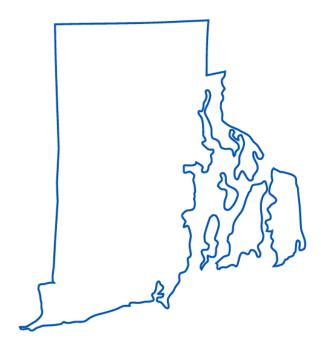# 2024 RHODE ISLAND SUMMER

UNDERGRADUATE RESEARCH SYMPOSIUM

Friday, July 26, 2024

UNIVERSITY OF RHODE ISLAND

CENTER FOR BIOTECHNOLOGY & LIFE SCIENCES
FASCITELLI CENTER FOR ADVANCED ENGINEERING
PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

Sponsored by

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2024 RHODE ISLAND SUMMER UNDERGRADUATE RESEARCH SYMPOSIUM

8:00 – 9:00 AM **CHECK-IN & CONTINENTAL BREAKFAST**
- CENTER FOR BIOTECHNOLOGY & LIFE SCIENCE

POSTER SET-UP
- FASCITELLI CENTER FOR ADVANCED ENGINEERING
- PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

9:00 – 9:30 AM **WELCOMING REMARKS**
- CENTER FOR BIOTECHNOLOGY & LIFE SCIENCE

DR. BARBARA WOLFE
- PROVOST, UNIVERSITY OF RHODE ISLAND

MS. BARBARA J. NAUMAN, M.B.A
- INTERIM VICE PRESIDENT OF ACADEMIC AFFAIRS, COMMUNITY COLLEGE OF RHODE ISLAND

MR. NEIL STEINBERG
- CHAIR, RHODE ISLAND LIFE SCIENCE HUB

DR. KERRY LAPLANTE
- DEAN, COLLEGE OF PHARMACY, UNIVERSITY OF RHODE ISLAND

9:30 – 11:00 AM **POSTER SESSION A**
- FASCITELLI CENTER FOR ADVANCED ENGINEERING
- PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

11 AM - 12:30 PM **POSTER SESSION B**
- FASCITELLI CENTER FOR ADVANCED ENGINEERING
- PARAMAZ AVEDISIAN '54 HALL, COLLEGE OF PHARMACY

POSTER PRESENTATION SCHEDULE

*** PLEASE NOTE: Posters are to be set up prior to the welcoming remarks and should remain up until 12:30 PM. Posters are to be presented according to the schedule below.*

Session	Presentation Times
A	9:30 – 11:00
B	11:00 – 12:30

Poster numbers	Location
1-25 (A & B)	Fascitelli Center for Advanced Engineering, 1st Floor (FCAE – Toray)
26-49 (A & B)	Fascitelli Center for Advanced Engineering, Ground Floor (FCAE - LL)
50-73 (A & B)	Paramaz Avedisian '54 Hall, College of Pharmacy (Avedisian)

NOTE: an Author Index is located at the end of this document

POSTER SESSION A
9:30 – 11:00 AM

Fascitelli Center for Advanced Engineering, 1st Floor
A-1 to A-25

Fascitelli Center for Advanced Engineering, Ground Floor
A-26 to A-49

Paramaz Avedisian '54 Hall, College of Pharmacy
A-50 to A-73

Development of a MATLAB-COMSOL Integrated GUI for Designing Multimode THz Fibers

Ahmet Akosman[1] & Eliana Leventhal[2]

[1]Electrical Engineering, Roger Williams University, Bristol, RI
[2]Computer Engineering, Roger Williams University, Bristol, RI

The THz region, which spans from 0.1 to 10 THz, holds significant potential for applications in telecommunications, medical imaging, and spectroscopy due to its unique properties, such as low photon energy and high penetration depth. The overall goal of this research project is to design optical fibers for use in the terahertz region, run them through electromagnetic Multiphysics COMSOL simulations, and to fabricate the fibers using a 3D resin printer. COMSOL is powerful in computing intricate Multiphysics equations, however it is difficult and tedious to manually set up a simulation within the software. Thus, this project focuses on creating a graphical user interface (GUI) to integrate MATLAB and COMSOL, using COMSOL's live link server. This GUI allows the user to input a series of parameters for the geometry and material of the fiber, and the instructions for a simulation, then the GUI can then output data from the simulation; both numerically and graphically. With the developed GUI, a unique multimode THz negative curvature fiber design based on UV-cured photosensitive resin is proposed and analyzed in detail to reach over 100 modes below the figure of merit loss of 1 dB/m for potential 6G communication protocols.

Negative Curvature THz Fiber based Biosensor Design and Fabrication for Analysis of Blood Constituents

Julia Ward, Riley Como, Ethan Neidt & Ahmet Akosman

School of Engineering, Computing and Construction Management, Roger Williams University, Bristol, RI

Terahertz (THz) radiation has recently gained significant attention owing to its potential in sensing, detection, and communications applications. The unique interactions of THz signals with materials, particularly their strong absorption by water, have sparked interest in employing THz technology for cancer detection and biosensing applications. Among recent advancements, hollow-core negative curvature fiber topologies have emerged as a promising candidate for low-loss electromagnetic wave transmission and refractive-index-based sensing. This study aims to explore unique fiber geometries for optimized total loss and sensitivity, enabling improved broadband THz biosensing capabilities. Utilizing a finite element method based electromagnetic solver, comprehensive numerical analyses were executed to design and evaluate performance of elliptical and circular 5-tube negative curvature fiber geometries tailored for THz radiation. Fiber parameters including the core diameter, ring diameter, and cladding thickness were swept to determine the optimal geometry for achieving the lowest total loss. To assess refractive-index-based sensing, individual blood constituents were introduced into the fiber core region. Blood components including water, plasma, hemoglobin, RBCs, and WBCs were numerically examined as fiber core analytes. Uniform relative sensitivities exceeding 90% for all blood constituents are achieved for a broadband frequency interval of 0.5 to 2 THz centered at the targeted frequency of 1 THz. To evaluate the feasibility of fabricating these hollow core fiber designs, they were manufactured using an SLA Resin 3D Printer. Various printing parameters were optimized to create consistent prints. Image analysis software was used to determine what printing parameters resulted in the minimum wall thickness deviation within a print. In conclusion, unique fiber designs were developed to investigate their biosensing potential in blood constituents through THz radiation. The findings of this study pave the way for advancements in THz biosensing technology.

Developing Resources and Experiences to Make Augmented Reality More Accessible

Aidan Donnellan

Engineering, University of Rhode Island, Kingston, RI

When it comes to augmented reality or any emerging technology, it can be difficult for the public to imagine how these technologies can be used in or integrated into our lives if they can't get their hands on it themselves. This summer, I contributed to a project with the DWELL Lab to create a solution to that issue. Our goal was to develop a web-based augmented reality (AR) product where users could not only experience AR but also be able to create their own experiences. My job was to consolidate information about the existing AR.js (Etienne. et al, 2017) open-source library and create an MVP (Minimum Viable Product) as a proof of concept. An MVP is related to developing a mock-up that displays the main point or features that characterize the final product. One of the most important features for the MVP to include was multiple different ways to edit and develop an AR scene to make it more accessible. All models, placements, and animations can be fully done within the HTML file that runs the website but not everyone knows or should need to know how to code to experience AR. Using features already packaged with the library, the MVP gives the ability to edit, create, and augment an AR scene without the use of any code. Along with this, the website includes an intro tutorial that highlights buttons and features on the UI (user interface) to guide the user through making their first AR experience. The tutorial has visual and text elements to appeal to different learning styles. It was also imperative for people to have access to this technology from any device. With an app-based solution, implementing more nuanced and complex features is possible. However, more skills are required on both the consumer and developer sides to make the experience usable (Greene, 2018). While app-based solutions have the benefit of being more powerful, this barrier has the potential to dissuade first-time users who are the main target audience of our project. This led us to a web-based solution. This kept our product accessible, but most importantly "such a powerful technology, that can help people and leverage their creativity, should be free in some way" (Carpignoli. et al, 2023).

For the poster, I will explain the importance of accessibility for AR, discuss current progress on the project, plans, and provide an example of the website for demonstration.

What's the story? Developing engaging narratives to communicate scientific research

Sydney Barnett[1], Ellen Fritz[2] & Shaun Kirby[3]

[1]Environmental Science, Bryant University, Smithfield, RI
[2]Painting & Computational Technology, Rhode Island School of Design, Providence , RI
[3]RI NSF EPSCoR, University of Rhode Island, Kingston, RI

From detecting DNA sequences of invasive species living in local waters to reconstructing Block Island's glacial history to preserve its cliff sides from sea level rise. RI C-AIM research strives to answer important scientific questions regarding climate change in the Ocean State. There is a critical need for this research to reach diverse audiences outside the scientific community that hold a social, cultural and/or economic stake in the health of Narragansett Bay. Storytelling is one of the most powerful ways to inspire and encourage a more engaged and informed public. Personal stories can demystify the processes and results of scientific research, which is often inaccessible to those without the expertise. Science communication can offer new insights into how science stories are as relevant to the social fabric as any other news story on politics or pop culture. This project entails engaging with other SURF students to create journalistic pieces accompanied by artistic visuals that highlight their research, research significance, and experiences. We develop interview questions, conduct interviews, and craft narrative stories that effectively communicate the science of a given research topic, as well as people's personal pursuits and journeys.

The final project culminates in the form of a website, which contains all of the completed narrative stories and visuals ready for easy distribution.

https://web.uri.edu/rinsfepscor/2023/11/15/whats-the-story-developing-engaging-narratives-to-communicate-scientific-research-p23/

What is in your water? Water Filtration Activity for Grades Five and Six in RI Coastal Communities

Zulay Izazaga[1], Jillian Nash[1], Julia Gandrud[2] & Anabela Maia[1]

[1]Biology, Rhode Island College, Providence, RI
[2]RI STEAM Center, Rhode Island College, Providence, RI

Climate change is strongly affecting the port of Providence through sea level rise and extreme weather events including thermal expansion, and more prevalent flooding. At the same time, the surrounding South Providence and Washington Park neighborhoods are characterized by growing poverty levels and living costs, a high dependency on natural resources (drinking water, clean air) and inability to effectively adapt to changes in the climate. As flooding and heavy rain happen more frequently, storm water runoff increases, directly affecting the water quality of lakes and oceans in the community. Our team aims to help coastal community members understand and respond to the problems posed by climate change and how to become more resilient through educational activities focused on community concerns such as water quality and pollution. These instructional exercises can be used in the classroom for students in grades fifth through sixth, or easily adapted for community outreach events. These educational activities were designed to be low cost, hands-on, standalone and showcase a sample finished final product. We designed a water treatment lesson plan in which students may design, build, and test their own water filter device out of recycled water bottles, household objects (cotton balls, coffee filters, cups), different rock sizes, and sand. In addition to demonstrating how water in the community is made safe to drink, this project gives students a firsthand look at the work of environmental engineers, which is relevant to the Next Generation Science Standard 3-5-ETS1-2. This practice can help encourage kids to keep the waterways in the community clean and sensitized for water quality issues after flooding events. Engaging the community in these activities raises awareness of community concerns and allows community members to better understand the steps that may be taken towards making the community more resilient.

Measuring Biodiversity in Narragansett Bay with Environmental DNA Techniques

Emma Barry, Owen Finnegan, Andrew Hogan & Jeffrey Markert

Biology, Providence College, Providence, Rhode Island

Shed or excreted DNA fragments from fish can be quantified to 1) determine which fish species are present and 2) estimate species abundance. Our collaborators at Roger Williams University have obtained census counts of fish species from three habitats in Narragansett Bay with seine nets. Dr. David Taylor of Roger Williams University has recorded his fish counts, and we collected water samples at the same locations, days, and times as his crew deployed their nets. To test how well the abundance of species-specific DNA fragments correlates with the census counts, we learned to use quantitative PCR to measure the concentration of DNA left over in the water from five focal fish species native to Rhode Island: Winter Flounder, Summer Flounder, Bluefish, Black Seabass, and Tautog. We compared the presence/absence data and the DNA concentrations that we received from our qPCR results to Dr. Taylor's counts and found that analyzing water samples with qPCR detects more species than determining biodiversity by physically seeing the fish. We also found little correlation between the concentration of DNA in the water and the abundance of fish seen by Dr. David Taylor when studied globally among all three sites.

Identifying and Tracking Invasive Species in New England with Environmental DNA
Owen Finnegan

Biology, Providence College, Providence, RI

Invasive species are a widespread concern in the United States, impacting almost every ecosystem across the country. Their presence, either through human introduction or a changing habitat, threatens the stability of ecosystems and native organisms. Monitoring the areas most vulnerable to these invasive species is critical to promoting the health of these regions, but at times, it can be difficult to survey. Environmental DNA (eDNA) has been used to detect rare and invasive species in water bodies to identify where these organisms are present without physically identifying them. Environmental DNA is derived from cellular material that an organism has left behind in its habitat. Samples can be taken from a habitat, and eDNA can be extracted and amplified through quantitative polymerase chain reaction (qPCR) to identify a species. We worked in both marine and freshwater systems to test the effectiveness of qPCR on species invasive to New England: Basket Clams (Corbicula fluminea), Shore Crabs (*Hemigrapsus sanguineus*), and Mitten Crabs (*Eriocheir sinensis*). Our research team tested sites where these invasives were known to be found, according to the Rhode Island Department of Environmental Management, along with sites in the surrounding area to locate other affected water bodies. We plan to continue working with eDNA to determine if we can identify if the organism is present and estimate the number of individuals in a given area.

Mechanisms of viral resistance differ among closely-related marine cyanobacteria

Lily Winsten

Biology, Roger Williams University, Bristol, RI

Synechococcus spp. are unicellular cyanobacteria that play a critical role as primary producers in Narragansett Bay (NB). These cyanobacteria can be lysed daily by co-occurring viruses, yet *Synechococcus* abundance in NB remains high, ranging from 10^4 to 10^5 cells/mL during the summer. This indicates that *Synechococcus* must exhibit resistance to many of these viruses. Marine *Synechococcus* spp. lack the CRISPR-Cas gene editing system that often provides immune defense against viruses, suggesting that they instead possess other types of resistance mechanisms. These could include changes in cell surface receptors that prevent viral attachment as well as intracellular defense mechanisms that prevent viral replication within the cell. This study investigated the mechanisms of viral resistance present in closely related NB *Synechococcus* strains exposed to isolates belonging to two genetically distinct viruses (RIM8 and RIM34). Pairwise infection kinetics assays were conducted using four *Synechococcus* cell types and four different viruses all isolated from Narragansett Bay. Viral attachment to cells and replication within cells was quantified over a 48 hour time period utilizing qPCR. Two of the *Synechococcus* strains, NB621-04 and NB621-07, were susceptible to the four viruses, but displayed varying levels of both viral attachment and replication. The other two cell strains, NB621-11 and NB720-25, were resistant to all four viruses and no viral replication was observed. In some cases, the viruses could not attach to the cells, suggesting that resistance may be caused by changes in cellular receptors. However, some of the viruses could attach to the cells but could not replicate, indicating that resistance is likely due to an intracellular defense mechanism. To further characterize viral resistance, next steps will include experimentation to understand which steps in the viral life cycle are blocked within the cell. In addition, full genome sequences of the cells will be used to examine the cellular genetic mechanisms associated with resistance.

Phosphate Groove: Unlocking the Rhythms of Sedimentary Deposits in the Kickamuit and Taunton Rivers

Gabriella Wade, Brennan Foley, Jamie Wells, Gabriella Fabrizi & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

Phosphorus can be found in many different forms (organic and inorganic), in soils, water bodies, and ocean sediments (Franson and Jones, 2007). All living organism utilizes phosphorus in numerous metabolic cycles and as structural motifs (Downing et al. 2000). The bioavailability of phosphorus, a limiting nutrient in the environment determines the successful growth of organisms, having a significant impact on primary production, species distribution, and ecosystem structure (Ferrier-Pages et al., 2016). Freshwater deposition of free phosphorus ions occurs upon mixing with alkaline saline waters into marine sediments thus becoming a reservoir for loose and tightly bound forms that can be ecologically recycled within this niche.

 In this investigation, the concentration of total phosphate, inorganic phosphate, organic phosphate, and water-soluble phosphate was determined from pore waters extracted from Mt. Hope Bay marine core sediments. Surface water, filtered pore water samples, as well as extruded dried sediment segmented samples were analyzed for their salinity, pH, conductivity, nitrate, nitrite, and sulfate, via HACH® protocols. Elemental analysis by ICP and XRF spectroscopy were conducted following established methods. This study shows that as total organic sediment carbon increases, total phosphate content increases. Pore water-soluble phosphate increases with depth from the surface of the core. No relationship was determined for the ratio of bond inorganic phosphorus to iron, remaining relatively constant with the analysis. The pH of pore water becomes more alkaline with an increase in depth from the surface. This is also reflected in the change observed in nitrate and nitrite content going from an aerobic to an anoxic environment with increasing depth.

Perchlorate in Portraits: Quantifying the Disappearance of Perchlorate in Washed Martian Regolith Using Spectroscopic Instrumentation

Gabriella Fabrizi, Jamie Wells, Gabriella Wade, Brennan Foley & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

On Earth, perchlorate ions are found naturally in isolated deposits. However, on Mars, they are much more widely distributed (1-2 wt%). If plants were to be grown in Martian regolith containing >1 wt% perchlorate, growth would be stunted or halted entirely (Oze et al. 2021). Those plants that do grow would rapidly absorb the perchlorate, making them hazardous to human health upon ingestion. Three Regolith simulants from Exolith Labs® reflecting the elemental composition of Martian regolith were used to compare the efficacy of deionized water, HCl, Acetic Acid, and EDTA at removing 1 wt% perchlorate, sulfates, and nutrient metals. MGS-1 and MGS-1S regolith simulants are Mars Global Simulants that represent the average sediment composition across the Martian planet. MGS-1S is supplemented with additional sulfates. JEZ-1 regolith simulant is representative of the Equatorial Jezero Delta Crater, which is thought to be an ancient sea bed.

Since the concentration of perchlorate in washed samples is below the limit of detection of the Methylene Blue Chemical Spot Test, spectroscopic instrumentation is required to identify and quantify the loss of perchlorate and sulfates in the regolith simulant. ICP-OES permitted the successful quantification of nutrient metals, however chlorine and sulfur could not be quantified at the tested wavelengths. Using XRF, chlorine and sulfur were quantified from dried samples of regolith that had been fully washed. In addition, sulfates could be quantified with HACH® protocols as a proxy for perchlorate due to the similar solubilities of the two compounds. ATR-FTIR and HPLC-IC could both detect highly resolved perchlorate peaks in sediment washes, and HPLC-IC could also detect sulfate peaks. FTIR-DRIFTS and RAMAN spectra obtained from dried regolith exhibited too much background fluorescence for any reliable quantification of either perchlorate or sulfate.

Interactions Between Marine Bacteria Cobetia marina and Polystyrene Microplastics

Emma Murdock[1], Lauren Lamothe[2], Animesh Pan[2] & Geoffery Bothun[2]

[1]Biological Sciences, University of Rhode Island, Kingston, RI
[2]Chemical Engineering, University of Rhode Island, Kingston, RI

The Sea Surface Microlayer (SSML) is the interface between the surface layer of the ocean and the Earth's atmosphere. With rising amounts of plastic pollution globally, plastics are ending up in the ocean in large quantities. Most of these plastics enter the ocean in the form of macroplastics, and over-time are degraded into micro and nanoplastics (MPs and NPs), through chemical and physical degradation. Microplastics and nanoplastics then accumulate in the SSML, interacting with the organic components within it. Widespread research and understanding of the consequences of these particles is limited. The goal of this project is to determine the effects of plastics, specifically as they interact with marine bacteria Cobetia marina. Microplastics were used in this project, specifically for the size of the particles, as bacteria have a larger surface to aggregate. Understanding the interactions of MPs with this bacteria is crucial for providing insight into how marine life and ecosystems are affected by plastic pollution as a whole. Negative impacts on bacteria present a significant threat to humans as well, as larger marine life used for consumption, like fish and shellfish, will be consuming bacteria that colonizes plastics. The plastics used in this experiment were commercial 20 µm polystyrene beads. By introducing varying concentrations of plastics to the bacteria, an understanding of the bacterial interactions was gathered. Qualitative data was collected in the form of optical density, which measures the absorbance, indicating the growth or decay of bacteria in relation to the presence of plastics. Additional studies were done on the formation of exopolysaccharides (EPS), as well as the chemical changes to those substances.

Single Particle Tracking for Tumorigenic Cell Sensing

Hayden Reilly, Lauren Hubert, Aceer Nadeem, Ryan Poling-Skutvik & Daniel Roxbury

Chemical Engineering, University of Rhode Island, Kingston, RI

Single-Walled Carbon Nanotubes (SWCNTs) have been investigated for their use in biosensing applications due to their distinctive optical properties. Due to their ability to be functionalized, SWCNTs are able to be used as biocompatible, long-term sensing devices. These unique characteristics of SWCNTs make them an ideal tool to track how nanomaterials can impact the environment and living organisms. This study proposes a method for detecting various cell-type dependent intracellular properties through the tracking of SWCNT movement within cells. GT-15 ssDNA-SWCNTs were first introduced into tumorigenic and non-tumorigenic human epithelial breast cells (MCF7 - MCF10a) via the cell membrane where they entered the early endosomal pathways. Using near-infrared (NIR) fluorescence spectral fingerprinting the ssDNA-SWCNTs were tracked as they moved inside of the cells. Particle tracking was done via MATLAB code that quantified the dynamics of the SWCNTs inside of the cell types. Analysis was performed, and a statistical difference was determined between the SWCNTs in the tumorigenic cells and the non-tumorigenic cells. These findings provide evidence that this method of single-particle tracking can be used as a sensor of tumorigenic transformation.

Hillslope Position Influences Variations in Tree Growth Over Time

Sean Costello, Elsie Siris & Joel Singley

Biology, Marine Biology, and Environmental Science, Roger Williams University, Bristol, RI

Tree growth depends on interactions between adjacent vegetation, local climate, and landscape properties. In arid, semi-arid, and Mediterranean climatic regions, hillslope position has been recognized as an important mediator of annual tree growth and its resilience to hydroclimatic variation, such as periods of drought. This relationship has garnered less research in humid, temperate regions such as Rhode Island, despite the fact that post-glacial landscapes can exhibit large variability in subsurface properties over small spatial scales. To begin addressing this gap, we cored 42 oak trees along a hillslope in Tiverton, Rhode Island, during the summer of 2024. We used image analysis software to measure annual growth for each tree. Our preliminary analyses identified greater maximum and median annual ring widths for trees lower on the hillslope compared to their similarly aged, but smaller diameter, counterparts higher on the hillslope. We also found that the minimum annual ring width was approximately the same regardless of hillslope position, and despite systematic differences in tree size. Broadly, all trees exhibited reductions in annual ring width at older ages, but the magnitude of these signals varied among hillslope positions, with trees at lower positions displaying the largest age-related changes in growth. The greater median and maximum ring widths of lower trees may indicate that conditions were more favorable for rapid growth at the bottom of the hillslope, especially in the early stages of their lives. In trees located on the upper part of the hillslope, the smaller absolute range of ring widths could suggest that these trees grew more consistently, regardless of climatic conditions. Overall, these results reveal that hillslope position is an important control on interannual growth patterns of oaks in this area. This provides a basis from which we will extract and analyze other growth signals that are indicative of sensitivity to hydroclimatic variability over the past century. Ultimately this work will provide further insight into the relative importance of stand age, topography, and climate as controls on the resilience of local forests.

The effects of gonad development in Atlantic Sea Scallops due to the habitat integration of Green Sea Urchins

Karina Torres[1], Brendan Elba[2] & Coleen Suckling[2]

[1]Rhode Island College, Providence, RI
[2]University of Rhode Island, Kingston, RI

Green Sea Urchins (*Strongylocentrotus droebachiensis*) were stocked with Atlantic sea scallops (*Placopecten magellanicus*) in lantern nets for approx. 2 months at a scallop farm site located within Casco Bay, Gulf of Maine. The goal of the trial was to determine whether the sea urchin's grazing habit could be used to feed upon and reduce biofouling on aquaculture gear and scallop shells and enhance scallop growth. During dissecting of the scallops integrated with sea urchins it was observed that gonad development appeared to be more enhanced compared to controls without sea urchins. This poster will focus on understanding this further whether sea urchin integration can enhance sea scallop gonad presence and size, compared to the controls without urchins, which would likely be beneficial for increasing grower profit.

Polyester microfiber retention time in laboratory seawater conditions

Brooklyn Mitchell[1], Amara Pouv[2] & Coleen Suckling[3]

[1]Marine Biology, University of Rhode Island, Kingston, RI
[2]Fisheries, Animal, and Veterinary Science, University of Rhode Island, Kingston, RI
[3]Aquaculture and Fisheries, University of Rhode Island, Kingston, RI

Microplastics are any plastic less than five millimeters and greater than one micrometer in length. They are created when larger plastics break down from processes like weathering. It is known that microplastics are present in virtually all marine ecosystems, however the impacts of these emerging pollutants is still not entirely understood. We have conducted experiments observing the accumulation and retention of polyester microfibers in the Eastern Oyster, Crassostrea virginica, with variation in the total quantity of fibers ingested by individual oysters. The goal of this work is to understand the exposure of the oysters to these engineered microfibers, by measuring their retention in seawater after introduction into laboratory controlled aquaria. Microfibers were introduced at a concentration of 950 fibers/Liter, and seawater samples were collected at high frequency within a 24 hour period This work is important for improving methodological approaches and descriptions in future microplastics studies which need to better describe exposures to organisms.

Effect of Specimen Geometry on Material Behavior when Subjected to Biaxial Loading

Layhla Morales & David Taggart

Mechanical, Industrial and Systems Engineering, University of Rhode Island, Kingston, RI

Material response when subjected to differing stress states is needed for effective design of reliable mechanical components. Various experimental methods have been developed to determine material behavior. Experimental results are used to determine behavior when subjected to various load condition. Information about the initial elastic response of a material as well as when it is expected to fail is crucial for engineering design as it helps to determine the most efficient material for a certain application. The most common experiment in material testing is uniaxial testing, where a specimen is subjected to loading along one axis. For materials subjected to loading in multiple directions, biaxial loading is often needed. In a biaxial experiment, a specimen with a cruciform geometry is subjected to loads along two orthogonal axes. Several recent investigations have examined the effectiveness of various cruciform specimen geometries. Ideally, the specimen geometry should induce a region of uniform biaxial stress where the corresponding strain field can be measured. These strain measurements provide an accurate measure of the material behavior under biaxial stressing. In this study, a b 3D printed TPU material was subjected to both uniaxial and biaxial testing. For the biaxial cruciform specimens, several geometries were tested to determine which shape would give the most accurate results.

Spatial variation in mercury contamination in freshwater fish species across Rhode Island

Brianna Lotti[1], David Taylor[1], Jonathan Serbst[2], Jim Lake[2], Alan Libby[3] & Mariel Sorlien[4]

[1]Marine Biology, Roger Williams University, Bristol, RI
[2]Environmental Effects Research Laboratory, Atlantic Ecology Division, U.S. EPA, Narragansett, RI
[3]Division of Fish and Wildlife, RI DEM, West Kingston, RI
[4]Narragansett Bay Estuary Program, Providence, RI

Fish provide essential nutrients and proteins beneficial to human health, yet may pose certain risks due to contaminants in edible tissues. For example, mercury (Hg) is a widespread toxicant that bioaccumulates in fish muscle (filet) tissue. Accordingly, federal and state government agencies issue consumption advisories to minimize diet related Hg exposure. Fish consumption advisories, however, often fail to account for small-scale spatial variations in Hg contamination, especially in freshwater fishes. This study examined site-specific Hg concentrations in bluegill sunfish (*Lepomis macrochirus*), pumpkinseed sunfish (*L. gibbosus*), largemouth bass (*Micropterus salmoides*), chain pickerel (*Esox niger*), and yellow perch (Perca flavescens), all of which are commonly consumed freshwater species. Target fish were collected from 57 lakes and ponds throughout Rhode Island from 2007 to 2023 using an electrofisher and rod & reel. Muscle tissue was extracted from each fish and measured for total Hg concentration (ppm wet weight) using automated atomic-absorption spectroscopy. For each waterbody, fish Hg data were size standardized, and mean values were analyzed relative to water chemistry and surrounding land use patterns. Total Hg concentrations were inversely related to pH and the areal extent of medium-highly developed lands. These results are attributed to increased rates of bacterial methylation of Hg in acidified waterbodies. Moreover, developed and disturbed watersheds often have a net decrease in terrestrial-to-aquatic Hg transport due to the loss of deciduous forests. Aquatic environments adjoining disturbed landscapes also receive excessive nutrient and organic inputs, which lead to biogeochemical conditions that inhibit Hg bioavailability to the food web.

