MONMOUTH UNIVERSITY | SCHOOL of SCIENCE

11th ANNUAL SUMMER RESEARCH PROGRAM SYMPOSIUM

AUGUST 8, 2019

10:30 AM – 1:00 PM

ERLANGER GARDENS

MONMOUTH UNIVERSITY | SCHOOL *of* SCIENCE

Dear Friends,

I would like to take this opportunity to thank the supporters and university partners who contributed to the success of the 2019 Monmouth University School of Science Summer Research Program (SRP). Their contributions allow us to provide research opportunities for undergraduate and high school students by funding their summer salaries as research assistants, providing opportunities for students to travel to conferences and professional meetings to present their research, and acquire the supplies and equipment necessary to complete their research projects.

Without their collective philanthropy, the Summer Research Program would not be possible. I would also like to acknowledge the faculty from the School of Science who dedicated their time and offered their expertise to mentor participating students.

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

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

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Monmouth University's Office of the Provost provides the chief academic leadership, responsibility and support to all of the University's schools and centers of distinction.

Urban Coast Institute

The Urban Coast Institute supports greater engagement and integration of students and faculty in the areas of marine science and policy including providing funding for Summer Research Program projects conducted by students in Monmouth University's Marine and Environmental Biology and Policy (MEBP) Program.

MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

11th ANNUAL SUMMER RESEARCH SYMPOSIUM

Thursday, August 8, 2019

Presentations by Department

Department of Biology

BY-1 **Can Rainfall Predict Fecal Indicator Bacteria Levels At Monmouth County Surfing Beaches Near Stormwater Outfalls?**

Kelly Hanna, Victoria Lohnes, Erin Conlon, Skyler Post, Maria Riley and Ariel Zavala

Faculty Mentor: Dr. Jason E. Adolf

BY-2 **Characterizing Deoxygenation And Harmful Algal Blooms In Branchport Creek, New Jersey**

Skyler Post, Erin Conlon, Kelly Hanna, Victoria Lohnes, Maria Riley and Ariel Zavala

Faculty Mentor: Dr. Jason E. Adolf

BY-3 **Nutrient Pollution And Harmful Algal Blooms Take A Toll On Monmouth County Coastal Lakes**

Maria Riley, Ariel Zavala, Skye Post, Kelly Hanna, Erin Conlon and Victoria Lohnes

Faculty Mentor: Dr. Jason E. Adolf

BY-4 **Why Do Trees Fall: Assessing Storm Impacts On Tree Mortality**

Sarah Gillogly, Hunter Hostage, Lois Walton and Samantha Cavalli

Faculty Mentor: Dr. Pedram Daneshgar

BY-5 **Exploring Factors That Affect Red Mangrove Propagule Dispersal**

Hunter Hostage, Lois Walton, Sarah Gillogly and Samantha Cavalli

Faculty Mentor: Dr. Pedram Daneshgar

BY-6 **The Impacts Of Salt Flooding On Juvenile Maritime Tree Species**

Lois Walton, Sarah Gillogly, Hunter Hostage and Samantha Cavalli

Faculty Mentor: Dr. Pedram Daneshgar

BY-7 **Temporal Monitoring Of The Endangered Atlantic Sturgeon (*Acipenser oxyrinchus*) In Sandy Hook And Raritan Bay**

Lauren Kelly, Charles Vasas and Hannah Craft

Faculty Mentor: Dr. Keith Dunton

BY-8 **Cooperative Efforts To Determine The Demographics And Post-Release Survival Of Sharks Captured In The Recreational Land-Based Surf Fishery**

Charles Vasas, Lauren Kelly, Hannah Craft and Michael Ngyuen

Faculty Mentor: Dr. Keith Dunton

BY-9 **Secondary Structure Analysis by SHAPE-MaP of the EGFR pre-mRNA Transcript: Uncovering Novel Regions for RNA Anti-sense Targeted Therapy**

Ryan Fink and Sawyer Hicks

Faculty Mentor: Dr. Martin J. Hicks

BY-10 **Designing and Testing RNA Therapeutics to Block VEGFR2 and EGFR Activation in Human Glioblastoma**

Flobater Gawargi

Faculty Mentor: Dr. Martin J. Hicks

BY-11 **RNA THERAPEUTIC STRATEGIES TO BLOCK VEGEFR2 EXPRESSION AND ANGIOGENESIS IN GLIOBLASTOMA MULTIFORM**

Kinneret Hannah Kanik

Faculty Mentor: Dr. Martin J. Hicks

BY-12 **Generation A Gene Therapy To Alter Splicing Patterns Within The EGFR Gene And Reduce The Overexpression Of EGFR Within Glioblastoma Multiforme Tumors**

Rachel Kovach

Faculty Mentor: Dr. Martin J. Hicks

BY-13 **Synthesis Of An RNA-Therapy To Alter Overly-Expressed Tyrosine Kinase Receptors In Glioblastoma Multiforme**

Reina Montero

Faculty Mentor: Dr. Martin J. Hicks

BY-14 **Using Crispr-Cas9 For Genetic Editing Of The Gabra2 Gene In Fetal Alcohol Syndrome**

Paul Haines, Charlotte Kelly and Orli Weiss

Faculty Mentor: Dr. Cathryn L. Kubera

BY-15 **Examining The Role Of Fascin In Primary Brain Cancers**

Syed Mehdi Husaini and Esra Celik

Faculty Mentor: Dr. Cathryn L. Kubera

BY-16 **Use Of Enzymatic Ethanol Assay To Evaluate A *Gallus gallus* Model Of Fetal Alcohol Syndrome**

Nadine Khalil and Noelle Kubinak

Faculty Mentor: Dr. Cathryn L. Kubera

BY-17 **Effect Of Manuka Essential Oil On The Growth And Viability Of Human Fibroblasts**

Caitlin Cevasco and Mruga Parekh

Faculty Mentor: Dr. Dorothy Lobo

BY-18 **The Inhibiting Effects Of Select Essential Oils On The Growth Of Multidrug Resistant *Klebsiella pneumoniae* And *Pseudomonas aeruginosa***

Anadi Saini, Amanda Zappacosta and Ryan Terrany

Faculty Mentor: Dr. James P. Mack

BY-19 **The Inhibiting Effects Of Arborvitae, Cassia, Cinnamon Bark, Oregano, And Thyme Essential Oils (EOs) On The Growth Of Multidrug Resistant *Enterobacter cloacae***

Ryan Terrany, Anadi Saini and Amanda Zappacosta

Faculty Mentor: Dr. James P. Mack

BY-20 **The Inhibiting Effects Of Arborvitae, Cassia, Cinnamon Bark, Clove, Oregano, And Thyme Essential Oils (EOs) On The Growth Of Multidrug Resistant *Acinetobacter baumannii***

Amanda Zappacosta, Anadi Saini and Ryan Terrany

Faculty Mentor: Dr. James P. Mack

BY-21 **Variation In Reproductive Traits Among Mice Adapted To Different Regions Of The Americas**

Jesse Bragger, David Grossi and Tiffany Longo

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-22 **Using Environmental DNA (eDNA) To Track Black Sea Bass And Winter Flounder In A Controlled Tank Environment**

Sean Kuback and Karolina Szenkiel

Faculty Mentor: Dr. Megan Phifer-Rixey

BY-23 **Turtles Of Lake Takanassee: How Does This Assemblage Persist?**

Christiana E. Popo and Travis Kirk

Faculty Mentor: Dr. Sean C. Sterrett

BY-24 **Monmouth County Beach Nesting Bird Monitoring And Stewardship Program**

Mary Emich and Maya Paco

Faculty Mentor: Assistant Dean John Tiedemann
Collaborating Mentors: Christina Davis and Pam Prichard, NJDFW

Department of Chemistry and Physics

CE-1 **The Effect Of Small Molecules On The Stability Of G-Quadruplexes**

Christopher Bentsen

Faculty Mentor: Dr. Davis Jose

CE-2 **Unraveling The B To A Conformational Transition In Duplex DNA At Single Base Pair Resolution**

Michal M. Kalisz

Faculty Mentor: Dr. Davis Jose

CE-3 **Spectroscopic Evaluation Of Non-Canonical DNA Conformations**

Brianna Miller

Faculty Mentor: Dr. Davis Jose

CE-4 **Biochemical Characterization Of A G-Quadruplex Forming Sequence In The *C-Myc* Promoter**

Adriana Zelaya

Faculty Mentor: Dr. Davis Jose

CE-5 **Peptoid Macrocycles As Potential Anticancer Agents: The Role Of Ions In Conformational Equilibrium**

Amanda Prascsak, Santino Timpani, Thomas Melfi, Roxy Nicoletti and Olivia Enny

Faculty Mentor: Dr. Dmitri Kosenkov

CE-6 **Modeling Impact Of Intermolecular Interactions Of LPG-Alcohol Mixtures On Stability Of Phyllosilicates: Towards Improvement Of Drilling Fluids**

Santino Timpani, Amanda Prascak, Thomas Melfi, and Jessica L. Digregorio

Faculty Mentor: Dr. Dmitri Kosenkov

CE-7 **Selection Of An Aptamer To Bind 2-Hydroxyglutarate Through Selex**

Danielle Guillen

Faculty Mentor: Dr. Jonathan Ouellet

CE-8 **The Theophylline Riboswitch; Its Design And Implementation**

Mika Schievelbein

Faculty Mentor: Dr. Jonathan Ouellet

Department of Computer Science and Software Engineering

CSSE-1 **Hawks Code: Developing An Adaptive Pedagogical Compiler To Enhance Student Learning**

Joe Chung, Matt Cohen, Victoria Johnson, Todd Qualiano and Trisha Smith

Faculty Mentor: Professor Katie Gatto

CSSE-2 **Analysis Of Healthcare Prescription Data Using Graph Database, Graph Algorithms, Cloud Computing Services And Machine Learning Models**

Patricia S. Skora

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-3 **Exploring Robotics With The NAO Robot**

Anthony Vives and Jimmy Duong

Faculty Mentor: Dr. Jay Wang

CSSE-4 **Actiontime: A Web Application Motivating Children For Good Habits**

Allen Lu, Steven Cassidy and Wenjin Zhang

Faculty Mentor: Dr. Cui Yu

CSSE-5 **A New Calendar Application For Time Management**

Matt Mammano and Wenjin Zhang

Faculty Mentor: Dr. Cui Yu

CSSE-6 **Smartparking: Using Artificial Intelligence To Find Empty Parking Spaces**

Jason Yan, John Meyer and Wenjin Zhang

Faculty Mentor: Dr. Cui Yu

MONMOUTH UNIVERSITY | BIOLOGY

BY-1

CAN RAINFALL PREDICT FECAL INDICATOR BACTERIA LEVELS AT MONMOUTH COUNTY SURFING BEACHES NEAR STORMWATER OUTFALLS?

