

9th Annual Summer Research Program Symposium

August 10, 2017 10:30am – 1:00pm Erlanger Garden



School of Science

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The Math Learning Center provides students with assistance in all levels of mathematics. Peer tutors are available to help students solve problems and to review concepts.

MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

9th ANNUAL SUMMER RESEARCH PROGRAM SYMPOSIUM

Thursday, August 10, 2017

PRESENTATIONS BY DEPARTMENT

DEPARTMENT OF BIOLOGY

A-1 Use of Pomegranate Juice Extract and Apple Extract to Treat and to Inhibit Inflammation in Cancers of the Oral Cavity and Glioblastomas

Justin L. Badamo and Angela Rella

Faculty Mentor: Dr. Jeffrey L. Weisburg

A-2 Trends in the Abundance and Spatial-Temporal Variation of Sharks and Rays in New Jersey Coastal Waters

Gina Badlowski and Jarius C. Bradley

Faculty Mentor: Dr. Keith J. Dunton

A-3 Combating the Multidrug Resistant Bacterium ESBL-Escherichia coli Using Selected Essential Oils and Methyglyoxal

Jalize Canela and Eric Bryan

Faculty Mentor: Dr. James P. Mack

A-4 Assessing Coastal Lakes in Monmouth County

Erin Conlon and Daniel Gerdon

Faculty Mentor: James Nickels

A-5 Impacts of Salt on Juvenile Trees of New Jersey Maritime Forests

Jeff Dudek, Jeff Francis, and Kelsey Connelly

Faculty Mentor: Dr. Pedram Daneshgar

A-6 Engineering of an Immunogenic pre-*Trans*-splicing RNA (iPTR) to Block Growth and Reactivate the Immune System in Glioblastoma

Sarah Falotico, Nicole Sivetz, and Peter Nekrasov

Faculty Mentor: Dr. Martin J. Hicks

A-7 Examining the Role of Fascin in Primary Brain Cancers

Syed Mehdi Husaini and Faraz Jamal

Faculty Mentor: Dr. Cathryn Kubera

A-8 Characterization of GABA_A Receptor Subunit in Developing *Gallus gallus* Cerebellum

Charlotte Kelly, Nadine Khalil, and Victoria Reggio

Faculty Mentor: Dr. Cathryn Kubera

A-9 New Approaches to Studying Gene Expression

Bradley Kraft

Faculty Mentor: Dr. Megan Phifer-Rixey

A-10 Monmouth University Beach Nesting Bird Monitoring and Stewardship Program

Shannon M. Lavelle and Bridget N. McCormick

Faculty Mentor: Assistant Dean John Tiedemann Additional Mentors: Christina Davis and Meaghan Lyon, New Jersey Division of Fish and Wildlife

A-11 Variation in Reproductive Traits Among House Mice Adapted to Different Climates in the Americas

Tiffany Longo

Faculty Mentor: Dr. Megan Phifer-Rixey

A-12 Synthesis of a Mini-Reporter to Test RNA Therapeutic Strategies to Block VEGFR2 and Angiogenesis in Human GBM

Koushik Muralidharan, Kerianne Fuoco, Arbaz M. Khan, and Hemangi Patel

Faculty Mentor: Dr. Martin J. Hicks

A-13 RNA Therapeutic Strategies to Alter the EGFR Transcript in Human Glioblastoma Cells

Peter Nekrasov, Nicole Sivetz, and Sarah Falotico

Faculty Mentor: Dr. Martin J. Hicks

A-14 DNA Extraction from Atlantic Sturgeon Spine and Fin Tissue

Brian Reiss

Faculty Mentor: Dr. Megan Phifer-Rixey

A-15 Demographics of the Land-Based Recreational Hook-and-Line Shark Fisheries within New Jersey

Alex Salamone, Gina Badlowski, Marissa C. DeTorre, and Jarius C. Bradley

Faculty Mentor: Dr. Keith J. Dunton

A-16 Identifying Pathways with Signals of Global Regulation Linked to Environmental Adaptation in House Mice

Sebastian Vera

Faculty Mentor: Dr. Megan Phifer-Rixey

DEPARTMENT OF CHEMISTRY AND PHYSICS

A-17 Sampling Oxazole-Based Macrocycles for Binding to DNA

Alvaro Aquino and Omar Shah

Faculty Mentor: Dr. Yana Kholod

A-18 Monitoring Riboswitch Modulation via Fluorescent Gene Expression

Sonia Dadlani

Faculty Mentor: Dr. Jonathan Ouellet

A-19 Development and Isolation of Aptamer for 2-Hydroxyglutarate

Artiom Efimenko and Krima Patel

Faculty Mentor: Dr. Jonathan Ouellet

A-20 Analysis of Excitation Energy Transfer in Pigment-Protein Complexes with PyFREC Software

Grant Gillan

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

A-21 Conformational Analysis and Binding Affinity to DNA of Telomestatin Derivatives

Grant Gillan, Noor Abouchakra, and Sierra Neuman

Faculty Mentor: Dr. Dmytro Kosenkov

A-22 Intramolecular Carbon-Hydrogen Bond Activation at Rhenium(V) Pentahydride Centers

Brian Macalush and Andrew Petrou

Faculty Mentor: Dr. Gregory Moehring

A-23 Acrylamide Gel Stain to Quantify DNA Fragments

Shenin Siddiqui and James Tilton

Faculty Mentor: Dr. Jonathan Ouellet

DEPARTMENT OF COMPUTER SCIENCE and SOFTWARE ENGINEERING

A-24 Use of IoT (Internet of Things) Devices in Healthcare Marketing Services

Kerry Ann DeMeester and Megan Rapach

Faculty Mentor: Dr. Raman Lakshmanan

A-25 Tyreek, Tommy and Takahashi: Race, Names And You Tube's Search

Jonathan Downie and Samantha Inneo

Faculty Mentor: Professor Katie Gatto

A-26 Hurricane Sandy Coast Guard Emergency Response Serious Game

Veronica Granite, Aidan Brown, Evan Frederickson, and Ryan Gilmartin

Faculty Mentor: Professor Jodee Vallone

A-27 Hurricane Sandy Firefighter Emergency Response Serious Game

Veronica Granite, Mike Nelli, Erik Ossner, Phillip Tracy, and Matt Moran

Faculty Mentor: Professor Jodee Vallone

A-28 Business Intelligence and Analytics Portal and Mobile App for Healthcare Service

Daniel Kelly

Faculty Mentor: Dr. Raman Lakshmanan

A-29 Process Improvement for Rapid Response Activation

Michael Marmer and Ping-Jung Liu

Faculty Mentor: Professor Richard Eng

A-30 Sums Law Application

Stephanie Okereke

Faculty Mentor: Dr. William F. Tepfenhart

A-31 Augmented and Mixed Reality Experience (A Residential High Rise Building)

Mahmoud E. Shabana and Craig Holbrook

Faculty Mentor: Professor Martin von Grossman

A-32 Emergency Healthcare Service Workflow Modeling and Analysis

Jiarui Tian

Faculty Mentor: Dr. Jiacun (Jay) Wang

A-33 Goal Tracking and Awarding System for Children and Teens

Clark Wang, Kevin Yan, and Andrew Parise

Faculty Mentor: Dr. Cui Yu

DEPARTMENT OF MATHEMATICS

A-34 The Effect of Active Learning Techniques Utilizing Case Study Work in Anatomy and Physiology

Austin Alcott and Pavneet Kaur

Faculty Mentor: Dr. Richard Bastian

A-35 Statistical Analysis of Essential Oils and Methylglyoxal: A Possible Treatment for Inhibiting the Growth of Escherichia Coli

Kelsey Gripp and Dillon Henrichsen

Faculty Mentor: Dr. Richard Bastian

A-36 Statistical Analysis: How Salt Marshes are Impacted by Nitrogen Deposition Levels

Jennifer Minor, David DiMasi, and Brianna Berenato

Faculty Mentor: Dr. Richard Bastian

A-37 Statistical Analysis of the Effects of Active Learning on Third-Year Medical Students' Attention and Retention of Information

Jennifer Minor, David DiMassi, and Brianna Berenato

Faculty Mentor: Dr. Richard Bastian

A-38 The Boundedness of Systems of Difference Equations with Periodic Coefficients

