicate that this area is important for migrating Atlantic Sturgeon, and the high abundance of prey resources indicates an important feeding habitat. This might explain temporal aggregations in this region.

**DESIGN OF AN IMMUNOGENIC AND ANTI-EGFR RNA THERAPEUTIC TO ALTER
RNA AND PROTEIN EXPRESSION IN GLIOBLASTOMA MULTIFORME**

Sarah Falotico¹, Nicole Sivetz¹, and Peter Nekrasov²

¹Monmouth University Department of Biology

²Biotechnology High School

Faculty Mentor:

Dr. Martin J. Hicks, Department of Biology

The most common and lethal malignancy of the central nervous system (CNS) is glioblastoma multiforme (GBM). Due to the blood brain barrier (BBB) and the relatively immunologically privileged status of the CNS, clinical strategies have not improved the standard of care. Epidermal growth factor receptor (EGFR), a type of tyrosine kinase receptor, has been found to be overexpressed in as much as 60% of GBM tumors. Upon binding of its cognate ligand, EGFR promotes tumor growth and proliferation. The glioma-specific antigen, interleukin-13 receptor alpha variant 2 (IL13R α 2) is highly immunogenic, attracting cytotoxic Tcells to the tumor microenvironment. Therapeutically, delivery of this antigen to the tumor has the potential to bypass the BBB and reactivate the immune system toward GBM. In the current study, we have designed and cloned an immunogenic pre-trans splicing RNA molecule (iPTR) against EGFR. In a GBM tissue culture model, we measure the RNA and protein expression of the iPTR and compare to multiple anti-EGFR RNA therapies. In addition, we are developing assays to use ELISA to measure changes in EGFR protein expression. Genetic delivery of our highly immunogenic IL13R α 2 peptide using the iPTR has the potential to redirect the immune system to recognize and induce apoptosis in GBM cells.

DESIGN AND DELIVERY OF DNA ENCODING RNA THERAPEUTICS TO ALTER THE EXPRESSION OF ONCOGENIC TRANSCRIPTS IN GLIOBLASTOMA

Kevin Gallagher¹, Sarah Falotico¹, Nicole Sivetz¹, and Peter Nekrasov²

¹Monmouth University Department of Biology

²Biotechnology High School

Faculty Mentor:

Dr. Martin J. Hicks, Department of Biology

Glioblastoma multiforme (GBM) the most common central nervous system (CNS) malignancy with a median survival of only 14 months. It is characterized by increased activation of one or more tyrosine kinase receptors, particularly epidermal growth factor receptor (EGFR). This receptor is dysregulated in about 60% of GBM tumors. EGFR amplification, over-expression and constitutive activation leads to uncontrolled growth and proliferation of GBM. Although a great deal is known about the aberrant biology exhibited by EGFR-activated GBM, the application of therapies against the biologic processes is limited by the blood-brain barrier, which restricts systemically administered therapies from reaching the brain. Although anti-sense RNAs and small interfering RNAs can be used to target and silence gene expression, exogenously expressed RNAs are susceptible to extracellular and intracellular nucleases as well as activation of cellular immunity against foreign nucleic acids. To bypass these degradatory mechanisms, we take advantage of a natural noncoding RNA gene architecture and the miRNA expression pathway along with an anti-sense targeted approach to alter EGFR expression. In addition, we make use of a polycistronic delivery system to express RNAs targeting splicing and alternative poly-A signal /G-rich elements of the EGFR transcript. DNA delivery vectors were transfected into human GBM cell lines. Results show that our vectors were expressed at high levels with subsequent reduction in full-length EGFR mRNA expression and concomitant activation of alternative therapeutic isoforms. Current strategies include using the polycistronic delivery mechanism to target additional oncogenic transcripts and adapting to a mouse model of GBM.

**SYNTHESIS OF A MINI-REPORTER CONSTRUCT TO TEST GENE TRANSFER
OF RNA THERAPEUTICS.**

**Koushik Muralidharan, Arbaz M. Khan, Kerianne Fuoco, and Hemangi Patel
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Martin J. Hicks, Department of Biology

Glioblastoma multiforme (GBM), a grade IV tumor of the central nervous system, is the most common malignant primary brain tumor, and has a median survival of only 14 months. Poor survival is due to a lack of efficacy in current therapies, including radiation and chemotherapy, which is limited by the blood-brain barrier (BBB). GBM requires new blood vessels, which is essential for tumor growth and survival. Endothelial cells connect with each other and form the walls of new blood vessels, bridging the gap between the growing tumor mass and the established vasculature of the circulatory system. The membrane receptor that activates tumors to recruit endothelial cells to create new blood vessels is vascular endothelial growth factor receptor 2 (VEGFR2). In our lab, we are developing a novel therapy to alter the expression of the VEGFR2 receptor. Changes in VEGFR2 expression to block its activation would inhibit the development of new blood vessels. We are designing therapies to bypass the BBB and deliver the genetic sequences of anti-sense RNA molecules to alter the splicing pattern and expression of the VEGFR2 transcript, creating a soluble VEGFR2 decoy. 9 different antisense sequences were designed to target and block critical elements of the VEGFR2 pre-mRNA transcript, and were cloned into two different therapeutic platform vectors, pAAV-U7-smOPT and pAAV-PTM (contains a pre-trans splicing molecule). We have designed and are cloning a mini-reporter-system that contains the regulatory elements of VEGFR2 splicing. This system measures the efficacy of RNA anti-sense therapeutics to alter the splicing of the VEGFR2 transcript. The visual marker, eukaryotic green fluorescent protein is used to mimic the natural splicing product, whereas the red fluorescent protein, mCherry detects changes in the efficacy of our RNA anti-sense therapy.

DELIVERY OF THERAPEUTIC RNA MOLECULES TO ALTER EPIDERMAL GROWTH FACTOR RECEPTOR EXPRESSION IN GLIOBLASTOMA MULTIFORME

Nicole Sivetz¹, Sanjana Akula², Anjali Chakradhar³, Ester Teper², Lucy Zou⁴, Sarah Falotico¹, and Peter Nekrasov¹

¹Monmouth University Department of Biology

²Biotechnology High School, ³High Technology High School, ⁴East Brunswick High School

Faculty Mentor:

Dr. Martin J. Hicks, Department of Biology

Glioblastoma multiforme (GBM), the most common central nervous system (CNS) malignancy, is characterized by overexpression of the transmembrane tyrosine kinase epidermal growth factor receptor (EGFR). Activated EGFR promotes GBM tumor proliferation and growth. Current prognosis for patients receiving standard care is approximately fourteen months due to the aggressive nature of this cancer and the isolating abilities of the blood brain barrier. Our novel approach to deliver DNA encoding anti-sense RNA molecules to alter pre-mRNA splicing of the EGFR mRNA transcript in GBM cells has the potential to bypass this barrier. In the strategy presented, we have designed a pre-trans-splicing RNA molecule (PTRM) to deliver a polyadenylation signal (PAS) into the EGFR pre-mRNA transcript upstream of the exon corresponding to the transmembrane domain, altering the mature EGFR transcript. In our design, optimization of the EGFR antisense binding domain and a U7 snRNA-SmOpt localization signal will enable the PTRM to compete against the downstream 3' splice sites of the EGFR transcript, generating a shortened mRNA transcript. Additionally, antisense oligonucleotides (AOs) were designed to target critical splicing motifs along the EGFR pre-mRNA transcript to induce alternative splice variants. These shortened transcripts could translate into non-membrane bound soluble peptide decoys and inhibit activation of the EGFR pathway. The PTRM therapy construct and AOs were cloned into an adeno-associated viral plasmid vector and delivered to GBM cell lines. Total RNA was isolated from cells and reverse transcribed using a random primer mix and target-specific primers to generate cDNA. PCR with specifically pre-designed primer sets were used to detect therapy expression and alternative splicing of EGFR transcripts. Our novel approach to harness the cellular pre-mRNA splicing machinery and gene therapy to generate targeted therapeutics may be an effective strategy in the treatment of GBM.