Kelly Hanna[1], Victoria Lohnes[2], Erin Conlon[1], Skyler Post[1], Maria Riley[1] and Ariel Zavala[3]

[1]Monmouth University Department of Biology, [2]Monmouth University Department of History and Anthropology, [3]Monmouth University Department of Chemistry

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

Funding Source:
Surfer's Environmental Alliance

Abstract

Monmouth County is home to several locations for recreational activity, including surfing beaches, many of which are located near stormwater or coastal lake outfall pipes. Since the New Jersey Department of Environmental Protection (NJDEP) began its weekly Cooperative Coastal Monitoring Program (CCMP) in 1974, it has been evident that discharged water from the pipes may contain fecal indicator bacteria (FIB) known as *Enterococcus*. *Enterococcus,* found in mammalian intestinal tracts, signify that fecal matter containing other harmful bacteria, protozoa, and viruses, is also present in the water. The current allowable limit of the FIB is 104 CFU per 100 ml of water. Although the evidence of increased *Enterococcus* levels after high rainfall events is acknowledged, in-depth research providing numerical data for these correlations has yet to be published. Forecast models used to predict this data are also absent. This study will provide quantifiable data on the relationship between environmental conditions and *Enterococcus* levels, including time between rainfall events, at five sites between Long Branch and Asbury Park, New Jersey. FIB data was collected using an IDEXX Quanti-Tray system to determine the most probable number (MPN) and rainfall data was gathered from the NJDEP DW&S Rainfall Acquisition website. To date, the team has acquired rainfall data ranging from 0 to 1.4 inches 24 hours prior to sampling and MPN data ranging from <10 to 4,884. The project will continue to assess trends as it progresses through fall and winter in the hope of creating a forecast model to give surfers and beachgoers the ability to determine how safe the water is before travel to the beach. As FIB in coastal waters is a global issue, these models may prove applicable to future research and broader regions.

BY-2

CHARACTERIZING DEOXYGENATION AND HARMFUL ALGAL BLOOMS IN BRANCHPORT CREEK, NEW JERSEY

Skyler Post[1], Erin Conlon[1], Kelly Hanna[1] Victoria Lohnes[2], Maria Riley[1] and Ariel Zavala[3]

[1] Monmouth University Department of Biology; [2]Monmouth University Department of History and Anthropology; [3]Monmouth University Department of Chemistry

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

Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University School of Science; Monmouth University Biology Department

Abstract

Deoxygenation of coastal waters due to the presence of harmful algal blooms (HABs) is not only a local crisis but has been expanding globally. HABs occur more frequently when phytoplankton, an important marine primary producer, are exposed to high temperatures and high nutrients for an extended amount of time. As HABs become pervasive in coastal environments, hypoxic and anoxic water conditions increase, and both HABs and anoxic conditions are capable of causing fish kills.

Branchport Creek in the Shrewsbury River is known to be polluted and experiences frequent deoxygenation and fish kills. However, the phytoplankton and HABs in these waters have not been characterized. Our objective was to characterize the phytoplankton growing here to determine their role in the deoxygenation and fish kills observed in Branchport Creek. Over the course of twelve weeks, a series of stations along Sandy Hook Bay, the Navesink and Shrewsbury Rivers were sampled. *In situ* sampling with chemical and biological analyses on the water were performed. These include salinity, temperature, oxygen, pH, turbidity, chlorophyll, and light transparency in the water column. Upon testing these parameters in Branchport Creek, we found a drastic difference in the surface water and the bottom water. The surface was always well oxygenated, but the bottom water's oxygen was slim to none. Fish kills were also observed in this area. After using microscopy to identify the phytoplankton and harmful algae blooms throughout the estuaries, dinoflagellates were dominant in Branchport Creek, whereas diatoms were dominant in Sandy Hook Bay. Further research is needed to determine if the cause of these fish kills was from a harmful algae species or from the lack of oxygen in the system.

Determining this can provide insight to new management practices locally and globally.

BY-3

NUTRIENT POLLUTION AND HARMFUL ALGAL BLOOMS TAKE A TOLL ON MONMOUTH COUNTY COASTAL LAKES

Maria Riley[2], Ariel Zavala[1], Skye Post[3], Kelly Hanna[2], Erin Conlon[3] and Victoria Lohnes[3]

[1]Monmouth University Department of Chemistry, [3]Monmouth University Department of Biology; [2] Marine and Environmental Biology and Policy

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

Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University School of Science; Monmouth University Biology Department

Abstract

Issues regarding Harmful Algae Blooms (HABs) in freshwater environments have been surfacing nationwide in recent news leading researchers to believe that environmental factors have made the water susceptible to the growth of HABs. Coastal lakes often produce HABs, due to nutrient pollution, which can decrease the amount of oxygen present in the water, leading to the death of wildlife if oxygen levels are too low. The research was conducted in order to test the water quality of the Monmouth County coastal lakes by determining the levels of nutrients found in each lake. From late May to mid-July, research was done weekly by driving to the sites (Lake Takanasse, Deal Lake, Sunset Lake, Wesley Lake, Fletcher Lake, Sylvan Lake, Silver Lake, Lake Como, Spring Lake, and Wreck Pond) and reading measurements on the multiparameter water quality probe which showed the levels of dissolved oxygen, percent of oxygen, salinity, and temperature in the water. While reading the measurements, a secchi test was done to measure the clarity of the lake. At each individual lake, a sample was taken in a 60 ml vial to measure the Phycocyanin (PC) and chlorophyll levels using a Cyanofluor Fluorometer which was then processed at a Monmouth University research lab. A one-liter sample bottle was also taken and transported to the New Jersey Department of Environmental Protection (NJDEP) lab in Leeds Point, NJ to process the nutrient levels found in each of the lakes. Beginning in mid-June, HABs were detectable in certain lakes, such as Sunset Lake and Spring Lake, in comparison to others in which HABs did not grow, such as Lake Takanasse. However, Deal Lake was stagnant in the beginning of the season, but the data shows a rapidly increasing amount of growth within the past few weeks. The current data set received from the NJDEP shows that lakes containing HABs have low levels of both Nitrate and Ammonia in the water. The global increase of HABs within freshwater environments are continuously having a negative impact on various ecosystems by removing the nutrients needed for survival.

BY-4

WHY DO TREES FALL: ASSESSING STORM IMPACTS ON TREE MORTALITY

Sarah Gillogly[1], Hunter Hostage[1], Lois Walton[1] and Samantha Cavalli[2]
[1]Monmouth University Department of Biology
[2]Monmouth University Department of Mathematics

Faculty Mentor:
Dr. Pedram Daneshgar, Department of Biology

Funding Source:
Monmouth University School of Science

Abstract

Climate change models representing potential future weather patterns reported in the International Panel on Climate Change (IPCC) predict an increase in the frequency of extreme weather events. The effects of these new climate and weather extremes pose a hazard to many residential and commercial areas as a result of flooding, high winds, extreme heat, and extreme cold. Trees in these areas are particularly susceptible to mortality and tree fall during storms because of the tall heights, the amount of wind break they provide, poor soil conditions and the lack of dense vegetation around them that can reduce storm impacts. Data is needed to better understand which trees species are more susceptible to fall as well as what conditions may increase that susceptibility. In order to better predict and mitigate the potential damage caused by trees effected by more frequent and extreme storm events, we analyzed fallen trees post storm assessing several factors linked to survival. Uprooting and bole snaps are exacerbated by shallow rooting, weakened condition of the tree such as disease, pests, or vines, cutting or pruning practices, age, and soil composition. The aim is to create a database of fallen trees in the state of New Jersey to conclude what factors increase the likelihood of damage caused by fallen trees. This information will allow us to better advise stakeholders on what trees may be high risk and prescribe which trees should be selected and where they should be planted going forward.