Nathanial Rodriguez

Faculty Mentor: Dr. Zachary Kudlak

URBAN COAST INSTITUTE

A-39 Bathymetry and Flood Mapping of Lake Como, New Jersey

Thomas Candiloro

Faculty Mentors: Dr. Geoffrey Fouad and James Nickels

A-40 Seasonal Diet and Prey Selectivity of Atlantic Sturgeon in a Coastal Marine Aggregation

Marissa C. DeTorre

Faculty Mentor: Dr. Keith J. Dunton

A-41 3D Hurricane Escape Mobile Application Using New Jersey's Evacuation Routes

Roberto Tanenbaum

Faculty Mentor: Professor Jodee Vallone

A-42 3D Serious Building Game Demonstrating FEMA Methodologies to Reduce Severe Flood and Storm Damage to Homes

Luke Tomkus

Faculty Mentor: Professor Jodee Vallone

DEPARTMENT OF BIOLOGY

ABSTRACTS

USE OF POMEGRANATE JUICE EXTRACT AND APPLE EXTRACT TO TREAT AND TO INHIBIT INFLAMMATION IN CANCERS OF THE ORAL CAVITY AND GLIOBLASTOMAS

Justin L. Badamo and Angela Rella Monmouth University Department of Biology

Faculty Mentor: Dr. Jeffrey H. Weisburg, Department of Biology

Funding Source: Monmouth University School of Science

Nutraceuticals are defined as any products derived from food sources with extra health benefits in addition to the basic nutritional value found in foods. Pomegranate juice extract (PJE) has been shown to have antiproliferative and proapoptotic properties in breast cancer and prostate cancer. Another strong nutraceutical is apple extract (AE), which has been also shown to induce apoptosis in prostate cancer and colorectal cancer. In these experiments, we want to see if PJE and AE could selectively target and kill cancers of the oral cavity, using the human squamous carcinoma HSC-2 cells as compared to human normal gingival fibroblast cell HF-1, and glioblastomas, using the human glioma cell lines A172 and SKMG.

The association between inflammation and cancer has been studied widely so we want to determine if PJE and AE could inhibit vital proteins in the inflammatory process. The transcription factor NF-kB has been a key element in inflammation, and its activation have been shown to upregulate gene expression of other pro-inflammatory cytokines. Although NF-kB was first characterized in cells of the hematopoietic system, research has shown that NF-kB activation can occur in most cell types. Using PJE and AE on all of the cell lines, we want to observe if these nutraceuticals could inhibit or slow down the activation of NF-kB and prevent the inflammatory process. To do this, we needed to determine the sub-lethal concentration of AE and PJE. One of the major signaling molecules in activating inflammation is IL-1 β . IL-1 is an important mediator of inflammation in the CNS by its release from microglial cells, which have also been suggested as targets for its action. It has also been reported that oral cancers secrete interleukin-1 beta (IL-1 β), which promotes the proliferation. We want to examine if treating the cells with the individual nutraceutical can also inhibit the secretion of IL-1 β .

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

Gina A. Badlowski¹ and Jarius C. Bradley² ¹ Monmouth University Department of Biology; ²Rutgers University School of Arts and Sciences

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

Funding Sources: Monmouth University School of Science Monmouth University Urban Coast Institute

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 (long live, late maturing) making the understanding of their abundance and distribution patterns essential for both conservation and management issues (e.g. bycatch). The coast of New Jersey has been shown to have an abundance of shark and ray species but, patterns in the species as well as distributions are relatively unstudied. Through better comprehension of species dynamics along the coast of New Jersey, we can gain a greater understanding of their populations, distribution, and migratory habits and can allow for greater conservation and management.

In 1988, the New Jersey Department of Environmental Protection (NJDEP) initiated a bottom trawl survey to evaluate the state's fishery resources. This survey is conducted 5 times throughout the year encompassing the entire coast of NJ inshore of 30m, representing one of the longest running and comprehensive fishery surveys conducted along the east coast allowing long-term patterns of species to be identified. To understand these patterns in sharks and rays, their distributions were mapped and catch-per-unit (CPUE) was calculated. We identified patterns in 4 species of commonly captured sharks; Atlantic Angel Shark (*Squantina dumeril*), Sand Tiger Shark (*Carcharias taurus*), Dusky Shark (*Carcharhinus obscurus*), Thresher Shark (*Alopias vulpinus*) and 3 species of rays; Roughtail Stingray (*Dasyatis centroura*), Southern Stingray (*Dasyatis americanus*), and Spiny Butterfly Ray (*Gymnura altavela*). 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 is necessary for conservation (e.g. critical habitat use) and appropriate management actions for these species.

COMBATING THE MULTIDRUG RESISTANT BACTERIUM ESBL-ESCHERICHIA COLI USING SELECTED ESSENTIAL OILS AND METHYLGLYOXAL

Jalize Canela and Eric Bryan Monmouth University Department of Biology

Faculty Mentor:

Dr. James P. Mack, Department of Biology

Funding Sources:

Kevin Young '89; doTERRA; Global Essence; Monmouth University School of Science

Due to the overuse of antibiotics, multidrug resistant bacteria have become increasingly prevalent and difficult to control globally. Natural medicinal products are currently being studied for their antibacterial properties with the expectation that they will be effective in combatting multidrug resistance. Specific natural products, such as essential oils and methylglyoxal, are currently being utilized for medicinal purposes (Polly, *et al.*, 2014). Essential oils contain organic compounds such as aldehydes, phenols, ketones, and esters, and it is hypothesized that the composition of these oils play a significant role when treating antibiotic resistant infections (Nazzaro, *et al.*, 2013).

In this study, the essential oils cinnamon bark, cassia, oregano, and the key ingredient of Manuka Honey, methylglyoxal, were tested for their efficacy as emollients made with carrier oils in combating Extended Spectrum Beta Lactamase (ESBL)-*Escherichia coli*. This bacterium is resistant to penicillins and cephalosporins due to its ability to produce an enzyme, called beta-lactamase, which inactivates the antibiotic by catabolizing its key compound, the beta-lactam ring.

The effects of these essential oils and methylglyoxal in combating ESBL-*E.coli* were tested using the Kirby-Bauer Disk Diffusion Susceptibility Method. The inhibition zone produced by each essential oil was compared to that of the currently used antibiotics (Nitrofurantoin, Imipenem, Fosfomycin, and Ciprofloxacin) to determine which of the tested compounds would be most effective against ESBL-*E.coli*. Our *in vitro* results show that the emollients of essential oils, as well as methylglyoxal, inhibit ESBL-*E. coli* growth more-effectively than the antibiotics currently used.

References:

- 1. Nazzaro, F., Fratianni, F., De Martino, L., Coppola, R., & De Feo, V. (2013). Effect of essential oils on pathogenic bacteria. Pharmaceuticals, 6(12), 1451-1474.
- 2. Polly, Beow, Hu, & Swee (2014). Essential Oils, A New Horizon in Combating Bacterial Antibiotic Resistance. *The Open Microbiology Journal*, 6-14.

ASSESSING COASTAL LAKES IN MONMOUTH COUNTY

Erin Conlon¹ and Daniel Gerdon² ¹Monmouth University Department of Biology ²Ocean Township High School

> **Faculty Mentor:** James Nickels

Funding Sources:

Monmouth University School of Science Monmouth University Urban Coast Institute

Monmouth County has 12 coastal lakes located along the Atlantic Ocean shoreline, some of which are located in densely populated urban communities of Asbury Park, Neptune, and Long Branch. The coastal lakes have historically provided a variety of recreational opportunities for area residents and visitors and served as important habitats for fish and wildlife. Unfortunately, the intense development that surrounds the coastal lakes has degraded these aquatic ecosystems. Unnatural modifications to adjacent shorelines and riparian corridors along their tributaries and the introduction of a variety of pollutants from storm water and nonpoint source runoff, has resulted in degraded water quality, disturbed fish and wildlife habitats, and generated increased algae blooms and the invasions of nuisance aquatic plants. As a result, the majority of the county's coastal lakes suffer from neglect and are valued less for the natural resources and the recreational opportunities they offer and instead viewed as an element of a community's storm water drainage system.

The Urban Coast Institute (UCI) along with students from the School of Science have embarked on a project to assess and map coastal lakes in Monmouth County, working with local NGOs, and governmental bodies.