EXAMINING THE ROLE OF FASCIN IN PRIMARY BRAIN CANCERS

Mehdi Husaini and Esra Celik
Monmouth University Department of Biology

Faculty Mentor:

Dr. Cathryn Kubera, Department of Biology

As one of the main actin-bundling proteins found in the body, fascin plays an important role in maintaining many regulatory behaviors, such as proper cell-cell adhesion through cytoskeletal structures. It has been shown to play a role in a cell's motile and invasive properties, making it important to study in cancer cells due to their established overexpression of the protein. Upregulation of fascin in colorectal cancers leads to increased metastatic and invasive properties. Fascin has been previously identified in a set of genes that mediated breast cancer metastasis to the lungs and has been implicated in gallbladder, pancreatic, and prostate cancer as well. Primary brain cancers, which can be very aggressive, also seem to have elevated fascin levels that correlate with tumor grade but have not been studied to the degree of other cell lines, making this a somewhat non-traditional investigation.

In this project, we examine the role of fascin in neural cancers like neuroblastoma and glioblastoma. We characterized fascin gene expression in brain cancer cell lines using RT-qPCR to assess mRNA levels, and immunocytochemistry to determine relative protein abundance. Preliminary results show robust fascin mRNA expression in Neuro2a neuroblastoma and A-172 glioblastoma cells. Immunostaining of both total fascin and phosphorylated inactivated fascin was elevated in mouse Neuro2a neuroblastoma cells when compared to Human Embryonic Kidney cells (HEK-293), which have reportedly low fascin expression levels. A-172 cells also exhibit distinct fascin and phosphofascin localizations throughout the cytoskeleton. We have begun to evaluate whether overexpression of fascin increases motile properties of neuroblastoma and glioma cells in culture using a 3D gel matrix invasion assay to observe cell movement into unoccupied space in real time. Preliminary findings suggest that cell growth and movement can be observed in the collagen matrix after transfection with GFP and use of EGF as a chemoattractant.

**DEVELOPMENT OF A CRISPR-CAS9 PLASMID TARGETING
THE *GALLUS GALLUS* GENE GABRA2**

Charlotte Kelly

Monmouth University Department of Biology

Faculty Mentor:

Dr. Cathryn Kubera, Department of Biology

The gamma-aminobutyric acid type A (GABA_A) receptor is a ligand gated ion channel that controls aspects such as cell growth and proliferation within *Gallus gallus*. The GABA_A receptor is made up of five subunits, which can be a combination of 2 α (1-6) units, 2 β (1-3) units and a γ (1-3), δ , ϵ , Θ , or π unit.

This study focuses on the α 2 subunit of the GABA_A receptor gene, GABRA2. This seems to play a role in alcohol dependency and Fetal Alcohol Spectrum Disorders. Using CRISPR-Cas9, we aim to knockout expression of the GABRA2 gene in chicken cells to examine the importance of GABRA2 function. The CRISPR-Cas9 mechanism of gene manipulation works by making small-guide RNA (sgRNA) directed double-stranded breaks in the DNA to delete a small portion of the target gene to knockout its activity.

To knockout GABRA2 activity in *Gallus gallus* cells, a pU6-(BbsI)_CBh-Cas9-T2A-mCherry CRISPR-Cas9 (Cas9-mCherry) plasmid was utilized. The plasmid contains a Cas9 enzyme to cut the DNA, a fluorescent mCherry reporter, and a space to insert target sequences. sgRNA oligonucleotides that were created as target sequences for the gene were subcloned into the plasmid, which was then transfected into DF-1 chicken fibroblast cell culture to ascertain expression of the Cas9-mCherry. Once effective knockdown of GABRA2 is assessed in culture, the Cas9-mCherry plasmid will be employed *in ovo* to determine the effect of GABRA2 deletion on the migration and differentiation of granule cells in the developing embryonic cerebellum.

**CHARACTERIZING THE EXPRESSION OF GABA_A RECEPTOR SUBUNITS
IN DEVELOPING *GALLUS GALLUS* CHICK**

**Nadine Khalil and Victoria Reggio
Monmouth University Department of Biology**

Faculty Mentor:

Dr. Cathryn Kubera, Department of Biology

Exposure to alcohol during gestation may induce abnormalities like Fetal Alcohol Spectrum Disorders (FASD). One possible contributor could be premature activation of GABA_A receptors (GABA_AR) by embryonic exposure to ethanol. Furthermore, GABA_AR encoding genes like $\alpha 2$ have been linked to the possible development of alcohol dependency. To better understand this relationship, we investigated the expression of GABA_A receptor subunits in *Gallus gallus* chicks throughout embryonic development.

The expression pattern of GABA_A alpha (α) subunits 1-6 and beta (β) subunits 1-3 was assessed at six developmental time points: embryonic day (E) 7, 9, 11, 13, 15 and 17. In cerebellum at E7, only $\alpha 5$ and $\alpha 6$ were not detected. Focusing in on $\alpha 2$, expression was observed as early as E7 in the cerebellum, optic tectum, and forebrain, and expression continued throughout the remainder of embryonic development. Transcript expression was measured by reverse transcription quantitative polymerase chain reaction (RT-qPCR) performed on isolated mRNA from the cerebellum, optic tectum, and forebrain of E7 - E17 chick embryos.

The liver was also extracted at each time point and $\alpha 2$ expression was measured via RT-qPCR as a negative control. However, unexpected expression of $\alpha 2$ was present for the liver at most timepoints. Recent evidence suggests hepatic cells also have their own form of GABA signaling. To determine whether $\alpha 2$ detection in the liver is real or due to mRNA contamination during sample preparation, the expression of two transcripts was measured at each time point: GRIN1, whose expression is enriched in brain, and TAT, whose expression is enriched in liver. We would expect that expression of GRIN1 would be present in the forebrain, optic tectum, and cerebellum samples at each time point but not in liver, and expression of TAT would be present in the liver samples at each time point but not in brain.

THE USE OF ESSENTIAL OILS TO COMBAT *STREPTOCOCCUS PNEUMONIAE*

Eric Bryan

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Dr. James Mack, Department of Biology

Over the past several decades, multidrug resistant bacteria have become increasingly prevalent in nosocomial and community environments. This has drawn concern from a number of national health agencies including the CDC (CDC, 2017). As many antibiotics become less effective in treating many bacterial infections, the need for alternative ways of combating these resistant strains has grown significantly (Nikaido, 2010). Essential oils, which are metabolic products of many plant species, are of great interest to researchers due to their antimicrobial effects on many species of bacteria (Nazzaro, 2013). In this research project, the efficacy of using essential oils (specifically cinnamon, cassia, and oregano) to combat the bacterium *Streptococcus pneumoniae*, a species that is developing antibiotic resistance, was investigated using the Kirby-Bauer Disk Diffusion Susceptibility Test. This was done by aseptically pipetting each of the essential oils onto blank diffusion disks. These disks were then transferred onto media plates growing the bacterium and the plates were incubated. The zones of inhibition formed around the disks were measured and compared to Ciprofloxacin, an antibiotic standard currently used to treat infections caused by this bacterium. Results of these experiments showed that the tested essential oils (cassia, cinnamon, and oregano) had inhibition zones better than or equal to the standard Ciprofloxacin. The results indicate that these essential oils may be a potential alternative way for treating infections caused by *Streptococcus pneumoniae*.