Mercury content in the baleen plates of rorqual whales

Ava Cieplinkski[1], Max Ajemian[1], David Taylor[1] & Matthew Savoca[2]

[1]Marine Biology, Roger Williams University, Bristol, RI
[2]Hopkins Marine Station, Stanford University, Pacific Grove, CA

Mercury is a persistent environmental contaminant posing significant risks to wildlife health due to its propensity for bioaccumulation in organismal tissues. This study investigated total mercury concentrations in the baleen plates of rorqual whales (Family Balaenopteridae), specifically the Fin whale (*Balaenoptera physalus*), Blue whale (B. musculus), and Rice's whale (*B. ricei*). Archived baleen samples were sourced from the Smithsonian's National Museum of Natural History and analyzed for total mercury (Hg) content (ppm dry weight) using atomic absorption spectroscopy. Male Fin and Blue whales from the Antarctic, South Pacific region (1947-1948), with body lengths ranging from 21 to 24 m, exhibited mean Hg concentrations of 0.19 ± 0.05 ppm and 0.14 ± 0.01 ppm, respectively (n = 2 per species). In contrast, male and female Rice's whales from the Mid-Atlantic and Gulf of Mexico (1923-2009), with ranging from 5 to 13 m in length, demonstrated higher Hg burdens compared to their congeners, averaging 0.80 ± 0.66 ppm (n = 8). Rice's whales showed evidence of Hg bioaccumulation, as indicated by a positive relationship between Hg concentration and body size. Notably, size-standardized Hg levels in the 1923 Rice's whale sample was substantially higher compared to those from later years (1923 = 1.99 ppm; 1974-2009 = 0.39 ppm). The observed variations in Hg contamination across whale species likely reflect inter-specific differences in geographic location, migratory behavior, habitat use, and feeding ecology. Additionally, the reduction in Hg concentrations in Rice's whales post-1970 may be linked to global pollution control measures.

Molecular Assessment of Green and Brown Algal Diversity of the Punta Burica Peninsula, Pacific Panama

Ariana Medina & Brian Wysor

Biology, Marine Biology, & Environmental Science, Roger Williams University, Bristol, RI

Punta Burica is a small peninsula off the Pacific coast of Panama that is characterized by an intriguing mudrock substratum. This substratum supports diverse populations of macroscopic algae by virtue of creating pools for them to inhabit and by retaining water within the substratum, which appears to minimize desiccation for attached algae. The Punta Burica region has been poorly studied phycologically, but the first study of the region revealed some 20 new records from just 45 specimens of red algae. Here, we extend our understanding of the Pacific Panama marine flora by using DNA barcoding to establish the species richness of brown and green algae of the Punta Burica peninsula.

Examining Abundance and Taxonomic association of Plastic Degrading Genes in the Narragansett Bay

Aidan McCrillis, David Banks-Richardson & Ying Zhang

Cell and Molecular Biology, University of Rhode Island, Kingston, Rhode Island

The pollution of plastics has become a universal problem with an estimated 399,000 tons of plastic that has accumulated in the ocean. 69,000 tons are predicted to be microplastics, and this large proportion of microplastics makes it difficult to remove plastics from the ocean mechanically. One of the most promising solutions for this problem is to find plastic degrading genes (PDGs) in microbes and use these to degrade plastics in the ocean. In previous work, we identified over 9,000 PDGs from metagenomic data in the Narragansett Bay. Our goal for this project was to map the abundance of different PDGs over different seasons and characterize microbial taxa carrying plastic degradation pathways. To perform these analyses we mapped metagenomic sequencing reads from individual samples collected monthly over two and half years to assess changes in PDG abundance through time. Metagenome-assembled genomes were used to infer bacterial carries of PDG pathways and their abundances over time. We found that degradation of the Polyethylene glycol (PEG) plastics is the most abundant type of PDGs found in the Narragansett Bay, and that the abundance of PDG clusters are strongly correlated with each other, either positively or negatively. This indicates that many clusters could be encoded by the genome of taxonomic groups closely related in their abundance overtime. Our study also identified Proteobacteria and Bacteroidota as the main taxonomic groups hosting PDGs. Metabolic pathways were identified in metagenome assembled genomes for common intermediates of plastic degrading pathways, such as terephthalate (TP) and phthalate. For our differential abundance analysis we found that summer and fall samples were similar and that winter and spring were similar in their composition of PDGs.

Treatment of wet marine diesel exhaust with catalytic material based on perovskite photovoltaic incorporating mixed-valent vanadium oxide (V$_3$O$_7$)

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Diesel exhaust gases such as NO$_x$ and SO$_x$ are significant contributors to pollution in today's atmosphere. The International Convention for the Prevention of Pollution from Ships (MARPOL) Annex VI has a tiered system for regulating these gases from marine diesel engines. The current standard, Tier III, limits the NO$_x$ emissions based on a vessel's horsepower. Our approach is based on perovskite photovoltaic architecture using fluorine-doped tin oxide (FTO) glass substrates coated with four layers applied by doctor blading. The first two being a TiO$_2$ layer and a mesoporous TiO$_2$ layer, then a perovskite layer and V$_3$O$_7$ layer respectively. The perovskite layer solution was formed from 0.3481g FAI, 1.0125g PbI$_2$, 0.1465g PbBr$_2$, and 0.0449g methylammonium bromide (MABr) in 2mL (4DMF:1DMSO) and 105.2 μL cesium iodide (CsI) solution (9.7430 g CsI in 25mL DMSO) to activate in a conical vial. The mixed-valent vanadium oxide layer was formed by hydrothermal synthesis of 0.2275g vanadium oxide (V$_2$O$_5$) and 0.005g 4-aminophenol (H$_2$NC$_6$H$_4$OH) at 180°C for 48 hours. This poster highlights the substrates and materials formed and tested via XRD, XRF, and artificial exhaust seawater NO$_3^-$ and NO$_2^-$ Hach spectrometry.

Evaluating the Impact of BRUV Bait Height on Fish Behavior

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The use of BRUVS, or Baited Remote Underwater Video Systems, for ocean exploration and surveying is a relatively novel technique in the field of marine science. Advantages of BRUVS include being non-destructive, non-extractive, relatively inexpensive to build and operate, and relatively safe to operate. Still, BRUVS have some disadvantages, including the lack of standardization in design and methodology. Without standardization between BRUVS studies, the findings of any one study are limited in relevancy and comparability to others. The goal of this study is to find an optimal standard for one understudied aspect of BRUVS design: height of the bait arm above the sea floor. Optimizing this variable could contribute to future standardization of BRUVS methodology. In yet to be published deep-sea footage taken off the coast of Yaizu, Japan by a J-BRUVS, in which the bait arm was 1.5-1.8 meters off the seafloor, the vast majority of fish were seen lingering well below the bait. Among the several hundred individuals viewed in the 32 hours of footage, only two individuals were seen swimming upwards and interacting with the bait bag. With the camera mounted just above the bait arm facing the bait, fish remained obscured from the camera's clear frame of view, making accurate data collection difficult. Determining an optimal bait arm height to attract specific types of fish species could inform the experimental design of future BRUVS studies to improve the accuracy of data collected. A BRUVS, hereafter URI-BRUVS was designed, which can deploy bait at 20 cm, 40 cm, 60 cm, and 80 cm above the sea floor, in order to test the effects of different heights of bait deployment on fish behavior. URI-BRUVS has been tested at 11 meters in the waters of the Narragansett Bay in Rhode Island in July 2024. There are plans to deploy URI-BRUVS in deep-sea conditions (200 meters) off the coast of Cape Cod, Massachusetts, to collect data at several different bait heights in the following months. It is expected that the lowest bait height being tested, 20 cm above the sea floor, will be most optimal for maximizing the quantity and accuracy of data collection for carnivorous fish greater than 5.08 cm in length. The goal in determining the optimal height at which to deploy bait is to inform further standardization of future BRUVS designs.

Fouled fishing nets for use in construction materials

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Plastic marine debris is a major issue, having negative impacts on climate and species inhabiting the ocean. Converting plastic waste into construction materials is being carried out around the world to combat plastic pollution and help provide materials for various applications (e.g., paving walkways). The purpose of this study was to develop a method to analyze the impacts of utilizing dirty fishing nets in plastic block manufacturing. Abandoned fishing nets removed from Cuttyhunk Island, MA were used. The total mass of the fouled fishing net was 8150 grams. Macro fouling was collected by handpicking, and the rest was collected using a powerwash. Five one-liter samples of wash water were collected and analyzed in duplicate for three different tests. Each sample (handpicked and washed off fouling) and the cleaned fishing net were later weighed. The wash water was analyzed in accordance with the Standard Methods for the Examination of Water and Wastewater Solids method SM2540 to determine the mass of fouling present. Fourier-Transform Infrared Spectroscopy (FTIR) was used to characterize the composition of the nets. 186 g of macro foulers and debris (e.g., mussel shells, fishing hooks, feathers, sticks) were removed by hand. Results from the SM2540 Solids testing showed an average total solids of 0.89 g/L +/- 0.22 g/L (n=10). Total suspended solids had an average of 0.57 g/L +/- 0.11 g/L (n=10). Total dissolved solids had an average of 0.27 g/L +/- 0.06 g/L (n=10). Therefore, for the 7920 g sample of cleaned fishing net removed from Cuttyhunk Island, the total fouling (handpicked and washed off) by mass on the nets was estimated to be 230 g . FTIR results revealed polymers such as high-density polyethylene (HDPE), polypropylene (PP), polybutylene (PB) and nylon. Next steps include additional fouling quantification and characterization, manufacturing blocks containing clean and dirty fishing nets, and testing differences in compressive strengths between blocks containing clean and fouled fishing nets. These data will expand the consideration for use of fouled fishing nets as construction materials, potentially resulting in increased removal of marine debris from the ocean.

An investigation of the age of Pleistocene glacial deposits on Block Island Martha's Vineyard, Long Island, and Cuttyhunk Island using Optically Stimulated Luminescence

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Roughly 10 miles off the southern coast of Rhode Island, Block Island contains two shores of geological interest providing insight into regional Pleistocene glacial history. The outcrops found here give us a glimpse into the way sedimentary units which form the island have been stacked and distorted by glacial activity. Mohegan Bluffs on the southern shore boasts cliffs made of a recognizable stratigraphy consisting mainly of sand, silt, glacial diamicton, and conglomerate units overlying sections of gray clay. On the northeastern shore of Block Island is Clay Head. Here, the cliffs towering over the beaches consist of the same stratigraphic units, yet with better exposure of basal units, including abundant exposure of Cretaceous white sand and clay, which has been variably thrust and folded into the Pleistocene glacial sequence. We hypothesize that similarities in the sedimentary units and their deformation are due to relatively consistent depositional environments in front of and below a continuous margin of the North American Laurentide ice sheet during its advance and retreat in southern New England. The timing of ice advances and retreats is debated, without any well-constrained ages from the lower, more deformed glacial strata known as the Lower Drift, which can be correlated lithologically between Mohegan Bluff and Clay Head on Block Island and with equivalent strata on Martha's Vineyard, Cuttyhunk Island, and Long Island. Through Optically Stimulated Luminescence (OSL) dating, fine grains of quartz extracted from field samples can give us insight into the timing of deposition of Lower Drift units. The unique process of sample collection and preparation have been a focus in this project. We sampled basal and upper units of the Lower Drift (Jameco Formation and Hempstead Formation, respectively) across the four islands. We selected sample sites for relatively uniform grain size and composition, optimal depositional environments and lack of excessive disturbance by elements such as groundwater or iron oxides. Samples were prepared in a light-safe environment at the OSL lab at Utah State University, but due to the time-intensive nature of processing OSL samples, data from these samples are not yet known. Watercolor panoramas of the cliffs and relevant geologic units and features therein were also developed, especially from Clay Head at Block Island, in order to depict the complex glaciotectonic processes associated with the formation of Block Island.

Development of Aerosol Nanocomposite Microparticle (nCmP) Formulations Using Curcumin-Cyclodextrin Inclusion Complexes for the Treatment of Lung Cancer

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Lung cancer which can be categorized as small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC), is the leading cause of global cancer incidence and mortality, with approximately 2 million diagnoses and 1.8 million fatalities estimated. NSCLC is a heterogeneous class of tumors and represents approximately 85% of all new lung cancer diagnoses. Curcumin (CUR) is a type of polyphenol extracted from the rhizome of turmeric and it has multiple pharmacological activities, including anti-inflammation, antitumor, antioxidant, and antimicrobial activities. Curcumin has been widely studied for its anticancer properties via its effects on a variety of biological pathways involved in apoptosis, tumor proliferation, chemo- and radiotherapy sensitization, tumor invasion, and metastases. Curcumin was reported to have the capability to effectively inhibit tumor cell proliferation, migration, and invasion. However, the low aqueous solubility of curcumin limited its clinical application. Cyclodextrin is a kind of excipient widely used for pulmonary delivery which can increase solubility of hydrophilic drug and enhance bioavailability. Therefore, this project is to develop aerosol nanocomposite microparticle (nCmP) formulations with increased bioavailability using curcumin-cyclodextrin inclusion complexes to treat NSCLC. The scanning electron microscopy (SEM) images indicated that the nanoparticles were successfully prepared. The particle size and poly dispersion index (PDI) indicated that the nanoparticles were prepared with uniform size distribution. The negative zeta potential showed the stability of the nanoparticles was good. The thermal behavior of the nanoparticles was evaluated via differential scanning calorimetry (DSC). The drug loading (DL) and encapsulation efficiency (EE) demonstrated that curcumin was successfully loaded into the nanoparticles. The Bs type phase solubility diagram of CUR in -cyclodextrin indicated that an inclusion complex with limited water solubility was formed. In conclusion, the CUR loaded nanoparticles were formulated successfully and the solubility of CUR can be enhanced by forming an inclusion complex with -cyclodextrin.

Magnetic Biofouling Release in Polymer Composites

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Unmanned underwater vehicles for seafloor exploration encounter issues after biofouling such as increased weight, changed hydrodynamics and polymer degradation. Cleaning processes typically involve removing the robot from the water and physically scrubbing it, or treating it with a biocidal agent. These cleaning processes lead to instrument downtime as well as potential polymer degradation. Within the past few years, various materials have been developed to combat these issues, with underlying mechanisms inspired by nature. Such material solutions, however, are often intricate and are difficult to manufacture for implementation. We propose the fabrication of magnetic silicone composites that combine surface micropatterning and magnetically-generated undulatory motion to induce an anti-biofouling response which requires only a few steps to reproduce using commercially viable products.

Optimizing synthesis of magnetic nanoparticles for optimal bacterial biofilm penetration

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Magnetic nanoparticles can be used to remove biofilms from surfaces using alternating magnetic fields. This project studies how altering synthesis parameters during hydrothermal synthesis changes the size and magnetic properties of magnetic iron oxide nanoparticles. A positively charged polymer, polyethyleneimine, is used as a surfactant to control nanoparticle size and provide a surface chemistry that promotes bacterial biofilm internalization. The hydrothermal synthesis method was selected due to the compromise between synthetic simplicity, and nanoparticle performance. The parameters studied are the concentration of surfactant and iron reagent, reaction temperature and reaction time.

Effect of decreased snowpack on a rare frosted elfin butterfly (*Callophrys irus*) host plant

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In response to climate change, Earth's increased global temperature has caused less snowfall and earlier snowmelt in spring. These changes can alter the phenology of organisms such as plant leafing and flower blooming. This can harm species reliant on plants more sensitive to temperature changes. The frosted elfin butterfly (*Callophrys irus*) is a species of concern in 11 states, including RI and MA. These host plant specialists only lay eggs on small yellow wild indigo (*Baptisia tinctoria*) and wild lupine (*Lupinus perennis*). If neither plant emerges and develops leaves by the time butterflies are laying eggs, this would be catastrophic for the downstream population. To simulate the impact of climate change on yellow wild indigo, five 3m x 3m plots of three treatments (shoveled, trampled, and untouched) were established at Gavins Pond in Foxborough, MA. Wild indigo growing within the plots were measured and soil temperatures were logged biweekly. We predict that the growth of wild indigo plants and soil temperature will be greater in plots with decreased snowpack.

Determining Foraging Distances in a Fragmented Urban Landscape Via Mark-Recapture

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Pollinator populations are in decline, due in part to urbanization. While urban environments can support pollinator populations, habitat fragmentation can prevent pollinators from gathering proper nutrients. Connectivity between gardens is important in urban environments where spaces are separated by impervious surfaces. My research builds upon prior Bonoan Lab research on plant and pollinator richness/abundance and the unequal distribution of flowering plants, i.e., nutrients, through the seasons in on-campus bioswales (rainwater retention gardens). To survey floral abundance, I performed quadrat sampling along transects in the bioswales. To determine if bees can move between bioswales, I performed a mark-recapture study on *Bombus* (bumble bees) and the smaller *Agapostemon* (green metallic sweat bees). Data collected displays if bees on campus can move among gardens to balance nutritional intake. It focuses on the distances traveled by the bees and the number of bees in each garden as the flowers change throughout the seasons. This will allow campus, as well as urban areas, to create gardens suitable to support the pollinator populations throughout the year.

Impact of post-exercise hot or cold water immersion on blood pressure regulation in men and women

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Both hot and cold water immersion are promoted as recovery strategies after exercise, although most research to date has been done only in men. In this study we examined differences between men and women in blood pressure responses and autonomic recovery from post-exercise hot or cold water immersion. Methods: Fifteen participants (8 Males, 7 Females) performed three trials approximately one week apart. Each trial consisted of a 15 minute running warmup, followed by the participant running 8 intervals of 400m each, with a 1 minute break between. Once 8 intervals have been completed a cooldown of 15 minutes was done, followed by either cool water immersion (CWI; 30 min at 18°C), hot water immersion (HWI, 30 min at 40°C), or control (CON; 30 min seated rest). We collected systolic (SBP) and diastolic (DBP) blood pressure during pre exercise, post exercise, and in 12 hours using an automated blood pressure cuff. Results: Pre exercise, SBP was higher in men (131 ± 2 mmHg) compared to women (114 ± 2), as was DBP (Men: 73 ± 1; Women: 68 ± 1). In CON and HWI, DBP decreased 12h post-exercise in men (CON: -3mmHg [$p=0.02$]; HWI: -7mmHg [$p=0.05$]), but not women (CON: +2mmHg [$p=0.73$]; HWI: -4 mmHg [$p=0.14$]). After CWI, men experienced a larger increase in DBP (Pre: 71 ± 2; Post: 87 ± 2 mmHg; $p=0.003$) than women (Pre: 66 ± 2; Post: 72 ± 3 mmHg; $p=0.003$). SBP did not significantly change with any treatment for men or women. Conclusions: While CWI and HWI have both have an impact on blood pressure, there seems to be a higher impact in men than women regarding their diastolic blood pressure. Exercise alone or combined with HWI decreases diastolic BP in men more than women. Post exercise after CWI causes a greater hypertensive response for men compared to women. This can have a huge importance in understanding the impact of post-exercise hot or cold water immersion on blood pressure regulation in men and women.

Testing for color vision in peppermint shrimp, *Lysmata wurdemanni*, *L. boggessi*, and *L. jundalini*, using optomotor response

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Peppermint shrimp (*Lysmata wurdemanni*, *L. boggessi*, and *L. jundalini*), are cleaner shrimp that specialize in removing dead and diseased tissue, and parasites on reef fishes. Crustaceans have a range of visual abilities, from being color blind to having many visual pigments, but most of them are limited in their ability to discern colors. A rotating optomotor drum with vertical stripes of blue and red shades were used to document the behavioral responses of each of the *Lysmata* sp. to determine whether they have color vision. The specific shades of blue and red were selected to have the same relative photon catch, i.e., the shrimps' presumed known photoreceptor visual pigment absorbed the same amount of light reflected from these two colors. These photon catches were determined by assuming a maximum spectral absorption of the visual pigment of Lysmata sp. identical to published data on *L. amboinensis*, which has a single visual pigment at λmax=518 nm. To this visual pigment, the generated colors red (645nm, photon catch 0.435) and blue (400nm, photon catch 0.432), have no contrast. Each drum was rotated around a 15cm$\times$15cm cylindrical tank housing a single shrimp for two minutes at 6rpm. After the first minute, the direction of rotation was switched. A black and white striped drum was used as a control to verify the shrimps' behavioral response to moving stripes. A solid white drum acted as a second control verifying the shrimps' behavioral response in the absence of detectable visual stimuli. When presented with the black and white control drum, a positive behavioral response was observed, with shrimp swimming in the direction of the drum, including a reverse in drum spinning direction. A negative response, defined by either random swimming or no movement at all, was observed for the control white drum, but specifically for the colored red and blue drum. This response was seen in all three Lysmata sp., showing that *L. wurdemanni*, *L. boggessi*, and *L. jundalini* are color blind.

Exploring the effects of Gnao1 knockdown on health and longevity of NIH 3T3 cells

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Aging is associated with increased incidence of chronic health complications such as cancers, cardiovascular disease, neurodegenerative disease, and metabolic disorders. Knockdown of the G alpha subunit gpa-7, an ortholog to Gnao1 in mammals, has been shown to increase life span in *C. elegans* when the gene is knocked out of this model organism. Gnao1 is a G alpha subunit that, when activated by a G-protein coupled receptor, activates the enzyme adenylyl cyclase, resulting in the production of cyclic AMP (cAMP). The effects of knocking out Gnao1 in NIH 3T3 tissue culture cells were tested using short interfering RNA, in which quantitative PCR revealed a significant reduction in expression. We hypothesize that knockdown of the G alpha subunit will reduce adenylyl cyclase activity, resulting in decreased production of cAMP in phenotypes associated with healthier aging. Future studies will focus on quantifying the knockdown of the Gnao1 gene to evaluate whether the reduction in this G protein signaling results in an increased tolerance to stressors and/or an upregulation of markers associated with increased lifespan.

Testing MATLAB's App Developer for Convenient Development of Learning Tasks

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Research in reinforcement learning heavily involves the use of probabilistic learning tasks to discover patterns and trends in the ways our minds learn new things. These tasks are typically designed as simple games to allow for quick and convenient research to be done with either online or in-person participants. However, many of the tools used to program these tasks can become obsolete or no longer supported by recent OS updates within just a few years, creating issues with research collaborations, replication, and sharing of data and task designs. (For instance, Psychtoolbox, a few years ago a top choice for experimental design, has increasingly become difficult to run on modern OS; some of its replacements, including PsychoPy, are not necessarily much more robust to software and OS changes). Recently, MATLAB has upgraded their app designer software to allow for convenient development of cognitive and learning tasks, and their accessible deployment –partially through harnessing cloud infrastructure – across machines, labs, and platforms, without the need to install new software or toolboxes that may not necessarily function compatibly with newer technologies. We sought to discover the capabilities of the app designer software through its applicability to the creation of a commonly used probabilistic learning task, with the hope that it will allow for easier and more optimal use for in-person participants as well as online participants. Using the features made available by the MATLAB App Designer, we developed a reinforcement learning task which involves participants choosing between three different shapes, each of a different color, with each choice offering either +1 point, 0 points, or -1 points to their score. Point values are dependent on a feature of the shapes, either the shape itself or its color, and remain the same for seven trials. The visual design of the game was formed using the Design View on MATLAB's App Developer, where components like labels and images can be drag-and-dropped and adjusted, and functionality was added through the Code View to program app behavior. This project showcased the convenience and applicability of MATLAB's App Designer to the development of cognitive and learning tasks. The app's functionality further displays promise in its usability in tandem with other technologies like eye-trackers, or its ability to be deployed online for larger-scale participant seeking.

Anxiety and Uncertainty Impact Learning in a Naturalistic, Choose-Your-Own-Adventure Story Setting

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Most tasks in our daily lives, from driving, to choosing what to eat, to navigating social situations, rely on learning. Mathematically, learning in such tasks is often modeled via "reinforcement learning" (RL): learning how to behave to maximize expected benefits from our actions. This has often been studied in the lab through automated, game-like computer tasks, such as clicking through figures to discover the most rewarding pattern or choosing among visual stimuli to meet a task goal. But real-life learning in humans happens in more naturalistic settings, with artificial stimuli less frequently involved than day-to-day situations and objects. Our goal was to test human reinforcement learning patterns in a more natural, story-like scenario and analyze the impact of anxiety, uncertainty, and compulsivity on these patterns. 52 pilot participants completed an online "choose your own adventure", text-based task, in which their goal was to bake cupcakes for a picnic. The story included five "chapters" (or blocks), with each chapter having its own subgoal (e.g. "find the flour in a messy kitchen full of unlabeled containers"). Each block involved a series of choices with common underlying structure; participants could learn that structure from the way each choice moved their story along. For instance, a participant might learn that blue containers hold baking-related ingredients, while orange containers hold dried beans. Based on their choices, the story led them to discover, mix, and bake cupcake ingredients in a way that results in either good, mediocre, or bad cupcakes. We also collected data on participants' anxiety, intolerance of uncertainty, and obsessive-compulsive scores. Overall learning performance was mixed (with participants seemingly learning the best story choices yet choosing other paths in the story), reaction times correlated with accuracy, with better learners going through the story faster (r = -0.2919, p = 0.0358). Furthermore, reaction times early in the story were higher for participants who scored high on anxiety and IUS (r =-0.2816, p = 0.0432) (r = -0.3407, -0.2805, p = 0.0134, 0.0440). These results hint at potential impacts of anxiety and uncertainty on learning in a more naturalistic RL setting, but further edits may be needed to better convey the learning structure of the task in a story-like setting, as well as to understand the impact of compulsivity in such learning scenarios, and its interaction with anxiety and uncertainty.

Investigating pathways regulating size-dependent accumulation of mitotic activator Cdc25

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Cells maintain a characteristic size to function. Most cells control their size by delaying cell cycle transitions until they reach a threshold cell size. This suggests that cells sense their size and relay this information to cell cycle machinery, but the molecular mechanisms of how size is determined in any cell type is largely unknown. We use the fission yeast Schizosaccharomyces pombe to study cell size control because of their easy-to-measure rod shape and extensive genetic tools. Studies in fission yeast have revealed the core components regulating the cell cycle in eukaryotes. Fission yeast cells enter mitosis and divide at a threshold cell size due to regulated activation of cyclin-dependent kinase (Cdk1), in part through size-dependent nuclear accumulation of phosphatase Cdc25. Recent work showed that Cdc25 accumulates specifically with cell volume, as opposed to another aspect of cell size (e.g. cell surface area or cell length). However, the molecular mechanisms governing the accumulation of Cdc25 with cell volume remain unclear. In this study, we investigate the pathways that influence the nuclear accumulation of Cdc25. There are known gene deletion mutants that advance fission yeast cells prematurely into mitosis, causing smaller cell size. We hypothesized that these genes encode negative regulators of mitotic activator Cdc25. We tested this using quantitative live-cell fluorescence microscopy to measure the concentration of mNeonGreen(mNG)-tagged Cdc25 in the cytoplasm and nucleus of small size fission yeast mutants compared to wild-type. We utilized an ImageJ/MATLAB image analysis pipeline to rapidly measure cell/nuclear size and fluorescent intensities. We uncovered 6 mutants with increased Cdc25 levels compared to wild type, indicating that these genes may encode for negative regulators of Cdc25. Of these mutants, 4 are involved in glucose-sensing (Pka1, Git3, Git5, and Gpa2), one is a transcriptional regulator (Sol1), and one is a mRNA regulator (Pab2). We focused on understanding the mechanisms of how Pka1 might regulate Cdc25. Previous work suggested that an E3 ubiquitin ligase Pub1 is involved in targeting Cdc25 for degradation and that this is blocked in low glucose conditions. A relationship between Pka1 and Pub1 has not been explored. Through genetic assays and examination of protein stability we reveal a role for Pub1 and Pka1 in regulation of Cdc25. Our work uncovers conserved regulatory networks involved in cell size control.

Tube feet plasticity: comparative study between purple sea urchins (*Strongylocentrotus purpuratus*) from two distinct habitats

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Sea urchins are found in various habitats with different hydrodynamic intensities, from the more expose intertidal to the less expose subtidal. Studying the diverse patterns of distribution among urchins of the same species can be an important tool in further understanding animal plasticity in relation to marine organisms. As is the case with most echinoderms, their survivorship highly depends on their ability to adhere to the substrate, to protect themselves from dislodgement from predators and hydrodynamic forces. A group of appendages called tube feet are responsible for such important task of anchoring onto the substratum. Tube feet are compose of a stem and a flatten disc in the distal end. The disc contains adhesive and de-adhesive cells which provide urchins with temporary chemical adhesion. The main goal of the study is to determine if tube feet plasticity occurs between urchins of the same species, but found in different habitats. We studied the adhesive performance and tube foot morphology of purple sea urchins (*Strongylocentrotus purpuratus*) in two different microhabitats: Intertidal, where urchins are exposed to air and waves during low tides; and Subtidal, where urchins are always underwater and experience weaker hydrodynamic forces. We measured adhesive force of the disc (force required to detach a disc from a surface; N), stem breaking force (force required to break the stem; N), whole animal force (force required to detach a whole animal from a substrate; N), number of tube feet used during the pulls, and righting time (time required to right themselves when turn upside down; sec), The results of the study reveal no plastic response from the two populations. The groups diverged slightly in disc size, but we didn't find a significant difference in the other response variables. Our results put into question past studies that argue for a correlation between hydrodynamic force and tube foot plasticity. This study brings to light the importance of conducting more field research to assess tube foot plasticity in sea urchins.

Sea urchin disc tenacity estimations: Are we doing it right?

