MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

10th Annual Summer Research Program Symposium

August 9, 2018

10:30am – 1:00pm

Erlanger Gardens

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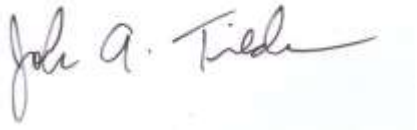

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The Math Learning Center provides students with assistance in all levels of mathematics. Peer tutors are available to help students solve problems and to review concepts.

MONMOUTH UNIVERSITY

SCHOOL OF SCIENCE

10th ANNUAL SUMMER RESEARCH PROGRAM SYMPOSIUM

Thursday, August 9, 2018

Presentations by Department

Department of Biology

B-1 A Comparison of Phytoplankton and Water Quality in Two Estuaries in Neighboring Watersheds of Monmouth County

Erin Conlon, Sydney Lucas, Skyler Post, Katelyn Saldutti

Faculty Mentor: Dr. Jason E. Adolf

B-2 Comparing the Phytoplankton Ecology of New Jersey Coastal Estuaries through Flow Cytometry

Skyler Post, Erin Conlon, Sydney Lucas, Katelyn Saldutti

Faculty Mentor: Dr. Jason E. Adolf

B-3 Nutrient Bioassay Experiments in Deal Lake Find Nitrogen Limiting To Harmful Algal Bloom Growth in the Summer Season

Katelyn Saldutti, Erin Conlon, Sydney Lucas, Skyler Post, Jack Campanella

Faculty Mentor: Dr. Jason E. Adolf

B-4 Plant Community Impacts on Northern Diamondback Terrapin Nest Site Selection and Success

Taylor Donovan, Kelly Hanna, Lois Walton, Christiana Popo, and Maria Riley

Faculty Mentor: Dr. Pedram Daneshgar

B-5 Temporal Monitoring of the Endangered Atlantic Sturgeon (*Acipenser oxyrinchus*) in Sandy Hook and Raritan Bay

Lauren Kelly, Charles Vasas, Troy Ohntrup

Faculty Mentor: Dr. Keith Dunton

B-6 Collaborative Efforts to Evaluate the Demographics and Post-Release Movements of Sharks Captured in the Recreational Land-Based Surf Fishery

Charles Vasas, Lauren Kelly, Troy Ohntrup

Faculty Mentor: Dr. Keith Dunton

B-7 Genetic Engineering of a miRNAs against VEGFR2 and EGFR to Reduce the Expression of Oncogenic Transcript in GBM

Andrew Gee

Faculty Mentor: Dr. Martin Hicks

B-8 Genetic Engineering of RNA Therapeutics to Alter the Splicing of VEGFR2 and EGFR Transcripts to Block the Growth of GBM

Michael Mazzucco, Flobater Gawargi, and Gowri Jagadeesh

Faculty Mentor: Dr. Martin Hicks

B-9 Secondary Structure Analysis by SHAPE-MaP of the EGFR and VEGFR2 pre-mRNA Transcripts: Uncovering Novel Regions for RNA Anti-sense Targeted Therapy

Ryan Fink

Faculty Mentor: Dr. Martin Hicks

B-10 Determining the role of the GABRA2 gene in a *Gallus gallus* Chick Fetal Alcohol Syndrome Model

Orli Weiss, Nadine Khalil, Esra Celik, and Samantha Perez

Faculty Mentor: Dr. Cathryn Kubera

B-11 Effects of Manuka and Kumquat Essential Oils on the Growth and Viability of Human Cancer Cell Lines

Jive Jacob and Subah Soni

Faculty Mentor: Dr. Dorothy Lobo

B-12 The Inhibiting Effects of Thymol, Carvacrol, and Cinnamaldehyde on Methicillin-Resistant *Staphylococcus Aureus* (MRSA) and Methicillin-Sensitive *Staphylococcus Aureus* (MSSA)

Anadi Saini and James Goldbeck

Faculty Mentor: Dr. James P. Mack

B-13 Breeding New Ideas: Establishing Colonies of New Wild Derived Mouse Strains

Tiffany Longo, Sebastian Vera, Summer Shaheed

Faculty Mentor: Dr. Megan Phifer-Rixey

B-14 Searching for Eastern Oysters (*Crassostrea virginica)* in the Navesink River and Sandy Hook Bay: An eDNA Approach

Katherine Banfitch and Jesse Bragger

Faculty Mentors: Drs. Megan Phifer-Rixey, Keith Dunton, Jason Adolf

B-15 Sources of Striped Bass *(Morone saxatilis)* in the Mixed-Stock Recreational Fishery in Northern Ocean County, New Jersey

Nikole Andre, Anjali Tampy, and Carleigh Engstrom

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

B-16 Monmouth County Beach Nesting Bird Monitoring and Stewardship Program

Mary Emich and Abigail Urbanak

Mentors: Assistant Dean John Tiedemann and Christina Davis, Meaghan Lyon, Pam Prichard – NJ Division of Fish and Wildlife

B-17 Use of Pomegranate Juice Extract and Apple Extract to Treat and to Inhibit Inflammation in Cancers of the Oral cavity

Michael R. Mazzucco and Noor Sarsar

Faculty Mentor: Dr. Jeffrey H. Weisburg

Department of Chemistry and Physics

CE-1 Unraveling the B to A Conformational Transition in Duplex DNA Constructs at Single Base Pair Resolution

Kirsten P. Lawson and Michal M. Kalisz

Faculty Mentor: Dr. Davis Jose

CE-2 Topographic and Biochemical Observation of a Stable G-Quadruplex

Brandon Rosenblum

Faculty Mentor: Dr. Davis Jose

CE-3 The Effect of Small Molecules on the Stability of G-Quadruplexes

Christopher Bentsen

Faculty Mentor: Dr. Davis Jose

CE-4 Novel Approach to Characterize I-R3 Deoxyribozymes Using Biochemical and Spectroscopic Analysis

Kushkumar Patel

Faculty Mentor: Dr. Davis Jose

CE-5 Exploring Oxazole- and Thiazole-based Macrocycle Binding to DNA

Kanwal Alam and Omar Shah

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

CE-6 Modeling Impact of Intermolecular Interactions of LPG—Alcohol Mixtures on Stability of Phyllosilicates: Towards Improvement of Drilling Fluids

Amanda Prascsak, Santino Timpani, Tom Melfi, and Gary Prato

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

CE-7 Acidolysis of Rhenium(I) Alkylcarbonate Complexes and Cytotoxicity of the Acidolysis Products

Arbaz M. Khan, Charmi Patel and Emily Tumbaco

Faculty Mentors: Dr. Gregory A. Moehring, Dr. Datta Naik and Dr. Jeffrey Weisburg

CE-8 Isolation of an Aptamer that Binds 2-HG

Danielle Guillen

Faculty Mentor: Dr. Jonathan Ouellet

CE-9 Isolating RNA Aptamers That Bind A30P Alpha-Synuclein and NEDD4

Darrel D'Souza and Jonathan Shen

Faculty Mentor: Dr. Jonathan Ouellet

CE-10 The Theophylline Riboswitch; Its Design and Implementation

Mika Schievelbein

Faculty Mentor: Dr. Jonathan Ouellet

Department of Computer Science and Software Engineering

CSSE-1 **Constructing 3D Panoramas**

Steven Cassidy, Mahmoud Shabana, Nianqi Tian

Faculty Mentors: Professors Gil Eckert and Jim Nickels

CSSE-2 **Designing a Virtual Reality Simulation to Illustrate the Effects of Impervious Surfaces from Urbanization on the Barnegat Bay Watershed**

Tess Hintelmann, Matt Rodriguez, Elise Winkley, Lauren Winkley

Faculty Mentor: Professor Kate Gatto

CSSE-3 **Designing a Virtual Reality Simulation to Demonstrate How Eutrophication Stimulates *Aureococcus anophagefferens* Blooms and its Effect on Marine Life in the Barnegat Bay**

Frank D'Agostino, Erik Ossner, Jackson Perry, Gregory Stickle and Christian Szablewski-Paz

Faculty Mentor: Professor Kate Gatto

CSSE-4 **Copay Services for Healthcare Providers as CRM Application**

Jessica Zemartis

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-5 **Statistical Analysis on Pharmacy Claim Payments to Detect Anomalies**

Kimberly Bianchi

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-6 **Social Networking Mobile Application to Aid in Recovering from Substance Abuse**

Michael Karolewicz

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-7 **Comparing SQL and NoSQL Database Systems**

John Neppel

Faculty Mentor: Dr. Jiacun Wang

Department of Mathematics

MA-1 **Statistical Analysis on Alfaxalone and Its Effects on Lab Rats and Bootstrapping With Small Sample Sizes**

