Thursday 9/28/23
3 PM - 5 PM

+

Friday 9/29/23
11 AM - 1:30 PM

Student Research Poster Session 2023

Sigma Xi
The Scientific Research Honor Society

Swarthmore


Results: Transient Absorption
Strongest Wavenumbers & Corresponding Coherence
Methods
Experimental Timeline (days)
PND 0 Pups born
PND 8 Cross-fostering
PND 20 Open Field Test
PND 21 Light-Dark Box
PND 22-26 Barnes Maze
Addition of Cholesterol
Zeta Potential:
DMPC:DMPG: -14.2 ± 2 mV
DMPC:DMPG:PEG: -11.5 ± 1 mV
PEGylated lipids are necessary for in vivo liposome survivability. They prevent aggregation, increase homogeneity and helps hide the liposome from the body's immune system.
DMPE-PEG2000 (PEG)
Methodology
Results
ETS Binding Site Deletions
None
ATMs Only
TVCs + ATMs
TVCs Only
1096
1055
E1 Del
E2 Del
E3 Del
E4 Del
Conclusion
Drug-Induced Conformational Changes
Summary and Future Directions
References
Round 0
Round 1
Round 2
Round 3
Round 4
Round 5
Round 6
Round 7
with an aqueous interior. They are useful drug delivery vehicles, able to safely administer toxic drugs or fragile nucleic acids. Recently liposomes have been used to deliver mRNA in the Covid vaccines.
liposome
drug-loaded liposome
targeted liposome
"stealth" liposome
I characterized the effect that various components have on basic liposome properties. Across 9 different formulations, I measured liposome size, surface charge, and model drug uptake.
Formation of Liposomes
Experiment:
- Injection into NAc using stereotaxic coordinates
- Trial & error
- 100 μm thin slices via vibratome
- Image using green fluorescence
Further Progress this Semes
Method: Image labelled CA
during a reward task

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Today, Sigma Xi has nearly 60,000 members in over 500 chapters in the U.S., Canada and other countries, including Switzerland, Thailand, Lebanon, New Zealand and Australia. Sigma Xi chapters are found wherever scientific research is undertaken in universities, colleges, industrial research facilities and government laboratories. Recent presidents of Sigma Xi have included Nobel laureate Frederick Robbins, National Medal of Science winner Kumar Patel, presidential science advisor Neal Lane, and National Science Foundation Director Rita Colwell.

For more information, visit www.sigmaxi.org.

SIGMA XI
THE SCIENTIFIC RESEARCH HONOR SOCIETY

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3	Elizabeth Agyei	Nick Kaplinsky (professor)	Building a Heat Inducible Fluorescent System in *C. reinhardtii* Using Golden Gate Cloning
4	Abdullah Ali	Dr. Liliya Yatsunyk	Biophysical Characterization and Crystallization of TET25 in complex with TrisQ
5	Kaya Arusha	Boadi, K.D., Ellah, S.S., Kim, D., Bauer, C.M.	Does sibling presence mitigate impacts of fostering on degu HPA-axis development?
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9	Anusha Bhatia	Professor Dawn Carone	Designing a System to Induce HSATII Expression in HeLa and Tig-1 Cells
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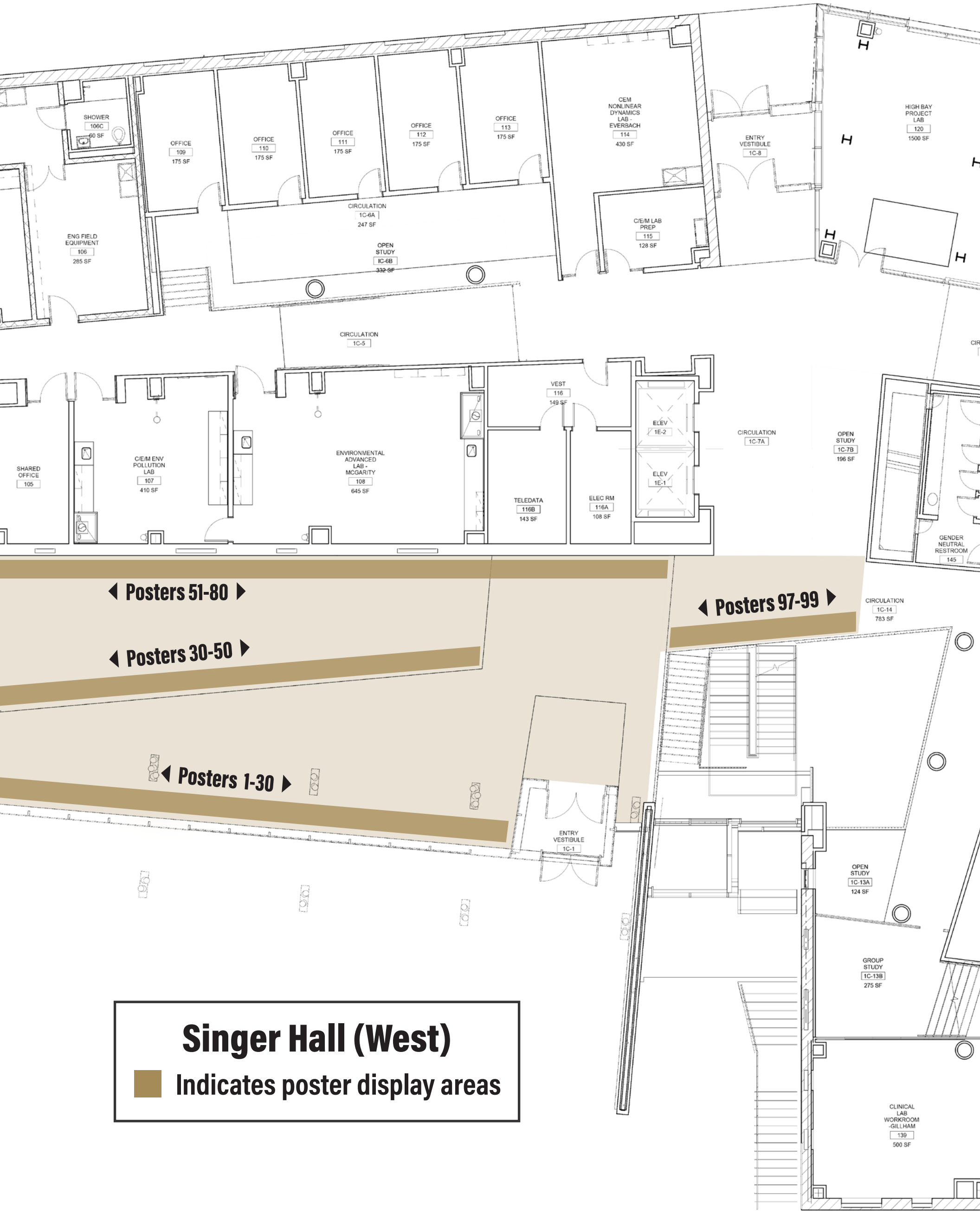

Singer Hall (West)

🟫 Indicates poster display areas

Analyzing Equity in EV Charging Station Access for Rural Areas

Ben Aaron, Donya Negahbani, Dr. Jason Hawkins

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The transition to electric vehicles (EVs) to reduce greenhouse gas (GHG) emissions has been a large part of climate policy. EV adoption relies on the charging stations that provide EVs with power, and the lack of charging infrastructure is a substantial obstacle to EV ownership for many consumers. With increasing incentives and goals for charging station construction, where public charging stations are placed impacts their utility, and unadvised planning could risk furthering the transportation infrastructure divide between rural and urban areas. This study examines the travel patterns of urban and rural areas to establish the varied need for charging stations and measures the equity of the existing public charging station sites across the United States. The use of job access as a measure of rurality reveals both the longer daily mileage traveled by people in rural areas and the influence of job accessibility on trip miles. Public charging stations, or electric vehicle supply equipment (EVSE), however, are concentrated in urban areas and still inaccessible for many consumers. The use of Lorenz curves and Gini coefficients gives a quantitative representation of current inequity and provides both a model for further equity analysis and a means of measuring policy success. Both the current lack of stations and the higher expected demand for public stations based on travel patterns highlight that more charging stations are especially needed in rural areas. These findings underline the need for policy decisions on the funding and placement of charging stations to be made with care to provide more equal access to EVSE and foster EV adoption everywhere.

Age-Dependent Variation in Home Range Sizes of *Bolitotherus cornutus*

Sarah Adebiyi, Dr. Vincent Formica

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The forked fungus beetle (*Bolitotherus cornutus*) is a species of beetle found in North America and known for its distinctive forked appearance. These beetles feed, inhabit, and mate on fungi growing on decaying wood, thus playing a pivotal role in nutrient cycling and the decomposition process within forest ecosystems. This study aimed to determine which intrinsic traits influenced the home range size of the forked fungus beetles. We hypothesized that older beetles, found in both young and old populations, would have larger home ranges due to heightened aggression and increases familiarity with their fungal environments. Consequently, we predicted that these older beetles would visit and live on more fungus brackets than their younger counterparts. Data was obtained from past researchers who documented the movements of the beetles in man-made enclosures for the span of three years. The modified dataset comprised 414 beetles, including 105 tenerals, 213 two-year-old beetles, and 96 individuals aged three years or older. Age structures were categorized as young (tenerals and 106 two-year-old beetles) and old (107 two-year-old and 96 three-year-old). The dataset included various traits, such as age, social partner age, population age structure, elytra (wing) length, sex, and spatial coordinates. Home ranges were computed using kernel density estimations from R's adehabitatHR package, which allowed for home range calculations for each individual beetle with a 65% kernel density. Our results revealed that 2-year-old beetles, irrespective of population structure, had the largest home range sizes. None of the other traits significantly predicted home range size. Interestingly, social partner age and population structure did not affect home range size as anticipated. The finding that two-year-old beetles in both the young and old population age structure had the largest home ranges aligns with the concept of the "middle age advantage," which suggests that unique benefits linked to this intermediate developmental stage, including enhanced agility and mobility, could facilitate essential activities like foraging, mating, and resource access. The discovery of this "middle age advantage" raises compelling questions and sets the stage for further exploration. Future research endeavors can delve deeper into unraveling the precise mechanisms underlying the “middle age advantage” and its broader implications. Although the precise advantages of larger home ranges remain uncertain, it is plausible that they enhance mate access and increase opportunities for successful egg laying, potentially contributing to overall fitness. This study sheds light on the relationship between age and home range sizes in forked fungus beetles, thus providing valuable insights into the ecological significance of the forked fungus beetles and their role in shaping forest ecosystems.

