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MONMOUTH
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SCHOLARSHIP WEEK

23rd ANNUAL

SCHOOL OF SCIENCE

STUDENT RESEARCH

CONFERENCE

APRIL 18, 2025

Featuring Poster Presentations
of Student Research

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



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MONMOUTH
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SCHOLARSHIP WEEK

School of Science Student Research Conference

Friday April 18, 2025

E 201

Science Building Multipurpose Room

Agenda

- | | |
|----------------------------|--|
| 10:00 am – 11:00 am | Registration and Poster Set-up |
| 11:00 am – 11:15 am | Welcome and Opening Remarks

Dean Joe Coyle |
| 11:15 am – 11:45 am | Keynote Address

KerryAnn Kelly '18 '19M |
| 11:45 am – 1:45 pm | Poster Presentations of Student Research
From the School of Science |
| 1:45 pm – 2:30 pm | Closing Remarks
Presentation of the Dean's Awards
for Excellence in Undergraduate Research

Dean Joe Coyle |

SCHOOL OF SCIENCE
2025 STUDENT RESEARCH CONFERENCE

DEPARTMENT OF BIOLOGY

BY-1 Comparing Citizen Scientist and Laboratory eDNA Protocols: Assessing DNA Yield and the Impact of Shipping Time

Alexis Baumgartner, Jason Adolf, Erin Conlon
Faculty Mentor: Dr. Jason Adolf

BY-2 First Record of the Sea Anemone *Actinia equina* (Cnidaria: Anthozoa) on the Mid-Atlantic Coast of the United States

Diederik Boonman¹, Craig Stephen Wilding², James T. Carlton³ and Jason E. Adolf¹
Faculty Mentor: Dr. Jason Adolf

BY-3 Fish Community Analysis using eDNA Metabarcoding Data from New Jersey's Coastal Lakes

Dylan DiBella
Faculty Mentor: Dr. Jason Adolf

BY -4 Characterization of *Sarracenia purpurea purpurea* Communities in the New Jersey Pine Barrens

Paul X. Santarsiero and Sage M. Phelps
Faculty Mentors: Dr. Pedram P. Daneshgar and Dr. Kevin P. Dillon

BY-5 Critical Analysis of U.S. Federal Plastic Laws and Regulations

Nitika Girish and Marelyn Natividad
Faculty mentor: Dr. Peter Jacques

- BY -6** **Cypress Essential Oil Limits Proliferation and Activates Apoptosis Signaling**
- Angelo Prado, Nicholas Tamburro, Michael Catalfumo, Michael DeCarlo, and Warda Chowdhury**
Faculty Mentor: Dr. Dorothy Lobo
- BY-7** **Hypoxia Decreases Proliferation of Fibrosarcoma Cells And Activates JNK**
- Michael Catalfumo and Nicholas Tamburro**
Faculty Mentor: Dr. Dorothy Lobo
- BY-8** **Isolating Polyethylene-Degrading Bacteria from Populated Jersey Shore Waterfronts**
- Alexa Ford, Julia Mandarino, Joe Pellicone, and Matt Snyder**
Faculty Mentor: Dr. Karen Pesce
- BY-9** **Assessing Nesting and Reproductive Vulnerabilities of Diamond-backed Terrapins at Sandy Hook National Recreation Area, Fire Island National Seashore, and Sagamore Hill National Historic Site**
- Kathryn A Marshall, Rebecca J. Berzins, Karissa I. Hough, and Sean C. Sterrett**
Faculty Mentor: Dr. Sean Sterrett
- BY-10** **The Use of Nutraceuticals (Piperine and Soursop) to Selectively Treat Cancers of the Oral Cavity**
- Julia Rice**
Faculty Mentor: Jeffrey H. Weisburg, Ph.D.
- BY-11** **Addressing Antimicrobial Resistance Using Endophytic Fungi As A Source Of Novel Anti-Infective Compounds**
- Sophia Guagliano, Alexander Kalina and Nicole Secondino**
Faculty Mentor: Professor Jon Polishook

BY -12

Antibiotic Potential of Endophytic Fungi from Avocado (*Persea Americana*) skins and Tamarind (*Tamarindus indica*) Shells

Jenifer Yax-Monroy, Nicole Raczkowski, Estellsy Acuahuatl and Joseph Pellicone

Faculty Mentor: Professor Jon Polishook

DEPARTMENT OF CHEMISTRY AND PHYSICS

**CE-1 CurveIQ: A Systematic and Rigorous Approach for Assessing the
Thermodynamic Stability of Macromolecular Structures**

**Omar W. Ahmed
Faculty Mentor: Dr. Davis Jose**

**CE-2 A Spectroscopic Evaluation of the B to A Conformational Transition in
Duplex DNA Using Fluorescent Base Analogues**

**Maria J. Hernandez Campos, Noureen Qureshi and Samantha LeCrone
Faculty Mentor: Dr. Davis Jose**

**CE-3 Investigating Local Conformational Changes from Ligands on G-
Quadruplex Complexes Using Fluorescent Base Analogues**

**Macklin Jugan and Matthew Finkelstein
Faculty Mentor: Dr. Davis Jose**

**CE-4 An Investigation of the Substitution Behavior and the Cytotoxicity of
Quinoline-8-Carboxaldehyde and Related Complexes**

**Lyndsey Buren
Faculty Mentor: Dr. Greg Moehring**

CE-5 Isolation of an Aptamer Selective to Glucose

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

CE-6 PLMVd and Circular RNA

**Anahi Menendez
Faculty Mentor: Dr. Jonathan Ouellet**

CE-7 Hammerhead Ribozyme Cleaving its RNA Substrate

**Ashley Salguero
Faculty Mentor: Dr. Jonathan Ouellet**

DEPARTMENT OF COMPUTER SCIENCE AND SOFTWARE ENGINEERING

CSSE-1 Beyond Accuracy: A Mock AI Audit For Fair And Transparent Insurance Cost Prediction With Low-Code And No-Code

Sushika Reddy Gade

Faculty Mentor: Professor Arup Das

CSSE-2 PARKSHARK Administration: The Future Of Campus Parking Management

Michael Ivanicki, Gianna Rao, Jodan Elysee, Maheen Ghaffar, Ryan Basile, Brendan Curiale

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-3 PARKSHARK Intelligence: Precision Parking Powered By Smart Data

Omar Ahmed, Zakariya Ahmed, Jenna Esposito, Nicholas Genardi, Flavia Daniels, Garrett Boag

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-4 PARKSHARK Mobile: Transforming Campus Parking With Smart Technology

Andrew McGovern, Anjali Narang, Aaila Arif, Bryn Bijur, Tennessee Tremain, Adnan Hoti