NEW APPROACHES TO STUDYING GENE EXPRESSION IN HOUSE MICE

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Studying gene expression can help us understand evolutionary processes such as speciation and adaptation. Recently, next-generation sequencing of RNA transcripts (RNA-Seq) has expanded the scope of gene expression analyses from a handful of genes to the entire genome. However, as generating sequence data has become cheaper and faster, the computational requirements of RNA-Seq have become challenging. The most commonly used method of analyzing RNA-Seq data applies direct alignment of short segments of RNA to a reference genome, requiring significant computational resources. In contrast, the recently developed programs Kallisto and Sleuth work together analyze RNA-Seq data quickly on a typical desktop computer. Because it is so fast, the data can be re-sampled or “bootstrapped” to quantify uncertainty. In this study, we first aimed to compare the requirements and results for Kallisto and Sleuth with bootstrap values of 100 vs. 1000. Then, we applied the method to data for which transcript level gene expression analysis had been time-prohibitive. For example, we compared gene expression among house mice derived from cold and warm adapted populations in the eastern U.S. We found that additional bootstraps provided little additional information, but increased time requirements by >10 fold. Importantly, we found that transcript level analysis provided valuable additional insight over and above gene-level analyses of gene expression. Overall, our results suggest that Kallisto and Sleuth may be considered as useful tools for quantifying and analyzing RNA-Seq data with limited computational resources, especially for time-prohibitive analyses of differential expression at the transcript level.

**VARIATION IN REPRODUCTIVE TRAITS AMONG HOUSE MICE
ADAPTED TO DIFFERENT CLIMATES IN THE AMERICAS**

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Although house mice, *Mus musculus domesticus*, are not native to the Americas, they have quickly adapted to diverse climates. For example, body size and nesting behavior are two traits linked to fitness that vary among populations from different latitudes, and those differences have a genetic basis. However, little is known about differences in female reproductive traits among populations. Reproductive traits have a direct impact on fitness and there are predictions from life history theory regarding how the seasonality of resources can affect allocation to reproduction. In this study, we analyzed breeding data from colonies of mice derived from populations in Canada, New York, Brazil, Florida, and Arizona. To best address the effects of inbreeding and of potential maternal effects, we first focused on first and second generations of wild-derived mice. Female reproductive traits including age at first litter and average litter size were compared among the five colonies. We found that litter size varied among climates; mice from the cooler regions (Canada and New York) produced larger litters than mice from the warmer regions (Brazil, Florida, and Arizona). This pattern suggests that mice from climates with limited breeding seasons may invest more effort in a given litter. Despite potential impacts of inbreeding and passive artificial selection, these trends persist into the sixth generation of lab bred mice. These findings lay the groundwork for additional genetic dissection of reproductive effort including pup size.

DNA EXTRACTION FROM ATLANTIC STURGEON SPINE AND FIN TISSUE

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The Atlantic Sturgeon, *Acipenser oxyrinchus oxyrinchus*, is an anadromous fish listed under the US Endangered Species Act. Along the East Coast, it spawns predominately in the Hudson, Delaware, and James rivers. It is estimated that there been a 99.5% loss of population in the Hudson River area since 1890. This population crash has been primarily attributed to anthropogenic activities that endanger both the fresh-water juveniles and the salt-water adults. Smaller populations are vulnerable to the effects of inbreeding and genetic drift that can lead to decreased genetic diversity impacting future generations. The goal of this project was to determine if standard methods for the extraction of DNA from tissues could be easily amended with a liquid nitrogen grinding step to extract DNA from archaic bony spine samples. We found that while high quality, high concentration DNA could easily be extracted from fin clips stored in ethanol, only low quality, low concentration DNA could be extracted from spines. While this DNA may be adequate for some genetic screens, future work will focus on testing more sophisticated methods for extracting DNA from archaic bone samples. The ongoing goal of this project is to assess genetic change in Atlantic Sturgeon populations and aid the conservation efforts.

**IDENTIFYING PATHWAYS WITH SIGNALS OF GLOBAL REGULATION
LINKED TO ENVIRONMENTAL ADAPTATION IN HOUSE MICE**

Sebastian Vera

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Dr. Megan Phifer-Rixey, Department of Biology

House mice from different climates in the Americas show strong evidence of environmental adaptation, including differences in gene expression. Here, the goal was to determine if there was evidence for differences in global regulation of pathways in mice from different environments. To do this, we used existing data on gene expression for lab-raised mice derived from different climates and gene pathway data. We identified all the genes in all annotated pathways for mice and determined whether expression was greater in cold climates vs warm climates or vice versa for each gene. We repeated this for different tissues. Then, we used a binomial test to determine whether, in each pathway, more genes than expected were responding in the same direction. In each tissue, we identified a number of pathways that show concerted changes between the populations, including some related to traits known to differ between the populations. In particular, we found overwhelming evidence of pathway level differences in expression in fat tissue and body weight is a trait that stands out as a major difference in morphology between these populations. Future analyses will include applying this method to classes of genes known to affect phenotypes in mice and to genes associated with ontology categories.

LIPID RAFT DYNAMICS DURING CO-USE OF ALCOHOL AND STIMULANTS

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Faculty Mentor:

Dr. Dennis Rhoads, Department of Biology

Binge consumption of alcohol is intensified by co-use of stimulants such as caffeine and amphetamine, the active ingredient in Adderall. Our lab is attempting to model co-use of alcohol and stimulants in adolescent Long-Evans rats. Earlier studies showed that administration of caffeine or amphetamine with ethanol resulted in decreased severity of subsequent alcohol withdrawal symptoms. If withdrawal symptoms are masked by stimulants, individuals would presumably have lost an important “cue” for emerging alcohol dependency. A prime candidate for brain interactions between alcohol and stimulants is the NMDA glutamate receptor. Cellular dynamics for this receptor may be controlled in part by its localization to lipid rafts. Lipid rafts were isolated as detergent resistant membrane fragments from forebrain regions of adolescent rats that were fed alcohol alone or in combination with a stimulant. Pair-fed rats with no additions to the diet and rats receiving stimulant alone served as controls. Western blotting was used to identify the raft marker flotilin and NMDA receptor. Two fractions were confirmed to contain flotilin and there was a marked increase in the less buoyant of the two fractions from rats consuming alcohol. Both raft fractions contained NMDA receptor with correspondingly higher levels in the less buoyant fraction from rats consuming alcohol. Location of NMDA receptors in an “alcohol-sensitive” raft fraction may help account for its upregulation during chronic alcohol consumption. Interestingly, these increases in the less buoyant raft fraction were eliminated when rats were consuming caffeine with alcohol. We conclude that caffeine alters alcohol-sensitive lipid raft dynamics to prevent elevation in NMDA receptors and this could contribute to the reduction in alcohol withdrawal severity characterized previously. This model may help explain differences in alcohol addiction patterns as they relate to co-use of alcohol and stimulants.