BY-5

EXPLORING FACTORS THAT AFFECT RED MANGROVE PROPAGULE DISPERSAL

Hunter Hostage[1], Lois Walton[1], Sarah Gillogly[1] and Samantha Cavalli[2]
[1]Monmouth University Department of Biology
[2]Monmouth University Department of Mathematics

Faculty Mentor:
Dr. Pedram Daneshgar, Department of Biology

Funding Source:
Monmouth University School of Science

Abstract

Mangroves, woody species that persist in the intertidal zone, are globally threatened as only seven percent of the original populations remain. Restoring and protecting mangroves has been challenging because so much about their natural history is still unknown. For example, little is understood about propagule dispersal of red mangrove (*Rhizophora mangle*), the most common mangrove species in the Caribbean. Red mangroves are viviparous, which means that the seeds germinate and the embryo grows on the parent plant before dispersal. Once dispersed the young plant or propagule is able float in water for extended periods of time until it settles and roots. In our lab, we have been exploring the factors which affect propagule dispersal, which include tidal flow, rate of water flow, location of the drop, timing of the drop and density of the mangroves. This summer we have explored how mangrove stilts may affect water flow and thus affect dispersal distance. To do this, we developed a flow through system which can be used in any moving shallow body of water to assess how mangrove stilt density affects rate of flow and thus mangrove dispersal. Our system consists of a contained observable area of one square meter in which water flows through pvc pipes, which are placed into the area in randomly determined locations are used to simulate mangrove stilts. To measure the rate of flow we used both a flow meter as well as timing a ball floating through the system. Our preliminary results suggest that flow is impacted by mangrove stilts in high densities and that the arrangement of stilts may also play a role.

BY-6

THE IMPACTS OF SALT FLOODING ON JUVENILE MARITIME TREE SPECIES

Lois Walton[1], Sarah Gillogly[1], Hunter Hostage[1] and Samantha Cavalli[2]
[1]Monmouth University Department of Biology
[2]Monmouth University Department of Mathematics

Faculty Mentor:
Dr. Pedram Daneshgar, Department of Biology

Funding Source:
Monmouth University School of Science

Abstract

Maritime forests are coastal wooded habitats representing the apex of dune succession found within range of salt spray. Their proximity to the ocean makes them more vulnerable to climate change induced impacts such as sea level rise and increased storm events which would lead to prolonged periods of flooding. In order to determine the potential impacts of flooding on Mid-Atlantic maritime tree species, we conducted two greenhouse experiments where we treated juveniles of eight tree species with different levels of salinity, as well as different frequencies of salt flooding in two randomized block designs. It was hypothesized that the conifer species would be more salt tolerant than the broad-leaved species as needles and scales have a lower rate of water loss, making them less vulnerable to salt stress. In addition, we predicted that the salt impacts would become more detrimental as the salinity level and frequency of flooding is increased, given the harmful effects salt has on plant physiology. A health index was created to assess the overall health, and a score was given to each individual biweekly over the duration of the growing season. Preliminary results suggest that salt flooding is most detrimental to the trees at a concentration of 10-15 ppt and when the increased flooding frequency is increased compared to our current rates. In addition, it is evident that the species have evolved different strategies to combat salt stress, and that ultimately some may be better able to withstand the increased flooding that sea level rise and extreme weather events may bring to maritime forests. The impacts will be further studied throughout the growing season through various response variables including leaf water potential, growth rate, and chlorophyll content, and all trees will be harvested before leaf senescence begins.

BY-7

TEMPORAL MONITORING OF THE ENDANGERED ATLANTIC STURGEON (*Acipenser oxyrinchus*) IN SANDY HOOK AND RARITAN BAY

Lauren Kelly, Charles Vasas and Hannah Craft
Monmouth University Department of Biology

Faculty Mentor:
Dr. Keith Dunton, Department of Biology

Funding Source:
Monmouth University Urban Coast Institute

Abstract

Sandy Hook Bay (SHB) and Raritan Bay (RB) are urbanized waterbodies located within close proximity of known Atlantic sturgeon coastal aggregation and freshwater spawning sites. While Atlantic sturgeon have been historically documented to occur in SHB, no formal surveys have been conducted to identify their presence/absence. The purpose of this project was to determine the presence/absence and seasonality of sturgeon within SHB through the use of acoustic telemetry. Working cooperatively with Naval Weapons Station Earle, six acoustic receivers were deployed in spring of 2016 to cover a portion of SHB. The array was expanded in 2019 with 13 acoustic receivers were deployed throughout RB and surrounding water bodies to monitor for previously tagged Atlantic Sturgeon. A total of 181 uniquely tagged individual Atlantic sturgeon were detected (n~187,000 detections). Sturgeon were detected in all months monitored but showed higher abundances in spring and fall. Some sturgeon displayed long residency times within the bay. Sturgeon largely came from the New York Bight (NYB) Distinct Population segment, but some came as far as south as Chesapeake Bay (MD) and Edisto River (SC), indicating that multiple DPSs utilize the area. This suggests that Sandy Hook Bay may be an important late spring – early summer habitat so proper protection may be needed to protect against localized anthropogenic threats (eg., vessel interactions, commercial fishing, dredging) that may pose possible negative interactions with sturgeon.

BY-8

COOPERATIVE EFFORTS TO DETERMINE THE DEMOGRAPHICS AND POST-RELEASE SURVIVAL OF SHARKS CAPTURED IN THE RECREATIONAL LAND-BASED SURF FISHERY

Charles Vasas[1], Lauren Kelly[1], Hannah Craft[1] and Michael Ngyuen[2]
[1]Monmouth University Department of Biology
[2]Stockton University Department of Biology

Faculty Mentor:
Dr. Keith Dunton, Biology Department

Funding Source:
Monmouth University Urban Coast Institute

Abstract

With the increasing popularity of recreational land-based shark fishing, a greater understanding and characterization of the species captured and their demographics is needed. Along the coast of New Jersey, this land-based shark fishery occurs largely during the summer months. We worked directly with the professional guide industry to classify the demographics of this shore based fishery. In 2017-2018, 182 individual sharks were captured consisting of 135 Sandbar Sharks (*Carcharinus plumbius*), 35 Sand Tiger sharks (*Carcharias taurus)*, 11 Dusky Shark (*Carcharinus obscurus*), and 2 Spinner shark (*Carcharhinus brevipinna*). A sub-set of individuals (n=9 Sand Tiger and n=13 Sandbar shark) were surgically implanted with Vemco V-16 acoustic transmitters. All acoustic tagged sharks were detected post-release, some as far south as North Carolina, leading to a 100% post release survival rate for our captured sharks. In 2019 88 sharks were captured consisting of three species (Sandbar sharks n=58, Sand Tiger sharks n=27, and Blacktip sharks (*Carcharhinus limbatus*) n=3). Of these sharks a subset of individuals (n=23 Sandbar, n=2 Sand Tiger and n=2 Blacktip) were surgically implanted with Vemco V-16 acoustic transmitters. This work on the classification of this recreational fishery and acoustic tagging to understanding post release survival and coastal movements provides us with the information needed to monitor this emerging fishery. Further understanding of the population demographics of this specific shark fishery, as well as migratory pathways along the coast of New Jersey can be used to support management and conservation efforts for this coastal shark fishery.

BY-9

SECONDARY STRUCTURE ANALYSIS BY SHAPE-MAP OF THE EGFR PRE-MRNA TRANSCRIPT: UNCOVERING NOVEL REGIONS FOR RNA ANTI-SENSE TARGETED THERAPY

Ryan Fink
Monmouth University Department of Biology

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

Funding Source:
Bristol-Myers Squibb

Abstract

Pre-mRNA splicing is the process whereby precursor messenger RNA (pre-mRNA) is processed into mature mRNA by removing introns and joining exons. The pattern of intron removal, and exon juxtaposition determines the characteristic of the translated protein. We have developed a gene therapy vector that delivers antisense RNA to block critical splicing elements of the pre-mRNA transcript of overexpressed tyrosine kinase receptors, specifically, epidermal growth factor receptor (EGFR). EGFR is overexpressed in 60% of glioblastoma multiforme brain tumors and leads to cell proliferation. To optimize targets within the EGFR transcript, we are using tools to characterize the EGFR pre-mRNA structurome. The technique is called selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). The SHAPE reagent (1M7) reacts with the 2' hydroxyl of RNA molecules when the RNA molecule is in a conformationally flexible position creating a 2' O-adduct. The modified RNA is reverse transcribed, incorporating mismatches at the acylated positions; a comparison of unmodified to modified RNA will allow us to determine RNA nucleotides that are involved in secondary structure, part of RNA-binding-protein complexes, or single stranded. Single stranded RNAs and RNAs with minimal structure are a preferential target of our therapy. We hypothesize that the secondary structure of the RNA will determine the most effective way to therapeutically alter the splicing of the EGFR pre-mRNA. A DNA construct containing the targeted region of the EGFR transcript; exon 10, intron 10 and exon 11 (E10_I10_E11) was created and transcribed *in vitro* using T7 polymerase. The E10_I10_E11 RNA was separated by denaturing polyacrylamide gel electrophoresis, purified, renatured and acylated using 1M7. The acylated E10_I10_E11 and non-acylated control RNA were sequenced using the third generation sequencing platform Oxford Nanopore MinIon. These experiments will help uncover targetable regions within the EGFR transcript.