Faculty Mentor: Dr. Raman Lakshmanan

CSSE-5 Cybersecurity Challenges and Solutions in the Metaverse: Penetration Testing, AI Spoofing and Phishing, and the Impact of Emerging Identity Verification Technologies

Gurmeet Singh

Faculty Mentor: Dr. Weihao Qu

CSSE-6 Forecasting Climate Trends: A Multi-Source Analysis of Global Climate Change Using NLP, Topic Modeling, and Time Series Forecasting

Krishna Khandelwal

Faculty Mentor: Dr. Jiacun Wang & Professor Arup Das

CSSE-7 Luxé: A Virtual Fashion Platform

**Estania Blanc Doblas
Faculty Mentor: Dr. Cui Yu**

CSSE-8 Monmouth University Tutoring Services

**Mar Elbanna, Sean Fritz, Ez Racancoj, Vincent Tuberion, Justin Vunic
Faculty Mentor: Dr. Cui Yu**

DEPARTMENT OF MATHEMATICS

MA-1 Water Quality Across Monmouth County Coastal Lakes

**Alexander Metz, Anthony Stirone, Brandon Govea, and Olivia Fowles
Faculty Mentors: Dr. Jason Adolf & Dr. Richard Bastian**

MA-2 Invasive Plant Species Effect On Terrapin Nest Sites

**Vincent Macri and Jason Sullivan
Faculty Mentors: Dr. Richard Bastian and Dr. Pedram Daneshgar**

MA-3 An Analysis of the Pelvis Over Time

**Sarah Henry, Malea Horn-Attanasio, and Matthew Muller
Faculty Mentors: Dr. Hillary Delprete and Dr. Richard Bastian**

**MA-4 Harmonic Content of String Networks: A Physical Application of Quantum
Graphs**

**Miriam Abecasis
Faculty Mentor: Dr. Torrey Gallagher**

**MA-5 Periodic Analysis of Simulated Orbits Using the Fast Fourier Transform
(FFT)**

**Jason French and Felipe Marcal
Faculty Mentor: Dr. Torrey Gallagher**

DEPARTMENT OF BIOLOGY

BY-1

**COMPARING CITIZEN SCIENTIST AND LABORATORY eDNA
PROTOCOLS: ASSESSING DNA YIELD AND THE IMPACT OF
SHIPPING TIME**

Alexis Baumgartner, Jason Adolf, Erin Conlon

Department of Biology and Urban Coast Institute

Faculty Mentor: Dr. Jason Adolf

ABSTRACT

This study aimed to evaluate two questions: How effective is the citizen scientist's eDNA sampling method in obtaining quality DNA results compared to the standard lab method? And is shipping time causing lower DNA quality when using the citizen scientist method? Three groups of five water samples were collected from the same body of water: the first for the standard lab method (LP), the second for the standard citizen science method (CRT), and the third for the citizen science method without shipping time (CF). All samples underwent the same extraction, amplification, and detection procedures and received values for the quantity of DNA fragments found, taxa richness, and the relative abundance of a specific species. A total of 44 taxa were identified among all three filter types. CF identified 6 unique taxa, CRT identified 2 unique taxa, and LP identified 3 unique taxa. A significant difference in taxa richness and DNA concentration was found between the citizen science method without shipping time (CF) and the standard citizen science method (CRT). No significant difference in richness and DNA concentration was observed between CRT and LP or between CF and LP. By enabling the general public to participate in scientific sampling, the scientific community can greatly expand the scope of data collection. However, it is essential to ensure that the data collected by citizen scientists maintains high quality to support credible research outcomes.

BY-2

FIRST RECORD OF THE SEA ANENOME ACTINIA EQUINA (Cnidaria: Anthozoa) ON THE MID-ATLANTIC COAST OF THE UNITED STATES

Diederik Boonman¹, Craig Stephen Wilding², James T. Carlton³ and Jason E. Adolf¹

Department of Biology

Faculty Mentor: Dr. Jason Adolf

ABSTRACT

Members of the genus *Actinia* are familiar members of rocky shore communities across much of the world. However, to date, no *Actinia* species have been reported from the North American continent. Here, we report *Actinia* from an approximately 22 km length of the New Jersey, US shoreline, where it was first discovered in 2021. Morphology and DNA barcoding data (mitochondrial cytochrome c oxidase I and nuclear internal transcribed spacer) indicate that these populations are *Actinia equina*. The presence of these populations close to major ports in New Jersey, New York, and Philadelphia suggests a probable introduction from shipping activities.

BY-3

**FISH COMMUNITY ANALYSIS USING eDNA METABARCODING DATA
FROM NEW JERSEY'S COASTAL LAKES**

Dylan DiBella

Department of Biology

Faculty Mentor: Dr. Jason Adolf

ABSTRACT

Coastal lakes are unique ecosystems, containing mostly freshwater with some saltwater influence from nearby oceans. Little research has been conducted looking at the current state of fish assemblages in New Jersey's coastal lakes. Investigating coastal lake fish communities is essential for understanding the health, function, and conservation of this ecosystem. We used R-Studio to analyze eDNA metabarcoding data collected from two of New Jersey's coastal lakes, Deal Lake and Sunset Lake. Using this data, we were able to identify what species' DNA were present in the lakes and calculate the relative abundance of each species identified. The abundance of species varied greatly between the two lakes. The most abundant species in Deal Lake were bluegill (*Lepomis macrochirus*), American gizzard shad (*Dorosoma cepedianum*), and white perch (*Morone americana*) and the most abundant species in Sunset Lake were brown bullhead (*Ameiurus nebulosus*), pumpkinseed (*Lepomis gibbosus*), and golden shiner (*Notemigonus crysoleucas*), respectively. We conducted multivariate analyses using environmental data collected alongside the eDNA metabarcoding data. This allowed us to investigate how factors such as season, location, and water quality influence the coastal lake fish communities. These findings emphasize the need for further research investigating fish communities in coastal lakes and the factors that influence community composition.

BY-4

**CHARACTERIZATION OF *Sarracenia purpurea purpurea* COMMUNITIES
IN THE NEW JERSEY PINE BARRENS**

Paul X. Santarsiero and Sage M. Phelps

Department of Biology

Faculty Mentors: Pedram P. Daneshgar and Kevin P. Dillon

ABSTRACT

The northern purple pitcher plant (*Sarracenia purpurea purpurea*) is a carnivorous plant species found in the New Jersey Pine Barrens. To survive and reproduce in soil that is nutrient poor and acidic, the purple pitcher plant employs carnivory to capture insects, thus supplementing its nutrient supply. The insects are captured in specific water-filled phytotelma: large cone shaped leaves, or “pitchers”. Insects attracted to the pitcher plant for its water source, fragrance, rewards, or its associated biotic community could eventually fall in, drown, and then become a source of nutrients for the plants. Purple pitcher plants are classified as inactive carnivores as they do not directly digest the insects but instead rely on a diverse community of microbes to break down the insects. This project aims to better understand the microbial community composition and dynamics of pitchers across the Pine Barrens. Seasonality, local environment, plant health, and external sources were examined as predictors of community composition. In June and July 2024, seven field sites throughout the NJ Pine Barrens were established for periodic monitoring and sampling. In June/July and October 2024, pitchers and pitcher fluid were sampled to characterize the microbial populations through cultivation-dependent and cultivation independent characterization. Bacteria including *Chromobacterium vaccinii*, *Rahnella aquatilis*, and others were cultivated and isolated from pitchers plants. Marker-gene surveys characterizing the bacterial (16S rRNA gene) and fungal (ITS region) communities were conducted as well. This preliminary work will shed light on factors affecting community assembly, succession and dynamics.

