**MONMOUTH UNIVERSITY**
SCHOOL OF SCIENCE

**MONMOUTH UNIVERSITY**
STUDENT SCHOLARSHIP WEEK

# 22nd ANNUAL

# SCHOOL OF SCIENCE STUDENT RESEARCH CONFERENCE

# APRIL 12, 2024

## Featuring Poster Presentations of Student Research

**Department of Biology**
**Department of Chemistry and Physics**
**Department of Computer Science & Software Engineering**
**Department of Mathematics**

# School of Science Student Research Conference

## Friday April 12, 2024

**E 201**
**Science Building Multipurpose Room**

### *Agenda*

| | |
|---|---|
| **9:00 am – 10:00 am** | **Registration and Poster Set-up** |
| **10:00 am – 10:10 am** | **Welcome and Opening Remarks** |
| | **Assistant Dean John Tiedemann**<br>**Interim Dean Joe Coyle** |
| **10:10 am – 10:30 am** | **Keynote Address** |
| | **Dr. Kevin Dillon, Lecturer - - Department of Biology**<br>**Monmouth University Class of 2015** |
| **10:30 am – 12:30 pm** | **Poster Presentations of Student Research**<br>**From the School of Science** |
| **12:30 pm – 1:00 pm** | **Closing Remarks**<br>**Presentation of the Dean's Awards**<br>**for Excellence in Undergraduate Research** |
| | **Interim Dean Joe Coyle** |

# SCHOOL OF SCIENCE
# 2024 STUDENT RESEARCH CONFERENCE

**DEPARTMENT OF BIOLOGY**

**BY-1**     **Microbial Community Composition Analysis In Coastal Lakes Of New Jersey As An Indicator Of Harmful Algal Bloom Formations**

**A. Diederik Boonman Morales**
**Faculty Mentor: Dr. Jason Adolf**

**BY-2**     **Using eDNA To Determine The Presence Of An Overwintering Population Of Striped Bass In The Manasquan River**

**Christopher Reigel and Gildon Smith**
**Faculty Mentors: Dr. Jason Adolf , Dr. Sam Chin and John Tiedemann**

**BY-3**     **Effects Of Elevated Wind Exposure On New Jersey Juvenilie Maritime Trees**

**Madison N. Jubick**
**Faculty Mentor: Dr. Pedram Daneshgar**

**BY-4**     **Spatial And Temporal Patterns Of The Prohibited Atlantic Angel Shark, *Squatina dumeril*, Within The Mid-Atlantic Bight**

**Jessica Maguire**
**Faculty Mentor: Dr. Keith Dunton**

**BY-5**     **Creation Of A Hypoxic State In HT-1080 Fibrosarcoma Cells Decreases Proliferation And Activates JNK**

**Michael Catalfumo and Nicholas Tamburro**
**Faculty Mentor: Dr. Dorothy Lobo**

**BY-6**     **Cypress Essential Oil Treatment Decreases Viability And Activates JNK In Fibroblasts**

**Michael Catalfumo, Nicholas Tamburro, and Angelo Prado**
**Faculty Mentor: Dr. Dorothy Lobo**

# DEPARTMENT OF CHEMISTRY AND PHYSICS

**CE-1**      **Unlocking Student Engagement: Exploring Autonomy, Competence, And Relatedness In The Stem Flipped Classrooms**

         **Rachel Ludwick**
         **Faculty Mentor:  Dr. Nikita Burrows**

**CE-2**      **Investigating Ligand-Induced Local Conformational Changes Of Fluorescently Labeled G-Quadruplex Structures**

         **Alexa Houseknecht and Maxwell Rosen**
         **Faculty Mentor: Davis Jose**

**CE-3**      **Single Proton Tight Coupling In The Bacterial Flagellar Motor**

         **Anna Medici, Maddison Beahm, Claudia Decker, Andrew McGovern, and Caden Kesselring**
         **Faculty Mentor: Dr. Ilyong Jung**

**CE-4**      **Isolation Of An Aptamer Selective To Glucose**

         **Deirdre Campbell**
         **Faculty Mentor: Dr. Jonathan Ouellet**

**CE-5**      **Creating A Cost Efficent Method To Determine Theophylline Riboswitch Activation**

         **Thomas Hintelmann, Olivia Enny, Mika Schievelbein, and James Tilton**
         **Faculty Mentor Dr. Jonathan Ouellet**

**CE-6**      **The Catalytic Chemistry Of The I-R3 DNA Enzyme Through Ion Promoted Cleavage**

         **Madison Pellerito**
         **Faculty Mentor: Dr. Jonathan Ouellet**

**DEPARTMENT OF COMPUTER SCIENCE AND SOFTWARE ENGINEERING**

**CSSE-1**      **ParkShark**

           **Davian Albarran, Bryan Le, Andrew McGovern and Tyler Gennaro and Gianna Piroso {Department of Communications}**
           **Faculty Mentor: Dr. Raman Lakshmanan**

**CSSE-2**      **Kicks Corner**

           **Ryan Berenger, Devin Brattvet, Ryan Hassmiller**
           **Faculty Mentor: Dr. Raman Lakshmanan**

**CSSE-3**      **RunSignUp Dynamic Leaderboard Project**

           **Vincent Loretta and Connor Bennett**
           **Faculty Mentor: Dr. Raman Lakshmanan**

**CSSE-4**      **A Machine Learning Approach To Mitigate Injuries In Collegiate Tennis Players**

           **Francisco Erramuspe Álvarez**
           **Faculty Mentor: Dr. Weihao Qu**

**CSSE-5**      **Penetration Testing Operating Systems: Exploiting Vulnerabilities**

           **Evan Gardner**
           **Faculty Mentor: Dr. Weihao Qu**

**CSSE-6**      **A Domain Specific Language For Differential Privacy SQL**

           **Killariben Limbachiya, Gnanika Yalamanchili and Kavya Varma Palukuru**
           **Faculty Mentor: Weihao Qu**

**CSSE-7**      **Static Analysis Tools Detecting Dll Injections And Checking File Integrity**

           **Jack Berkowitz**
           **Faculty Mentor: Weihao Qu**

**CSSE-8**     **Ingredient Lens: Food Recognition And Recipe Generation**

**Dmitry Bezborodov, John Costa, Andrew Catapano, Jack Berkowitz**
**Faculty Mentor: Dr. Cui Yu**

**CSSE-9**     **DEVSLIST: A Recruitment Platform For Developers**

**Joseph Furmanowski, Evan Gardner, Tyler Gennaro, and Daniel Lawrie**
**Faculty Mentor: Dr. Cui Yu**

# DEPARTMENT OF MATHEMATICS

**MA-1**     **Analyzing The Effectiveness Of Monmouth University's
Math Placement Exam**

**Malea Horn-Attanasio, McKayla Miksza and Rachel Vassallo
Faculty Mentor: Dr. Richard Bastian
Client: Dr. Susan Marshall, Department of Mathematics**