The first phase started this year is to map lakes for water depth and potential accumulated sediments. The work is being conducted using a newly acquired autonomously controlled surface vessel (ASV). The ASV, which is 5ft long and weighs less than 100lbs, allows easier access to shallow water lakes instead of the traditional method of boat equipment and personnel. Surveys are run with a line spacing of 75ft. Depth data is collected at approximately 0.5ft intervals. Once completed and processed, depth data can be printed on a map or exported to Google Earth.

The information is valuable for the towns because it provides current conditions information. In many cases these data have not been collected in more than 40 years.

IMPACTS OF SALT ON JUVENILE TREES OF NEW JERSEY MARITIME FORESTS

Jeff Dudek, Matt Francis, and Kelsey Connelly Monmouth University Department of Biology

Faculty Mentor: Dr. Pedram Daneshgar, Department of Biology

Funding Sources: Monmouth University School of Science Monmouth University Urban Coast Institute

Maritime forests are coastal woodland communities often found on barriers islands that persist in the presence of salt spray. These forests are important as their strong root systems help to maintain barrier islands, which protect shores from large storms. The proximity to salt water, along with a sandy soil composition, produce a hostile environment for seedling establishment and subsequent growth, but the fate of these seedlings is important as they represent the future canopy of the forest. Which tree species are more susceptible to salt stress during the seedling stage has yet to be explored for maritime forests in the Mid-Atlantic. We tested the salt tolerance of commonly found juvenile maritime forest species through exposure to salt spray and saltwater flooding and documented plant recovery.

In order to determine which study species to use for the experiments, field sampling of the forest floor was conducted on New Jersey barrier islands, Sandy Hook, and Island Beach State Park. Five species, three deciduous and two evergreen species, were chosen for the study based upon greatest abundance. A greenhouse experiment was created to examine salt spray on these species under both shade and light conditions. A salt spray gradient was established in both light conditions to test the species tolerance to salt. Additionally, a separate saltwater flooding experiment was designed to test the impacts of different submergence lengths in brackish water. Growth and physiological data (photosynthesis rates) were used to assess the impacts of the treatments. Preliminary results suggest that the evergreen species are more adapted to the presence of salt than deciduous species. This information might be important in the future in determining potential succession within the forest.

ENGINEERING OF AN IMMUNOGENIC PRE-*TRANS*-SPLICING RNA (IPTR) TO BLOCK GROWTH AND REACTIVE THE IMMUNE SYSTEM IN GLIOBLASTOMA

Sarah Falotico¹, Nicole Sivetz¹ and Peter Nekrasov² ¹Monmouth University Department of Biology, ²Biotechnology High School

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

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

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 T-cells 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. The iPTR has the potential to synergistically block growth and reactivate the immune system toward the tumor microenvironment. In a GBM tissue culture model, we use reverse transcription of RNA to synthesize cDNA and use PCR to detect changes in transcript expression. 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.

EXAMINING THE ROLE OF FASCIN IN PRIMARY BRAIN CANCERS

Syed Mehdi Husaini and Faraz Jamal Monmouth University Department of Biology

Faculty Mentor: Dr. Cathryn Kubera, Department of Biology

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

As one of the main actin bundling proteins found in the body, fascin plays an important role in maintaining many regulatory behaviors. It is vital for proper cell-cell adhesion through cytoskeletal structures and has been shown to play a role in a cell's motile and invasive properties. Fascin is an important protein to study because its overexpression is seen in various cancers. Previous literature has shown that upregulation of fascin increased the metastatic and invasive properties of colorectal cancer cell lines. Additionally, fascin has been identified in a set of genes that mediated breast cancer metastasis to the lungs, and has been implicated in gallbladder, pancreatic, and prostate cancers as well. Primary brain cancers, which can be very aggressive, also seem to have elevated fascin levels that correlate with tumor grade. 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. Furthermore, immunostaining of both total fascin and phosphorylated 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 immunostaining in cytoskeleton at the distal margin of extended processes.

To evaluate whether overexpression of fascin increases motile properties of neuroblastoma and glioma cells in culture, in the future we plan to use a three dimensional gel matrix invasion assay to observe cell movement into unoccupied space in real time.

CHARACTERIZATION OF GABA_A RECEPTOR SUBUNIT EXPRESSION IN DEVELOPING Gallus gallus CEREBELLUM

Charlotte Kelly, Nadine Khalil, and Victoria Reggio Monmouth University Department of Biology

Faculty Mentor: Dr. Cathryn Kubera, Department of Biology

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

Fetal Alcohol Spectrum Disorders (FASD), which occur among 2-5% of the United States population, results as a consequence of fetal exposure to ethanol during gestation. In the developing cerebellum, Fetal Alcohol Syndrome has been shown to cause an array of abnormalities such as reduced cell numbers and deficits in coordination and functional control. Fetal ethanol exposure can also cause premature activation of GABA receptors, whose encoding genes have been linked to the possible development of alcohol dependency. However, the molecular mechanisms in which prenatal alcohol exposure leads to structural and functional defects in the developing cerebellum are still unclear. Through the genetic manipulation of GABA_A receptor subunits in *Gallus gallus* chick embryos, we will be able to better understand the underlying mechanisms leading to FASD.

The first goal of this study was to determine expression levels of the GABA_A receptor subunit genes in the developing cerebellum of embryonic day 7 (E7) chicks. DNA oligo primers were designed for amplification of GABA_A receptor alpha subunits 1-6 and beta subunits 1-3. Subunit expression was measured by extracting RNA from the cerebellums of E7 chick embryos and performing reverse transcription quantitative polymerase chain reaction (RT-qPCR). Isolated messenger RNA was reverse transcribed to create copy DNA, and then quantitative PCR was performed in order to amplify these genes. In addition to GABA_A alpha subunits 1-6 and beta subunits 1-3, samples were probed for two controls: Xeno RNA and the cytoskeletal gene beta-actin. Complementary DNA was detected for alpha subunits 1-4 as well as all beta subunits. No complementary DNA was detected for alpha subunits 5 and 6.

NEW APPROACHES TO STUDYING GENE EXPRESSION

Bradley Kraft Monmouth University Department of Biology

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

Funding Sources:

Monmouth University School of Science

Studying gene expression has the potential to help us understand evolutionary processes such as speciation and adaptation. Recently, next-generation sequencing of RNA transcripts (RNA-Seq) has allowed us to study gene expression across entire genomes rather than just a small handful of genes. 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 requires direct alignment of short segments of RNA to a reference genome. This alignment must take into account several million short reads for multiple samples across exon breaks. Therefore, such analyses generally require access to high performance computing resources. However, the recently developed programs Kallisto and Sleuth work together to quantify and analyze RNA-Seq data quickly on a typical desktop computer. In addition, 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. Specifically, we compared expression levels of transcripts among lab-raised house mice derived from cold and warm adapted populations in the eastern U.S. We found that increasing the number of 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 genelevel analyses of gene expression.

MONMOUTH UNIVERSITY BEACH NESTING BIRD MONITORING AND STEWARDSHIP PROGRAM

Shannon M. Lavelle and Bridget N. McCormick Monmouth University Department of Biology

Mentors:

Assistant Dean John Tiedemann, Department of Biology Christina Davis and Meaghan Lyon, New Jersey Division of Fish and Wildlife

Funding Sources:

New Jersey Division of Fish and Wildlife Conserve Wildlife Foundation of New Jersey

Once common along the Atlantic coast, Piping plover (*Charadrius melodus*) populations were decimated by hunting for the millinery trade in the early 20th century. The Migratory Bird Treaty Act of 1918 stopped the hunting of these birds and the population recovered to some extent. Unfortunately, in the past several decades, the population has declined dramatically due to disturbance of nesting habitat and breeding conditions. Least terns (*Sternula antillarum*), American oystercatchers (*Haemtopus palliates*), and black skimmers (*Rynchops niger*) share the same nesting habitat as piping plovers and are also being faced with threats of population decline. The piping plover is a protected species under the Federal Endangered Species Act. Along the Atlantic coast it is designated as threatened, which means that the population will continue to decline if not protected. In New Jersey, piping plovers, least terns, and black skimmers are considered endangered and American oystercatchers are considered a species of concern. Factors contributing to declines of these species include:

- Disruption of natural coastal processes that create and renew nesting habitats due to commercial, residential, and recreational development of coastal areas;
- Human disturbance associated with recreational beach use;
- Predation and harassment by gulls, crows, raccoons, skunks, foxes, pets, and feral cats.