BY-10

DESIGNING AND TESTING RNA THERAPEUTICS TO BLOCK VEGFR2 AND EGFR ACTIVATION IN HUMAN GLIOBLASTOMA

Flobater Gawargi
Monmouth University Department of Biology

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

Funding Source:
Bristol-Myers Squibb

Abstract

Glioblastoma multiforme (GBM), is the most common and aggressive malignant primary brain tumor with a median survival of 14 months. Current therapies are limited by the blood brain barrier. Epidermal growth factor (EGFR) and Vascular Endothelial Growth Factor receptor 2 (VEGFR2) are crucial for cancer cell survival. In our lab we are developing an innovative therapy that can bypass the blood brain barrier by developing RNA therapies to alter the splicing mechanism of the EGFR and VEGFR2 gene to reduce or block its activation, thus stop tumor cells from growing. Eleven Antisense sequences were designed to target the EGFR gene and nine Antisense sequences for VEGFR2, to potentially block their activation. The Antisense sequences were cloned into pAAV-U7-smOPT. In addition, multiple cloning strategies and protocols were used to clone the exonic splicing silencer 4G-quadruplex into our therapy vector. In addition, another aspect of this research is to isolate multiple tyrosine kinase receptors mRNA from GBM cancer cells, clone the cDNA into a T7 expression vector to transcribe control RNA to use in our high throughput sequencing experiments. Multiple cell lines including U87 and SK-MG cell line are being cultured and transfected with our novel therapies. Total mRNA was collected, analyzed, and compared to same cell lines without treatment. The collected data will allow the research to move toward a mouse model using adeno-associated virus (AAV) vector which was chosen based on its non-pathogenic and integrative features.

BY-11

RNA THERAPEUTIC STRATEGIES TO BLOCK VEGEFR2 EXPRESSION AND ANGIOGENESIS IN GLIOBLASTOMA MULTIFORM

Kinneret Hannah Kanik
Monmouth University Department of Biology

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

Funding Source:
Bristol-Myers Squib

Abstract

Glioblastoma Multiform (GBM) is an aggressive malignant brain tumor. Patients with GBM tend to have an over-expression of the tyrosine kinase receptor protein, Vascular Endothelial Growth Factor Receptor 2 (VEGFR2), which promotes the growth of new blood vessels, angiogenesis. VEGFR2 activation plays a major role in pathological angiogenesis and development of solid tumors, such as GBM. Our lab is developing antisense RNA therapy to alter VEGFR2 protein expression. More specifically, my role is to develop a gene therapy, encoding an antisense RNA that will induce a therapeutic isoform of the VEGFR2 protein. This will alter the pre-mRNA splicing pattern of the exons of VEGFR2 transcript, effectively prohibiting the receptor from binding to the cell membrane. We hypothesize that determination of the secondary structure of VEGFR2 Exon 13_Intron13_Exon14 will unravel the most effective way to approach synthetically altering the splicing of the VEGFR pre-mRNA. To develop my project, I have learned and carried out basic molecular biology protocols specific to the Hicks lab. In order to characterize VEGFR2 and EGFR transcripts, I grew and maintained GBM cell lines, isolated cytoplasmic and nuclear RNA, and reverse transcribed the RNA to generate complimentary DNA (cDNA). To isolate the EGFR isoform, I designed quantitative PCR (qPCR) primers, and tested a new VEGFR2 primer sets. Using these primer sets, I have evaluated tyrosine kinase receptor expression in GBM cell lines, HEK293 and SKMG3. To verify the product size of qPCR and PCR, I ran an agarose gel electrophoresis. Through these experiments, I have contributed to distinct projects in the Hicks Lab as well as gained expertise to initiate experiments to develop my own individual project to evaluate VEGFR2.

BY-12

GENERATION A GENE THERAPY TO ALTER SPLICING PATTERNS WITHIN THE EGFR GENE AND REDUCE THE OVEREXPRESSION OF EGFR WITHIN GLIOBLASTOMA MULTIFORME TUMORS

Rachel Kovach
Monmouth University Department of Biology

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

Funding Source:
Bristol-Myers Squibb

Abstract

Glioblastoma Multiforme (GBM) is an aggressive, malignant brain tumor that originates in glial cells. Glial cells provide insulation and support for neurons that transmit signals within the brain. Those diagnosed with GBM, on average, survive 12-15 months after diagnosis with a 5-year survival rate of 5%. 60% of those diagnosed with GBM exhibit overexpression of Epidermal Growth Factor Receptors (EGFR), which play a part in the proliferation of the glial cells that exist within the brain and central nervous system. It's the overproduction of these wild type EGFR that cause the proliferation of the cancer cells. We hypothesize that altering the splicing patterns of the gene that codes for EGFR will reduce the over expressions of EGFR wild types and ultimately reduce the growth of GMB tumors. To create different versions of the therapy to test, restriction digest cloning was used to ligate many different antisense sequences to multiple versions of the same backbone DNA sequence; one ligated therapy per backbone. We create different versions of these therapies to test which version will work the best in reducing the over expression of EGFR. We want to test these therapies in vitro; to do this we had to grow up GMB cancer cells (SKMG-3) to test our therapy in. The cells were grown up in a media consisting of DMEM with 10% FBS. Nuclear extraction is performed on HEK-293T cells so that the necessary nuclear material (including the hnRNP- h protein) are present in the SKMG-3 cells for the therapy to be tested. The therapy is introduced into the cells through transfection. Once transfected, the samples are run through an EMSA to test whether the protein of interest interacts with our therapy to suppress the overexpression of EGFR.

BY-13

SYNTHESIS OF AN RNA-THERAPY TO ALTER OVERLY-EXPRESSED TYROSINE KINASE RECEPTORS IN GLIOBLASTOMA MULTIFORME

Reina Montero
Monmouth University Department of Biology

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

Funding Source:
Bristol-Myers Squibb

Abstract

Glioblastoma Multiforme (GBM) is a prominent form of brain cancer that encompasses formation of gliomata in astrocytes and oligodendrocytes of the central nervous system (CNS). This form of brain cancer has a mortality rate of 15 months. Treatments are limited due to the blood-brain barrier, and resistance to current medical treatments. Tyrosine Kinase Receptors (TKRs) are key players in the proliferation and development of GBM. Examples include, the vascular endothelial growth factor receptor (VEGFR) and epidermal growth factor receptor (EGFR). VEGFR is responsible for the formation of new blood vessels and EGFR leads to an increase in tumor size. DNA transcription occurs within the nucleus to produce pre-mRNA that is modified by splicing, polyadenylation, and capping to form mature mRNA which is translated into protein by the ribosome. Our strategy aims to deliver a gene therapy that will be targeted to the nucleus of tumor cells and transcribed to take on the function of disrupting splicing reactions in TKR genes. My project focuses on altering splicing with the goal of disrupting the expression of the transmembrane domain in EGFR. Without this transmembrane domain, EGFR will bind to its ligand without EGFR pathway activation (ligand sequestration). This dominant negative receptor is termed the soluble decoy. To ensure that our therapy interacts with hetero-ribonucleoprotein H and blocks splice site recognition, I performed various EMSA experiments that verify RNA-protein binding affinity and the formation of RNA-protein complexes. Mammalian cell cultures were grown and transfected to produce hnRNP H, cells were lysed, the protein isolated and dialyzed. RNA therapy was generated by T7 transcription, followed by RNA extraction and purification. Therapeutic RNAs were incubated at various protein concentrations. Reactions were run through a non-denaturing gel to separate molecules and verify the formation of RNA-protein complexes.

BY-14

USING CRISPR-CAS9 FOR GENETIC EDITING OF THE GABRA2 GENE IN FETAL ALCOHOL SYNDROME

Paul Haines[1], Charlotte Kelly[1] and Orli Weiss[2]
[1]Monmouth University Department of Biology
[2]Cornell University

Faculty Mentor:
Dr. Cathryn L. Kubera, Department of Biology

Funding Sources:
Bristol-Myers Squibb; Monmouth University Biology Department

Abstract

Fetal Alcohol Spectrum Disorders (FASDs) are a group of conditions that lead to learning disabilities, heart defects, and craniofacial abnormalities due to premature exposure to alcohol. The most severe form of the condition is Fetal Alcohol Syndrome (FAS). Variations of the GABRA2 gene have been associated with alcoholism and may play a role with alcohol in the development of FASDs. The gene causes protein expression of the α2 subunit of gamma-aminobutyric acid type A ($GABA_A$) receptor. We are using CRISPR-Cas9 technology to cause gene knockout of the GABRA2 gene in *Gallus gallus* brain thereby creating a model by which to examine this possible underlying mechanism of FAS. To do this, we used a CRISPR-Cas9 plasmid vector and engineered them to encode GABRA2 gene-specific guide RNAs. To cause gene knockout, we are using three different CRISPR-Cas9 plasmids to edit exons of the GABRA2 gene in different locations. We believe using all three plasmids together will cause a synergistic effect leading to efficient gene knockout of GABRA2. To determine gene knockout efficiency from each plasmid, each plasmid was separately transfected *in vitro* into *G. gallus* DF-1 fibroblast cells. Each plasmid contains a fluorescent mCherry reporter which was expressed in the DF-1 cells indicating successful transfection and possible genetic editing of the chicken genome. More research needs to be done in order to determine successful genetic editing of GABRA2 in tissue culture before employing the CRISPR-Cas9 plasmids *in ovo* to determine the effect of GABRA2 gene knockout in the developing brain of embryonic chicks.

BY-15

EXAMINING THE ROLE OF FASCIN IN PRIMARY BRAIN CANCERS

Syed Mehdi Husaini and Esra Celik
Monmouth University Department of Biology

Faculty Mentor:
Dr. Cathryn L. Kubera, Department of Biology

Funding Sources:
Bristol-Myers Squibb; Monmouth University Biology Department

Abstract

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 as well as a cell's motile and invasive properties, making it important to study in cancer cells due to established fascin overexpression. Upregulation of fascin in colorectal and breast cancer cells leads to increased metastatic and invasive properties, and the protein 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, disrupting the traditional ideology behind the investigation.