**MA-2**     **Defining A Cancer Cluster**

**Kyle Broesler, Anthony Stirone and Matt Wolyn
Faculty Mentor: Dr. Richard Bastian
Client: Dr. Pedram Daneshgar, Department of Biology**


**MA-3**     **Preliminary Analysis In Understanding Problem Behavior In Dogs And Cats**

**Abby Eck and Adrian Cieniewicz {Department of Business}
Faculty Mentor: Dr. Richard Bastian
Client: Dr. Lindsay Mehrkam, Department of Psychology**


**MA-4**     **Statistical Analysis Of The TPLO On Canine Meniscus Tears**

**Jane Zink, Anna Dos Santos {Department of Chemistry & Physics} and
      Sarah Henry {Department of Biology}**

**Faculty Mentor: Dr. Richard Bastian
Client: Drs. Garrett Davis and Aixa Gonzalez, Red Bank Veterinary Hospital**


**MA-5**     **A Numerical Investigation Of An Adaptive Power Series Approximation
To Compartmental Models**

**Brooke Tortorelli
Faculty Mentor: Dr. Joseph Coyle**


**MA-6**     **An Exploration Into The Lattice Heronian Kites And Rhombi**

**Eliana L. Joskowski
Faculty Mentor: Dr. Susan H. Marshall**

# DEPARTMENT OF BIOLOGY

# MICROBIAL COMMUNITY COMPOSITION ANALYSIS IN COASTAL LAKES OF NEW JERSEY AS AN INDICATOR OF HARMFUL ALGAL BLOOM FORMATIONS

**A. Diederik Boonman Morales**
**Department of Biology**

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

## ABSTRACT

Coastal lakes are vital ecosystems, providing numerous ecological benefits, and to the local communities. However, the health of these ecosystems is threatened and facing gradual degradation due to human activities, polluted water runoff, and Harmful Algal Bloom formations. HABs are complex phenomena that impact waterbodies and can have ecological and anthropogenic impacts. Genomics approaches of microbial community composition can improve our ability to monitor and understand HAB dynamics. Here, eDNA samples collected from three coastal lakes in 2021 and 2022 were analyzed by 16s meta-barcoding to examine the spatial and temporal distribution of microbial community composition. Through NMDS ordinations and K-means clustering, the composition can be reduced to a single variable that can more easily be analyzed and spatially represented. A pipeline was created to seamlessly run the same process to analyze future samples. This study will contribute to the conservation and management of these critical ecosystems, providing a better understanding of the roles of microbial communities in coastal lake ecology.

BY-2

# USING eDNA TO DETERMINE THE PRESENCE OF AN OVERWINTERING POPULATION OF STRIPED BASS IN THE MANASQUAN RIVER

**Christopher Reigel and Gildon Smith**
**Department of Biology**

**Faculty Mentors: Dr. Jason Adolf and Dr. Sam Chin, Department of Biology**
**and**
**Assistant Dean John Tiedemann, School of Science**

## ABSTRACT

Along the Atlantic coast of the United States, there are four geographically specific striped bass spawning grounds that contribute to the migratory population: the Hudson River, Chesapeake Bay, Delaware River, and the Roanoke River. Migratory individuals from each of these stocks comingle as they move north to foraging and nursery grounds in spring/summer and return south to overwintering grounds in fall. As water temperatures cool in late November and early December, striped bass begin to move into overwintering habitats. These habitats include natal rivers/tributaries, non-natal rivers and bays, and nearshore aggregations ranging from New Jersey to North Carolina. Inshore overwintering habitats may be vulnerable to environmental impacts that could alter these habitats and endanger overwintering contingents of the population. Early spring landings of striped bass by anglers in the Manasquan River indicate that an overwintering contingent of striped bass may be present. Identifying overwintering habitats is important for developing adequate protections for this species. Here we present the results of qPCR analysis of water samples collected in the Manasquan River. Striped bass DNA concentration determined by this method may allow for overwintering fish to be detected noninvasively, providing an alternative to capture for assessing presence.

# EFFECTS OF ELEVATED WIND EXPOSURE
# ON NEW JERSEY JUVENILIE MARITIME TREES

**Madison N. Jubick**
**Department of Biology**

**Faculty Mentor: Dr. Pedram Daneshgar, Department of Biology**

## ABSTRACT

As climate change becomes a rising issue in modern science, long term effects on ecosystems and wildlife are still being investigated. Specifically, the increased frequency and intensity of storms raises concerns for disturbances in vital forest habitats. The following greenhouse experiment was conducted to replicate increased wind levels on five New Jersey native maritime forest tree species and monitor the effects on development and growth. Species were selected following a survey within Sandy Hook Gateway National Recreation Area, Sandy Hook NJ, which favored The Silver Maple (*Acer saccharinum*), Atlantic White Cedar (*Chamaecyparis thyoides*), Shortleaf Pine (*Pinus echinata*), Virginia Pine (*Pinus virginianna*), and the Pin Oak (*Quercus palustris*). A total of 75 trees seedlings (15 per species) were randomized equally into three treatments of 25 (n=25). Treatment levels included: 0 hours of wind per day (C), 3 hours of wind per day (A), and 6 hours of wind per day (E). Growth variables including tree height (cm), stem diameter (cm), and overall health were assessed for baseline comparison. At the conclusion of the experiment, trees were harvested for root, leaf, and stem biomass. A series of four bootstrapped ANOVA tests were performed to determine the percent change in each variable for all species on a group and individual treatment level. The results of the study show Virginia Pine and Silver Maple exclusively displayed a significant change over time, and supported the original hypothesis stating increased wind exposure will reflect negatively on tree growth. However, the remaining species failed to reject the null hypothesis stating there will be no change, causing the hypotheses to not be fully accepted. Overall, more information is needed to determine the true impact of amplified wind exposure on maritime forests.

# SPATIAL AND TEMPORAL PATTERNS OF THE PROHIBITED ATLANTIC ANGEL SHARK, *Squatina dumeril*, WITHIN THE MID-ATLANTIC BIGHT

**Jessica Maguire**
**Department of Biology**


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

## ABSTRACT

Globally, Angel sharks (*Squatina* spp.), are one of the most threatened species of sharks with more than half of the 22 extant species currently classified as Threatened on the IUCN red list. Atlantic angel sharks (*Squatina dumeril*), are a "data deficient" species that ranges along the east coast of the US and is currently federally prohibited from being harvested. Distribution of this species along the east coast varies with depth and season. The objective of this study was to evaluate the spatial and temporal distribution of Atlantic angel sharks in the Mid-Atlantic Bight, through analysis of long-term coast wide offshore bottom trawl surveys conducted by the New Jersey Department of Environmental Protection (NJDEP), Southeast Atlantic Monitoring and Assessment Program (SEAMAP), Northeast Atlantic Monitoring and Assessment Program (NEAMAP), and National Marine Fisheries Service (NMFS). Surveys were conducted seasonally and ranged from the Gulf of Maine to Cape Canaveral, FL which covers the Atlantic angel shark's entire geographic range. The highest, Angel shark captures occurred off southern New Jersey in the summer season (n=94), in water depths less than 30 m. A small subset of sharks (n=5) was surgically implanted with Vemco acoustic transmitters to evaluate long-term movements within this region. Sharks were detected at 22 different sites (n=1,388 unique detections) along the coast with most of the detections occurring off MD and NC. This information shows strong northerly summer and southerly winter migrations. Data also showed that Atlantic angel sharks migrated away from nearshore habitat in early October and were almost exclusively found deeper than 20 m by November Since Atlantic angel shark populations with the US are "data deficient", this information is important in the understanding and conservation of this species.