Kimberly Bianchi and Samantha Cavalli

Faculty Mentor: Dr. Richard Bastian

MA-2 **Statistical Analysis on the Absence of Fire in an Ecosystem That Should Have Fire**

Justine Kukowski, Peri Trembley and Michael McGuigan

Faculty Mentors: Dr. Richard Bastian and Dr. Pedram Daneshgar

MA-3 **Statistical Analysis on the Use of Active Learning in Anatomy and Physiology**

Justine Kukowski, Peri Trembley and Michael McGuigan

Faculty Mentors: Dr. Richard Bastian and Dr. Bernadette Dunphy

MA-4 **Statistical Analysis of Dog-Owner Behavior in Play Parks**

Melissa Culmone and Alexandria Halloran

Faculty Mentors: Dr. Richard Bastian and Dr. Lindsay Mehrkam

MA-5 **Perfect Pyramids: The Search for Heronian Simplexes in Higher Dimensions**

Nathaniel Rodriguez

Faculty Mentor: Dr. Susan Marshall

DEPARTMENT OF BIOLOGY

B-1

A COMPARISON OF PHYTOPLANKTON AND WATER QUALITY IN TWO ESTUARIES IN NEIGHBORING WATERSHEDS OF MONMOUTH COUNTY

Erin Conlon[1], Sydney Lucas[1], Skyler Post[1], Katelyn Saldutti[2]
[1]Monmouth University Department of Biology
[2]Rutgers University Department of Marine and Coastal Sciences

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

Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University School of Science; Monmouth University Department of Biology; ICFNJ Targeted Gene Delivery Fund

Abstract

The Navesink and Shrewsbury estuaries offer an ideal system for comparative studies due to their similar geomorphology, yet different watershed characteristics. These estuarine systems converge and flow out into Sandy Hook Bay, making them the optimal estuaries to observe the effects of freshwater inputs on phytoplankton composition. Over the course of twelve weeks, five boat trips were taken to obtain water samples at twenty-one designated stations, each 1.6 kilometers apart, reaching from the tips of the rivers all the way to the outer edge of Sandy Hook Bay. These locations were tested for different parameters, including salinity, temperature, dissolved oxygen, and Secchi depth. Each sample was also processed at the lab for chlorophyll *a*, turbidity, *in vivo* fluorescence, flow cytometry, and preserved using Lugol's. The results of each parameter were graphed on scatterplots to observe possible correlations. Overall, there was no significant difference between systems in chlorophyll *a* biomass and no significant correlation between chlorophyll a and salinity, however a correlation between temperature and chlorophyll *a* was found ($r^2 = 0.10$, $p = 0.002$). The sites found to have extremely high chlorophyll levels were investigated further using the Lugol's samples to determine the taxonomy of the organisms responsible. These data give an idea of how each parameter affects the types of phytoplankton that culminates in the different systems. Comparing these two estuaries has shown that the Shrewsbury River has a more saline, less turbid environment better suited for chlorophyll growth within its upper tributaries. Further research is needed to accurately track the growth of chlorophyll within the neighboring estuaries of the Navesink and Shrewsbury, for instance, how chlorophyll a is spatially distributed within each system.

B-2

COMPARING THE PHYTOPLANKTON ECOLOGY OF NEW JERSEY COASTAL ESTUARIES THROUGH FLOW CYTOMETRY

Skyler Post[1], Erin Conlon[1], Sydney Lucas[1], Katelyn Saldutti[2]
[1]Monmouth University Department of Biology
[2]Rutgers University Department of Marine and Coastal Sciences

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

Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University School of Science; Monmouth University Department of Biology; ICFNJ Targeted Gene Delivery Fund

Abstract

Phytoplankton have a tremendous impact on the ecosystem. They are beneficial in that they are the primary producers of the food web, converting sunlight to 'food energy' and driving ecological productivity. However, they are also responsible for harmful algae blooms, which can result in massive fish kills and a negative impact on the food web. To complement studies of bulk phytoplankton based on measuring Chlorophyll *a* in the water, the objective of this experiment was to characterize patterns of phytoplankton cell size and cell abundance in relation to salinity and chlorophyll *a* in Sandy Hook Bay, the Shrewsbury River, and the Navesink River. Flow cytometry was used to measure the fluorescence (color), diameter (size) and count (number) of cells for each sample. Results show that, in areas that have similar total phytoplankton biomass based on Chl *a* measurement the composition of the phytoplankton community could be different. Differences between the systems studied included that the abundance of nanoplankton in the Navesink River was higher than in the Shrewsbury and Sandy Hook Bay, suggesting a species composition difference between these neighboring estuaries. The results suggest that the phytoplankton composition substantially varies between the Shrewsbury River, Navesink River, and Sandy Hook Bay despite similarities in total phytoplankton biomass. These data can be used to understand the mechanisms causing phytoplankton blooms, and potentially analyze their effect on the ecology of the estuaries.

B-3

NUTRIENT BIOASSAY EXPERIMENTS IN DEAL LAKE FIND NITROGEN LIMITING TO HARMFUL ALGAL BLOOM GROWTH IN THE SUMMER SEASON

Katelyn Saldutti[1], Erin Conlon[2], Sydney Lucas[2], Skyler Post[2], Jack Campanella[3]
[1] Rutgers University, Department of Marine and Coastal Science
[2] Monmouth University, Department of Biology
[3] Biotechnology High School

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

Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University School of Science; Monmouth University Department of Biology; ICFNJ Targeted Gene Delivery Fund

Abstract

Cyanobacteria are microscopic, photosynthetic, opportunistic organisms that can be problematic to both marine and freshwater habitats. With favorable growth conditions - ample sunlight, warm water, and readily accessible nutrients - cyanobacteria form harmful algal blooms (HABS) that discolor lakes a striking blue-green and negatively affect entire lake ecosystems from the bottom up. Cyanobacteria species *Microcystis* and *Anabaena* common to these blooms and identified in this study produce neurotoxins and hepatotoxins linked to very serious human health consequences. Instruments like the handheld Cyanoflour used in this experiment detect and measure phycocyanin (PC), a photosynthetic pigment specific to cyanobacteria, relative to total chlorophyll biomass (PC:Chl) to indicate bloom occurrence, allowing researchers to separate and track CyanoHABs distinct from bulk phytoplankton.

Five nutrient bioassay experiments were conducted in this fresh water coastal lake to determine nutrient limitation on algal growth. Anthropogenic nutrient inputs commonly attributed to the over-application of fertilizers and storm water runoff, were simulated by the addition of nitrogen (NO_3), ammonia (NH_4), and phosphorous (PO_4) individually and combined in Redfield ratio requirements (16:1). Triplicate samples of lake water were subjected to 7 nutrient treatments representing single and combination additions of NO_3, NH_4, and PO_4 and incubated over a five-day period. Measurements of phycocyanin (PC) pigment, chlorophyll (Chl), and PC: Chl fluorescence were analyzed for statistical significance ($p < 0.05$) and found nitrogen to be limiting in the summer season with appreciable growth in treatments containing ammonia. Further, NH4 additions appeared to specifically enrich cyanobacterial HAB species in Deal Lake water samples. Microscopic analysis of preserved samples suggests a succession pattern between *Anabaena* and *Microcystis* during a bloom event. Empirical understanding of nutrients supporting growth, water quality monitoring, informed management, and public knowledge is critical to mitigating the effects of cyanobacterial harmful algal blooms.

B-4

PLANT COMMUNITY IMPACTS ON NORTHERN DIAMONDBACK TERRAPIN NEST SITE SELECTION AND SUCCESS

Taylor Donovan, Kelly Hanna, Lois Walton, Christiana Popo, and Maria Riley
Department of Biology

Faculty Mentor:
Dr. Pedram Daneshgar, Department of Biology

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

Abstract

Northern diamondback terrapins *(Malaclemys terrapin terrapin),* a unique species found within estuarine systems of the Atlantic coast, have been listed as species of concern in New Jersey due to evidence of decline. While several factors, both natural and anthropogenic, are to blame for these declines, nest site degradation and loss may be the most detrimental to the success of future populations because of the strong nest site fidelity exhibited by terrapins. Disturbances, land alteration and the invasion of problematic species such as *Phragmites australis* seem to be driving nest site degradation, but their definitive impacts on nest site selection and success have yet to be explored.