The New Jersey Division of Fish and Wildlife (NJJDFW), Endangered and Nongame Species Program is responsible for monitoring and management of these species. Each summer Monmouth University interns assist NJDFW with this work including:

- Conducting surveys of Monmouth County beaches to assess nesting activity;
- Monitoring and providing protective management of nest sites to reduce effects of human disturbance;
- Determining nesting success including the fate of chicks and causes of nest failures; and,
- Providing public outreach, especially during periods of heavy recreational beach usage.

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

Tiffany Longo Monmouth University Department of Biology

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

Funding Source:

Monmouth University Summer Scholars Program

Although the house mouse, *Mus musculus domesticus*, is not native to the Americas, it has evolved and adapted to many different regions within a short amount of time. Mice are well known for their reproductive ability, but little is known about differences in their reproductive traits among diverse climates of the Americas. Identifying significant differences in reproductive traits is central to understanding adaptation, so we addressed this question by analyzing breeding data collected from wild-derived colonies of mice from Canada, New York, Brazil, Florida, and Arizona. We focused on the first and second generation of lab bred mice to control for environmental variation seen in wild-caught individuals and to reduce the effects of inbreeding in later generations. We compared traits like age at first litter, average pups in each litter, sex ratio, etc. among the five colonies. Our results identified that litter sizes varied significantly between the colonies. Specifically, litter size was larger for mice from the cooler regions (Canada and New York) than mice from the warmer regions (Brazil, Florida, and Arizona). Future work will focus on determining if there are also differences in pup weight among colonies. Interestingly, we found that while there were differences in success rates for breeding among colonies, those differences were not affected by season as might have expected given patterns in the wild.

SYNTHESIS OF A MINI-REPORTER TO TEST RNA THERAPEUTIC STRATEGIES TO BLOCK VEGFR2 AND ANGIOGENESIS IN HUMAN GBM

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

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

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

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 survival depends on the formation of new blood vessels, which is essential for the exchange of wastes and nutrients. 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. 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.

RNA THERAPEUTIC STRATEGIES TO ALTER THE EGFR TRANSCRIPT IN HUMAN GLIOBLASTOMA CELLS

Peter Nekrasov¹, Nicole Sivetz², and Sarah Falotico² ¹Biotechnology High School, ²Monmouth University Department of Biology

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

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

Therapies for glioblastoma multiforme (GBM), the most common central nervous system malignancy, are limited by the blood-brain barrier (BBB) and therapeutic persistence. Tyrosine kinase receptors (TKRs), such as epidermal growth factor receptor (EGFR), are overexpressed in GBM cells and drive cell proliferation. Previous research examining aberrant transcripts in cancers has identified alternative intronic polyadenylation within intron 15 of the EGFR transcript, resulting in truncated isoforms that lack the EGFR transmembrane domain. Untethered from the membrane, the soluble extracellular EGFR decoy sequesters growth factors in the tumor microenvironment. To take advantage of this natural phenomenon, we are developing a strategy to bypass the BBB to deliver to the tumor a vector that persistently expresses anti-EGFR RNA therapy. We engineered a pre-trans-splicing therapeutic RNA with a polyadenylation signal and a pre-mRNA splicing localization signal (U7-smOPT) to splice into and halt the EGFR transcript, preventing the translation of the transmembrane domain. Multiple binding domains, complementary target sequences playing a large role in *trans*-splicing efficiency, were designed by predicting strong branch points, splice sites, and polyadenylation elements within intron 15 of the EGFR transcript. Using the HiFi Assembly cloning method, target sequences were designed *in silico* and generated for insertion into the therapy vector. After glioblastoma cells were transfected with a therapy vector, RNA was isolated and converted to cDNA. Multiple primers were designed to detect splicing efficiency.

DNA EXTRACTION FROM ATLANTIC STURGEON SPINE AND FIN TISSUE

Brian Reiss Monmouth University Department of Biology

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

Funding Source:

Monmouth University School of Science

The Atlantic Sturgeon, *Acipenser oxyrhinchus*, 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.

DEMOGRAPHICS OF THE LAND-BASED RECREATIONAL HOOK-AND-LINE SHARK FISHERY WITHIN NEW JERSEY

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

Funding Sources: Monmouth University School of Science Monmouth University Urban Coast Institute

Popularity of recreational, land-based, hook-and-line shark fishing has steadily increased amongst recreational fishermen in past years and primarily targets prohibited species. Because of the general nature of the fishery (catch-and-release, land-based, night-time fishing) collection of fishery demographics, as well as enforcement can be difficult. To gain a better understanding of this fishery within New Jersey, we enlisted the help of a local fishing guide service to participate as a voluntary angler to tag (dart tags) and collect biological information (sex and length) on the sharks captured and released among 2 well known fishing areas within the Atlantic Ocean and Delaware Bay. The volunteer angler conducted 12 excursions and captured and released 53 sharks including 20 Sand Tiger (Carcharias Taurus) (n= 8 males, 9 females, and 2 unknown) 31 Sandbar shark (Carcharinus plumbius) (all females) and 1 Dusky Shark (Carcharhinus obscurus)) with significantly smaller sharks captured in the Bay location. Of these sharks captured, we also surgically implanted long-term (10-year) acoustic transmitters in 9 Sand tiger and 6 Sandbar sharks to gain a better understanding of their long-term movements and habitat use as well as post-release survival within this fishery. Overall, this information will allow for better management and conservation efforts to take place on these critical species that play a major role in the ocean ecosystem.

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

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

Funding Source:

Monmouth University School of Science

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 pathway data from the Kyoto Encyclopedia of Genes and Genomes (KEGG). We identified all the genes in all annotated pathways for mice and determined whether expression was greater in cold climates versus 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 way. 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.

DEPARTMENT OF CHEMISTRY AND PHYSICS

ABSTRACTS

SAMPLING OXAZOLE-BASED MACROCYCLES FOR BINDING TO DNA

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Faculty Mentor: Dr. Yana Kholod, Department of Chemistry and Physics

Funding Source:

Monmouth University School of Science

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. Specifically, a set of three oxazole-based macrocycles have been considered. Different molecules of this class, depending on their structure and substituents, bind highly selectively to certain DNA forms (e.g., double-helix, parallel, anti-parallel, G-quadruplex and mixed-type hybrid structures). Therefore, such oxazole-based macrocycles can be selected for optimal binding to specific DNA forms, and subsequent targeted inhibition of telomerase in cancer cells.

In the course of the SRP program, the first stage of the project that includes a comprehensive sampling of various conformations of the preselected oxazole-based macrocycles has been performed. The molecules under study are large and have a complex structure. Therefore, we started with building initial structures of those molecules with GaussView software.

When those initial molecular structures were built, they were pre-optimized using the Molecular Mechanics methods as implemented in GaussView. The molecular structures looked reasonable from a chemical point of view after that procedure. At the next stage, each molecular structure was optimized to achieve a geometry that corresponded to an energy minimum using Quantum Mechanical methods called Hartree-Fock (HF) method and density functional theory (DFT) in the computational chemistry program package Gaussian09. Specifically, we used the HF method for a geometrical optimization, and the DFT method (as implemented in the B3LYP functional) for a precise electronic energy calculation of that optimized molecular structure. The procedure was repeated for each molecular conformation.

The energies for those structures show the stability of those conformations. In general, the lower the electronic energy, the more stable the molecular structure is, and it is therefore more likely to exist in reasonable quantities in a reaction mixture, thus allowing the molecular structure to bind to DNA.

MONITORING RIBOSWITCH MODULATION VIA FLUORESCENT GENE EXPRESSION

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Faculty Mentor:

Dr. Jonathan Ouellet, Department of Chemistry and Physics

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

This summer, I continued a cloning project that was initiated by a former student, however there was missing genetic information in the sequencing. My main goal was to use the pHL 1278 plasmid to create a reporter system for the theophylline riboswitch. From this, a ratiometric fluorescent tool would be made to test the activity of the riboswitch. Upon completion, this project would provide a core tool used in other projects.

A riboswitch is a structural domain rooted within a non-coding sequence of mRNA. It's in a position that interferes with the translation based on the presence of a specific ligand. Theophylline is a small molecule, similar to caffeine, that is used in inhalers for treatment of asthma. More importantly, to know if the RNA has bound to theophylline, an expression platform needs to be paired with the aptamer to observe the modulation of fluorescent gene expression.