We previously characterized fascin gene expression in brain cancer cell lines using RT-qPCR and immunocytochemistry to determine relative protein abundance, where preliminary results show robust fascin mRNA and protein presence in Neuro2a neuroblastoma and A-172 glioblastoma cells when compared to controls such as Human Embryonic Kidney cells (HEK-293), which have reportedly low fascin expression levels.

Current findings have allowed us to move into manipulating fascin expression to assess its effects on cell motility using a 2D invasion assay. Using a Biotek Cytation 5 multi-mode plate reader, we have accumulated extended time-lapse imaging of cancer cell invasion across varying fascin expression conditions. These video montages have allowed us to conduct computerized evaluation of whether fascin overexpression increases cell motility related to metastasis and invasion, while using the designed invasion assay to observe cell movement into unoccupied space in real time. This project provides a visualization of the effect of varying fascin expression on the motile properties of primary brain cancer cell lines in hopes of identifying a therapeutic target.

BY-16

USE OF ENZYMATIC ETHANOL ASSAY TO EVALUATE A *Gallus gallus* MODEL OF FETAL ALCOHOL SYNDROME

Nadine Khalil and Noelle Kubinak
Monmouth University Department of Biology

Faculty Mentor:
Dr. Cathryn L. Kubera, Department of Biology

Funding Sources:
Bristol-Myers Squibb; Monmouth University Biology Department

Abstract

Fetal Alcohol Spectrum Disorder (FASD), which results from prenatal exposure to alcohol, is a wide-spread condition impacting 2-5% of infants in the United States. Distinctive craniofacial abnormalities and symptoms that develop from FASD include widening of the eyes, flat nose, thin upper lip, learning disabilities, and heart defects. Here we use a *Gallus gallus* model to study FASD. On embryonic day seven (E7), when cerebellum development begins, 20% ethanol, 50% ethanol or PBS was injected into the air sac of the egg during the *in ovo* method, whereas in the *ex ovo* method 20% ethanol, 50% ethanol or PBS was added topically. The cerebellum controls mobility, coordination, balance and speech, all of which may become impaired as a result cellular apoptosis in the cerebellum following embryonic alcohol exposure. In our FASD model, tissue and egg white samples were harvested on E8.

An enzymatic Ethanol Assay was performed on egg white samples from ethanol- or PBS-treated eggs to determine alcohol concentration. The Assay measured reduction of NADH from nicotinamide-adenine dinucleotide (NAD+) through two separate enzymatic reactions: aldehyde dehydrogenase mediated oxidation of ethanol to acetaldehyde, followed by alcohol dehydrogenase mediated conversion of acetaldehyde to acetic acid. The Cytation 5 plate reader was used to collect readings of NADH absorbance of 340 nm, which is directly related to the amount of ethanol in the sample. Preliminary assay results indicate successful detection of ethanol in positive controls and standard curves, as well as in egg white samples collected 24 hours post ethanol treatment.

In addition, chicks developing *ex ovo* were video recorded to observe the effects of alcohol on the intrinsic reflex behavior that developing chicks begin to display on E6. Pre- and post-treatment movies will be assessed for frequency and duration of reflex bouts to determine the effect of alcohol on embryonic movements.

BY-17

EFFECT OF MANUKA ESSENTIAL OIL ON THE GROWTH AND VIABILITY OF HUMAN FIBROBLASTS

Caitlin Cevasco[1] and Mruga Parekh[2]
[1]Northeastern University Department of Biology
[2]Monmouth University Department of Biology

Faculty Mentor:
Dr. Dorothy Lobo, Department of Biology, Monmouth University

Funding Sources:
Kevin Young ’89; Monmouth University School of Science

Abstract

Manuka oil is popular in many skincare products because of its antibacterial and anti-inflammatory properties that treat several skin conditions. Previous work at Monmouth University indicated manuka essential oil had inhibitory effects on bacteria growth. Subsequent work in this laboratory demonstrated that proliferation of fibrosarcoma (HT-1080) and cervical adenocarcinoma (HeLa) cells was also negatively affected by manuka essential oil treatment. The goal of this work was to test the effect of manuka essential oil on normal human fibroblasts. To conduct the experiment, normal human fibroblasts (CUA-4) were grown on 24-well plates and subconfluent cultures were treated with varying concentrations of manuka essential oil for 24 hrs. A trend was found that as the concentration of oil increased, cell proliferation, measured by direct cell counting, decreased in a dose-dependent manner with a concentration of 100 µg/ml decreasing proliferation 23% in comparison to control cells. In support, MTT assays were also performed, and cells treated with manuka essential oil also demonstrated decreased viability using this assay. Similarly, a concentration of 100 µg/ml resulted in a 26% decrease in viability compared to the control. Further testing to determine if observed cell death is a result of apoptosis will be performed.

BY-18

THE INHIBITING EFFECTS OF SELECT ESSENTIAL OILS ON THE GROWTH OF MULTIDRUG RESISTANT *Klebsiella pneumoniae* AND *Pseudomonas aeruginosa*

Anadi Saini[1], Amanda Zappacosta[1], and Ryan Terrany[2]
[1]Monmouth University Department of Biology; [2]Rutgers University

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

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

Abstract

Multidrug resistant bacterial infections have become a global issue within the past century due to the overuse of many broad-spectrum antibiotics. Antibiotic resistance develops through the evolution within a bacterial species that cause the medication to no longer have its original effectiveness. According to the CDC (2013), 2 million people in the US contract a multidrug resistant infection annually.

Initially, 81 essential oils (EOs) were tested at 100% concentration on Mueller Hinton II agar using the Kirby-Bauer Disk Diffusion Test. This was done to determine which essential oils had inhibiting effects on the growth of multidrug resistant *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Of the 81 essential oils that were tested, arborvitae, cassia, cinnamon bark, cypress, and oregano effectively inhibited the growth of *Klebsiella pneumoniae*. Cassia, cinnamon, and cumin EOs inhibited the growth of *Pseudomonas aeruginosa*. To determine the minimum inhibitory concentration (MIC) of these select essential oils, dilutions were made using jojoba oil. The zones of inhibition were measured for all plates after 24 hours of incubation at 37°C. In addition, time of efficacy testing was performed at 30-minute intervals to determine the minimum amount of time required to record the maximum zones of inhibition of these significant essential oils at 100% concentration.

The zones of inhibition from select EOs at 100% concentration were compared to the zones created by the antibiotic disks containing the leading medically prescribed antibiotics for its respective bacterium. Regarding *Klebsiella pneumoniae*, arborvitae, cassia, cinnamon bark, cypress, and oregano outperformed the antibiotic Imipenem. For *Pseudomonas aeruginosa*, cassia outperformed the antibiotics Meropenem, Imipenem, and Amikacin. All MIC values were determined to be values less than 25% concentration for both bacteria. These results show that low concentrations of these EOs can successfully inhibit the growth of *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* in vitro.

BY-19

THE INHIBITING EFFECTS OF ARBORVITAE, CASSIA, CINNAMON BARK, OREGANO, AND THYME ESSENTIAL OILS (EOs) ON THE GROWTH OF MULTIDRUG RESISTANT *Enterobacter cloacae*

Ryan Terrany[2], Anadi Saini[1] and Amanda Zappacosta[1]
[1] Monmouth University Department of Biology; [2] Rutgers University

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

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

Abstract

Antibiotic resistance in many species of bacteria has become a major global concern. Through rapid evolution, many antibiotics used in past years have become ineffective in the treatment of multidrug resistant bacterial diseases. The widespread overuse of antibiotics has only escalated this increasingly prevalent antibiotic resistance. It is hypothesized that some natural products such as essential oils may be a valuable alternative in treating multidrug resistant bacteria such as *Enterobacter cloacae* (*E. cloacae*).

Initially, 81 essential oils (EOs) were tested at full concentration on Mueller Hinton II agar using the Kirby-Bauer Disk Diffusion Test. This was done to determine which essential oils had inhibiting effects on the growth of multidrug resistant *E. cloacae.* Of the 81 essential oils that were tested, arborvitae, cassia, cinnamon bark, oregano, and thyme inhibited the growth of *E. cloacae*. To determine the minimum inhibitory concentration (MIC) of these select essential oils, various dilutions were prepared using jojoba oils. The zones of inhibition were measured for all plates after 24 hours of incubation at 37° C. In addition, time of efficacy testing was performed at 30-minute intervals to determine the minimum amount of time required to visually record the maximum zones of inhibition of these significant essential oils at 100% concentration.

All of the MICs for the five EOs tested were below 25% for *E. cloacae*. The zones of inhibition for cassia and cinnamon bark were greater than those of the leading antibiotics Imipenem and Meropenem. These EOs and their antimicrobial components could possibly be used in nosocomial settings to treat this multidrug resistant bacterium. These results strongly suggest that cassia and cinnamon bark essential oils are able to outperform Imipenem and Meropenem at inhibiting *E. cloacae* in vitro.