Building a Heat Inducible Fluorescent System in *C. reinhardtii* Using Golden Gate Cloning

Elizabeth Agyei, Nick Kaplinsky (professor)

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This summer, I focused on creating a heat induced fluorescent system in *C. reinhardtii* that would allow me to run thermotolerance assays and observe their results using fluorescent light. My lab previously built up a similar system in *A. thaliana* to study thermotolerance and the effect of different mutations on how *Arabidopsis* reacts to heat. To create this system, I first endeavored to build a plasmid construct with a promoter from Chlamy that is highly expressed at 40 C and with DNA fragments, including a blue fluorescent protein, from a modular cloning kit designed for Chlamy. I transformed bacteria with the construct, isolated the plasmids, then transformed Chlamy and plated the transformants on a plate with antibiotic. After successful transformation of Chlamy with the construct, I isolated two bacterial colonies containing said construct and sequenced them. I found that the sequences from the isolated plasmid were different than what was expected. As a result, I run an electrophoresis gel to determine if the desired sequence was present in any of my bacterial colonies and received a positive result. Therefore, the next directions of this research involve identifying which colonies contain the desired construct and isolating the plasmid.

Biophysical Characterization and Crystallization of TET25 in complex with TrisQ

Abdullah Ali, Dr. Liliya Yatsunyk

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G-quadruplexes (GQ) are non-canonical DNA structures that can have various genomic consequences based on their formation and location within the genome. Telomeric sequences have potential to form GQs and stabilizing these structures using small molecule ligands is desired. This is to prevent the development of cancerous diseases. Research into solving the structure of GQs and their complexes with small molecule ligands may allow for the development of novel anticancer therapeutics. Here, we study a telomeric sequence from *T. thermophila* (TET25) complexed with the ligand TrisQ. Biophysical characterization revealed a change in topology when adding TrisQ from hybrid to parallel along with increased thermal stability of the TET25 sequence. Crystallization was successful with resolutions as high as 1.64 Å with the structure being close to solved (Rwork/Rfree = 0.2671/0.2692).

Does sibling presence mitigate impacts of fostering on degu HPA-axis development?

Arusha, K.S., Boadi, K.D., Ellah, S.S., Kim, D., Bauer, C.M.

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This study examined how the presence of siblings affects endocrine stress response development in cross-fostered offspring of a social rodent, *Octodon degus*. We hypothesized that remaining with siblings mitigates the stress of fostering. Pups were either not cross-fostered (controls), cross-fostered at postnatal day 8 without siblings (single cross-foster), or cross-fostered at postnatal day 8 with the rest of their birth litter (complete cross-foster). One day after fostering and later at weaning, cortisol was measured at baseline and stress-induced levels, and dexamethasone was used to assess negative feedback efficacy. We predicted that stress response reactivity would be highest in single cross-fostered pups, lowest in controls, and moderate in complete cross-fostered pups. Specifically, we predicted that single cross-fostered pups would have higher stress-induced cortisol levels and weaker negative feedback than their complete cross-fostered counterparts. This investigation will contribute to our understanding of how family instability impacts postnatal stress response development.

Designing a Cell Synchronization Method for Studying Receptor Trafficking Dynamics in the Later Stages of Mitosis

Aryan Ashraf, Danelle Devenport, Bradley Davidson, Dawn Carone

Devenport Lab, Princeton University; Davidson Lab, Swarthmore College; Carone Lab, Swarthmore College ▪ aashraf1@swarthmore.edu

The planar cell polarity receptor Celsr1 exists at polar ends of the membranes of murine keratinocytes, and, during cell division, Celsr1 is internalized in vesicles during early mitosis and then recycled back to the cell membrane during and/or after cytokinesis. However, the exact trafficking dynamics of Celsr1 in these later mitotic stages are still ill-defined, as it seems that Celsr1 is recycled back to the membrane randomly before becoming more polarized from the influence of some internal cue. It is also difficult to properly assess the roles that some proteins play in this process, as inhibiting proteins of interest, such as the aurora kinases (AurK), leads to consequences like prometaphase arrest that render the cell unable to undergo those later stages. This study sought to design a method to synchronize cell division with the goals of 1) determining the time frames for the later stages of mitosis and 2) finding the window where the cells are in late-metaphase or early-anaphase. It was additionally hypothesized that AurKs could be inhibited in dividing cells past the stage of prometaphase and metaphase without inducing mitotic arrest.

Using a one-step drug treatment protocol with the CDK1 inhibitor RO-3306 and a quantification method developed from similar synchronization experiments with HeLa cells, the time frames for the later mitotic stages were identified for murine keratinocytes by quantifying fixed cells taken at multiple time points following drug treatment. The late

metaphase/early anaphase window was then determined from this information, and synchronized keratinocytes were treated with AurK inhibitors during this window to assess what effects the absence of aurora kinases would have on the trafficking of Celsr1 and, in turn, elucidate what roles they are playing in this process. Unfortunately, due to poor transfection efficiency, no effects of AurK activity on Celsr1 trafficking patterns were observed, but none of the dividing cells were arrested, indicating that aurora kinase inhibition during the determined window was successful. Experiments will have to be repeated with cells with a greater transfection efficiency or cells from a stable line transfection to be able to see any effects aurora kinase activity has on Celsr1 trafficking patterns. This synchronization method could also be applied to other cell types and other receptor trafficking dynamics.

Quantifying Competitive Binding of Adsorbates to Silver Nanoparticles

Iris Barone, Kathryn Riley

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Silver nanoparticles (AgNPs) have an increased use in the medical and commercial field because of their antimicrobial properties. Because of their small size, they easily diffuse into the environment where they can enter waste water treatment plants, for example. Once they enter the environment, the AgNPs can interact with biomolecules or natural organic matter to form coronas. These coronas form when adsorbates bind to the AgNP surface which changes several properties of the nanoparticle such as size, surface charge, and binding behavior. Citrate coated nanoparticles were studied in three different sizes: 10, 20, and 40nm particles. Two adsorbates were studied: Bovine Serum Albumin (BSA) and Suwannee River humic acid (SRHA). BSA was chosen as the model protein and SRHA as the natural organic matter. K_a values were obtained using UV-vis spectroscopy of the nanoparticles with each adsorbate individually. K_a values of BSA while the nanoparticle was precoated with SRHA were also quantified. The size and surface charge of the nanoparticles with the different binding conditions (single and multi-adsorbate) were quantified using dynamic light scattering (DLS). Indications of corona formation include an increase in the nanoparticle diameter and surface charge. The secondary structure of the BSA was quantified with the different binding conditions using circular dichroism (CD). Our initial findings are that BSA is denatured by the nanoparticles alone and SRHA alone. This denaturation is then amplified when the BSA is in solution with the AgNPs and SRHA. Future work will consist of further characterization of the single and multi-adsorbate systems using capillary electrophoresis (CE). Nonequilibrium capillary electrophoresis of equilibrium mixtures (NECEEM) will be used to quantify the binding and rate constants of the different adsorbate conditions.

Estimating The Number Of Morphological Rate Partitions In A Phylogenetic Tree

Student Researchers: Jialun (Joyce) Ben, Zachary Potthoff, Pradip Sharma Poudel, Anhad Singh. Professor: Steve Wang

In a phylogenetic tree, each branch can be thought of as having a true underlying rate of evolution. These rates are unknown, but they may be estimated from the observed number of character changes and the estimated duration of each branch. Given a tree with N_B branches, there may be as few as one rate of evolution (if all branches have the same rate) or as many as N_B rates (if each branch has a different rate).

Here, our goal is to estimate the number of distinct rates of evolution in the tree when the observed data are discrete counts of character changes. First, we describe an exhaustive search algorithm that examines each possible partition of k rates assigned to contiguous non-overlapping regions of the tree, where k ranges from 1 to N_B. For each possible partition, we calculate how well it fits the observed data using AIC. The partition with the smallest AIC provides an estimate for the number of distinct rates, their magnitudes, and their corresponding regions of the tree. This exhaustive search algorithm is guaranteed to find the best-fitting partition, but it is impractically slow for trees with large numbers of tips (i.e., approximately 20 or more).

We next describe two fast algorithms that can be applied to large trees: a forward (splitting) algorithm that starts by assuming that all branches have the same rate and then checks whether adding additional rates improves the fit, and a backwards (merging) algorithm that starts by assuming each branch has a different rate and checks whether merging contiguous branches improves the fit. We compare these fast algorithms with the exhaustive search algorithm and assess their performance on simulated datasets. Finally, we apply our methods to a dataset of lungfish fossils to better understand their evolutionary dynamics.