# CREATION OF A HYPOXIC STATE IN HT-1080 FIBROSARCOMA CELLS DECREASES PROLIFERATION AND ACTIVATES JNK

**Michael Catalfumo and Nicholas Tamburro**
**Department of Biology**

**Faculty Mentor: Dr. Dorothy Lobo, Department of Biology**

## ABSTRACT

Hypoxia is characterized as a state in which tissues become oxygen deprived. Under hypoxic conditions, proteins called Hypoxia-Inducible Factors (HIFs) become activated to turn on the expression of important genes.Cobalt chloride ($CoCl_2$) has been used in many cell types to stimulate the activation of HIF-1$\alpha$ and thus chemically mimic creation of a hypoxic environment (Sanchez and Cardenas, 2019). The purpose of this study was to determine if $CoCl_2$ could create a hypoxic environment in HT-1080 fibrosarcoma cells, and how this would affect proliferation. Confluent cultures of HT-1080 cells were treated with either 100 µM or 250 µM of $CoCl_2$ for 1 hour, 4 hours, or 24 hours. Using western blot analysis, it was determined that HIF-1$\alpha$ expression could be detected at 1 hour with 250 µM of $CoCl_2$ and at 4 hours with 100 µM of $CoCl_2$. Maximal expression of HIF-1$\alpha$ occurred after 24 hours. To study the effect pf $CoCl_2$ treatment on proliferation, HT-1080 cells were plated onto 24-well plates and were treated with 100 µM or 250 µM of $CoCl_2$ for 24 hours. Untreated cells served as the control. All cells were counted using trypan blue dye exclusion.  100 µM $CoCl_2$ treatment decreased proliferation by 9%, while cells treated with 250 µM $CoCl_2$ resulted in a 40% decrease of proliferation. Therefore, $CoCl_2$ creates a hypoxic environment for HT-1080 cells, and decreased proliferation of these cells. Western blotting was performed to determine if the expression of the JNK stress pathway was increased in $CoCl_2$-treated cells. Prolonged hypoxia does appear to activate JNK in HT-1080 fibrosarcoma cells. Potential downstream targets of this activation, including transcription factors, other signaling molecules, and tumor stem cell markers will be tested to determine if JNK signaling during hypoxia is involved in their regulation.

# CYPRESS ESSENTIAL OIL TREATMENT DECREASES VIABILITY AND ACTIVATES JNK IN FIBROBLASTS

**Michael Catalfumo, Nicholas Tamburro, Angelo Prado**
**Department of Biology**

**Faculty Mentor: Dr. Dorothy Lobo, Department of Biology**

## ABSTRACT

Cypress oil is an essential oil derived from evergreen coniferous trees native to Southern Europe and Western Asia. Cypress oil exerts anticancer properties due to their natural terpenes which induce apoptosis and cell cycle arrest, in turn limiting tumor growth and metastasis. The components of cypress essential oil include a total of 20 constituents which represent 98.1% of the oil. The major components of this oil include: α-pinene (48.6%), δ-3-carene (22.1%), limonene (4.6%) and α-terpinolene (4.5%). To determine the effect of cypress essential oil on cell proliferation, CUA-4 normal fibroblasts were treated with increasing concentrations of the oil and the effects on proliferation and viability were determined. Proliferation was measured by direct cell counting using trypan blue dye exclusion, and it was found that increasing concentrations of cypress essential oil decreased proliferation. Likewise, an MTT assay was performed to ascertain viability of treated cells, and it was determined that high concentrations of cypress essential oil also decreased viability. The decreased viability may be due to the activation of stress-signaling resulting in apoptosis. Western blot analysis was used to detect cleavage of the apoptosis marker protein PARP, and preliminary results indicate the treatment with cypress essential oil does stimulate apoptosis in CUA-4 normal fibroblasts. Additionally, Western blotting has confirmed that the JNK signaling pathway, which is a stress-response pathway, was activated following treatment with cypress essential oil. Subsequently, treatment of cancerous fibrosarcoma cells will be performed to determine if the effects of treatment differ in these cells.

# XEROPHILIC AND XEROTOLERANT FUNGI AS A SOURCE OF NOVEL ANTIBACTERIAL COMPOUNDS

**Alexandra Decaro, Hridmita Hasan, Alex Kalina and Isabella Torres**
**Department of Biology**

**Faculty Mentor: Adjunct Jon Polishook, Department of Biology**

## ABSTRACT

Xerophilic and xerotolerant microfungi, those filamentous fungi that can grow at or tolerate a low-water availability and typically cause food spoilage, were isolated from unprocessed or raw honey, a sugary food produced by bees from nectar and purchased in local grocery stores as a model for natural product discovery. Each undiluted honey was spread on multiple G18 agar plates to select for fungal species able to grow in a low-water availability environment for up to 21 days. Any emerging fungal growth was subcultured onto malt extract agar slants and incubated at room temperature (20-22C) until significant hyphal growth was observed. From 15 honey samples, over 200 fungal isolates were recovered representing 40 morphotypes, based on macroscopic features. Some of the fungal genera isolated include *Aspergillus*, *Penicillium*, *Talaromyces* and multiple non-sporulating strains. These fungal morphotypes were then regrown on cornmeal, malt-extract, potato dextrose and G18 agar petri plates for 10 days at room temperature. The antibiotic potential of these morphotypes was assessed by placing agar discs of each morphotype / production agar on top of a gram-positive and gram-negative bacterial strain embedded in a triptase soy agar plate. Antibiotic evaluation was assessed by the size of any zone of inhibition after overnight incubation at 37C. The zones of inhibition will be compared to commercially available antibacterial compounds to determine novelty. Further studies may include fungal identification based on microscopic features and/or phylogenetic analysis.