In this study, we investigated the plant communities associated with newly laid terrapin nests along the New Jersey coast to determine the impacts of disturbance, land alteration and plant invasions on nests. It was hypothesized that site alterations and plant invasions have made sites less suitable for nesting and for the success of future populations. At each nesting site, the plant community was surveyed and the habitat was described in regards to disturbance and invasions. To determine the impacts of the plant community on nest temperature, iButtons were installed in each nest within the 24 hours of the nest establishment. Preliminary results suggest that terrapins do not select sites based on the plant communities and the site fidelity rules selection. The final impacts of site selection on the nests will be assessed upon hatching when temperature and plant biomass data and percent of eggs hatched are analyzed this fall.

B-5

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

Lauren Kelly, Charles Vasas, Troy Ohntrup
Department of Biology

Faculty Mentor:
Dr. Keith Dunton, Department of Biology

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

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 2018 with ten acoustic receivers were deployed throughout RB and surrounding water bodies to monitor for previously tagged Atlantic Sturgeon. A total of 139 uniquely tagged individual Atlantic sturgeon were detected (n=68,344 detections) in SHB through early spring 2018. 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 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 (e.g., vessel interactions, commercial fishing, dredging) that may pose possible negative interactions with sturgeon.

B-6

COLLABORATIVE EFFORTS TO EVALUATE THE DEMOGRAPHICS AND POST-RELEASE MOVEMENTS OF SHARKS CAPTURED IN THE RECREATIONAL LAND-BASED SURF FISHERY

Charles Vasas, Lauren Kelly, Troy Ohntrup
Department of Biology

Faculty Mentor:
Dr. Keith Dunton, Department of Biology

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

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 this shore based fishery. In 2017, 12 land-based excursions captured 53 individual sharks were captured consisting of 20 Sand Tiger (*Carcharias taurus)*, 31 Sandbar Shark (*Carcharinus plumbius*), and 1 Dusky Shark (*Carcharinus obscurus*). A sub-set of individuals (n=9 Sand Tiger and n=6 Sandbar shark) were surgically implanted with Vemco V-16 acoustic transmitters. In 2018, 9 land-based excursions 49 individual sharks were captured consisting of 9 Sand Tiger, and 40 Sandbar shark. A sub-set of individuals (n=7 Sandbar shark) were surgically implanted with Vemco V-16 acoustic Transmitters. All acoustic tagged sharks were detected post-release, as far south as North Carolina, suggesting high survival rates within the fishery. Our work on classification of the fishery and acoustic tagging to understanding post release survival and coastal movements will continue throughout the 2019 season as well as working with the guide service to develop best and safe release practices. Further understanding 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.

B-7

GENETIC ENGINEERING OF A MIRNAS AGAINST VEGFR2 AND EGFR TO REDUCE THE EXPRESSION OF ONCOGENIC TRANSCRIPT IN GBM

Andrew Gee
Department of Biology

Faculty Mentor:
Dr. Martin Hicks, Department of Biology

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

Abstract

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, which are limited by the blood-brain barrier. A common aberration in GBM is the overexpression and constitutive activation of the epidermal growth factor receptor (EGFR) and upregulation of angiogenesis through the VEGFR2 pathway. In addition, miRNA cluster 17-92 is often upregulated in various cancer types, including GBM and has been implicated in tumor cell survival, apoptosis suppression and tumorigenesis. Each of the distinct miRNAs of the miRNA cluster 17-92 have distinct and possibly synergistic function in promoting oncogenic characteristic associated with a cancerous phenotype. Alteration of the targets of miR 17-92 could prove to be an effective therapy combatting cancer growth and proliferation using the RNA the interference pathway. In order to alter the targets of miR 17-92 from their native state to sequences against EGFR and VEGFR2, a pAAV backbone was cloned with a synthetic nucleotide sequence to target various regions of the EGFR mRNA transcript and named miRIP1-antiEGFR. In order to additionally target VEGFR2, the targetscan program was used to consider known miRNAs putatively targeting VEGFR2 and the chosen sequences were substituted into the miRIP1-antiEGFR vector with care taken to maintain the same secondary structure as the wild type 17-92 cluster, tested MFOLD program. Cloning of the new sequences was achieved by using restriction endonucleases to cut in pre-designed sites between each separate miRNA present in the miRIP1-antiEGFR. Synthetic sequences representing miRNAs targeting VEGFR2 were cloned using restriction endonucleases. This newly assembled miR cluster in pAAV backbone was designated AG1
This altered 17-92 cluster will be used for future testing in transfection into GBM cells and evaluation of RNAi potency by comparing levels of VEGFR2 and EGFR transcripts and protein. Dam-/ Dcm- E. coli were used to replicate the existing pAAV-IP1 plasmid due to one restriction enzyme BclI, being blocked by DNA methylation.

B-8

GENETIC ENGINEERING OF RNA THERAPEUTICS TO ALTER THE SPLICING OF VEGFR2 AND EGFR TRANSCRIPTS TO BLOCK THE GROWTH OF GBM

Michael Mazzucco, Flobater Gawargi, and Gowri Jagadeesh
Department of Biology

Faculty Mentor:
Dr. Martin Hicks, Department of Biology

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

Abstract

Glioblastoma multiforme (GBM), a grade IV tumor of the central nervous system, is the most common malignant primary brain tumor, having a median survival of only 14 months. Poor survival is due to a lack of efficacy in current therapies which is limited by the blood-brain barrier. GBM tumors are characterized by angiogenesis, which is essential for tumor growth and survival. To develop a new treatment, our lab has designed an RNA therapeutic vector against the pre-mRNA of the pro-angiogenic transcripts, EGFR and VEGFR2. This therapy induces alternative splicing leading to shortened mRNA transcript isoforms, which translate into soluble decoy proteins as opposed to the canonically spliced full-length transmembrane receptor. These soluble decoys competitively bind the EGF or VEGF growth factors, without activation of the intracellular tyrosine-kinase phosphorylation signaling pathway. Targeting of key splicing elements by RNA antisense therapeutics is complemented by the molecular cloning of a heterogenous ribonucleoprotein recruitment domain into the RNA therapeutic vector, effectively silencing the site by artificial intronic redefinition. By transfection into GBM cell lines, EGFR and VEGFR2 protein expression will be measured by flow cytometry and ELISA RNA expression will be evaluated by MinION nanopore sequencing. Currently, we are developing methods to isolate and purify recombinant poly-histidine tagged hnRNP proteins using Ni-Nitriloacetic acid column. Efficacy of the hnRNP proteins to bind the RNA therapeutic molecule will be tested using the Electrophoretic Mobility Shift Assay (EMSA), and a super-shift EMSA using an antibody against the poly-histidine tagged protein. In addition, we will extract RNA from the EMSA gel and reverse transcribe to confirm therapeutic RNA binding. Transfection of mammalian expression vectors in tissue culture will also be performed and subsequently measured by RNA and protein assays. Once the therapy RNA-hnRNP protein interactions are confirmed, future steps include cloning of a serine-arginine (SR) protein recruitment domain to act as a splicing enhancer, directing the spliceosome to a desired splice site or intronic poly-adenylation site to increase synthesis of EGFR and VEGFR2 soluble decoy isoforms.

B-9

SECONDARY STRUCTURE ANALYSIS BY SHAPE-MAP OF THE EGFR AND VEGFR2 PRE-MRNA TRANSCRIPTS: UNCOVERING NOVEL REGIONS FOR RNA ANTI-SENSE TARGETED THERAPY

Ryan Fink
Department of Biology

Faculty Mentor:
Dr. Martin Hicks, Department of Biology

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

Abstract

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, which are limited by the blood-brain barrier. A common aberration in GBM is the overexpression and constitutive activation of the epidermal growth factor receptor (EGFR), observed in 57% of all GBM. EGFR upregulation stimulates the PI3K/AKT signaling pathway which sustains tumorigenesis. Alternatively, our lab developed a novel therapeutic approach; (Hicks et al. 2016) which delivers a gene directly to the CNS using an adeno-associated virus gene transfer vector to encode either RNA or protein therapeutics. Our current approach is to deliver an RNA molecule with complementarity to critical splicing elements of the EGFR pre-mRNA transcript. Thus, inducing alternative isoforms and driving a reduction in mRNA. Furthermore, alternative splicing is regulated by secondary structure of the pre-mRNA nascent transcript (Soemedi et al. 2017). To improve our therapeutic strategy, we have begun experiments to analyze the EGFR secondary structure using 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 (Weeks et al. 2018) 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 are a preferential target of our therapy. SKMG3 cells were exposed to the SHAPE reagent under three conditions: in-cell, cell-free, and denatured. RNA was extracted, reverse transcribed, PCR amplified, and will be sequenced on a MinION nanopore platform. The three data sets will be compared using ShapeMapper2 (mutational profiling) to deduce the secondary structure, including reactivity profiles of EGFR pre-mRNA.