Designing a System to Induce HSATII Expression in HeLa and Tig-1 Cells

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Human Satellite II (HSATII) is a type of tandemly repetitive non-coding DNA found near the centromeres of several human chromosomes. Different HSATII subfamilies vary in sequence and are found on distinct chromosomes. Analyses of RNA-seq data containing HSATII sequences suggest that specific subfamilies may be prone to overexpression in some cancer cells. Further, several HSATII sequences are differentially expressed across cancer cell types. While HSATII is often expressed in cancer cells, it is transcriptionally silent in normal cells. When HSTII is expressed, the HSATII RNA form foci and subsequently bind and redistribute MeCP2, a methyl-CpG binding protein that regulates gene activity. Previous research demonstrated that constitutive expression of HSATII randomly inserted into the Tig-1 (healthy fibroblast cells) and HeLa (cervical cancer cells) genomes leads to cell division defects. This project aims to design a system that allows for easy insertion of different HSATII sequences into a specific location in the genome to compare the phenotypic consequences of expression of various HSATII subfamilies. We employed a gene editing technology called TALENs to direct the HSATII sequence to the AAVS1 safe-harbor locus. This locus is transcriptionally active and allows expression of the inserted sequence without impacting nearby endogenous genes. The TALENs donor plasmid utilizes a Dox-inducible system, so adding a chemical called doxycycline induces gene expression of the inserted sequence. However, the donor plasmid contains a gene for GFP (green fluorescent protein), so we needed to swap the GFP gene for our sequence of interest, HSATII. To clone HSATII into the plasmid, we added restriction enzyme sites to the HSATII sequence via PCR, digested the HSATII sequence and donor plasmid with restriction enzymes, and ligated the HSATII sequence and plasmid backbone. The plasmid was transformed into E. coli, and several bacterial colonies were screened via colony PCR. We isolated plasmid DNA from a few promising colonies and confirmed successful cloning of HSATII into the plasmid via DNA sequencing. The HSATII plasmid was then stably transfected into HeLa cells via lipid-mediated transfection, and doxycycline was added to induce expression. Future directions include examining HSATII expression in transfected HeLa cells by conducting RNA fluorescence in-situ hybridization to visualize expression and RT-qPCR to quantify relative expression. Other next steps involve transfecting Tig-1 cells with HSATII and analyzing effects on cell division. Further, since we successfully cloned an HSATII sequence into the TALENs donor plasmid, we can repeat cloning to generate plasmids with HSATII sequences from different subfamilies and transfect them into HeLa and Tig- 1 cells to compare the varying consequences of expression of different HSATII subfamilies.

Thai pronouns in diachronic perspective: Origins, change, and the Prestige Cycle

Kanyarin Boonkongchuen

Thai is renowned for its large and complex pronominal system, which has been the subject of research in various subfields including sociolinguistics (Saisuwan 2016), syntax (Aroonmanakun 2000), and historical linguistics (Matsuyama 1962; Strecker 1984). Thai is divergent from other closely related Tai languages, which have relatively simpler pronominal systems, and a straightforward 10-term pronoun paradigm has been reconstructed for Proto-Tai (Strecker 1984). Thai pronominals are also notable because they appear to violate binding Condition C (Chaiphet and Jenks 2020), which Jenks (2022) accounts for by proposing that Thai pronominals are actually complex indices that fall into three subclasses: 1) true personal pronouns, 2) referentially dependent anaphors, and 3) expanded indexicals. However, previous studies still leave gaps between our theory of the synchronic syntax, the sociolinguistic usage of Thai pronouns, and a more full account of how such a dramatic typological shift took place in Thai over centuries.

Focusing on Jenks' *true personal pronouns* category, in this study we begin to fill this gap by detailing how the Thai pronominal system has expanded and diversified through language contact and social stratification over the course of several hundred years, and connect these changes to specific sociohistorical influences. We have compiled a database of all discussion of pronominal terms in extant pedagogical and reference works starting from the 17th century, and continuing to the work of Haas in the mid-20th century, which helped spark a dramatic increase in focus on Thai by Western linguistic scholars, and the development of linguistics as a discipline in domestic Thai universities.

Classification of infant fNIRS data improves prediction of cognitive development 18 months later

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One goal of research on developmental adversity is the early identification of children at risk for later adverse outcomes. While surveys and cognitive testing provide important metrics of development and risk, they can also be limited by their reliance on a child's cooperation with instructions or parents' accurate reports. We tested whether a classifier for fNIRS data, collected during a passive task at 6 months old could be used to predict developmental outcomes at 24 months. fNIRS improved prediction accuracy by 12% over using only Mullen scores at 6 months.

Quantitative Separation of Polystyrene Nanoparticles in Environmental Matrices using Capillary Electrophoresis

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Currently, about 400 million tonnes (800 billion pounds) of plastics are being produced yearly worldwide. As this plastic decays whether it be degradation from UV light, mechanical degradation, or other means, nanoplastics are released into the environment. Due to their size, nanoplastics interact uniquely with the environment when compared to macroscale plastics, particularly in how they attach to larger particles in the soil and can be transported through the environment. Additionally, nanoplastics have substantial potential for toxicity due to physical changes, including photooxidation, chain scission, leaching, and biotic weathering, which occur uniquely in different media and are dependent on the surface chemistry of the nanoplastics. Although much research is currently underway, we still know very little about the mechanism by which nanoplastics move, their toxic effects, and the mechanism of toxicity. For these reasons, nanoplastics have become an emerging pollutant. A comprehensive understanding of nanoplastic aggregation is important to evaluate how they interact with and move through the environment which will ultimately affect their environmental fate. While macroscale plastics have been widely studied, additional studies and analytical techniques are needed to explore the interactions between nanoplastics and the environment. As a result, we have developed a method that employs capillary electrophoresis (CE) for the separation of nanoplastics of different sizes (50, 100, or 200 nm) or different surface coatings (bare, amino, or carboxyl) with vastly improved peak resolution, analysis time, and detection sensitivity compared to other commonly used techniques. Additionally, we will show preliminary data for plastic-clay heteroaggregate quantification.

Parental Provisioning to Offspring Across Maternal Age Groups in Rotifers

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In many animal species, offspring from older mothers have shorter lifespans, worse health, and lower reproduction than offspring of younger mothers. One current hypothesis is that these maternal age effects are caused by a decrease in parental provisioning to embryos as maternal age increases. To assess whether maternal provisioning of energy to embryos changes with maternal age, we measured hatching rate, starvation tolerance, egg and neonate size, and egg lipid content in eggs and offspring from young and old mothers in the rotifer *Brachionus manjavacas*. Prior to each experiment, two generations of maternal age synchronization were performed to be certain that the F2 generation (the experimental mothers) came from mothers of known ages (F0 ≤ 5d, F1 ≤ 6d). In the first experiment, three parameters were observed in the F3 generation from four different maternal age groups (3d, 6d, 9d, 11d): hatching rate, or the number of eggs that hatched over the span of ten hours; starvation tolerance, or how long these hatched neonates survived without food; and the sizes of eggs and neonates. During the second experiment, the neutral lipid content was measured from eggs of 3- and 11-day old mothers using a microplate assay. Although a higher portion of eggs hatched from young mothers than old mothers, suggesting lower investment by older mothers, egg and neonate size and neonate starvation tolerance

increased with increasing maternal age, suggesting greater provisioning by old mothers. Our results illustrate the importance of using the appropriate measure to assess maternal provisioning and it's age-related effects on offspring health and lifespan.

Looking Out for the Little Guy: Species Distribution Modelling of *Nannothemis Bella*

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Nannothemis bella Uhler 1857 (Odonata:Libellulidae), the smallest dragonfly in North America, inhabiting bogs and sedge fens across their distribution, which spans from Quebec south to Florida, and west to Minnesota and Louisiana. While common in the northern part of their range, *N. bella* is of conservation concern in the southern populations where they are disjunct and rare. Previous research has focused on male territorial behaviour with little consideration to the ecology and population dynamics within the species. To fill this knowledge gap, we constructed species distribution models (SDMs) to define factors in habitat suitability and determine projected future habitat. Our present-day SDMs indicate the dominant environmental elements determining habitat suitability include rate of temperature fluctuations, peak summer temperature, precipitation, and soil pH. Our projected SDM for 2050 predicts a significant decrease in habitat suitability throughout the entire range of *N. bella*. As such, *N. bella* is a species of conservation concern and conservation measures must be put into place as soon as possible. In addition, future genetic data will be analysed for further insights into gene flow between populations.

Function-First Synthesis: Solventless Synthesis of FROMPable Fragrant Mixtures in Continuous Flow at Scale

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Function-first synthesis underlines desired functions of products as the driving goal instead of structures, which in theory accelerates scientific discovery through bypassing steps of extended purification and speciation. Herein, we demonstrate the possibility and benefits of function-first synthesis by synthesizing intentional mixtures that can undergo frontal ring-opening metathesis polymerization (FROMP; such mixtures are thus described as FROMPable) to produce materials with a pleasant odor and good thermomechanical properties post-cure. FROMP is a controllable and energy efficient reaction mechanism that has allowed for a novel polymer formation pathway. Dicyclopentadiene (DCPD), a byproduct of petroleum refining, has shown to be a commercially available FROMPable monomer that produces a sturdy post-cure material. However, it is malodorous and largely disliked. As such, we chose to carry Diels-Alder reactions between DCPD and vinyl acetate (VA) to produce 5-norbornen-2-yl acetate (NB-OAc) as our main product in the mixture – which is known to be FROMPable and possesses a pleasant, fruity odor – as well as its cyclic adducts with cyclopentadiene (CP-NB-OAc). We adopted continuous flow chemistry, a micro-reactor system that allows for precise reaction environment adjustment, as our reactor. With temperature, pressure, retention time, and feed composition readily adjustable, we were able to carry out solventless Diels-Alder reactions with minimal purification between DCPD and VA to produce FROMPable mixtures in large scale, i.e., 1L/day.

Products that reacted solventlessly from DCPD:VA=1.2:1 as the starting material, 90 bar pressure, 4- minute retention time, and 280°C – 345°C temperatures with a 5°C increment were collected and characterized. As reaction temperature increases, the resulting product mixture exhibited increased viscosity and fragrance. FROMP was observed in all samples upon mixing with Grubbs 2nd generation catalyst and frontal heating. A higher DCPD:VA ratio (1.5:1) led to blockage inside the flow reactor coil. ^{1}H NMR spectra and GC-MS results revealed the presence of DCPD, Tricyclopentadiene, Tetracyclopentadiene, NB-OAc, CP-NB-OAc adduct, and CP-CP-NB-OAc adduct, the latter two barely present in the preceding literature, as well as an equilibrium closer to products with increasing temperature. FROMP velocity and differential scanning calorimetry (DSC) results of post-cured material revealed a negative relationship between FROMP performance / thermomechanical properties of post- cured material and reaction temperature, and a positive relationship between the degree of polymerization and reaction temperature. On top of the fine product-function tunability of continuous flow chemistry, the possibility and the efficient nature of function-first synthesis are thus demonstrated.