# BRAIN REGIONAL ANALYSIS OF RESISTANCE TO ALCOHOL-INDUCED UPREGULATION OF NMDA RECEPTORS IN THE ADHD-LIKE SHR STRAIN

**Sarah A. Henry, Department of Biology**

**Faculty Mentor: Dr. Dennis E. Rhoads, Department of Biology**

## ABSTRACT

Prior work in our lab investigated behavioral and biochemical interactions between prolonged alcohol (ethanol) consumption and co-use of amphetamine, a stimulant, in adolescent Long-Evans (LE) rats. Because stimulants are prescribed to treat attention-deficit hyperactivity disorder (ADHD), these studies eventually included the Spontaneous Hypertensive Rat (SHR), an experimental model for adolescents with ADHD, and their respective control strain, Wistar-Kyoto (WKY). From this work, we have evidence that: 1) amphetamine co-use attenuates alcohol withdrawal symptoms in LE and WKY control strains; 2) the NMDA subtype of glutamate receptor is upregulated and likely responsible for withdrawal symptoms in LE rats; and 3) the SHR strain is resistant to both NMDA receptor upregulation and development of alcohol withdrawal behaviors. The purpose of the present study is to fill gaps in this SHR work by analyzing individual brain regions, testing for effects of amphetamine as well as ethanol, and examining the control WKY brain for ethanol-induced upregulation of NMDA receptors. Brain regions had been frozen previously, including rats that had consumed a control diet or a diet supplemented with alcohol, amphetamine, or alcohol and amphetamine. Based on previous behavioral studies, we hypothesized: 1) that these treatments would have no effect on more selective brain regions of SHRs, and 2) NMDA receptor upregulation would be observed with WKY rats. Brain regions were subjected to subcellular fractionation, polyacrylamide gel electrophoresis (SDS-PAGE), and Western blotting with antibodies against the NMDA receptor and the enzyme GAPDH as a loading control. Results so far indicate no differences among treatment groups in NMDA abundance in hindbrain, cerebral cortex, and subcortical forebrain regions of SHRs. If extrapolated to human adolescents, our work suggests the diagnosis of an alcohol use disorder among those with an ADHD diagnosis might be complicated by the absence of alcohol withdrawal symptoms.

# PROBING LIPID BILAYER DYNAMICS AS A MECHANISM FOR INHIBITION OF NEUROTRANSMITTER TRANSPORT BY UNSATURATED FATTY ACIDS

**Joseph Kurzeja and LeConte Stover, Department of Biology**

**Faculty Mentor: Dr. Dennis E. Rhoads, Department of Biology**

## ABSTRACT

The purpose of this research was to determine if Excitatory Amino Acid Transporter 3 (EAAT3) is located within lipid rafts in brain membranes and if unsaturated fatty acids (UFA) alter this location. EAAT3 plays an important role in controlling levels of glutamate, the major excitatory neurotransmitter in the brain. Past work showed that EAAT3 was inhibited by UFA which could be elevated locally through phospholipase A2 signaling or more generally during stroke. Those studies led to the proposal that fatty acids have this effect by perturbing the membrane lipid environment of the transporter. For the present study, we hypothesized UFA exposure might inhibit the transporter by altering the preferred location of EAAT3 between raft and non-raft regions of brain membranes. Initially, raft preparations were tested for the presence of EAAT3 and flotilin following polyacrylamide gel electrophoresis (SDS-PAGE) and Western blotting. EAAT3 was most abundant in non-raft portions of the membrane. When raft and non-raft membranes were prepared after exposure to the UFA oleic acid, there was no detectable change in the distribution of EAAT3 between raft and non-raft fractions. Immunoprecipitation using beads coated with flotilin to enrich for flotilin-based rafts confirmed some degree of co-localization with EAAT3. Again, pre-exposure to the UFA oleic acid had little or no effect on the apparent amount of flotilin-based raft isolated, nor on co-localization with EAAT3. Thus, the hypothesis that lipid bilayer dynamics might serve as the medium for an alteration of lipid-protein interactions necessary for EAAT3 function was not supported. However, what emerged through this analysis was an effect of oleic acid on the relative amount of dimeric vs monomeric EAAT3. Although these results are preliminary, they lead us to a new hypothesis that UFA are inhibiting the formation of a more active dimeric form of the transporter.

**BY-10**

**VIA DISC NP ALLOGRAFT SOLUTION FOR DEGENERATIVE DISC DISEASE**

**Gioanna Curci, Department of Biology**

**Faculty Mentor: Assistant Dean John Tiedemann, School of Science**

**ABSTRACT**

Degenerative Disc Disease (DDD) is the deterioration of the intervertebral discs, which causes back pain. Nutrition, genetics, lifestyle, and injury can accelerate disc degeneration. By age 60, most people will have some disc degeneration, but not everyone is suffering from pain. Regenerative medicine, which focuses on developing new treatments to heal tissues and organs and restore function due to aging, disease, or damage, is one solution to helping those with DDD. Via Disc NP, an injectable allograft, intends to supplement a patient's tissue loss due to intervertebral disc degeneration and help relieve pain. In addition, Via Disc NP offers treatment in a minimally invasive manner. This study conducted at Jasper Spine Institute aimed to determine if Via Disc NP helps reduce patients' pain. Patients were routinely followed, and pain was assessed on a visual analog scale (VAS). The results of this study at Jasper Spine Institute show whether patients had pain relief after receiving the Via Disc NP treatment.

# DEPARTMENT OF CHEMSITRY AND PHYSICS

# UNLOCKING STUDENT ENGAGEMENT: EXPLORING AUTONOMY, COMPETENCE, AND RELATEDNESS IN THE STEM FLIPPED CLASSROOMS

**Rachel Ludwick**
**Department of Chemistry and Physics**

**Faculty Mentor: Dr. Nikita Burrows, Department of Chemistry and Physics**

## ABSTRACT

The flipped classroom model facilitates student engagement by leveraging pre-class learning to enable deeper exploration of concepts during dynamic, collaborative peer-to-peer in-class activities guided by instructors. While research on its cognitive benefits remains varied, consistent findings highlight a positive student experience. However, understanding the underlying reasons for this positive experience remains elusive. This study employs self-determination theory to examine how the fulfillment of autonomy, competence, and relatedness needs contributes to student experiences in the flipped classroom. Through semi-structured interviews and inductive coding, this research unveils the pivotal role of these psychological needs across pre-class, in-class, and post-class activities, shedding light on the mechanisms driving student satisfaction in this educational approach.