B-10

DETERMINING THE ROLE OF THE GABRA2 GENE IN A *Gallus gallus* CHICK FETAL ALCOHOL SYNDROME MODEL

Orli Weiss, Nadine Khalil, Esra Celik, and Samantha Perez
Department of Biology

Faculty Mentor:
Dr. Cathryn Kubera, Department of Biology

Funding Sources:
Monmouth University School of Science; Bristol-Myers Squibb; Drs. Margaret Ann and Stephen Chappell/The Stars Challenge; Monmouth University Department of Biology

Abstract

Fetal Alcohol Spectrum Disorder (FASD) is a condition that leads to learning disabilities, heart defects, and craniofacial abnormalities due to premature exposure to alcohol. This disorder affects 2-5% of infants in the United States. Studies show *Gallus gallus* to be an effective model organism for the study of Fetal Alcohol Syndrome. The purpose of this project is to determine the role of the GABRA2 gene in embryonic cerebellar development and the cerebellar defects seen in individuals affected by FASD. A model for FASD was developed through air sac injections of 20% ethanol in *Gallus gallus* eggs at embryonic day 7 (E7). Also, CRISPR vectors were constructed to target and knock down the activity GABRA2 *in vitro* in avian DF-1 fibroblast cells. In this study, CRISPR vectors were successfully constructed to contain scrambled and target sequences for the GABRA2 gene. Avian DF-1 cells were successfully transfected *in vitro* using the CRISPR vectors. The next step would be to assess the CRISPR knockdown of GABRA2 in these cells. Tissues from control and FASD model chicks were collected during different embryonic stages (E9, E11, & E13), which will be used in RNA extraction to determine the presence of the GABRA2 expression in the samples obtained. Histology slides were also obtained for immunostaining to assess the amount of cell death and proliferation.

B-11

EFFECTS OF MANUKA AND KUMQUAT ESSENTIAL OILS ON THE GROWTH AND VIABILITY OF HUMAN CANCER CELL LINES

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

Abstract

Since research on the effects of essential oils on human cell lines is limited, the goal of this project was to treat various cancer cells lines with manuka and kumquat oils at different concentrations and ascertain the effects on cell proliferation. The two cancer cell lines tested were fibrosarcoma (HT-1080) cells and adenocarcinoma (HeLa) cells. Manuka oil is popular in many skincare products because of its antibacterial and anti-inflammatory properties that treat several skin conditions. However, manuka oil also contains an active ingredient that is commonly found in herbicides and is potentially toxic to human cells at certain concentrations. Kumquat oil has many properties that make it a dietary treatment against cancer and other maladies such as heartburn and gallstones. To conduct the experiment, both cell lines were grown on 24-well plates and subconfluent cultures were treated with varying concentrations of manuka oil and kumquat oil for 24 hrs. A trend was found that as the concentration of oil increased, cell viability, measured by direct cell counting, decreased. In support, MTT assays are currently being performed, and preliminary results of HT-1080 cells treated with manuka oil also demonstrated decreased viability using this assay. Further testing to determine if observed cell death is a result of apoptosis will be performed. We are also going to test normal fibroblast cells (CUA-4) and hopefully see a difference in how the oils effect these cells, as well as treating cells with other oils that are not well studied, including cypress oil and tangerine oil.

B-12

THE INHIBITING EFFECTS OF THYMOL, CARVACROL, AND CINNAMALDEHYDE ON METHICILLIN-RESISTANT *Staphylococcus aureus* (MRSA) AND METHICILLIN-SENSITIVE *Staphylococcus aureus* (MSSA)

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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

Antibiotics have revolutionized the way infectious diseases have been treated over the past century. Unfortunately, certain microorganisms have adapted and evolved to become resistant to many of these antibiotics. According to the CDC, two million people are infected from drug resistant bacteria in the US annually; the most prevalent cases coming from MRSA and MSSA in healthcare facilities. Due to the indiscriminate and overuse of antibiotics, options to control multidrug resistant bacterial infections have become limited. Essential oils, which are metabolic products of many different plant species, have antimicrobial effects on many species of bacteria.

Of the many components found in several essential oils known to be bactericidal towards MRSA and MSSA, nine major components were chosen to test their individual activity against these bacteria. The nine components were carvacrol, geraniol, eugenol, geranic acid, alpha-pinene, benzaldehyde, methyl salicylate, trans-cinnamaldehyde, and thymol. These components were tested on Mueller Hinton II agar using the Kirby Bauer Disk Diffusion Test to determine their effectiveness at inhibiting the growth of MRSA and MSSA. A series of emollients of different concentrations were prepared of each component using jojoba oil as the medium. Five microliters of each of the emollients were aseptically pipetted onto 6 mm blank discs. These plates were then incubated at 37 °C for 24 hours to allow the bacteria to grow and the zones of inhibition to develop. The zones of inhibition were then measured in millimeters. Of the nine components tested, three components worked significantly better than two of the antibiotics that are currently being used to treat patients with MRSA and MSSA vancomycin (Vancocin) and trimethoprim-sulphamethoxazole (Bactrim). The three components are thymol, carvacrol, and cinnamaldehyde. The minimum inhibitory concentrations (MIC's) of these three components were then determined and compared to one another. The results show that emollients of thymol, carvacrol, and cinnamaldehyde in jojoba oil can successfully inhibit MSSA and MRSA in vitro growth better than Vancocin and Bactrim.

B-13

BREEDING NEW IDEAS: ESTABLISHING COLONIES OF NEW WILD DERIVED MOUSE STRAINS

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Faculty Mentor:
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Funding Sources:
Monmouth University Summer Scholars Program; Office of the Provost; Monmouth University School of Science; Monmouth University Department of Biology

Abstract

Although house mice, *Mus musculus domesticus*, are not native to the Americas, they have quickly adapted to diverse climates. For example, body size and nesting behavior are two traits linked to fitness that vary among populations from different latitudes, and those differences have a genetic basis. This invasive species has become an important model organism for studying human biological processes, but laboratory strains lack some of the genotypic and phenotypic variation in natural populations. This summer, we have established colonies of wild-derived mice originating from New York, Brazil, Arizona, Florida, and Canada. Each of these strains have been inbred for at least ten generations. In addition to body size, we have found differences in litter size among mice from different climates. Reproductive traits have a direct impact on fitness and predictions from life history theory suggest seasonality of resources can affect reproductive allocation. We plan to build on previous work by comparing pup size and litter size among the colonies at later stages of inbreeding. In addition, we are interested in measuring the effects of high fat diets on body size in all of the strains. The mouse model of diet-induced obesity has become an important tool for understanding the relationship between high fat Western diets and the development of obesity. We will be screening our strains for response to high fat diet to determine if they may be a useful model for diet induced obesity reflecting genetic diversity not present in classical inbred strains. Together, these studies will provide novel insight into the interaction between environment, genetic diversity, and fitness and potentially provide new strains for studying diet induced obesity.

B-14

SEARCHING FOR EASTERN OYSTERS (*Crassostrea virginica)* IN THE NAVESINK RIVER AND SANDY HOOK BAY: AN EDNA APPROACH

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

Abstract

Eastern oysters (*Crassostrea virginica*) are critical ecosystem engineers and, as filter-feeders, have a key role in maintaining water quality. Once common in local waters, Eastern oysters have declined significantly since the mid-1990's. Because of their ecological importance, restoration efforts have been implemented in the Navesink River and Sandy Hook Bay. Notably, in the spring of 2018, an oyster was collected in the Navesink River. Nevertheless, the overall success of restoration programs is difficult to assess. Traditional methods to detect populations of oysters, especially when they are in small numbers, can be costly and inefficient. Using environmental DNA (eDNA) offers a fast and relatively low-cost alternative. eDNA refers to free DNA molecules that are released from organisms into the environment. eDNA is increasingly being used in marine environments for invasive and rare species detection, monitoring particular species, and characterizing community composition when traditional methods are expensive and/or prohibited. Here, we use an eDNA approach to determine if Eastern Oysters can be detected in water samples collected from the Navesink River and Sandy Hook Bay. Water samples were collected, filtered, and DNA was extracted following published protocols. Quantitative PCR (qPCR) was then used to screen for the presence of oysters within the Navesink River and Sandy Hook Bay. Preliminary findings suggest any oyster populations in these areas are too small and/or patchy to be detected with this method. However, additional optimization may increase the sensitivity of the assay and this method may be useful for future restoration efforts.

