MONMOUTH UNIVERSITY

SCHOOL of SCIENCE

SUMMER RESEARCH PROGRAM

2025 SUMMER RESEARCH PROGRAM SYMPOSIUM AUGUST 7, 2025

MONMOUTH UNIVERSITY | SCHOOL of SCIENCE

Dear Friends and Colleagues,

I would like to take this opportunity to thank the supporters and university partners who contributed to the success of the 2025 Monmouth University School of Science Summer Research Program (SRP). Your contributions allow us to provide impactful research experiences for undergraduate students by funding their summer salaries as research assistants, acquisition of the supplies and equipment necessary to complete their research projects, and providing opportunities for students to travel to conferences and professional meetings to present their research. Without your collective philanthropy and support, the Summer Research Program would not be possible.

I would also like to acknowledge the faculty from the School of Science who dedicated their time and offered their expertise to mentor participating students this year. We aim to provide meaningful experiences outside traditional classroom settings, and this event is crucial in reaching this goal.

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

Joe Coyle,
Dean Monmouth University School of Science

2025 Summer Research Program
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The School of Science Summer Research Program (SRP) would not be possible without the support of the Departments of Biology, Chemistry and Physics, Computer Science and Software Engineering, and Mathematics as well as a number of other University offices, programs, and supporters including the following:

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Monmouth University's Office of the Provost provides the chief academic leadership, responsibility and support to all of the University's schools and centers of distinction. The Provost Office provides stipends to faculty that participate as mentors to our Summer Research Program student research assistants.

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The School of Science Dean's Advisory Council provides key input to the School's strategic planning process and annual support for the Summer Research Program. Council members include:

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Bruce Kratz is a technology executive with over 35 years of experience leading software engineering teams. He currently serves as Vice President of Development at RunSignup, a platform for race registration, fundraising, and ticketing.

Over his career, Bruce has held senior roles at companies including IBM, Hewlett-Packard, Bluestone Software, Princeton Softech, Sparta Systems, and NextGen Healthcare. He also founded and operated his own software services companies earlier in his career. As CTO of Sparta Systems, he led engineering and product growth efforts that contributed to two successful Private Equity exits.

A Monmouth University alumnus with a B.S. in Computer Science, Bruce has served on the School of Science Dean's Advisory Committee and continues to advise early-stage tech companies and investors. In his spare time he serves as a Captain with the Marmora Volunteer Fire Company right outside of Ocean City NJ, where he lives with his wife Lynn and their two children.

2025 Summer Research Program Symposium

Edison Science Building – Room E 201

Thursday, August 7, 2025

10:00 a.m. – 1:00 p.m.

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Symposium Agenda

10:00 a.m. – 10:15 a.m.	**Welcome** **Dean Joe Coyle**
10:15 a.m. – 10:30 a.m.	**Opening Remarks** **Bruce Kratz '89**
10:30 a.m. – 12:00 p.m.	**Poster Session**
12:00 p.m. – 12:15 p.m.	**Closing Remarks** **Dean Joe Coyle**
12:15 p.m. – 1:00 p.m.	**Lunch and Networking**
1:00 p.m.	**Adjourn**

Project Abstracts

Department of Biology

SRP – 1 **Discovering Marine Vertebrate Biodiversity And Seasonality Using Edna Along The New Jersey Coastline**

Harmony Lighty
Monmouth University Department of Biology

Faculty Mentor: Dr. Jason Adolf

SRP – 2 **Restoration Revealed: Edna And Water Quality As Indicators Of Coastal Ecological Health**

Emma Owendoff Najarian
Lehigh University College of Health

Faculty Mentor: Dr. Jason Adolf

SRP – 3 **Development and Testing of a Novel qPCR Assay for Endangered Atlantic Sturgeon Environmental DNA (eDNA) in Continental Shelf Waters**

Christopher Reigel
Monmouth University Department of Biology

Faculty Mentor: Dr. Jason Adolf

SRP – 4 **Phosphorylation Of JNK By Cypres Essential Oil In Both Normal Fibroblasts And Fibrosarcoma Cells**

Warda Chowdhury[1], Bianca Farro[2], Hermoine Kissoon[1], Carmen Lobo[3]
[1] Biology Department, Monmouth University, [2] Brown University, [3] Saint John Vianney High School