SOURCES OF STRIPED BASS (*MORONE SAXATILIS*) IN THE MIXED-STOCK RECREATIONAL FISHERY IN NORTHERN OCEAN COUNTY, NEW JERSEY

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Monmouth University Department of Biology**

Faculty Mentor:

Assistant Dean John Tiedemann, School of Science
Director, Marine and Environmental Biology Policy Program

There are three major Atlantic coast spawning grounds for striped bass - the Hudson River, Chesapeake Bay and its tributaries and the Delaware River system. Individuals from each of these stocks comingle within the migratory population of striped bass moving along the coast although the relative contribution of each spawning stock to the migratory population fluctuates annually. As a result, the coastal striped bass recreational fishery is a mixed-stock fishery and anglers in New Jersey may be catching fish from any of the striper's geographically distinct spawning areas during the spring and fall migratory runs.

The primary objective of this project is to use genetic stock discrimination techniques to identify the stock-specific origin of striped bass in the fall fishery in northern Ocean County, New Jersey and estimate the relative contribution of individual spawning stocks to the fishery centered on this region. To accomplish this, small pieces of pelvic fin tissue are removed from angled fish and processed to yield DNA for characterization of genetic variation among individuals of the same species.

This fall, 84 fish were sampled by volunteer anglers while surf fishing from beaches of Ocean County. Typical surf fishing gear with artificial lures was the predominant mode of fishing. Upon landing a striped bass, anglers followed a standard procedure for obtaining fin clips. Their samples were subsequently dropped off at local bait and tackle shops, picked up weekly, and transferred to the lab at Monmouth University. Once delivered to our lab total DNA was extracted and quantified from the fin clip samples using DNA purification and isolation kits. The resultant purified DNA is ready for the Polymerase Chain Reaction (PCR) to amplify the DNA. Once amplified, the DNA is sequenced and a genetic "fingerprint" of the population (stock) the fish came from is identified.



Department of Chemistry and Physics
Abstracts

**UNRAVELING THE B TO A CONFORMATIONAL TRANSITION
IN DUPLEX DNA CONSTRUCTS AT SINGLE BASE PAIR RESOLUTION**

Kirsten P. Lawson

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Faculty Mentor:

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The transition of the standard B-form DNA helix to A-form DNA was first seen by X-ray imaging of DNA fibers. Over time, the structures of B and A DNA were further characterized with many higher resolution crystal structure. Significant characteristically different properties of B form and A form DNA include helical differences per base pair of 3.4Å for B form and ~2.9Å for A form, sugar pucker is C2'-endo for B and C3'-endo for A form and far less hydration of A form. Observations of protein and nucleic acid complexes indicated that B-DNA is commonly converted to A-DNA upon binding of proteins. The transition of B-DNA double helix to A-form is essential for biological functions as recognized by the presence of A-form DNA in many protein-DNA complexes. Recently it was proposed that the shorter length of the A-form DNA compared to the B-form DNA might play an important role in duplex DNA packaging in bacteriophages and that this conformational change might itself serve as the source of the large forces generated by the DNA packing motors. While it is known that the B to A conformational transition occurs, the specifics, like where in the DNA it originates, how it propagates and detailed step-by-step mechanism involved are still unknown. By using site-specifically labeled synthetic oligonucleotides, our aim is to explore the local and global conformational changes in this highly biologically relevant transition. After characterizing the B to A transition in duplex DNA, our aim is to compare the A-form conformation in DNA duplex with that found in DNA-RNA hybrid as well as DNA-protein complexes. Further we will introduce small organic molecules to enhance the stability of these structures and will use computational modeling to support our observations.

**A SPECTROSCOPIC APPROACH TO UNDERSTAND THE STRUCTURAL
INTRICACIES OF NON-CANONICAL NUCLEIC ACID CONFORMATIONS**

Brandon C. Rosenblum and Jacqueline R. Evans
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Faculty Mentor:

Dr. Davis Jose, Department of Chemistry and Physics

A molecular level understanding of the structure and function of the macromolecular machines of gene expression is a major theme of Biology. The local conformations of individual nucleic acid bases are important components in processes fundamental to gene regulation. In this project our focus is to elucidate the structural complexities of unusual DNA conformations such as G-quadruplexes and T-loops at single base resolution. G-quadruplexes and T-loops are unusual nucleic acid structures found mainly at telomeres, the multiple repeats of guanine rich sequences found at the linear eukaryotic chromosome ends. G-quadruplex (the four stranded nucleic acid secondary structures) formation can affect chromatin architecture and regulation of replication, transcription and recombination and has been associated with genomic instability, genetic diseases and cancer progression. We are using fluorescent base analogues to study the local conformations of individual bases at specific locations and cyanine dyes inserted into the sugar-phosphate backbone to monitor the backbone motions of different G-quadruplex and T-loop structures. Using these approaches we can compare the structure and stability of various G-quadruplex and T-loop forming nucleic acid sequences and the results will shed light into the conditions that stabilize these secondary structures. Using a variety of spectroscopic characterizations such as UV spectroscopy, Circular Dichroism (CD), and fluorescence, the formation of different nucleic acid structures can be studied for stability, both locally as well as globally. The results obtained should help to clarify the basic science behind many genetic diseases and cancers and will, we hope, be useful in developing therapeutic drugs as well as helping to formulate new methods to treat these diseases.

EXPLORING OXAZOLE-BASED MARCOCYCLE BINDING TO DNA

Omar Shah

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Faculty Mentors:

Dr. Yana Kholod, Department of Chemistry and Physics

Dr. Dmytro Kosenkov, Department of Chemistry and Physics

The presented research is devoted to a computationally-aimed selection of small organic molecules, called ligands, that have shown potential as anti-cancer drugs with low toxicity. Different ligands, depending on their structure and substituents, bind highly selectively to certain DNA forms. In the current work, a small set of oxazole-based macrocycles has been selected as a starting point, to explore the potential of these molecules for optimal binding to specific DNA forms, and subsequent targeted inhibition of telomerase in cancer cells. A comprehensive sampling of various conformations of the preselected oxazole-based macrocycles has been performed, and later followed by molecular docking. The density functional theory (as implemented in the B3LYP functional) has been employed for geometry optimization of the selected conformations. At the next stage, molecular docking methods, embedded into the AutoDock4 program, has been used to explore the ligand interactions with DNA. Currently, our group is working on predicting the DNA-ligand interactions for other oxazole-based macrocycles.

**ANALYSIS OF EXCITATION ENERGY TRANSFER IN PIGMENT-PROTEIN
COMPLEXES WITH PyFREC SOFTWARE ANALYSIS OF EXCITATION ENERGY**

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Dr. Dmytro Kosenkov, Department of Chemistry and Physics

Discovery of fundamental mechanisms of photosynthesis and further advancements of solar cell technology requires the understanding of kinetics of electronic excitations and associated excitation energy transfer (EET) in pigment-protein complexes. Electronic couplings (EC) and rates of EET in pigment-protein complexes have been calculated and analyzed based on the Förster theory, analyzing the resulting spectral overlap of donor emission and acceptor absorption. The calculations have been carried out with the PyFREC (Python Fragment Electron Coupling) software which enables evaluation of EC and EET in a complex molecular system by splitting the system into individual coupled fragments (e.g., bacteriochlorophylls) based on their molecular geometry. UV-Vis spectral analysis was also carried out with TD-DFT methods on each fragment using Gaussian09 software to calculate the twenty lowest singlet excited states of each bacteriochlorophyll molecule of study. The information derived from each calculation is necessary in understanding the photosynthetic nature of each pigment-protein complex.