Through molecular cloning, PCR, DNA purification, etc., the DNA corresponding to a riboswitch that is known to bind to theophylline was inserted into the pHL 1278 plasmid between the mCherry and GFP fluorescent genes. The final cloned plasmid contained a promotor, mCherry gene, riboswitch, and the GFP gene. Recently, the sequencing for this cloned plasmid was received and analyzed. A functional assay will be done to test the activity of the riboswitch. Upon induction, mCherry is constitutively expressed whereas GFP's expression is dependent on the presence of theophylline. This allows for a ratiometric fluorescent measurement to be made for mCherry vs. GFP.

In the future, the GFP gene in plasmid pHL 1720 will be replaced with the Kanamycin resistance gene. The GFP gene allows for visual results whereas the Kanamycin resistance gene kills any unwanted bacteria, allowing it to be more accurate. Later, this system will be used to convert aptamers into riboswitches.

DEVELOPMENT AND ISOLATION OF AN APTAMER FOR 2-HYDROXYGLUTARATE

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Faculty Mentor:

Dr. Jonathan Ouellet, Department of Chemistry and Physics

Funding Sources:

Bristol-Myers Squibb Monmouth University School of Science

Currently, one of the most effective ways of diagnosing cancer is through examination of intracellular components to determine whether or not the cell contains specific molecules, known as oncometabolites. These oncometabolites, which are produced only in the aftermath of metabolic events taking place within cancerous cells, serve as biological markers for distinguishing cancerous cells from normal, healthy cells. These biomarkers set the basis of our research project, which is developing an RNA aptamer against the oncometabolite 2-hydroxyglutarate, a molecule derived from the Krebs's cycle of certain gliomas and lymphomas.

We have designed a sequence for the RNA aptamer to complex with a hammerhead ribozyme to form a molecule capable of catalyzing self-cleavage upon binding to 2-hydroxyglutarate, otherwise known as an aptazyme. In order to generate the most successful aptamer for 2-hydroxyglutarate, our large sample pool of DNA is then subjected to stringent selection by introducing a method of Systematic Evolution of Ligand by Exponential Enrichment, or simply referred to as the SELEX cycle. With SELEX, we are able to narrow down the wide range of DNA combinations, a number which is close to that of Avogadro's number of possibilities, to a few that are selected for to be the most effective aptamers. The developed aptamer within the human genome can subsequently function as a biosensor, regulating gene expression for a cellular toxin to ultimately destroy any cancerous cell presenting 2-hydroxyglutarate.

Currently, the project has successfully completed 15 cycles of SELEX and are proceeding with the sixteenth cycle. We have completed bacterial cloning of the G_{11} aptamers, followed by a functional assay to test the effectiveness of our selected aptamers. Unfortunately, all of G_{11} samples being tested were determined ineffective because of the fact that the aptamers cleaved without the presence of 2-HG. The next step of the project is to continue with the SELEX cycle until positive selection of SELEX shows more progression towards higher percentage of cleavage.

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

Grant Gillan

Monmouth University Department of Chemistry and Physics

Faculty Mentors:

Dr. Yana Kholod and Dr. Dmytro Kosenkov, Department of Chemistry and Physics

Funding Sources:

Sparta Systems Monmouth University School of Science

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 Fenna – Matthews – Olson pigment-protein complex have been calculated and analyzed based on the Förster theory. 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.

CONFORMATIONAL ANALYSIS AND BINDING AFFINITY TO DNA OF TELOMESTATIN DERIVATIVES

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Faculty Mentor: Dr. Dmytro Kosenkov, Department of Chemistry and Physics

Funding Sources:

Sparta Systems Monmouth University School of Science

Telomestatin is a macrocyclic hexaoxazole that has shown promising anti-cancer capabilities in its telomerase inhibitory activity through G-Quadruplex DNA (gqDNA) stabilization¹. Telomestatin derivatives are studied for better understanding of the binding properties of macrocyclic molecules to gqDNA. Conformations of macrocycles containing two to four monomer subunits of thiazole or oxazole with varying functional groups were built and pre-optimized in gas-phase at the M06-D3/6-31G* level of theory, followed by optimization in a PCM solvent (acetonitrile) at the M06-D3/6-31+G** level. The thermochemical analysis of each optimized structure, the relative stability of each isomer were evaluated through the calculation of Gibbs free energy that, in particular, includes the entropy due to molecular vibrations within the system. Molecular docking calculations of the most stable macrocyclic structures were carried out in order to assess their interactions with gqDNA.

References:

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INTRAMOLECULAR CARBON-HYDROGEN BOND ACTIVATION AT RHENIUM(V) PENTAHYDRIDE CENTERS

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Faculty Mentor:

Dr. Gregory Moehring, Department of Chemistry and Physics

Funding Source:

Monmouth University School of Science

Rhenium(VII) heptahydride complexes readily exchange hydride ligands with molecules such as benzene, water, alcohols, amines, or between separate rhenium(VII) heptahydride centers. Those same rhenium(VII) centers catalyze a variety of small organic molecule transformations through the activation of C-H bonds within the small molecules. Much less has been reported on the ability of rhenium(V) pentahydride centers to exchange hydride ligands with other sources of hydrogen. A report described hydrogen exchange occurring at a rhenium(V) pentahydride center supported by bidentate phosphine ligands where one of the phosphine centers was dangling unbound. Our work investigates the previously unreported intramolecular hydrogen exchange that is found for several rhenium(V) pentahydride complexes where the metal center is supported by a primary amine ligand in addition to two PPh₃ ligands. The three new complexes described here include primary amine ligands with a second dangling amine or alcohol functional group. In the cases of all of these new complexes, hydride ligands undergo a fluxional exchange between coordination sites as well as an exchange of hydride ligands with the ortho protons of the PPh₃ ligands. A second exchange process is observed involving the ortho protons of the PPh₃ ligands and hydrogen from at or near the dangling end of the primary amine ligand. The net of the exchange processes makes some PPh₃ protons, some hydride ligands, and some of the protons from the primary amine ligand equivalent in the ¹H NMR spectrum at higher temperatures. At lower temperatures separate proton resonances are observed for all of the exchanging protons. The proton exchanges are observed by two dimensional EXSY NMR experiments and the results of those experiments are used to determine the activation energies for the exchange processes

ACRYLAMIDE GEL STAIN TO QUANTIFY DNA FRAGMENTS

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Faculty Mentor: Dr. Jonathan Ouellet, Department of Chemistry and Physics

Funding Sources: Bristol-Myers Squibb Monmouth University School of Science

To understand the structure/function relationship of many nucleic acids, kinetics of the DNA is monitored over time and separated on acrylamide gels using radioisotope phosphorus-32. Currently, nucleic acid kinetics is observed mainly through the use of radioactivity. However, using radioactivity raises safety concerns and heavy regulations. Therefore, this project is focused on determining which dye is best fitted to quantify a small quantity of short DNA fragments on urea-denaturing polyacrylamide gels.

To observe the DNA fragments, DNA (70 nucleotides) are separated by a polyacrylamide gel. Next, the DNA in the gel is fixated and saturated with different dyes. Afterwards, the gel is destained in a manner that allows only the DNA to be stained and the rest of the gel to remain clear. This method allows the DNA to be detected under white light or ultra violet light as well as under light and dark background. With the help of the dye, DNA at different concentrations can be observed and quantified using the software image (ImageJ) to do densitometry analysis on a picture of the gel. As of now, DNAs (70 nucleotides) have been observed with Methylene blue, SybrGold, and GelRed dyes.

Many different dyes will be used to find the ultimate dye that would give the best result to observe DNA and the function and structure of nucleic acids. Once set with DNA, this technique could be used to monitor kinetics of DNA cleavage. More importantly, it could be used in the field of RNA kinetics to monitor the RNA cleavage of ribozymes. In the future, more dyes with DNAs (70 nucleotides) as well as other different lengths of DNAs will be used for observation.

DEPARTMENT OF COMPUTER SCIENCE AND SOFTWARE ENGINEERING

ABSTRACTS

USE OF IOT (INTERNET OF THINGS) DEVICES IN HEALTHCARE MARKETING SERVICES

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Faculty Mentor:

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

Funding Source:

The Macaluso Group

Pharmaceutical product marketing includes sampling of prescription medications to physicians. This sampling is done by sales representatives while visiting physicians. There are industry and governmental guidelines and regulations to track and report this accurately. This process costs over \$16 billion per year and is getting more expensive with new regulations being introduced that vary from state to state.