Faculty Mentors: Dr. Dorothy Lobo and Dr. James Mack

SRP – 5 **The Effects of Essential Oils (EOs) on the Growth of Multidrug Resistant Bacterium Staphylococcus epidermidis**

Alexandra Decaro
Monmouth University Department of Biology

Faculty Mentor: Dr. James Mack

SRP – 6 **Mapping Dopaminergic Circuits Underlying Aggression In The *Drosophila* Brain**

Aiswarya L. Raghavaraju[1], Sarah A. Henry, Edward A. Kravitz
[1]Department of Biology, Monmouth University, West Long Branch, NJ.
[2]Department of Neurobiology, Harvard Medical School, Boston, MA.

Faculty Mentor: Dr. Saheli Sengupta

SRP – 7 **Evaluating The Thermal Environment Of Easter Box Turtles (*Terrapene Carolina*) In A Suburban Island**

Olivia Fowles
Monmouth University Department of Biology

Faculty Mentor: Dr. Sean C. Sterrett, Department of Biology and Dr. Dane Ward, Department of History and Anthropology

SRP – 8 **Measuring Diamond-Backed Terrapin (*Malaclemys Terrapin*) Body Size From Drone Imagery**

Victoria O'Malley
Monmouth University, Department of Biology

Faculty Mentor: Dr. Sean Sterrett

Department of Chemistry and Physics

SRP – 9 **A Spectroscopic Study of the B to A Conformational Transition in Duplex DNA**

Noureen Qureshi, Samantha LeCrone, and Tomas Barry
Monmouth University, Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose

SRP – 10 **Unravelling Ligand-induced Local Conformational Changes in G-Quadruplexes Using Fluorescent Base Analogues**

Daniel Flynn and Macklin Jugan
Monmouth University, Department of Chemistry and Physics

Faculty Mentor: Dr. Davis Jose

SRP – 11 **Transcription Of Hammerhead Ribozyme And Spinach Aptamer To Measure With Fluorescence**

Ashley Salguero
Monmouth University Department of Chemistry and Physics

Faculty Mentor: Dr. Jonathan Ouellet

SRP – 12 **Investigating baby spinach RNA aptamer fluorescence with DHFBI to measure G-quadruplex stability**

Rina Lee[1], Melanie Morales-Paz[2], Julianna Proscia[2]
[1]: Case Western Reserve University, Biochemistry
[2]: Monmouth University, Department of Chemistry and Physics

Faculty Mentor: Dr. Jonathan Ouellet

Department of Computer Science and Software Engineering

SRP – 13 GArel: Relational Reasoning for Mutable Arrays

William Judd
University of Illinois Urbana-Champaign[4]

Faculty Mentor: Dr. Weihao Qu

SRP- 14 Sentinel LLM: A Clinical Q&A Chatbot for Early Sepsis Detection

Brooke Tortorelli , Miriam Abecasis, Isaac Sasson, Sophia Velandia, and Thomas Farrell
Monmouth University

Faculty Mentor: Dr. Jiacun Wang

Department of Mathematics

SRP - 15 **Solutions to Compartmental Modeling**

Elise Cantu[1], Chris Tsimbinos[2]
[1]Rowan University, [2]Wake Forest University

Faculty Mentor: Dr. Joseph Coyle

SRP – 16 **Detection of a Mystery Planet Using Orbital Deviations**

Adina Kestenbaum[1] , Felipe Marcal, Jason Sullivan, Matthew Walter[2]
[1]University of Michigan, [2]Monmouth University

Faculty Mentor: Dr. Torrey Gallagher

SRP – 17 **Beyond Heronian Shapes: Lattice *N*-Gons**

Katie Wallace
Episcopal High School

Faculty Mentor: Dr. Susan Marshall

DEPARTMENT OF BIOLOGY

SRP-1

DISCOVERING MARINE VERTEBRATE BIODIVERSITY AND SEASONALITY USING EDNA ALONG THE NEW JERSEY COASTLINE

Harmony Lighty

Monmouth University Department of Biology

Faculty Mentor: Dr. Jason Adolf, Monmouth University Department of Biology

Funding Sources:

Monmouth University School of Science; New Jersey DEP Resource Monitoring Initiative (RMI)

Abstract

Environmental DNA (eDNA) is an emerging tool that allows researchers to detect the presence of species in aquatic environments. This is possible through the collection of water samples, which are used to analyze the genetic material that is shed by organisms. This method is non-invasive compared to traditional methods that require capture, and an improvement as many marine species are difficult to track through traditional methods. eDNA helps researchers identify the distribution of species along the New Jersey coastline and how their presence may vary seasonally.