MICROWAVE ASSISTED SYNTHESIS OF QUINAZOLINES

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Faculty Mentor:

Dr. Massimiliano Lamberto, Department of Chemistry and Physics

Epidermal growth factor receptor (EGFR) upregulation is closely associated with tumor metastasis, treatment resistance, and poor patient prognosis in a variety of malignancies. This widely-expressed tyrosine kinase activates critical signaling pathways to promote cell survival and proliferation, thus EGFR is an attractive therapeutic target. The development of EGFR inhibitors compounds, such as erlotinib and gefitinib, has resulted in agents with antitumor activity in several cancer models, yet toxicity and mutation-mediated resistance remain major obstacles. To address these issues, the protein structure of tumor-specific EGFR isoforms can be exploited during inhibitor development to increase drug efficacy and selectively differentiate tumor cells from normal cells expressing wild-type EGFR. A number of substituted quinazolines have been previously demonstrated to be potent EGFR inhibitors but their synthesis schemes can be lengthy and complex. Here, we propose utilizing rapid microwave-assisted synthesis to access a variety of scaffold compounds with previously demonstrated efficacy against EGFR activity, among other applications. This strategy not only produces compounds in comparable or even increased yields compared to traditional synthesis techniques, but microwave-assisted chemistry enables more facile adjustment of these inhibitor structures to subsequently alter their biological activities

CLONING OF T7 RNA POLYMERASE

Karla Clavelo

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Dr. Jonathan Ouellet, Department of Chemistry and Physics

This project is centered around cloning the coding sequence for the T7 RNA polymerase bacteriophage within the plasmid pUC19. This bacteriophage is known for being highly specific for its T7 phage promoter, meaning it will transcribe DNA that is linked to its promoter. This quality makes T7 RNA polymerase ideal for producing RNAs and directing gene expression within cells. The plasmid pUC19 was used along with DNA inserts for the T7 RNA polymerase. The DNA inserts, labeled A, B, C, and D were amplified with PCR and then purified through agarose gel. The inserts C and D were combined into CD and inserted into pUC19 after digestion with HINDIII and PSTI restriction enzymes. The CD insert and pUC19 were ligated using T4 DNA ligase and then transformed using BL21 E. coli competent cells. Currently, the transformations have yielded no bacterial colonies so the protocol for PCR of DNA inserts, digestions, purifications, and ligations have been redone. Ultimately, all DNA inserts will be ligated into pUC19 and transformed into E. coli. Considering the central dogma of molecular biology, we are working with DNA that will be transcribed into RNA and eventually translated into a protein. This will effectively amplify the T7 RNA polymerase.

SELECTION OF AN APTAMER THAT BINDS GLUCOSE

Emma Stowell

Monmouth University Department of Chemistry and Physics

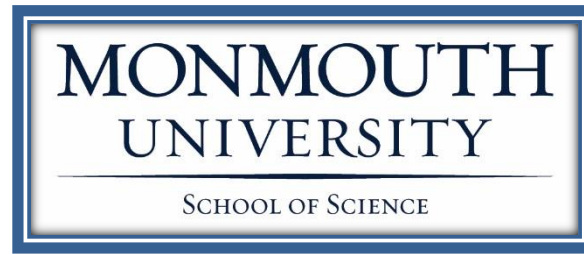
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Type 1 diabetes is a metabolic disease which occurs when the pancreas does not produce enough insulin, resulting in high blood sugar levels. It can be a debilitating condition, as the most popular form of treatment involves regular injection of insulin. Furthermore, the medical and financial burden of diabetes is only increasing. Because of these factors, there is an immense need for research and development to mitigate issues pertaining to type 1 diabetes.

This project explores the development of an aptamer, a type of RNA molecule, which binds specifically and selectively to glucose. To develop the aptamer, systematic evolution of ligands by exponential enrichment (SELEX) was used. However, after sequencing it was found that the aptamer was not binding glucose selectively. Thus, more stringent SELEX conditions were implemented. After four generations of stricter SELEX, a decrease in RNA which binds to molecules other than glucose and an increase in RNA which binds to glucose was seen. This indicates that the aptamer pool became more selective to glucose and these results are explored in the poster. However, SELEX will be continued until the most selective aptamer is isolated.

Once the most selective aptamer is isolated, it will be converted to a riboswitch. The riboswitch will then have the ability to regulate the production of insulin in the presence of glucose. This technology could lead to the development of a new treatment method for type 1 diabetes that would be both less stressful and pain free for patients.



Department of Computer Science and Software Engineering
Abstracts

**MONMOUTH MEDICAL CENTER SURGEON RESIDENCY PROGRAM
EVALUATIONS MOBILE APP**

Kalyna Reda

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Faculty Mentor:

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

Monmouth Medical Center (part of Robert Wood Johnson Barnabas Health) Surgery Residency program trains residents and molds them into future surgeons. Throughout this 5-years training process, evaluations are required for improving both the residents' skills and the attending surgeons teaching techniques. With the shift in use of technology, the current paper-based forms are out of date and either not filled or done at a much later time losing valuable information that could have been captured at the time of evaluation. Monmouth Medical Center Director of Surgery approached CSSE department to see if there a way to make the process more efficient using mobile phones and tablets. Upon searching the app store, there is nothing on the market for doctors to use to evaluate the intensive training that goes on. In this project, we developed a mobile app to increase evaluation completions would improve training programs tremendously. Both the trainee and trainer could see where he or she can improve and track his or her progress. Being that this has not been developed before, the results are unknown and limitless. We hope that the application would result in an increase in usage of the evaluations, a way for the administrators to view all evaluations, and the evaluations being filled out electronically in less than a minute. The app is scheduled for presentation to surgeons at Monmouth Medical in coming months, and possibly to top surgeons in the country at a national surgeons conference later this year.

IT LAB ASSISTANT APPLICANT WEBSITE AND DATABASE

Paul Miceli

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Faculty Mentor:

Professor Jan Rohn, Department of Computer Science and Software Engineering

As time goes on, it is important to digitalize the things that we do. This makes it easier to manage the tasks that need to be done. In this case, IT Lab Assistant Applications were done by paper and the need for a better way to deal with applications was needed. This project's main goal is to develop a website that will allow IT Lab Assistants to apply for a position and then store the applicant information into a database. The database is to be used for creating a schedule in which a lab assistant is assigned to each course section based on their qualifications, preferences, and availability. There are three main objectives for this project: have a website so that students can enter information and apply to be an IT Lab Assistant, store the information into a database, and create reports based on criteria on the application. The results of this project will be a better way to apply and manage IT Lab Assistant applications.

INTERACTIVE CAMPUS MAP FOR MONMOUTH UNIVERSITY

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Faculty Mentor:

Dr. Daniela Rosca, Department of Computer Science and Software Engineering

The purpose of this project, developed as a Software Practicum project by four senior Software Engineering students, in collaboration with Geographic Information Systems Professor Geoffrey Fouad, is to design and build an online interactive campus map that will allow students and visitors to easily navigate Monmouth University campus. It is being implemented as a prototype that can be used as a proof of concept to potentially be built upon by other student groups in the future. The interactivity of the map will help users (current students, prospective students, faculty, visitors, etc.) clearly visualize the campus and gain a better understanding of campus facilities, where they are located, and what they have to offer. The map identifies important campus elements, including buildings, sports fields and recreational areas, paths and walkways, and parking lots. It also contains several optional layers that show the locations of additional campus amenities, such as restrooms, computer labs, dining options, and Monmouth University Police Department “Blue Buttons”. In addition to displaying information about areas of interest on campus, this application also provides an important feature, which calculates walking directions between two selected map locations, and estimates the time to navigate from one location to the other. The map application was developed using the classic Waterfall software process model. This is a sequential model, consisting of requirements, design, implementation, testing, and maintenance phases. Technologies learned by the students and utilized for the development of the map are as follows: JavaScript, HTML, and CSS programming languages, ESRI technologies including ArcMap, ArcGIS Server, and ESRI JavaScript 4.6 API, as well as Node.js, RESTful services, and Proxy. The ultimate goal of this project is to develop a highly intuitive, interactive map of the Monmouth University campus that will replace the static image currently used on the school’s website.