In the future, the project can be extended by varying reaction parameters besides temperature. With the established methodology for continuous flow chemistry, reactions between DCPD and other similar compounds than VA can be studied systematically in order to achieve chemical diversity with desired functions.

Regression methods for constructing species distribution models for eagle use in the continental United States

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Species distribution models (SDMs) are a statistical approach that uses species abundance and environmental data to predict species' distribution across an area of interest. An SDM can take the form of a generalized linear model, generalized additive model, or kernel density estimation. Our research focuses on using existing SDM frameworks to model and analyze eagle distribution across the continental United States. We will use an SDM to better predict eagle minutes at wind facilities in the United States. Our SDM will allow for the extrapolation of existing data to predict the distribution of golden and bald eagles at any proposed wind facility site prior to its construction. These predictions can be used in partnership with US Fish and Wildlife Service to inform take permit decisions for wind farms. Eagle take permits are required for wind farms to operate due to fatal collisions of bald and golden eagles with wind turbines. Our research seeks to understand the relationship between eagles and wind farm locations while minimizing the time and funding resources associated with the data collection required. This work was completed as part of the NSF REU at Ursinus College, funding courtesy of Grant #1851948.

Confirming the Change in Mass Loss Rate of Zeta Pupis Over 19 Years

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The mass loss rate of zeta Pupis has increased around 40% in data from Cycle 1 (which contain an observation taken 19 years before Cycle 19 data) to Cycle 19 (which contains a dozen observations that spread over 1 year) by Chandra Space Telescope, as proposed by a former research project. We use a different method to access this change, by calculating Sigma* value which is related to the mass loss rate, and run a statistical analysis about how significant the change is.

We make improvements to our past absorption model and fit the Chandra data with the model to generate the Sigma* value. We plot the Sigma* from Cycle 19 vs. the time . By comparing the weighted average of Cycle 19 data with Cycle 1 data, and analyzing its statistical significance, we found that there is a significant increase around 30% from Cycle 1 to Cycle 19, and the data within Cycle 19 is fairly consistent with each other.

Effect of D2 Antagonist Raclopride on Feeding Behavior and Motivation in Mice Models

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Motivation to seek and consume specific foods is thought to change as a result of experience. Previous work from rodents and humans has suggested that prolonged consumption of palatable, highly caloric foods leads to reduced motivation to seek less palatable, low-calorie foods as well as reduced expression of dopamine D2 receptors (D2R) in the brain. Based on both observations, it has been suggested that reduced D2R activation *causes or underlies* reduced motivation for low-calorie foods. Indeed, systemic pharmacological blockade of D2Rs by raclopride and haloperidol has been observed to reduce appetitive motivation during a short assessment (30 minutes) of food motivation, but the effect of raclopride on longer measurements of food motivation has yet to be assessed. Thus, we used a 24-hour resetting closed-economy progressive ratio task to measure continuous performance variables related to chow intake and motivation before and after multiple daily injections of saline and raclopride in male and female mice. Although we expected the raclopride to reduce motivation to seek and consume chow across days, we saw no consistent effects when we looked at performance binned into 24-hour blocks. We have just begun additional analyses to look at smaller time bins, and it seems raclopride might have reduced chow intake during the light part of the animal's day (approximately 12 hours after injection). This finding is extremely encouraging as it suggests chow intake might have been differentially impacted during the night and day. We plan to conduct further analyses at the greater temporal resolution to better understand whether/how long the drug affected intake and motivation variables and/ or whether there was compensatory eating behavior at night to offset the decreased intake during the day.

Swept Away: Risk of dislodgement during barnacle cyprid surface exploration

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Many sessile marine organisms disperse via planktonic larvae, which must settle and adhere to surfaces to recruit onto new habitats. The fusiform cyprid larvae of barnacles explore surfaces by bumping, walking, and turning while leaving adhesive footprints. During metamorphosis, cyprids raise their bodies off the substratum into an upright position. Using dynamically-scaled models of the cyprid of *Tetraclita japonica*, we measured the forces and torques experienced by cyprids on surfaces exposed to ambient flows. The Reynolds numbers of the cyprids and models ranged from 123 to 1230, calculated using water speeds measured at the height of cyprids in fouling communities and on intertidal rocks (0.13 to 1.3 ms-1). Cyprids in different orientations (anterior, posterior, or broad-side towards flow) and tilt angles (0°, 48°, and 90°) were tested. Preliminary analysis showed that the drag pushing cyprids downstream was greatest when they were oriented broadside to the flow, and when they were oriented 90° to the substratum during metamorphosis. Depending on orientation and tilt angle, cyprids can be dislodged from surfaces by being spun around or pushed downstream by ambient flow, or by being peeled off the surface. Thus, resisting both torques and forces are important in adhering to surfaces. Our work showed that the risk of dislodgement for small planktonic organisms not only depends on ambient flow, but also on their orientations and behaviors.

Expression Patterns of Human Satellite DNA in Cancer Cells and Neural Stem Cell Differentiation

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Human satellite II (HSATII) is a type of human satellite DNA, which are tandem repeats that compose 8-10% of the genome. HSATII is dormant in normal somatic cells but highly expressed in some cancer cell lines. Studies have found that HSATII expression in osteosarcoma cells (U2OS) can form focal accumulations which recruit various DNA regulatory proteins that consequently disrupt genome stability. Why are HSATII sequences conserved in the genome if they are only expressed in cancer cells? Emerging studies of HSATII expression in early development explore this question.

Certain characteristics of HSATII expression led us to hypothesize that HSATII is expressed in the process of neural stem cell (NSC) differentiation from embryonic stem cells (hESC). We took a binary approach to test this hypothesis: We performed a differential gene expression analysis on RNA sequencing data collected from differentiated neural cells, and we conducted RNA fluorescence *in-situ* hybridization on differentiating NSCs. We found expressions of HSATII and HSATIII (another type of human satellite DNA) during the process of NSC differentiation using both approaches.

This is one of the first studies to detect human satellite DNA expression in early development and the process of differentiation. Our results showed that HSATII and HSATIII are expressed at low levels during NSC differentiation compared to cancer cells. This leads us to postulate

that HSATII expression in early development is low and regulated, but its expression becomes unregulated in cancer cells, thereby resulting in genome instability.

The Neural Correlates of Covert Attention

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The slope of the EEG power spectrum has been associated with a variety of sensory and cognitive processes, as well as demographic differences such as age and psychiatric conditions. However, until recently, it has often been disregarded in favor of the study of periodic brain activity, such as alpha and the other frequency bands. So, further research is required to understand its role in cognitive performance. In this analysis, we examined the changes in aperiodic slope and alpha power during a task of covert visual attention, and compared their predictive power in regards to task performance.

In order to improve our understanding of the extensive collection of existing neuroscience data, this analysis used data from a neurofeedback experiment conducted by Schneider et al (2020). In this study, participants were instructed to covertly attend to one side of a screen, and respond when a target appeared on either side of the screen. Many previous studies with this paradigm showed that alpha lateralization, the difference in alpha power between hemispheres, changes based on the direction of attention. So, in the original experiment, Schneider used alpha lateralization to provide real-time feedback to their participants.

Our analysis confirmed several of the original study's findings, including decreased alpha power in the hemisphere contralateral to the direction of attention. Differences in aperiodic slope between attention conditions were smaller, but in the same direction, as differences in alpha power. Additionally, linear mixed models showed that while both alpha and slope lateralization were significantly associated with reaction time, alpha had a stronger predictive effect. These results confirm previous findings that alpha power is a strong correlate of covert attention, and imply that aperiodic slope is likely a correlate as well.

Task design may influence results of behavioral task used to study depression

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Understanding the mechanism behind which depression influences perception is of growing interest within the field of psychology. To study this relationship, many studies utilize a behavioral task in which participants rate emotional facial expressions on a continuous scale from sad to happy. Prior studies have found that depressed individuals exhibit a negative bias, a tendency to view things as more negative then they truly are, when evaluating emotion compared to their non-depressed counterparts. Our current study aims to understand the cognitive mechanisms underlying these behavioral findings. In this study, task design was manipulated to gain insight on how context effects influence perception. Faces were presented to participants in either a blocked or mixed design. In the block design faces were presented grouped by their respective valence meaning a subject might see a series of happy faces followed by a series of sad faces. The mixed design presented happy and sad faces intermixed. Our first hypothesis was that faces presented in the block condition would be rated closer to neutral relative to faces in the mixed condition. Our second hypothesis was that this effect would vary as a function of valence. To test these hypotheses, two surveys administered through the online platform Prolific to n=150 participants. One survey implemented a between-subject design and the other a within-subject design allowing us to vary which participants received the blocked condition, mixed condition or both. Participants were required to rate a series of faces on a scale ranging from very sad to very happy. Ultimately it was found that task design does appear to have an effect on ratings as it was observed that in the block condition, there was a trend towards neutral. Happy faces were being rated sadder and sad faces were being rated happier. These results suggest that the design of the behavioral task does appear to have some degree of influence on the emotional ratings. Future directions include testing whether task design affects the relationship between negative bias and depression.

Convolutional Neural Network to Classify Book Covers

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Our research project sought to answer the question of whether or not a computer could “judge a book by its cover.” To achieve this, we developed a machine learning model that utilizes book cover image data to classify a book into one of 30 genres. On top of this central goal, we also wanted to understand the mathematics behind artificial intelligence and the applications behind various machine learning models. To do so, we spent the first few weeks researching, following tutorials, and applying these methods to real-world datasets. This simultaneously allowed us to hone our skills when it came to optimizing our own model.