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Adhesives that are robust in wet conditions are highly demanded in industrial and biomedical fields. Many invertebrates, including echinoderms (i.e. sea urchins), use chemical adhesion to secure attachment to rough substrates which makes them good candidates for the development of bio-inspired adhesives. Sea urchins achieve attachment by using tube feet, which are appendages that grow in between the spines and, powered by the water vascular system, can extend and contract. Tube feet end in a disc that releases adhesive and de-adhesive secretions that allow for reversible chemical adhesion. The adhesive secretion remains in the substrate after detachment and, when stained, reveals a footprint. Traditionally, disc tenacity (disc adhesive force per unit area; Tdisc) is calculated by dividing the disc adhesive force (N) by the disc surface area (mm^2). This calculation of Tdisc assumes that every time a disc is used, the whole surface area of the disc secretes the adhesive secretion. However, footprints are often incomplete, suggesting that only part of the surface area of the disc was used for adhesion. Thus, estimating disc tenacity by dividing the disc adhesive force by the footprint area (Tprint) would provide a more accurate estimation of the true disc force per unit area. In this study, we estimated Tdisc and Tprint of four different species of sea urchin: *Strongylocentrotus purpuratus*, *Strongylocentrotus pallidus*, *Mesocentrotus franciscanus*, and *Strongylocentrotus droebachiensis*. Additionally, we estimated the correlation between disc surface area and footprint area. Our results showed that Tdisc and Tprint vary among species, with *S. purpuratus* having the highest Tdisc and *M. franciscanus* having the highest Tprint. We also found that disc surface area does not correlate with footprint area where *M. franciscanus* left the smallest footprint but had the largest disc surface area and *S. droebachiensis* left a large footprint but had a relatively small disc surface area. Collectively, these results suggest that published values of Tdisc may not represent sea urchins' true disc adhesive force per unit area. Thus, estimating the true disc tenacity is needed to improve our understanding of the adhesive capacity of sea urchins which can help inform the development of bio-inspired adhesives.

Production of Artificial Tendons Using Liquid Crystal Elastomers for Soft Exogloves

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Liquid crystalline elastomers (LCEs) are a class of materials that combine the elastic behavior associated with conventional elastomers with the stimuli responsive properties of anisotropic liquid crystals. Stimuli, such as heat or light, alter the mesogen orientation causing the LCE network to rearrange. In response to a stimulus, this material can change shape and demonstrate soft, reversible actuation. These mechanical and optical functions of LCEs make them suitable for potential technological applications like artificial tendons. The directional dependence of liquid crystal elastomers mimics soft tissues throughout the body, making it an ideal material for rehabilitation devices. Soft exo-gloves for patients who have lost full or partial control over their hands, is effective and essential for rehabilitation exercises. UV curing is an important step in tailoring these properties by controlling the cross-linking density and molecular alignment within the polymer network. LCE samples were photo-cured and programmed at 50%, 75%, and 100% strain, with samples demonstrating between 70% and 86% shape fixity when unloaded. This investigation into the UV curing process of LCEs, focuses on the effects of UV exposure parameters such as intensity, wavelength, and duration on the mechanical behavior and actuation capabilities of the material. Experimental results demonstrate how varying UV curing conditions influence the material's modulus, strain response, and shape-memory characteristics.

Quantifying the effect of environmental threat on food consumption in mice

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Universally, organisms must weigh hunger against competing motivations to prioritize behaviors directed toward the most pressing survival need. Understanding how the brain resolves these competing needs is a primary aim of our laboratory's research. Toward this goal, in this study we asked how three environmental threat modalities–contextual, olfactory, and visual– affect food-seeking behavior and consumption. We designed a series of experiments in which mice were presented with a choice between accessing food and avoiding a perceived predator threat. The animals' behavior was tracked and food consumption recorded to determine the degree to which the environmental threat suppressed hunger. Before all behavior trials, mice (n = 8) were food-deprived for 4-18 hours. In the open field test (OFT), food was taped in the center of a 56 cm2 chamber under two conditions–illuminated under high intensity light or not illuminated at all–taking advantage of mice's innate aversion to illuminated open spaces. Time spent in the center (threat zone) and food consumption in each 15 minute trial was quantified. In the predator odor assay (POA), food was placed directly adjacent to trimethylthiazoline (TMT), a component of fox feces to which mice demonstrate an innate fear. Each subject was tested on 4 hr food-deprivation and sated. Time spent in the predator odor zone and food consumed in each 15 minute trial was quantified. In the looming stimulus assay (LSA), food was placed in one quadrant of a chamber, directly underneath a projector which projects a rapidly expanding shadow onto the floor, meant to evoke the shadow of a predator from above. Each mouse was run on the LSA at variable stimulus intensities (low, medium, and high contrast). Time spent in the threat zone and food consumed in each 10 minute trial was quantified. Across all three experiments, our results indicate a complex interplay between hunger and fear, with variations in individual responses suggesting that both internal states and external cues significantly influence decision-making. Understanding the balance between these conflicting motivations can shed light on the decision-making processes and survival strategies of this animal model. With these behavioral assays established, we will next use optogenetics to ask how hunger-sensing neurons in the hypothalamus drive food-directed behavior under variable environmental threat.

The effect of pregnancy and maternity on behavioral motivations amidst environmental threat

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To survive in nature's complex and ever-changing environment, humans and animals alike must be able to balance competing incentives. In a setting where the motivations of fear and hunger are simultaneously present, the goal of this study is to understand specifically how pregnancy and maternity cause females to reprioritize competing needs. To accomplish this, we analyzed behavioral responses to the threat of predation and the presence of food in both food-deprived and sated pregnant and maternal mice. Each pregnant mouse, as well as a group of virgin controls, were initially run on two separate assays: the predator odor assay and the open field assay. In the predator odor assay, each mouse was either food-deprived for four hours or left sated prior to being placed in a plexiglass chamber for a total of 30 minutes. In the first half of the experiment, a tissue containing trimethylthiazoline (TMT)—a component of fox feces—was taped to one side of the chamber to elicit fear. Then, the interaction between fear and hunger was able to be analyzed in the second set of 15 minutes, during which a piece of food was placed adjacent to the tissue containing the predator scent. Similarly to the predator odor assay, each mouse was then run both sated and food-deprived in the open field chamber for 15 minutes. This experiment highlighted a mouse's innate fear of open spaces by taping a piece of food directly in the center of the chamber. Finally, the virgin control mice and the original pregnant subjects were again tested post-partum on the predator odor assay, allowing us to track behavioral changes seen in females after giving birth. When designing the experiment, we predicted that pregnant and maternal mice would spend less time in threat zones and consume less food than virgin controls due to hypersensitivity in the senses of pregnant and maternal mice. While our results reveal that pregnancy has no significant effect on motivated behaviors in the context of hunger and threat, maternity may reveal a correlation between a newfound responsibility as a mother, and a hesitation to risk individual safety to protect one's pups. The next direction we plan to take with this study is an analysis of behavior across the lifespan, particularly exploring an imbalance between motivated behaviors in juvenility.

Determining the probiotic potential of *Pseudoalteromonas rubra* against native pathogens.

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Tropical corals host diverse and specific microbiomes that modulate coral fitness, and many microbes play a protective role against pathogens. Two strains of the bacteria *Pseudoalteromonas rubra* (KB1 and CH007) were isolated from seawater and crustose coralline algae (CCA) in the temperate coral (*Astrangia poculata*) culturing tanks in Roger Williams University Wet Lab. *P. rubra* is thought to be protective to tropical corals, via production of the prodigiosins and N-acyl-homoserine lactones. Additionally, *P. rubra* induces larval settlement in at least one tropical coral species. *P. rubra* KB1 and CH007 inhibit growth of several species of *Vibrio*, including known coral, finfish, and shellfish pathogens. An exposure assay was conducted and *P. rubra* KB1 and CH007 were found to be not lethal to *A. poculata*. Exposure to *P. rubra* significantly altered the *A. poculata* microbiome composition, including increases in bacteria involved in sulfur cycling and likely antibacterial production. However, exposure also was correlated with decrease in known beneficial associates. Coral mucus and seawater microbiomes resembled one another at some, but not all, time points during exposure, and there was significant strain-dependent variation in the impact on *A. poculata* microbiome composition and diversity. These data lay the groundwork in developing *P. rubra* as a probiotic treatment and in understanding the molecular mechanisms of any benefit that *P. rubra* may confer to corals. Due to the resistance of *A. poculata* against *V. coralliilyticus* in the lab, the sea anemone, *Exaiptasia diaphana*, was selected as an experimental system to assess *P. rubra*'s capacity for disease prevention and/or mitigation. *Exaiptasia diaphana* was exposed to high concentrations (108 cells/ml) of the pathogen *V. coralliilyticus*, and dosed with *P. rubra* either before or after the *V. coralliilyticus* exposure. Preliminary data showed that pretreatment with *P. rubra* 12 hours before *V. coralliilyticus* did not reduce the *Vibrio*-induced mortality. However, anemones treated with *P. rubra* 12 hours after *V. coralliilyticus* exposure showed a decrease in mortality compared to those exposed to the pathogen alone.

Reactions of Corticosteroid Pharmaceuticals with Human Gut Microbiota-Derived Hydroxysteroid Dehydrogenases

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Enzymes from the gut microbiome are able to metabolize the food we eat, while also metabolizing different prescribed drugs. These drugs can be modified to be activated, like prodrugs, inactivated, or modified in a way that causes toxicity. Many reactions of the gut are uncharacterized, and identification of these reactions is important to identify the drug interactions and their products. In this study, 20-hydroxysteroid dehydrogenase enzymes known to modify cortisol were the focus, chosen for their reactivity and efficiency for modifying corticosteroids. The enzymes used were expressed by human gut microbes *Bifidobacterium adolescentis* and *Agathobaculum desmolans* (formerly *Butyricoccus desmolans*), which are denoted as WP_008310233.1 (WP-233) and WP_051643274.1 (WP-274) respectively. The efficiency of the reactions was determined by enzyme kinetics in different buffers. UV-Vis spectrophotometry indicates that WP-233 is more efficient than WP-274 at reducing several tested corticosteroids. These findings add to the growing base of knowledge of reactions catalyzed by enzymes found in gut microbiota and help to further the advances made towards personalized healthcare.

Gut Microbiota-Derived 17-Hydroxysteroid Dehydrogenase Interactions with Corticosteroid Drugs

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The proteins found in gut microbiota are capable of metabolizing not only the food that we consume, but also commonly prescribed pharmaceuticals. These pharmaceuticals can be transformed to activate, deactivate, or create toxic metabolites. The specific reactions that take place are widely undocumented, indicating a need to identify potential drug interactions and their products. This study focuses on the metabolic enzymes such as "desmolase" enzymes and 17-hydroxysteroid dehydrogenases (HSDHs), which are known to modify corticosteroids to produce androgenic compounds, and other HSDHs known to modify unique positions around the steroid core. Of the proteins we have tested, we have observed that a 3/17-HSDH from *Crenobacter intestini*, (UniProt ID A0A4T0V530, CI317) is capable of reducing norethisterone, a contraceptive. The efficiency of the enzymatic with certain corticosteroids was determined using UV-Vis spectrophotometry, indicating that CI317 displays 3-hydroxysteroid dehydrogenase activity with norethisterone. These findings add to the growing understanding of reactions catalyzed by enzymes found in gut microbiota and help to further the advances made towards personalized healthcare.

Development of Virtual Reality Setup for Drone Physical Human Robot Interaction Experiments

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Physical Human-Robot Interaction (PHRI) is one of the most interesting fields which could potentially contribute towards knowledge and technological advancement. Mobile robots, robotic arms, are all highly studied, however, due to safety concerns, when it comes to unmanned aerial vehicles (AUVs) it is a field that is still underexplored. The aim of this research project is to use a Robot Operating System (ROS) with Unity software to create a simulation environment in which a human subject can interact virtually with the real physical environment. Particularly, the human subject will wear a VR headset to interact with a simulated hovering drone while the real sense of haptic touch for such interaction will be provided and measured by a real physical robotic arm outside the proposed virtual environment, and invisible to the user. Our framework requires not only communication between the virtual reality and simulated drone, but also having the robotic arm be able to communicate with the drone within the simulation and vice versa. In contrast to previous studies in human-UAV physical interaction, our closed-loop framework will enable us to measure and evaluate the interaction forces within a safer testbed condition to eventually guide the development of a real PHRI drone. Our final goal is a Unity simulation interfaced with the robotic arm. Over this research project, we have evaluated available open source packages that offer Unity drone simulations, have compatibility with Ubuntu, are compatible with the ROS version operating the robotic arm (melodic), and provide other robotics related simulations. Among those, we selected ZeroSim because it meets these requirements. In addition, the robotic arm is also controlled by a different desktop computer, which means the Ubuntu laptop with the Unity simulation needs to be interfaced with the desktop to offer communication between the drone within the simulation and the physical robotic arm. At the current stage of development, we achieved ROS-enabled robotic simulations on Unity. In the future, we are planning to establish the communication between the robotic arm and the simulation. We need to ensure that while ROS controls the drone in the simulation, the arm performs the proper movements to emulate the drone trajectory. The usage of virtual reality through Oculus also needs to be incorporated. Eventually, we plan to use the developed platform for human subject experiments in drone PHRI.

Quantifying cysteine reactivity using small molecules

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Many protein and peptide functions are regulated by the reactivity of the cysteine side chain. Determining cysteine nucleophilic reactivity is thus crucial for understanding many biological processes, elucidating the metallodrug-protein interactions, and designing covalent drugs. Methods for systematically quantifying cysteine reactivity are, however, not well established. Recently, we created a library of small molecules to quantify cysteine nucleophilicity under physiologically relevant conditions. By manipulating the molecules' structural parameters, we aim to use these probes to quantify cysteine nucleophilicity and explore its correlation with the protein's local environment.

Testing the dominance of Arrhenius: How social behavior and environmental temperatures interact to regulate the supply and demand of energy in social groups

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A foundational concept to biology and chemistry states that temperature has an exponential effect on reaction rates, including the anabolic and catabolic reactions of cellular and organismal metabolism. This concept has been quantified by a few different models including the law of Arrhenius, all which preserve the assumption that the rates of reactions depend on temperature in an exponential way. For an ectotherm like an ant, the law of Arrhenius suggests its metabolic rate should be an exponential function of temperature, potentially even independent of any social behaviors in ant colonies. To test whether or not these theories are valid for social insects, we measured pavement ant (*Tetramorium immigrans*) metabolic rates using flow-through respirometry (indirect calorimetry) as colonies (N=6) were housed within aluminum chambers placed on a peltier-effect plate to ramp their temperature from 10-40 degrees C.

After verifying that the exponential model was the best fit for the colony data, we calculated Q10 values as a method of comparing the thermal sensitivity of colonies with and without brood (eggs, larvae, and pupae). We found that the Q10 of colonies with brood did not significantly differ from colonies without brood ($p = 0.9$). Colonies with brood averaged a Q10 of 1.93 (95% CI: 1.76 - 2.11), and similarly, colonies without brood averaged a Q10 of 1.93 (95% CI: 1.75 - 2.10).

Development of Rare Cell Identification of Medulloblastoma Cancer Cells from Blood

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Medulloblastoma is the most common malignant brain tumor in children. Currently, there are four main subgroups of medulloblastoma, which include WNT, SHH, GP3, and GP4. Each subgroup varies in its genetic characteristics and prognoses. Thus, patients need staging tests to determine subtype, metastasis potential, and treatment strategies. Yet, sampling for staging is a high-risk procedure for the patient. The next frontier of diagnosis and staging is liquid biopsy and we collaborate with a group at Massachusetts General Hospital developing a microfluidics device for detecting medulloblastoma from blood draws. As with the design of the liquid biopsy device, computational tools for analyzing transcriptomics and genomics from liquid biopsy are not well-developed. Our long-term goal is to use single-cell RNA sequencing, scRNA-seq, of liquid biopsies to define biomarkers and computational tools to identify medulloblastoma cancer cells. Medulloblastoma cells in blood can represent less than .003% of the product. We set out to test and develop robust statistics for outlier detection and leverage them for rare cell identification. To test rare cell identifiers in scRNA-seq, we combined three publicly available data sets that processed medulloblastoma patient samples through scRNAseq and annotated the cells present. In total, there were 28,361 cells from 54 medulloblastoma patients varying in age and subgroup. Next, we set out to have cells from this comprehensive medulloblastoma cell atlas integrated with publicly available whole blood scRNAseq data to test rare cell identification methods to improve liquid biopsy for this vulnerable population of cancer patients.

Use of Ko-143 to evaluate Breast Cancer Resistance Protein (BCRP) as a potential mechanism for Perfluoroalkyl substance (PFAS) absorption in the gut

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Perfluorinated alkyl substances (PFAS) are a class of synthetic chemicals widely used in consumer products and industrial processes due to their water repellency, heat resistance, and chemical stability. PFAS exposure is linked to adverse health outcomes such as elevated cholesterol levels, immunosuppression associated with reduced vaccine response, endocrine disruption, cancer, and liver injury. PFAS are highly absorbed from the gastrointestinal tract (GIT) and distributed to tissues, such as the liver. The mechanisms by which PFAS are absorbed are unclear but permeability, and transporters such as Breast Cancer Resistant Protein (BCRP) are hypothesized. In vitro studies indicate that Perfluorooctane sulfonic acid (PFOS), Perfluorooctanoic acid (PFOA), Perfluorobutanesulfonic acid (PFBS), Perfluorohexanesulfonic acid (PFHxS), and Flourotelomer sulfonic acid (6:2FTS) are human BCRP substrates. Ko143 is a known inhibitor of BCRP. Herein, it was hypothesized that Ko143 could inhibit BCRP, thereby reducing PFAS efflux from the enterocytes, and resulting in higher PFAS absorption in mice. To investigate whether PFAS as substrates of intestinal Bcrp, in vivo, C57BL/6J 10-week male mice, n=6/treatment group, were administered a single oral 10mL/kg dose of either a vehicle solution (1mL DMSO diluted with hydroxypropyl methylcellulose (10mg/mL) and 5%(v/v) Tween-80, and further diluted 1:1 with a 5% glucose solution) or a 10mg/mL Ko143 in vehicle dosing solution. 30 minutes later all mice received a single oral 10mL/kg dose of a 0.5mg/mL PFAS cocktail consisting of 1:1 ratios of PFOS, PFOA, PFBS, PFHxS, and 6:2FTS. Tissues were collected 1 hour after administration of the PFAS cocktail. Plasma, liver, lung, kidneys, brain, and duodenum were collected and snap-frozen in liquid nitrogen. Plasma and liver samples underwent the QuEChERS (Quick, Easy, Cheap, Effective, Rugged, and Safe) extraction method to prepare for Liquid chromatography-mass spectrometry (LC/MS) analysis. Plasma and liver concentrations of PFOS, PFOA, PFBS, PFHxS, and 6:2FTS in the control group versus the Ko143 group showed no significant difference in PFAS concentrations, suggesting that BCRP may not be a critical mechanism for PFAS absorption in the GIT.

Etheno-5-methylcytosine is Repaired by the Human Enzyme ALKBH2

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Epigenetic regulation and DNA damage has been linked to the cause of many disorders such as type 2 diabetes, neurodegeneration, obesity, and many types of cancers. Organisms have evolved to mitigate the accumulation of DNA adducts in the body through enzymatic pathways. The AlkB family proteins belong to the α-Ketoglutarate (α-KG)/Fe(II) dependent class of enzymes with nine identified human homologues (ALKBH1-8 and FTO). ALKBH2 has been shown to repair DNA damage, specifically etheno adducts by direct reversal repair (DRR) with a preference for double-stranded (ds)-DNA. Exocyclic etheno adducts are highly mutagenic DNA lesions that are formed by reactions of DNA with products of lipid peroxidation (LPO) or the carcinogen vinyl chloride and its derivatives, such as chloroacetaldehyde (CAA). Specifically, 3,N4-etheno-5-methylcytosine (ε5mC) can be formed by the reaction of CAA and 5- methylcytosine (5mC), an epigenetic modification. ε5mC has been reportedly more abundant than 3,N4-etheno-cytosine (εC) due to 5mC's nucleophilic nitrogen making it prone to carcinogenic electrophiles. The 16mer ε5mC was synthesized from 5mC with incubation of CAA and purified on a reverse phase HPLC C18 column and identified by Mass Spectrometry. Our results showed that ALKBH2 can convert ε5mC to 5mC with a repair ratio of 54%. These results are important as they reveal a new target for epigenetic damage related to a variety of disorders.

Navigating the Squid Retina: The Role of Motor Proteins in Visual Processing

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The squid visual system is exceptional in its ability to adapt to varying light levels. In humans, contraction and expansion of the pupil allow differing levels of light to enter into the retina. The adaptation in squid is facilitated by the movement of pigment granules within photoreceptor cells in the retina. These granules, small oval-shaped organelles, travel along microtubules from the base of the cell to the tip in response to changes in light intensity acting as molecular sunglasses. Motor proteins are responsible for the movement of these granules although the specific motor proteins responsible for this movement have not yet been identified. Our research aims to identify and understand the distribution of these motor proteins and their binding sites on pigment granules.

To investigate this research question, we paired indirect antibody labeling with a combination of confocal and wide-field fluorescent microscopy techniques. By labeling light and dark adapted retinal cells, we aimed to fluorescently track the motor proteins responsible for pigment granule migration. We tested common motor proteins including a variety of dyneins, myosins, and kinesins. Surprisingly, we have yet to identify a motor protein which co-localizes with the pigment granules themselves. However, we found evidence that suggests conventional kinesin and myosin 7 may be attached to the microtubules instead. Our findings suggest that the proteins responsible for pigment granule movement are either not included in our hypothesized group of candidates, or that the proteins attach to the microtubules and are split from the pigment granules during the cell fixation process. Further research at both the light and electron microscopy level will delineate where the motor proteins attach to regulate movement of pigment granules along the microtubules. Identifying the role and distribution of specific proteins within retinal cells will provide valuable insight into this mechanism and inspire further research into the role of these motor proteins in sub-cellular transport across various organisms.

Variations in Organophosphate Ester Concentrations in Atmospheric Particulate Matter in Klamath Falls, OR

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Air pollution continues to be a major environmental concern not only to the ecosystem but human health as well. Changes in atmospheric particulate matter (PM) from both natural (wildfire) and anthropogenic (winter home heating) sources can adversely affect human health while also indicating the severity of the harmful chemicals the air contains. Organophosphate esters (OPES) are an example of pollutants which have a wide range of uses within consumer products including flame retardants, plasticizers, and herbicides. Despite its rural location, areas such as Klamath Falls, Oregon, are susceptible to increased levels of PM due to the effects of wildfire season in the summer months, woodstoves for home heat in the winter months, and their geographic "basin" structure, all contributing to the increase of these chemicals within the air throughout the year. Filter-based samples of PM less than 2.5 microns in aerodynamic diameter (PM2.5; inhalable size fraction) were analyzed for 35 OPEs and novel-OPEs. Results suggest a diverse array of sources and correlations between compounds and meteorological parameters. Correlation with elevated air quality index (AQI) was also investigated.

Source Allocation and Ratio Analysis of Polycyclic Aromatic Hydrocarbons and Organophosphate Esters in Providence, RI

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The Port of Providence is a substantial urban center with a variety of industries and businesses, each with diverse modes of transportation. Such urban centers are often documented as containing a multitude of pollutants that significantly contribute to air pollution and negatively impact environmental health. Among the main pollutants and markers of pollution in urban environments are polycyclic aromatic hydrocarbons (PAHs) and organophosphate esters (OPEs). PAHs are consistent byproducts of incomplete combustion, including petroleum and coal combustion, vehicle emissions, cigarette smoking, and wood burning, all of which make PAHs most commonly and readily found in densely populated urban and industrial areas. OPEs are incorporated into consumer products as flame retardants and plasticizers which also makes them typically located in urban environments that contain large populations and multiple industries and factories. Since the Port of Providence is a potential hot spot for PAHs and OPEs, filter-based sampling was done on the roof of a building in the heart of the Port with samples of both total suspended particulate (TSP) and particulate matter less than 2.5 microns (PM2.5) being collected to determine the atmospheric concentration of 13 target PAHs and 35 target OPEs and NOPEs (novel OPEs). Using ratios of the concentrations of select and specific PAHs, a variety of possible sources of PAH were determined which indicates a diverse blend of sources of pollution at the Port of Providence. Additionally, meteorological data collected at the sampling sites was correlated with the concentrations of multiple OPEs to uncover a specific trend between solar radiation and OPE concentration that has room for further research.

Stochastic Simulations of Transcranial Electrical Stimulation for Neurodegenerative Disease

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Parkinson's Disease (PD) continues to be one of the most prevalent forms of neurodegenerative disease both globally and in the United States. As PD has no known cure, a vital focus of biomedical research is on mitigating patient symptoms, which for this condition are highly debilitating through parkinsonisms, as well as dementia and neuropsychiatric problems that can present in later stages of this disease. One such therapy that has shown great success in addressing symptoms of PD is transcranial electrical stimulation (TES), a non-invasive neurostimulation technique that modifies neuronal excitability for targeted brain regions. Further, when coupled with techniques from the fields of mathematical modeling and computation simulation, TES efficiency can be enhanced via patient-specific computer visualizations and predictions of electrical energy magnitude and distribution within the head cavity. A limitation of these simulations, however, is an absence of the uniqueness and variability of cranial tissue conductivities that inherently exist among different individuals; as these conductivities are an integral parameter in these simulations, their utility fundamentally depends on them. To address this issue, a stochastic mathematical model of TES has been implemented. The basis of the mathematical model is Laplace's Equation coupled with boundary conditions that emulate TES electrode functioning, and numerical solutions are achieved using the finite element method. A python-based software framework has also been developed, and is used to execute 10,000 Monte Carlo experiments on an MRI-derived three dimensional head geometry, for each of three distinct electrode montages commonly used in PD TES. Results highlight the importance of incorporating conductivity uncertainty within patient-specific simulations of TES. Furthermore, our approaches and software framework are flexible, providing easy adaptation to alternative TES electrode configurations and in silico experimental parameters. We hope that this work will continue to help optimize therapeutic treatments for patients of neurodegenerative disease.

Changes of cytoskeleton structure and nuclear homeostasis altering chromatin organization

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Amyotrophic Lateral Sclerosis (ALS) is a devastating neurodegenerative disorder that primarily affects motor neurons in the brain and spinal cord. Emerging evidence suggests that alterations in cytoskeletal structure may play a crucial role in the pathogenesis of ALS, though the precise mechanisms remain unclear. The cytoskeleton is composed of many fibers including F-actin (filamentous actin), which is essential for cell motility, division, and structural support. F-actin interacts closely with the nucleus through the LINC (Linker of Nucleoskeleton and Cytoskeleton) complex, which connects actin filaments to the nuclear envelope. Underneath the envelope, the nuclear lamina provides structural support, organizes chromatin, and is involved in DNA replication and cell division. Within the context of ALS, we explored the hypothesis that altering cytoskeletal structure and disrupting nuclear homeostasis may be linked to changes in chromatin organization leading to cellular dysfunction. To investigate this, we utilized Human Embryonic Kidney 293 (HEK293) cells treated with various drugs. Dimethylsulfoxide (DMSO) served as the control, while Latrunculin B (Lat B) was used to disrupt the actin cytoskeleton, Intramimic-01 (IMM-01) to promote F-actin polymerization, and Sodium Arsenite ($NaAsO_2$) as a cytoskeletal unrelated stressor. We then used immunofluorescence staining with specific antibody markers, including Phalloidin to visualize F-Actin, Lamin B and RanGAP1 to visualize the nuclear envelope, H3K9 di- and tri-methylation, H3K9 acetylation, and H3K27 trimethylation, to visualize changes to chromatin compaction and organization. We found that when altering the cytoskeleton by using IMM-01 to increase actin polymerization, the H3K9me histone light intensity decreases therefore relaxing chromatin structure and making DNA more accessible to transcription factors and RNA polymerase. Our image analysis provides insights into a potential correlation between cytoskeletal dynamics and chromatin organization.

Examining the Development of Alzheimer Disease like Symptoms in a Rabbit Model Of Cerebral Palsy

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Cerebral palsy (CP) is a group of disorders that affect movement, muscle tone, and posture, often resulting from brain damage due to perinatal insults like hypoxia-ischemia (HI). In the US, about 10,000 babies are born with CP annually. Adults with CP are at an increased risk of developing Alzheimer's disease (AD) later in life compared to those without CP. To better understand the link between early-life insults and the development of AD, we conducted a study combining the HI rabbit model of CP and the high-cholesterol diet rabbit model of AD. We hypothesized the injury to the developing fetus in the HI rabbits would multiply the effect of the high cholesterol diet, and as the HI rabbits on a high-cholesterol diet age, they would exhibit exacerbated AD-like symptoms. To study this, fetal rabbits were subjected to 40 minutes of hypoxia in utero at 70-80% gestation or a sham surgery. Once the rabbit kits were weaned, they were placed on either a high-cholesterol diet with copper in their drinking water or a normal diet with distilled drinking water. We used novel object location, novel object recognition, and eyeblink conditioning to assess learning and memory deficits at 2 months of age and 7 months of age. Western blots for glial fibrillary acidic protein (GFAP) and beta-amyloid were used to analyze potential protein expression changes in the frontal cortex. The results will provide insight into how early-life insults interact with other risk factors to affect later development of AD. In the future, we plan to age rabbits to 18 months because age is a critical factor in the onset of AD. These future studies with older subjects may provide more insight and a deeper understanding of the relationship between early-life HI and later neurodegenerative changes.