MYXR

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MYXR is a software application that allows entertainment industry professionals to stay connected with their clients, improve their process, provide a marketing solution, manage and increase communication between businesses and clients, and create a dynamic way for guests to interact with each other before, during, and after an event. Communication is a huge problem in the entertainment industry, whether the event owner requires the timeline of an event to be changed, guests request and vote on multiple songs to a DJ during an event, or guests need to reach out to the business owner.

For the MYXR team's Software Practicum class, we focused on the core features of the application that comprise a live chat feed, song request system, and management of the event timeline. The team plans on continuing to update the project features after graduation, and convert the project into a commercial application.

Throughout the process of creating the application, the MYXR team has undertaken an agile development process, including iterative planning, designing, and requirements gathering, comprehensive coding, and testing including black box, white box, and UX testing over multiple sprints. MYXR is currently an iOS application, developed in xCode with Swift. The database was securely stored and encrypted with Firebase. The team plans to develop the app for Android as well, and release them to the Android Google Play Store and iOS AppStore.

In completing the project, the team hopes to mitigate the common issues mentioned above, making the businesses more efficient overall, and allowing guests to enjoy the event even more.

The MYXR team has presented their project at the ThinkTank challenge in November 2017, hosted by Monmouth University and won 3rd place. The team is planning on presenting at Monmouth's Hawk-Tank Challenge in April 2018, and is actively involved into identifying possible investors into the project.

TRUFISHING MOBILE APPLICATION

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Faculty Mentor:

Dr. Daniela Rosca, Department of Computer Science and Software Engineering

The primary purpose of this application is to bring a social media aspect to the fishing community, as well as attracting new members. The application's goal is to bring users together in a fun way and revive the fishing culture among the youth. It is designed in the form of a game in order to attract the younger population. The game will have a point system to reward the winning user of said challenge. Challengers can be invited by friends who create the challenges with a set of rules. In order to win challenges, the challengers must capture themselves catching a fish based on the rules. Users will also be able to go back and view their catches via a catch feed. The system will be linked to Facebook and other social media platforms in order to share catches and fishing experiences.

The client of the project is TruFishing, a startup for the users of the fishing community. The project is currently being built by a team of engineers from Monmouth University. Their process involved working with the owner of TruFishing to design, implement, and fine tune a TruFishing application for iOS framework. The app was built in Xcode using Swift 3 with a backend in Google Firebase. The team used an Agile process to design and develop the application over the course of the 2017-2018 school year. Five sprints were planned to complete development of the application by the end of the 2018 Spring semester. At the end of each sprint, the team produced a deliverable to share with the owner of TruFishing for feedback and approval. By the end of the project, the team gained knowledge of the work necessary to develop an application from the ground up, dealing with a real customer, and building a product that started with a vague idea and transformed it into a real application.

AMERICAN SIGN LANGUAGE RECOGNITION AND SPEECH

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When the transmission of verbal messages is impossible, people often shift to sign languages. It can also assist in situations where writing, as well as typing, is difficult. Therefore, sign language is vital in aiding communication among people with disability. This special group of individuals finds it hard to communicate with people who do not understand the sign language. At certain times, miscommunication often leaves the sender and receiver of a message frustrated and helpless. The American real-time sign language recognition system (ASLRS) can reduce these communication obstacles (Garcia & Viesca, 2016). It utilizes Convolutional Neural Networks that are critical in translating a user's video to text. The objectives and goals of the project is to leverage computers in the improvement of communication between people with disabilities in speaking and others in an effective way, especially for everyday purposes. This will depend on and use the American Sign Language (ASL). Furthermore, achieving a quick response from the computer in translating the sign language is paramount, as effective communication depends on the information being conveyed in a real-time fashion. This translation of the signs into their corresponding letters will have to be fine-tuned to allow for natural timing shifts between gestures, and should not require the user to take long pauses between gestures, as that may cause an unnatural feeling. In this project, we are using Google Inception version (3) Architecture, which is a deep learning technique to allow the system to discern which sign language gesture is being conveyed and map that to the alphabet through the use of a camera attached to the system. In conclusion, deep learning algorithm is the best fit field for solving complex problems such as recognizing sign language at the present time. It gives us freedom to control and consume a large amount of datasets that a single human brain may be unable to contain and the translation of sign language to letter and speech is our main goal in this project.

MONMOUTH UNIVERSITY'S SCHEDULING ENVIRONMENT (MUSE)

**Joey Baldasari, Michael Hunt, Stephen Kresevic,
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Monmouth University Department of Computer Science and Software Engineering

Faculty Mentor:

Dr. Cui Yu, Department of Computer Science and Software Engineering

There exist current and potential issues with how Monmouth University students pick classes. This “picking” process is often quite time-consuming, especially for freshman and/or transferred students. Some students rely heavily on their advisors. The efficiency and effectiveness is an issue. Although there is no statistical data regarding the validity of the statement, unfortunately there is always a possibility of miscalculated class schedulings. To make class selection simpler and easier, we build a prototype, Monmouth University’s Scheduling Environment (MUSE), which is to provide at least one generated schedule for a desired semester. The user (student) will log into the webpage that will securely analyze their audit and match the courses needed with courses in a semester. This version of the prototype will at least have features including class filters, week day and time filters, general professor information and filters, and matching full/part time credit requirements. Despite the potential success of this prototype, the following, but not limited to, may not be including upon release: automatic registration after advisor approval, suggested classes by semester, efficient major/minor program recording and analyzing, and efficient mass web traffic control. This prototype will heavily rely on student audit, which isn’t always accurate; for this reason, users still should discuss the generated schedule(s) with their advisor before registering. MUSE is targeted to benefit students who have the newly structured audits and is meant to be the start of Monmouth University’s official automatic scheduling system.

XANADU: A CONVENIENT WEB-BASED OCR TOOL

**Matthew Fullerton, Anthony Hamill, William Jones, Thomas Reilly, and Luke Tomkus
Monmouth University Department of Computer Science and Software Engineering**

Faculty Mentor:

Dr. Cui Yu, Department of Computer Science and Software Engineering

In the modern world, many wish to convert physical, text-based documents to an editable text document that they can save for the sake of the document's longevity, manipulation, digital searching procedures, and more. Our project is to develop such a software application, named as XANADU. In this project, we choose to exploit the use of Optical Character Recognition (OCR), which translates written text to editable text. We also try to provide a simple and intuitive route for users with the aforementioned intent. To bring these ideas to fruition, XANADU uses Google's open source OCR library (dubbed 'Tesseract') to convert images of text to editable text documents. This application is designed to be web-based and adaptable to fit any device screen, providing a clean and intuitive interface with the use of the Angular framework. To achieve good accuracy, our implementation is added with image processing techniques, and a natural language processing algorithm to filter the resultant text through refinement and error checking. Our main image processing technique uses a cropping tool, which will allow users to crop their photos before being interpreted by Tesseract in order to gain better accuracy. Once Tesseract returns the text, it will go through the natural language processing algorithm to correct any grammatical errors. Our goal is to build a convenient Web-based OCR Tool, which has improvement upon existing technologies by returning more accurate results and providing superior user experience for all that desire it.