# INVESTIGATING LIGAND-INDUCED LOCAL CONFORMATIONAL CHANGES \ OF FLUORESCENTLY LABELED G-QUADRUPLEX STRUCTURES

**Alexa Houseknecht and Maxwell Rosen**
**Department of Chemistry and Physics**

**Faculty Mentor: Davis Jose, Department of Chemistry and Physics**

## ABSTRACT

DNA sequences rich in guanines readily fold to form quadruplex structures (GQs), which are bound by Hoogsteen-type hydrogen bonding of four guanine nucleotides (G4). GQs are important structural components in many physiological functions, including limiting telomerase activity seen in 85-90% of human tumor cells. Telomerase activity can be influenced by introducing small molecules that can interact with GQs. This interaction of small molecules can alter the stability and local conformations of the GQ at the guanine tetrad level, which in turn can affect the telomerase activity and cancer progression. To identify changes in the local conformations of the telomeric sequence upon interaction with small organic molecules, we incorporated 6-methylisoxanthopterine (6MI), a circular dichroism (CD)-active fluorescent base analogue of guanine in place of guanine at distinct positions in the human telomeric GQ sequence. Several variations of DNA sequences were used to monitor the conformational changes at different locations of the GQ structure using UV-Vis, CD, and fluorescence spectroscopic methods. Past studies investigated the binding of TmPyP4 (5,10,15,20-Tetrakis-(N-methyl-4-pyridyl) porphyrin), a telomerase-inhibiting ligand, to the GQ but only addressed their interaction in a global conformational perspective. In this study, we used fluorescent base analogues to track the local conformation at individual G-tetrad levels using spectroscopic methods. The results demonstrated an initial stabilization followed by destabilization of the human telomeric DNA sequence with increasing ratios of TmPyP4, whereas the modified strands showed stabilization or destabilization depending on the position of the probe. The results suggest that site-specific fluorescent probes can monitor the global and local structure and stability changes in GQs upon ligand binding. Understanding the effect of different drugs on the local GQ conformation will help to develop targeted drugs to treat cancer and other telomere-related diseases.

# SINGLE PROTON TIGHT COUPLING IN THE BACTERIAL FLAGELLAR MOTOR

**Anna Medici, Maddison Beahm, Claudia Decker, Andrew McGovern,
and Caden Kesselring**
**Department of Chemistry and Physics**

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

## ABSTRACT

Cell motility is a fundamental process crucial for various biological and physiological functions. At the heart of bacterial locomotion lies the bacterial flagellar motor (BFM), a highly efficient biological rotary motor. Understanding the mechanism behind torque generation in this motor is pivotal for elucidating numerous biological phenomena. The BFM, found in most bacteria, harnesses the power of protons ($H+$) in *Escherichia coli* (*E. coli*) or sodium ions ($Na+$) in Vibrio alginolyticus to generate torque, propelling cell movement. Compromising at least 40 different proteins, the BFM features a basal body connected to the flagellum via a flexible hook, surrounded by three cell envelopes and four protein rings forming the rotor. Notably, the Cytoplasmic ring (C-ring) and Supermembranous ring (MS-ring) constitute the torque generation site, composed of subunits FliG, FliM, and FliN. The precise movement relationship between the MS-ring and C-ring remains uncertain, though they are commonly assumed to rotate together. In *E. coli*, the presence of one to at least eleven torque-generating units known as stators along the C-ring perimeter has been observed. Each stator comprises copies of MotA and MotB forming proton transmembrane channels. These stators function independently, facilitating rotor rotation through conformational changes in MotA induced by proton flow. Experimental investigations, including high-concentration L-arabinose and resurrection experiments, were conducted to measure motor speed in real-time and estimate the associated proton count per motor revolution. Results indicate a single proton can generate enough force to produce the minimum torque, 4.3 Hz, required for a 13.7° rotation. As the *E. coli* cells incorporated more stators, their motor speeds increased stepwise at about 4 Hz. A singular proton exerts enough torque to complete one of the 26 discrete steps to complete a full flagellar rotation which supports a single-proton-based tight coupling mechanism.

CE-4

# ISOLATION OF AN APTAMER SELECTIVE TO GLUCOSE

**Deirdre Campbell**
**Department of Chemistry and Physics**

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

## ABSTRACT

Diabetes is a disease that hundreds of million people live with daily throughout the world. Although this is disease is typically not fatal, it can be if not treated properly. The day to day life of a person with diabetes consists of blood sugar monitoring by finger pricks, insulin injections and strict diet. The research for a glucose aptamer would be the first step to eliminate the need for all of this. This project uses Systematic Evolution of Ligands by Exponential Enrichment, or SELEX, to select RNA that binds specifically glucose. The process is a cycle beginning with a PCR from a pool of millions and billions different DNA sequences, then transcription to RNA, negative selection, positive selection, and reverse transcription back to DNA. The conclusion of the reverse transcription is the beginning of the next generation where each generation becomes more selective to glucose. Eventually the RNA would be sequenced and converted to a riboswitch. A riboswitch is a sequence of untranslated mRNA that can bind a specific ligand, in this case glucose, and transmit a signal to the expression platform to start the reaction to make a protein. For this project, the riboswitch would begin the production of insulin only in the presence of glucose. By making insulin outside of the pancreas, diabetes patients would no longer need insulin injections or constantly monitor their blood sugar levels. The project is currently on its 26th generation and is continuing to move forward. Once we obtain a high ratio of positive over negative cleavage percentages we will begin the process to clone DNA and individually test sequences to find an aptamer that cleaves only in the presence of glucose.

# CREATING A COST EFFICENT METHOD TO DETERMINE THEOPHYLLINE RIBOSWITCH ACTIVATION

**Thomas Hintelmann, Olivia Enny, Mika Schievelbein, James Tilton, Jonathan Ouellet**
**Department of Chemistry and Physics**

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

## ABSTRACT

A riboswitch is a small piece of RNA in structure that binds a molecule to itself to turn on or turn off a gene. As a result, riboswitch regulation provides an opportunity to develop targeted therapies for various diseases. Currently one of the only ways to determine activation of a riboswitch in an organism is to perform Fluorescent Activated Cell Sorting (FACS). This machine requires a large amount of upkeep and a trained technician to use. Most smaller research universities do not have the resources to be able to use this type of machine which greatly limits the amount of research that can be performed on riboswitches. This project is built based on 3 different cloning methods: Gibson assembly, golden gate assembly, and PCR assembly. To test this, the lab is currently taking plasmids and performing these assemblies using fluorescent genes, GFP-UV and mCherry, as well as the sequence for the theophylline riboswitch. Once these genes are cloned, the hope is to view under UV light which of the fluorescent genes are expressing. The amount of expression will be quantified using ratio-metric fluorescence. If GFP-UV and mCherry express this will tell that the theophylline riboswitch is active. If only mCherry is active this will tell theophylline is riboswitch is inactive. These measurements can be used to measure activation of other riboswitches as well.