The Association of Repetitive Negative Thought with Physical Symptoms of Depression

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Repetitive negative thought (RNT) is associated with symptoms of depression and anxiety, but past research has primarily focused on its association with psychological, rather than physical symptoms of depression (Spinhoven et al., 2018; Taylor & Snyder, 2021). This study aims to investigate the relationship between two types of RNT, worry and rumination, and physical symptoms of depression. Although worry is more commonly associated with anxiety and rumination is more commonly associated with depression, we hypothesized that both types of RNT would show associations with physical symptoms of depression, consistent with transdiagnostic models of RNT. Participants were 580 college students who completed several measures on a secure website as part of a larger study. Measures included the Penn State Worry Questionnaire (PSWQ; Meyer et al., 1990) and the rumination subscale of the Reflection Rumination Questionnaire (Trapnell & Campbell, 1999), which ask participants to answer questions about their tendency to engage in worry or rumination. Physical symptoms of depression were measured on the Diagnostic Inventory for Depression (DID; Zimmerman et al., 2003), which asks participants to rate the severity of each DSM symptom of depression over the past week. We ran a series of Pearson correlations to evaluate the relationship of worry and rumination to each physical symptom of depression. As we hypothesized, both types of RNT are related to physical symptoms of depression. Worry and rumination were each significantly related to increased severity of physical symptoms of depression including loss of energy, physical restlessness, decreased physical activity, appetite loss and increase, weight loss, and decreased sleep. All correlations were in the small to medium range. Only rumination was associated with increased sleep, and neither rumination nor worry was associated with weight gain. Results suggest that both worry and rumination might have important, and largely parallel, links to physical symptoms of depression. Rumination is frequently linked to symptoms of depression but the present results support a transdiagnostic view of RNT in which worry is also linked to these symptoms.

Common Factors in Individuals Experiencing Suicidal Thoughts

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Suicide rates increased over the course of the COVID-19 pandemic, especially among youth (Bridge et al., 2023). This series of tragedies generated more widespread attention towards the issue of suicide which remains one of the most important and vaguely understood issues in psychology. Our research aims to identify common factors reported by individuals who report thoughts of suicide. We proposed that these individuals would share a set of common positive factors.

To account for the limited time frame of the RI-INBRE SURF program, our research focused on secondary analyses of an existing dataset. This allowed us to polish our methods for further study of larger datasets. The dataset consisted of several self-report scales including the Penn State Worry Questionnaire (PSWQ), the Mood and Anxiety Symptoms Questionnaire (MASQ), and the Positive and Negative Affect Schedule (PANAS), which were administered to 580 undergraduate students on a secure website.

A Spearman's ranked correlation was performed on each of the scales to analyze the individual items' correlation with thoughts of death or suicide over the past two weeks, which was rated on a scale from 0 (not at all) to 4 (extremely). Our data is ordinal, not continuous; Spearman's correlation is suited to this type of data. We employed correlational heatmaps to identify which items in each scale and which subscales could be considered common factors of participants who report suicidal thought. These will be presented on our poster along with boxplots for significantly correlated items.

Our results indicated that four individual items (feelings of worthlessness, choking sensations, fear of death, and disgust with self) had moderate to strong positive correlations with recently experienced thoughts of suicide or death. Only one of the subscales (the PANAS guilt subscale), had a moderately strong correlation with suicidal thought.

We hope that this research will better equip clinicians to identify risk factors in their patients. We plan to apply a method similar to this one onto larger datasets, and datasets that include survivors of suicide attempts or those who have died by suicide, such as the National Comorbidity Survey (NCS) and the National Violent Death Reporting System (NVDRS). On top of that, we are seeking to use datasets which employ a binary YES/NO scale for suicide items which would provide an even clearer answer to our preliminary question.

Addictive Tendencies in a Mouse Model of Bipolar Disorder

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Bipolar disorder (BD) is a chronic mood disorder characterized by cycles in mood and energy. Individuals with BD are at a higher risk of comorbid substance use disorders (SUD). Studies have shown that a mutation of the ClockΔ19 gene in mice may be a valid rodent model for BD. The ClockΔ19 mouse model presents both face and predictive validity in its parallels to human bipolar disorder such as, disrupted circadian rhythms, hyperactivity, increased risk taking, addictive tendencies, and the impact of lithium on BD symptoms. Additionally, similar to an increase in rates of SUD in humans with BD, these ClockΔ19 mice have shown a greater preference for alcohol and cocaine than wildtype (WT) mice. One assay used to test for addictive tendencies is the sucrose preference test (SPT). The SPT consists of two phases, the baseline and the test. In the test phase, mice can choose to drink water or sucrose water. The findings from this test can answer questions on the presence of increased motivation and addictive tendencies in ClockΔ19 mice. In our lab we examine the differences in preference of sucrose water between male and female wildtype (WT), heterozygous (HET), and homozygous (HOM) mice. In a sample size of 18 mice, we found no significant difference between WT, HET, and HOM mice. These results may have been due to the concentration of sucrose. We used a concentration of 0.03% for 12 mice and 0.01% for 6 mice, both of which produced ceiling effect like results. In the future, we suggest a decreased sucrose concentration to possibly eliminate the ceiling effect and an increase in sample size.

Expression of Alpha 1C Sub-Unit in Circadian Mouse Model for Bipolar

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Bipolar disorder (BD) is a highly heritable chronic mood disorder characterized by manic episodes with cognitive deficits being an undertreated trait of the disease. These deficits are the best predicters of disease outcome and have begun to be studied in the CLOCKΔ19 mouse model which has good face and predictive validity for BD. In recent studies we have begun to show that the ClockΔ19 mouse model may serve as a valid model for translational study of the cognitive deficits reported by the clinical literature surrounding BD. In this study we seek to continue that research and elucidate the possible underlying molecular mechanisms of the deficits we observe. Several lines of evidence suggest that calcium (Ca2+) signaling is significantly associated with BD. The CACNA1C gene encodes for the alpha 1C subunit of L-type voltage gated calcium channels (VGCC) which is responsible for neuronal excitability. The strongest evidence for the association between Ca^{2+} signaling and BD is abnormalities in intracellular Ca^{2+} signaling found in platelets of BD patients. Supporting evidence from genome wide association studies (GWAS) also show a gain of function mutation in allele rs1006737 of CACNA1C gene being significantly associated with BD. This risk allele increases expression of CACNA1C in some areas of the brain leading to increased neuronal excitability exhibited by BD patients. In the current study we use a cohort of ClockΔ19 mice from our previous cognitive studies to examine the relative expression of CACNA1C in the prefrontal cortex (PFC) and hippocampus (HIPP) of (n=5) wild type, (n=3) heterozygous, and (n=3) homozygous ClockΔ19 mice. We expect that homozygous ClockΔ19 mice which have BD phenotypic traits will show increased expression of CACNA1C in the areas of the brain associated with cognitive the cognitive deficits seen in these mice. Furthermore, we expect that heterozygous ClockΔ19 will show increased CANA1C expression in these regions compared to wild types to a lesser extent then the homozygous mice as they are a translational representation of unaffected first degree relative of patients with BD. The results of the qPCR are currently being examined and might show a causative mechanism of the deficits previously seen in this mouse model of BD.

Muscle Fiber Type Composition In a Rabbit Model of Cerebral Palsy

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Cerebral palsy (CP) impacts approximately 2-3 per 1000 live births and involves lifelong motor disabilities, including impaired muscle function. CP is caused by developmental insults or injuries occurring perinatally, such as hypoxia-ischemia (HI). While extensive research has focused on the nervous system impacts of CP, the effects on skeletal muscle development remain underexplored. To do so, we are using a rabbit model of CP, which offers a closer approximation of human motor dysfunctions compared to rodents. This study tests the hypothesis that prenatal HI alters the muscle fiber type composition of the lateral gastrocnemius muscle, potentially exacerbating motor impairments in CP. We are comparing the muscle fiber type compositions of juvenile rabbits that experienced prenatal HI to that of age-matched sham-operated controls using immunohistochemistry and fluorescence microscopy techniques. Our findings will shed light on skeletal muscle adaptations occurring in CP and help develop targeted therapeutic strategies. This goes without saying, there is always more to do.

In vitro and *In vivo* Assessment of Kupffer cell-Targeted Nanoparticles for Treating Alcohol-related Liver Disease

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Alcohol-related liver disease(ALD) rate has been increasing; out of the 98,457 liver disease deaths, 46% involved ALD in 2022. ALD is resulted from chronic alcohol abuse that is associated with liver damage, further leading to hepatocellular carcinoma. The objective of this project was to develop nanoparticles (NPs) that can target Kupffer cells to deliver anti-inflammatory therapies against ALD. Polylactic-co-glycolic acid (PLGA), an FDA-approved biodegradable and biocompatible polymer, was used to encapsulate dexamethasone (DEX), an anti-inflammatory drug. The DEX-PLGA NPs were coated with pH-responsive biopolymer Carboxymethyl chitosan (CMC), which releases drugs in an acidic environment. The NPs were surface decorated with INT -777, a semisynthetic bile acid that targets G-protein coupled bile acid receptor (Gpbar1) expressed in Kupffer cells. The drug loaded particles were analyzed for their cytotoxicity and efficacy in targeting THP-1 and HepG2 cells that have similar characteristics as Kupffer cells and hepatocytes, respectively. In vitro, THP-1 and HepG2 were treated with varying concentrations of Lipopolysaccharides (LPS) and Ethanol (EtOH) to mimic the ALD condition when testing cell viability. Cellular uptake studies demonstrated that groups with the INT-777-containing NPs had higher uptake than the groups without the INT-777 NPs during inflammation (EtOH and LPS treatment). An ALD mouse model was developed using a standard liquid diet combined with 5% ethanol. Hematoxylin and eosin stained methods were used to confirm steatosis and periportal inflammation in the liver. No inflammation was observed in other tissues. NPs biodistribution 24 hours post-injection showed most of the NPs in the liver. Oil Red O staining resulted in having the most oil droplets in the liver tissues of the ALD mouse model that did not receive NPs treatment, while mouse models treated with NPs showed a similar pattern with healthy liver with a decrease in the amount of oil droplets. Furthermore, immunohistochemistry methods were used to detect Kupffer cell specific F4/80 markers and showed the nanoparticles were concentrated around Kupffer cells. The Cytochrome P450 2E1(CYP2E1) immunohistochemistry was used to show the metabolic enzyme induced by alcohol.

Tissue Engineering of Intervertebral Disc Using 3D Bioprinting

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Pain in the lower back has a strong connection to degenerative disc disease (DDD) and can be present as early as adolescence. Each year, over 266 million people experience DDD globally. Current treatments for artificial disc replacement involve the use of metal-based prosthetics. However, these prosthetics are made of rigid materials that limit mobility. Furthermore, they release metal particles into the body over time, due to wear and tear. This project provides insight into a new approach for replacing damaged intervertebral discs. The goal is to create a biocompatible tissue-engineered intervertebral disc using extrusion-based 3-dimensional bioprinting. In the human body, an intervertebral disc consists of a tough outer ring, the annulus fibrosus, which is made of collagen fibers and cartilage. The inner ring, nucleus pulposus, consists of a gelatinous material made of proteoglycans and water. The outer ring was printed using a hard biodegradable polymer, polycaprolactone (PCL). The printing parameters were at a speed, temperature, and pressure of 6 mm/s, 200 °C, and 500 kPa, respectively. The inner ring was printed using a soft gelatin methacrylate (GelMA)/ polyethylene glycol diacrylate (PEGDA) based hydrogel. The hydrogel (w/v) composition was 15% PEGDA, 5% GelMA, 0.5% lithium phenyl-2,4,6-trimethylbenzoylphosphinate (LAP), and 7% methylcellulose. A second hydrogel, varying only with its GelMA concentration at 3%, was also synthesized. The printability and characteristics of both hydrogels were then compared. The swelling behavior of both hydrogels in 1x PBS was characterized over a week-long period at room temperature (25°C) and body temperature (37°C). Using a rheometer, the rheological properties of both hydrogels were also assessed. Finally, mechanical properties were studied using a Material Testing System (MTS), and the hydrogel structure was imaged using EVOS microscopy.

Sleep Deficiencies and Proactive Versus Reactive Aggression Among Peripubertal Youth Receiving Intensive Psychiatric Services

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Background: Sleep deficiencies (e.g., insufficient duration, low quality) are common in childhood and adolescence and are linked with increased aggressive behavior. Research has shown that sleep deficiencies are more strongly related to reactive than proactive aggression. However, limited research has been conducted in peripubertal youth (9-12) with severe psychopathology nor integrated objective and subjective assessments of sleep. The purpose of the current study was to conduct a preliminary analysis exploring the association between objective and subjective sleep deficiencies and peripubertal youth proactive and reactive aggression in a sample of youth receiving treatment in a partial psychiatric hospitalization setting.

Method: A subsample of 14 peripubertal youth (ages 9-12) admitted to a mental health partial hospitalization program who participated in a sleep research study were included in the current study. The participants were 58% Non-Hispanic White, 17% Black, 17% Latino, and 8% Asian. Thirty-six percent identified as female, 29% as male, and 35% as non-binary. Youth completed two weeks of sleep assessment using multi-informant baseline questionnaires and daily diaries, as well as wearing a Fitbit Charge 5 to assess objective total sleep time based on activity and heart rate. The Proactive/Reactive Aggression scale for child-report was used to assess aggression. The pediatric self-report and parent proxy version of the PROMIS Sleep Disturbances subscale was used to assess subjective sleep deficiencies. Fitbit-derived total sleep time across two weeks was used for an objective assessment.

Results: Proactive and reactive aggression were positively correlated (r = .49). Higher objective total sleep time was correlated with lower reactive (r = -.20) but not proactive (r = .07) aggression. Parent and youth-reported sleep duration was largely uncorrelated with reactive or proactive aggression. Higher youth-reported sleep disturbances were related to higher levels of reactive (r = .34) but not proactive (r = .10) aggression. Conversely, higher parent-reported youth sleep disturbances were related to higher proactive (r = .51) but no reactive (r = .02) aggression.

Discussions: Findings show associations between sleep deficiencies and peripubertal proactive and reactive aggression. However, the strength and pattern of these associations depend on the informant and method. Results support the use of multi-informant and multi-method approaches to sleep

Brain Injury and Dating Violence Among Young Adults

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Introduction: Current literature has identified an association between dating violence and several types of brain injury, but there is a lack of research in young adults. Current literature focuses on brain injury in women who have experienced dating violence with a gap in research on males and sexual and/or gender minorities. This research aims to identify the association between dating violence and brain injury among young adults, with a focus on how this relationship varies across different sexual and/or gender identities.

Methods: The 2022 Rhode Island Young Adult Survey is a behavioral health survey targeting adults aged 18-25 who reside in Rhode Island for at least part of the year. Various recruitment methods were conducted including paid social media ads and the survey resulted in n = 1,022. Multivariable logistic regression assessed the relationship between dating violence and brain injury, adjusting for age, sexual and/or gender identity, race/ethnicity, and social status. An interaction term between dating violence and sexual and/or gender identity was added to the model to test for moderation.

Results: In the fully adjusted model, young adults who have experienced dating violence had significantly higher odds of having a brain injury (OR[95% CI]= 1.84 [1.01, 2.16]), compared to those who did not report dating violence. The interaction term was significant (p = 0.012) and predicted probabilities plot showed that in the presence of dating violence: for heterosexual males, the probability of brain injury decreased, for heterosexual females, the probability of brain injury slightly increased, and for sexual and/or gender minorities, the probability of brain injury dramatically increased.

Conclusion: Not only do findings support the association between dating violence and brain injury, but the odds of brain injury related to dating violence is much higher among heterosexual females and sexual and/or gender minorities. Translating research into practice, brain injury prevention in young adult heterosexual females and sexual and/or gender minorities should focus on the prevention of dating violence. Yet, males in this age group, who are most likely to experience brain injury, should have prevention efforts based on other risk factors. These findings can contribute to better tailored prevention, intervention and support strategies for young adults affected by brain injury, specifically by sexual and/or gender identity. Future efforts might in

Insomnia and Pornography Addiction in Rhode Island Young Adults

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Objectives. There is limited literature on pornography addiction in young adults, and even more so the role of insomnia in pornography addiction. Of the few studies that exist, this association was measured among adult men and veterans. More research is needed on this association among young adults and among those with other sexual and/or gender identities. This study examined 1) the association between insomnia and porn addiction and 2) whether this association varies across sexual and/or gender identities among Rhode Island Young Adults aged 18-25 years old.

Methods. This study uses data from the 2022 Rhode Island Young Adult Survey, which successfully recruited 1,022 young adults aged 18-25 who live in Rhode Island—for at least a part of the year. Pornography addiction and insomnia were measured by valid and reliable scales: Problematic Pornography Consumption Scale and the Insomnia Severity Index, respectively. Potential confounders measured and controlled for include age, sexual and/or gender identity, race/ethnicity, social status, and alcohol use disorder. Multivariable logistic regression was used to estimate the relationship between insomnia and porn addiction. An interaction term between sexual and/or gender identity (cisgender heterosexual males; cisgender heterosexual females; sexual and gender minorities) and insomnia was added to the model to assess potential moderation.

Results. Prevalence of pornography addiction was 6.2%, and highest among cisgender heterosexual males (17.3%). Prevalence of insomnia was 23.8%, and highest among sexual and/or gender minorities (30.5%), then cisgender heterosexual females (21.1%),then cisgender heterosexual males (11.3%). Young adults with insomnia, controlling for all confounders, had 2.51(95% CI: 1.53, 4.35) times the odds of pornography addiction compared to those without insomnia. The interaction term was significant (p<0.001) and the association was strong among cisgender heterosexual males but insignificant among other sexual and/or gender groups.

Conclusions. Insomnia is associated with porn addiction among young adults, particularly among cisgender heterosexual males. Future research should examine whether treatment of sleep-related disorders, such as insomnia, may impact an individual's dependence upon pornography, particularly among cisgender heterosexual males. Similarly, research is needed to understand the mechanisms of this relationship and why it is specific to cisgender heterosexual males.

Chemical Characterization of *Vibrio coralliilyticus* and its Secretome for the Identification of Bioactive Metabolites

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Vibrio coralliilyticus strain RE22 is a gram-negative, marine bacterium recognized for its pathogenicity towards marine invertebrates, especially oysters and coral. In oyster larvae, interactions with RE22 impact developmental processes and immune responses, which can be detrimental for both marine ecosystems and aquaculture systems alike. We hypothesize that RE22 employs membrane vesicles (MVs) in its attack against hosts and their microbiomes. Other Gram-negative bacteria, such as *Vibrio cholerae* are known to produce MVs carrying a wide array of molecular cargo—including toxins, outer membrane proteins involved in biofilm formation, immunomodulatory microRNAs, and specialized metabolites— to neighboring cells. In this study, we conducted a comparative metabolomic analysis between different RE22 culture fractions to deduce which secondary metabolites are packaged into MVs, transported through diffusion, or retained in the cells. Using ultracentrifugation, *Vibrio coralliilyticus* RE22 MVs were isolated from the filtered supernatant of broth cultures. The pelleted cells, MVs, and MV-free supernatants were extracted and prepped for analysis by liquid-chromatography tandem mass-spectrometry. Untargeted metabolomic studies were conducted using bioinformatics tools, such as Global Natural Products Molecular Social Networking (GNPS), SIRIUS, and Cytoscape. Immediate findings suggest differences among fractions regarding the presence of putatively annotated metabolites.

Investigating the Role of Serotonin in the Escalation of Alcohol Consumption

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Alcohol Use Disorder (AUD) is a chronic relapsing disorder, characterized by problematic patterns of alcohol use and is often comorbid with depression. Knowledge of the neurobiological mechanisms that control drinking behaviors, the expression of alcohol-associated memories and how these mechanisms are modulated by internal states is critical to understanding why these behaviors are resistant to change. *Drosophila* serves as an exceptional model organism because of its lower complexity, the similarity that exists in reward circuitry function, and the availability of neurogenetic tools that enable the analysis of neural circuits with exceptional spatial resolution. Like mammals, *Drosophila* escalate drinking and form an enduring preference for alcohol-associated cues, which persist despite aversive consequences. Previous work identified discrete neural circuits that underlie alcohol associated memories and their temporal requirements. These memories require the mushroom body, a learning and memory region, as well as DA modulation which shifts from an entire population during acquisition to two discrete DA subsets known to process memories with opposing valence. More recent work suggests a role for serotonin in consolidating alcohol associated memories. Interestingly, other work in mice suggests a role for serotonin in regulating voluntary consumption of alcohol. However, it is unclear if serotonin plays a role in regulating voluntary consumption in *Drosophila*. Here, we utilize the FLIC, a newly developed consumption assay to continuously measure alcohol-related feeding behaviors in flies. First, we characterized alcohol consumption across 5 days for different doses (10% and 15%) compared to sucrose to determine precisely when voluntary alcohol consumption begins to escalate. Continuous measurements were taken from previously starved flies (24 hours). Preliminary data suggest that flies develop preference for 15%, but not, 10% alcohol. Next, we intend to investigate the impact of chronic stress on alcohol consumption. We hypothesize that chronic stress will result in faster escalation of drinking, and this will be ameliorated by the administration of selective serotonin receptors inhibitors (SSRI). By experimentally investigating the role of serotonergic neurons in voluntary alcohol consumption, a clearer understanding of the underlying neural circuitry involved in the complicated relationship between AUD and internal states such as stress will be obtained.

Determining the DNA Repair Capabilities of Melanoma Derived Variants of Polymerase Theta

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There are numerous environmental factors that prompt damage to human DNA. DNA Polymerases are the main recourse for providing repair mechanisms to maintain the genetic integrity of our DNA when damage occurs. The human body has an abundance of DNA Polymerases which aid in the repair of double-strand breakage (DSBs), which result from exposure to ultraviolet light or irradiation, that are unique types of DNA damage. DNA polymerase theta (Polθ) is the major DNA repair polymerase in the pathway known as microhomology-mediated end-joining (MMEJ) repair pathway, a pathway that occurs any time within the cell cycle to repair DSBs but is often less accurate than the more classical pathways of nonhomologous end joining (NHEJ) or homologous recombination (HR). In this pathway, Pol θ has a unique role in which it identifies small homologies within the broken strands and aligns the sections for extension and repair. Pol theta is a large 290 kDa protein that contains an N-terminal helicase domain, a central domain, and a C-terminal catalytic polymerase domain. The exact domain that functions in MMEJ is not well understood. Previous studies have suggested that the activity is primarily in the central domain, but some activity is linked to the C-terminal Polymerase domain. Using only the C-terminal domain, we performed in vitro biochemical assays wild-type Pol θ and cancer-associated variants L2538R, E2406K, T2161I with several ssDNA strands of various lengths each containing internal microhomology to try and observe its aligning and extension abilities to observe the basic MMEJ function without the N-terminal portion of the protein. Our studies demonstrated that there is a higher occurrence of extensions and repair on shorter vs longer DNA strands and the mutants demonstrated a similar sequence of extension. Interestingly, the variants revealed a smudging pattern on DNA templates greater than 70nt suggesting either greater endonuclease activity or inconsistent DNA alignment and extension. This project lays the groundwork for future MMEJ assays using other cancer-associated located in both the central and N-terminal helicase domains to explore the role of key residues involved in this unique activity and the potential role for aberrant MMEJ activity in cancer.

Characterizing the Active Site Environment and Mechanism of Cancer Derived Variants of Human DNA Polymerase Theta

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DNA is regularly being damaged by numerous endogenous and external factors often leading to genomic instability and disease. There are several pathways through which damage is mitigated, all of which utilize DNA polymerases to repair damage, through replacing or bypassing the damaged nucleotide. DNA Polymerase Theta (Pol Theta) is one such enzyme that operates in DNA repair, known to be a low fidelity enzyme notorious for base mispairing, a driving factor in the promotion of genomic instability. How and why Pol Theta mis-incorporates is not well understood. To explore this and determine the mechanism of DNA polymerization, we can monitor the enzyme active site in real-time using a 2-aminopurine(2-AP) fluorescent modification at the templating base on our DNA substrate and observe changes in fluorescence during correct and incorrect nucleotide incorporation with a stopped-flow instrument. We observe that during correct nucleotide incorporation there is a decrease in fluorescent signal due to the pi stacking interactions that facilitate correct nucleotide alignment, while no observed fluorescence change is seen with incorrect nucleotide incorporation. Using the same technique, we observed real-time nucleotide incorporation with cancer derived variants L2538R and E2406K, both exhibiting similar fluorescent quenches in the presence of correct nucleotide. While L2538R behaves similar to WT, E2406K experiences a unique increase in fluorescence when presented with the incorrect nucleotide. To further examine the active site environment, we have moved the 2-AP probe to a +1 position and observed an increase in fluorescence followed by a rapid decrease as incorporation of the correct nucleotide occurs, again a trend that is absent in the presence of incorrect nucleotide for both WT and the variants. We hypothesize that this is consistent with nucleotide binding and subsequent release of the DNA product. Combining with our biochemical data this suggests that the E2406 residue plays a critical role in nucleotide selection and alignment for accurate base pairing, highlighting its potential impact on overall fidelity and mutagenesis.

Investigating the Effects of Different Isoforms of COX7A on Mitochondrial Supercomplex (mSC) Assembly and Modulation of Mitochondrial Reactive Oxygen Species Production

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Introduction: The mitochondrion, the major cellular organelle for energy production via oxidative phosphorylation, is composed of four electron transport chain complexes; I, II, III and IV, that are responsible for transporting electrons to molecular oxygen. The assembly of these multi-protein structures into one large complex known as a supercomplex (SC), is thought to enhance energy production efficiency by minimizing electron leakage, which reduces the production of reactive oxygen species (ROS). Maintaining redox balance is critical in the heart, where excessive ROS can induce oxidative stress and impair cardiac function. A protein of interest identified in multiple tissues that promotes mitochondrial supercomplex (mSC) assembly is COX7RP (also known as COX7A2L). We have previously shown that the overexpression of COX7RP reduces ROS production in heart cells via promoting SC assembly. However, COX7RP is one of three COX7A isoforms that are mutually exclusive for incorporation into mSC. The other Cox7A isoforms expressed in the heart are COX7A1 and COX7A2, and their role in mSC formation and ROS production is unknown.

Methods: Vectors for adenoviral (AdV) overexpression and lentiviral CRISPR-mediated gene knockdown of COX7RP, COX7A1, and COX7A2 were designed using Vectorbuilder. Adenoviral COX7A overexpression sequences had silent mutations to render them CRISPR resistant and were expressed with mRFP670nano. Plasmids were isolated from *E. coli* stocks, purified and transfected into HEK 293 cells using Lipofectamine 3000. Cells were cultured in DMEM supplemented with 10% Fetalgro in a CO2 incubator at 37°C.

Results: HEK293 cells transfected with pac1-linearized purified Adv-COX7A1, COX7A2, and COX7A2l plasmids displayed distinct viral plaques demonstrating successful viral propagation. Subsequent passages and infection of HEK293 cells showed increasing expression and infection efficiency of all viruses. Future experiments will be focused on generating COX7A1, COX7A2, and COX7A2L knock-out cell lines using retroviral methods.

Conclusion: 4 distinct AdV were generated and produced, which will be indispensable in determining the role of different COX7A isoforms in modulating ROS and mitochondrial SC formation. Future studies will uncover the role of overexpression of these specific adenoviruses in COX7A null cell lines. Understanding the roles of COX7A1 and COX7A2 on SC assembly and ROS modulation is currently an unmet need in cardiac pathophysiology.

The Fanconi Anemia Proteins are Required for Effective Thrashing Behavior in *C. elegans*

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Fanconi anemia (FA) is a rare human genetic disease characterized by birth defects and increased risk for cancer and bone marrow failure. It affects roughly 1 in 136,000 individuals.   In recent years we have observed an increase in neurological symptoms among FA patients. These include limb weakness, papilledema, seizures, and irreversible loss of neurological function. These symptoms are referred to as Fanconi anemia neurological syndrome (FANS). The molecular basis of FANS is poorly understood.

Our lab is using the model nematode *C. elegans* as a model to understand the role of the FA proteins in nervous system development. *C. elegans* is an outstanding model for the study of the nervous system because it maintains a complete nervous system, has a short period of 4 days to go from egg to adult, and can reproduce genetically identical offspring asexually.

In this study, we have analyzed the effects of mutation of the FA pathway on the ability of animals to thrash (swim) in liquid media. Thrashing is a rhythmic movement that *C. elegans* perform when submerged in liquid, a movement controlled by the VB and VA cholinergic neurons as well as the VS gabaergic neurons. Differences in the frequency of thrashes could indicate a defect in the function of these sets of neurons. Thrashing was analyzed on days 1, 4, and 11, allowing us to monitor this behavior across the lifespan.

In the assay, thrashing was analyzed in four different strains of *C. elegans*: a wild-type N2 strain, fcd-2 mutant, fnci-1 mutant, and a strain that is mutant in both fcd-2 and fnci-1, under unstressed conditions and following exposure to hydroxyurea from egg to larval stage 2 (L2), a developmental time period when neurogenesis occurs. Hydroxyurea is a ribonucleotide reductase inhibitor that depletes cellular nucleotides resulting in DNA replication stress. We determined that deletion of the FCD-2 and FNCI-1 genes results in reduced thrashing compared to wild-type N2 animals, particularly under conditions of DNA replication stress. Furthermore, differences in the levels of thrashing became more pronounced in mutant animals with aging. Our results indicate that the FA proteins play an important role in *C. elegans* thrashing behavior and suggest that the FA proteins may play an important role in the development and function of VB and VA cholinergic and VS gabaergic neurons. Our studies provide potentially important mechanistic insight into the molecular origins of FANS.