BY-5

CRITICAL ANALYSIS OF U.S. FEDERAL PLASTIC LAWS AND REGULATIONS

Nitika Girish and Marelyn Natividad

Department of Biology

Faculty mentor: Dr. Peter Jacques

ABSTRACT

Plastic pollution has become a global issue, affecting ecosystems, wildlife, and human health. The widespread use of plastic, particularly single-use items, has led to an overwhelming amount of waste that has been difficult to manage. Most plastics are non-biodegradable, causing them to accumulate in oceans, rivers, and landfills. Marine life has been very vulnerable, as animals tend to ingest or become entangled in plastic debris. Beyond environmental harm, plastics contain harmful chemicals that can also enter the food chain, into our systems. Addressing this crisis has become important in order to maintain our planet and shift towards a sustainable future.

This research examines the evolution and impact of federal plastic-related laws and regulations, with a particular focus on the relevant provisions outlined in the United States Code of Federal Regulations (CFR). As plastic waste and pollution continue to pose significant environmental challenges, federal regulations have become a critical tool in managing plastic production, disposal, and recycling. This study analyzes the structure and scope of existing federal policies governing plastic materials, from production standards to waste management and recycling mandates. Special attention is given to the Environmental Protection Agency's (EPA) role in regulating plastic waste, as well as the U.S. Food and Drug Administration's (FDA) oversight of plastic materials used in food contact applications. The research also explores recent legislative efforts to strengthen plastic pollution mitigation, including the Plastic Waste Reduction Act. By evaluating the effectiveness of these regulations, this study seeks to provide a comprehensive understanding of federal plastic pollution policy, its enforcement mechanisms, and its potential for driving sustainable practices in the plastic industry. The findings contribute to ongoing debates on the need for reform in federal plastic laws, offering recommendations for more effective regulation and governance of plastic materials in the United States.

BY-6

**CYPRESS ESSENTIAL OIL LIMITS PROLIFERATION AND ACTIVATES
APOPTOSIS SIGNALING**

Angelo Prado, Nicholas Tamburro, Michael Catalfumo, Michael DeCarlo, and

Warda Chowdhury

Department of Biology

Faculty Mentor: Dr. Dottie Lobo

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. These include: α -pinene (48.6%), δ -3-carene (22.1%), limonene (4.6%) and α -terpinolene (4.5%) which are the main components comprising 79.8% of the oil. A cell line of HT-1080 (fibrosarcoma) cells were treated with cypress essential oil at different concentrations and the effects were determined. Proliferation was measured by direct cell counting using trypan blue dye exclusion and MTT assay. Proliferation of HT-1080 fibrosarcoma cells demonstrated a significant decrease with increased concentration of cypress essential oil. In addition, high concentrations of cypress essential oil also decreased MTT activity which therefore confirmed a decrease in viability due to essential oil treatment. To determine if the decrease in viability was due to apoptosis, PARP cleavage was measured, and confirms apoptosis in both normal fibroblasts and fibrosarcoma cells. Apoptosis also appears to be correlated with the activation of JNK in both cell lines, indicating that this stress-signaling pathway is activated by cypress essential oil treatment.

BY-7

HYPOXIA DECREASES PROLIFERATION OF FIBROSARCOMA CELLS AND ACTIVATES JNK

Michael Catalfumo and Nicholas Tamburro

Department of Biology

Faculty Mentor: Dr. Dorothy Lobo

ABSTRACT

Hypoxia is characterized as a state in which tissues become oxygen deprived. Under hypoxic conditions, proteins called Hypoxia-Inducible Factors (HIFs) become activated, and in turn, regulate the expression of downstream genes. Cobalt chloride (CoCl_2) has been used in many cell types to stimulate the activation of HIF-1 α and thus chemically mimic creation of a hypoxic environment. The purpose of this study was to determine if CoCl_2 could create a hypoxic environment in HT-1080 fibrosarcoma cells, and to determine the effect of hypoxia on downstream signaling and 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 α 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 α occurred after 24 hours. To study the effect of 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 with untreated cells serving 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.

BY-8

**ISOLATING POLYETHYLENE-DEGRADING BACTERIA FROM
POPULATED JERSEY SHORE WATERFRONTS**

Alexa Ford, Julia Mandarino, Joe Pellicone, and Matt Snyder,

Department of Biology

Faculty Mentor: Dr. Karen Pesce

ABSTRACT

The world is currently producing about 430 million tonnes of plastic per year, which is contributing to the widespread pollution. Synthetic plastics such as polyethylene (PE) and polypropylene (PP) are particularly problematic because of their resistance to natural degradation processes and their tendency to breakdown into microplastics. Microplastics can accumulate in landfills or natural environments, particularly in aquatic ecosystems, where they pose significant risks to biodiversity and human health. In the human body, microplastics can cause damage to the respiratory, nervous, immune, and gastrointestinal systems. Polyethylene is a commonly used plastic component in food packaging. Certain bacterial species, such as *Pseudomonas*, contain an *alkB* gene that encodes for alkane-1-monooxygenase, which seems to play a key role in polyethylene degradation. Soil and water samples were collected from 7 sites through Monmouth and Ocean Counties in NJ and analyzed to determine if polyethylene degrading bacteria were present. Bacteria were cultured in minimal media supplemented with low-density polyethylene (LDPE). DNA was isolated and PCR of the *alkB* gene was conducted. Bacterial *alkB* genes were found in five of the nine sites - Compton Creek, Lake Lefferts, Shark River, Swimming River Park, and Windward Beach. The presence of this gene suggests that local microbial communities have the necessary metabolic capabilities to break down LDPE. These findings emphasize the potential for biological solutions to plastic pollution, particularly in natural environments.