**CE-6**

**THE CATALYTIC CHEMISTRY OF THE I-R3 DNA ENZYME THROUGH ION PROMOTED CLEAVAGE**

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

**ABSTRACT**

Deoxyribozymes are synthetically engineered short ssDNAs that function in hydrolyzing RNA. More recently, a small ssDNA enzyme was engineered to break the phosphodiester bond in DNA, that are important to the long-term storage of genetic information. For the single-stranded I-R3 DNA enzyme, the catalytic core of 17 nucleotides forms an asymmetrical bulge when it is annealed to its single-stranded DNA substrate. When this structure is in the presence of $Zn^{2+}$ under neutral pH, the substrate strand will be cleaved between two adenosines in positions A15 and A16, resulting in a 5' product and 3' product. At the discovery of the I-R3 DNA enzyme, $Zn^{2+}$ promoted cleavage activity, while $Cd^{2+}$, $Co^{2+}$, $Cu^{2+}$, $Ni^{2+}$, $Mn^{2+}$, $Ca^{2+}$, and $Mg^{2+}$ did not promote the cleavage activity to occur. This project is designed to study the cleavage behaviors of the I-R3 DNA enzyme through substituting different metal ions for zinc ions based on their similarities in atomic radii size to that of the zinc ions. The current hypothesis is that metal ions of similar atomic radii size to zinc ions may promote the cleavage activity of the I-R3 DNA enzyme. The chosen metal ions will be added to 100 pmol DNA enzyme, 10 pmol DNA substrate, 50 mM HEPES pH 7.05, and consistent salt concentrations after an initial annealing period. The sample will be quenched with a denaturing solution, ran on an acrylamide gel, and stained with SYBR gold to be analyzed by photodensitometry to find the percentage of cleavage. Understanding the correlations between metal ions and cleavage of the I-R3 DNA enzyme would have a significant impact on the understanding of deoxyribozymes and their overall catalytic function. This research could also have further biological and medicinal applications with targeting and cutting single-stranded viral DNA, such as parvoviruses.

# DEPARTMENT OF COMPUTER SCIENCE
# AND
# SOFTWARE ENGINEERING

CSSE-1

PARKSHARK

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

**ABSTRACT**

A common issue commuter college students deal with on a daily basis is struggling to find available parking at their college campuses. In addition, they are essentially forced to start their commute as early as possible before their upcoming classes, in hopes of finding a preferable parking spot.

With the implementation of a new parking app service, known as "ParkShark", we can revolutionize the commuter parking experience to make it stress free. This innovative service, with its integration of software, hardware known as "SharkTag", and cloud-based service, uses Bluetooth technology and GPS hardware to track parking spot occupancy in campus parking lots in real time. ParkShark significantly reduces the amount of time spent trying to locate open spots by giving students precise information about parking occupancy on a mobile app. SharkTags are stored in students' vehicles, acting as passive devices. It communicate with satellites to transfer data to the app in an accurate and efficient manner. The user interface of ParkShark shows real time parking spot availability updates, allows students to upload their personal information and class schedules, and offers GPS navigation, actuated by our custom backend that integrates with our database.. All of which allows students to plan and manage their commutes accordingly. ParkShark offers students an effective, user-focused solution to the persistent problem of finding parking spots, marking a new approach in campus parking management. ParkShark has the potential to take the lead as the preferred parking app for college commuter students across the country due to its innovative technology.

CSSE-2

# KICKS CORNER

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**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science
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## ABSTRACT

E-commerce and resell markets have become a focal point for many. We have seen companies like Amazon, StockX and Ebay become the powerhouses of the online shopping industry. All of us have an interest in athletic shoes and have gone through the issue of trying to navigate different websites trying to find the best price on a pair of shoes. This is where we got the idea to create Kicks Corner.

Our project will allow users to browse shoes along with being shown popular and recently searches shoes and see prices from multiple online shoe resell websites and purchase shoes from those websites directly from Kicks Corner. Registered users will also be able to trade shoes they own – sell or trade with users. Once a user uploads their shoes they can be used to make a trade within Kicks Corner. Users will be able to list shoes in their collection to trade which will be placed on the trade screen. Kicks Corner includes a messaging system where users will have the ability to message each other about trade details which can be seen under the user's account. Kicks Corner is a full-stack web application developed using Codeigniter php framework and using an opensource API in nodeExpress framework for searching popular shoes on the internet. The goal of Kicks Corner is to provide users with an all-in-one application where they can get the best deal on a pair of shoes or trade for another pair they want more.

# RUNSIGNUP DYNAMIC LEADERBOARD PROJECT

**Vincent Loretta and Connor Bennett**
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**Faculty Mentor: Dr. Raman Lakshmanan, Department of Computer Science and Software Engineering**

## ABSTRACT

RunSignup is a popular platform that provides a variety of services to clubs and organizations hosting running, bicycling, and endurance events, and fundraising campaigns. Users who choose to host a race are provided ample tools to create and manage their event registrations, payments, event scoring, and results publishing in the RunSignup platform. Specific to race events, race directors can view race finishing data scored by an electronic bib chip timing or manual entry, allowing all users to view relevant race data in a presentable leaderboard format.

RunSignup tasked us with creating a web application that allows users to navigate to their desired race and view race data. This was accomplished by utilizing RunSignup's public API and setting up our own unique and efficient query API implemented using GraphQL query language. The graphQL service is based on python Flask application framework. The frontend is React application coded in JavaScript, HTML, CSS, acting as GraphQL client. The frontend React application is responsible for querying GraphQL service for information to be displayed.

The RunSignup Dynamic Leaderboard allows users to navigate to their desired race by searching for their race of choice and choosing the events and result sets they would like to view. Upon selection, users can view either the individual or team results for their desired race making this application perfect for use at track meets or cross-country events. Race participants, audience members, and organizers can view the RunSignup Dynamic Leaderboard via the internet to see race results as they come in and can even project it onto a big screen to fully showcase the leaderboard to all individuals in attendance of a meet.

# A MACHINE LEARNING APPROACH TO MITIGATE INJURIES IN COLLEGIATE TENNIS PLAYERS

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**Faculty Mentor: Dr. Weihao Qu, Department of Computer Science
and Software Engineering**

## ABSTRACT

The aim of this research is to leverage Artificial Intelligence (AI), to bridge the gap between rapid technological advancements and their application in sports performance. Despite the widespread adoption of AI technologies in various sectors, their integration into sports performance optimization and injury prevention remains underexplored. This study focuses on utilizing AI to analyze and interpret collegiate tennis player's data—such as weight, workload, nutrition, and sleep—to accurately predict injury risks and enhance athletes' career longevity through optimized rest and training regimens.

To address this challenge, we propose to develop a Deep Learning algorithm capable of predicting potential injuries and future performance metric. We employed a methodology involving the distribution of 8 WHOOP devices among D1 tennis players of both genders and the comprehensive user data includes sleep duration, workout/match intensity and length, and physiological parameters. The study further explores the application of tailored advice generated by the ChatGPT API to mitigate identified injury risks, thereby offering a novel approach to personalized athlete care and training optimization.