BY-20

THE INHIBITING EFFECTS OF ARBORVITAE, CASSIA, CINNAMON BARK, CLOVE, OREGANO, AND THYME ESSENTIAL OILS (EOS) ON THE GROWTH OF MULTIDRUG RESISTANT *Acinetobacter Baumannii*

Amanda Zappacosta[1], Anadi Saini[1] and Ryan Terrany[2]
[1]Monmouth University Department of Biology; [2]Rutgers University

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

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

Abstract

The discovery of antibiotics has transformed the way modern medicine treats bacterial infections. In recent years, the overuse of these drugs has resulted in many bacteria evolving to become resistant rendering many antibiotics ineffective. According to the CDC (2013), 7,300 people are infected with *Acinetobacter baumannii* (*A. baumannii*) per year. These people are typically hospitalized individuals with weakened immune systems, especially those in intensive care unit (ICU) and neonatal intensive care unit (NICU) settings.

Initially, 81 essential oils (EOs) were tested at 100% concentration on Muller Hinton II agar using the Kirby-Bauer Disk Diffusion Test to determine which essential oils had inhibiting effects on the growth of multidrug resistant *A. baumannii*. Of the 81 EOs tested, arborvitae, cassia, cinnamon bark, clove, oregano and thyme were very effective in inhibiting the growth of this bacterium. To determine the minimum inhibitory concentration (MIC) of these select essential oils, various dilutions were prepared using jojoba oil. The zones of inhibition were measured for all plates after 24 hours of incubation at 37°C. In addition, time of efficacy testing was performed at 30-minute time intervals to determine the minimum amount of time required to visually record the maximum zones of inhibition of these significant essential oils at 100% concentration.

The current leading prescribed antibiotics for *A. baumannii* are Colistin and Ampicillin/Sublactam. Colistin yielded a 15 mm zone of inhibition and Ampicillin/Sublactam yielded in a 23 mm zone of inhibition. All six of the select EOs had zones of inhibition greater than the antibiotics Colistin and Ampicillin/Sublactam at 100% concentration. All of the MICs for the above essential oils were determined to have values below 16%. These results confirm that low concentrations of the six EOs can inhibit bacterial growth of *A. baumannii* in vitro better than the current leading antibiotics.

BY-21

VARIATION IN REPRODUCTIVE TRAITS AMONG MICE ADAPTED TO DIFFERENT REGIONS OF THE AMERICAS

Jesse Bragger, David Grossi and Tiffany Longo
Monmouth University Department of Biology

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

Funding Sources:
Monmouth University Biology Department; Monmouth University School of Science; TriBeta Biological Honor Society

Abstract

Although house mice, *Mus musculus domesticus*, are not native to the Americas, they have quickly adapted to a wide range of 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 been shown to have a genetic basis. Reproductive traits have a direct impact on fitness and life history theory predicts that both body size and climatic seasonality have the potential to affect reproductive investment. Here, we investigate whether litter size and pup weight vary among mice from different climates using new wild-derived mouse strains originating from New York, Brazil, Arizona, Florida, and Canada. We find significant differences in litter size among laboratory bred mice from these populations, both in early and later generations of inbreeding. Preliminary data also suggest differences in pup size among mice derived from these locations. Overall, mice from higher-latitude locations tend to have larger litters and larger pups. These findings suggest that reproductive parameters may be either directly or indirectly selected on as populations of house mice adapt to more seasonal, temperate climates. To identify additional phenotypic and genotypic variation, two new projects are being launched, a survey of local populations in New Jersey and a study testing differences in activity levels and behaviors typical of predator avoidance.

BY-22

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

Sean Kuback[1] and Karolina Szenkiel[2]
[1]Monmouth University Department of Biology, [2]Barnard College

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

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

Abstract

Environmental DNA (eDNA) from water samples can be used to study marine and aquatic communities without the potentially negative impacts of traditional methods like electrofishing or trawling. However, the potential of eDNA sampling is limited without controlled studies that test the sensitivity of different eDNA detection methods and that establish key parameters like shedding and decay rates. The purpose of this project is to use metabarcoding to track eDNA in a controlled tank experiment including Black Sea Bass, *Centropristis striata*, and Winter Flounder, *Pseudopleuronectes americanus*. Water samples were obtained at regular intervals prior to, during, and after the residence of the fish in the tank and were filtered by collaborators. We then extracted DNA from the filters following protocols to limit contamination. Nested PCR was then performed on the extracted DNA samples to check for contamination and assess the presence/absence of species-specific eDNA at different time points. Results showed no evidence of contamination and indicated that Black Sea Bass DNA was detectable in water samples collected while fish were in the tanks and for some time following fish removal. These extractions will now be used to build amplicon libraries for next generation sequencing. Once complete, metabarcoding results will be combined with qPCR results from collaborators to compare sensitivity and estimate shedding and decay rates.

BY-23

TURTLES OF LAKE TAKANASSEE: HOW DOES THIS ASSEMBLAGE PERSIST?

Christiana E. Popo and Travis J. Kirk
Monmouth University Department of Biology

Faculty Mentor:
Dr. Sean C. Sterrett, Department of Biology

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

Abstract

Highly urbanized, coastal areas represent a challenge for organisms that require moving across landscapes to complete their lifecycle. Freshwater turtles are a vertebrate group that requires movement to disperse to other habitats, find suitable nesting areas, and seek refuge during extreme climatic events (e.g. drought, floods). For long-lived vertebrates, a sustainable and functional population may be indicated by a normally distributed size class or an estimate of $\lambda \geq 1$ (i.e. population growth rate). However, large population estimates without evidence of recruitment may result in a population that is unable to persist over time. We surveyed a freshwater turtle assemblage using baited hoop traps in a spatial capture recapture framework, in four different sections of Lake Takanassee, Long Branch, NJ, in June 2019. Each individual captured was identified, measured, weighed, uniquely marked and released at its point of capture. We made 115 total captures of 100 individuals. We were able to detect four species; eastern painted turtle, snapping turtle, red-eared slider and eastern musk turtle; which are commonly found in urban freshwater habitats. Snapping turtle made up 36% of our individual capture but 86% of the total turtle mass (596 lbs. total). After analyzing our preliminary results, we found that one turtle moved between lakes in less than a week, indicating that migration between lake sections is possible. Further sampling events will be required to estimate species abundance in Lake Takanassee. The goal of this study is to understand if these common species can functionally persist in a highly urbanized landscape with threats such as roads, pollutants, landscape fragmentation, human interference and watershed modifications.

BY-24

MONMOUTH COUNTY BEACH NESTING BIRD MONITORING AND STEWARDSHIP PROGRAM

Mary Emich and Maya Paco
Monmouth University Department of Biology

Mentors:
Assistant Dean John Tiedemann, School of Science
Christina Davis and Pam Prichard, New Jersey Division of Fish and Wildlife

Abstract

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)* and American oystercatchers *(Haemtopus palliates)* share the same nesting habitat as piping plovers and are also being faced with similar threats resulting in population declines.

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 and least terns 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; and predation and harassment by gulls, crows, raccoons, skunks, foxes, pets and feral cats.

The New Jersey Division of Fish and Wildlife (NJDFW) Endangered and Nongame Species Program is responsible for monitoring, management, and stewardship of these species in New Jersey. Working as endangered species interns, we assisted the NJDFW with their beach nesting bird stewardship program in Monmouth County this summer by conducting surveys of Monmouth County beaches to assess nesting activity; monitoring and providing protective management of nest sites in Monmouth County to reduce effects of human disturbance; determining nesting success at each site including the fate of chicks and causes of nest failures; and providing public outreach, especially during periods of heavy recreational beach usage.

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CE-1

THE EFFECT OF SMALL MOLECULES ON THE STABILITY OF G-QUADRUPLEXES

Christopher Bentsen
Monmouth University Department of Chemistry and Physics

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

Funding Sources:
Bristol-Myers Squibb; Summer Research Program at Monmouth University

Abstract

Telomeres are repetitive Guanine rich sequences at the ends of chromosomes that play a crucial role in protecting critical gene coding proteins from getting attacked and lost through cell division. The human telomere consists of a sequence of nucleotides, TTAGGG, that starts near the end of the duplex DNA and continues as a single strand. This single strand intrudes into the duplex DNA to form a T-Loop, which resembles a cap. Inside the cap, the Guanine rich sequence forms a G-Quadruplex structure, which is where our research is focused. The two important abnormalities that are directly correlated to the malfunction of telomeres are cancer and premature aging syndromes. The malfunctioning of telomeres results from many factors and the stability of the G-Quadruplexes is one of them. In the current research, we are introducing several types of small molecules, one of which is the porphyrin-based class of small molecules, to study the effect of ligand-induced stabilization/destabilization of these non-canonical DNA structures.

Incorporation of several classes of ligands have been introduced in two ways. Ligands under study were either incubated with the annealed DNA for 1 hour and or annealed with the DNA. Depending on the way these ligands are introduced has shown variances in the thermal stability of the G-Quadruplex. As the next step, we will introduce fluorescent probes wither on the DNA or on the ligands to identify how the ligands bind to the DNA and the structural changes caused by it. The final test will be the introduction of a helicase to analyze the true stability of the G-Quadruplex. This study will be useful in developing new therapeutic methods for treatment of diseases including cancer and genetic diseases such as Bloom syndrome, Werner syndrome, and Fanconi anemia.

CE-2

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

Michal M. Kalisz
Monmouth University Department of Biology

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

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

Abstract

The transition of the standard B-form DNA helix to A-form DNA was first seen by X-ray imaging of DNA fibers in 1953. Over time, the structures of B and A DNA have been further characterized with many higher resolution crystal structures. 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. Even though it is known that the B to A conformational transition occurs, the specifics like where in the DNA it originates, how it propagates, and the detailed step-by-step mechanism involved is still unknown. By using site specifically positioned fluorescent oligonucleotides, we explored the local and global conformational changes in this highly biologically relevant transition. Our results showed that by using 2-Aminopurine (2-AP), a fluorescent analogue of Adenine, we could monitor the local and global conformational change simultaneously.