The goal of this project is to analyze previously collected eDNA samples from the New Jersey coastline from several previous projects. This will allow us to identify marine vertebrate species' spatial and temporal distribution, focusing specifically on the non-fish category of marine vertebrates that have not previously been analyzed. This data is necessary for informing conservation strategies, improving conservation and management, and enhancing monitoring efforts in response to climate change and coastal development.

SRP-2

RESTORATION REVEALED: eDNA AND WATER QUALITYAS INDICATORS OF COASTAL ECOLOGICAL HEALTH

Emma Owendoff Najarian
Monmouth University Department of Biology, Lehigh University College of Health

Faculty Mentor: Dr. Jason Adolf, Monmouth University Department of Biology

Funding Sources:
Monmouth University School of Science; AKRF Gansevoort Monitoring contract to Monmouth University

Abstract

Environmental DNA (eDNA) is genetic material shed by organisms that allows non-invasive ecological monitoring of aquatic systems and detection of species presence and richness in environmental samples, offering insight into biodiversity and ecological health.

Water samples were collected from multiple sites with varying levels of restoration from the Atlantic Highlands Marina in New Jersey through the Hudson River. Restored sites included areas within the Gansevoort Peninsula in Manhattan in which oyster castles were implemented to support biodiversity and habitat rehabilitation, while the unrestored sites through the Hudson River and Pier 25 remained largely untouched. At each of the 22 sample sites, about a liter of water was collected for eDNA analysis and tested for water quality parameters, including temperature, dissolved oxygen, conductivity, salinity, pH, turbidity, PE, chlorophyll, and Secchi depth. eDNA from these samples was extracted and will be processed using metabarcoding to identify aquatic species present in each sample, highlighting biological diversity across the different sample types.

Although data collection and analysis are presently ongoing, this project aims to determine whether environments with implemented restoration efforts support richer or more stable ecological systems compared to unrestored ones. With the integration of molecular processes and environmental parameter monitoring, this research utilizes eDNA as a complementary method for tracking ecological changes and examining restoration effectiveness.

The findings of this study may support future targeted, data-driven approaches to coastal habitat management and provide a baseline for future monitoring. This project contributes to efforts to refine and expand restoration implementation and assessment in coastal habitats.

SRP-3

DEVELOPMENT AND TESTING OF A NOVEL QPCR ASSAY FOR ENDANGERED ATLANTIC STURGEON ENVIRONMENTAL DNA (EDNA) IN CONTINENTAL SHELF WATERS

Christopher Reigel

Monmouth University School of Science, Marine and Environmental Biology and Policy Program

Faculty Mentors: Dr. Jason Adolf & Ms. Elizabeth Clark, Biology Department

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

NOAA-NMFS-NEFSC 2024 Earmark Ecological Resilience in the Hudson-Raritan (PIs Jason E. Adolf and Tony MacDonald)

Abstract

The Atlantic sturgeon, *Acipenser oxyrinchus oxyrinchus*, is an endangered anadromous fish of historic ecological and commercial importance. Atlantic sturgeon are currently monitored using traditional surveying methods such as gillnetting and acoustic telemetry, which can be costly and logistically challenging to undertake, making it difficult to effectively monitor this species across their broad range. Environmental DNA (eDNA) has emerged as a useful complementary tool to traditional surveying for many aquatic species. A qPCR probe-based assay for the monitoring of Atlantic sturgeon has been published, but the authors concluded that the assay was not designed for use in low population density areas, making it less suitable for monitoring sturgeon during the time they are migrating through continental shelf waters. The objective of our study is to develop an optimized probe-based qPCR assay for Atlantic sturgeon that can successfully detect their presence in ocean water samples. Optimization measures included making the assay amplicon length shorter and modifying qPCR protocols. We have validated this assay *in silico* and are further validating it against DNA extracts from Atlantic sturgeon and closely related/cohabitating species (e.g. shortnosed sturgeon, menhaden, river herring, gizzard shad), as well as field samples where Atlantic sturgeon have been verified by capture or metabarcoding methods. Development of a more sensitive qPCR assay for Atlantic sturgeon will better allow tracking of this important species throughout its natural range.