After that, we developed a basic version of the model which took in an image and outputted a prediction. We used a Convolutional Neural Network, which is a type of network that works especially well for image classification problems. Initially, it did not work great, as we had yet to optimize the model. However, we saw significant improvements after incorporating and modifying our own pre-trained model. We verified this by running scripts to confirm the performance of the model. Another roadblock we encountered was our model performing well in training and built- in testing, but poorly in practice. We were able to resolve this by plotting the model’s performance in a graph known as a confusion matrix and then using the pattern we saw to fix the issue. Once we fixed the issue, the model worked as well in practice as it did in testing.

The model had about a 26% accuracy on the testing set, which is significantly higher than what a random guess would suggest (3%). This number jumps up to 46% when measuring if the correct answer was present in the top three most likely predictions. To make our research more accessible, we made a website that lets users upload their own image of any book cover of their choosing. It uses the model we created to give the top 5 most likely predictions in the form of a pie chart. The website is available at https://www.cs.swarthmore.edu/~adas3/judgethisbook/.

Effects of Adolescent Social Isolation on Neurobiological Responses to Opiates and Drugs of Abuse

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The substance use disorder epidemic has troubled the United States for decades. While trends have gradually worsened in recent years, a sharp increase in illicit drug use and opioid-related overdoses followed the onset of social isolation during the COVID-19 pandemic. A population that is of particular concern in regards to social isolation is adolescents seeing as how neuronal development during teenage years is substantially strengthened by social interactions. To understand how adolescent social isolation stress may alter neurobiological responses to opiates and drugs of abuse like heroin, we worked with collaborator Dr. Brianna George from Wake Forest School of Medicine. Dr. George placed rats in either group housed or socially isolated conditions. Then, rats from both groups were placed in heroin self-administration chambers and had their heroin-seeking behavior recorded. After establishing that socially isolated rats demonstrated more drug-seeking behavior than group housed counterparts, individuals then underwent investigator administered heroin of escalating doses via intraperitoneal injections. After 36 hours post-injection, the rats were humanely euthanized and brains were shipped to Swarthmore College, where we proceeded to dissect rat brain tissue. We dissected the nucleus accumbens, medial and rostral medial prefrontal cortex, orbitofrontal cortex, basolateral amygdala, hippocampus, and lateral hypothalamus - brain regions that are involved in reward and decision making circuitry. RNA isolations were performed to then conduct quantitative polymerase chain reaction (q-PCR). While q-PCR results indicate that the targeted genes are not significantly affected by treatment of heroin in conjunction with social isolation, there might be other ones that are. To analyze the complete set of genes within the dissected brain regions, we hope to perform RNA sequencing using core facilities at the University of Minnesota. We anticipate receiving results by early October.

AlgoArt: A Platform for Algorithmically Generated Artwork

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Computer science and art are two disciplines with incredible potential for overlap, yet hobbyists and professionals alike from both fields often struggle to explore this intersection. The AlgoArt project seeks to address this by bringing together artists and programmers to create algorithmically generated artwork through a user-friendly online platform. AlgoArt began in the summer of 2022 as an open-source framework for creating drawing algorithms. The algorithms procedurally draw basic shapes and use parameters for detailed customization. Based on these algorithms, the research team created the AlgoArt platform (algoart.org), which consisted of two parts: (1) a creator studio for real-time artwork generation and parameter customization and (2) a digital gallery for displaying and reviewing generated artworks. AlgoArt is designed to be user- friendly for artists who may be new to programming but complex enough for experienced programmers to explore in depth. During the summer of 2023, we redesigned the website and laid the groundwork for a server-side image generation API. The new version of the AlgoArt platform works

more intuitively, incorporates new features, and looks aesthetically better than the previous prototype. The API, when fully integrated, will allow verified users to schedule mass image generation on the server according to specified parameters. This work was completed using HTML, CSS, JavaScript, PHP, and MySQL. Work on this project will continue into the future to provide artists and programmers with a platform to explore the possibilities of computer-generated artwork.

Bounding the Size of Sets of Similar Permutations

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Motivated by anticode problems in coding theory and similar questions in information theory we analyze the implications of permutation similarity. We analyze permutation similarity using a metric where we subtract the length of the longest common subsequence between two permutations from the total length of the permutations. In particular, we set out to find the maximum number of elements that can be contained in a set of permutations on $[n]$ where every permutation is within similarity k of every other permutation in the set. We let $f_k(n)$ denote that maximal size.

We were able to prove $f_0 = 1$ and $f_n = f_{n-1} = n!$. We showed a general lower bound of $\frac{n!}{(n-k)!}$ by construction. We were also able to show that the upper bound for f_1 and f_2 is also $\frac{n!}{(n-k)!}$. The fact that this value is equal to the lower and upper bounds are equal in these special cases is promising. We were able to find a general upper bound of about $216^k \frac{n!}{(n-k)!}$ for any n and k. We conjecture that with continued work we can further reduce the leading term but have shown that we would require a broadly different strategy to reduce it below 2^k. We suspect that the actual upper bound is $\frac{n!}{(n-k)!}$ from the special cases we proved explicitly, our code written to evaluate small values, and by analogy to other problems in the field.

Exploring Website Resources Shared Within Online Health Communities (OHCs) In Response to Help-Seeking Posts by Women with Intimate Partner Violence (IPV) Experiences

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One in three women worldwide are abused by their intimate partners. Many women with intimate partner violence (IPV) experiences seek help anonymously in online health communities (OHCs) instead of through legal or police services. As OHC members often share websites to answer each other's questions, we investigated the categories of websites shared and how relevant they are to the type(s) of help requested by original posters (OPs). We extracted posts and comments from the r/domesticviolence subreddit on Reddit, including only help-seeking posts written by self-identified adult women with IPV experiences, with at least one website shared in the corresponding comments. Websites were annotated by topic and used to iteratively develop a codebook. Then, shared websites were categorized as "relevant" or "irrelevant" to the type(s) of help sought by OPs. Help-seeking posts were annotated for characteristics including post length, mentions of choking, and specific versus general questions. We used a chi- squared test to find that posts with specific questions received more relevant websites (p=0.023), while all other variables were found insignificant ($p>0.05$). A total of 170 website links were categorized into eight subjects, the top three being 1) General IPV Resources (34.7%); 2) Financial, Healthcare, Housing, and Food Support (10%); and 3) Safety Warnings (5.9%). This study provides insight into the informational needs of women with IPV experiences that are currently addressed by website-sharing, which could be utilized to create a digital tool that automatically suggests relevant website resources in OHCs.

Lens Modeling of a Gravitationally-Lensed Dusty Star-Forming Galaxy

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In recent decades, groundbreaking research unveiled a novel class of galaxies known as dusty star-forming galaxies (DSFGs), characterized by their exceptionally high rates of star formation. Yet despite their large star formation rates, these galaxies remained elusive in large optical wavelength surveys due to their dust-obscured nature. The dust within DSFGs absorbs light in the ultraviolet and optical regions and re-emits the energy in the far-infrared/submillimeter spectrum. In this study we present a potential lens model using carbon monoxide data from the NOrthern Extended Millimeter Array (NOEMA) for a strongly gravitationally-lensed DSFG first discovered in the Atacama Cosmology Telescope (ACT) 470 deg^2 equatorial field survey. We used the *lensmodel* (Keeton 2011) and *pixsrc* (Tagore & Keeton 2014) software to delense the image of the DSFG and obtain a pixelated reconstruction. The results presented here are preliminary as we need a complementary dataset to confirm the foreground mass in the system. Once completed, this lens model promises to shed invaluable light on the DSFG's physical properties, significantly advancing our understanding of the intricate processes governing galaxy formation and evolution.

Interactive Exercises for Dive into Systems

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This project sets out to create interactive exercises for the free online computer systems textbook, Dive into Systems (DIS). Originally a non-interactive text, DIS is now extended with a highly visualized and interactive exercise book that aims to enhance educational effectiveness by providing top-quality resources to students from all backgrounds nationwide.

The overall target of our project is to introduce various facets of interactivity. To achieve this goal, we use Runestone Academy, an open-source platform for building interactive textbooks, as our exercise book host. We are allowed to create various types of exercises with some pre-built functionalities. However, in order to satisfy the specific pedagogical needs of computer system topics, we further modified Runestone.

Compared to the vanilla Runestone release, our improved version can further support infinite randomly generated exercises based on crafted algorithms. We also extended our efforts to research question quality and content visualization, so that every generated question best aids understanding.

Pedagogically, we empirically discovered fundamental characteristics of interactive exercises that best support students' learning. We concluded that our question bank needs to cover as many circumstances and concept subtleties as possible and that we need consistent and color-coding instruction for students' learning experiences.

Modeling Effects of Sound Deprivation on Auditory Neurons

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Cochlear Implants (CI) are a relatively new medical implant that can give people who experience a certain type of deafness a parallel experience to hearing. Cochlear Implants bypass the inner ear's cochlea and electrically stimulate the first layer of auditory nerves directly. Those with bilateral CI's have been shown to have a less precise sound localization ability - this is due majorly to hardware limitations. As such, CI's are forced to approximate a sound's location into sparse, discrete spaces. Humans can detect ITDs as small as 10 microseconds, while humans with a CI can detect ITDs around 100 microseconds. The human auditory processing pathway has a section of neurons that are responsible for sound localization - these are called the MSO neurons. They are the first stage in the pathway that take input from both the left and the right ear and measures the Interaural Time Difference (ITD). It has been previously observed (in avian neurons that are equivalent to a human's MSO neuron) that as a neuron spends more time without a stimulus, the neuron undergoes physiological changes to adapt and become more sensitive to future potential stimuli. Our research question was to model how these physiological changes affect MSO neuron firing rates, as well as how that increased sensitivity affects the precision of sound localization.