CE-3

SPECTROSCOPIC EVALUATION OF NON-CANONICAL DNA CONFORMATIONS

Brianna Miller
Monmouth University Department of Chemistry and Physics

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

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

Abstract

The B-DNA to A-DNA transition is associated with the continuation of cell processes such as cell reproduction. B-DNA is the most common conformation of DNA, present in aqueous solutions, and is the most stable conformation of DNA. A-DNA is present in dehydrated solutions and helps protect the cell from harsh conditions and makes buried parts of DNA available for interactions. In this study, the B to A conformational was achieved either by partial dehydration of the DNA using increased ethanol concentration or by introducing spermine and spermidine, two polyamines found in all eukaryotic cells. Our aim is to characterize the B-DNA to A-DNA transition achieved by different strategies using spectroscopic methods and study the pathway in each of these methods. To observe the B-DNA to A-DNA transition, a circular dichroism (CD) spectrometer was used in which the changes in absorption of the left circularly polarized light and right circularly polarized light are monitored. A sample of 60% ethanol with a buffer solution and a DNA sequence with 25 base pairs was used to initiate the titration. The transition peaked around 270 nm, which displayed a conformation transition around 73.9% ethanol in the solution. As a next step our aim is to introduce spermine or spermidine to the system at different ethanol percentages and monitor the spectral changes observed during this conformational transition at various intervals. This will help us to understand the fundamentals of the long known B to A DNA conformational transition.

CE-4

BIOCHEMICAL CHARACTERIZATION OF A G-QUADRUPLEX FORMING SEQUENCE IN THE *C-MYC* PROMOTER

Adriana Zelaya
Monmouth University Department of Chemistry and Physics

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

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

Abstract

G-quadruplexes are secondary structures formed by Guanine rich nucleic acid sequences that can be defined as parallel, anti-parallel or hybrid depending on the sequence and cations involved. Proteins that interact with quadruplexes have been associated with aging disorders or cytotoxicity towards tumor cells. The effect is based on the stability of G-quadruplex, which in turn is determined, by a variety of factors. Using biophysical techniques, our aim is to characterize the properties of G-quadruplexes and its interaction with small molecules, which can in future, used as therapeutic drugs to target specific G-quadruplex sequences. For this study we used the G-quadruplex forming Pu27 sequence within the c-Myc promoter. c-Myc is a regulator of the cell cycle and proliferation and Pu27 can negatively regulate its transcription. Our results showed that the formation of the G-quadruplex can be tracked by the Circular Dichroism (CD) signal and the stability of the quadruplex increases as the concentration of the salt increases. In future, we are planning to introduce small organic ligands to either increase or decrease the stability of these G-quadruplexes.

CE-5

PEPTOID MACROCYCLES AS POTENTIAL ANTICANCER AGENTS: THE ROLE OF IONS IN CONFORMATIONAL EQUILIBRIUM

Amanda Prascsak, Santino Timpani, Thomas Melfi, Roxy Nicoletti and Olivia Enny
Monmouth University Department of Chemistry and Physics

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

Funding Source:
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Abstract

In the field of cancer research, the toxicity of anti-cancer drugs is an urgent problem. Ligands, which are small organic molecules, have been proposed as potential anti-cancer drugs, since they bind to DNA macromolecules in telomeres to inhibit tumor growth. The cytotoxicity of these potential drugs is estimated based on the selectivity of their binding to specific DNA conformations. The current research focuses theoretically modeling ligands that have shown promise as anti-cancer drugs with low toxicity. Specifically, various oxazole and thiazole peptoid macrocycles are being considered. Different molecules belonging to this class, depending on their structure and substituents, bind in an extremely selective fashion to certain DNA forms, like the double-helix, parallel, anti–parallel, G-quadruplex, and mixed–type hybrid structures. Such oxazole/thiazole-based macrocycles can be chosen for optimal binding to these specific DNA conformations, and therefore, the subsequent targeted inhibition of telomerase in cancer cells.

To study conformational equilibrium in those designated sets of oxazole and thiazole peptoid macrocycles and to explore effects from the surroundings, focusing on the role of cations, a computational chemistry study has been conducted. Initially, a comprehensive sampling of various conformations for the predetermined oxazole/thiazole-based macrocycles was performed. Low energy conformations have been located for neutral peptoid macrocycle molecules as well as for their complexes with one and two sodium ions. The simulations have been conducted in solution to replicate the effects of the environment. It has been determined that sodium ions stabilize certain conformations significantly. Furthermore, we anticipate that the inclusion of cations in our ongoing examination of ligand-DNA binding will promote strong affinity of the ligands under study to DNA molecules.

CE-6

MODELING IMPACT OF INTERMOLECULAR INTERACTIONS OF LPG-ALCOHOL MIXTURES ON STABILITY OF PHYLLOSILICATES: TOWARDS IMPROVEMENT OF DRILLING FLUIDS

Santino Timpani, Amanda Prascak, Thomas Melfi and Jessica L. Digregorio
Monmouth University Department of Chemistry and Physics

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

Funding Source:
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Abstract

In recent years of fracking, the issue of borehole failures from shale instability has been increasing. Shale instability is caused by intermolecular interactions of polar water-based drilling fluids with shale minerals. Identifying this issue, it was proposed to use liquefied petroleum gas (LPG) based drilling fluids in fracking. LPG is a mixture of propane, butane, and other nonpolar components that can be safely recovered from the borehole. This project aims to solve issues of shale instability by improving a waterless fracking method that uses LPG-alcohol mixtures instead of water-based drilling fluids. Using computational chemistry methods, such as density function theory (DFT) and fragment molecular orbital theory (FMO) intermolecular interactions between components of LPG mixtures and phyllosilicates that create shale instability were identified and analyzed. In addition, further analysis of intermolecular interactions completed via examining bond length and bond angles of each LPG-component orientation with the Phyllosilicate. These non-covalent interactions include Coulomb electrostatic, polarization, exchange-repulsion, and dispersion. Bulk steric factors that influence LPG-phyllosilicate interactions are also taken into consideration.

By using quantum DFT calculations, optimum configurations of the molecules separately and bound in the gas-phase are predicted. Performing an FMO investigation of the optimized LPG-based mixtures and phyllosilicate crystals will allow us to understand which intermolecular interactions are most prevalent in these components. Future plans consist of studying the thermodynamic characteristics (e.g. solubility) of phyllosilicates in LPG-polyol mixtures using the statistical thermodynamics methods based on the conductor-like screening model for realistic solvents (COSMO-RS) approach. If successful, it may be possible to integrate the results into the field of fracking to solve the issue of borehole failures from shale instability and to provide safe waterless drilling fluid.

CE-7

SELECTION OF AN APTAMER TO BIND 2-HYDROXYGLUTARATE THROUGH SELEX

Danielle Guillen
Monmouth University Department of Chemistry and Physics

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

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

Abstract

Glioma and Acute Myeloid Leukemia are both cancers that have been linked to the formation of 2-HydroxyGlutarate (2-HG) during the Krebs Cycle. A point mutation on Arginine 132 of IDH1 enzyme causes a gain of function that converts α-Ketoglutarate (α-KG), the correct metabolite, into 2-HG, an inhibitor. Up to 86% percent of patients with excess levels of 2-HG have been found to have tumors relating to the above cancers. The goal of this research is to isolate an aptamer, or a single strand of RNA, that can bind to the 2-HG molecule with high specificity and accuracy. Through cycles of SELEX, Systematic Evolution of Ligands by Exponential Enrichment, a large pool of randomized RNA sequences can be narrowed down until eventually, only the addition of 2-HG to the RNA pool shows a high percentage of cleavage, while also showing little to no cleavage with the addition of random molecules, like magnesium. Once an aptamer is found, it will then be cloned, by use of a plasmid, and incorporated into a riboswitch, that will act as the mechanism to turn on and off translation of a desired gene to create a biosensor or cancer therapy.

CE-8

THE THEOPHYLLINE RIBOSWITCH: ITS DESIGN AND IMPLEMENTATION

Mika Schievelbein
Monmouth University Department of Chemistry and Physics

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

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

Fluorescence Activated Cell Sorting, or FACS, is a method that was used to convert the theophylline aptamer into a riboswitch. This method could theoretically be used to convert other discovered aptamers into riboswitches, however it is a costly method and is only available to those with the high-tech, expensive FACS machines. The theophylline riboswitch was previously discovered by implementing the Theophylline aptamer with random sequences into a specifically-designed plasmid and using a FACS machine to sort the cells.

We can structure a new system that would select only the sequence containing the theophylline riboswitch without the use of a FACS machine. To do so, we place a pool of sequences containing the aptamer, which is linked to the Shine Dalgarno with random nucleotides, into a plasmid and transform the plasmid into bacteria cells. Then, the use of replica plating along with screening selects the cells that only contain the plasmid with the correct riboswitch sequence. By doing so, we confirm that this system is efficient in converting aptamers into riboswitches without the need for a FACS machine.