B-15

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

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Faculty Mentors:
Assistant Dean John Tiedemann, School of Science and Dr. Megan Phifer-Rixey, Department of Biology

Funding Sources:
Berkeley Striper Club; Monmouth University Urban Coast Institute; NSF BEACON; Monmouth University Department of Biology

Abstract

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

The primary objective of this project is to use microsatellite genotyping to identify the stock-specific origin of striped bass in Ocean County, New Jersey and estimate the relative contribution of individual spawning stocks to the fishery in this region. First, during fall 2017 and spring 2018 volunteer anglers from beaches in Ocean County collected fin clips and morphological data from >120 fish. Next, DNA was extracted from fin clips using DNA purification and isolation kits. Despite extended time between collection and extraction, DNA concentration and quality was generally acceptable for Polymerase Chain Reaction (PCR). Extracts were then used to successfully test established multiplex microsatellite PCR protocols. After the full set of microsatellite PCRs have been generated, genotypes will then be used to assign individual fish to spawning grounds using publicly available population genetics programs. These data can then be used in future management plans to protect important spawning areas and maintain breeding populations.

B-16

MONMOUTH COUNTY BEACH NESTING BIRD MONITORING AND STEWARDSHIP PROGRAM

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Mentors:
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Christina Davis, Meaghan Lyon, Pam Prichard New Jersey Division of Fish and Wildlife

Funding Sources:
New Jersey Division of Fish and Wildlife Endangered and Nongame Species Program; Conserve Wildlife Foundation of New Jersey; Monmouth University School of Science

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 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 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;
- 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. This summer as endangered species interns, we assisted the NJDFW with their beach nesting bird stewardship program in Monmouth County 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.

B-17

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

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Faculty Mentor:
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Funding Sources:
Bristol-Myers Squibb; Monmouth University School of Science;
Monmouth University Department of Biology

Abstract

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). The association between inflammation and cancer has been studied widely so we want to determine if PJE and AE could inhibit vital signaling of 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 the human squamous carcinoma HSC-2 cells and human normal gingival fibroblast cell HF-1, 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 pathways that activates NF-kB is epidermal growth factor (EGF). We want to quantify the EGF receptors (EGFR) to ovserve its over-expression in the HSC-2 cells verse HF-1 cells. By quantifying EGFR on the cells, we can determine, to a degree, the strength and intensity of the immune response.

DEPARTMENT OF CHEMISTRY AND PHYSICS

CE-1

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

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Faculty Mentor:
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Funding Sources:
Monmouth University School of Science;
Monmouth University Department of Chemistry and Physics

Abstract

The transition of the standard B-form DNA helix to A-form DNA was first seen by X-ray imaging of DNA fibers. Over time, the structures of B and A DNA were further characterized with many higher resolution crystal 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. While it is known that the B to A conformational transition occurs, the specifics, like where in the DNA it originates, how it propagates, and detailed step-by-step mechanism involved are still unknown. By using site specifically positioned fluorescent oligonucleotides, our aim is to explore the local and global conformational changes in this highly biologically relevant transition. Further, the local conformational tracking using fluorescent probes allows us to compare the A-form conformation in DNA duplexes with that found in DNA-RNA hybrid as well as DNA-protein complexes. Eventually we will introduce small organic molecules to enhance the stability of these structures and will use computational modeling to support our observations. Our results showed that using 2-Aminopurine (2-AP), a fluorescent analogue of Adenine, we could monitor the local as well as global conformational change simultaneously. Additionally we found that spermidine, a poly cationic amine, found in living cells can drive the duplex DNA into an alternative conformation in presence of ethanol. Our hypothesis is that spermidine binds to the grooves of the DNA and induce a conformational change that is neither A nor B form, but something similar to a triple helix. Currently we are exploring various ethanol and spermidine concentrations to characterize this novel transition.

CE-2

TOPOGRAPHIC AND BIOCHEMICAL OBSERVATION OF A STABLE G-QUADRUPLEX

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

Funding Sources:
Monmouth University School of Science;
Monmouth University Department of Chemistry and Physics

Abstract

A molecular level understanding of the structure and function of the macromolecular machines of gene expression is a major theme of Biology. The local conformations of individual nucleic acid bases are important components in processes fundamental to gene regulation. In this project, our focus is to elucidate the structural complexities of unusual DNA conformations such as G-quadruplexes and T-loops at single base resolution. G-quadruplexes and T-loops are unusual nucleic acid structures found mainly at telomeres, the multiple repeats of guanine rich sequences found at the linear eukaryotic chromosome ends. G-quadruplex (the four stranded nucleic acid secondary structures) formation can affect chromatin architecture and regulation of replication, transcription and recombination and has been associated with genomic instability, genetic diseases and cancer progression.

Herein, we propose a series of structures present at the telomere that could be used as a therapeutic target to limit the abnormalities occurring in biological processes. Telomeres are repetitive guanine rich sequences at the ends of chromosomes that play a crucial role in protecting critical gene coding proteins and maintaining the genome integrity. This specific sequence of DNA that is guanine rich at the end of telomere consists of various non-canonical DNA structures such as G-quadruplex and T-loops. The aim of this project is to elucidate the structural intricacies observed at the telomeric end of the chromosomes using various spectroscopic approaches. Using a custom synthetic oligonucleotide containing eight guanines that forms a very stable parallel guanine tetraplex in the presence of the K^+ ion we showed that there is no pH depends on this oligonucleotide. Further, our results demonstrated that Poly Acrylamide Gel Electrophoresis (PAGE) can serve as a way to purify various structures formed by this oligonucleotide and our aim is to characterize these different structures using absorbance and circular dichroism spectroscopy techniques.

CE-3

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

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

Funding Sources:
Monmouth University School of Science;
Monmouth University Department of Chemistry and Physics

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 looks like 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 can be due to many factors and the stability of the G-Quadruplexes is one among them. In the current research, we are introducing porphyrin based small molecules to study the effect of ligand-induced stabilization/destabilization of this non-canonical DNA structures. Incorporation of ligand L1 showed that this small molecule interact with the DNA in different ways depending on the way the molecule is introduced. When it is annealed with the DNA, this polycationic small molecule binds to the single strand DNA and forms a less stable G-Quadruplex perhaps by hindering the close association of the guanine tetrads. When the ligand is not annealed with the DNA and instead incubated for 1 hour after the DNA is annealed, it binds to an already formed G-Quadruplex and further stabilizes the structure. The difference in melting points deduced from thermal melting experiments and DNA secondary structure obtained from spectroscopic experiments supported our hypothesis. This study will eventually be useful in designing and developing new therapeutic methods for the treatment of many diseases including cancer and other genetic diseases such as Bloom syndrome, Werner syndrome and Fanconi anemia.

CE-4

NOVEL APPROACH TO CHARACTERIZE I-R3 DEOXYRIBOZYMES USING BIOCHEMICAL AND SPECTROSCOPIC ANALYSIS

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Dr. Davis Jose and Dr. Jonathan Ouellet, Department of Chemistry and Physics

Funding Sources:
Monmouth University School of Science;
Monmouth University Department of Chemistry and Physics

Abstract

DNAzymes, also known as deoxyribozymes or DNA-based enzymes, are single-stranded DNA molecules with catalytic activity. DNAzymes are isolated from random-sequencing DNA pools using in-vitro selection and many that catalyze a diverse range of chemical transformations have been identified. Most deoxyribozymes cleave in the presence of magnesium ions (Mg^{2+}); however, the deoxyribozyme that is being studied cleaves only in the presence of zinc ions (Zn^{2+}), which is very uncommon. The goal of this project is to identify how the zinc chloride catalyzes the bimolecular I-R3 (Class 1 Representative 3) that was discovered by SELEX (Systematic Evolution of Ligands by Exponential Enrichment). We use a novel fluorescent-based assay to understand the interaction modes of $Zn2^{+}$ with I-R3 DNAzyme and the mechanism of DNA cleavage by this enzyme. There are multiple fluorescent probes that can be used; however, the selected probes for this project are 2-aminopurine (2-AP) and 6-methyl isoxanthopterin (6-MI). 2-Aminopurine is analogous to adenine while 6-methyl isoxanthopterin is analogous to guanine. Currently, we incorporated 2-AP within the cleavage site of the substrate to follow the kinetic rate. Our Results showed that the presence of 2-AP fluorescent probe did not interfere with the cleavage of the DNA and opens up a new technique to study this complex biological interaction. In the future, our aim is to use multiple combinations of the fluorescent probes to have a better understanding of the functional mechanism of I-R3 deoxyribozyme and its interaction with Zn^{2+} and other cations with a similar atomic radius.