A Developmental Exploration of Home-School Mismatch and its Implications for Latinx Family Closeness

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Higher education emphasizes independence and self-exploration, which can clash with the traditions of students who are the first in their families to attend an American four-year institution (i.e., first-generation college students). As students further develop their independence in higher education, they might find themselves in conflict with family expectations. The present study focuses on 24 Latinx, first-generation college (FGC) students from immigrant families, who participated in semi-structured interviews discussing their journey through higher education. We employed grounded theory and AI-driven tools to conduct thematic analysis. We identified four developmental changes: *Hard Interdependence*, *Hard Independence*, *Expressive Independence*, and *Expressive Interdependence*. Despite previous research that portrays FGC students as static, our findings suggest that FGC students experience dynamic changes while transitioning into institutions that emphasize independence. We introduce a developmental perspective for understanding how FGC students change and adapt, highlighting the role family plays in shaping their college experiences. Yet, academic institutions fail to integrate and recognize the value of family in the lives of students. Thus, this work illuminates the need to redesign interventions that move beyond traditional, education-centric strategies towards an approach that addresses the multifaceted needs of students, both inside and outside higher education.

Modification of anti-tetranor-PGDM antibody and development of Enzyme-Linked Immunosorbent Assay

Masaki Fujishiro

[Background and Purpose] We previously reported that urinary levels of tetranor-PGDM, the final metabolite of Prostaglandin D2, reflected the severity of food allergy symptoms. To apply our findings to clinical diagnosis of food allergies, we produced anti-tetranor-PGDM antibodies and developed an enzyme-linked immunosorbent assay (ELISA) using these antibodies. However, human urine contains numerous contaminants that influence the measurement of tetranor-PGDM levels, resulting in higher values than the actual concentrations. In this study, we aimed to construct an ELISA for more precise measurement of tetranor-PGDM concentrations in human urine by modifying the amino acids in existing antibodies to enhance specificity.

[Methods and Results] The 3D structure of anti-tetranor-PGDM antibody was predicted by means of homology modeling using sequence information of existing antibodies. We identified on the tertiary structure five hydrophobic patches, characterized by densely packed hydrophobic amino acids. Subsequently, we selected 17 amino acids with significant solvent-accessible surface areas for modification, replacing them with highly hydrophilic serine and aspartic acid residues. In practice, point mutant plasmids were synthesized through PCR and In-Fusion cloning, which were then transfected into HEK293T cells to produce mutant antibodies. Urine samples obtained from food allergy patients underwent protein removal and solid-phase extraction using Oasis PRiME HLB columns. PGDM concentrations were measured via competitive ELISA using the modified antibodies. As a result, we obtained six modified antibodies that more accurately approximated the values obtained with liquid chromatography with tandem mass spectrometry (LC-MS/MS). Furthermore, we observed further enhancement when multiple amino acids were mutated. Among them, one exhibited better agreement with the measurements by LC-MS/MS, with a trendline slope of 1.2 and an intercept of 4.2, as opposed to the parent antibody's values of 1.4 and 7.9, respectively. The correlation increased from 0.49 to 0.70.

[Conclusion] In this study, we modified anti-tetranor-PGDM antibodies based on conformational modeling and patch analysis, leading to the development of a competitive EIA method that can more accurately measure tetranor-PGDM concentrations in human urine.

Wnt Signaling Regulates Stem Cell Proliferation During Ciona Robusta Heart Growth

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Wnt signaling is a conserved pathway with numerous developmental roles including regulating heart formation and growth. Its contributions have not been fully characterized, so we investigated how Wnt signaling affected heart growth in *Ciona robusta* (a chordate of the tunicate phylum). In *Ciona* juveniles, heart growth is driven by a distinctive group of cardiac progenitors known as the undifferentiated line (UL). These progenitor cells are thought to divide and give rise to the different kinds of cell types found in the Ciona heart. Recent single-cell RNA sequencing studies indicate that Wnt receptors (Ciona orthologs to Frizzled4) and target genes (*Ciona* orthologs to Axin2 and LGR5) are expressed in the UL. To determine any contribution of Wnt signaling to UL division, a Wnt inhibitor (IWR-1-

endo) and vehicle (DMSO) were applied to the juveniles 7 days post fertilization (dpf) for 24 hours, respectively. For the pulse group, Ciona juveniles were then exposed to EdU (a stain to visualize cell division) for 30 minutes followed by rinsing and immediate fixation. For the chase group, after 30 minutes of Edu stain, Ciona juvenile animals were allowed to grow for a 36-hour chase followed by fixation. Then, all samples were stained with DAPI to label cell nuclei. The pulse and chase experiments showed a significant increase in EdU-labeled ULs without a significant increase in the total number of ULs. These results indicate that the Wnt signaling pathway suppresses cardiac progenitor proliferation, while a Wnt-independent mechanism maintains the UL length. This experiment has begun to outline the role of Wnt signaling in coordinating the dynamics of progenitor division for proper organ growth.

Effects of Temperature on Metal Recovery from Spent Lithium-Ion Batteries Using the Microbiome in Corn Silage

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Recovery of valuable metals from spent lithium batteries presents an important way to achieve a sustainable development and circular economy. Conventional metallurgical methods are costly and harmful for the environment, while the more sustainable bioleaching method is not time efficient. The objective of this study is to evaluate the effect of temperature (thermophilic and mesophilic) on the reductive bioleaching of cathode materials using corn silage fermentation. Acidogenic fermentation of corn silage without any inoculum was operated under thermophilic (55°C) and mesophilic (35°C) conditions. On day 16, black mass was added to the reactor to start the leaching process. Results showed that mesophilic temperatures (35°C) were more efficient for reductive bioleaching using corn silage than thermophilic temperatures (55°C), with Co and Ni leaching efficiency of 48% and 68% in mesophilic treatment after 19 days (day 16 to day 34), respectively, while only 22% and 27% in thermophilic treatment. Lactic acid and acetic acid were the main acid species during the entire process, reaching 3300 mg/L and 2736 mg/L in the mesophilic reactors, respectively, while the thermophilic reactor only reached around 1000 mg/L and 2364 mg/L after the black mass was added. The thermophilic reactor had higher levels of reducing sugars, especially after the addition of black mass to the reactors, but the rate of acidogenesis was slow compared to the mesophilic reactors. These results indicated that the acids and reducing sugars during reductive bioleaching of. This study demonstrated an efficient, low cost and green leaching system for critical metals recovery from spent lithium-ion batteries.

Characterizing Neuropathy Target Esterase in *Dugesia japonica*

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OP-induced delayed neuropathy (OPIDN) is a syndrome characterized by the distal degeneration of axons in central and peripheral nervous systems, caused by exposure to organophosphorus compounds (OPs), a class of chemicals commonly found in insecticides. Similar degeneration is observed in diseases such as Alzheimer's disease and Parkinson's disease. Neuropathy target esterase (NTE) is known to be the target protein of OPs for the initiation of OPIDN. Although OPs can inhibit NTE, only neuropathic OPs cause OPIDN.

Besides its role in OPIDN, NTE seems to play important roles in lipid metabolism and development. However, there is still a lot unknown about the protein, such as its exact functions and the etiology of OPIDN after the protein is inhibited.

The goal of my project is to characterize NTE in *Dugesia japonica*, a species of asexual freshwater planarians, whose regeneration ability and amenability for rapid screening make them a good model organism for toxicology studies. By comparing the gene sequences encoded for human NTE and planarian NTE, we found that the protein is well conserved, justifying the use of *D. japonica* to study NTE. First, to quantitatively measure NTE activity in *D. japonica*, we are adapting a biochemical assay which involves a colorimetric reaction to indicate hydrolysis of a known substrate, phenol valerate. NTE activity is experimentally defined as phenol valerate hydrolase activity that is inhibited by the neuropathic OP mipafox but not by the non-neuropathic OP paraoxon. Because there are published protocols for measuring NTE activity in other organisms, i.e. adult hen brains, the first step is running a positive control to show that we can get reproducible results and that the adapted protocol is working. I encountered many problems and could not detect significant NTE activity in adult hen brains, which could be caused by a lot of variables, such as the freshness of the hen brain supply, purity of chemicals, sample inhibition time. Once the positive control confirms the reliability of our protocol, I will measure NTE activity in *D. japonica*. While I continue to optimize the biochemical assay, in parallel, I am performing NTE gene knockdown in planarians through RNA interference. I will use behavioral screening to investigate if there are any behavioral defects in worms with decreased NTE expression compared to controls, to get insights on the physiological functions of NTE. Furthermore, I am using techniques of whole mount in situ hybridization and antibody staining to visualize where the gene and the protein, respectively, are expressed in *D. japonica*. This project will contribute to characterizing planarians as an invertebrate model system in toxicology studies and further the understanding of NTE and causes of neurological diseases.

Symphony of Motion: The Story of How Robotic Manipulators Moves

Justin Gonzalez

This project is an in-depth examination of a six-degree-of-freedom (6-DOF) robotic arm manipulator with a focus on forward and inverse kinematics, kinematic differentiation, and algorithmic control for trajectory planning. The robot specifically used was the Jaco2 made by the company Kinova. The research addresses communication with the robot through an Application Programming Interface (API), allowing the implementation of algorithms and a more user-friendly interface. In addition, this project provided the fundamental algorithms and code for the Jaco2 robotic arm in the Brain in Silicon lab to be used in future research.

We start by establishing a detailed understanding of the forward and inverse kinematics of the 6-DOF robotic arm manipulator. By developing mathematical models and algorithms, the study enables precise control of the end-effector position, and later checks the accuracy with the software development kit (SDK).

Incorporating kinematic differentiation into the analysis allows for real-time angular velocity and enables dynamic control and coordination of the robotic arm. This dynamics plays an important role in achieving smooth movements and avoiding dead zones. Dead zones are spaces within the robot’s workspace that the robot cannot pass through as it would run into a physical obstacle or singularities.