**ASSESSING NESTING AND REPRODUCTIVE VULNERABILITIES OF
DIAMOND-BACKED TERRAPINS AT SANDY HOOK NATIONAL
RECREATION AREA, FIRE ISLAND NATIONAL SEASHORE, AND
SAGMORE HILL NATIONAL HISTORICAL SITE**

Kathryn A Marshall, Rebecca J. Berzins, Karissa I. Hough, and Sean C. Sterrett

Department of Biology

Faculty Mentor: Dr. Sean Sterrett

ABSTRACT

The Diamond-backed Terrapin (*Malaclemys terrapin*; DT) is the only turtle species found in coastal, brackish waters in the U.S., across its range from Massachusetts to Texas. DT faces significant challenges due to human recreation, climate change, and road mortality, which disproportionately affect nesting females. We used beach nesting surveys and camera traps at three National Park Service sites to map the spatial distribution of nests, quantify the female breeding population, and identify nesting vulnerabilities of DT. In 2023, we observed 13 live adult terrapins and 277 depredated nests at Sandy Hook National Recreation Area. In 2024, we observed 10 live adults and 205 depredated nests at Fire Island National Seashore and Sagamore Hill National Historic Site. While predators like red foxes and raccoons were identified, human activities, especially recreational use of nesting areas, emerged as a significant threat, especially at Sandy Hook. During the study, we observed 203 leashed and unleashed dogs, with some engaging in behaviors such as digging, barking, or splashing within designated search zones. These findings underscore the need for enhanced, seasonal proactive conservation measures to mitigate the impacts of both natural and anthropogenic threats on DT, especially with the looming threats of climate change.

BY-10

**THE USE OF NUTRACEUTICALS (PIPERINE AND SOURSOP) TO
SELECTIVELY TREAT CANCERS OF THE ORAL CAVITY**

Julia Rice

Department of Biology

Faculty Mentor: Jeffrey H. Weisburg, Ph.D.

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. Piperine, an extract from black pepper, is an alkaloid with a long history of medicinal use. In fact, it exhibits a variety of biochemical and pharmaceutical properties, including chemopreventive activities without significant cytotoxic effects on normal cells. It has been shown to inhibit multidrug resistance by modulating drug efflux transporters like P-glycoprotein, thereby enhancing the bioavailability and efficacy of various therapeutic agents. Piperine consists of a conjugated piperidine ring and a methylenedioxy functional group, which contribute to its ability to modulate biological pathways, particularly in reactive oxygen species (ROS) generation, enzyme inhibition, and cellular signaling. Piperine has been shown to have these antiproliferative and proapoptotic properties in breast cancer cell lines. Another strong nutraceutical is Graviola, also known as soursop. The active components of soursop, primarily Annonaceous acetogenins (AAGs), are a group of long-chain fatty acid derivatives with terminal γ -lactone rings and multiple hydroxyl functional groups. Acetogenins, such as annonacin and bullatacin, inhibit complex I of the electron transport chain (ETC) in mitochondria, increasing superoxide (O_2^-) and hydrogen peroxide (H_2O_2) production. Soursop has been also shown to induce apoptosis in breast and colorectal cancer cell lines. In these experiments, piperine and soursop will be used to see if they could selectively target and kill cancers of the oral cavity, using the human squamous carcinoma HSC-2 cells as compared to human normal gingival fibroblast cell HF-1. Initial findings with piperine have shown that it selective kills HSC-2 cancer cells (IC₅₀ 80 mg/mL) while sparing the HF-1 normal cells (IC₅₀ 750 mg/mL). As the production of reactive oxygen species is a typical mechanism of action of nutraceuticals, cellular protective processes in these cell lines will also be determined.

ADDRESSING ANTIMICROBIAL RESISTANCE USING ENDOPHYTIC FUNGI AS A SOURCE OF NOVEL ANTI-INFECTIVE COMPOUNDS

Sophia Guagliano, Alexander Kalina, and Nicole Secondino

Department of Biology

Faculty Mentor: Professor Jon Polishook

ABSTRACT

The global overprescription of antibiotics has led to a significant issue: antibiotic resistance. In 2019, deaths associated with bacterial antimicrobial resistance were estimated to be the twelfth leading cause of death, surpassing HIV and malaria. The Food and Agricultural Organization projects that if current trends continue, antibiotic resistance could become the leading cause of death by 2050. Microbial natural products have historically been a rich source of new antimicrobial compounds, beginning with the discovery of Penicillin in 1928. Endophytic microfungi are nonpathogenic symbiotic fungi that live within plant tissues. This study aims to isolate and identify endophytic microfungi that produce novel antimicrobial compounds with potential medicinal applications.

In this study, endophytic fungi were isolated from the skins of avocados (*Persea americana*) purchased from local supermarkets and imported from the Americas. Segments of surface-sterilized avocado skin were added to selective fungal growth media. Any emerging growth was isolated on malt extract agar slants. From a total of 108 isolates, 48 fungal morphospecies were recovered based on their visual growth characteristics. Each representative isolate was regrown on several production media for 10 and 21 days. At each interval, agar discs from each plate were added to media embedded with gram-positive *Staphylococcus epidermidis* and another with gram-negative *Escherichia coli*. Any zones of inhibition were measured and compared to commercially available antibacterial compounds to evaluate their novelty.

A total of 29 zones of inhibition were observed among the 48 isolates studied. 11 fungal morphospecies, including several *Fusarium* species, demonstrated antimicrobial activity. To further identify the strains, ITS sequences were obtained through DNA extraction, amplification via PCR and purification, and subsequent sequencing. The sequences were then compared to the NCBI BLAST database. Future studies will involve regrowing the active fungal strains in larger quantities to chemically isolate the active compounds for natural product identification.

BY-12

ANTIBIOTIC POTENTIAL OF ENDOPHYTIC FUNGI FROM AVOCADO (*PERSEA AMERICANA*) SKINS AND TAMARIND (*TAMARINDUS INDICA*) SHELLS

Jenifer Yax-Monroy, Nicole Raczkowski, Estellsy Acuahuitl and Joseph Pellicone

Department of Biology

Faculty Mentor: Professor Jon Polishook

ABSTRACT

With the rise of antibiotic resistance, researchers are driven to find new antimicrobial compounds sourced from nature, including endophytic fungi, those commensal microorganisms inhabiting plant tissue. In this study, endophytic fungi were isolated from locally sourced Avocado (*Persea americana*) skins and Tamarind (*Tamarindus indica*) shells using (selective) Bandoni's Sorbose with cyclosporine agar to reveal their fungal diversity. From 78 avocado and tamarind derived fungal cultures, 30 different species were identified based on gross morphological appearance (morphospecies). Some isolates were readily identifiable species, such as *Penicillium sp.* and *Aspergillus niger*, based on their morphology and microscopic features. The other fungal strains exhibited a wide range of color and textures. These variations highlight the distinct morphological traits that aid in species characterization. Understanding these physical differences is essential for linking specific fungal isolates to potential antimicrobial properties. Antimicrobial assays data is provided and could elucidate deeper insights into the bioactive compounds produced by these fungi and their potential efficacy against microbial pathogens, *S. epidermiditis* and *E. coli*. Future studies would include species identification using DNA isolation, ITS sequencing and NCBI Blast searches