SRP-4

PHOSPHORYLATION OF JNK BY CYPRES ESSENTIAL OIL IN BOTH NORMAL FIBROBLASTS AND FIBROSARCOMA CELLS

Warda Chowdhury[1], Bianca Farro[2], Hermoine Kissoon[1], Carmen Lobo[3]
[1] Biology Department, Monmouth University, [2] Brown University, [3] Saint John Vianney High School,

Faculty Mentor: Dr. Dorothy Lobo and Dr. James Mack,
Biology Department, Monmouth University

Funding Sources:
Monmouth University School of Science; Biology Department

Abstract

Cypress oil is an essential oil derived from evergreen coniferous trees native to Southern Europe and Western Asia. 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. Some of these components have demonstrated anti-cancer properties, but little is known about their effects in fibroblasts. Prior to our recent studies, both HT-1080 fibrosarcoma cells and CUA-4 normal human fibroblasts display reduced expansion and viability after treatment with cypress essential oil. Apoptosis was provoked in the two cell types (which was shown by PARP cleavage). Our focus for this project was to test the involvement of the stress signaling protein JNK in the trigger of apoptosis. Both the fibrosarcoma cells and fibroblast were treated with cypress oil. Proteins were then extracted and used for western blot analysis to determine whether JNK was activated. The JNK proteins remained constant after treatment in normal fibroblasts while the level of JNK decreased after fibrosarcoma cells were treated. Activation of JNK in both cell types was still able to be identified although the level of total JNK was low in the fibrosarcoma cells. For further research, it may be possible to impede the activity of JNK with the help of chemical inhibitors or overexpression of phosphatases in order to test whether apoptosis could be reduced.

SRP-5

THE EFFECTS OF ESSENTIAL OILS (EOS) ON THE GROWTH OF MULTIDRUG RESISTANT BACTERIUM STAPHYLOCOCCUS EPIDERMIDIS

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

Funding Sources:
Monmouth University School of Science, Department of Biology
Mr. Kevin Young ('89)

Abstract

Amid the sterile laboratories of modern medicine, a more ominous pattern is unfolding: the rise of multidrug-resistant bacteria—conjured not by alchemy, but by the chronic overprescription and mechanistic misuse of antibiotics. As conventional treatments falter and resistance outpaces pharmaceutical innovation, researchers are beginning to turn back toward nature's more ancient therapeutic laboratory that predates modern medicine (Lawless, Julia. *The Illustrated Encyclopedia of Essential Oils*. Element, 1995). Essential oils (EOs), long revered in herbalist circles and whispered about in the margins of traditional healing, are now being examined through the lens of scientific inquiry for their potential to counteract these microbial adversaries (Lawless, Julia).

In this study, I focused on five essential oils—arborvitae, cassia, cinnamon bark, melaleuca, and thyme—tested against the multidrug-resistant bacterium *Staphylococcus epidermidis*. These oils emerged as frontrunners from an initial screening of 119 EOs at full strength, each showing notably potent antimicrobial activity. To temper their intensity, each was diluted with jojoba oil, a neutral carrier known for its skin-like compatibility.

The oils were then compared with six commonly prescribed antibiotics for *S. epidermidis*: Amikacin, Ceftriaxone, Colistin, Imipenem, Meropenem, and Tigecycline. Antibacterial efficacy was measured using the Kirby-Bauer Disk Diffusion Method, and Minimum Inhibitory Concentrations (MICs) were recorded.

The results were nothing short of compelling. Arborvitae, cassia, and cinnamon bark exhibited greater inhibition of bacterial growth than the antibiotics tested, suggesting a potent synergy of volatile compounds working in concert—perhaps guided by more than mere chemistry. While these findings stand firmly within the framework of empirical science, they also evoke a reverence for the botanical wisdom woven into nature's plant etymology. In an era where resistant pathogens outpace our synthetic remedies, the old-world magic of plant medicine may yet offer its quiet, powerful resistance.