The interconnectedness of epigenetic alterations and mitochondrial dysfunction during the aging process

Dakota Hunter, Sydney Bartman, Jaime Ross & Giuseppe Coppotelli

George & Anne Ryan Institute for Neuroscience, University of Rhode Island, North Kingstown, RI

Age-related illnesses have markedly increased over the last few centuries alongside the dramatic increase in human longevity as advancements in medical care and hygiene practices have developed. Aging can be defined as a time-related decline in physiological functions required for survival and reproduction. The aging process is accompanied by an accumulation of damage to macromolecules, organelles, and cells, which ultimately leads to organ/tissue dysfunction and death. Currently, twelve hallmarks of aging have been defined, and our study aims to investigate the interconnectedness of epigenetic alterations and mitochondrial dysfunction during the aging process. These two hallmarks of aging have also been highly implicated in the development of several age-related diseases, such as metabolic disorders, forms of cancer, as well as neurodegenerative diseases including Alzheimer's disease. Using the innovative ICE (inducible changes to epigenome) mouse model, which has shown a link between epigenetic alterations induced by DNA damage and premature aging, we can directly test in cells whether such alterations in the epigenetic landscape can affect mitochondrial function. Ongoing studies aim to compare possible changes in mitochondrial morphology, membrane potential, electron transport chain expression, generation of reactive oxygen species (ROS), as well as mitochondrial fusion and fission. Live-cell imaging, immunocytochemistry, flow cytometry, and western blot techniques are being used to investigate these differences. Findings from this project will greatly contribute to the present understanding of the aging process and will identify potential biochemical markers and/or targets for aging interventions.

An inducible system for overexpressing TAG-1 in developing motor and sensory neurons

Adam Xu, Kathleen Meininger, Sienna Partipilo & Alexander Jaworski

Neuroscience, Brown University, Providence, RI

During nervous system development, spinal motor neurons (MNs) project their axons to various targets in the body periphery. The molecular mechanisms that guide MN axons to their appropriate targets remain incompletely understood. Previously, we have shown that the cell adhesion molecule TAG-1 prevents MNs from misrouting their axons into the dorsal root ganglia (DRG). TAG-1 is expressed both in the sensory neurons of the DRG and in MNs, and global deletion of TAG-1 causes MNs to misproject their axons into the DRG. However, deletion of TAG-1 only in MNs results in fewer misprojections, suggesting that TAG-1 derived from other sources helps guide motor axons past the DRG. One potential source is the DRG itself, and we hypothesize that DRG-derived and MN-derived TAG-1 synergize to guide MNs past the DRGs and to their appropriate targets. In order to test this, we sought to independently manipulate TAG-1 expression in the MNs and DRGs. Here, we use mouse genetics and quantitative immunohistochemistry of embryo tissue sections to evaluate methods for manipulating cell-type specific TAG-1 levels. While we have established methodology to delete TAG-1 specifically in MNs, we demonstrate that several Cre transgenic lines fail to efficiently delete TAG-1 in the DRG. As a solution, we present a doxycycline-controlled Tet-On gene expression system for modulating TAG-1 levels in the MNs and the DRG. Utilizing an optimized version of this system in global TAG-1 knockouts will enable further exploration of cell type-specific TAG-1 functions in motor neuron axon guidance.

POSTER SESSION B
11:00 AM – 12:30 PM

Fascitelli Center for Advanced Engineering, 1st Floor
B-1 to B-25

Fascitelli Center for Advanced Engineering, Ground Floor
B-26 to B-49

Paramaz Avedisian '54 Hall, College of Pharmacy
B-50 to B-73

Development Of Dual-Comb Ultrafast Erbium Fiber Lasers Using Homemade Graphene-Based Saturable Absorbers

Nathan Arduino, Matthew Silvay & Ahmet Akosman

Engineering, Roger Williams University, Bristol, RI

In this study, an ultrafast erbium laser was built using homemade 2-dimensional saturable absorbers. There are several components utilized in the laser's setup, beginning with a 980nm pump, providing the system with up to 700mW of optical power and protected using an isolator. This source then connects to the main laser cavity, which consists of a fiber WDM (wavelength division multiplexer), 0.90cm of Liekki erbium gain fiber, 1m of PMF (polarization maintaining fiber), approximately 11m of SMF (single mode passive fiber), a graphene saturable absorber, a 1550nm fiber isolator to control the flow of light within the system, and a 10% fiber output coupler to control the amount of energy released from the cavity. In order to minimize loss in the cavity, the vast majority of laser components were spliced together wherever possible. Fibers were connectorized at the input and output of the cavity, PMF, and the ferrule connection where the saturable absorber is deposited. The laser cavity was analyzed through the use of several devices, such as an optical power meter, oscilloscope, and optical spectrum analyzer. These devices allowed for measuring power output from the laser cavity for a range of source currents and identifying the resulting pulses from mode-locked signals.

The saturable absorbers used within this laser cavity were hand-made in the lab using the method known as liquid phase exfoliation. The 2d saturable absorber materials developed for the laser cavity include graphene, molybdenum disulfide, and a molybdenum disulfide/graphene mixture. Solutions containing a combination of the powdered materials and an IPA/water mixture were prepared, then placed in an ultrasonic processor, and lastly placed into a centrifuge resulting in the 2d saturable absorbers suspended in liquid solutions. The quality of these solutions was then tested to determine the concentration and thickness of the 2d materials. This study shows promise in finding an easy, efficient method for preparing high-quality 2d saturable absorbers for achieving mode-locking in laser systems.

Evaluating Conditions Contributing to Freshwater and Atmospheric Microplastic Inputs into Narragansett Bay

Ally Fennell[1], Kate Zmich[2], Ella Membrino[1] & Lillian Jeznach[1]

[1]School of Engineering, Roger Williams University, Bristol, RI
[2]College of Environmental and Life Sciences, University of Rhode Island, Kingston, RI

Microplastics pollution is a widespread and growing concern for the entire world, especially for Rhode Island due to the high urban land cover and the importance of surrounding marine life to the local economy. This study aims to look at how different conditions affect the freshwater concentrations and atmospheric fluxes of different types of microplastics to the Narragansett Bay. A custom designed atmospheric microplastic deposition collector installed on campus and used to measure atmospheric microplastic fallout. Freshwater samples were collected at different sites along three major rivers in Rhode Island. The river samples were digested using potassium hydroxide since they contained greater concentrations of organic matter than the atmospheric samples. All samples were stained with nile red. The stained samples fluoresce under a blue light, which allowed for easier microplastic counting and identification under the microscope. Blank samples were collected and analyzed for all freshwater and atmospheric samples. Data was analyzed to understand conditions contributing to increases or decreases in microplastic freshwater concentrations and atmospheric fluxes. Atmospheric microplastic fluxes were analyzed with respect to wind speed. For freshwater samples, microplastic concentrations were compared at different locations along the river relative to wastewater treatment plants and their proximity to urban/rural locations. Based on the analysis, the majority of microplastic particles in both the atmospheric and freshwater samples were fibers then fragments. In addition, greater atmospheric fluxes were measured at lower wind speeds. Data thus far do not indicate significantly greater microplastic concentrations downstream of wastewater treatment plants. This project is part of a larger long-term microplastic sampling campaign involving undergraduate researchers to develop a database of freshwater and atmospheric microplastic data. This research will help to better understand microplastic distributions across the state which is needed in order to develop effective solutions and technology to combat the abundance of microplastics that are a growing global and local issue.

Enhancing AR Accessibility Through Alt-Text: A Case Study of a Stormwater Management Tour

Novena Kapisa

Art and Sciences, University of Rhode Island, Kingston, RI

This summer, I contributed to an innovative project with the DWELL Lab in partnership with the Providence Stormwater Innovation Center at Roger Williams Park. Our goal was to create an augmented reality (AR) walking tour that maps and models green stormwater infrastructure sites, producing educational AR installations for public environmental education. My role involved writing descriptions for particular Points of Interest (POIs). A POI is a specific location where people can see specific content or information. Along the way, I realized we could improve accessibility by adding alt text to the AR experience.

Alt text (alternative text) is important for making digital content accessible, especially for people using screen readers. Alt text, typically used for describing images, can also serve an important role in AR applications (Edwards. et al, 2023). Text, images, and 3D elements in AR can be hard for people with visual impairments, cognitive disabilities, or different learning styles because they might not be clear without additional context. By adding alt text to the project, communication designers can create a foundation for a more inclusive AR experience. So that educational AR content is available to more people, including those with visual impairments or different learning needs, we can promote equal opportunity for environmental education and increase public engagement with stormwater management issues. This approach should reflect the understanding that accessibility should be both responsive to individual user needs and a fundamental aspect of communication design (Strantz, 2021). It not only benefits users with visual impairments but also improves the experience for a variety of people, like those in remote areas, those who can't afford on-site visits, or those affected by severe weather (Heilig. et al, 2024). By creating this additional layer of information, designers can significantly improve the tour's accessibility.

For the poster, I will explain what alt text is and its importance for accessibility, discuss potential challenges it might face, and provide an example from my project that can be used to demonstrate how to create effective alt text. Working on this project taught me a lot about making tech-based education more inclusive. By thinking about accessibility from the start, designers can create AR experiences that are both educational and inclusive.

Augmenting Environmental Education: Creating Inclusive AR Experiences with Adobe and Hoverlay

Calder Puckett

Art and Sciences, University of Rhode Island, Kingston, RI

This summer, I worked in the DWELL Lab and collaborated with the Providence Stormwater Innovation Center at Roger Williams Park on an exciting project. We are developing an augmented reality (AR) walking tour that showcases green stormwater infrastructure sites, offering educational AR installations for public environmental education. My role focused on creating the AR experience using Adobe software, ensuring that the content was engaging and informative.

Throughout the project, I worked with members of the Stormwater Innovation Center to create an informative poster designed to educate the public about watershed protection. The poster, titled "How to be a Good Citizen of the Watershed," highlights various actions individuals can take to contribute to a healthier watershed. From planting rain gardens to minimizing chemical use, each small action contributes to a larger environmental impact. The poster also includes calls-to-action, encouraging community involvement through volunteering and citizen science.

For the poster presentation, I will discuss the process of designing the AR experience and the informative poster, emphasizing the importance of collaboration and community engagement. This project underscored the significance of creating educational tools that are both visually appealing and accessible to a diverse audience. By integrating AR technology and informative visuals, we aim to enhance public understanding of stormwater management and promote proactive environmental stewardship.

As emphasized in the Handbook of Scientific Communication, effective science communication requires that "science professionals, communicators, and a broader public must work together to slow the spread of misinformation, to generate action based on scientific knowledge, and to ensure that all audiences read and critically examine scientific findings for bias"(Mallete 2022) This collaborative approach is vital for creating impactful and inclusive educational experiences.

Using Diatoms to Explore Coastal Resiliency with Middle School Students

Jillian Nash[1], Zulay Izazaga[1], Julia Gandrud[2] & Anabela Maia[1]

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[2]RI STEAM Center, Rhode Island College, Providence, RI

The coastal regions of Rhode Island, notably the port of Providence, face significant challenges due to climate change. Neighboring communities are not well-equipped to grapple with these challenges, especially since the residents of Providence County (in cities like Pawtucket, Cranston, Warwick, Woonsocket) are consistently on the lower end of the socioeconomic scale. While there are other interventions available to combat localized flooding and excessive heat, education surrounding climate change and coastal resilience is limited. In response to these multifaceted challenges, we have developed lesson plans aimed at educating K-12 students about coastal resilience in Rhode Island. These lesson plans are designed to help students understand the impacts of climate change in their communities and explore practical solutions to enhance resilience. Our educational activities align with several Next Generation Science Standards, incorporate art education and are crafted to be engaging, multi-disciplinary, and cost-effective. This lesson plan focuses on diatoms present in major bodies of water as indicators of water health. In this lesson, students will observe diatom samples from their local community waters and learn more about these organisms and their role as bioindicators, creatively express their findings using artistic techniques, and learn the significance of diatoms in water health. The students will use readily available sculpting or building materials (clay, LEGO, paper, etc) to create 3-dimensional interpretations of the diatoms they will observe, focusing on an individual diatom specimen. The writing portion of this activity will take approximately 10 minutes, then the remainder of their class period (between 30 and 50 minutes depending on the school) to craft their diatom sculptures. This lesson plan fulfills Next Generation Science Standard RST.6-8.7; "Integrate quantitative or technical information expressed in words in a text with a version of that information expressed visually (e.g., in a flowchart, diagram, model, graph, or table)". This activity emphasizes critical topics such as water quality, pollution, and familiarity with local ecology. This literacy standard involves integrating technical information with visual representations. The summative project where students build 3D models of diatoms effectively demonstrates this integration by transforming textual or quantitative data about water quality into physical models Through this initi

An Assessment of Environmental DNA for Estimating Population Density

Andrew Hogan

Biology, Providence College, Providence, RI

Environmental DNA (eDNA) is obtained from shed organic material, and can be used as an indicator of biodiversity and species abundance within an ecosystem. In this project, we studied the behavior of environmental DNA samples in estuarine environments. We first designed a qPCR probe for Mummichogs (Fundulus heteroclitus) and used it to conduct two experiments. In the one, water samples were taken from tanks at the EPA's Atlantic Coastal Environmental Sciences Division Laboratory in Narragansett. Each tank contained a different number of fish of relatively similar sizes, allowing for the total biomass of the tank to be estimated. By quantifying the DNA in each tank, a relationship relating biomass and DNA concentration was discovered. There was an increase in DNA as fish biomass increased. Secondly, the rate of decay of eDNA in environmental water samples was determined by testing water samples on the day of collection as well as three, six, and nine days later. As time progressed, the DNA concentration of detectable DNA initially increased before suffering a sharp decline sometime around the sixth day. These projects can be used to support and validate other eDNA experiments, either through the experimental usage of eDNA samples or through the meaning of experimentally obtained data samples.

Stuck Between a Cow and a Plant Place; Analysis of EHEC Attachment Mechanisms on Bovine Cells and Plants

Luke Neri, Ryan Cielo, Joshua Rykiel & Matthew Moreau

Biology, Providence College, Providence Rhode Island

Enterohemorrhagic *Escherichia coli* (EHEC) is a dangerous and common pathovar of *E. coli* due to its large host range and production of Shiga toxin; a toxin that damages blood vessels resulting in local and systemic tissue damage. EHEC transmission to humans occurs through various hosts, most commonly cattle and produce products. Super shedder (SS) cattle infected with EHEC shed at a rate three log higher than regular shed rates, causing SS isolates to account for almost 96 percent of EHEC in the environment. SS isolates of *E. coli* have a distinctive phenotype; producing high levels of biofilm and have strong, aggregative adhesion patterns on bovine recto-anal junction squamous epithelial (RSE) cells. To better understand the mechanisms responsible for this change in phenotype, comparative transcriptomics were performed via RNA sequencing on SS and non-SS isolates attached to RSE cells. To determine if the mechanisms that drive SS-isolates unique adherence phenotypes on RSE cells correlate to the ability (and alterations in ability) to attach to other vehicles of transmission, namely spinach and lettuce, we took a previously determined mutant library of SS and non-SS EHEC isolates and examined their attachment and biofilm formation on leafy greens. To test adherence, we developed a leaf attachment assay where 1.5 cm spinach disks were inoculated with 107 CFU of the SS and non-SS mutants and parents for 4 hours. Leaf discs were then homogenized, and cells were plated on media to determine the number of adherent bacterial cells. Because *E. coli* form biofilms once attached to these leaves, these same mutants were further tested on their ability to form biofilms in spinach and lettuce lysates via the crystal violet method. Based on the data, attachment and biofilm formation of EHEC are strain, host, and temperature dependent. One exception to this result was the ΔyfaL mutant, which up until this point was identified as a hypothetical protein, has a conserved phenotype across both SS and non-SS isolates for attachment and biofilm formation. The analysis of this data is critical to identifying what genetic factors may play a role in the attachment and biofilm formation of SS and non-SS strains of *E. coli*. This data can be utilized to identify further genes of interest correlated to attachment to create a more diverse mutant library with the possibility of creating therapeutics to target EHEC attachment rather than antibiotic treatments to treat EHEC post-infection

Bacteriophage-host interactions are influenced by genetic variation in genomic islands

Michaela Johnson & Marcia Marston

Biology, Roger Williams University, Bristol, RI

T7-like bacteriophages that infect coastal cyanobacteria are ubiquitous in marine environments, where they impact the composition, evolution, and mortality of their hosts. Often these phages are very host-specific using tail-fibers, known as receptor binding proteins, to recognize and attach to lipopolysaccharide (LPS) features on the host's surface. Previous studies have described the T7-like phage genome as having three genomic islands where an abundance of horizontal gene transfer occurs. In particular, tail-fibers genes are observed to have the highest rate of transfer. We have isolated and sequenced 24 *Synechococcus*-infecting T7-like phages from Narragansett Bay, Rhode Island to identify genes that may be important in phage-host interactions. In this study we aimed to characterize a gene in the second genomic island that was extremely divergent among the sequenced isolates with only 14% to 47% predicted amino acid sequence identity. To explore possible functions of the gene, we utilized AlphaFold2 to make 3D models of single polypeptides and their corresponding homotrimers. Despite the amino acid variation, the predicted protein structures were all very similar, with the predicted shape suggesting that these proteins might serve as receptor binding proteins. Host range analysis was performed by setting up pairwise cross-infection assays using 6 *Synechococcus* cell types. A distinct infection pattern was seen; all the phages could infect a *Synechococcus* in clade I (MV1320), but only some could infect a *Synechococcus* in clade VI (WH8018). An infection kinetics experiment was then conducted to assess how the different gene variants may influence phage infection dynamics, such as attachment to cells and replication in host cells. For this assay, four T7-like phages were added to host cells (MV1320) and multiple samples were collected over a 48-hour period. At each time point the cells were removed via filtration and the extracellular DNA was quantified using a qPCR assay. We found the four phages showed different levels of both attachment to the cells and replication within the host cells. Further analysis of the function and content of genes located in the other islands will aid in the understanding of how the exchange of genetic material between phages impacts interactions with host cells.

Nutrient Extraction from Martian Regolith Simulants to Establish Their Suitability as a Substrate for Plant Growth

Jamie Wells, Gabby Fabrizi, Gabriella Wade, Brennan Foley & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

Mars is a prime candidate for future exploration and potential long-term human habitation but presents significant challenges to on-planet sustainable plant growth. Understanding the composition of plants and the essential nutrients they require is crucial for assessing their growth potential on Mars. Terrestrial plants depend on a complex mixture of macronutrients (N, P, K, Ca, Mg, and S) and trace micronutrients (Fe, Mn, Zn, Cu, Mo, B, Cl, and Ni). The Mars regolith is amenable to these nutrients, though lacking carbon, which can be supplemented. The greater challenge is the high levels of toxic perchlorate (2% wt) distributed through the planet's surface, making it unsuitable for plant growth.

To address this challenge, we tested three different Martian soil simulants formulated in Exolith Labs® to explore nutrient extraction on pretreated, perchlorate-removed, regolith. The simulants' metallo nutrients were extracted by either washing or leaching (2g/(20mls x 5)) with DI water, hydrochloric acid (1M), or acetic acid (1M). These small extraction techniques were then compared to a bulk wash extract (50g/500mls) to see whether a solid stock fertilizer mix could be prepared for growth supplementation of Martian soil similar to the commercial product Jackpot®. Our experimental findings using ICP, FTIR, XRF, and XRD spectroscopy indicate that washing was a more efficient method, and although H_2O has limited efficacy in nutrient extraction, HCl and acetic acid solutions significantly enhanced the release of essential nutrients from the simulants. Furthermore, the three simulants were unsuccessful in making a fertilizer mix that contained all of the essential nutrients needed to sustain plant life. However, H_2O was the best solution for extracting a mix containing the highest concentration of a number of these essential nutrients.

This study also examined the physical properties of the simulants, including sedimentation rates, water holding capacity, and bulk density. These properties are critical for efficient nutrient extraction and as a potential substrate for viable plant growth. Regolith MGS-1S has the most nutrient-rich regolith as well as the most efficient and timely nutrient extraction because of its high concentration of soluble SO4- anion and larger particle composition. MGS-1 and JEZ-1 have slower extraction efficiencies because their smaller particle size composition allows for greater water holding capacities and slower leach flow.

Estuarine Sediment in the Kickemuit River: Analysis of Raw, Decarbonized, Decarbonated, and Acid-Washed Samples Using XRD, XRF, ICP-OES, DRIFTS, and Raman

Brennan Foley, Gabriella Wade, Gabriella Fabrizi, Jamie Wells & Stephen O'Shea

Chemistry, Roger Williams University, Bristol, RI

The Kickemuit River in Rhode Island is a major freshwater input for Mount Hope Bay estuary, and it is a major source of nutrients notably the limiting organic and inorganic phosphorus forms. Phosphorus on entering the more basic saline waters precipitates and deposits within the estuarine sediment bound to Ca and Fe, becoming ecological locked and recycled in this niche. This study analyzed the concentration of metal ions [Fe, Ca, Mg, Al] and their mineral structures by a suite of spectroscopic instrumentation XRD, XRF, ICP, DRIFT, and Raman within the bay sediment and contrasted this with concentration of water soluble and bound phosphates extracted from the sediment. Segmented (25 cm) core samples (1 M) were collected from six different sites from the Kickemuit and Taunton rivers, and Mount Hope Bay. The segmented samples were dried (100°C 24hrs), ground, sieved (#20 mesh size), and were heated (550°C 4hrs) to determine the total organic carbon from loss on ignition and further heated (1000°C 5hrs) to determine total carbonate content. The release of the different forms of phosphorus upon treatment (water and acid washes) was determined by the ascorbic acid chemical spot test. The samples analyzed by spectroscopic instruments and chemical spot tests were compared to the 1646a NIST reference estuarine sediment standard. XRF scans of whole and treated segmented sieved samples identified the presence and an abundance of Fe, Ca, Si, Mn, Al, and Cu metal ions. Further instrumental XRD analysis identified the acid washed decarbonated sample having a high concentration of bound phosphates in the form of ferric phosphate [$FePO_4$] and apatite [Ca_5PO_4]. XRD spectra also revealed the abundance of aluminosilicates such as kaolinite [$Al_2Si_2O_5(OH)_4$], gibbsite [$Al(OH)_3$], and feldspars [$KAlSi_3O_8$], [$NaAlSi_3O_8$], [$CaAl_2Si_2O_8$]. FT-IR DRIFTS analysis of overlaid comparative spectra from each phase of the sediment treatment and extraction shows loss of sulfate, carbonate, and phosphate ions. Raman spectroscopy indicated that heating the dried sediment to a 1000°C altered the mineral composition and species. ICP-OES was used to identify the concentration of suspended and water-soluble metals and phosphorus directly within filtered pore water and those extracted from the sediment by either aqueous or acid wash. The latter acid wash being more potent extractant of metals and phosphorus ion.

Environmental Transformation of Microplastics from Consumer Plastics and their Physicochemical Properties

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Plastics waste pollution has emerged as a profoundly concerning threat to the marine ecosystems. Plastics that find their way into the ocean break down into microplastics (MPs) (with maximum size of 5 mm and a minimum size of 1 μm) and nanoplastics (NPs) (with size of < 1μm). In coastal ecosystems, these plastics have been shown to accumulate within the sea surface microlayer, which is a thin gel-like layer containing biological molecules, organic pollutants, microorganisms, and inorganic particles. Secondary MPs and NPs account for the bulk of plastic particles in marine ecosystems and are formed by photochemical and mechanical degradation and they have attracted ample attention for their considerable hazards. To better understand the fundamental physicochemical properties of MPs and NPs in their colloidal regime, further research is required. As continuation of our previous study in this work a mechanical procedure was used to generate size fractionated MPs (10-22 μm and 22-50 μm) from pristine and weathered (UVA light 340 nm exposure) single use expanded polystyrene foam plates via colloidal ball milling followed by sieving. The morphology of the created MPs was determined using Field Emission Scanning Electron Microscope (FE-SEM) imaging and the size distribution of the fabricated MPs were also characterized using Particle Size Analyzing (PSA) and Image-J analysis. Finally, to identify the chemical compositions of MPs we have used Fourier Transformation Infrared Spectroscopy (FTIR). These characterized MPs can be utilized in future experimentation to gain a new understanding of how MPs and bacteria interact with the environment around them.

Quantum well formation on carbon nanotube surface via a peroxide- mediated reduction of aryl diazonium salts

Jayden St. Louis, Aceer Nadeem & Daniel Roxbury

Chemical Engineering, University of Rhode Island, Kingston, RI

Single-walled carbon nanotubes (SWCNTs) have emerged as promising candidates for diverse biomedical applications due to their distinctive fluorescence properties and their ability to respond to environmental changes. These attributes make them particularly effective in bio-sensing. The conventional use of aryl diazonium salts for covalent functionalization often involves harsh conditions that can considerably limit biocompatibility and scalability. Conducting a reaction with single-stranded DNA-wrapped SWCNTS and aryl diazonium salts using hydrogen peroxide as a reducing agent makes use of mild conditions, can be monitored real time with fluorescence analysis, and is scalable and more biocompatible. Presence of quantum well defects on the SWCNT surface leads to the emission of a new more intense fluorescence peak (E11*) compared to the normal E11 emission peak. The intensity of the E11* peak increases as the reaction continues, presumably due to more quantum well defects being created on the SWCNT surface. More fluorescent SWCNT solutions will in theory allow for enhanced sensing capabilities and less SWCNT concentrations being employed in various applications, such as the development of wearable textile sensors or biosensors for intracellular microenvironment monitoring. Furthermore, obtaining significant fluorescence measurement while using less SWCNTs is germane to use in cells as it would be less disruptive to the cell environment as well as less likely to have any cytotoxic effects. In terms of electrospinning wearable textiles, maintaining fluorescence while using less SWCNTs may allow for better control of the interior polymer solution in core-shell fibers and could potentially limit undesired results such as SWCNT aggregation.

Climate Change Alters Thermal Dynamics of Rhode Island Lakes

Elsie Siris, Sean Costello, & Joel Singley

Biology Marine Biology, and Environmental Science, Roger Williams University

Lakes are vital freshwater resources that, as reservoirs of water and energy, are sensitive to changes in climate across timescales. Past research has demonstrated that climate change has already impacted lake temperatures and mixing, especially in relatively large and deep lakes around the world. Comparatively, Rhode Island lakes and ponds are relatively shallow with small surface areas. The combination of these features may result in unique sensitivity to climate not captured by prior studies. To further investigate this, we used the General Lake Model (GLM), a one dimensional energy and water balance model, to simulate thermal dynamics of two representative lakes. Specifically, we parameterized our models to represent the bathymetry of Deep Pond and Watchaug Pond, which are both located in southwest RI, have similar maximum depths (~11 m), and markedly different surface areas (8 and 233 hectares, respectively). We then forced the models with historical hourly meteorological data from Warwick, RI to generate daily temperature profiles of both lakes. Our preliminary analysis of these simulations reveal that from 1970–2023, mean surface temperature, number of days stratified per year, and resistance to mixing of surface and bottom waters have all likely increased for both lakes. Notably, we found evidence that the larger lake may have experienced a more substantial change in annual mixing patterns, especially in terms of the occurrence, strength, and persistence of summer stratification. Overall, our preliminary work suggests that climate change may have already altered the thermal dynamics of lakes and ponds in RI and, importantly, that the extent of changes in mixing regimes may differ depending on size-depth characteristics. This study serves as a foundation from which we will further validate model performance and assess the seasonally-specific changes in thermal dynamics and ecosystem consequences among many RI lakes.

Identifying whether sea urchin species can easily access external biofouling when housed inside oyster aquaculture gear.

Naomy Robalo Moreno, Brendan Elba & Coleen Suckling

College of the Environment and Life Sciences, University of Rhode Island, Kingston, RI

Biofouling has been a challenge in the shellfish aquaculture industry as they build up on the outside and inside of gear causing the water flow and flushing of metabolic byproducts to reduce. This can stunt the growth and survival of commercial organisms. In aquaculture, the removal of biofouling creates a substantial part and cost of farming effort and growers are looking for solutions to reduce biofouling and effort. The integration of sea urchins with shellfish like oysters has received a lot of recent interest. They graze continuously on hard surfaces like oyster bags and oyster hsellsfeeding on commonly associated biofouling species. Previous studies have shown success in reducing biofouling when sea urchins were integrated with shellfish but with mixed results on reducing external biofouling of aquaculture gear. What remains unknown is whether all species of urchin can access and consume external biofouling which this study addresses. A pilot study was conducted to further understand the feeding behavior of sea urchins on biofouling on the external aquaculture gear surface. Two species were observed: the Atlantic Purple sea urchin (*Arbacia punctulata*) and green sea urchin (*Strongylocentrotus droebachiensis*), by enclosing individuals into mesh boxes comprised of biofouled oyster mesh and measuring biofouling and observing sea urchin feeding behavior.