DEPARTMENT OF CHEMISTRY AND PHYSICS

**CurveIQ: A SYSTEMATIC AND RIGOROUS APPROACH FOR
ASSESSING THE THERMODYNAMIC STABILITY OF
MACROMOLECULAR STRUCTURES**

Omar W. Ahmed

Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose

ABSTRACT

The structure and stability of biological macromolecules, including nucleic acids and proteins, are influenced by various factors, such as temperature, solvent conditions, pH, salt concentrations, and the presence of relevant small molecules. Historically, thermal denaturation curves have been used to monitor the stability of macromolecules as a function of temperature under different conditions. Spectroscopic methods, including UV-visible absorbance spectroscopy, circular dichroism, and fluorescence spectroscopy, can be employed to experimentally determine the melting profile of macromolecules. For nucleic acids, the nearest neighbor model is the most common approach for analyzing and interpreting the experimentally obtained denaturation profiles. Analyzing the experimentally determined thermal denaturation curves and comparing them with theoretically predicted values provides insights into the structural details of the molecules. However, analyzing the experimentally determined melting curves is a multifaceted and multivariate process involving numerous regression and error analysis steps. Previously developed thermal denaturation fitting software, such as MeltWin and MeltR, can be utilized to obtain consistent and reliable thermal fitting curves and support data extraction. However, since MeltWin is no longer maintained and MeltR limits user involvement, we created CurveIQ, an open-source thermal denaturation software package that is highly user-friendly and allows users to control the selection parameters according to the experimental conditions. Additionally, CurveIQ can analyze and extract the thermodynamic parameters of biological macromolecules not only from data collected by UV-visible spectrophotometers but also from circular dichroism and fluorescence spectroscopic methods.

**A SPECTROSCOPIC EVALUATION OF THE B TO A
CONFORMATIONAL TRANSITION IN DUPLEX DNA USING
FLUORESCENT BASE ANALOGUES**

Maria J. Hernandez Campos, Noureen Qureshi and Samantha LeCrone

Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose

ABSTRACT

The transition of the standard B-form DNA helix to A-form DNA was first seen by X-ray imaging of DNA fibers in 1953. Over time, B and A DNA structures have been further characterized by many higher-resolution crystal structures. The transition of B-DNA double helix to A-form is essential for biological functions as recognized by the presence of A-form DNA in many protein-DNA complexes. Recently, it was proposed that the shorter length of the A-form DNA compared to the B-form DNA might play an essential role in duplex DNA packaging in bacteriophages and that this conformational change might itself serve as the source of the large forces generated by the DNA packing motors. Even though it is known that the B to A conformational transition occurs, the specifics, like where in the DNA it originates, how it propagates, and the detailed step-by-step mechanism involved, whether mismatches and abasic sites influence the transition, are still unknown. We explored the local and global conformational changes in this highly biologically relevant transition using site-specifically positioned fluorescent oligonucleotides where 2-Aminopurine, the fluorescent base analogue of adenine, was site-specifically introduced. Our results showed that we could simultaneously monitor the local and global conformational change using 2-AP.

INVESTIGATING LOCAL CONFORMATIONAL CHANGES FROM LIGANS ON G-QUADRUPLEX COMPLEXES USING FLOURESCENT BASE ANALOGUES

Macklin Jugan and Matthew Finkelstein

Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose

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-methylisoxanthopterin (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 be used as an “intrinsic sensor” to 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.

**AN INVESTIGATION OF THE SUBSTITUTION BEHAVIOR AND THE
CYTOTOXICITY OF QUINOLINE-8-CARBOXALDEHYDE AND
RELATED COMPLEXES**

Lyndsey Buren

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Faculty Mentor: Dr. Greg Moehring

ABSTRACT

This work focuses on the preparation and properties of mononuclear rhenium(I) tricarbonyl complexes, which are stabilized by three carbonyl ligands. Such complexes have applications or potential in catalysis, especially the electrocatalytic reduction of carbon dioxide to carbon monoxide, electroluminescence, nuclear medicine, cytotoxins, and cell imaging agents. Three carbonyl ligands stabilize the neutral rhenium(I) centers which are usually supported by a monodentate and a bidentate ligand.

Reports of acyl-stabilized rhenium(I) tricarbonyl centers are rare. Reports of rhenium(I) tricarbonyl centers stabilized by the oxygen of an aldehyde group are even less common. There is only one report of the ligand quinoline-2-carboxaldehyde, stabilizing neutral rhenium(I) tricarbonyl complexes. Recent work in our lab has found that neutral rhenium(I) tricarbonyl complexes stabilized by an acyl-metallated bidentate ligand can be prepared using quinoline-8-carboxaldehyde (Q8carboxal) as a reactant. Q8carboxal can also act as a bidentate ligand in its neutral form by donating electron density from the aldehyde oxygen. There are no known previous reported reactions between Q8carboxal and rhenium carbonyl complexes however.

A particular focus of this work has been the preparation and characterization of complexes with the form $\text{ReBr}(\text{Quin-8-C(O)R})(\text{CO})_3$ (where Quin is quinoline or a halide-substituted quinoline and $\text{R} = \text{H}$ or Me) The labile substitution of the neutral bidentate ligand Quin-8-C(O)R was studied under pseudo first order conditions in either DMSO or acetonitrile. The activation barrier, under such conditions was found to be only slightly more than 20 kcal/mol at room temperature. Future work for this project will include structural characterization of one example complex, photophysical studies of the new complexes, and cytotoxicity tests of the new complexes against an oral cancer cell line and a normal oral cell line.

ISOLATION OF AN APTAMER SELECTIVE TO GLUCOSE

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ABSTRACT

Diabetes is a disease that hundreds of million people live with daily throughout the world. Currently there is not a long-term cure for diabetes. The day-to-day life of managing the disease 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 finding a cure for diabetes. 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.

PLMVd AND CIRCULAR RNA

Anahi Menendez

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ABSTRACT

The Peach Latent Mosaic Viroid (PLMVd) is a viroid that infects peach trees. This viroid has a unique ability to self-cleave and self-ligate *in vivo*, using rolling circle amplification (RCA). The purpose of our research is to use these properties of PLMVd to produce circular RNA. The use of circular RNA to diagnose is especially popular because it is believed that the circular structure protects the molecule from the immune system, specifically from degradation by exonucleases. For this reason, it is necessary to find an accessible and cost-efficient method to produce circular RNA and study its properties.