We anticipate that our findings will demonstrate the significant benefits of AI in transforming athlete training and health management. The expected outcomes include an accurate algorithm for injury risk prediction and the ability to deliver customized injury prevention advice. This technology benefits both athletes and coaches. Athletes can better understand and manage their training load, optimizing performance while minimizing injuries. Coaches gain valuable insights into athletes' stress levels, enabling them to tailor training programs for maximum benefit and longevity, and modify their lineups to get the most competitive team for upcoming matches.

**CSSE-5**


**PENETRATION TESTING OPERATING SYSTEMS:**
**EXPLOITING VULNERABILITIES**

**Evan Gardner**
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**Faculty Mentor: Dr. Weihao Qu, Department of Computer Science**
**and Software Engineering**

**ABSTRACT**

In today's digital age where technology permeates every aspect of human civilization the safeguarding of critical data stored on devices like phones, computers, and tablets against unauthorized access has emerged as a paramount concern. As we increasingly depend on these devices for both productivity and personal affairs, the question of how to protect the vast collections of sensitive information they contain becomes crucial. Information safety against unauthorized access is a critical area in cybersecurity which is addressed through the discipline of penetration testing. This practice involves security researchers simulating adversarial attacks to assess the defenses of various technological systems, including web applications, operating systems, networks, and more, to secure sensitive data from malicious entities. This research focuses on exploring operating systems, specifically Windows and Linux, without requiring login credentials, utilizing specific methods like command combinations in languages such as BASH within the terminal to access admin accounts. These command combinations are made in conjunction with penetration testing devices including a USB Rubber Ducky to emulate keystrokes on a machine emphasizing speed and efficiency. This research highlights significant security vulnerabilities that, if exploited, could lead to severe consequences not just for individual devices but for entire networks and critical infrastructures such as core businesses, schools, or governments. By identifying and mitigating these vulnerabilities the research is planned for the application of our findings to strengthen security protocols that aim to bolster our technological defenses. Strengthening security protocols includes introducing system administration security enhancements creating a futile ability to access the root terminal from an unauthorized state. Thus, this contribution to safeguarding digital domains against continuously evolving cyber threats ensures the safety and integrity of individual and collective digital functions.

# A DOMAIN SPECIFIC LANGUAGE FOR DIFFERENTIAL PRIVACY SQL

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**Faculty Mentor: Weihao Qu, Department of Computer Science**
**and Software Engineering**

## ABSTRACT

The wide use SQL language and its urging privacy needs make it a hot research topic, in particular, at the industry level. The research project focuses on developing a specialized language, DPDSL, for differential private querying to enhance privacy protection in data queries. It aims to address the challenges faced in ensuring privacy in data queries, especially when using standard SQL methods. By introducing concepts like potential risky queries, customized privacy budget management at the column level, and noise addition strategies, the project aims to provide a systematic way to detect and rewrite queries to ensure data security while maintaining query expressiveness and flexibility.

Significant difficulties with differential private querying systems have been noted by earlier researchers. These difficulties mostly relate to efficiently managing privacy budgets and making sure that noise is applied appropriately to safeguard sensitive data. Existing techniques, such as Chorus, are limited by budget management and SQL-style complexity.
To overcome this, we propose DPDSL, a specialized language enabling column-level customization of privacy budget management. Based on the language, we have a query rewriting tool which rejects potentially dangerous queries. By introducing ideas like query rejection and personalized budget management, it also expands the flexibility of querying while establishing new benchmarks for sensitive data security. Through the concept of differential private querying—which includes introducing controlled noise to query results to disguise sensitive information while allowing for meaningful analysis, our system presents a novel method for protecting sensitive data. We plan to evaluate our system in the real-world databases.

# STATIC ANALYSIS TOOLS DETECTING DLL INJECTIONS AND CHECKING FILE INTEGRITY

**Jack Berkowitz**
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**Faculty Mentor: Weihao Qu, Department of Computer Science
and Software Engineering**

## ABSTRACT

Dynamic Link Libraries(DLLs) are components in the Windows operating systems, used for code modularity, rescue, and efficient resource management across different applications. For instance, most famous applications use the pop-up windows function, which adopts DLLs to save time and reduce the repetition of code. DLLS are dynamic in nature because they are accessible to all applications. However, this dynamic nature also introduces security vulnerabilities, most known is injection techniques. DLL injection involves the insertion of malicious code in the DLL address space. Allowing attackers to manipulate or even compromise system behavior.

This issue has not been fully understood, there is no tool to detect potential risks that some programs may cause for the DLLs, which may allow unauthorized access to windows machines. To prevent that event from occurring, the need to validate the location of these files is needed. To fill this gap, we propose a system which is able to statically detect potential risky DLLs of arbitrary apps on a Window machine. Our system finds out these "risky" DLLs by comparing the locations of DLL Files that are referenced by a program to a past list of DLLs. Static analysis over these lists, any deviations or alterations in their locations can be found, indicating potential tampering or injection. This approach enhances systems security by enabling the identification of unauthorized modifications to critical DLL files. Our system will be evaluated on real Windows machines under certain injection attacks on DLLs on various commonly used software such as Steam, Chrome, Facebook and so on.

# INGREDIENT LENS: FOOD RECOGNITION AND RECIPE GENERATION

**Dmitry Bezborodov, John Costa, Andrew Catapano, Jack Berkowitz**
**Department of Computer Science and Software Engineering**

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

## ABSTRACT

Artificial Intelligence (AI) is at the forefront of modern computer science, playing a crucial role in various aspects of our lives such as information retrieval, entertainment choices, and targeted advertising. It also has infinite applications that can transform industries and daily tasks. One such application is training AI to recognize human faces, animals, and objects in images. Our AI Food Recognition Application aims to use AI image recognition to identify a food item and provide a recipe on how to make it.

The application prioritizes user-friendliness and ease of use. After a user uploads a photo, the Image Classification Model recognizes the dish and provides a recipe on how to prepare it. The project's architecture consists of a cloud database as the backend, along with APIs that can invoke and utilize the model for dish identification. Each user can create an account that stores a history of their generated recipes, as well as their allergies and dietary restrictions, which can be set in their account settings to personalize their recipes. Once the dish is analyzed and a recipe is generated, logged-in users can conveniently store all generated labels and recipes in their account's history, accessible for future reference. This personalized approach significantly enhances user engagement and satisfaction, making the AI Food Recognition Application a handy tool for food lovers and cooking enthusiasts.

CSSE-9

# DEVSLIST: A RECRUITMENT PLATFORM FOR DEVELOPERS

**Joseph Furmanowski, Evan Gardner, Tyler Gennaro, Daniel Lawrie**
**Department of Computer Science and Software Engineering**

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

## ABSTRACT

The DevsList web application aims to simplify the job and internship search process for students and developers while providing employers with an efficient way to identify qualified candidates. This topic was chosen after recognizing the challenges faced by Monmouth's CSSE students in securing internships. Many students have discussed their struggles in finding job opportunities and differentiating themselves from other applicants. Some students even found that their employers expressed complaints about difficulties finding suitable candidates. The root of these challenges is the limitations of existing job search platforms. Many of these platforms lack essential features considered crucial in the job search process. For instance, popular platforms like LinkedIn lack interactive job maps and a simplistic application process.