In our project, we plan to modernize the prescription sampling process by using IoT (Internet of Things) devices to accurately track sampling in a secure and cost-effective manner. We have developed a proof-of-concept kiosk hardware and software combination with of IoT buttons, a Raspberry Pi computer with a touch screen display, wireless connectivity to Internet for the buttons and computer and cloud computing software application. The kiosks can be deployed in physician's offices for samples ordering. Each button represents a prescription drug and upon pressing the button, the physician will be asked to confirm their purchase either on the touch screen or a mobile app. Orders can be viewed by the physicians from the touch screen display or mobile app, which provides pertinent information such as order number and status, making easier to track. Limitations can also be placed on the buttons to control the quantity and frequency of orders. The software uses advanced cloud computing technologies and services. It is deployed in Amazon Web Services with enhanced security to meet all regulatory and compliance requirements, and scalability for widespread deployment.

Future research will include productizing the kiosk hardware and software for commercial deployment. Using IoT devices, Raspberry Pi computer, and cloud computing software technologies, we are making prescription samples ordering as simple as pressing a button!

TYREEK, TOMMY AND TAKAHASHI: RACE, NAMES AND YOU TUBE'S SEARCH

Jonathan Downie¹ and Samantha Inneo² ¹Winston Preparatory School ²Point Pleasant Boro High School

Faculty Mentor: Professor Katie Gatto, Department of Computer Science and Software Engineering

Funding Sources: Independent College Fund of NJ Johnson & Johnson Monmouth University School of Science

Our research is an exploration of racial/gender perception as expressed via the search algorithm of YouTube. The focus of the analysis is on the sentiment based on creator made video tags, and variation of video tagging shown to various groups.

The search criteria used are a randomly selected sub-set of common names given to babies with mothers of varying racial backgrounds, according to US Census data based on births in the city of New York. An analysis of top results will be part of the project.

Data collected for analysis includes Meta data from page source such as video title, keywords, and tags to provide a picture as close to what You Tube shows as possible. Keyword analysis versus an established list of word sentimentality will be used to create a numeric score.

The project will result in a website that will allow end users to test their own names against perception.

HURRICANE SANDY COAST GUARD EMERGENCY RESPONSE SERIOUS GAME

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Faculty Mentor:

Professor Jodee Vallone, Department of Computer Science and Software Engineering

Funding Sources:

Independent College Fund of New Jersey; Johnson & Johnson Monmouth University School of Science; Monmouth University Urban Coast Institute

The Urban Coast Institute works to educate the public on the effects of certain conditions on coastal regions. On October 29, 2012 Hurricane Sandy brought \$75 billion dollars in destruction to the East Coast with 80 mph winds, high flood water, and widespread rain.

The purpose of this development project is to inform the public on how the Coast Guard responds to emergency situations like Hurricane Sandy. The mini games included are inspired by real events, such as the sinking of the HMS Bounty that took place during the storm, and are set in a landscape based on real locations, such as Sandy Hook Bay and the mainland. The player is tasked with using a patrol boat to navigate debris littered seas to reach the three (3) rescue missions. A time allotment of twenty (20) minutes is given to complete the task.

The User Interface (UI) features a functioning mini map, timer, objective marker, level completion counter, and health gauges. The large and treacherous 3D environment is the platform for the mock rescue missions that take place in the game. One of the three missions takes place in the bay while the other two take place on Sandy Hook's flooded out land. Back-end programming and gameplay allows the player to traverse a dangerous hurricane affected environment by boat. The player starts in first person until they reach the patrol boat. At this point, the player's view is changed to top down for the duration of travel between each level. Once a new level is reached, the first person perspective returns until the rescue is completed.

HURRICANE SANDY FIREFIGHTER EMERGENCY RESPONSE SERIOUS GAME

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Faculty Mentor:

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Funding Sources:

Independent College Fund of New Jersey; Johnson & Johnson Monmouth University School of Science; Monmouth Urban Coast Institute

The Urban Coast Institute works to educate the public on the effects of certain conditions on coastal regions. On October 29, 2012 Hurricane Sandy brought \$75 billion dollars in destruction to the East Coast with 80 mph winds, high flood water, and widespread rain. One of the most devastated areas affected by Hurricane Sandy was Breezy Point in Queens, New York. This peninsula received a deadly combination of rain, flooding, and high winds that created a raging electrical fire which destroyed 122 homes and damaged 22 others.

In this educational game players control one of the emergency responders to this blaze in a setting modeled after the real-life Breezy Point. Armed with a fire hose the player must work against the clock and hurricane-like conditions to put out as many fires as you can in a limited amount of time. Players will need to act fast and efficiently in order to improve their score.

The game simulates an environment resembling that of Breezy Point during Hurricane Sandy in order to give players an understanding of the situation. In addition to this, arcade style elements such as in game pickups and puzzle aspects have been included to boost entertainment and replay-ability. This mini-game will give players a well-rounded experience by portraying a real-world event through a 3D environment.

BUSINESS INTELLIGENCE AND ANALYTICS PORTAL AND MOBILE APP FOR HEALTHCARE SERVICE

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Faculty Mentor:

Dr. Raman Lakshmanan, Department Computer Science & Software Engineering

Funding Source

The Macaluso Group

Data collected on healthcare services originate from multiple sources – patients, healthcare providers, payers, external services for patient eligibility verification. The effectiveness of the service is measured using Key Performance Indicators (KPI) consisting of data gathered from above sources and Service Level Agreements (SLA) to perform the service. A prior research project identified methods to convert data from multiple sources into a Meta data representation for analytics engine to visualize the data. In this research, we customized the visualization with a web portal application and a mobile app for branding the service and present a better user experience in interacting with the analytics data.

The web portal application was developed in Java programming language as a servlet under Tomcat web service technology for cloud deployment. The servlet simplified the user interaction to portal using point-and-click to analyze the data. The servlet supports future extensibility using dynamic construction of portal menus and navigation without any changes to underlying Java code. A native iOS iPad app in Swift language was also developed to interface with the analytics data. The iOS app has a different look-and-feel optimized for touch interface.

The servlet application is currently in use by end users and has been received favorably. The iOS app is in test and future work on this project will bring that into production.

PROCESS IMPROVEMENT FOR RAPID RESPONSE ACTIVATION

Michael Marmer¹ and Ping-Jung Liu² ¹Monmouth University Department of Computer Science and Software Engineering ²Wesleyan University/Dartmouth College

Faculty Mentor:

Professor Richard Eng, Department of Computer Science and Software Engineering

Funding Sources:

DefinedLogic Monmouth University School of Science

A local medical center uses Rapid Response Teams (RRTs) to address sudden changes in patient conditions before they become a crisis. The task was to analyze the RRT data to understand whether RRTs were being activated appropriately. Three months of data from a dataset were explored to better predict the need for calling an RRT. The dataset, however, was missing necessary vital information to help determine the cause for an RRT. By conducting literature research, more objective ways were found to better predict when a patient has a significant health status change. The National Early Warning Score (NEWS), published by the Royal College of Physicians in 2007, was proposed. The NEWS categorizes seven physiological parameters, or vital signs, and aggregates a score which determines the necessary interventions for a patient. NEWS not only finds strong correlations in predetermining behaviors in patient conditions, but can also determine the longevity of patient conditions. Research also indicates that determining factors such as physical symptoms, primary patient condition, prevalent medical history, and medicine administered can be strong indicators of change in patient health status. A new template was fashioned to help illustrate necessary patient information that help could determine a sudden change in patient health status. Based on the information provided by the new template, use case scenarios were conducted to demonstrate the historical trends of patient vital signs. In the next steps of the project – with the assistance of further data being provided – machine learning algorithms and the new template are to be implemented into a mobile application to help process necessary patient information in near-real-time.

SUMS LAW APPLICATION

Stephanie Okereke

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Faculty Mentor:

Dr. William F. Tepfenhart, Department of Computer Science and Software Engineering

Funding Sources:

Monmouth University Department of Computer Science and Software Engineering

Unfortunately, complex laws in the United States compel individuals to ignore them rather than comprehend them. As a result, those who either understand the laws are lawyers or lawmakers. Therefore, people will be taken advantage of because they cannot understand the law. The computer program that I am creating, or Sums Law, will facilitate better understand of the law by outputting a simplified yet precise summarization of any law.