The goal is to integrate a target gene into PLMVd so that when the viroid self-ligates into a circular structure, it will also circularize the inserted gene. A transformation will be done to incorporate a dimer of PLMVd (including the target gene) plasmid into bacteria. In theory, the bacteria should then continuously transcribe dimers of the PLMVd and circularize, thereby circularizing the with the inserted gene. To retrieve the circular RNA from the bacteria, a magnetic bead primer will be utilized.

HAMMERHEAD RIBOZYME CLEAVING ITS RNA SUBSTRATE

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ABSTRACT

Hammerhead ribozymes are small self-cleaving RNA molecules with significant potential in genetic therapy due to their catalytic RNA-cleaving activity. Understanding their enzymatic mechanism is essential for optimizing their therapeutic application and broadening our understanding of the RNA cleavage mechanism. These ribozymes function by inducing site-specific cleavage of RNA sequences, making them valuable tools for targeted gene regulation and antiviral strategies.

This project aims to develop a simple and affordable kinetic assay for cleaving activity to study hammerhead ribozyme activity using SYBR Gold gel staining. The assay will allow for real-time observation of RNA cleaving events, providing insight into the ribozyme's catalytic efficiency and structural dynamics. The study focuses on the cleavage efficiently by using the gel staining dye SYBR Gold. Additionally, the research will explore key factors influencing ribozyme activity, such as ionic concentration, temperature, substrate, and sequence specificity, to optimize reaction conditions.

Furthermore, this research explores the potential application of hammerhead ribozymes, particularly in targeting viral RNA genomes, such as those of certain viral infections, such as HIV, by targeting its RNA sequences.

**DEPARTMENT OF COMPUTER SCIENCE
AND
SOFTWARE ENGINEERING**

CSSE-1

**BEYOND ACCURACY: A MOCK AI AUDIT FOR FAIR AND
TRANSPARENT INSURANCE COST PREDICTION WITH LOW-CODE
AND NO-CODE**

Sushika Reddy Gade

Department of Computer Science & Software Engineering

Faculty Mentor: Professor Arup Das

ABSTRACT

The increasing adoption of machine learning (ML) in insurance pricing raises critical concerns regarding fairness, transparency, and regulatory compliance. Recent regulations, such as the New York City Automated Employment Decision Tool (AEDT) Law and Colorado’s AI Insurance Pricing Regulation, highlight the need for systematic AI audits to ensure fairness and mitigate bias in high-stakes decision-making.

This study conducts a mock AI audit of an XGBoost-based ML model for medical insurance cost prediction, going beyond traditional accuracy metrics such as R^2 score and RMSE. Instead, we emphasize fairness, bias detection, and model explainability, employing SHAP (Shapley Additive Explanations) and LIME (Local Interpretable Model-agnostic Explanations) to assess feature influence—such as smoking status, age, and BMI—and detect biases. If bias is identified, we explore mitigation strategies, including fairness constraints and feature adjustments, to enhance equitable decision-making.

A key innovation of this study is its focus on democratizing AI auditing through low-code and no-code platforms, making fairness assessments accessible to business analysts, regulators, and decision-makers without coding expertise. These platforms provide intuitive visual tools, enabling broader stakeholder participation in AI governance and regulatory compliance.

Our findings contribute to a best-practices framework for AI audits, emphasizing that ML models must be evaluated not only for accuracy but also for their societal and ethical impact. By integrating regulatory compliance, fairness assessments, and explainability techniques within a low-code/no-code framework, this study presents a novel and practical approach to ensuring transparent, fair, and accountable AI systems in insurance pricing and beyond.

CSSE-2

**PARKSHARK ADMINISTRATION: THE FUTURE OF CAMPUS
PARKING MANAGEMENT**

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Department of Computer Science and Software Engineering

Faculty Mentor: Dr. Raman Lakshmanan

ABSTRACT

The ParkShark Patrol iPad application and the ParkShark Admin web portal are auxiliary applications for the ParkShark service that assist in the monitoring and management of parking lots, parking passes, and traffic policy enforcement on campus. These apps contribute to the ultimate goal of ensuring a safer and easier parking experience on campus for students and faculty. The ParkShark Patrol iPad app allows traffic officers to monitor parking spots in their surrounding area in real time as they drive through parking lots; the “Patrol View” map displays the live statuses of all parking spots within a chosen radius of an officer’s vehicle. The Patrol iPad app also allows officers to issue and print tickets, view and update in-depth information about each parking spot and vehicle, and receive live parking lot occupancies, closures, and announcements. The ParkShark Admin web portal is utilized by the police headquarters to streamline overall parking management. This web portal allows administrators to view the statuses of all lots and spots on campus, as well as close entire parking lots or specific rows and spots for any construction or events. Administrators can also send announcements to all campus users for important updates such as closures and inclement weather, assign ParkShark tags to users and replace lost or damaged ones, and track and update parking tickets and their paid or unpaid statuses. By combining real-time monitoring, ticket management, and communication features, the ParkShark Admin web portal and ParkShark Patrol iPad app offer a scalable and user-friendly solution for police departments in addressing the challenges of campus parking management.

CSSE-3

**PARKSHARK INTELLIGENCE: PRECISION PARKING POWERED BY
SMART DATA**

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Boag**

Department of Computer Science and Software Engineering

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ABSTRACT

ParkShark Intelligence is the backbone of our parking system, integrating a custom database, APIs, and a differential GPS station to provide precise real-time tracking of parking spot occupancy. The system processes the locations of vehicles on campus to accurately guide users to available spots and support administrative parking management. To achieve high accuracy, we use a custom-built GPS station that corrects standard satellite data, which typically has an error margin of up to 10 meters. Our station reduces this error to just 0.02 meters (2 centimeters) using differential GPS error correction calculations. The GPS station was calibrated by collecting satellite data over several days from a fixed-position antenna, synthesizing it to get a precise location. We developed embedded software for the GPS station to receive satellite coordinates, compute the correction factor, and stream to the database for use in real-time vehicle tracking. The ParkShark relational database models and links various elements such as users, tags, spots, lots, tickets, and announcements. This interconnected structure ensures seamless communication between system components and supports API calls that are utilized by the various apps. The ParkShark APIs serve as the communication bridge between the database and the front-end applications. The API accepts the location that a user chooses to park in and passes it back to our smart server, which analyzes the location and matches it with the correct parking space. The API allows users to view synchronized data for all parking availability, as well as access and update their schedules and accounts. For administrators, the API provides more in-depth information for every parked vehicle and facilitates communication of closures, tickets, and announcements between traffic officers and the police headquarters. By combining these technologies, ParkShark Intelligence delivers a precise, efficient, and scalable solution, transforming campus parking into a seamless experience.