Filter Feeding as a Direct Pathway for Microplastic Consumption in Humpback Whales (*Megaptera novaeangliae*)

Lindsey Reimels[1], Sarah Davis[2], Andrew J. Davies[2] & Coleen Suckling[1,3]

[1]Biological Sciences, University of Rhode Island, Kingston, RI
[2]Fisheries, Animal and Veterinary Sciences, University of Rhode Island, Kingston, RI
[3]Biological Oceanography, University of Rhode Island, Kingston, RI

Limited research has been conducted on the relationships between baleen whales and microplastics (MPs), which is a critical knowledge gap in advocating for these and other species' conservation. Previous studies have suggested that a majority of MPs found in the tissues of baleen whales is a result of trophic transfer via food ingestion. However, due to the prevalence of MPs in the waters in which baleen whales feed, as well as the comparable characteristics of MPs and potential prey species, it is likely that baleen whales ingest MPs not only through ingestion of prey but also directly through the act of filter feeding. To test this hypothesis, I developed a 3D model of a humpback whale baleen rack and exposed it to MPs by mimicking filter feeding in a laboratory setting. This allowed me to effectively observe the retention rate of MPs by the baleen rack, simulating the amount of MPs that would be trapped in the mouth and likely swallowed during feeding. The results illustrate that the morphology of a baleen rack is consistent in trapping MPs indicating that MPs may be consumed directly through the mechanisms of filter feeding alongside trophic transfer. The data revealed by this study exposes a need to reevaluate our knowledge on the entirety of MPs being consumed by baleen whales during feeding.

FEATool: A Student-Friendly Option for Finite Element Analysis

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Finite element analysis (FEA) is a numerical method that has applications in many different engineering disciplines including stress analysis, heat transfer, mass transfer, fluid flow and electromagnetics. In this project, use of the FEATool software package for stress analysis is explored. Modeling results include stresses, strains, and displacements, each of which can be reported separately in the x and y directions. In a specific example, FEA results are applied to compare theoretical modeling results to values discovered through experimentation.

For engineering students, use of FEA software often requires navigating complex modeling steps, both in terms of creating models and extracting useful information from the results. Much of the commercially available FEA software is complicated to use and pose a steep learning curve for students with little prior experience. A recently developed software, FEATool, provides accurate analysis while breaking down the analysis into very simple steps that help students to better understand the process and importance of FEA. Due to its ability to model a variety of field problems, FEATool can be used in a variety of engineering courses.

This poster includes an overview of FEATool, an example of how FEATool was used to model biaxial tension sample geometries, and ways students and teachers can use FEATool in their engineering classes, coursework, design projects and research studies.

Maternal mercury transfer from pregnant spiny (*Squalus acanthias*) and smooth (*Mustelus canis*) dogfish to their pups through differing reproductive strategies

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Mercury (Hg) is a bioaccumulative contaminant that can be transferred from pregnant females to developing embryos (i.e., intrauterine maternal Hg transfer); thus, leading to health deficits in offspring. This study examined Hg transfer in the ovoviviparous spiny dogfish (*Squalus acanthias*) and viviparous smooth dogfish (*Mustelus canis*). Female dogfish were collected from Narragansett Bay, Rhode Island Sound, and Block Island Sound via rod & reel, gillnet, and trawling. In the laboratory, intrauterine pups were excised from pregnant dogfish, after which samples of mother and pup muscle tissue were analyzed for total Hg concentrations ([Hg] in ppm dry weight) using automated atomic-absorption spectroscopy. Maternal muscle [Hg] was positively related to TL within both species, indicating bioaccumulation of the contaminant in mature females. Muscle [Hg] as a function of age followed similar trends between both species, however, Hg bioaccumulation was much higher in males than females for both species indicating the offloading of Hg to pups in females. Smooth dogfish pups exhibited higher muscle [Hg] than spiny dogfish pups, indicating a viviparous reproductive strategy results in higher amounts of Hg offloading than ovoviviparity. There existed a significant positive relationship between maternal and pup muscle [Hg] within smooth dogfish however no such relationship was exhibited in spiny dogfish. These results suggest that maternal Hg transfer occurs in both spiny and smooth dogfish, and the viviparous reproductive strategy of smooth dogfish results in higher amounts of Hg offloading to pups than the ovoviviparous strategy of spiny dogfish.

Mercury bioaccumulation in top-level predatory fishes from marine and freshwater environments

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Mercury is a widespread environmental contaminant that poses a threat to human and wildlife health. Mercury concentrations ([Hg]) may be elevated in fish tissues due to individual bioaccumulation and biomagnification in the food web. This study examined Hg bioaccumulation rates in striped bass (SB) and largemouth bass (LMB): top-level predatory fishes in marine and freshwater environments. SB, LMB, and their prey were collected in Rhode Island waters from 2006 to 2023 using rod & reel, electrofishing, and trawling methods. Age (yr) was determined for each fish based on measurements of total lengths (TL; cm) in the laboratory (LMB: 15-57 cm, 1-18 yr, n = 412; SB: 26-105 cm, 2-12 yr, n = 231). Muscle tissue excised from SB and LMB, as well as prey whole bodies, were analyzed for total [Hg] (ppm wet weight) using automated atomic-absorption spectroscopy. Total [Hg] of SB were significantly lower than LMB despite no difference in the species' trophic position, as calculated from stable nitrogen isotopes, and SB being older and larger in body size. Prey of LMB (juvenile conspecifics, sunfishes, and crayfish) had higher [Hg] compared to SB prey (forage fish, squid, and crabs), which may explain interspecific differences in Hg contamination. Growth dilution and variations in feeding and excretion rates may also contribute to higher [Hg] in LMB relative to SB. Lastly, total [Hg] of legally harvestable LMB and SB routinely exceeded the US EPA threshold level; thus, frequent consumption of either species may adversely affect human health.

Molecular Characterization of *Bryopsis* species richness in the Western North Atlantic

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Bryopsis is a species rich genus of siphonous green algae known for its feathery and sometimes iridescent appearance. There are two species of *Bryopsis* in Rhode Island (*Bryopsis plumosa* and *B. hypnoides*) but preliminary DNA Barcoding data suggest at least three species are present. Given their potential for causing environmental problems through biological invasion, and their pharmacological potential, being able to identify species is critically important. My project attempts to clarify *Bryopsis* species richness by assessing DNA sequence variation from specimens collected throughout the Western North Atlantic, which is home to 13 species of the 59 known worldwide.

Mapping the Geographic Distribution of Foraminifera Protists from Sedimentary Samples

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Foraminifera, a diverse group of single-celled microeukaryotes characterized by their intricate shell (called the "test") structures, serve as crucial indicators in marine environments and are invaluable in environmental monitoring. This research project investigates the genetic variation of foraminifera in marine sedimentary samples across diverse geographical locations around the globe using metabarcoding data. This enhances our understanding of foraminiferal diversity, providing insights into their history and their responses to environmental shifts. A Snakemake pipeline was used for the analysis of large datasets compiled from literature and from sequencing data obtained at the Zhang lab. Comparative analyses highlight the range of diversity and variation in foraminifera around the world, and show their potential role as indicators of environmental change. Understanding the distribution and grouping patterns of foraminifera is essential for reconstructing past climatic conditions and predicting future marine ecosystem dynamics.

An Electrochemical Biosensor to Screen Oysters for *Perkinsus marinus*

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Mollusk disease-causing protists affect the ecology and economy of Narragansett Bay marine communities and their habitats. *Perkinsus marinus* is the causative agent of Dermo disease in oysters. The detection of this pathogenic protist informs aquaculturists about the distribution and abundance of Dermo disease but current methods are time-consuming and costly. Electrochemical biosensing is an emerging, cost-effective technique that could provide real-time detection in the field. A *P. marinus* DNA-coated electrode and a redox indicator were used with a custom-built potentiostat to measure the current response under applied potential for various targets. The constructed biosensor was able to specifically distinguish complementary and non-complementary oligonucleotides at pM detection levels. Future tests will include the identification of *P. marinus* in treated and non-treated oysters which will confirm the potential of the device as a practical screening tool for real-time detection.

Measuring Growth And Grazing Of Marine Heterotrophic Bacteria On The Northeast Shelf Using Flow Cytometry

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Marine heterotrophic bacteria are the most abundant, diverse and metabolic active organisms in ocean environments. They are essential contributors of carbon and energy to higher trophic levels and in remineralizing organic matter and nutrients, form the microbial loop, and thus play a key role in oceanic carbon cycles and planktonic food webs. While abundances of heterotrophic bacteria are routinely measured in oceanographical surveys, measurements on bacterial growth and grazing rates are sparse. These measurements are essential to understanding how heterotrophic bacteria contribute to planktonic food webs and ecosystem functioning. The present study aimed to measure bacterial growth and grazing from samples collected as part of the Northeast Shelf Long Term Ecological Research (NES-LTER) project. During the spring 2024 NES-LTER cruise, routine dilution experiments were performed, which were originally designed to measure the growth of marine phytoplankton and grazing rate by microzooplankton. Using this readily available procedure, we collected and preserved bacteria samples at each time point and treatment. When back on shore we 1) developed a lab specific method to quantify bacterial abundances using the Guava EasyCyte Flow Cytometer, 2) applied these methods for the analysis of bacterial growth and grazing using samples collected on EN715, and 3) in the future, will include these rates as routine measurements within the NES-LTER project. Having access to these stocks and rates from future cruises will give further insight into the flow of organic matter in planktonic food webs within the economically and ecologically important NES waters. This preliminary analysis will set the base for routine monitoring of heterotrophic bacteria, contributing information about their spatial, temporal, and seasonal dynamics to the NES-LTER project.

Recycling Waste Plastic into Plastic-Sand Composite Building Materials

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Plastic waste is a major global problem affecting environmental and human health, especially for developing countries that lack proper recycling infrastructure. One potential solution is to use waste plastics for building materials (e.g., bricks and pavers) by mixing shredded waste plastic with sand, melting, and compressing it in a mold. This study identified 1) factors that affect the strength of the bricks and 2) the methods for conducting UV accelerated weathering on the bricks. A literature review was conducted to determine which parameters should be used. Google Scholar was used to identify a total of 22 papers relevant to the strength of the bricks. Data recorded included: type of plastic; plastic:sand ratio; grain size; melting temperature; molding pressure; curing time; and compressive strength. Thirteen articles relevant to UV accelerated weathering of the bricks were identified. Data recorded included: type of material; duration of trial; and cycle methods. ASTM and ISO standards for accelerated weathering was also researched. From the compressive strength analysis, few trends were identified because many variables changed from study-to-study. Consequently, the effects of the plastic:sand ratio, which was reported in 95% of studies, showed no trends. Molding pressure, whose effects were not investigated in any of the 22 studies, was significant because the average compressive strength of bricks compressed by workers with a tamping rod was 9.9 MPa but bricks compressed with machines at higher pressures averaged 33.5 MPa of strength. However, the pressures exerted by the machines during molding ranged from 0.2-10 MPa and there were no trends in strength across that range. Two studies showed that strength increased with curing time up to 28 days, but most did not consider it based on untested assumptions that strength would not increase past 24 hours. Based on distribution of the data in this review it is recommended to investigate the plastic:sand ratio between 20:80 and 30:70, the molding pressure between 0.5 and 10 MPa, and the curing time between 24 hours and 28 days. For the accelerated weathering, it is recommended to comply with ASTM D2565: Standard Practice for Xenon Arc Exposure of Plastics Intended for Outdoor Applications, because it is well studied and the standard most closely applicable to plastic-sand composites. These recommendations could aid in improving the quality of bricks and understanding their environmental impact.

Identifying Potential Bacterial Food Sources of Anaerobic Ciliates from Rhode Island Coastal Benthic Habitats

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The benthic zone of Narragansett Bay and Rhode Island coastal ponds host a diverse community of microorganisms, playing an important role in nutrient cycling within oxygen-depleted environments. A common and conspicuous member of sediment microbial communities are anaerobic ciliates, which act as grazers of other microbes. Here, we investigated the potential microbial food sources of four anaerobic ciliates originating from the Pettaquamscutt River and Napatree Saltpond in Rhode Island, and Oyster Pond in Falmouth, Massachusetts. Twelve distinct bacterial morphotypes were isolated from the anaerobic ciliate cultures. Following isolation, 16S rRNA gene sequencing was used to classify the bacteria present. Of these distinct morphotypes, six families of taxa were classified: Vibrionaceae, Paracoccaceae, Shewanellaceae, Pseudomonadaceae, Sphingomonadaceae, and Enterobacteriaceae. Characterization of the bacterial communities that co-occur with anaerobic ciliates provides a foundation for further understanding the ecological interactions between these two domains of life in marine and estuarine sediments.

Development Electrospun Fibers Loaded with Curcumin Nanoparticles and Cyclodextrin Inclusion Complexes for Temporal Drug Release

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Lung cancer is one of the deadliest forms of cancer, with treatment challenges stemming from poor drug solubility and stability, leading to inefficient chemotherapeutic delivery. This study addresses these challenges by exploring the benefits of cyclodextrin (CD) inclusion complexes, nanoparticle delivery, and electrospun fibers, using acetalated dextran (Ac-Dex) and polyvinyl alcohol (PVA) to enhance drug administration. CD forms host-guest complexes that improve the solubility and stability of encapsulated compounds. In this work, curcumin (CUR) models a poorly water-soluble drug in CD inclusion complexes and nanoparticles (NP). CUR-CD inclusion complexes and CUR NP are synthesized and integrated into electrospun fibers. Preliminary solubility data indicates that cyclodextrins enhance curcumin's solubility. CUR NP exhibits appropriate size, polydispersity index (PDI), surface charge, morphology, drug loading, and encapsulation efficiency, as determined by dynamic light scattering (DLS) and scanning electron microscopy (SEM). Thermal analysis using differential scanning calorimetry (DSC) reveals that curcumin is more bioavailable when encapsulated in nanoparticles and electrospun fibers. The presence of CD in the fibers improves their encapsulation efficiency and releases guest molecules in a controlled manner. This controlled release can reduce the frequency of drug administration, increase patient compliance, and maintain chemotherapeutic drug levels over time. These findings suggest that CD inclusion complexes and NP-loaded electrospun fibers have significant potential in drug delivery applications, including lung cancer treatment, and pave the way for developing more efficient drug delivery systems that can enhance treatment outcomes, reduce side effects, and improve the quality of life for patients.

Synthesis of PEG-Coated Magnetic Nanoparticles for Drug Delivery

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The synthesis of PEG-coated magnetic nanoparticles using the hydrothermal method plays a significant role for drug delivery applications. Autoclaves are used to synthesize magnetic nanoparticles in aqueous media at high temperatures and high pressures. The hydrothermal method has the advantage of controlling the size and shape of the particles to better their magnetic and biological properties in the human body. The significance of using polyethylene glycol is due to its biocompatibility, stealth properties and its stability in blood circulation for the human body. In this study, it was important for us to see what the most effective way of coating PEG on the surface of our particles is. While doing so, it was also crucial to maintain the shape and size of the magnetic nanoparticles to help penetrate tumor tissues effectively. These magnetic nanoparticles can be binded to drugs and antibodies that are inserted into the bloodstream and can be directed to a specific tumor using an external magnetic field. Our research contributes to the development of targeted drug delivery systems to treat cancer tumors.

Low Frequency Rotating Magnetic Field Apparatus Designed for Magnetic Nanoparticle Application

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Rotating magnetic fields have been proposed as an activation mechanism for magnetic micro- and nanoparticles. When excited by a rotating magnetic field, magnetic particles rotate and translate, exerting mechanical forces and torque on the surrounding medium. This behavior can be exploited for multiple applications such as anticancer treatments, fluid mixing and antibacterial processes.

There is currently no commercially available setup for the application of rotational magnetic fields. Presented here is the construction of a rotating magnetic field apparatus. The prototype allows the application of low frequency (1-10 Hz) rotating magnetic fields with tunable strengths (2-27 mT). This system uses a brushless motor, controlled by Arduino and an ESC, to rotate permanent magnets. The device can be operated via a computer or as a stand alone system through a touchscreen graphical user interface, and the rotational speed is measured live using a tachometer. The rotating magnetic field apparatus is ready to be used to test the performance of magnetic nanoparticles in removing marine bacterial biofilms.

The Effects of Integrated Pest Management on Honey Bee Behavior and Colony Level Health

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Honey bees face threats from many directions, but the most pressing is the parasitic mite Varroa destructor. One popular method of combatting Varroa is adding drone comb, which forces the colony to raise larger, mite-preferred male bees. While this method reduces colony-level mite numbers, it may add unnecessary colony-level stress as drones are nutritionally expensive to raise, particularly in nitrogen. Our research investigates how forcing the hive to raise drones for mite management affects honey bee population growth, foraging behavior, and nutrition. We accomplished this by estimating adult bee population and area of drone brood, examining foraging behavior of the bees before, during, and after management with drone comb, and sampling bee-collected pollen and nectar for nutritional analysis using colorimetric assays and elemental analysis (ongoing). These data will help us to understand unintended effects of integrated pest management and how to further support honey bees, allowing us to tell a complete story about how integrated pest management affects these important pollinators.

Autonomic Recovery from Post-exercise Cold Water Immersion

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Athletes often use various recovery methods such as cold water immersion (CWI) to enhance training outcomes. The effect of CWI on the autonomic nervous system remains uncertain, and it is unclear whether CWI positively or negatively impacts autonomic recovery as reflected by blood pressure and heart rate variability (HRV). Purpose: We examine the effects of cold water immersion (CWI) on blood pressure response and autonomic nervous system recovery in active individuals following an intense bout of exercise. Methods: 15 active individuals participated in two separate, randomized trials. These trials included an interval exercise (~8 km treadmill running with 8x400m intervals) followed by a 30-minute treatment of either CWI (30 min at 18°C) or control (CON; 30 min seated rest). Systolic (SBP) and diastolic (DBP) blood pressure as well as HRV were assessed three times during each trial session: before exercise (Pre), immediately after exercise and treatment (PostTx), and 12 hours post-exercise (12hPost). These variables were measured using the Finapres® NOVA hemodynamic monitoring system, a clinical grade non-invasive continuous blood pressure monitor. Results: SBP increased following the CWI treatment (PostTx = 128 ± 4 mmHg) as compared to pre exercise values (Pre = 124 ± 4 mmHg), however it returned to baseline 12 hours post treatment (12hPost= 122 ± 3 mmHg). Similarly, DBP increased following the CWI treatment (DBP PostTx = 79 ± 2, DBP pre = 69 ± 1 mmHg), but came back to baseline values 12 hours post treatment (DBP 12hrPost = 69 ± 1 mmHg). SBP and DBP were not different from baseline (Pre) at any time point in CON. With CWI, HRV increased post-treatment (rMSSD Pre: 73 ± 11 ms; PostTx: 98 ± 12 ms) but returned to pre-exercise values the following morning (12hPost: 72 ± 10 ms). Conclusions: Post-exercise CWI causes a transient increase in blood pressure and HRV, but does not cause any prolonged changes in autonomic function and blood pressure regulation. Since both blood pressure and HRV measurements returned to their baseline values after treatment, the effects of CWI are limited in duration. Although the increase in HRV post-treatment may be interpreted as beneficial, the concurrent rise in blood pressure may be concerning for individuals with compromised cardiovascular health.

The Impact of Post-Exercise Hot Water Immersion on Blood Pressure and Autonomic Recovery

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Hot water immersion (HWI) has been recognized as an effective post-exercise recovery method, specifically associated with enhanced heat tolerance and improved aerobic performance. However, it is unknown how HWI impacts an individual's blood pressure response and autonomic nervous system post-exercise. Autonomic activity can be reflected and measured through Heart Rate Variability (HRV), Blood Pressure (BP), and Baroreflex Sensitivity (BRS). PURPOSE: To examine the impact of Post-exercise HWI on blood pressure and autonomic measures on well trained individuals after a bout of intense exercise. METHODS: 15 active individuals took part in 2 randomized trials consisting of interval exercise (~8k treadmill running of 8x400m intervals), followed by 30 minutes of treatment of either hot water immersion (HWI; 30 min at 40C) or time control (CON; 30 min seated recovery). Systolic (SBP) and diastolic (DBP) pressure, and autonomic measurements were taken pre-exercise (Pre), immediately post-treatment (PostTx), and the following morning (12hrPost). RESULTS: SBP was not significantly different at any time point, but tended to decrease 12hrPost with the inclusion of HWI (Pre= 120±4, PostTx= 120±4, 12hrPost= 117±4 mmHg) compared to control measures (Pre= 125±4, PostTx= 121±4, 12hrPost= 121±4 mmHg). DBP decreased from baseline measures with the inclusion of HWI (Pre= 73±2, PostTx= 70±2, 12hrPost= 68±2 mmHg) in comparison to control measures (Pre= 71±1, PostTx= 73±1, 12hrPost= 70±1 mmHg). RMSSD tended to decrease immediately Post-HWI, but returned to baseline 12hrPost (Pre= 73±21, PostTx= 53±14, 12hrPost= 67±25 ms). HF/LF Ratio values did not show significant changes, but had a tendency to decrease immediately Post-HWI (Pre= 0.35 ± 0.08, PostTx= 0.31 ± 0.05, 12hrPost= 0.31 ± 0.08). BRS decreased immediately Post-HWI, but had a tendency to return towards baseline values by 12hrPost (Pre= 14±4, PostTx= 10±2, 12hrPost= 13±1 ms/mmHg). CONCLUSION: Post-Exercise HWI causes a prolonged decrease in BP values as opposed to exercise alone. However, this decrease is not explained by changes in BRS or autonomic balance, as measured by HRV. This decrease in BP could be beneficial for individuals engaging in exercise to optimize cardiovascular health.

Investigating the effect of rapamycin and 2,5 dideoxy adenosine on the lifespan of *Brachionus plicatilis*

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Understanding the basic biology of aging and underlying molecular events that result in deterioration of physiology may lead to treatments for chronic age-related health conditions in people. Rotifers (*Brachionus plicatilis*) are microscopic aquatic organisms recently developed by our lab as a model organism for studying metabolic and biochemical pathways implicated in the aging process. Rotifers have previously been used in ecotoxicology as sentinels for monitoring water quality given their heightened sensitivity to waterborne contaminants. Based upon this application, we hypothesize that rotifers are excellent models in screens to identify drugs capable of extending health and longevity. Other advantages of this model organism include a short laboratory life span of 2-3 weeks and parthenogenic reproduction resulting in genetically identical generations. Through the utilization of high-throughput robotic drug discovery and hypothesis driven experimentation, we test the effect of pharmaceuticals such as rapamycin and 2,5 dideoxy adenosine on the lifespan of rotifers to target adenylyl cyclase activity as well as the target of rapamycin (TOR) kinase pathway with previous literature suggesting an expansion of lifespan. We provide evidence that rotifers are effective model organisms for pharmacologic screens in discovery of new drugs capable of affecting lifespan or other phenotypes of interest.

Characterizing the Molecular Mechanism of Lifespan Extension in *Caenorhabditis elegans* via gpa-7 Depletion

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Aging is a universal biological process that all organisms undergo, but relatively little known of the molecular events that underpin the pathophysiology of age-related decline. *Caenorhabditis elegans* (*C. elegans*) are model organisms for aging as their genes can be knocked down easily using RNA interference. The protein coding gene gpa-7 is predicted to be a G protein alpha subunit involved in the activation of adenylyl cyclase. Our lab discovered that gpa-7 knockdown increases the lifespan of *C. elegans*. We assessed whether long-lived gpa-7 deplete worms have reduced reproduction rates compared to worms on control RNAi. The gpa-7 animals did not exhibit a reduced rate of reproduction compared to the control. Since we predict that loss of gpa-7 decreases adenylyl cyclase activity, we evaluated the effect of the adenylyl cyclase inhibitor 2',5' dideoxyadenosine on *C. elegans* life span. Future directions include evaluating whether the gpa-7 knockdown results in nuclear localization of the FOXO transcription factor DAF-16, which has been associated with other long-lived worms.

Using Machine Learning to Classify and Look Deeper Within Big Data in Psychopathology

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Mental health disorders, such as depression, anxiety, and obsessive-compulsive disorder (OCD), have significant impacts on individuals' daily lives and overall well-being. However, the precise neural and cognitive mechanisms behind many such disorders are not yet understood, partly due to current symptom-based approaches to psychopathology classification, and partly due to the complexities of disorder presentation and potential neural substrate.   This is where algorithms such as computational factor modeling and machine learning come into play: these methods can look deeper within large datasets to understand complex relationships and patterns not visible in smaller data or using simple descriptive statistics. Computational psychiatry has proposed novel insights into disease classification, through the use of big data tools that can incorporate not just behavioral and clinical data, but genetic, environmental, and physiological factors. In the current study, we applied machine learning classification and regression algorithms on two big mental health data sets to understand and predict the roots and outcomes of mental health disorders. First, we trained a series of classifiers using MATLAB's classification learner on an open online dataset (Mental Health Disorders) with n =638 participants with different diagnoses, to identify which of 28 physiological, psychological, and social markers (e.g. "feeling nervous", "weight gain", "having a close friend") are most predictive of diagnosis. Second, we used a dataset provided by our collaborator Dr. Emily Gentes, which included clinical questionnaire data from n=580 participants on a total of 615 items. We wrote a classifier to predict individuals' greatest worry (e.g. "school", "health and safety", "social relationships"). Classifier accuracies ranged from 31-55%, with School/Career and Family/Social Relationships worries predicted most accurately, and the top three overall predictor items included: feeling calm, feeling stressed not knowing the future, and feeling cheerful. While results may have been biased by class imbalance (most participants had worried about the school/career category), these results highlight the potential of machine learning in mental health research, offering new insights into the factors contributing to mental health disorders.

Investigating the effects of the mTORC1 pathway inhibition in developmental cerebellar pathology associated with NPC1 deficiency

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Deficiency of the NPC1 protein causes the lysosomal storage disease Niemann-Pick Type C (NPC), triggering early neurodegeneration and juvenile death. Previously, our laboratory found that microglia, the resident phagocytic cell of the brain, are significantly affected during development in a Niemann-Pick Type C (NPC) disease mouse model. In the NPC1 deficient mouse, changes in microglia morphology, proliferation, phagocytic activity, and expression of developmental proteins precede cerebellar Purkinje Cell (PC) death. Given that lack of NPC1 induces overactivation of the mTORC1 pathway in other types of cells, we interrogated if early changes in NPC1 mutant microglia were due to overactivation of the mTORC1 pathway. Our experimental approaches included measuring in microglia the phosphorylation of S6 (pS6), a downstream kinase phosphorylated by mTORC1, using immunofluorescence at early and late postnatal developmental stages. We also treat NPC1 mutant mice with the drug Rapamycin, an inhibitor of the mTORC1 pathway from postnatal age 10 (P10) to P21 (weaning age). Our results showed higher levels of pS6 in NPC1 mutant microglia compared to wild-type (WT) mice at early stages of postnatal development when microglia are not completely matured. The inhibition of the mTORC1 pathway was confirmed by the decreased levels of pS6 immunoreactivity in microglia from P21 NPC1 mutant mice treated with Rapamycin. Analysis of microglia morphology showed decreased total length and arborization and increased mean diameter in Rapamycin-treated NPC1 microglia compared with WT mice. Preliminary results also suggest a decrease in microglia number, while the volume of presynaptic terminals from climbing fibers that innervate PC dendrites was increased in Rapamycin-treated NPC1 cerebella. Additionally, the decreased myelination of PC axons found in NPC1 deficient mice was prevented by Rapamycin treatment. Our preliminary results suggest that Rapamycin treatment affects microglia proliferation and growth in NPC1 deficient mice and improves neuropathological changes that precede neurodegeneration in this NPC mouse model.

Cell size control under changing environments

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Cells maintain their size to function in their ecological and organismal context. Environmental factors influence the size of cells of both unicellular and multicellular organisms. For example, starvation leads to reduced cell size of *Drosophila*, rats, and yeast. Most cells control their size by delaying cell cycle transitions until they reach a threshold cell size, suggesting that cells connect their growth and cell cycle signaling. The molecular mechanisms of how cells adapt their size to different environmental conditions remains unclear. We use fission yeast as a model system to study cell size control because they have an easy-to-measure rod shape, extensive genetic tools, and use the same genes and proteins as human cells do for cell division. Fission yeast enter mitosis and divide at a threshold cell surface area due to size-dependent activation of Cyclin-dependent kinase (Cdk1). Recent work suggests this regulation is achieved by scaling the accumulation of mitotic activators with different aspects of cell size or growth. There is surface area-dependent accumulation of the protein kinase Cdr2, a Wee1 inhibitory kinase. Mitotic activator Cdc25 accumulates in the nucleus specifically with cell volume, while Cdc13 (Cyclin) nuclear concentration scales with cell cycle time. Such an integrated system likely provides robust and dynamic properties for size control upon changes to individual pathways or size parameters. How cell surface area (Cdr2), time (Cyclin/Cdc13), and cell volume-sensing (Cdc25) pathways function under low nutrient or stress conditions has been unknown. Using our high-throughput image analysis pipeline we measured the geometry of dividing cells grown under osmotic stress, oxidative stress, and low nutrient conditions. We used genetic assays using cells with reduced or increased Cdc25 (volume), Cdc13 (time), or Cdr2 (surface area) levels to test the contribution of these pathways. We find that Cdc25 (volume) and Cdc13 (time) sensing pathways are necessary for cell adaptation and increased cell volume under oxidative stress. Interestingly, the cell surface area (Cdr2) pathway was not required for cell adaptation and increase in cell surface area in osmotic stress or low nutrient conditions. These findings suggest that there may be back-up pathways for cell surface area sensing under these conditions. Our work identifies the role of size control pathways in cell adaptation to changing environments.