SRP-6

MAPPING DOPAMINERGIC CIRCUITS UNDERLYING AGGRESSION IN THE *DROSOPHILA* BRAIN

Aiswarya L. Raghavaraju[1], Sarah A. Henry[1], Edward A. Kravitz[2]
[1]Department of Biology, Monmouth University,
[2]Department of Neurobiology, Harvard Medical School

Faculty Mentor: Dr. Saheli Sengupta
Monmouth University Department of Biology

Funding Sources: Monmouth University School of Science, Department of Biology

Abstract:

Dopamine (DA) is a key neuromodulator regulating aggression across species. Yet, our understanding of DA-specific neural circuits and molecular mechanisms underlying this behavior remains incomplete. A major challenge is that DA influences multiple behaviors (such as sleep, locomotion, and motivation), making it difficult to isolate its specific role in aggression. We used the fruit fly (*Drosophila melanogaster*) to study DA-specific aggression circuits. The fly brain contains ~200,000 neurons and offers extensive genetic tools for manipulating specific cell types and neural circuits. Fruit flies display aggression using stereotypical motor programs that are easily quantifiable. We studied male aggression, which consists of distinct motor programs. Of them, lunging is the predominant aggressive motor program, characterized by males rearing up on their hind legs and striking opponents with their front legs. This genetically hardwired behavior serves as an excellent readout for studying neural control of aggression. Like humans, fruit flies use DA as a neuromodulator that signals through different receptor subtypes. Understanding how individual DA-receptor types contribute to aggression is essential for comprehensively understanding dopaminergic regulation of this behavior. Using the UAS-GAL4 binary expression system, we activated a subset of neurons expressing the dopamine 1-like receptor 2 (Dop1R2) receptor in the fly brain. Dop1R2 receptor stimulates adenylyl cyclase and calcium signaling. Thermogenetic activation of Dop1R2 neurons using a temperature-sensitive cation channel dTrpA1 enhanced lunges in male fights. Expression analysis using UAS-mCD8::GFP reporter revealed labeled neurons in multiple brain regions, including the fan-shaped body (FB), a key structure within the central complex. FB regulates sensory integration, motor control, and sleep homeostasis, but its role in aggression remains unclear. Using the FlyWire connectome database, we identified FB neurons matching the morphology of the FB neurons labeled by our GAL4 line, and predicted its synaptic partners. Future work will test these predictions experimentally to define the circuits through which DA modulates aggression.

SRP-7

EVALUATING THE THERMAL ENVIRONMENT OF EASTER BOX TURTLES (*TERRAPENE CAROLINA*) IN A SUBURBAN ISLAND

Olivia Fowles
Monmouth University, Department of Biology

Faculty Mentors: Dr. Sean Sterrett, Monmouth University, Department of Biology; Dr. Dane Ward, Monmouth University, Department of History & Anthropology

Funding Sources:
Monmouth University School of Science; Summer Scholars Program

Abstract

Eastern box turtle (*Terrapene carolina*) populations are in decline in New Jersey partly due to fragmentation and destruction of their habitats caused by human development and related activities. Understanding the habitat selection of eastern box turtles allows for more informed protection of this species' preferred habitats. Ectothermic species such as eastern box turtles rely on external sources of heat or refugia to thermoregulate, making the thermal signature of their habitat vital for their survival and reproduction. To investigate the relationship between eastern box turtle habitat selection and the ambient temperature of their environment, a fragmented suburban ecosystem in New Jersey that contained a range of thermal conditions was examined. Temperature was sampled in twenty-nine locations throughout the study site in a variety of different habitat types and twenty-four eastern box turtles were tracked using radiotelemetry from June through August 2023. Using empirical Bayesian regression kriging, predictive maps of average temperature throughout the study site in weekly intervals were created from temperature sampling data as well as land surface temperature and normalized difference vegetation index (NDVI) derived from satellite imagery. While maps were unable to be generated for several weeks of sampling due to lack of satellite images, the completed maps depict the variation of temperature throughout the landscape as a result of differing habitat conditions, as well as how temperature varied throughout the study site temporally. Further study is required to understand how the movements of the tracked eastern box turtles is related to the predicted temperature of their environment.