CSSE-4

PARKSHARK MOBILE: TRANSFORMING CAMPUS PARKING WITH SMART TECHNOLOGY

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ABSTRACT

ParkShark is an innovative software system that revolutionizes campus parking by replacing traditional parking permits with custom-built digital tags and providing real-time parking lot and spot availability for both users and administrators. Available on both iPhone and Android, the ParkShark mobile app pairs and communicates via Bluetooth Low Energy (BLE) with the digital ParkShark Tag, which sends real-time GPS data to the app. The mobile app then communicates this data to our backend server, which uses tag locations to determine the availability status of every individual parking spot. The ParkShark app receives data from the backend server and provides users with a hands-free UI/UX that displays parking lot capacities, parking spot availability, campus closures, and announcements. Additionally, users can input their campus arrival times and preferred lots, as well as manage their vehicle and tag information. The ParkShark Tag acts like the EZ-Pass of campus parking, providing users with a hands-free device that “does the work for you” in reporting user parking. Each tag pairs with one user’s mobile device, ensuring privacy of communication between a user’s phone and mobile app. The tag is programmed with custom software that encodes and sends GPS data and can receive signals from the mobile app to know when to pair, when to turn on, when to send GPS data, and when to turn off, ensuring power efficiency. The communication of GPS information and commands between the ParkShark Tag and ParkShark mobile app are essential to providing a system that can suggest to a user where they should park when they are arriving on campus.

CSSE-5

**CYBERSECURITY CHALLENGES AND SOLUTIONS IN THE
METAVERSE: PENETRATION TESTING, AI SPOOFING AND
PHISHING, AND THE IMPACT OF EMERGING IDENTITY
VERIFICATION TECHNOLOGIES**

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Faculty Mentor: Dr. Weihao Qu

ABSTRACT

Cyberterrorism encompasses a wide range of attacks aimed at stealing credentials, money, or tricking targets into clicking malicious links that lead to harmful content. Often, content that appears harmless, such as social media videos presented as entertainment or informational material, can disguise a hidden agenda. These attacks include, but are not limited to, spoofing, phishing, and AI-generated deepfakes. As open-source AI software becomes increasingly accessible to the public, such attacks have skyrocketed, with deepfakes posing a particular threat. AI clones of credible personalities are being misused to promote products, political ideologies, or streams of thought designed to manipulate public opinion. While previous scams were easily recognizable due to obvious red flags, such as foreign phone numbers, suspicious email addresses, or malicious looking links, the sophistication of these attacks has grown exponentially with AI.

As this study demonstrates, even experts in computer science and technology have been fooled by such attacks with 100% success under certain conditions. One particularly concerning use of AI is voice cloning, which has been employed to impersonate children calling their parents, pleading for financial help to get them out of prison. This is just the beginning of AI-driven attacks, and as such, public awareness and education in cybersecurity have become critical to protect individuals from falling victim to these evolving threats. Multistage, advanced phishing attacks are also a growing concern, as they often do not involve clickable links or immediate goals. Instead, they aim to subtly manipulate targets into adopting specific beliefs or behaviors. Digital brainwashing through cyberterrorism is becoming increasingly common, as unsuspecting social media users consume content that unknowingly promotes a hidden agenda. This silent form of cyberterrorism is often dismissed as misinformation or fake news, underestimating the harm it causes and continues to cause due to widespread public ignorance.

CSSE-6

FORECASTING CLIMATE TRENDS: A MULTI-SOURCE ANALYSIS OF GLOBAL CLIMATE CHANGE USING NLP, TOPIC MODELING, AND TIME SERIES FORECASTING

Krishna Khandelwal

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Faculty Mentor: Professor Arup Das & Dr. Jiacun Wang

ABSTRACT

This project presents a comprehensive analysis of climate change by integrating data from scientific publications (Nature Climate Change) and media outlets (New York Times). Web scraping techniques were employed using Firecrawl to collect articles, followed by natural language processing methods including exploratory data analysis (EDA), word clouds, sentiment analysis with VADER, and topic modeling using BERTopic with UMAP embeddings. Additional datasets—such as global Air Quality Index (AQI), Earth warming temperatures, and disaster records—were merged for deeper correlation analysis. A transformer-based summarizer (Flan-T5) was used to generate concise abstracts from scraped content. Finally, time series forecasting using RNN and LSTM models was applied to predict global trends in AQI, disaster frequency, and temperature anomalies over the next three years. This multi-layered approach highlights the intersection of climate science and media narratives while offering predictive insights into future climate patterns.

CSSE-7

LUXÉ: A VIRTUAL FASHION PLATFORM

Estania Blanc Doblas

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ABSTRACT

Luxé is a creative web platform redefining how people engage with fashion online. This web app lets users upload their clothing items to a virtual closet, share outfit posts, join weekly and monthly styling competitions with community voting, and play with fashion using a stylist tool including adjustable avatars.

Luxé's core is a strong, contemporary technology platform meant to provide a smooth and safe fashion experience. Built with Node.js and Express.js, the backend handles everything from user authentication to contest logic, while Firebase Authentication ensures secure sign-ins. Firestore enables real-time interactions, such as new outfit posts, contest votes, or follower notifications, delivering instant updates without delay. Meanwhile, Firebase Storage keeps high-resolution images of clothing and fashion uploads securely stored and ready to showcase. A custom-built RESTful API connects the frontend and backend, ensuring smooth interactions across the platform.

Luxé takes digital fashion a step further with Unreal Engine's MetaHuman integration, allowing users to visualize their outfits on hyper-realistic 3D avatars, bringing style to life like never before. Behind the scenes, the program maintains a modular architecture, neatly organizing middleware, utilities and route handlers for simple upgrades and scalability. By blending advanced technology with fashion creativity, Luxé redefines the online fashion experience.

CSSE-8

MONMOUTH UNIVERSITY TUTORING SERVICES

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Department of Computer Science and Software Engineering

Faculty Mentor: Dr. Cui Yu

ABSTRACT

Computer Science, Software Engineering, and Information Technology tutors at Monmouth University have identified a need for a more structured system that allows students to connect with university tutors and schedule appointments in advance. Currently, students visit the tutoring center without prior notice, limiting the time available for tutors to prepare relevant materials and resources. To enhance the tutoring experience, a custom-built system has been developed to streamline appointment scheduling and improve accessibility to academic support.

Monmouth University Tutoring Services is a proprietary web-based application designed to facilitate seamless appointment scheduling, allowing students to specify the subjects they need help with and describe the challenges they are facing. Additionally, the system supports the upload of class notes and study materials, fostering a peer-based study environment. It utilizes HTML and CSS to create a modern, user-friendly interface accessible across various devices. JavaScript and Node.js provide essential functionality – enabling features such as dynamic search bars, file storage and retrieval, and appointment scheduling. Python facilitates automated content aggregation in our website through means of web scraping and HTML parsing. Google Firestore, a NoSQL database, supports user registration and file tracking, ensuring a personalized experience for site users.