Adhesive Performance: A comparative Study of Sea Urchins *Strongylocentrotus purpuratus* and *Strongylocentrotus pallidus*

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Sea urchins possess hundreds of small, fleshy mobile appendages called tube feet. Each tube foot is connected to the animal by a proximal stem and ends in a distal disc. The disc secretes an adhesive for attachment and a de-adhesive for detachment allowing for temporary adhesion. The coordination of these tube feet allows sea urchins to evade predators, find food, and withstand hydrodynamic forces. This study compares the adhesive performance of the two species to determine if their contrasting habitats influence their adhesion capabilities. The purple sea urchin, *Strongylocentrotus purpuratus*, is usually found in the more exposed intertidal zones, while the white sea urchin, *Strongylocentrotus pallidus*, typically inhabits deeper and more sheltered subtidal regions. Adhesive performance of these species was evaluated by measuring 1) whole animal adhesive force (N; force needed to remove an urchin from a substrate after attachment), 2) disc adhesive force (N; force required to detach a disc from a surface), 3) stem breaking force (N; force required to cause material failure of the stem), and behavioral aspects such as 4) righting (sec; time required for an urchin to flip itself in the right position if placed on its backside), and 4) the number of tube feet used for whole animal adhesion. Our results show that *Strongylocentrotus purpuratus* outperformed *Strongylocentrotus pallidus* in all static adhesive measurements (disc adhesive force, stem breaking force, whole animal adhesion). However, righting response was similar among species. Notably, *S. purpuratus* also exhibited greater variability in the response variables measured, suggesting potential adaptations to the fluctuating conditions of intertidal habitats. The study findings indicate that species found in different habitats have contrasting static adhesive performance, highlighting the ecological adaptability of sea urchins across diverse environments.

Sea Urchin Tube Feet Skeletal Morphology and Its Correlation with Disc Tenacity

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Echinoids, such as sea urchins, use specialized appendages called tube feet that secrete adhesive and de-adhesive materials for temporary attachment. Tube feet enables them to accomplish critical tasks such as withstanding hydrodynamic forces and foraging for food. These small and numerous appendages consist of a proximal mobile and extendable stem and a distal disc that chemically adheres to the substratum. The disc is supported by a calcified structure called a rosette. The rosette contains claw-like structures called ossicles that are arranged in a ring and vary in number between species. The ossicle's stereom is made up of solid trabecules and pores. Previous studies hypothesize that the ossicle skeletal density (relative proportion of the area of the trabecules and pores) correlates with the urchin's ability to attach to surfaces, but has never been tested. In our study, we evaluated the ossicle area (mm2), ossicle skeletal density (%), counted the number of ossicles per disc, and calculated maximum disc tenacity (maximum force per unit area of the disc [MPA]) of four species of sea urchins with distinct adhesive abilities: red urchin, *Mesocentrotus franciscanus*; purple urchin *Stronglyocentrotus purpuratus*; green urchin, *Stronglyocentrotus droebachlensis*; and white urchin, *Stronglyocentrotus pallidus*. Tube feet discs were collected and treated with bleach to reveal the internal rosette enclosed by the disc. The ossicles were mounted on a stud and imaged with scanning electron microscopy (SEM). The ossicle's area and skeletal density was measured using the ImageJ software. We found that red urchins have a higher skeletal density, followed by white, purple, and green urchins in a decreasing order which matched the discs' maximum tenacity results. These results suggest a correlation between disc tenacity and ossicle skeletal density in sea urchins, where denser ossicles result in stronger disc attachment to surfaces. The number of ossicles per disc and ossicle area varied among species but did not correlate with rosette skeletal density or disc tenacity. Our findings show that adhesive performance in sea urchins is influenced not only by the adhesive secretion, but also by the morphology of the calcified structure of the discs. Thus, incorporating an assessment of the rosette in sea urchin adhesive studies is needed to fully understand its adhesive performance.

Artificial Tendons from Liquid-Crystal Elastomers

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Liquid-crystal elastomers (LCEs) are unique materials that display a reversible shape change property under an external thermal stimulus. By utilizing this shape change property of LCE's, we develop an LCE that mimics the mechanical characteristics of a tendon. To create this LCE, we need to first optimize the LCE's chemical ratios of its thiol-acrylate and acrylate-acrylate crosslink network which control the mechanical properties. Second, we characterize these LCE's; that is to measure the mechanical properties of the LCE to compare to that of a tendon. The optimization step is split into two parts; the first part is done by adjusting the ratio of the two thiol-functionalized monomers EDDET and PETMP, particularly the PETMP since that monomer is what facilitates the thiol-acrylate crosslinks. The second part is adjusting the amount of excess acrylate (RM257), this affects the acrylate-acrylate crosslink density which controls the reversible memory of the LCE. The characterization of the LCE's is done by using a TA® Instruments DHR20 Rheometer to measure the stress, strain and contractile force of the LCE as well as its storage and loss moduli. By analyzing the characterization data, we can then compare the results to that of a tendon and find which LCE performed closest and adjust any ratios if needed to further optimize the LCE.

Understanding competing fear and hunger motivations through correlating neural activity and behavior

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To ensure the greatest rate of survival and overall benefit in nature, both animals and humans must manage competing motivations to alter behavior in different environments. Analyzing the balance between fear and hunger survival motivations, this study investigates different hunger intensities and predator odors in their effects on food consumption and behavioral responses to threat. Mice (n=20) were run on a predator odor assay (POA) in which they were exposed to four odor conditions over the course of multiple trials: no odor, a fox feces component known as trimethylthiazoline (TMT), coyote urine, and bobcat urine. Preceding each trial, mice were food deprived for 4 or 18 hours and the weight of each mouse was recorded to target a 5-10% body weight reduction. In each 30 minute trial, the mouse first was exposed to the predator odor confined to one end of the chamber for 15 minutes. After this initial exposure, the second 15 minute period included the introduction of a piece of food adjacent to the predator odor. Following each trial the amount of food consumed and time spent in the threat zone surrounding the predator odor were analyzed. Results from the studies were highly variable: there were no clear fear and hunger behaviors between different odors or across different time deprivations. To identify a neural correlate of this behavioral variability in response to predator odor, we investigated activity in the bed nucleus of the stria terminalis (BNST), a region of the brain known to process innate olfactory threat stimuli. Mice (n=5) were re-exposed to TMT and were then perfused. Brains were sectioned and sections containing the BNST were stained with a primary antibody to the immediate early gene cFos and a secondary antibody conjugated to a fluorescent protein. Prominent cFos expression in the BNST indicated that this region responds to TMT. cFos expression was quantified and correlated with the animal's food consumption to ask if greater BNST activation corresponds with a greater behavioral response to predator odor. Our results provide insight into a complex fear and hunger dynamic and contribute to our understanding of how these competing motivations are balanced in the brain. Future experiments in our lab will use different concentrations of TMT to manipulate fear in order to better assess the effect of environmental threat on food-seeking behavior.

Interplay of Division and Metabolism in Uropathogenic *Escherichia coli*

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Uropathogenic *Escherichia coli* (UPEC) cause 80% of urinary tract infections. Many UPEC strains enter a metabolite-dependent, non-proliferative state of dormancy, called quiescence, when cultured *in vitro*. During infection, UPEC are thought to form quiescent intracellular reservoirs in bladder epithelial cells, which may help evade antibiotics. In a genetic screen to identify mutants defective for quiescence, we discovered that the cell division regulator ZapE, an ATPase important for division in *E. coli* during stress, is essential for UPEC to enter the quiescent state. Entry into quiescence also requires a complete tricarboxylic acid (TCA) cycle, and deletion of SdhA, which encodes a subunit of succinate dehydrogenase (SDH), prevents quiescence, and promotes proliferation. To determine if ZapE directly interacts with SDH, we performed a bacterial two-hybrid (BACTH) assay using ZapE and SdhA fusion proteins. We observed that ZapE interacts with SdhA alone and that the interaction is stabilized by additional SDH components. ZapE interacting with both cell division machinery and oxidative metabolism suggests that there is crosstalk between these two fundamental and essential pathways that has gone previously unreported. To further investigate the interaction between ZapE and SDH, we used AlphaFold2, an artificial intelligence-based system to predict protein structure, to find potential interaction sites. We then evaluated each predicted site using the BACTH assay. We found that mutating residues 184-187 of ZapE to alanines prevented an interaction with SdhA. Finally, we purified the ZapE mutant protein, ZapE(184-187AAAA), to test it for function in vitro. These results are important for understanding regulatory mechanisms among two essential pathways in UPEC, cell division and TCA cycle metabolism, which may underlie recurrent urinary tract infections.

Detection and Quantification of *Escherichia coli* in Shellfish by Combined MPN-qPCR Method

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There is substantial need for the rapid and efficient detection and quantification of *Escherichia coli* and other fecal coliforms in shellfish intended for human consumption. Outbreaks of diarrhea, hemorrhagic colitis, and Hemolytic Uremic Syndrome (HUS) in humans have been associated with *E. coli* outbreaks, most commonly the O157:H7 strain due to its production of pathogenic Shiga-toxins. The current FDA- approved most probable number (MPN) method used for quantifying pathogenic *E. coli* in shellfish is outdated and can take up to four days to complete. In this project, two triplex quantitative Polymerase Chain Reaction (qPCR) assays were developed using previously published primers and probes. These assays are intended to be combined with the overnight enrichment from the standard FDA MPN method for the detection and quantification of the pathogenic O157:H7 *E. coli* strain. The assays were validated against known amounts of Shiga-toxin producing O157:H7 from cultures and confirmed to detect the strain. This streamlined qPCR-MPN method will be troubleshooted and validated with known amounts of O157:H7 E. coli through spiking experiments and later used to enumerate *E. coli* from summer shellfish collections. These qPCR assays will eventually be offered as part of the standard diagnostic methods in the Aquatic Diagnostic Laboratory at Roger Williams University.

Exploring the Role of Azoreductase Enzymes in Drug Metabolism: Implications for Personalized Medicine

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The gut microbiome is home to trillions of microorganisms, some of which have been shown to metabolize xenobiotics such as drugs and food dyes. However, people can metabolize drugs differently because each person has a unique microbiome with different microorganisms. If this relationship was better understood, doctors could prescribe different drugs to patients depending on the unique metabolic potential of their microbes. Still, we do not know the effects of all bacteria or enzymes in the microbiome; many are understudied, including enzymes in the azoreductase IPR003680 family. We studied the metabolic effects of two azoreductases found in *Escherichia coli* (UniProt ID P41407) and Alistipes sp. CHKCL003 (UniProt ID A0A143XFE8). For the enzyme P41407, we found activity on several substrates, including methyl red and ethyl red; for the enzyme A0A143XFE8, we found enzymatic activity on the substrates methyl red, ethyl red, phenol blue, HMND (5-hydroxy-2-methylnaphthalene-1,4-dione) and sunset yellow. We also sought to test the mechanism of these enzymes, as there is only some evidence for its support. We propose that azoreductases do not directly reduce the azo bonds. Instead, they act as quinone reductases and require a quinone-like intermediate to form in azo compounds before reducing them. To support this mechanism, we synthesized three 4-(4-R-phenyl)-diazenyl)phenol compounds, which were able to be reduced by azoreductase enzymes. Each compound had a different substituent attached to the non-phenol-containing benzene ring; we hypothesize that the rate of azoreduction should not be electronically affected by the substituent due to our proposed mechanism. Enzyme kinetics assays showed similar enzymatic rates of reduction with these dyes. Overall, exploring how different drugs and azo compounds can react with different azoreductase enzymes is important for advancing personalized medicine.

Comparative biochemical analysis of zebrafish and human DNA polymerase theta function

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DNA Polymerase Theta (Pol θ) is a DNA repair enzyme that holds a significant role in repairing broken DNA strands through a specific type of microhomology-mediated end joining (MMEJ) called polymerase theta-mediated end joining (TMEJ). Within this specific type of DNA repair, Pol θ is prone to inducing DNA mutations. However, despite this inherent ability to generate mutations, Pol θ itself is crucial for cell survival, as loss of Pol θ function has been observed to be detrimental to cell survival. With this contradiction between necessity of the enzyme and its susceptibility to induce mutations, leads one to question: is this protein beneficial or a hinderance? Recently, there have been multiple POLQ gene variants found in patient isolated melanoma tumors, suggesting a potential role in melanoma carcinogenesis. However, there is currently no connection between Pol θ and melanoma.

To better understand Pol θ and its potential in carcinogenesis, we propose generating a zebrafish Pol θ melanoma model. For our study of Pol θ we have chosen zebrafish since they are a well-established melanoma model and have homologous genes to humans. However, no functional studies of zebrafish Pol θ have been completed.

To this end, we cloned and purified the polymerase domain from zebrafish Pol θ and compared its function to the polymerase domain of human Pol θ to determine if these proteins have a similar function. This is important because if the Pol θ behaviors are similar, more tools could be created to study Pol θ activity, specifically the activity of how particular variants of Pol θ work. The similarities between human and zebrafish Pol θ could also allow for zebrafish transgenic Pol θ lines to be generated. We conducted four assays to determine the similarity of zebrafish Pol θ to the human homolog. First, circular dichroism (CD) melting spectrum to assess protein structure similarities; second, a primer extension assay to determine if Pol θ was able to complete repair through incorporation of nucleotides; third, a CPD bypass assay to determine if zebrafish Pol θ can bypass CPD damage; and fourth, an MMEJ repair assay to determine if zebrafish Pol θ can fix double strand breaks. Based on these experiments, it has been concluded zebrafish and human Pol θ do express similar behaviors. With this information, we can move forward in the process of using the zebrafish animal model by generating variants of Pol θ in zebrafish.

Neural Network Robotic Swarms: Communication, Mapping, and Navigation

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The goal of this work is to develop a swarm of autonomous robots capable of efficiently mapping and navigating environments while imposing real-world constraints on communication and external sensors. This system leverages neural networks to enhance decision-making and adaptability in robotic swarms, particularly in scenarios where communication and sensor data are limited. Applications include search and rescue, environmental monitoring, and exploration of unknown or hazardous areas. This project utilizes ROS 2 (Foxy) on Ubuntu 20.04 for integrating neural networks with robotic control. Each robot is controlled by a Deep Neural Network trained using reinforcement learning, with independent training for each network. Input data for each network includes robot ID, lidar readings, odometry, and orientation, along with the same data shared to and from robots within a communication distance threshold. The network features multiple hidden layers and two output nodes for linear and angular velocities, managing dynamic data flow and emulating short-range communication. The reward function is computed using ground truth and other available data to provide an evaluation and improvement of each individual network. Training occurs in varied environments with obstacles and different robot numbers to ensure robustness. The system can save and load neural network configurations for continuous improvement. Although specific performance metrics and results are not yet available, there has been a noticeable improvement in robot behavior through an early reward algorithm, which discouraged actions such as falling over, crashing, and stagnation. Current efforts focus on implementing the concept and development of tools for metrics evaluation and training guidelines. Future work aims to enhance swarm efficiency and adaptability. The software architecture provides many opportunities for algorithmic improvement, including the inclusion of a genetic algorithm setup in which the best networks are selected at each training episode while poorly performing networks are discarded. Additionally, new features like multiple data jump capabilities and the implementation of advanced reinforcement learning techniques prioritizing recent data and encouraging predictive assumptions about robot positions and environmental conditions are planned.

Novel phosphines for the Appel-type reactions

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Among marketed drugs derived from natural products, 69% contain hydroxyl functional groups. Moreover, sugars and natural amino acids, such as serine and threonine, also bear the hydroxyl group. The ubiquity of the hydroxyl group makes it a convenient synthetic handle for modification of drug-like compounds for improved bioactivity. The Appel reaction is a widely used transformation that converts an alcohol into an alkyl halide, by using a phosphine and a halogen source, such as carbon tetrachloride or iodine. Conventionally, triphenylphosphine is employed in the Appel reaction; despite its low cost and ready availability, triphenylphosphine cannot promote the Appel reaction under some conditions, particularly when alcohol substrates are in very low concentrations. Here, we present our study to improve the Appel reaction's efficiency by optimizing the electronic and geometric parameters of phosphines.

Brachyponera: kinematics of an ultra fast antennal interaction between needle ants

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The impressive organization and cooperation of social insect societies is thought to be largely a result of the ability for the individuals within colonies to communicate with each other, exchanging and processing information. Ant communication uses chemical, mechanical, and visual modalities and often involves interaction through antennal contacts. While observing the Rhode Island population of needle ants (*Brachyponera chinensis*), we observed a novel interaction behavior. We are calling the behavior a "vibe check" and are working to quantify and describe its natural history. For this project, we analyzed the trajectories of automatically tracked coordinates on body segments recorded at high magnification and at 1000 frames per second. The tracking was conducted using Deep Lab Cut, a free and open-source, python-based, artificial intelligence software package for animal pose estimation. Through our analysis, we were able to quantify the speeds of individual antennae, infer patterns of alternating movement between the pair of interacting individuals, and compare the kinematics of this behavior with other ultra-fast movements across the animal kingdom.

Aggressive Glioblastoma Evolution

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Glioblastoma multiforme (GBM) is the most common and deadliest of malignant primary brain tumors in adults. The three subtypes of glioblastomas are primitive neuronal, mesenchymal, and classical (astrocytic-like). Common mutations in genes found among GBM patients are in EGFR, IDH1, RB1, TP53, MYCN, and MDM2. GBM invades the nearby brain tissue, but the blood brain barrier prevents metastasis outside of the brain. Metastasis outside of the nervous system, extraneural, is rare, representing less than 2% of cases1. The mutations and genomic alterations that drive extraneural brain metastasis are not-well defined, highlighting the need for further research into this aggressive metastatic form of GBM. To elucidate genomics alterations behind extraneural metastasis, we studied a highly aggressive GBM patient through whole genome sequencing. This study is unique as the GBM case presented with metastasis in both the blood (323 days) and the rib (343 days). Samples were collected at initial biopsy through time of death to analyze mutations that drove GBM, clonal evolution of the subtypes present at diagnosis, and the presence of extrachromosomal circular DNA (eccDNA). We discovered missense, nonsense, and intron mutations within the commonly mutated GBM driver genes. In most tumor samples, MDM2 had a gain in copy number, and PTEN, CDKN2A, and CDKN2B presented with a loss in copy number. We followed each clone throughout its evolution, and discovered eccDNA may drive extraneural metastasis.

Comparative Analysis of Pediatric and Adult Blood Composition

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As sequencing technologies and computational tools improve, blood diagnostics are becoming more common place in cancer detection and staging. Our lab's goal is to harness computational analytics of brain cancer evolution and novel microfluidics platforms to enable improved staging throughout an entire clinical treatment course in a relatively non-invasive form of serial biopsy. However, we study varying forms of brain cancer and although a majority are adults brain cancers represent the second most common form of pediatric cancer. Although it is well-defined that cardiac function, blood volume, and normal hemoglobin levels are age-dependent the single cell transcriptomic landscape of children versus adults remains under-investigated. This research investigates the composition of blood in pediatric and adult populations, in order to further define the transcriptomic differences in blood components for future liquid biopsy discoveries. Through unification of publicly available single cell RNA sequencing (scRNAseq), we collected transcriptomic profiles of 2 adult individuals and 8 pediatric individuals representing 68,842 and 43,219cells. Key blood components, including red blood cells, B-cells, T-cells, platelets, and hemoglobin were annotated. We then examined blood composition changes from childhood to adulthood. The creation of a whole blood cell atlas and the valuable insights into composition changes between adults and pediatric samples, will guide future work on computational analytics of liquid biopsy in brain cancer patients.

Enabling Persistent Observation with Autonomous Underwater Vehicles

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Coastal water changes rapidly, necessitating diverse observation platforms, as small-scale processes like harmful algae blooms and shelf water intrusion challenge traditional buoy systems. Autonomous underwater vehicles (AUVs) could bridge the observational gap and address these rapidly evolving processes, but the current boat-based AUV operations are inefficient due to weather dependency and boat demands. Enabling AUVs with underwater resident capability could serve as potential relief to this challenge. In order to enable AUV residency, a mechanism to maintain system power levels must be developed. This project explores using AUVs with underwater docking stations to recharge their batteries towards persistent AUV operation and weather-independent monitoring. In order to prove this concept, the software Stonefish and the middleware ROS2 were used to create a 3D virtual environment of a stationary ROV and controller-operated docking AUV. In this simulation, the dimensions of the docking station were derived using the same ratio as average car size to parking garage space. Additionally, a basic frame and ROV were designed to support the docking station. This three-part assembly was imported into the simulation as a static object, while the AUV was imported as a dynamic object. An important quantifiable component of the simulation was the tuning of a Proportional Integral Derivative (PID) controller such that the AUV responds effectively to operator inputs. This AUV controller was tuned to control 4 degrees of freedom: pitch (rotation about y axis), yaw (rotation about z axis), depth (change in z direction) and surge (change in x direction). Based on the success of the simulation, a docking station using the simulated dimensions will be built and deployed to test manual docking of a real world AUV. Future developments of this project will include the charging mechanism and implementation of full vehicle autonomy.

Pinpointing Two Precursor Proteins of Alzheimer's Disease: Amyloid Precursor Protein and Presenilin

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Amyloid precursor protein (APP) in its cleaved form, beta-amyloid protein (Aβ), is a causal agent in familial Alzheimer's Disease (AD). Mutations in presenilin (a hypothesized catalyst of this cleavage) have been discovered in families affected by this devastating disorder. While the Aβ plaques formed as a result of these mutations have been heavily studied in recent years, little is known about the location and relationship of APP and presenilin before this cleavage process occurs. As such, the research presented here aims to characterize the locations of APP and presenilin within the neurons of goldfish spinal cord tissue. Additionally, this research builds on the working hypothesis that APP is localized in synaptic vesicles for trafficking purposes. Employing immunocytochemistry in combination with confocal light microscopy, we conducted two double labeling experiments, comparing the distribution of (i) APP with the synaptic vesicle protein SV2, and (ii) APP with presenilin. Our results suggest that APP is not located within the synaptic vesicles, as we do not observe a consistent overlap of APP and SV2 fluorescent markers. Images labeling APP and presenilin showed a punctate staining for APP consistent with the theory that APP is in discrete regions of the nervous system. However, presenilin showed a broader distribution through the spinal cord tissue. We observed inconsistent colocalization between the two proteins. This finding was surprising to us as presenilin is thought to be part of a four-protein complex that cleaves APP. To further investigate these results, we have started to prepare samples for transmission electron microscopy, which will clarify the conclusions drawn from imaging at the light microscopy level. Through characterizing the locations of APP and presenilin within the neuron, this work aims to provide insight into their relationship and their role in Alzheimer's Disease.

Seasonal Trends of Polycyclic Aromatic Hydrocarbons (PAHs) in Atmospheric Particulate Matter at Providence College, Providence, RI

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Polycyclic Aromatic Hydrocarbons (PAHs), among other pollutants, are a significant concern due to their carcinogenic and mutagenic properties. PAHs, primarily produced by incomplete combustion processes, can efficiently sorb to particulate matter (PM), posing significant health risks. Urban environments, with dense populations and higher levels of vehicular and residential emissions, are particularly vulnerable to high PAH levels.

Providence, Rhode Island, the third-most populated city in New England, serves as an important urban center in the region. Providence, known for its substantial household heating during the colder months and high transportation emissions due to its location along the I-95 corridor and proximity to the Port of Providence, is an appropriate location to study seasonal variations in PAH concentrations. Previous research has indicated that urban areas contribute significantly to PAH levels, which are impacted by temperature, relative humidity, and meteorological conditions.

In this study, the seasonal changes of PAH concentrations were analyzed in ambient air at Providence College, an urban site in Providence, Rhode Island. This study attempts to discover significant seasonal trends in PAH emissions by analyzing the relationship between temperature, relative humidity, and PAH levels. The findings will help improve our understanding of air quality dynamics and develop strategies to reduce PAH-related health hazards in urban settings.

Spatial Variability and Source Apportionment of Polycyclic Aromatic Hydrocarbons Across an Urban Atmospheric Gradient

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Atmospheric particulate matter, an indicator of pollution, can contain harmful chemicals that can pose a harmful impact on human and environmental health. Particulate matter that is in the urban environment in Providence, Rhode Island was collected in filter-based samples that will be extracted and analyzed to detect concentrations of specific polycyclic aromatic hydrocarbons (PAHs), which are anthropogenic markers of incomplete combustion. Filter-based samples of total suspended particulate (TSP) and particulate matter less than 2.5 microns in aerodynamic diameter (PM2.5) have been collected at two locations in Providence, RI- at the Port of Providence and at Providence College (PC). Samples were extracted through pressurized liquid extraction and blown down to a volume that can be analyzed by gas chromatography coupled with mass spectrometry to detect concentrations of 13 different PAHs. The concentrations of organic compounds found in the samples across the two locations in Providence were compared to one another based on diagnostic ratios of isomeric PAHs. These calculated diagnostic ratios can provide insight to potential source attribution to particulate matter sampled. Further exploration of statistical differences in the diagnostic ratios across locations was performed to investigate source variance in suburban versus urban environments.

A Machine Learning Based Approach for Creating Mathematical Models of Intracellular Signaling Pathways with Application to Neurodegenerative Disease

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Degenerative diseases of the nervous system have tremendous prevalence in populations across the entire world. In the United States alone, approximately 10 million individuals suffer from Parkinson's disease, Alzheimer's disease, or amyotrophic lateral sclerosis. Despite tremendous progress by the research community to progress neurological therapies and our comprehension of the pathogeneses of these diseases, intracellular mechanisms by which they operate remain highly elusive. In support of this challenge, mathematical modeling and computer-based simulation has shown to successfully augment laboratory research in the discovery of neurodegenerative disease characteristics and mechanisms at the intracellular level. Nevertheless, the complexity of these models coupled with unknown signaling kinetics is highly problematic, as without appropriate values for these unknowns, the models are incomplete and unusable. To address this issue, we present a novel, informatics-based approach that can identify proper model kinetics with tremendous speed and accurately and demonstrate this approach using a mathematical model of a dopaminergic neuron intracellular signaling pathway with application to Parkinson's disease. Our approach synthesizes data science principles including collection, screening, cleaning, and balancing of 100 million realizations of model kinetic tuples with a host of diverse machine learning algorithms including Gaussian, logistic, neighbor, tree, ensemble, support vector, and neural network methods. Results show that a well-structured neural network can classify model kinetic tuples with accuracy in excess of 96%, and in addition, reach speeds that are four orders of magnitude faster than traditional screening approaches. Furthermore, our methods are generalizable, and can be seamlessly extended to alternative neurodegenerative modeling applications. It is our hope that this work will help synergize mathematical modeling and biomedical research, thereby facilitating a greater understanding of the pathogenesis, progression, and treatment options for neurodegenerative disease.

Impacts of Cytoskeletal Alterations on Subnuclear Bodies: Implications for Amyotrophic Lateral Sclerosis

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The cytoskeleton, a dynamic network of protein filaments, plays a pivotal role in maintaining cellular structure, facilitating intracellular transport, and regulating numerous cellular functions. Manipulating the network highlights its critical influence on subnuclear bodies, specialized structures within the nucleus such as nucleoli, Cajal bodies, and nuclear speckles, which are essential for various aspects of gene expression and RNA processing. Cytoskeletal alterations are a common pathological feature of Amyotrophic Lateral Sclerosis (ALS), a progressive and fatal neurodegenerative disorder that primarily affects motor neurons. In prior studies, it has been shown that an hexanucleotide GGGGCC repeat expansion in the C9orf72 gene is the most frequent genetic cause of ALS in Europe and North America. Mutations in this gene account for about 25-40% of familial cases and approximately 6% sporadic ALS. In past studies, altered nuclear envelope, the framework of the nucleus, has been shown as the key pathogenic event in C9orf72-linked ALS in cellular models, as well as post mortem patient tissue and mice. In this study, Human Embryonic Kidney cells (HEK 293), were used to see if alterations of the cytoskeleton impacts nuclear bodies using targeted drugs, such as Latrunculin B and Intramimic-01. When cells were treated with these targeted drugs, actin polymerization was either inhibited or increased. Fibrillarin, a protein that plays an essential role in ribosome biogenesis inside the nucleolus, was found to be significantly less than the control DMSO-treated cells when actin polymerization was increased. Similarly, we found that SMN, a protein involved in splicing machine assembly, was significantly lower in cells treated with both drugs in comparison to the control. Cajal bodies play a crucial role in biogenesis and assembly of small nuclear ribonucleoproteins and contain proteins and RNA molecules essential for the cell. Increased mechanical tension can lead to displacement or reorganization of Cajal bodies within the nucleus, while decreased tension can possibly impact snRNP and snoRNP. To test whether similar alterations could be seen in the context of ALS, HEK 293 cells were transfected with C9orf72 G4C2 expanded repeat. Similar alterations of nuclear bodies, such as fibrillarin, were identified in the C9orf72 treated cells confirming our hypothesis.

Quantification of VGluT1+ synapses onto motor neurons in a Rabbit Model of Cerebral Palsy

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Cerebral Palsy (CP) is the most common motor disorder in children, leaving many with lifelong non progressive motor impairments, with pain as the most common comorbidity. The most common type of CP, spastic CP, is classified by increased muscle tone (hypertonia) and exaggerated reflexes (hyperreflexia). CP is often caused by a prenatal hypoxia-ischemia (HI) injury. This injury can affect the developing corticospinal tract (CST), a major neuronal pathway responsible for movement control.