CE-5

EXPLORING OXAZOLE-AND THIAZOLE-BASED MACROCYCLE BINDING TO DNA

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Funding Sources:
American Chemical Society – Petroleum Research Fund Research; Corporation for Science Advancement – Cottrell Scholar Award; Monmouth University School of Science; Monmouth University Creativity Grant;
Monmouth University Department of Chemistry and Physics

Abstract

The presented research is devoted to a computationally-aimed selection of small organic molecules (ligands) that have shown potential as anti-cancer drugs with low toxicity. Different ligands, depending on their structure and substituents, bind highly selectively to certain DNA forms. In the current work, a small set of oxazole- and thiazole-based macrocycles have been selected to explore the potential of these molecules for optimal binding to specific DNA forms, and subsequent targeted inhibition of telomerase in cancer cells. Initially, a comprehensive sampling of various conformations of the preselected oxazole- and thiazole-based macrocycles have been performed. The density functional theory (as implemented in the B3LYP functional) has been employed for geometry optimization of the selected conformations. At the next stage, molecular docking methods, embedded into the AutoDock4.2 program, have been used to explore the ligand interactions with DNA.[1] Each low-energy conformation resulted from our DFT optimization has been docked to a double stranded dodecanucleotide d(CGCGAATTCGCG) obtained from the Protein Data Bank. The results of the simulations will be presented, including the most probable docked structures and binding energies. Currently, our group is working on refining the DNA-ligand binding energies using fragmentation-based quantum chemistry methods, namely the Fragmentation Based Method (FMO).[2]

1. Yana Kholod, Erin Hoag, Katlynn Muratore, and Dmytro Kosenkov „Computer-Aided Drug Discovery: Molecular Docking of Diminazene Ligands to DNA Minor Groove“, J. Chem. Educ., 2018, 95(5), 882-887, DOI: 10.1021/acs.jchemed.7b00989
2. Gary Prato, Samantha Silvent, Sammy Saka, Massimiliano Lamberto, and Dmytro Kosenkov „Thermodynamics of Binding of Di- and Tetrasubstituted Naphthalene Diimide Ligands to DNA G-Quadruplex“, J. Phys. Chem. B, 2015, 119(8), 3335-3347, DOI: 10.1021/jp509637y

CE-6

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

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Funding Sources:
American Chemical Society – Petroleum Research Fund; Research Corporation for Science Advancement – Cottrell Scholar Award; Monmouth University School of Science; Monmouth University Department of Chemistry and Physics

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 are identified and analyzed. These non-covalent interactions include Coulomb electrostatic, polarization, exchange-repulsion, and dispersion. Bulk steric factors that impact LPG-philosilicate 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 philosilicate crystals will allow us to understand which intermolecular interactions are most prevalent in these systems. 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 a safe waterless drilling fluid.

CE-7

ACIDOLYSIS OF RHENIUM(I) ALKYLCARBONATE COMPLEXES AND CYTOTOXICITY OF THE ACIDOLYSIS PRODUCTS

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Dr. Jeffrey H. Weisburg, Department of Biology

Funding Source:
Monmouth University School of Science;
Monmouth University Department of Chemistry and Physics

Abstract

Organometallic compounds have been known to contribute to many significant advances in the medicinal field. One of its most significant advances is its contribution in the battle against cancer. Cis-platin, an organometallic compound with a platinum center, is the most commonly used cytotoxin in cancer treatment. However, there is a need to expand to other organometallic compounds and their potential cytotoxic properties due to resistant cell lines and significant side effects.

This research focuses on Rhenium(I) centered organometallic compounds supported by one α-diimine ligand, three carbonyl ligands, and a sixth ligand. In this research there is an emphasis on a rhenium complex with a sixth alkyl carbonate ligand. This ligand arises from the reflux of dirheniumdecacarbonyl in pentanol under an atmosphere of carbon dioxide. The alkyl carbonate ligand containing rhenium complex can be used in substitution reactions with a variety of acids such as difluoroacetic acid, chloroacetic acid, hexanoic acid, benzene sulfonic acid, tetrafluoroboric acid, benzoic acid, and a pyridinium salt.

Prior research has reported that the pentylcarbonate containing 2,2'- bipyridine and 1,10 phenanthroline complexes have cytotoxic properties. Knowing this, it is hypothesized that compounds with similar structures synthesized through substitution reactions will also have cytotoxic properties. Acidolysis reaction products are characterized by IR and NMR spectroscopy to verify the compound's structure. Their cytotoxic properties are also tested through in-vitro analysis using an oral cancer cell line, HSC-2, and a normal oral cell line, HF1. These results will, hopefully, give us a better understanding of the mechanism behind the cytotoxic properties of the compounds.

CE-8

ISOLATION OF AN APTAMER THAT BINDS 2-HG

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

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

Abstract

Glioma and Acute Myeloid Leukemia are both cancers that have been linked to the formation of 2-HydroxyGlutarate (2-HG), during the third step in the Krebs Cycle. When a point mutation to Arginine 132 of IDH1 enzyme causes a gain of function that converts α-Ketoglutarate (α-KG), the correct metabolite, into 2-HG, an inhibitor. One of the carbonyl groups is converted into a hydroxyl during an added step. Up to 86% percent of patients with excess levels of 2-HG have been found to have tumors, what if there was a way to stop the formation the tumor and the production of 2-HG?

Through the development of a biosensor, we can do exactly that. The goal of my research is to isolate an aptamer, or a single strand of RNA, that can bind to 2-HG with high specificity and accuracy. Once an aptamer is found, it can then be cloned into a plasmid and added to a riboswitch, which acts as a mechanism to turn on and off translation of the desired genes we place in the plasmid. In the case of this project, snake venom is a likely gene that will be activated by the binding of 2-HG. This will effectively kill any cell that can cause cancer.

Through cycles of SELEX, Systematic Evolution of Ligands by Exponential Enrichment, a pool of randomized RNA sequences is narrowed down, until eventually 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. The implementation of a biosensor that can destroy precancerous cells would revolutionize the medical field.

CE-9

ISOLATING RNA APTAMERS THAT BIND A30P ALPHA-SYNUCLEIN AND NEDD4

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Faculty Mentor:
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Funding Sources:
Monmouth University School of Science: Summer Research Program

Abstract

Parkinson's disease (PD) is a neurodegenerative disorder which negatively affects movement. Symptoms of PD are caused by the death of dopamine producing neurons in the brain. Researchers have found that neuronal death in hereditary PD is likely caused by the buildup of mutant A30P alpha-synuclein (a-syn), which forms clumps known as Lewy bodies. Previous research also suggests that A30P a-syn can be targeted for lysosomal degradation by an E3 ubiquitin ligase, NEDD4. This study involves developing a dual RNA aptamer structure consisting of an aptamer for NEDD4 and an aptamer for A30P a-syn connected by an RNA linker. The end goal is to develop these two aforementioned aptamers and deliver them to the brain via AAV, where the aptamers will bind to NEDD4 and a-syn, stabilizing enzyme-substrate interaction and helping NEDD4 specifically target a-syn instead of the many other proteins it can ubiquitinate.

In order to isolate the NEDD4 and A30P a-syn aptamers, we conducted Systematic Evolution of Ligands by Exponential Enrichment (SELEX). To do this, hammerhead ribozymes with a variable stem 2 (each consisting of 30 random nucleotides) were used. Ribozymes cleave when the aptamer (randomized) region binds to a substrate, allowing binding aptamers to be easily separated from non-binding ones. Once transcribed from DNA to RNA, the ribozymes went through negative selection to remove aptamers that bound to NEDD4 and a-syn analogues. Next, RNA was subject to positive selection to isolate aptamers that bound to NEDD4 and a-syn. By repeating the SELEX cycle multiple times, we can purify the initial RNA pool to only include aptamers showing high specificity to solely the target substrates. Once development of these aptamers is complete, a therapy that targets the root cause of the disease, not just the symptoms, can be developed, revolutionizing the way we treat PD.

CE-10

THE THEOPHYLLINE RIBOSWITCH; ITS DESIGN AND IMPLEMENTATION

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

Abstract

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 the aptamer with random sequences into a plasmid and transform the plasmid into bacteria cells. Then, replica plating along with screening selects the cells that only contain 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 converted into its riboswitch, the system of ratiometric fluorescence will allow for testing of the riboswitch's function. This is because a designed plasmid containing coding for two fluorescence proteins on either side of the inserted riboswitch will give the availability 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.

DEPARTMENT OF
COMPUTER SCIENCE & SOFTWARE ENGINEERING

CSSE-1

CONSTRUCTING 3D PANORAMAS

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Funding Sources:
Monmouth University Urban Coast Institute; Monmouth University Department of Computer Science and Software Engineering; Aerial Applications

Abstract

Natural disasters cause significant structural damage to important community infrastructure. To help expedite fast structural recovery, companies such as Aerial Applications use drone technology to help repair crews locate and identify crucial infrastructure such as power lines in need of immediate repair. Since drones are limited to taking photographs or short videos, the challenge is to take this data from the drone and recreate the landscape for future analysis.