I am creating an application, mainly on smartphone devices, that prompts the user to select major law topics (i.e. Civil Rights), search the key number, or type in a few phrases. To do this, I am harvesting data from websites, specifically from law.cornel.edu, so that the application displays condensed and simplified versions of the law. If necessary, the program will also replace difficult vocabulary of the summarized version for simple synonyms.

In addition, I aim to polish the interface of the program so that it is simple enough for anyone to use. Also, this application will be free because I do not want to deter the user from using this helpful resource.

AUGMENTED AND MIXED REALITY EXPERIENCE (A RESIDENTIAL HIGH RISE BUILDING)

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Faculty Mentor:

Professor Martin von Grossmann, Department of Computer Science and Software Engineering

Funding Sources:

DefinedLogic Monmouth University School of Science

The objective of the project was to utilize innovative tools and development activities to understand and apply findings from the research conducted to develop a mixed reality experience. A Tishman Spire high rise building located in San Francisco, California was identified as the venue to produce the mixed reality application and experience. The requirements for our project consist of creating a virtual 3D model of the exterior of a building and have it launch on a mobile device when the camera is aimed at a physical target. The target chosen to launch the application is a blueprint for the building, noting the relevance to the experience. The students designed the interior and exterior of the building. They utilized the development tool, Unity, to primarily create the components of the 3D models of the building. The students used the augmented reality tool set, Blippar, to launch and program the models and animations to create the experience from our target while incorporating the Unity models. The students used a variation of agile development methodologies to define the process and stay organized. All aspects of the project have been built through careful development and testing within the time constraints of the SRP.

Upon aiming the mobile device camera at the blueprint, the user is able to interact with the exterior of the building as it appears on top of the blueprint. The 3D image of the building superimposed on a real object (in this case a blueprint) will demonstrate a form of augmented reality. The user will then have the option to touch a portion of the building, within the construct of the application, which will become highlighted to produce an interior view of that area. Once inside, the experience will transition from augmented reality (AR) to virtual reality (VR) and the user will be able to navigate around the inside of the area that is designed. The combination of AR and VR therefore results in a Mixed Reality (MR) development.

EMERGENCY HEALTHCARE SERVICE WORKFLOW MODELING AND ANALYSIS

Jiarui Tian

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Faculty Mentor:

Dr. Jay Wang, Department of Computer Science and Software Engineering

Funding Sources:

WorkWave Monmouth University School of Science

The quality of care in the emergency department of a hospital is dependent on efficient clinical workflow, which depends on time and resource allocation during each step of treatment. Although workflow management technology for the automation of organizational healthcare processes has received considerable attention, more work on the timeliness analysis of emergency healthcare is needed. This idea is the starting point of our research: analyzing the timing performance and resource requirements of emergency healthcare service. The first step is to model the emergency health care workflow using resource-oriented workflow Petri net theory. We choose a real-world emergency treatment of stroke as a specific case study. Based on Dr. Wang's previous research, I refined the whole workflow and involved resources to make it more practical and began the simulation part of the project.

Existing simulation tools, such as MATLAB Petri Net Tools package and open-source tool PIPE, can simulate timed Petri nets, but are unable to simulate resource-oriented Petri net. For this reason, I simulated the workflow based on T-time Petri nets, using MATLAB Petri Net Tools. At this step, the process of analyzing timing performance assessment has been implemented. We further decided to develop a specific resource-oriented Petri net simulation tool to analyze resources requirement. Our currently developed simulation tool has implemented the simulation of T-time Petri net.

The goal of the next step is to implement the Resource-oriented Petri net with multi-thread programming techniques, making it more suitable for the analysis of real-world healthcare workflow analysis.

GOAL TRACKING AND AWARDING SYSTEM FOR CHILDREN AND TEENS

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Faculty Mentor:

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

Funding Sources:

WorkWave Monmouth University School of Science

Technology has evolved to become incorporated in every foreseeable field of study. However, the exponential rate at which technology is growing has also blinded many from the negative effects that have emerged. Improper usage of technology affects society in many harmful ways. With the younger generation growing up in this age of tech frenzy, many parents have found it a struggle to keep their children away from distractions of the Internet, and instead focused on schoolwork and healthy hobbies. This problem is the focus of our research. The goal of our project is to create a web application tool to help people, especially children and teens, organize their time and manage their screen time.

This application supports users to set their goals and tasks, different from the regular experience of existing calendar or appointment tools. For example, in this application, one can set a daily task of 'Go to bed by 10pm,' and a special goal of 'No video game for a month.' Users are awarded for accomplishing these set tasks and goals. Parents and teachers can use this tool to train their kids/students for better time management, positive habits, and self-discipline. MySQL, PHP, HTML, CSS, JQuery, and JavaScript are used for implementation. Soon we will have classmates and friends to test the application. Further enhancements are expected in the future.

DEPARTMENT OF MATHEMATICS

ABSTRACTS

THE EFFECT OF ACTIVE LEARNING TECHNIQUES UTILIZING CASE STUDY WORK IN ANATOMY AND PHYSIOLOGY

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Client: Dr. Bernadette Dunphy, Department of Biology

Funding Sources:

Monmouth University Math Learning Center Monmouth University School of Science

Inclusion of active learning techniques, specifically case study work, resulted in learning gains as noted by increased scores on a national standardized exam. Active Learning is a method that can be used in a classroom that directly involves students in the learning process. This method can include case study presentation and analysis, students using the whiteboard during discussions, or small group discussion in class. This type of metacognitive learning is successful in documented gains in the more difficult integrative physiological processes.

Metacognitive learning research has been done, however, we were primarily interested in the use of active learning in upper level anatomy and physiology classes. This integration would not only benefit the student's learning of physiological processes, but also give them a platform to build the knowledge of different human systems, and integrate that knowledge throughout the two course series.

It is hypothesized that through the use of active learning students will better learn the material with the result being an increased score on the HAPS exam, a national comprehensive examination. The students' scores on this exam were recorded in the spring 2016 (n=25) and spring 2017 (n=17) semesters. A student's t-test was used to compare each semester to the national average. Using this test, in both semesters the students scored significantly higher than the national average. This difference can be attributed to active learning, and has shown that active learning is a better technique than traditional learning in Anatomy and Physiology.

STATISTICAL ANALYSIS OF ESSENTIAL OILS AND METHYLGLYOXAL: A POSSIBLE TREATMENT FOR INHIBITING THE GROWTH OF ESCHERICHIA COLI

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Client: Dr. James Mack, Department of Biology

Funding Sources:

Monmouth University Math Learning Center Monmouth University School of Science

Various bacteria have become resistant to antibacterial drugs. Dr. Mack and his research student Joseph Kellett tested three essential oils and methylglyoxal to see how they would react with E. coli in comparison to six different antibiotics. The three essential oils were cassia, cinnamon bark, and oregano and they were combined with jojoba oil, olive oil, and coconut oil in order to help dilute them in the petri dishes. A zone of inhibition measured in millimeters was recorded from each petri dish where the bacteria had stopped growing from whatever substance was added.

The response variable for our statistical analysis was the zone of inhibition. Our first task was to test for normality. After running several tests and checking histograms, we concluded that the data was not normal. We had to run non-parametric tests because they do not have the normality assumption. We ran three tests comparing two medians, three medians, and five medians. The groups were broken and compared by the Wilcox test of two medians and the Kruskal Wallis test for multiple comparisons. We found that the methylglyoxal was significantly different from everything but the cassia essential oil. The other oils were just as effective as the antibiotics. We also ran power tests and determined that a greater sample size would be needed to get more valid results.

STATISTICAL ANALYSIS: HOW SALT MARSHES ARE IMPACTED BY NITROGEN DEPOSITION LEVELS

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Client: Dr. Pedram Daneshgar, Department of Biology

Funding Sources:

Monmouth University Math Learning Center Monmouth University School of Science

Salt marshes are coastal wetlands that are flooded and drained by salt water brought in by tides. Dr. Pedram Daneshgar is a terrestrial ecologist and biology professor at Monmouth University. This research was done in hopes of publishing a note on salt marshes and nitrogen deposition. Nitrogen deposition refers to nitrogen displacement naturally via the nitrogen cycle. There were six sites of salt marshes all located in the mid – Atlantic region, and six treatments types.