In conclusion, this study offers an extensive investigation of the 6-DOF robotic arm manipulator, covering forward and inverse kinematics, kinematic differentiation, API integration, trajectory planning, and dead zone avoidance. The research outcomes have significant implications for the field of robotics, offering a framework for precise, efficient, and safe robotic arm manipulation in various industrial and research applications.

Investigating the Role of the Lateral Habenula in Itch and Scratch Behavior

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Itch is an uncomfortable sensation that elicits the desire to scratch. Despite the aversive quality of itch, scratching itself evokes a pleasurable experience mediated by the midbrain reward center. However, the neural mechanisms controlling the initiation and termination of scratching behavior are poorly understood. The lateral habenula (LHb) is pivotal in negatively regulating motivated behavior due to its robust ability to modulate aminergic neurons. Hence, we analyzed the lateral habenula and its downstream projection targets to better understand its role in terminating the itch-scratch cycle. I used a combination of mouse genetics and trans-synaptic viruses to allow visualization of neurons stimulated by a pruritogen and their postsynaptic targets. Both contralateral and ipsilateral itch-activated LHb neurons projected to the rostromedial tegmental nucleus (RMTg) and dorsal raphe nucleus (DRN). In addition, we analyzed the function of LHb neurons in chronic itch by chemogenetically inhibiting LHb neurons using an inhibitory DREADD. Mice were repeatedly exposed to squaric acid dibutyl ester (SADBE) leading to the development of contact dermatitis, and spontaneous scratching was recorded pre- and post-injection of the DREADD ligand. Mice exhibited increased scratching behavior following the administration of the DREADD ligand contrary to an acute itch model which displayed a reduction in scratching behavior. Our study reveals how the lateral habenula impacts the itch-scratch cycle and may provide direction for novel antipruritic therapies.

On the reactivity of $(\mathrm{TriNOx}^{3-})\mathrm{M}$ with OH, NH, and CH bonds.

Vivian Guo

Metal-ligand cooperative chemistry is an exciting area of research that has given rise to new methods for the activation of bonds. We recently reported the preparation of the aluminum-nitroxide complex $(\mathrm{TriNOx}^{3-})\mathrm{Al}$ and the gallium-nitroxide complex $(\mathrm{TriNOx}^{3-})\mathrm{Ga}$ and demonstrated its MLC chemistry. In this contribution we will discuss our continuing work in the reactivity of the $(\mathrm{TriNOx}^{3-})\mathrm{Al}$ and the $(\mathrm{TriNOx}^{3-})\mathrm{Ga}$ complexes with O-H, N-H, and C-H bonds.

Effects of OSU6162 on Limited Access Binge Eating

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Binge Eating Disorder (BED) is the most prevalent eating disorder, contributing to obesity, metabolic syndrome, feelings of depression and shame, and other negative effects. It is characterized by loss of control binge eating, or consuming a large amount of calories in a short period of time, and it disproportionately affects women. With only one FDA-approved

drug for BED, further research is needed to understand its associated neural circuits and explore their modulation for the improvement of patient outcomes. Thus, we sought to implement a mouse model of BED and test a promising pharmacological intervention. We chose the limited access model described in Wu et al. (2021) because the model had been used as a proof-of-concept for a successful human case study of deep brain stimulation for the treatment of BED. According to the published model, providing male mice with daily limited access (one hour) to high-fat diet (HFD) will cause them to develop a stable pattern of binge eating within 10 days: mice will consume greater than 50% of their total daily calories from HFD with less than 15% variation in HFD intake across days. We implemented this model in our lab by providing groups of male *and female* mice with access to a HFD for only one hour each day across 13 days. As expected, the male and female mice developed a pattern of binge eating, but it did not stabilize within the time period tested. Despite this, we still tested whether OSU6162, a novel drug that had previously been shown to reduce binge eating in a distinct rat model, would reduce binge eating in our model. We found that intraperitoneal injection of OSU6162 had no significant effect on binge consumption. This negative result may suggest that our binge model could be improved, or that the drug may not be as potent as originally thought.

Exploration of parameters for carbon nanotube separations via automated fluorescence titration

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Single-wall carbon nanotubes (SWCNTs) have a variety of useful optical, electronic, thermal, and mechanical qualities that would be ideally harnessed for various applications, including biotherapeutics, sensors, and energy storage. However, synthetic methods do not produce single SWCNT species but rather mixtures of various species which limit their utility for some of their potential uses. Therefore, the efficient and reproducible separation and refinement of specific species is an intensely sought after objective. One such separation system is aqueous two-polymer phase extraction (ATPE) which utilizes the difference in solvation energies in each of the two polymer phases to distribute a specific SWCNT species into a specific polymer phase. Interestingly, one can track these phase transitions using fluorescence spectroscopy. Previous NIST research has shown that the presence of various third components can shift these extractions to more favorable conditions. Utilizing a novel automated fluorescence titration technique, the exploration of this massive phase space becomes vastly more attainable. This project focuses on the addition of various salts and third surfactants to attempt to shift ATPE to more industrially favorable conditions.

Regional Oceanic Modeling of Ocean Current Energy Potential

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Ocean currents are a potential source of renewable energy, especially in locations like the Florida Straits, where the strong and consistent Gulf Stream contains vast quantities of energy. Therefore, this is a prime location for deployment of ocean current turbines (OCTs), a new technology that can be used to harvest ocean current energy. For OCTs to be used most effectively, a strong understanding and accurate characterization of the target currents are needed. For example, ocean currents often produce powerful eddies, which are circular currents that can lead to changes in current velocity and direction, two critical factors for energy potential. For this project, a numerical model based on the highly advanced Regional Ocean Modeling System (ROMS) is used to simulate ocean circulation including currents, tides, and mixing in the Florida Straits. The objectives are to understand and characterize ocean currents and estimate the current energy density in the Florida Straits, gaining knowledge which will be useful for assisting in selecting the best location for placement of OCTs.

Three numerical simulations were performed: the first did not include tidal forcing; the second did include tidal forcing; and the third was identical to the second but with increased background viscosity. As both tides and viscosity affect the model's simulation of currents and eddies, this leads to changes in predicted energy density. Results from the different models were compared to each other as well as data from ADCP (Acoustic Doppler Current Profiler) buoys, focusing on the current speed and power density in the Florida Straits. Model power density overall is higher than derived from the *in situ* observations. Among the three versions, the second simulation most accurately predicted the energy at the mooring locations. In addition to revealing the usefulness of the tidal forcing, this also suggests that lowering the viscosity could lead to an even more accurate power estimate. As ROMS continues to develop, it will remain extremely valuable to potential ocean current energy projects.

Biophysical characterization of DNA sequences with the potential to form five-tetrad G-quadruplexes

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G-quadruplexes (GQs) are noncanonical DNA secondary structures composed of stacks of guanine- tetrads. They are found often in oncogene promoters and have therapeutic potential as a drug target. Although many three- and four-tetrad GQs have been well characterized, sequences with the potential to form more than four tetrads have not. Here, we investigate sequences with four stretches of five guanines connected by TT, TTT, TTA, and TTTT loops. Biophysical characterization of these sequences indicates that they all fold into G-quadruplexes with all adopting predominantly an antiparallel conformation—only LM11 and LM16 also had strong hybrid contributions. A native-PAGE gel revealed that variants LM1-11 are relatively homogeneous, and UV-vis melting experiments show that all the LM sequences are folded and stable under physiological temperatures. To investigate whether LM sequences contain five G-tetrads, we deleted a guanine at the 3' end for three sequences, after which we observed a small drop in melting temperature. The results are not sufficient to firmly establish the number of G-tetrads. If we do eventually discover that five-tetrad GQs exist, then sequences with the potential to form them can be better therapeutic targets than their three-tetrad counterparts, as the relative rarity of five-tetrad GQs would provide more selectivity to the drugs that target them.

Intron Retention and Arabidopsis thaliana Thermotolerance

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Intron retention (IR) is a phenomenon occurring during the transcription process. After DNA is transcribed into pre-mRNA, introns are spliced out. The remaining exons form the final mRNA product. However, if IR occurs, some introns will be retained in the final mRNA, prohibiting translation of normal proteins. The presence of IR reduces functional expressions of genes and can result in overestimation of gene expressions.

IR plays an important role in *Arabidopsis thaliana* thermotolerance. *A. thaliana* seedlings, after acclimation at 37°C, can survive a subsequent temperature of 45°C. This is referred to as acquired thermotolerance. However, when the acclimation temperature is increased to 40°C, seedlings fail to acquire thermotolerance. Experiments show that heat shock protein 17.6 (HSP17.6) has lower and slower expression pattern at 40°C compared to 37°C. This trend is common among heat-induced genes and could be caused by IR.

In our study, we compared two programs, IRFinder-S and JUM, used for detecting IR. RNA-seq data from *A. thaliana*, growing under room temperature, 37°C, 38°C, 39°C, and 40°C, were analyzed. Both programs identified genes that showed significantly higher intron levels at 40°C than that at 37°C. These genes are enriched for functions related to heat shock response. However, there are hundreds of genes that are identified by only one program because IRFinder and JUM call IR based on different algorithms. Analysis demonstrated that IRFinder-S generated more biologically relevant better calls than JUM.

We used the IR ratio generated by IRFinder-S to adjust the exon count level in order to obtain the functional expression level of each gene. Both the non-adjusted and adjusted gene expression levels at 37°C and 40°C were compared through DESeq2. New groups of genes with differential expression levels between these two temperatures, were identified after the adjustment The reduction of expression level of group of genes due to IR may explain the failure to acquire thermotolerance at 40°C.