Photogrammetry is a technique used commonly to map areas and objects with the input of photographs. This science is useful in constructing 3D models from 2D images using intricate algorithms that involve matching key features between images, as well as calculating and estimating the camera's position. These algorithms carry over to point cloud development, which is the plotting of key features into a 3D environment from these images. The end product is a detailed mesh of the area that was photographed by a drone flying in a specific flight pattern.

Although photogrammetry might seem to be a narrow field of study, our group has come across many sub-fields that comprise this science. A few of these are multi-view geometry, epipolar geometry, complex linear algebra computations, and homography. We tasked ourselves with researching, analyzing, and in some cases reprogramming code from existing applications that implemented these technologies in an effort to improve or re-think how Aerial Applications could envision an alternative method for their service.

To this end, we are developing an alternative method of reconstruction by combining existing technologies with a different presentation layer using panorama imaging to develop a 3D reconstruction of the photographed area.

CSSE-2

DESIGNING A VIRTUAL REALITY SIMULATION TO ILLUSTRATE THE EFFECTS OF IMPERVIOUS SURFACES FROM URBANIZATION ON THE BARNEGAT BAY WATERSHED

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

Abstract

The Barnegat Bay Watershed includes part of Ocean and Monmouth County in New Jersey. The populations of these counties have been rapidly growing each year and more than doubles throughout the summer months. Increased urbanization creates more housing, buildings, and pavement. Materials such as asphalt and concrete from roads are impervious to water, meaning water that previously percolated into the ground and returned to the bay now floods roads and flows on the surface. The flowing water carries the chemicals and materials it encounters, such as fertilizers and pesticides, and brings them into the bay as runoff. The introduced chemicals and nutrients disrupt the ecosystem, contributing to the Barnegat Bay's problem of eutrophication and causing brown-tide algal blooms. Understanding the trend in urbanization and its effect on algal blooms is crucial in resolving the issue of runoff pollution.

Virtual reality allows people to visualize the change in urbanization of the watershed over a long period of time. A simulation was created in Unity 4.7 to demonstrate how the number of impervious surfaces increases overtime, their distribution, and how they impact algal bloom events. The team gathered urbanization data of the Barnegat Bay Watershed from 1995 to 2016. The data modeled instances of blooms over time. The simulation was displayed on the Oculus Rift and Google Daydream, allowing users to interact with the environment and see the effects of long-term urbanization in accelerated time.

The goal of the project is to educate the general public on the impact residents have on the Barnegat Bay Watershed. The simulation can be used to transport high school classrooms and community organizations onto the watershed so they can witness change over a long-period of time. As a result, the team learned methods of portraying scientific data and relationships in an interactive and educational medium to be used as a teaching tool.

CSSE-3

DESIGNING A VIRTUAL REALITY SIMULATION TO DEMONSTRATE HOW EUTROPHICATION STIMULATES *Aureococcus anophagefferens* BLOOMS AND ITS EFFECT ON MARINE LIFE IN THE BARNEGAT BAY

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

Abstract

The Barnegat Bay is a significant body of water in New Jersey, serving as a key estuarine habitat for species that reside there. Long-term nutrient pollution from nonpoint sources has made the system eutrophic, increasing the risk of algal blooms, such as brown-tide blooms from *Aureococcus anophagefferens*. The increase in algal concentration reduces the amount of sunlight and dissolved oxygen entering the water, disrupting the ecosystem and killing a majority of fish and submerged aquatic vegetation.

With the advent of virtual reality, new methods of modeling eutrophication of the Barnegat Bay have become possible. A simulation was created in Unity 4.7 to demonstrate the relationship between several parameters, such as temperature, turbidity, and dissolved oxygen, and how they impact different types of marine life in the bay. The team gathered data from the northern part, central part, and southern part of the Barnegat Bay. The data determined likely outcomes for the water quality and whether an algal bloom occurs. The simulation was displayed on the Oculus Rift and Google Daydream, allowing users to interact with the environment and change parameters to see varied scenarios.

The goal of the project is to educate the general public on the severe state of the Barnegat Bay. The simulation can be utilized to immerse high school classrooms and community organizations into the depths of the Barnegat Bay so they can witness these complex interactions and gain a visual understanding of the situation. As a result, the team learned methods of portraying scientific data and relationships in an interactive and educational medium to be used as a teaching tool.

CSSE-4

COPAY SERVICES FOR HEALTHCARE PROVIDERS AS CRM APPLICATION

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Funding Source:
The Macaluso Group

Abstract

This project focused on the feasibility of migrating current copay services healthcare provider web portals used by physicians into a Customer Relationship Management (CRM) platform to provide an integrated service with other physician services. Critical requirement in this effort is the safeguarding of patients' personal and health information privacy to meet the PCI (Payment Card Industry) and HIPPA (Health Insurance Portability and Accountability Act) standards.

The project used Salesforce.com CRM platform to develop a physician services application. In order to remain compliant with the privacy limitations of the field, we utilized RESTful web services exchange data with backend services in a secure manner. The application was developed using Apex programming language, JavaScript, and HTML, and custom components for JSON and networking for REST API interfaces. The application implemented major functionalities needed in a copay services application – patient enrollments, review of benefits, submission of benefits claims, review of claims data in detail, and communication with patients.

The result of this work has been a proof-of-concept that demonstrates what the CRM platform is able to do natively and what can be accomplished using custom components and web services code to exchange data with external systems.

CSSE-5

STATISTICAL ANALYSIS ON PHARMACY CLAIM PAYMENTS TO DETECT ANOMOLIES

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Funding Source:
The Macaluso Group

Abstract

For patients in need of expensive pharmaceutical drugs, affordability can be a concern for many. Insurance companies (payers) cover the cost of the drugs to varying degrees based on a patient's medical coverage plan and deductible limits, with any remaining amount being the patient's copay responsibility. However, the amount of coverage can vary based on the patient's resident state, the pharmacy filling the prescription, and agreements between the payer and pharmacy. By using data from prior years for various drugs, this research project attempts to setup the underlying statistical models to detect variations in patient copay amounts for drugs at the state, pharmacy, and payer levels.

To statistically analyze the research question, various steps had to be taken. To look at the average amount paid for each state, analysis of variance (ANOVA) tests were needed. For the ANOVA tests to be valid, the data had to be normal. The data was found not to be normal, therefore the Non-Parametric Kruskal Wallis Test was used with the Conover Iman Test of Multiple Comparisons as a follow up. These tests are similar to the ANOVA tests except they compare the median values rather than the mean. This process was repeated for each individual state comparing the pharmacies, and then for each individual pharmacy comparing the payers. Using R-Studio, a statistical analysis tool, software was developed to import data and statistically analyze the variabilities in patient copay amounts. The user is able to select which states to focus on as well as which pharmacies within the specific state and which insurance companies. A map of the states, median plots, and boxplots are all automatically created as well to allow more visuals while comparing the amount paid per state, pharmacy, or insurance company.

In the near future, the methodologies developed in this project will be deployed to a cloud computing environment to analyze data in real time. This will be followed by additional research into use of Machine Learning classification and regression algorithms to predict trends in claims adjudication.

CSSE-6

SOCIAL NETWORKING MOBILE APPLICATION TO AID IN RECOVERING FROM SUBSTANCE ABUSE

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Funding Source:
The Clean Living Community

Abstract

Recovery from substance abuse often requires both professional and social support. While professional support can be purchased, social support cannot. Professional cannot be alongside their patients at all times to provide the constant support needed, and the professional-client relationship limits the scope of appropriate actions on behalf of the professional.
This project involved design and development of a social networking application for iOS mobile devices to aid in the patient's search for social support. The application allows users to "connect" with other users in recovery in order to share social support. The application will present the users with possible "connections" which are ordered by closeness in location and personal compatibility. When creating an account for the application, users complete a personality survey, in which the results are stored and used to find other users whom answered similarly. Users may also search out "mentors," other users that have been recovered for more than 3 years that have volunteered to provide mentorship to those seeking it out. Users may privately communicate through an instant message format. Users may also RSVP to events, which are opportunities for users to gather together in to share support through activities in person. Such events are created by other users that wish to share their time. The application uses Google Firebase as a backend database service, which handles issues regarding user authentication, application scalability and data security.

Future research would include offering more services to users and targeted advertising for outside firms to support users in recovery. Using the phone in everyone's pocket, it has never been easier to find support in recovery!