SRP-8

MEASURING DIAMOND-BACKED TERRAPIN (*MALACLEMYS TERRAPIN*) BODY SIZE FROM DRONE IMAGERY

Victoria O'Malley

Monmouth University, Department of Biology

Faculty Mentor: Dr. Sean Sterrett, Monmouth University, Department of Biology

Funding Sources:

Monmouth University School of Science; Department of Biology

Abstract

Diamond-backed Terrapins (*Malaclemys terrapin*) are the only brackish water-adapted turtle species native to North America. Due to various anthropogenic impacts including road mortality, crab trapping and overcollection, *M. terrapins* are declining across their range. However, the decline is not unique to their species because many turtle species globally are declining. This emphasizes the need for better methodologies to be developed in order to learn faster than the species are declining. While traditional sampling methods can be invasive and time consuming, the field of drone ecology can counter these challenges. Drone ecology is a novel field that allows for a relatively unbiased and non-invasive approach for understanding population dynamics. The objective of this project is to develop and evaluate methods that use drone imagery to measure the body size of *M. terrapin* to further understand population dynamics. Especially for vulnerable populations, a non-contact approach to gain insights into a population's integrity is beneficial. Flight procedures included capturing various photos with a standard drone model, the DJI Phantom 4 Pro, at many heights above a known *M. terrapin* breeding aggregation. The photographs were then analyzed with a widely available software system, ImageJ, so that individuals could be identified and measured using the ground sampling distance, a measure that takes into account the height and camera sensor. The data captured via drone was compared to data recorded via traditional sampling methods to compare the methodologies for measuring *M. terrapin* populations. To validate the ability to measure shells via drone imagery, an accuracy test was done to compare known measurements to recorded drone measurements. Furthermore, the same aggregation was measured at varying heights to understand how height can impact accuracy of the measurements. Drone ecology has the potential to provide a new approach to learning about vulnerable wildlife populations without direct contact.

DEPARTMENT OF CHEMISTRY AND PHYSICS

SRP-9

A SPECTROSCOPIC STUDY OF THE B TO A CONFORMATIONAL TRANSITION IN DUPLEX DNA

Noureen Qureshi, Samantha LeCrone, and Tomas Barry
Monmouth University, Department of Chemistry and Physics

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

Funding Sources:

Monmouth University School of Science, Department of Chemistry and Physics

Abstract

The transition from the standard B-form DNA helix to A-form DNA was first observed through 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. The experiments were conducted on three different strands, with probes placed at a) the end of the duplex, b) the middle of the duplex, and c) with a mismatch of bases. Our results showed we could induce B to A transition in all these strands, and simultaneous monitoring of local and global conformational change is possible with the incorporation of 2-AP.

SRP-10

UNRAVELLING LIGAND-INDUCED LOCAL CONFORMATIONAL CHANGES IN G-QUADRUPLEXES USING FLUORESCENT BASE ANALOGUES

Daniel Flynn and Macklin Jugan

Monmouth University, Department of Chemistry and Physics

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

Funding Sources:

Monmouth University School of Science, Department of Chemistry and Physics

Abstract

G-Quadruplexes (GQs) are crucial structural components located in the telomeric regions of eukaryotic chromosomes. Telomerase activity, which plays a vital role in cancer progression and aging, can be affected by introducing small molecules that interact with GQs. 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 showed that the ligands' effect on the GQs' stability depends on the probe's position. Further, the study demonstrated 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.

SRP-11

TRANSCRIPTION OF HAMMERHEAD RIBOZYME AND SPINACH APTAMER TO MEASURE WITH FLUORESCENCE

Ashley Salguero

Monmouth University Department of Chemistry and Physics

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

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

Abstract

In our investigations, we utilize *in vitro* for kinetic studies of hammerhead ribozyme activity. As well as exploring the folding of the Baby Spinach aptamer.

Hammerhead ribozymes, small self-cleaving RNA molecules, hold significant promise in genetic therapy due to their intrinsic catalytic RNA-cleaving activity. A comprehensive understanding of their enzymatic mechanism is crucial for optimizing therapeutic applications and elucidating the intricate RNA cleavage process. These ribozymes achieve site-specific cleavage of target RNA sequences, making them valuable tools for precise gene regulation and innovative antiviral strategies.