After an aptamer has been successfully converted into its riboswitch, the system of ratiometric fluorescence will allow for testing of the riboswitch's function. This is done by designing a plasmid, pTRFlac, that contains genes for two fluorescence proteins on either side of the inserted riboswitch. Currently, the methodology to engineer pTRFlac is by cloning in pUC18, since the plasmid already contains a lactose operon. The plasmid pHL1720 already contains the correct sequence for mCherry, followed by theophylline riboswitch and GFP. This segment is amplified by PCR and cloned into pUC18, resulting in the desired plasmid pTRFlac. The two florescent proteins, mCherry and GFP will provide the ability to measure the riboswitch's function through fluorescence readings.

Both of these systems are the key to innovating the next step in creating synthetic riboswitches.

MONMOUTH UNIVERSITY | COMPUTER SCIENCE *and* SOFTWARE ENGINEERING

CSSE-1

HAWKS CODE: DEVELOPING AN ADAPTIVE PEDAGOGICAL COMPILER TO ENHANCE STUDENT LEARNING

Joe Chung, Matt Cohen, Victoria Johnson, Todd Qualiano and Trisha Smith
Monmouth University Department of Computer Science and Software Engineering

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

Funding Sources:
Independent College Fund of New Jersey/Johnson & Johnson;
Monmouth University School of Science

Abstract

HawksCode is a pedagogically focused Java compiler designed with web-based challenges that are designed to align with the course objectives of object oriented programming courses at Monmouth University. The challenge bank is designed to accommodate the following courses: CS 175 (Introduction to Computer Science I), CS 176 (Introduction to Computer science II), and CS 205 (Data Structures & Algorithms).

The web-based compiler is designed to provide a series of curriculum-based challenges to supplement the existing Computer Science learning experiences offered at Monmouth University. By integrating with the university's existing single sign on system, students are able to track their progress through challenges and receive custom resource recommendations to help meet their personal learning needs.

The System is designed in Java using the Spring MVC framework. The compiler's user interface is built with HTML/CSS and JavaScript which uses Thymeleaf to facilitate data transfer between the front-end and back-end. User-input is passed to pre-designed Java files designed to ensure the challenge is complete via the correct method, compiles those files, and runs the program if compiled successfully to check to see if the student completed the challenge as described.

The site is protected using the Pac4j security library, and users are authenticated with Monmouth University's federated login system. The student's login credentials are used to track which challenges they have completed.

CSSE-2

ANALYSIS OF HEALTHCARE PRESCRIPTION DATA USING GRAPH DATABASE, GRAPH ALGORITHMS, CLOUD COMPUTING SERVICES AND MACHINE LEARNING MODELS

Patricia S. Skora
Monmouth University Department of Computer Science and Software Engineering

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

Funding Source:
d2m Solutions

Abstract

Fraud and anomaly detection in large datasets using Machine Learning models have become more prominent in recent years. Credit card issuers have used Machine Learning systems that are able to detect unusual account activity in almost real time. In this project, research was conducted to construct a graph and relationships model using millions of mock data of relevant entities – prescribers, patients, pharmacies, prescriptions and fulfillment - to see if the same principles that work for major credit card companies could work in drug delivery; targeting anomalies in the prescription realm, like doctors overprescribing the same drug to a single patient or pharmacies filling too many prescriptions for a patient.

Neo4j was used as the underlying graph database deployed in Amazon Web Services (AWS). Mock data was created using an online service, tens of thousands of data objects each day. Data was processed automatically using AWS S3 storage, event triggers to execute AWS Lambda functions, creating new nodes and relationships in the database. To query the database and make the system more user friendly, a web portal was developed using Flask and Bootstrap to allow users to interact with graph database. Neo4j provides a graph algorithm library that incorporates many unique calculations that could be run against graph data, like degree centrality, page rank, and Louvain modularity to find outliers in data using machine language extensions to graph algorithms.

For future research, the numeric embeddings of the nodes in the database and the algorithms could be fed into a machine learning model using Keras and Tensorflow to research if the system could learn the patterns of different anomalies and fraud. Eventually, after thousands of records and numerous, trial and error, and weeks of training time, the program should be able to detect anomalies in real-time.

CSSE-3

EXPLORING ROBOTICS WITH THE NAO ROBOT

Anthony Vives and Jimmy Duong
Monmouth University Department of Computer Science and Software Engineering

Faculty Mentor:
Dr. Jay Wang, Computer Science and Software Engineering Department

Funding Sources:
Monmouth University School of Science; Monmouth University Department of Computer Science and Software Engineering

Abstract

The NAO, the humanoid robot, is a product of SoftBank Robotics. For the means of this project the NAO v6 robot, the most current version, was utilized to conduct our research in speech recognition, communication, and body movement. The use of speech recognition and communication will allow the robot to act as a tour guide for students and visitors of the university. The robot will attempt to answer questions about the Computer Science & Software Engineering Department and draw attention and interest in what a major in Computer Science or Software Engineering may offer. The robot will have the ability to move by displaying signs of emotion, it can greet others, and dance. These actions will be triggered by voice commands and help make the robot appear more appealing to the public. We will utilize the SoftBank Choregraphe Suite and a wireless network router to connect and load programs on the robot. Through the use of Choregraphe's built in tools and drag and drop interface, one can use canned code snippets or create custom snippets in Python to manipulate the robot as needed. This project only scratches the surface of what NAO is capable of and has many more sensors to take advantage of to have the robot act alone or with other robots. The NAO robot is a great learning tool to better understand robotics and how to develop the software that makes the robots act and feel like human beings.

CSSE-4

ACTIONTIME: A WEB APPLICATION MOTIVATING CHILDREN FOR GOOD HABITS

Allen Lu[1], Steven Cassidy[2] and Wenjin Zhang[2]
[1]High Technology High School
[2]Monmouth University Department of Computer Science and Software Engineering

Faculty Mentor:
Dr. Cui Yu, Computer Science and Software Engineering

Funding Source:
Independent College Fund of New Jersey/Johnson & Johnson

Abstract

Some children require motivation to ensure that they learn how to work consistently towards a goal and complete tasks in a timely manner. Psychology has shown that rewards can be used to reinforce positive behavior, especially in young children. ActionTime is a web application that is created with this goal in mind. Adults such as parents and teachers can create challenges for groups of their children or students. These challenges consist of a task that can be completed in stages while tracking progress - which would be approved by the challenge sender - along the way. Challenges can come in three different forms: self, direct, or public. Public challenges are available for all users while direct challenges are sent by one user to either a group or another user. Self-challenges allow users to set their own goals. Each challenge is also described by a ranking among the users who are working on or have completed the challenge. This ranking system motivates children to complete the challenge efficiently and with their best efforts. Once a challenge is completed, the sender can provide a reward. These rewards can come in the form of points or prizes. ActionTime is developed with a PHP framework known as Laravel which allows simplification of the backend communication and database access. The web pages also use bootstrap, allowing for a responsive design. This web application hopes to enhance the learning and development in children at an early age. By using motivation to encourage positive behavior, ActionTime aims to help children become independent and efficient, thereby promoting success later in life.

CSSE-5

A NEW CALENDAR APPLICATION FOR TIME MANAGEMENT

Matt Mammano[1] and Wenjin Zhang[2]
[1]Point Pleasant High School
[2]Monmouth University Department of Computer Science and Software Engineering

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

Funding Source:
Independent College Fund of New Jersey/Johnson & Johnson

Abstract

In this project, a new web application is developed to aid students with difficulty to manage their time. There are three steps to use the application. The first step is to insert all of the available free time that one has during typical weeks. This can be edited afterwards but it does remain the same for each week afterwards till further updates. The second step is to input new tasks or upcoming events that require work, such as homework and tests. At last, a schedule is automatically generated to suggest how to utilize free time to complete tasks or to prepare for future events. While this application exploits existing calendar open source, a lot of adjustments are coded to make the application easy to use. Backend database is implemented to store free time, tasks and events. The main challenge of this project is to design a logic that can make time management as efficient as possible, and yet flexible to adapt. Many people suffer from weakness in organization and planning. This application aims to alleviate the problem.

CSSE-6

SMARTPARKING: USING ARTIFICIAL INTELLIGENCE TO FIND EMPTY PARKING SPACES

Jason Yan[1], John Meyer[2] and Wenjin Zhang[3]
[1]High Technology High School; [2]Red Bank Regional High School;
[3]Monmouth University Department of Computer Science and Software Engineering

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

Funding Source:
Independent College Fund of New Jersey/Johnson & Johnson

Abstract

Most people have probably experienced the hassle of parking space scarceness. The goal of this research project is to create a mobile application that can automatically identify parking spots that are available. To achieve this goal, there are two main challenges to solve: setting up an overview of parking space and identifying empty parking spots. First, the detection of the empty parking spaces is split into two parts: the photo segmenting of the parking lot and the detection of cars. In an effort to lower the set-up requirement, the program in this study requires only the four bounding coordinates of the parking lot, automatically masks out the undesirable colors, blurs the lines with Gaussian blur, detects edges with Canny edge detection, distinguishes lines with Hough line transformation, and groups lines together in order to detect the horizontal and vertical lines running across the parking lot. With these lines, the parking lot can be successfully segmented and the picture of each parking spot can be obtained for car detection. Secondly, to identify empty parking spots, a convolutional neural network model is used to detect whether there is a car in each parking spot. Based on the classic convolutional neural network model, VGG16, proposed by K. Simonyan and A. Zisserman in 2014, we extend and train it with a large database of pictures of parking lots, reaching an accuracy of 98% on the validation dataset. For end users, the mobile application displays the picture of parking lots, indicating the empty and taken spots. SmartParking is a project aimed at creating a smart and easy-to-use application that gives users the opportunity to simply look at their phone and see which parking spots are available.