The vision for DevsList is to serve as an all-in-one solution that eliminates the need to navigate between various websites when searching for the right job. The goal is to assist individuals facing difficulties finding jobs and provide them with a seamless experience, avoiding the challenges that many students have encountered. DevsList aims to be a valuable resource for all aspiring and current software engineers, helping them discover meaningful career opportunities, internships, and freelance projects. The implementation of this application utilized several current techniques, including NEXT.js, Tailwind CSS, MySQL, web scraping, and more.

# DEPARTMENT OF MATHEMATICS

# ANALYZING THE EFFECTIVENESS OF MONMOUTH UNIVERSITY'S MATH PLACEMENT EXAM

**Malea Horn-Attanasio, McKayla Miksza and Rachel Vassallo**
**Department of Mathematics**

**Faculty Mentor: Dr. Richard Bastian, Department of Mathematics**

**Client: Dr. Susan Marshall, Department of Mathematics**

## ABSTRACT

This project examines the effectiveness of Monmouth University's Math Placement Exam in assigning students to their first math courses by looking at the students' midterm and final grades in their assigned courses. Designed by Dr. Susan Marshall, the chair of the math department at Monmouth University, this project's data consists of 124 students, who either scored a 1, 2, 3, or 4 on the exam which determined their place in a specific level course. The data was analyzed by class, and students who received a grade of a C- or higher were considered to be successfully placed in their course by the exam.

# DEFINING A CANCER CLUSTER

**Kyle Broesler, Anthony Stirone and Matt Wolyn**
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**Faculty Mentor: Dr. Richard Bastian, Department of Mathematics**

**Client: Dr. Pedram Daneshgar, Department of Biology**

## ABSTRACT

Cancer is at the forefront of importance in the United States due to its frequency among the population. For that reason, it is crucial to do research to get a better understanding and ultimately get closer to finding cures. To this end it is essential to understand certain factors that can go into someone potentially getting cancer. A few possible ways can be genetics, stress, physical factors, or even environmental factors. The goal of this study is to determine if there are any clues to what defines a cancer cluster for a given area. In this observational study, cancer counts were taken from 2016 to 2020 by the CDC relative to the population within each state. Cancer counts were given for forty-eight specific areas within the United States, detailing cancer cases for the total population, five different ethnicities, and two genders within the given areas. The forty-eight areas are mostly states, with Puerto Rico and the District of Columbia being the exceptions. The five ethnicities consist of Asians, Native Americans, African-Americans, Hispanics, and Whites. This study employs Poisson Regression, which is a statistical test that models the relationship between the expected count of data and explanatory variables that are believed to influence the count. Determining how to categorize a cancer cluster can be difficult, but certain explanatory variables like gender, ethnicity, and area can potentially change the outlook on how cancer arises.

MA-3

# PRELIMINARY ANALYSIS IN UNDERSTANDING PROBLEM BEHAVIOR IN DOGS AND CATS

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**Department of Business**

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**Client: Dr. Lindsay Mehrkam, Department of Psychology**

## ABSTRACT

Owners face many challenges when it comes to taking care of their pets. To understand why these problems occur, a survey was conducted on various questions pertaining to pet demographics, attachment levels, problem behavior levels, owner demographics and attitudes towards behavior programs. The survey was sent to an email contact list and posted through social media by the Monmouth University Polling Institute. A sample of 196 dog owners and 143 cat owners was collected. Various hypotheses will be carried out in order to understand if pet demographics and attachment levels predict the problem behavior level. These conclusions can then benefit trainers for creating behavior programs to aid in the challenges owners face based on the demographics of the pet.

# STATISTICAL ANALYSIS OF THE TPLO ON CANINE MENISCUS TEARS

**Jane Zink**
**Department of Mathematics**

**Anna Dos Santos**
**Department of Chemistry & Physics**

**Sarah Henry**
**Department of Biology**

**Faculty Mentor: Dr. Richard Bastian, Department of Mathematics**

**Client: Dr. Garrett Davis and Dr. Aixa Gonzalez, Red Bank Veterinary Hospital**

## ABSTRACT

One of the most common surgical procedures performed on canines is the tibial plateau leveling osteotomy, or TPLO, which incises a portion of tibia bone for stifle joint realignment following a cranial cruciate ligament tear (CCL). In some of these canines, a meniscus tear may occur in the stifle following the TPLO, thus necessitating a second surgery which exacerbates recovery for the canine and introduces financial complications for the owner. This project serves to identify canine predispositions and procedural variations in the TPLO that may raise the risk of post-surgery meniscus tears, in hopes that protocol modifications may be adopted to help prevent the second tear. Statistical techniques like logistic regression are used to analyze veterinary hospital records, investigating relationships between variables such as pre- and post-operative tibial plateau angles (TPA), blade size, and canine weight for their ability to predict the probability of a meniscus tear. It is hypothesized that during incision, if the TPA is insufficient in leveling the tibia, instability may occur as the stifle readjusts and may increase the risk of a meniscus tear.

**MA-5**

# A NUMERICAL INVESTIGATION OF AN ADAPTIVE POWER SERIES APPROXIMATION TO COMPARTMENTAL MODELS

**Brooke Tortorelli**
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**Faculty Mentor: Dr. Joseph Coyle, Department of Mathematics**

## ABSTRACT

Compartmental modeling is frequently used as a model technique when the variables of interest can be grouped into distinct categories or compartments. This is typically the case when simulating the spread and behavior of infectious diseases.

When the resulting differential system is coupled in a nonlinear way, numerical techniques are often the only way to approximate the true solutions. Here, we employ a power series approximation demonstrating a way to estimate the radius of convergence as part of an adaptive technique for long term approximations.

# AN EXPLORATION INTO THE LATTICE HERONIAN KITES AND RHOMBI

**Eliana L. Joskowski**
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**Faculty Mentor: Dr. Susan H. Marshall, Department of Mathematics**

## ABSTRACT

A quadrilateral is *Heronian* provided that each side length and the area are integers, and it is *lattice* if it can be placed in the xy-plane so that its vertices have integer coordinates. Building on previous student work with parallelograms, we discovered not all Heronian rhombi are lattice, and we found necessary and sufficient conditions for a Heronian rhombus to be lattice based only on its side length and area. We then explored Heronian kites with two right angles, commonly known as *Heronian right kites*. We determined that there are infinitely-many Heronian right kites but not all are lattice. We proved a necessary and sufficient condition for Heronian right kite to be lattice based solely on its side lengths, which allowed us to show that there are infinitely-many lattice Heronian right kites. Our next direction is to study Heronian kites in general.