The CST participates in synaptic competition, the developmental process in which one synapse affects the stability and survival of another. Neurons in the CST compete with Ia afferents, sensory fibers responsible for monitoring and controlling reflexes, for synapses onto motor neurons. Rabbit kits, when exposed to an HI injury in utero, mirror CP in humans. Previous studies using this rabbit model of CP have shown sprouting of CGRP+ (calcitonin gene related peptide) afferent fibers in the spinal cord after an HI spinal cord injury and thinning of the CST. Using the HI rabbit model of CP, we studied sprouting of 1a afferent synapses onto motor neurons. We hypothesized thinning of the CST is accompanied by greater sprouting of Ia afferents onto motor neuron somas in the lumbar spinal cord of HI rabbit kits than in sham rabbit kits. Ia afferents are excitatory glutamatergic sensory neurons that express vesicular glutamate transporter 1 (VGluT1) at their axon terminals.We used immunohistochemistry to label VGlut1+ synapses onto the somas of choline acetyltransferase (ChAT)+ motor neurons in the lumbar spinal cord of both HI and sham postnatal day 18 rabbits.

We found HI rabbits have a greater amount of VGluT1+ synaptic contacts (16.66 +/-1.436, n = 3 sections) onto motor neurons than sham rabbits (9.383 +/- 1.660, n = 3 sections). These findings suggest that greater amounts of VGluT1 synaptic contacts of 1a afferents onto motor neurons could lead to exaggerated reflexes as seen in patients with CP.

Examining Repetitive Negative Thought Among Individuals with Eating Disorders

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Repetitive negative thought (RNT), encompassing both rumination and worry, has been increasingly recognized as a significant factor in eating disorders. Research has shown that people with bulimia and binge eating disorder report higher levels of RNT than the general public (Palmieri et al., 2021). While rumination has been both concurrently and prospectively linked to eating disorder symptoms, the relationship between worry and eating disorders remains less explored (Smith et al., 2018), although anxiety disorders are a common psychological comorbidity among these patients (Rosenbaum & White, 2013). The present study aims to examine the level of worry in individuals with a lifetime history of anorexia, binge eating disorder, and bulimia compared to those with no history of eating disorders.

Analyses were carried out in the National Comorbidity Survey Replication (NCS-R), a nationally representative household survey comprising 3,725 participants collected between 2001 and 2003. Worry was measured by two items ("How often did you find it difficult to control your worry or anxiety/nerves?") and ("How often were you so nervous or worried that you could not think about anything else, no matter how hard you tried?") rated on a scale from 1 (never) to 4 (often). The presence or absence of a lifetime history of anorexia, binge eating disorder, and bulimia was defined by DSM diagnostic criteria.

Consistent with our hypothesis we found that individuals who endorse a history of binge eating disorder or bulimia report more worry than those who do not endorse any history of eating disorders. Individuals with either of these disorders report a higher frequency of times it is hard to control worry/anxious/nervous emotions, along with a higher frequency of being so nervous that they could not think of anything else. There were no significant differences in either worry variable between individuals with anorexia and those with no history of eating disorders, which we attribute to the small sample (n = 11) of individuals reporting a history of anorexia. Follow-up analyses suggest that these results are not solely due to eating-related worries, or comorbidity with generalized anxiety disorder (GAD). These findings indicate that worry management strategies could be beneficial in the treatment of eating disorders.

Mental Health and Environmental Factors for Unaccompanied Children in the United States

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Unaccompanied minors are children under 18 years old, who have migrated to the United States (US) and are without a guardian. Recent research shows an increase in unaccompanied minors arriving to the US, mainly migrating from Guatemala, Honduras, and El Salvador. In 2023, the Office of Refugee Resettlement (ORR) reported 118,938 unaccompanied minors arrived in the US (ORR, 2024). Unaccompanied children experience trauma before, during, and after their migration, which research shows is associated with substantial mental health issues (Cardoso et al., 2017). This exploratory study aims to address a gap in research on unaccompanied children's mental health and evaluate how a child's environment is associated with their mental health. Data was collected using a survey with the Patient Health Questionnaire (PHQ-9), Sense of Community Index (SCI), and various demographic variables (e.g. age, sex, country of origin). All data was collected in partnership with a Rhode Island nonprofit organization, Dorcas International, between February 2024 and June 2024. The unaccompanied children who completed the survey were all receiving case management services from Dorcas International. The PHQ-9 is a 9-item instrument that measures the severity of depressive symptoms, and scores range from 0-27. (Kroenke et al., 1999). In addition, the SCI measures a participant's sense of community, and includes four subscales: meeting needs, influence, membership, and shared emotional connection (McMillan & Chavis, 1986). The sample includes n=51 unaccompanied children. Most children in the sample identify as male (76.47%) and the mean age is 16.35 years old (SD=1.52). Most children migrated from Guatemala (78.43%) and over half the sample are separated from both parents (58.7%). The mean depression score in the sample is 1.11 (SD= 2.09), and 7.84% of the sample meet criteria for moderate depression. Children from Guatemala report greater symptoms of depression (M=1.4; SD= 2.28), compared to children from other countries (M=.10; SD=.30) (p<.05). The highest sense of community is reinforcement of needs (M= 9.56; SD= 5.13) and the lowest sense of community is perceived membership (M= 8.23; SD=5.30). The results suggest that, while unaccompanied children report their environment is able to meet their immediate needs, there is a lower sense of perceived membership in the community. The results can inform the development of clinical services to help facilitate integration in the US.

Reliability of Automated Scoring of The Novel Object Recognition Task in a Mouse Model of Bipolar Disorder

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Bipolar disorder (BD) is a chronic mood disorder characterized by shifts in mood and energy. Several studies suggest the ClockΔ19 mouse may be a valid model of BD. We seek to further validate the ClockΔ19 model through our investigation of cognitive deficits that are present in human bipolar disorder using cognitive tasks such as novel object recognition. We currently use a manual scoring process to analyze behaviors in a series of cognitive tasks. Following this study, we aim to automate our behavioral scoring process using EthoVision XT to analyze behavior in ClockΔ19 mice. EthoVision XT is a video tracking software used for tracking and analyzing movement and behaviors in rodents. By using automated video tracking software such as EthoVision XT, we can analyze a wider range of behaviors at a much higher efficiency. While initial investments into video tracking software are costly, decreased labor hours involved with manual scoring offsets high software costs. Alongside these benefits of automated scoring, there is increased consistency and reliability in removing the possibility of differences between scorers in the manual scoring process. Several studies have suggested automated behavioral scoring can produce near identical results as manual scoring in rodents. In this study, we compare manual and automated behavioral scoring in the novel object recognition task (NOR) with a reliability test. We found no significant difference between manual and automating scoring using EthoVision XT.

Behavioral Differences in a Mouse Model of Bipolar Disorder

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Bipolar Disorder (BD) is an undertreated chronic mood disorder characterized by episodes of mania and depression, leading to significant shifts in mood, concentration, and activity levels. A genetic model for BD, involving the mutation of the ClockΔ19 gene, provides insights into the rapid mood cyclicity found in human populations. The ClockΔ19 mouse model is a circadian rhythm-based model which features BD-like phenotypes, such as increased risk-taking behavior, addictive tendencies, hyperactivity, mood cycling and disrupted circadian clocks. ClockΔ19 mice display mood cyclicity on a 24-hour basis. Our goal is to further validate the behavioral phenotypes of the ClockΔ19 mouse model as a pre-clinical model for BD. A crucial factor in checking for validity in mouse models has been to develop assays that can be used for continuous automated home-cage assessments to analyze complex mouse behaviors. Home-cage monitoring (HCM) allows us to test the overall behavior of a mouse to validate the ClockΔ19 model for further studies on treatments for BD. In our lab, we are looking for trends in activity that further reassure the phenotypic profile of the Clock19 mouse model, such as an increase in hyperactivity, disturbed sleep, and mood cyclicity, similar to what is seen in humans with BD. Our preliminary findings show that a far deeper understanding of mouse mutant phenotypes can be established by monitoring behavior in their home- cage over one or more light and dark cycles. While there are notable trends of sex-specific and phenotypic differences in behaviors, our sample size currently, is considerably small. Ultimately, we hope to understand the correlation of specific behaviors with genetic and phenotypic variations by using automated and multimodal measurements enabled by HCM.

Muscle Spindle Development in a Hypoxia-Ischemia Rabbit Model of Cerebral Palsy

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Cerebral palsy (CP) is a group of non-progressive developmental disorders resulting from perinatal neurological injury. Motor and sensory deficits, including hyperreflexia and spasticity, characterize CP. Unlike the majority of CP animal models, rabbits that undergo prenatal hypoxic-ischemic (HI) injury replicate these motor deficits. The development of muscle spindles, the most prominent proprioceptors, may contribute to hyperreflexia and proprioceptive deficits observed in CP. This study examines muscle spindle development across the early postnatal period in the HI rabbit model as compared to age matched controls. We hypothesize that HI injury will alter muscle spindle morphological development. Specifically, as this model has increased reflex activity, HI rabbits are expected to have increased muscle spindle density. In addition, muscle spindle capsule thickness and size are expected to be altered in the HI rabbit model. Immunofluorescent staining of neurofilament and synaptic vesicle glycoprotein 2 were utilized to visualize muscle spindle morphology in the calf muscle, soleus. Hematoxylin and eosin staining of soleus cross-sections was performed to supplement this analysis by measuring muscle spindle capsule thickness. These findings will characterize muscle spindle morphological development in a rabbit model of CP and direct future work to elucidate its effects on motor function.

Investigating the Effects of Nanoparticle-based Treatments on an Alcohol-Related Liver Disease (ALD) Liver-Chip Model

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Since 2016, alcohol-related liver disease (ALD) has been the leading cause for liver transplants in the United States (US). In 2022, ALD accounted for approximately 45,000 deaths, about 46% of all documented liver disease deaths that year. ALD causes inflammation in the liver that, over time, leads to cirrhosis and progressive loss of liver function, often even leading to hepatocellular carcinoma. In 2019, 50.3% of all cirrhosis deaths in the US were alcohol-related. A key challenge in liver disease treatment is the non-specific nature of the therapies, resulting in toxicity in other organs. In this research, we developed and characterized biodegradable, biocompatible poly(lactic-co-glycolic acid) (PLGA) polymer-based nanoparticles (NPs) for drug delivery into the acidic and inflamed ALD environment. The NPs were conjugated with INT-777 - a semi-synthetic bile acid agonist specific to the Takeda G protein-coupled receptor 5 (TGR5) expressed on Kupffer cells in the liver. INT-777-mediated TGR5 activation can inhibit the pro-inflammatory cytokine production of Kupffer cells, which are known to play a role in liver inflammation progression. Representing ALD using microphysiological liver models allows researchers to accurately study liver disease and investigate the effects of therapeutic drugs. Therefore, the drug delivery system was tested using the Emulate liver-chip module. This model recreates the physiology and mechanical forces cells experience within the body. Human HepG2 liver carcinoma cells were seeded in the top epithelial channel to represent hepatocytes. Differentiated human THP-1 monocytic cells were seeded in the bottom endothelial channel to represent Kupffer cells. The cells were treated with a combination of lipopolysaccharide and ethanol to induce ALD-associated inflammation. Fluorescent dye-loaded NPs were used to visualize uptake by differentiated THP-1 cells using confocal microscopy. Encapsulation and release of the encapsulated anti-inflammatory drug was assessed by UV-Vis spectrometry. Finally, a treatment study was carried out to assess the therapeutic effects of the NPs in the liver-chip model.

Purification and Characterization of DNA Oligonucleotides Containing Site-Specific Modifications

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Oligonucleotides are essential tools in chemical, biological, and medical research. Synthetic oligonucleotides have become fundamental technologies in the pharmaceutical and biotechnology fields, playing a key role in applications ranging from diagnostics to therapeutics. This study focuses on the purification, characterization, and comparison of two modified oligonucleotides: 16-nucleotide oligomers (16-mer) with 6-methyladenosine (m6A) and 1-methyladenosine (m1A) modifications. The aim is to remove impurities from automated solid-phase synthesis and other sources. Using Reverse Phase High-Performance Liquid Chromatography (RP-HPLC) and Anion Exchange-HPLC, these DNA oligomers were isolated from their crude samples. Subsequent identification and characterization were performed using Liquid Chromatography-Mass Spectrometry (LC-MS). In line with previous studies on oligonucleotide separation and characterization, this experiment highlights the importance of incorporating advanced analytical methods for precise and accurate results. These methods include, but are not limited to, tandem mass spectrometry (MS/MS), Exonuclease Digestions with Matrix-Assisted Laser Desorption Ionization (MALDI-TOF), enzymatic analysis, analysis of trace elements, hydrophilic interacting chromatography (HILIC), and nuclear magnetic resonance (NMR). These advancements, combined with a range of bioanalytical techniques, provide researchers with a comprehensive toolkit for improved separation and thorough analysis of oligonucleotides, paving the way for new discoveries and applications.

Exploring the Association of Adversity Dimensions and Emotion Management in Youth

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Background: Emotion management refers to managing emotions to meet social expectations and to adapt flexibly. Although there is evidence that suggests adversity is a predictor of poor emotion management, previous studies have relied on specificity and cumulative risk approaches to adversity. Since adversity can be experienced in multiple types, dimensional models may elucidate the specific developmental correlates of different types of early life experiences. Previous research has assessed adversity dimensions (i.e., experiences of threat or deprivation) and their associations with emotional processing, which revealed that threat experiences were associated with select emotions (i.e., anger) of emotional processing. The current study explored how these dimensions of adverse experiences may influence emotion management in a sample of peripubertal youth with severe psychopathology.

Methods: Participants were admitted to a children's partial hospitalization program with severe psychopathology. The final sample was n = 397, with participants predominantly identifying as White (80%) and male (55%) with a mean age of 10.21 (SD = 1.53). Experiences of youth adversity was assessed by parent report on the Adverse Childhood Experiences questionnaire (ACE-Q). Items were categorized into either threat or deprivation dimensions based on the nature of the adversity. The youth's emotion management was assessed by parent report on the Children's Emotion Management Scale with subscales of anger, sadness, and worry.

Results: Regression analyses revealed that deprivation, but not threat, predicted parent report of sadness inhibition (β=.152, p<.05, 95% CI [.056, .394]). Neither deprivation nor threat predicted worry inhibition. Deprivation, but not threat, predicted parent report of anger inhibition (β=.138, p<.05, 95% CI [.028, .308].

Conclusion: These findings show an association between parent report of deprivation experiences and parent report of youth sadness management but not youth report. Additionally, threat experiences did not predict any report of emotion management. This suggests that specific dimensions of adversity (i.e., deprivation) may increase the likelihood that youth with these experiences may struggle with managing their own emotions, specifically sadness, possibly indicating a need for higher level of care. Findings from this study have the potential to inform clinical interventions for youth with experiences of adversity and emotion regulation dif

Internet Gaming Disorder and Prescription Drug Misuse: Associations by Student Status

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Internet gaming disorder is a multifaceted issue that is not well understood as surveillance studies do not routinely measure video game use and video game addiction. This study among young adults aimed to examine the association between gaming addiction and prescription drug abuse along with whether that relationship varies by student status. The 2022 Rhode Island Young Adult Survey included N=1,022 students between the ages of 18 to 25 who had lived in Rhode Island, with n=124 lifetime prescription drug misusers (12.1%) included in this study. Logistic regression models were used to estimate the association between gaming addiction and odds of prescription drug misuse by student status. With each additional unit in gaming addiction score the odds of prescription drug misuse increased by 6% (OR[95%CI]=1.06 [1.02,1.10]). In the fully adjusted model, the interaction between student status and gaming addiction score was significant at p=0.044. Student status was linked to a greater probability of prescription drug misuse as gaming addiction score increased with this association being weaker among non-students. The rising popularity of video games coupled with the high prevalence of prescription drug misuse throughout college campuses may promote co-occurring behavior. Efforts should be taken to impose strict guidelines on the sale of controlled substances and/or limit video game usage among young adults. Further research is necessary to understand the underlying mechanisms regarding gaming addiction and its relation to prescription drug misuse among young adult student populations.

Investigating the Biosynthetic Potential of *Pseudoalteromonas rubra* Strain CH007

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Crustose coralline algae (CCA) are a group of calcifying red algae that grow on coral reefs worldwide and have been shown to induce coral larval settlement. The marine bacterium *Pseudoalteromonas rubra* has been repeatedly isolated from CCA and may promote induction of coral larval settlement due to its production of specialized metabolites.

In this study, compounds produced from *Pseudoalteromonas rubra* strain CH007, isolated from CCA growing in the culture tanks at Roger Williams University, were purified using multiple chromatographic methods. The resulting fractions were investigated using high performance liquid-chromatography coupled with tandem mass-spectrometry (HPLC-MS/MS). CH007 was found to produce a series of pigmented molecules known as the prodiginines. Bioactivity testing of fractions enriched in prodiginines revealed antimicrobial properties against the fish pathogen *Vibrio anguillarum* strain M935m and the causative agent for Juvenile Oyster Disease, *Roseovarius crassostreae*.

Vibrio coralliilyticus and *Phaeobacter inhibens* Membrane Vesicles Modulate Biofilm Formation

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Oyster hatcheries in Eastern United States face infection from the deadly marine pathogen, *Vibrio coralliilyticus* strain RE22. The putative probiotic, *Phaeobacter inhibens* strain S4 has been used to mitigate host infection with *V. coralliilyticus* RE22. It is hypothesized that membrane vesicles (MVs) may serve as delivery systems for compounds responsible for the probiotic effect. MVs that package biologically active components can influence diverse cellular processes, such as cell-to-cell communication, stress responses, antimicrobial resistance, horizontal gene transfer, and immune evasion, among others. It has also been hypothesized that MVs play a role in the inhibition of biofilm formation. Biofilms are a community of microorganisms that adhere to a surface, multiply and form an exopolymeric matrix that shields the bacteria from immune recognition and provides antimicrobial resistance. In this study, we investigated the effect of MVs on biofilm formation using crystal violet staining and confocal microscopy assays. MVs were isolated from 200 mL cultures of *V. coralliilyticus* RE22 and *P. inhibens* S4 harvested after 24 hours. A decrease in biofilm formation by *P. inhibens* S4 was observed when exposed to *V. coralliilyticus* RE22 MVs exceeding 1.2×10^9 particles/mL. Similarly, *V. coralliilyticus* RE22— exhibited decreased biofilm formation when exposed to *P. inhibens* S4 MVs exceeding 1.4×10^8 particles/mL. Our preliminary conclusion is that MVs dosed at higher concentrations have greater inhibitory properties of biofilm formation. Future studies will include liquid-chromatography tandem mass-spectrometry for chemical characterization, transmission electron microscopy for bacteria visualization, and the use of BioTek Cytation 5 as an alternative biofilm fluorescence quantification method.

Investigating the impact of chronic isolation on alcohol consumption

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Social interactions and the development of social bonds are considered a basic human need equivalent to the need for food, water, sleep, and shelter. The absence of social interactions can have significant mental and physical health consequences. For example, recent reports suggest that social isolation in humans is associated with increased risk of depression, anxiety, suicide, premature death, and the development of alcohol use disorder (Parigi 2014). Understanding the impact of social isolation is particularly important in a post pandemic world where millions of people experienced chronic social isolation. Strikingly, the need for social interactions is not unique to humans- a multitude of organisms are social from humans, to rodents, and fruit flies, however, precisely how chronic social isolation affects the brain and behavior is unclear. Here we capitalize on the fruit fly, *Drosophila melanogaster*, to investigate the effects of chronic isolation. *Drosophila* are the ideal model organism because they have a simple nervous system that supports complex behaviors, they have a short life cycle, but reproduce in large numbers, and can be genetically modified in a variety ways. Previous work demonstrates that chronic isolation disrupts sleeping patterns and increases the expression of genes that signal starvation in *Drosophila*. Similar work in mice and humans report that social isolation induces activity in brain regions associated with hunger. However, how chronic social isolation impacts voluntary alcohol consumption is not understood. In this study we intend to measure the effects of chronic social isolation on voluntary alcohol consumption. *Drosophila* will first be provided with a rich social experience (200 flies) for 3-5 days and then either isolated for seven days or housed in groups of 25 same or mixed sex flies. Subsequently flies will be placed in the Fly Liquid-Food Interaction Counter (FLIC), to continuously measure feeding behaviors for three days. We hypothesize that chronically isolated flies will prefer to consume alcohol when given a choice between 15% alcohol and 5% sucrose. By understanding the impact of chronic isolation, we can develop strategies to counter its effects and reduce its severity.

Altered Activity of Human DNA Polymerase Theta in Cancer-Derived Variants

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DNA Polymerase Theta (Pol θ) is an enzyme tasked with the repair of damaged DNA. In patients with more advanced stages of melanoma cancers, they were found to be more likely to have mutations in their Pol Q (the gene that codes for Pol θ), suggesting a correlation between the mutations and cancer development. We looked at two specific patient mutations in POLQ—N2424I and N2035K—and assessed how the mutations impacted the function in comparison to the non-mutated protein (Wildtype). N2424I is a mutation that occurs in the nucleotide binding or fingers domain of Pol θ, and changes from the polar uncharged amino acid Asparagine to the non-polar amino acid Isoleucine. This mutation was found in a sun-exposed tumor from a patient who also had a mutation in their BRCA2 gene. Mutations in the BRCA gene hinder the cell's capability to carry out homologous recombination, which means Pol Q may become the primary resource for repairing double-strand breaks through the microhomology mediated end joining pathway. N2035K, which is also derived from a sun-exposed tumor, occurs in the exo-nucleus domain, and Asparagine is changed to Lysine, which is polar and charged. The mutated proteins were expressed and purified from *E.coli* cells. Once purified, we used circular dichroism to test the structural integrity of the mutations and determined that the mutations did not affect the global structure. Through DNA primer extension assays on a variety of DNA substrates, we identified several differences in the DNA polymerase function of the variant. Most notably N2035K was less successful at bypassing and extending UV damaged DNA, a common function of Wildtype. This suggests the amino acid change could affect the overall DNA repair ability of Pol theta and could play a potential role in carcinogenesis.

How the semantic ambiguity of suffixes affects the ease which we read complex words

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Semantic ambiguity causes difficulty for readers because it has been shown to delay comprehension. There has been much research on the role of ambiguity at the level of the word, but ambiguity also exists at the sub-lexical level, such as that of the morpheme. Many words comprise more than one morpheme. In investigating how we read multi-morphemic words it is crucial to determine whether words are recognised via decomposition into stem and affix and whether affixes are represented in lexicon independent of the stems to which they are attached. How does morphemic ambiguity influence recognition of complex words? How are ambiguous affixes represented in the lexicon? We examined these questions by analyzing data from the English Lexicon Project (ELP). We asked whether response time to recognize a word is influenced by the consistency with which a suffix letter pattern appears in real suffixed words. We found that complex words (e.g. walkable) show an effect of semantic consistency, while monomorphemic words that contain a letter pattern that is identical to that of an affix, but crucially does NOT function as an affix in that word (e.g. table) do not show this effect. Our goal is now to identify patterns of brain activity that reflect these processing differences. To do so we have designed an ERP lexical decision study using frequency-matched complex word stimuli, examining whether a suffixed word can be primed by a word sharing only the suffix letters in a masked priming paradigm. We predict that we will see brain activity that is consistent with easier processing for high-consistency prefixes but not for low-consistency prefixes.

Characterizing Nucleotide Dependency for the Interaction between Cell Division Proteins FtsA and FtsN

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In *Escherichia coli*, the cytoskeletal protein FtsZ promotes the formation of a division septum at the cell center and assembles into a large polymeric structure called the Z-ring. Coordination between FtsZ in the ring and other division proteins, including FtsA, which anchors FtsZ to the cytoplasmic membrane, and FtsN, a bitopic membrane protein ending in a peptidoglycan binding SPOR (sporulation-related repeat) domain, directs PG synthesis. FtsA polymerizes in the presence of ATP, forming dynamic polymers that assemble and disassemble with cycles of ATP hydrolysis. FtsN is known as the trigger for septation and, through its interaction with FtsA, may bridge early and late stage division through activation PG synthases in the periplasm. This study aims to characterize the functional interactions between FtsA and FtsN in reconstituted systems in vitro. FtsN binds to peptidoglycan and recruits FtsA, and ATP increases the amount of FtsA recruited. FtsA hydrolyzes ATP to yield ADP, which accumulates in the reaction. Therefore, we established an enzyme-based system comprising acetate kinase and a phosphate donor to replenish ATP in reactions where ATP depletion may impact the interaction. We compared the amount of FtsA-FtsN complexes assembled on peptidoglycan under varying nucleotide conditions. This work is important for understanding how the essential cell division machinery assembles in bacteria and provides a platform to evaluate conditions that may inhibit division through disrupting the FtsA-FtsN complexes.

Modulation of serotonin receptor 2c in a rabbit model of cerebral palsy

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Cerebral Palsy (CP) is the most common physical disability in children, affecting 1 in 500 live births. One cause of CP is perinatal hypoxic-ischemic (HI) injury to the brain and spinal cord. Individuals with CP experience muscle hypertonia and hyperreflexia. The neurotransmitter serotonin (5-HT) plays a major role in modulation of muscle function, coordination, and movement. The role of 5-HT in perinatal injury is not fully understood; but elevated levels of 5-HT may contribute to development of muscle spasticity in the HI rabbit model of CP that we used in this study. Our group is interested in how different 5-HT receptors affect perinatal development of the motor system. 5-HT receptor 2c (5-HT-2c) is an excitatory receptor which we hypothesized may play a role in modulation of neuromuscular activity after HI. We hypothesized that 5HT-2c receptor expression is increased in motoneurons after prenatal HI injury. To better understand how 5-HT-2c is expressed in motoneurons, we performed immunohistochemistry on postnatal day 5 slices of surgical sham control and HI lumbar spinal cord tissue. The spinal cord segments were then imaged as Z-stack photomicrographs, and further analyzed to measure mean fluorescence intensity of 5-HT-2c in motoneurons to determine if receptor 2c is upregulated or not in our CP model. We found that the level of 5-HT-2c expression in motoneurons was different between groups (P=0.007, Welch ANOVA), with lower 5-HT-2c expression in HI motoneurons compared to sham motoneurons (P=0.007, Tukey's post-hoc test). These preliminary results indicate that neonatal motoneurons downregulate 5-HT 2c after prenatal HI injury. Therefore, the composition of 5-HT receptors on motoneurons are impacted following perinatal HI injury to the brain and spinal cord. Future studies will examine whether 5-HT-2c receptor expression is related to motor dysfunction, which can be extremely variable between kits exposed to prenatal HI.

Characterizing the Biogeochemical Relationships Between Manganese-Metabolizing Bacteria in Rhode Island Soils

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Bacteria that use extracellular metals as terminal electron acceptors during anaerobic respiration are common in soil. We are investigating how consortia of bacteria influence the biogeochemistry of soil manganese. Manganese reduction in soil is detected using PVC film coated with brown paint consisting of oxidized manganese species. Soil manganese reduction solubilizes and removes the brown paint from the sensor. Bacteria on the sensor are sampled using a sterile cotton swab and isolated by streaking them to single colonies on 0.2 X lysogeny broth (LB) plates. We have isolated a pool of over 40 bacteria that can individually remove brown paint from the sensors and identified them using 16S rRNA gene sequencing. As expected, some isolates are predicted to be manganese-reducing bacteria. Surprisingly, some of the isolates are predicted to be manganese-oxidizing bacteria. That manganese-oxidizing bacteria can remove oxidized manganese paint suggests a synergistic relationship between manganese-reducing and manganese-oxidizing bacteria in the soil. We are currently testing the hypothesis that bacteria in the soil are cooperating to metabolize the oxidized manganese on the sensor. This will be accomplished by measuring the rates of manganese paint removal for individual isolates and comparing these rates to those observed when we co-inoculate cultures with pairs of manganese metabolizing bacteria. We reason that these pairs are likely to synergize because the reduction of manganese produces a substrate that manganese oxidizers can utilize for their metabolism. Ultimately, this experiment will aid in understanding the metabolic relationships between different manganese-metabolizing bacteria in soil and the complex biogeochemistry of an ecological system.

Updating Oncology Drug Brand Names on HemOnc.org for Improved Usability

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Generic drug names provide a standardized reference, but brand names are often more familiar to patients and healthcare providers, facilitating clearer communication and reducing the risk of medication errors. HemOnc.org, a comprehensive knowledge base of evidence-based cancer treatments, lacks updated information on the brand names of many oncology drugs. This project aims to update the brand names to improve the practical usability and make the resource as broadly inclusive as possible. We conducted a comprehensive search on hemonc.org for FDA-approved and marketed oncology drugs, focusing on the period from 2000 to 2012. Our approach involved an extensive web search to identify all possible brand names associated with each generic name. We categorized the drugs based on dosage, formulation, and routes of administration. Each brand name was meticulously verified for accuracy and discrepancies were resolved through discussion and cross-referencing with sources. The validated information was compiled into a spreadsheet, which will subsequently be updated on the HemOnc.org website to enhance the database. We identified 67 oncology-related drugs approved by the FDA between 2000 and 2012. The number of drugs identified per year ranged from 3 to 12, covering 12 years. The number of brand names per drug varied widely, with some drugs having as few as one brand name and others having up to 18 brand names. During the verification process, all identified discrepancies were resolved through thorough discussion and cross-referencing with reliable sources. There were 17 drugs in our dataset for which no new brand names were identified and updated. The systematic update of oncology drug brand names on HemOnc.org significantly enhances the database's utility for healthcare providers, researchers, and patients. Our work underscores the importance of maintaining up-to-date drug information in medical databases to keep pace with the evolving pharmaceutical landscape.

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