This system aims to make it easier for students to seek academic assistance while allowing tutors to be better prepared with relevant resources. By improving accessibility and organization, this platform enhances the overall effectiveness of tutoring services at Monmouth University.

DEPARTMENT OF MATHEMATICS

MA-1

WATER QUALITY ACROSS MONMOUTH COUNTY COASTAL LAKES

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Department of Biology and Mathematics

Faculty Mentors: Dr. Jason Adolf & Dr. Richard Bastian

ABSTRACT

Assessing water quality is critical for understanding the health of aquatic ecosystems and is necessary for making informed management decisions. Monmouth County contains a system of coastal lakes that have been degraded by pollution and other human activities and have been the subject of several restoration efforts from management organizations over the past decade. The goal of this research is to establish whether the current restoration practices are helping these coastal lakes, or if managers need to try other strategies to improve the health of the lakes. Citizen scientists have been collecting water quality data from 10 coastal lakes in Monmouth County since May 2019. This data being collected by citizen scientists highlights the importance of community involvement, which enhances research accuracy and improves policy decisions. There is variability between lakes in terms of water quality, sample size and location within the water body, as well as seasonally and annually. Seven parameters including temperature, conductivity, turbidity, and pH were tested to assess water quality. These parameters were used not only to compare the difference between lakes, but also to observe the seasonality among each lake and across the duration of the study thus far. Analysis of variance (ANOVA) tests were used to determine whether there were differences between the lakes, as well as differences over time. The results of this study can be used to design more effective restoration strategies that can be applied to coastal lakes throughout New Jersey, not just Monmouth County.

MA-2

INVASIVE PLANT SPECIES EFFECT ON TERRAPIN NEST SITES

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Departments of Mathematics and Biology

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

ABSTRACT

The northern diamondback terrapin is a species of terrapin native to the East Coast of the United States. Understanding factors that impact the nest sites of these creatures is imperative in ensuring the long-term sustainability of the species. Like many other reptilian species, the temperature of the terrapin's nest sites impact what gender their hatchlings will be, called temperature-dependent sex determination. If temperatures of the nest sites tend in one direction, so too will the gender of the turtles. Temperatures below 27.7 °C will produce males and temperatures above 31 °C will produce females. Invasive species, such as *Phragmites australis*, along with other plants, are quickly dominating once optimal nest site locations. Little is known about how the different plant species affects terrapin nesting. With data collected from past field work, including the temperature of eleven different terrapin nest sites and various different measures of plant species in the immediate area surrounding these sites, this study aims to determine the effects these plants have on the terrapin nest sites. Specifically, this study will aim to conclude if more plants around a nest site leads to a lower nest site temperature. The results of this study are important in ensuring the long-term survivability of the northern diamondback terrapin and dictating what, if any, human interference needs to happen in order to ensure their longevity.

MA-3

AN ANALYSIS OF THE PELVIS OVER TIME

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Faculty Mentors: Dr. Hillary Delprete and Dr. Richard Bastian

ABSTRACT

This study examines sexually dimorphic pelvic characteristics to evaluate the impact of political turmoil on an osteological collection from Coimbra, Portugal. The dataset comprises 62 Caucasian females and 79 Caucasian males born between 1839-1905, representing a relatively isolated population with minimal influx and efflux. Sex and birth year are used as predictors to analyze variations in pelvic depth and reproductive-related dimensions, such as the anteroposterior diameter of the inlet, midplane, and outlet, transverse diameter of the midplane, and bispinous diameter. Preliminary ANOVA with bootstrapping suggests inter- and intra-cohort variation within and between males and females born in different periods, suggesting that some ecological and/or cultural factors—such as nutrition—may have contributed to pelvic disparities. Means plots characterize cohorts' change in pelvic morphology over time and suggest that sex and birth year are primarily responsible for shaping these trends. Findings from this study may be extrapolated to future research analyzing the influence of sociocultural factors on pelvic morphology, such as nutritional deficits experienced by K-8th grade children during the Covid-19 pandemic.

MA-4

**HARMONIC CONTENT OF STRING NETWORKS: A PHYSICAL
APPLICATION OF QUANTUM GRAPHS**

Miriam Abecasis

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Faculty Mentor: Dr. Torrey Gallagher

ABSTRACT

If we know the sound a string makes, can we determine its length? This question forms the basis of our research. We began by analyzing this scenario and then moved on to examining cases where two and three strings are attached at a node. We determined that the harmonics of the one-string system will be of a specific form that depends on the string length. We then studied two attached strings and determined that a two-string system produces the same harmonic spectrum as one string whose length equals the sum of both strings. Our goal then became physically constructing these systems to observe the extent to which a physical model agreed with our theoretical model.

Beginning with the one-string case, we determined what our system should sound like with the error that accompanies experiments done in the real world. Moving on to the two-string scenario, we had to figure out how to concatenate two strings without affecting the integrity of the system. We did this by looping two strings together and twisting them until the system resembled a single string. We then wrote code analyzing the harmonics of our system and determining the validity of this method of concatenation.

PERIODIC ANALYSIS OF SIMULATED ORBITS USING THE FAST FOURIER TRANSFORM (FFT)

Jason French and Felipe Marcal

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Faculty Mentor: Dr. Torrey Gallagher

ABSTRACT

On September 23, 1846, Johan Gottfried Galle pointed his telescope at the sky and intentionally observed, for the first time in history, the planet Neptune. This remarkable feat was not easy to achieve. Alexis Bouvard had previously published astronomical tables predicting the orbit of Uranus. Astronomers noticed that the true trajectory of Uranus was slightly deviated from Bouvard's predictions. Mathematicians Urbain Le Verrier and John Couch Adams interpreted these deviations as the effects of a massive gravitational body dwelling past the orbit of Uranus. By comparing Uranus' trajectory to its theoretical orbit, Le Verrier located Neptune within 1 degree of its true position!

The objective of this project is to simulate a similar scenario: we will imagine we are on a planet that is alone in its star system, but we observe that our planet's orbit deviates from our theoretical calculations. What information can we deduce about the mystery planet that must also dwell in our star system? We use numerical integration in Python to simulate these star systems and draw numerical conclusions.

Utilizing the Fast Fourier Transform (FFT), we examined multiple three body systems with different parameters. An interesting relationship between the tallest peak of the FFTs was found when varying both distance and mass of the external body. Upon varying the mass of the external body, the height of the tallest peak increased proportionally to the mass change. When varying the distance, the height of the tallest peak changed with an inverse square relationship to the distance. These relationships suggest that the height of the tallest peak is directly related with the force from the external object. This study aims to further evaluate the relationships seen on the FFT that can be leveraged to identify parameters such as the velocity, mass, and distance of the mystery planet.