Three separate datasets were analyzed. For the normal response variables, a one-way ANOVA (Analysis of Variance) was used to see if there was a statistically significant difference between the sites, and then between the treatments for each of the response variables. For the first two datasets, the results show significant differences between the sites but not for the treatments. For the third dataset, the results show statistically significant differences between the treatments but not for the sites. Since some of the response variables were not normal in this dataset, a Non-Parametric Test (Independent-samples Kruskal-Wallis Test) was used. The Independent- samples Kruskal-Wallis Test is the nonparametric version of one-way independent ANOVA.

STATISTICAL ANALYSIS OF THE EFFECTS OF ACTIVE LEARNING ON THIRD YEAR MEDICAL STUDENT'S ATTENTION AND RETENTION OF INFORMATION

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Client: Dr. Sarah Smithson, OB/GYN, Monmouth Medical Center, Long Branch, NJ

Funding Sources:

Monmouth University Math Learning Center Monmouth University School of Science

Active learning involves techniques that are used to engage the audience during a lecture. Examples of active learning include case-based learning, discussions with the students, and bringing students up to the board. Dr. Smithson is an OB/GYN who works at Monmouth Medical Center. She is looking at active learning and its effects on her third-year medical students' ability to pay attention and retain information. Dr. Smithson offered a lecture on ovarian cancer in two different ways: with active learning and without. She then immediately gave her students a quiz on the information that was presented to them, had them fill out a questionnaire on their own attentiveness, and had a neutral observer also rate them on how attentive they seemed to be during the lecture. A week later, Dr. Smithson gave her students the same quiz (delayed quiz) to see how well they retained the information.

Because these data collected were not normal, non-parametric tests for significant differences between the active learning and the non-active learning groups were used. The non-parametric tests were the Wilcoxon matched-pair rank (for related samples, such as the immediate and delayed quiz score) and Mann-Whitney U test (for independent samples, such as the active and non-active learning groups). The results show that active learning did not have an effect on the four scores individually. However, the distribution of the active learning group is not the same for the two quiz scores.

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THE BOUNDEDNESS OF SYSTEMS OF DIFFERENCE EQUATIONS WITH PERIODIC COEFFICIENTS

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Funding Sources: Monmouth University Math Learning Center Monmouth University School of Science

Difference equations are the discrete analogue of differential equations. Whereas differential equations model the evolution of a system in continuous time, difference equations model the evolution of a system in discrete time. Such equations are important because they can approximate some differential equations, they are usually easier to solve computationally, and because there are many systems which operate solely in discrete time (e.g., population growth, Markov chains).

In our project, we examine the boundedness character of systems of difference equations. Systems of difference equations are two or more difference equations that are dependent on each other. Essentially, we attempt to determine whether there are solutions to these systems, given an initial set of parameters that grow to infinity. We study two systems, which are known as (12, 23) and (12, 8), and find that (12, 23) is always bounded (there are no solutions that grow to infinity); however, we are unable to determine whether (12, 8) is bounded or unbounded. Though, we suspect that (12, 8) is unbounded and have conjectures for its unboundedness.

URBAN COAST INSTITUTE

ABSTRACTS

BATHYMETRY AND FLOOD MAPPING OF LAKE COMO, NEW JERSEY

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Faculty Mentors: Geoffrey Fouad, Geographic Information Systems Program James Nickels, Urban Coast Institute

Funding Sources:

Urban Coast Institute Heidi Lynn Sculthorpe Summer Research Grant Santander

The storage capacity of Lake Como, New Jersey is unknown since a bathymetric survey has not been performed after the effects of Hurricane Sandy. An accurate estimate of the lake's storage capacity is critical for flood planning of surrounding communities. For this reason, a survey was conducted to collect high-density depth readings of the lake. The points were connected using a triangulated irregular network to create a bathymetric surface of the lake bottom. The surface was used to estimate the maximum storage capacity of the lake, which was compared to a previous survey. Flooding at different heights of the lake was also mapped using the newly created bathymetric surface. This surface will be instrumental to run flood simulations in preparation for future storms.

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

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Funding Source:

Urban Coast Institute Heidi Lynn Sculthorpe Research Grant Santander Monmouth University School of Science

Atlantic Sturgeon, Acipenser oxyrinchus, is a federally protected species that undergoes large coastal migrations. Aggregations of Atlantic Sturgeon are known to occur in several coastal locations that include large seasonal aggregations in the spring and fall off the coast of New York, which largely consist of sub-adults from the Hudson River. To understand potential reasons why sturgeon aggregate, seasonal changes in diet as well as prev availability were examined within this known aggregation. Stomach contents of Atlantic Sturgeon were collected through non-lethal gastric lavage in the spring (n=28) and fall (n=39) of 2013 and compared against benthic invertebrate samples collected simultaneously (spring, n=24; fall, n=24). Overall, sturgeon had 66 species of prey items identified available to them but consumed only 28 species of these items. In both seasons, gammarid amphipods, Ampelisca verrili, proved the most important prey item, with the highest Index of Relative Importance (IRI) values; accounting for the most abundant weight, frequency, and abundance of all prey taxa. In addition to gammarids, sturgeon consumed considerable numbers of polychaete; *Glycera spp.* and *Nepthys spp*, as well as crustaceans; Squilla empusa. Atlantic sturgeon showed an opportunistic feeding behavior due to slight variations in diet seasonally with macroinvertebrate prey availability as seen in the increase of importance of polychaete species from fall to spring. Selective analysis, in comparing the availability of prey items compared to consumed prey items, shows that the sturgeon are actively selecting amphipod species, especially Ampelisca Verrili while opportunistically feeding on most polychaetes in this aggregation. Concurrent studies indicate that this area is important for migrating Atlantic Sturgeon, and the high abundance of prey resources indicates an important feeding habitat which aids in explaining temporal aggregations in this region. The identification of essential foraging areas is an important step in future management of the species.

3D HURRICANE ESCAPE MOBILE APPLICATION USING NEW JERSEY'S EVACUATIONS ROUTES

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Funding Sources:

Urban Coast Institute Heidi Lynn Sculthorpe Research Grant Santander

A coast-wide disaster could happen at any moment, such as Hurricane Sandy in late 2012. This unfortunate event impacted many states from Florida to Maine, and severely damaged New Jersey. It is our goal to prevent loss of life and damage by developing a hurricane escape routing mobile application. Aside from taking measures to help prevent hurricane damage to their homes, people can take matters into their own hands by evacuating coastal towns safely. Evacuations routes are spread throughout the states, but people may not be aware of their existence. This prompts a problem: how can we educate people about using the evacuation routes to escape from a hurricane?

We developed a 3D hurricane escape game for PCs with real world roads, evacuations routes and select buildings in New Jersey based on Homeland Infrastructure Foundation-Level Data (HIFLD) and Mapbox. The user will be able to use GPS directions, select a starting location, and race against the clock to arrive at one of many predetermined safe locations in New Jersey. While this program will not simulate Hurricane Sandy, it will allow the user to get a sense of what route to take and what the potential driving conditions could be during a storm.

3D SERIOUS BUILDING GAME DEMONSTRATING FEMA METHODOLOGIES TO REDUCE SEVERE FLOOD AND STORM DAMAGE TO HOMES

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Urban Coast Institute Heidi Lynn Sculthorpe Research Grant Santander

Superstorm Sandy caused extensive property damage to homes on the eastern coast of the United States in late 2012, encouraging many homeowners to make improvements with the aim to mitigate future storm damage. Some mitigations are obvious, such as raising the home from ground level with stilts or ground level garages to prevent flood related water damage. Other potential damage mitigations recommended by FEMA are less obvious however, such as particular types of foundations, flood openings, shingles, utility placement, and more.

The FEMA Home Builder's Guide to Coastal Construction is a lengthy, technical document that, while necessary to contractors and architects who rely upon it, is obscure outside those groups, and therefore does not accessibly demonstrate the effects of its recommendations.

Our Unity 3D serious game provides users with an open-ended simulation wherein they can design houses that may attempt to meet FEMA coastal construction recommendations. We simulate a severe storm with heavy flood, wind, and rain forces against the home the user constructs, and provide feedback in terms of meeting various game goals related to home value and storm damage.