CSSE-7

COMPARING SQL AND NOSQL DATABASE SYSTEMS

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

Funding Source:
Discovery Data

Abstract

The purpose of this research assignment was to explore the benefits and drawbacks of relational (SQL) and non-relational (NoSQL) database systems. To conduct the research, I loaded fields of data, courtesy of Discovery Data, into MySQL and MongoDB. I observed the differences in schema and wrote two Java programs to measure and compare query execution time between the systems.

By running the programs, I observed that MongoDB executed administrative commands faster than MySQL. Queries for data retrieval especially proved to be much faster. I also noted that complex queries were easier to execute for MySQL than MongoDB.
I have also learned in my research that relational databases are beneficial in storing structured and static forms of data. Relational databases are also effective at maintaining data integrity by being **ACID** compliant; an acronym for a set of properties that ensure the database safeguards its data when administrative tasks are carried out and when system failure occurs. The drawbacks of include issues with scalability and inflexible schema.

Non-relational databases are effective in storing unstructured and dynamic forms of data. Non-relational databases effectively store data entries in their own unique format without altering the schema of the entire database. Non-relational databases also have the added benefit of effective horizontal scalability, meaning that they can accommodate growing data by sharing across multiple servers. The main disadvantage of non-relational databases is that they do not preserve data integrity as well as relational databases. Non-relational databases prioritize fast data availability over consistency. This property can lead to discrepancies in data when transactions are carried out.

DEPARTMENT OF MATHEMATICS

MA-1

STATISTICAL ANALYSIS ON ALFAXALONE AND ITS EFFECTS ON LAB RATS and BOOTSTRAPPING WITH SMALL SAMPLE SIZES

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Funding Source:
Julianne McCready, Red Bank Veterinary Hospital

Abstract

Respiratory infections can be very common among pet rats, and they often need to undergo procedures to help them become healthy. In order to know the severity of the infection, x-rays are needed. When performing an x-ray, regular anesthesia has been used to prep the rats in the past, but it puts a lot of stress on the rats which can potentially cause cardiovascular side effects. Alfaxalone has been labeled for intravenous injection in dogs, cats, and other species but there is little information available about the use of it in pet rats. By using data from her experiment, Dr. Julianne McCready is trying to figure out whether Alfaxalone is a safe and effective way to sedate rats without putting them under anesthesia.

To statistically analyze her research question, various steps had to be taken. Due to the small samples sizes of nine and two, comparing the vitals of healthy lab rats to sick lab rats was difficult to accomplish. After researching different methods, we bootstrapped our data in order to analyze the results. Bootstrapping allowed for us to create confidence intervals and hand calculate p-values to test the significance of each comparison.

MA-2

STATISTICAL ANALYSIS ON THE ABSENCE OF FIRE IN AN ECOSYSTEM THAT SHOULD HAVE FIRE

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Dr. Pedram Daneshgar, Department of Biology

Funding Sources:
Monmouth University Department of Mathematics;
Monmouth University Department of Biology

Abstract

The Pitch Pine tree (*Pinus rigida*) is a tree whose reproductive cycle needs the presence of fire. The heat from fire is what causes the pine cone from this species to open and release seeds. In NJ's Pinelands, controlled fires are conducted regularly to both get rid of litter and help species reproduce. However, NJ's Maritime forests showed no signs of controlled fires happening. To compare both populations, tests were both run directly under the 49 tested trees and 10 meters away from the trees. The variables tested included the number of juveniles in the tested radius, litter depth, the trees age, height, width, and the soil.

To do a statistical analysis on this data, several tests were done. First, descriptives of both the predictor and response variables were taken. Next a test of Normality was done on the data. Mother Nature is not a normal place, and most of the variables were not either. An independent ample t-test requires normality, however the client wished for these tests to be run on the data despite the lack of normality in the data. Finally, a correlation test was used to find out if there was any correlation between any of the variables.

MA-3

STATISTICAL ANALYSIS ON THE USE OF ACTIVE LEARNING IN ANATOMY AND PHYSIOLOGY

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Abstract

Anatomy and Physiology is a required class for many science majors. The course material can be difficult for students to learn as there is a lot of information that needs to be memorized and used. As a result, different methods have been used to teach these classes to find the best way to teach the students. One of these methods was implemented by Dr. Dunphy starting in 2016 in her Anatomy and Physiology classes. She used an active learning approach through case studies which involves students more in what they are learning. At the end of the semester, students were tested using the HAPS exam which is a national standardized test for Anatomy and Physiology classes. To measure the effectiveness of her approach, the students' HAPS scores from her class were examined. This was done with 2016, 2017, and 2018.

To do the required statistical analysis on this data, several tests were done. Initially, the HAPS scores for each year were tested for normality; they passed. The first test run was a 1-sample t-test to compare the HAPS national average to the class averages from Dr. Dunphy. 2016 and 2017 showed a significant difference from the national average, while 2018 did not. Similarly, another t-test was run to compare the HAPS national average to the class scores for all three years combined into one. This test showed a significant difference. Another test run was an ANOVA to compare the scores for each of Dr. Dunphy's classes between all three years. The results showed that not all three classes had the same mean score, so post hocs were run to assess which class was different. 2017 and 2018 were shown to be significantly different from each other. Overall, it seems that Dr. Dunphy's approach results in better HAPS scores.

MA-4

STATISTICAL ANALYSIS OF DOG-OWNER BEHAVIOR IN PLAY PARKS

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Dr. Lindsay Mehrkam, Department of Psychology

Funding Sources:
Monmouth University School of Science;
Monmouth University Department of Mathematics

Abstract

Dog parks can be found throughout the nation and are not only beneficial for communities, but also for the physical and mental wellbeing of pet dogs. These locations allow dogs to exercise and play off-leash in controlled and supervised environments, as well as interact with other canines. This study was conducted in the hopes of providing insight into aggressive dog behavior to ultimately make dog parks safer through the influence of policy. Throughout this study there were 400 different dogs and 950 play bouts observed in two dog play parks. Dr. Mehrkam conducted her study and received her data from March to November of 2017. This observational study involved daily 30-minute recordings of play and involved the work of four coders.

We hoped to find behaviors that can predict aggressive interactions between dogs. Using those key behavior precursors to aggression, we needed to determine if owners are missing important factors that can lead to aggression. To see how the environment of the play park changes dog attitudes, we compared types of dog parks in terms of both aggression and owner interaction. Using Chi-Square and Two Proportion testing, we concluded that the proportion of dog interactions that lead to aggression is higher in more crowded dog parks. Also, 71.9% of precursor behaviors we found lead to aggression were missed by owners that did not interact with their dogs during bouts.

MA-5

PERFECT PYRAMIDS: THE SEARCH FOR HERONIAN SIMPLEXES IN HIGHER DIMENSIONS

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Dr. Susan Marshall, Department of Mathematics

Funding Source:
Monmouth University Summer Scholars Program

Abstract

Simplex is the general term for an *n*-dimensional triangle. For a simplex to be Heronian, it must have non-negative integer (hyper) volume and be composed of lower dimensional Heronian simplexes. We refer to these integral Heronian simplexes as "perfect pyramids". For example, in dimension 0, a perfect pyramid is any point. In dimension 1, any line of integral length is a perfect 1-pyramid, and in dimension 2, any triangle with integral side lengths and integral area is a perfect 2-pyramid. In dimension 3, any triangular pyramid with integral side lengths, surface area, and volume is a perfect 3-pyramid.

It's well known that dimensions 0, 1, 2, and 3 have infinitely many perfect pyramids. In fact, mathematicians such as Euler and Carmichael have devised methods to generate all Heronian 2-simplexes; others, such as Kurz, improved the speed at which Heronian 2-simplexes can be generated. However, the existence of higher-dimensional Heronian simplexes is an open question, and our research focuses on the search for higher-dimensional Heronian simplexes. Do there exist any 4-dimensional perfect pyramids? It's been shown that almost-perfect 4-pyramids exist by Buchholz, where he constructed a 4-simplex with integral side lengths and volume but non-integral surface area. However, none have succeeded in constructing any perfect 4-pyramid.

To find these 4-simplexes, we attempted to close the gap on Heronian 3-simplexes since it is unknown whether all perfect 3-pyramids are known. We ran extensive computer searches and found strong evidence to suggest that 4(iii), a specific possible configuration for a perfect 3-pyramid, is unlikely to exist. We also found seemingly novel methods to generate Heronian isosceles triangles. However, we were unable to show the existence of any perfect 4-pyramids or complete the list of possible configurations for Heronian 3-simplexes.