Department of Mathematics
Abstracts

ANALYSIS OF IRREGULAR PATTERNS IN TIDAL ELEVATION

Dillon Henrichsen

Monmouth University Department of Mathematics

Faculty Mentor:

Dr. Joseph Coyle, Department of Mathematics

Normal tidal patterns have an underlying smooth periodic oscillating, or sinusoidal, behavior. In the case of irregular phenomenon such as storm related situations, the usual pattern may be temporarily disrupted. In this project we attempt to identify irregular tidal elevation patterns by analyzing the Discrete Fourier Series over fixed periods of time. In particular, we consider the change in the Discrete Fourier Coefficients between periods of time with relatively normal patterns to that of known disruptions. The data we analyze is taken from a tidal gauge located on the Shrewsbury River at Sea Bright, NJ (USGS 01407600).

**ANALYZING THE EFFECTIVENESS OF THE 2010 NEW JERSEY
EMERGENCY OPERATION PLAN MANDATE**

**Taylor Donovan and Dillon Henrichsen
Monmouth University Mathematics Department**

Faculty Mentor:

Dr. Richard Bastian, Department of Mathematics

Client:

Lt. Christopher York, Rumson, NJ Police Department

This analysis was conducted to determine if the 2010 New Jersey Emergency Operation Plan Mandate had any impact on the rates of school violence, vandalism, drug use, and weapons use in both AB and IH districts in the New Jersey school system. The Emergency Operation Plan was a statewide program implemented to ensure the safety and wellbeing of students of all ages in emergency response situations. The plan required fire, active shooter, and shelter in place drills to occur at each school at least twice per year. The aim of this study was to determine if the plan mitigated the number of school violence, vandalism, drug use, and weapons use reports, and also to determine if there was a difference in incidences reported from AB or IJ districts. School districts within the state are assigned a letter grade based on the funding available to them through the state. To compare the number of reports from years before the mandate to the years following the mandate, a chi-square analysis and Poisson regression will be run. This project was designed in coordination with Lieutenant York of the Rumson Police Department.

STATISTICAL ANALYSIS: DOG-OWNER BEHAVIOR IN PLAY PARKS

Melissa Culmone and David DiMasi
Monmouth University Department of Mathematics

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics

Dr. Lindsay Mehrkam, Department of Psychology

Dog parks can be found throughout the nation and are not only beneficial for communities, but also for the physical and mental wellbeing of pet dogs. These locations allow dogs to exercise and play off-leash in controlled and supervised environments, as well as interact with other canines. It is speculated that typical dog owners are likely unaware of the actual indicators of aggressive behavior that can be seen within dog play. This study was conducted in the hopes of not only distinguishing such “red flag” indicators, but to also provide insight into proper owner intervention and ultimately make dog parks safer through the influence of policy. There were 400 different dogs and 950 play bouts observed in two dog play parks throughout the duration of the study. It is hypothesized that some of the 68 play behaviors of interest can be determined to be specific precursors to aggression. Dr. Mehrkam conducted her study and received her data from March to November of 2017. This observational study involved daily 30 minute recordings of play and involved the work of four coders.

STATISTICAL ANALYSIS OF SPORT LEADERSHIP BEHAVIOR, ATHLETE SATISFACTION AND GROUP COHESION AMONG DIVISION 1 FEMALE COLLEGIATE SOCCER PLAYERS IN THE U.S.

**Rebecca Klee, Alyssa Parker, and Larissa Russo
Monmouth University Department of Mathematics**

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics
Coach Kristine Turner, Department of Athletics

Kristine Turner is the head coach of Monmouth University's women's soccer team and is currently studying the relationship between sport leadership behavior, athlete satisfaction, and group cohesion. She hypothesizes that sport leadership behavior is significantly correlated with athlete satisfaction and group cohesion. Additionally, she hypothesizes that sport leadership behavior is a significant predictor of athlete satisfaction and group cohesion. Athlete satisfaction is a positive emotional state linked to athletic experiences and outcomes, sport leadership behavior is a term for leadership characteristics exhibited by sport administrators, sport managers, coaches, and athletes, and cohesion is the process of a group unifying and sticking together to pursue a common goal. The data for this analysis was collected from nationally validated surveys that were distributed to various division 1 female collegiate soccer teams. Among the surveys distributed were the Sport Leadership Behavior Inventory (SLBI), Group Environment Questionnaire (GEQ), and Athlete Satisfaction Questionnaire (ASQ). The SLBI, GEQ and ASQ were designed to measure and assess self-rated leadership characteristics, individual perception of team involvement, and individual satisfaction of athletes, respectively. The survey responses were based on the Likert scale. The independent variable (sport leadership behavior) and the dependent variables (athlete satisfaction and group cohesion) were derived from the survey responses. To analyze this data, linear-regressions were performed, and correlation coefficients were calculated and tested for significance. The results of this analysis will describe the relationship between sport leadership behavior, athlete satisfaction and group cohesion among division 1 female collegiate soccer players in the United States.

STATISTICAL ANALYSIS ON THE EFFECTS OF ESSENTIAL OILS ON BACTERIA

Justine Kukowski

Monmouth University Department of Mathematics

Eric Bryan

Monmouth University Department of Biology

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics

Dr. James Mack, Department of Biology

Bacteria are becoming more and more resistant to antibiotics; this has resulted in treatments becoming ineffective. A new treatment will need to be developed in time to combat various infections. It has been said that essential oils have stronger effects on controlling bacteria than antibiotics; they may be the next new treatment. The effects of different essential oils on bacteria were studied and compared to an antibiotic, Ciprofloxacin. The essential oils were Cassia, Cinnamon, and Oregano. The effectiveness was determined by measuring inhibition zones for each with bacteria; the bigger the inhibition zone, the more effective the treatment.

To do a statistical analysis on this data, several tests were done. Initially, the data was tested for normality. When it did not meet normality, nonparametric tests were used to compare the median values between the essential oils. The test that was used was a Kruskal-Wallis test in which it was determined that the median values were not equal across all essential oils. To determine which median values were different, post-hoc tests were run on all possible pairwise comparisons. The median inhibition zone for Ciprofloxacin was statistically smaller than any of the essential oils, and the median inhibition zone for Cassia was statistically smaller compared to Oregano. Therefore, it was determined that all essential oils work better than Cipro and among the essential oils Cassia was least effective.

**STATISTICAL ANALYSIS ON EDUCATING STUDENTS WITH
AUTISM SPECTRUM DISORDER**

**Justine Kukowski and Nicole Cimaglia
Monmouth University Department of Mathematics**

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics
Dr. Stacy Lauderdale, Monmouth University School of Education

Educating Students with Autism Spectrum Disorder has been given the reputation of being challenging. Though this may be true, could it be because our teachers are not properly trained to work with these students? In teaching students with Autism Spectrum Disorder, there are evidence based practices that educators should follow. In this study, Dr. Lauderdale is investigating if the evidence based practices are being implemented, the level of knowledge teachers have of autism and what factors affect this knowledge. This will be done using APERS self-assessments filled out by teachers from five different school districts, as well as, APERS assessments filled out by in-class observers. The results from this study are intended to develop a model that can be used to train teachers in the evidence-based practices for students with autism.