The Baby Spinach aptamer is a synthetically engineered RNA molecule that transforms RNA visualization in living cells. This aptamer functions as a genetically encodable, fluorogenic tag for RNA, analogous to Green Fluorescent Protein (GFP) for proteins. Its unique functionality arises from its specific interaction with the non-fluorescent ligand, 3,5-difluoro-4-hydroxybenzylidene imidazolinone (DFHBI). Upon folding into its defined three-dimensional conformation, which critically involves the formation of a G-Quadruplex, the aptamer creates a precise binding pocket. This interaction significantly enhances DFHBI's quantum yield, inducing bright green fluorescence.

After transcription, Urea-PAGE purification and quantification by absorbance, the concentrations were 1.62μM, 3.97μM and 9.47μM for the Hammerhead Ribozyme, Hammerhead Substrate and the Baby Spinach Aptamer respectively.

The concentrations were too low for a ribozyme activity. However, a single melting temperature denaturation of the Baby Spinach Aptamer-DFHBI by fluorescence was performed, leading to a Tm of 48.0ºC.

The next steps would involve hammerhead kinetics as well as more baby spinach melting denaturation using chemical compounds that could potentially (de)stabilize the G-Quadruplex structure.

SRP-12

INVESTIGATING BABY SPINACH RNA APTAMER FLUORESCENCE WITH DFHBI TO MEASURE G-QUADRUPLEX STABILITY

Rina Lee[1], Melanie Morales-Paz[2], Julianna Proscia[2]

[1]: Case Western Reserve University, Biochemistry
[2]: Monmouth University, Department of Chemistry and Physics

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

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

This project characterized a baby spinach RNA aptamer that fluoresces upon binding to the small-molecule, analogous to the green fluorescent protein fluorophore, DFHBI. The aptamer's fluorescence served as an indicator for structural integrity and functional folding, specifically, its G-quadruplex conformation.

To assess proper folding and fluorescence activation, DFHBI was added in a 100:1 molar ratio to RNA. Unbound DFHBI remains non-fluorescent due to internal rotation, dissipating absorbed energy as heat. When bound to the G-quadruplex structure in the RNA, this rotation is restricted, resulting in the dye releasing energy by emitting light at a higher wavelength-producing fluorescence.

Fluorescence was measured at 503 nm (excitation at 466 nm) using a cuvette-based assay. A temperature scan from 2˚C to 65˚C showed strongest fluorescence at low temperatures, indicating proper and stable G-quadruplex folding. A decrease in signal with increasing temperature reflected RNA unfolding and structural destabilization. From these graphs, melting temperatures (Tm) were determined through first-derivative analysis of fluorescence curves, reinforcing reversed folding behaviors between cycles. The melting temperature was determined as 45.5ºC.

These results validate the proper transcription, purification, and conformational integrity of the baby spinach RNA aptamer. Additionally, this system demonstrates the utility for real-time structural RNA analysis.

DEPARTMENT OF COMPUTER SCIENCE AND SOFTWARE ENGINEERING

SRP-13

GAREL: RELATIONAL REASONING FOR MUTABLE ARRAYS

William Judd
University of Illinois Urbana-Champaign

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

Funding Sources:
NSF CRII 2451348

Abstract

We present GArel, a novel relational type and effect system designed to reason about general relational quantitative properties involving mutable arrays in a functional programming context. GArel extends prior work on relational cost analysis, particularly building upon ARel, by enabling more expressive and precise reasoning over array-manipulating programs.

A central challenge in analyzing such programs is identifying the appropriate information to track about mutable arrays to support accurate relational reasoning. GArel addresses this by allowing customizable relations within the array information β, facilitating fine-grained and context-sensitive relational comparisons. Furthermore, it introduces a parameterizable grading mechanism that generalizes beyond relative cost, enabling the system to verify a broad spectrum of quantitative relational properties.

In addition to the theoretical framework, we implement a relational type checker for GArel, with a strong emphasis on performance and automation. Our implementation integrates advanced SMT solvers and employs an optimized algorithmic formulation of the type system, which significantly improves type-checking efficiency and scalability. The result is a powerful and practical tool for reasoning about quantitative behavior in programs that manipulate mutable arrays, advancing the state of the art in relational program analysis.