To do a statistical analysis on this data, several different tests needed to be done. The data did not meet the assumption of normality, meaning that nonparametric tests needed to be done to get results. To compare the APERS self-assessments with the APERS observer assessments, a Wilcoxon Signed-Rank test was done. To assess the use of EBPs and how well these implementations were done, two different Chi-Square tests were run. In addition, a power analysis was done to figure out the necessary sample size to get significant results.

**β -HYDROXY- β -METHYLBUTYRATE EFFECT OF PHYSICAL PERFORMANCE
ON ATHLETIC POPULATIONS**

**Shannon McAleer and Anthony Hamill
Monmouth University Department of Mathematics**

Faculty Mentor:

Dr. Richard Bastian, Department of Mathematics

β -hydroxy- β -methylbutyrate (HMB) claims to be a physical performance nutritional supplement. Supplementation of HMB has reportedly resulted in improved body composition, muscle strength, aerobic capacity, and recovery from exercise. Studies have had mixed results. Some demonstrate an enhancement in physical performance while others do not. Characteristics of the studies such as training regimens, nutrition, study populations, and general methodology has led to these mixed results. As opposed to the other studies, which used samples from recreational or novice participants, this study focuses on athletic populations. These populations consisted of either professional or collegiate athletes from multiple sports. Therefore, the primary purpose of this review is to examine supplementation of HMB in athletic populations. The literature was systematically reviewed via Medline among others. Pending availability and homogeneity of the literature, the study will potentially investigate the magnitude of effect via meta-analysis. It is hypothesized supplementing with HMB will not provide additional benefits in athletic performance when macronutrient intake is matched.

STATISTICAL ANALYSIS OF OCEAN WAVE HEIGHTS IN THE EAST COAST

Jennifer Minor and Kimberly Bianchi
Monmouth University Department of Mathematics

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics
Dr. Thomas Herrington, Monmouth University Urban Coast Institute

Every year between the months of June and November, ocean waves have been seen to have more energy due to the amount of hurricanes that come across the shore. It is already known that there is a seasonality with wave heights, meaning that during the winter season, the average wave height is lower than that of the summer. By using data from a hindcast collected off the shore of New Jersey from 1980 - 2015 and buoy data from a buoy located relatively in the same spot off the coastline of New Jersey, Dr. Tom Herrington is trying to figure out whether the ocean waves from this past year, 2017, are significantly different than those in the past. Wave heights were recorded twice every hour for the buoys and once every hour with the hindcast.

To statistically analyze his research question various steps had to be taken. To look at the average wave heights across the years 1980 to 2017, analysis of variance (ANOVA) tests were needed. For the ANOVA tests to be valid the data had/has to be normal. The wave heights were found not to be normal, therefore an independent sample Kruskal - Wallis Test was used which does not have data normality as an assumption.

STATISTICAL ANALYSIS OF SYNOVIAL FLUID IN CANINES WITH CCL TEARS

Jennifer Minor

Monmouth University Department of Mathematics

Tiffany Longo

Monmouth University Department of Biology

Faculty Mentor:

Dr. Richard Bastian, Department of Mathematics

Client:

Dr. Lindsay Nussbaum, DVM, Red Bank Veterinary Hospital

A tear in the cranial cruciate ligament (CCL) can be devastating to a dog's mobility. The CCL is a group of ligaments that stop a dog's knee from twisting or overextending. Once the ligament is torn, walking for a dog can become painful. When a dog presents these symptoms of a CCL tear such as lameness, there are several tests used to diagnose the problem. These tests include a physical examination of the leg, an X-ray of the injury, and surgery. Surgery is the one test that is accurate when predicting if the dog had a torn CCL or not. Since surgery is costly, our client, Dr. Nussbaum, is trying to find other ways in which a diagnosis of a CCL tear can be made without having to resort to surgery. One of these ways is examining the relationship between blood and synovial fluid. Our client, Dr. Nussbaum, took measurements of the lactate, glucose, alkaline phosphatase (ALP), and electrolytes present in both the blood and synovial fluid of the dog.

To analyze her research question, various steps had to be taken. Since the predictor and response variables were continuous a linear regression test was used. There are various assumptions for a linear regression model. If any one of these assumptions are violated the linear regression test is not valid. The results show that blood levels of glucose, lactate, sodium, and chloride statistically significantly predict the synovial fluid levels of glucose, lactate, sodium, and chloride.

**STATISTICAL ANALYSIS OF THE RELATIONSHIP BETWEEN DYADIC PLAY
STRUCTURE IN DOGS AND OWNER BEHAVIOR**

**Larissa Russo and Kelsey Gripp
Monmouth University Department of Mathematics**

Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics

Dr. Lindsay Mehrkam, Wayne D. McMurray School of Humanities and Social Sciences

There has been minimal research on how type of play exhibited by dog-dog dyads affect owner behavior in a naturalistic setting. Dr. Mehrkam, a psychology professor at Monmouth University, is interested in the relationship between observational owner behavior and interactions between domestic dogs. In a public off-leash dog park, type of play and owner behavior preceding and following the onset of specific play bouts were recorded. The size of the dogs, approximate length of play bout, and number of people in the park at the time of each play bout were also recorded. Dr. Mehrkam hypothesizes that there is an association between antecedent owner behavior (behavior preceding play bout) and the type of play between dogs. Additionally, she hypothesizes that there is an association between consequential owner behavior (behavior after onset of play bout) and the type of play between dogs. She was also curious to determine if there are associations between antecedent owner behavior and length of a play bout, type of play and the number of people in a park, and type of play and the relative or absolute size of dogs. To analyze this data, various chi-square tests were performed. The key results of this analysis indicate that there is a significant relationship between dyadic play structure in dogs and owner behavior in a naturalistic setting.

VARIATIONS IN VIOLENT CRIME

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Faculty Mentors:

Dr. Richard Bastian, Department of Mathematics
Dr. Marie Mele, Wayne D. McMurray School of Humanities and Social Sciences

In 2011, the city of Trenton faced a budget crisis and, as a result, one-third of the city's police force was laid off. At the time, the city's violent crime rate was ranked the 5th highest in the state. The present study aims to examine the effects of this police force reduction by comparing crime between 2010 and 2012. Researchers will analyze the characteristics and rates of violent crimes, such as homicide, robbery, and aggravated assault, within the city. Statistical techniques with include chi-square and logistic regression.

MANGROVE ECOSYSTEMS AND FRAGMENTATION IN THE BAHAMAS

Michael Welch

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Dr. Richard Bastian, Department of Mathematics

Dr. Pedram Daneshgar, Department of Biology

Mangrove forests are ecosystems of great biological diversity comprising hundreds of species, such as algae, mollusk, crustacean, fish, insects, reptiles, birds, and mammals. Because of their sensitivity to the cold, they are essentially found on the coastlines of the tropics and the subtropics. These mangrove trees are very important, as their intricate network provides shelter to an abundance of oceanic species and also provides them food. While being cautious about the preservation of these ecosystems, fragmentation—the process or state of being broken into small or separate pieces, may have an effect on the way the mangroves continue to provide shelter and food. This project examines these fragmentations in the Bahamas. In the Bahamas there are eight different sites with three transects each, and ten points per transect. The number of healthy and sick red seedlings, red saplings, and red adults are recorded. After finding the mean for each species on each site, we are going to compare the means to each other, hoping to find some differences. The results of the project will answer what effect fragmentation has, if at all, on mangrove ecosystems. Also, if an effect is found, new ways to care for mangroves must be explored to keep them from going extinct. Mangroves support an abundant amount of marine life, so without them, other marine life could decline as well.