SRP-14

SENTINEL LLM: A CLINICAL Q&A CHATBOT FOR EARLY SEPSIS DETECTION

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Funding Source:
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Abstract

Sepsis is a critical medical condition that arises when the body's response to infection causes life-threatening organ dysfunction. Despite heightened awareness and protocol-driven management strategies, early diagnosis remains a persistent challenge in clinical practice, especially in high-pressure settings like emergency departments and ICUs. Nurses, as frontline responders, are pivotal in identifying early signs but often work under cognitive overload and protocol ambiguity.

Large language models (LLMs) represent frontier neural network techniques that use self-supervised learning algorithms to process and understand human languages or text. This project aims to develop Sepsis Sentinel LLM, an interactive clinical chatbot fine-tuned on sepsis-specific knowledge. Built on compact, decoder-only transformer models like Phi-2 or Mistral-7B, and hosted in a lightweight Gradio interface, this tool will be designed to sit at the nurses' station to assist with real-time clinical queries. Students will complete the end-to-end machine learning pipeline—from data collection to fine-tuning, testing, and deployment—with a strong emphasis on safety, groundedness, and clinical relevance.

DEPARTMENT OF MATHEMATICS

SRP-15

SOLUTIONS TO COMPARTMENTAL MODELING

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

Abstract

The spread of diseases has become an annual occurrence where the impact can be on a global scale. One method used to predict the spread of diseases is the SIR model, which categorizes the population into one of three compartments. A person can be susceptible to the disease (s), currently infected with the disease (i), or recovering from the disease (r). As time goes on, people will move from s to i, from i to r, from r to s, and then the cycle will repeat. The SIR model consists of a set of equations relating the rates of change of each compartment state, with the three states. This research intended to predict the long-term behavior of the three states in the SIR model with initial values for each variable, as well as outlined parameters. Using the series solutions of each variable, we employ Newton's method to approximate solutions. We considered what happens when the parameters are also changing over time, in addition to the variables. This includes the derivation of the equilibrium state for each of the variables. Our results suggest that the dependence between the parameters and states is stable. This can be used to shed more light on how certain diseases progress within any given population and how certain changes in the parameters alter that progression. Furthermore, this can serve as the baseline to analyze how herd immunity and/or vaccination rates affect the spread of diseases.

SRP-16

DETECTION OF A MYSTERY PLANET USING ORBITAL DEVIATIONS

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Faculty Mentor: Torrey Gallagher, Department of Mathematics

Funding Sources: Monmouth University School of Science

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 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 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 live in our star system? We use numerical integration in Python to simulate these star systems and draw numerical conclusions along with some fun animations of the orbiting bodies.

In particular, we plot the deviations of our home planet from its theoretical orbit and, using the Fast Fourier Transform, we are able to draw some conclusions about the orbital period of the mystery planet. Additionally, we use the instances of maximal deviation to find patterns with the mystery planet's orientation relative to our home planet with the hope of determining exactly where to point our telescope in the sky.

SRP17

BEYOND HERONIAN SHAPES: LATTICE *n*-GONS

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Funding Sources:
Monmouth University School of Science; Mathematics Department

Abstract

Heronian *n*-gons are polygons with n vertices, integer side lengths, and integer area. A lattice *n*-gon is a polygon that can be placed into the *xy*-plane so that the vertices are integer coordinates. Previous SRP students have studied the question of when Heronian quadrilaterals can be transformed to this integer placement using Fricke's method; however, his process requires an already rational placement.

Given a lattice *n*-gon, the distance formula implies that the distance squared between any two vertices must be an integer that can be written as a sum of two squares. This places a restriction on what lengths the diagonals can be in a Heronian lattice shape: integer norm. Additionally, Pick's Theorem tells us that lattice polygons must have rational area; specifically, an integer or rational number with denominator two.

This summer we proved the converse: *n*-gons with rational area and vertices that create integer norm sets are lattice polygons. This is done with an initial rotation to make previously irrational coordinates rational and then applying Fricke's method, if necessary. This expands the types of polygons that are known to be lattice beyond Heronian shapes. In this process, we discovered an infinite family of right triangles with irrational side lengths that are lattice and a method to translate *n*-gons with irrational side lengths and irrational coordinates to either a rational or integer placement.