A Screen for Soil Secondary Metabolites that Promote Phosphorus Bioavailability

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Conventional agriculture is highly dependent on phosphate fertilizers, which can lead to eutrophication and biodiversity loss. Phosphorus can be especially challenging to manage as it often adsorbs to iron in the soil, rendering it unavailable to plants. Certain rhizobacteria offer potential solutions as they produce redox-active metabolites (RAMs) that are capable of reducing iron and solubilizing phosphorus in the process. Lab-based studies have shown that in the model bacterium *Pseudomonas*, RAM production is regulated by phosphorus bioavailability. However, the extent to which phosphorus- regulated RAMs are produced by bacteria in agricultural fields remains unknown. To determine how common this was, we developed a screen that uses a colorimetric assay for iron reduction (the ferrozine assay) as a proxy for RAM production and applied it to bacterial strains isolated from the rhizosphere of tomato plants. Screens were conducted on bacteria grown under high and low phosphorus. Isolates that reduced iron were further identified through 16S sequencing. Several isolates from our samples reduced iron under low phosphorus including various natural *Pseudomonas* isolates. These results offer promising avenues for developing biofertilizers using RAM producing bacteria and future work would enhance our understanding of secondary metabolites' role in macro-nutrient cycling.

Non-destructive Performance Comparison of Li-Ion 2032 Coin Cells for Non-ambient Temperature Applications

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Coin cell batteries have long found diverse applications in small consumer products. Rechargeable lithium-based coin cells are now commercially available offering an eco-friendly alternative, but their use is not as widespread. Performance of these batteries under non-ambient temperature conditions is important for many applications, but note widely investigated. We report on a non-destructive, temperature-dependent performance comparison of three different commercially available, rechargeable 2032 coin cell models. Batteries were cycled galvanostatically over at least 100 cycles at three different temperatures: 60°C, 24°C, and 0°C. In-situ data collection was performed using temperature-controlled test chambers. We observed the highest initial capacity in higher temperature cycling but a faster capacity fade. During room temperature cycling we also observe an increase in initial capacity over the first ~40 cycles that may be consistent with a similar phenomenon observed in Li-ion pouch cells with graphite anodes. Differential capacity analysis was performed to determine the mechanism of cell deterioration and investigate the rise in capacity. Detailed results from temperature-dependent electrochemical cycling, along with X-ray diffraction and scanning electron microscopy analysis, will be presented to explain differences in cell performance across battery models and temperatures.

Designs of Vibration and Pressure Sensors Using Interferometry

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The application of interferometry with lasers and optical fibers allows accurate measurements of sensitive changes. We built a vibration sensor using a design of Michelson interferometer which was made up of an adjustable arm and a fixed arm, two sets of cube corners, a polarized beam-splitter, and a detector. A positive relationship was found between the change in effective path length difference and a large-scale change in the intensity of the two-beam interference fringe pattern after proper alignment. We also built a Mach-Zehnder interferometer with two plane mirrors, a beam splitter and a micron viewer with a monitor to observe the dynamics of circular fringe patterns. Comparisons and analysis of the two vibration sensors were made.

On top of the Michelson interferometer, we assembled a gas compensator cell which consisted of sealed gas with a pressure bulb, and attached it to one arm to make a pressure sensor. The pressure change in the bulb alters the refractive index of the air and hence optical path length difference. An oscillating interference signal with increasing periods

was observed when the pressure decreased non-uniformly with a gas leakage. Further, we modeled the physical behavior of a four-core fiber by COMSOL to improve the sensibilities and other sensing possibilities like bending and twisting.

A Partial Resolution of Hedden's Conjecture on Satellite Homomorphisms

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Our research investigates the properties of the self-maps induced by pattern knots in solid tori on the smooth knot concordance group. We began by testing two-component links, one by one, to see which of them, if any, described patterns which induce homomorphisms on the knot concordance group. The initial goal of our research was to add small pieces of evidence to support Matthew Hedden's conjecture that the only patterns which induce homomorphism are those which induce the zero map, the identity map, or reversal. However, our goal changed somewhat as we started to recognize patterns in our findings, and we were eventually able to prove a stronger result, which resolves Hedden's conjecture for patterns of certain winding numbers.

We prove that if the winding number of a pattern is even but not divisible by 8, then the corresponding map is not a homomorphism, thus partially establishing Hedden's conjecture. This is the first result to obstruct all patterns of a given winding number from inducing homomorphisms.

Coupled electrochemical characterization of silver ions and silver nanoparticles released from nanoparticle-embedded textiles

Casey Jordan

Recently, there has been a notable increase in the popularity of engineered nanomaterials (ENMs) in the commercial and medical sectors. As the significance of ENMs becomes more evident, it is crucial to have easily accessible methods for measuring and analyzing the properties of nanoparticles, such as transformative mechanisms, biocompatibility, and toxicity. A deeper understanding of these properties will facilitate better-informed decisions regarding the safety and environmental impact of materials infused with ENMs. Nevertheless, modern analysis techniques tend to be costly and require extensive sample preparation. Consequently, we have developed an alternative, cost-effective method for analyzing silver nanoparticles (AgNPs) utilizing the electrochemical techniques of particle-impact voltammetry (PIV) and linear sweep stripping voltammetry (LSSV). These techniques allow us to simultaneously determine the concentration of both AgNPs and their dissociated ions in solution. The high resolution and rapidity of these methods enable kinetic experimentation and quantification of the relationship between ion release and AgNP concentration over time. This presentation will include data on the integration of these techniques, their accuracy and efficiency, as well as insights into the kinetics of AgNP and silver ion release.

Prostaglandin D_2 and J_2 Promote Cell Proliferation in Sebocytes (SEB-1)

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Androgenetic alopecia is a common form of hair loss that is linked to high levels of testosterone and is observed in both men and women. Despite its widespread effect, there is still much unknown about the hair loss mechanism in this type of alopecia. Previous studies have shown that prostaglandin D_2 is elevated in the scalp of patients with androgenetic alopecia and can also cause transgenic mice to develop alopecia. These mice have been reported to have sebaceous gland hyperplasia, identified by their unusually large sebocytes. Since sebocytes play a large role in regulating androgen homeostasis, it is impossible to ignore their role in hair loss. In this study, we investigated the effects of prostaglandin (PG) D_2, E_2, F_2, and J_2 on SEB-1, a sebocyte cell line. We show that out of the four, prostaglandin D_2 and J_2 promoted sebocyte proliferation, while prostaglandin E_2 and F_2 do not. These results suggest that signaling pathways involving PGD_2 and PGJ_2 may be a target for drug developers seeking treatment methods for androgenetic alopecia.

Formation of a left-handed G-quadruplex in KRAS proto-oncogene and interactions with ligand, NMM

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The G-Quadruplex (GQ) is a non-canonical DNA structure that is formed by pi-pi stacked guanine tetrads. Guanine residues act as hydrogen bond donors and acceptors via Hoogsteen base pairing to arrange into these tetrads. GQ motifs have been identified in promotor ribosomal and telomeric DNA regions as well as at the oncogene promoters, making GQ a valuable therapeutic target. GQs can adopt left and right-handed helical conformations, however, only a small number of left-handed GQs (LHG4) have been studied. We used a 12-nucleotide sequence: GGTGGTGGTGTG. This minimal motif is found as a transcript variant in the KRAS proto-oncogene on chromosome 11 and folds into an LHG4. The KRAS gene is involved in the RAS/MAPK signaling pathway which is essential for cell differentiation and proliferation. We have designed 8 variants of KRAS by adding either one or two nucleotides to each side of the 12-nucleotide KRAS sequence as it appeared in the original KRAS sequence. These variants were characterized with biophysical techniques like thermal difference spectra (TDS), circular dichroism (CD), UV-vis melt, and poly acrylamide gel electrophoresis (PAGE) to determine their folding and stability. Of the 8 variants, only one was a LHG4 while 4 variants were right-handed GQs and 3 no longer adopted GQ topology. UV-vis melt showed multiple transition states in the melting curves of all right and left-handed variants. N-methyl mesoporphyrin IX (NMM) is a porphyrin that selectively binds to GQs. LHG4s went from having multiple transition states to displaying only a single transition state. Furthermore, the addition of NMM induced the shift of KRAS and a left-handed variant from a left-handed to right-handed helicity. We succeeded in crystallizing a right-handed variant of KRAS. Currently we are attempting to solve the phase problem using molecular replacement. At the beginning of our work, we hypothesized that more than one KRAS variant would display left-handedness, however, this has not been the case suggesting that short LHG4 sequences are easily disrupted or unfavorable with the addition of nucleotide

overhangs. Our work with KRAS and its variants will help characterize the behaviors and design of LHG4s in different contexts including the addition of NMM. This may aid in the design of drugs targeting LHG4s in oncogene promoter regions.

Computed Tomography Reconstructions from Sparse Data with Deep Generative Models

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Computed Tomography (CT) is a pivotal medical imaging modality, providing cross-sectional views of the body using a rotating X-ray apparatus. While CT is invaluable for diagnosing conditions like COVID-19 and brain cancer, obtaining high-quality CT reconstructions necessitates dense projections, inadvertently increasing the X-ray dose and the potential risk to the patient.

Fortunately, deep neural networks offer a promising avenue, transforming sparse 2D projections into detailed 3D reconstructions when trained on analogous datasets. However, a prevailing challenge is that current deep learning methods require high- quality ground truth as input, which excludes fragile samples from the training dataset.

To address this dilemma, we have developed a self-supervised, probabilistic deep learning method: the Physics-Informed Variational Autoencoder. Our approach innovatively leverages structural similarities within the same dataset to fill in the gaps of sparse projection measurements, generating a dense reconstruction. The model has been rigorously trained on lung CT images from both COVID-19 and non-COVID-19 patients, as well as brain CT scans from patients with various types of hemorrhages, in both 2D and 3D modalities. We are in the process of validating our model's performance through integration with pre-existing classifiers to assess the accuracy and clinical relevance of our reconstructions.

Measuring the ecosystem services provided by farmers market vendors: a two-year study

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The Earth is warming at an alarming rate, resulting in heightened instances of drought, species extinction, and food scarcity. This worrisome shift coincides with an unprecedented rate of human-driven transformations to natural ecosystems, eclipsing all comparable periods in human history. Ecosystems provide important benefits to humans—collectively referred to as ecosystem services (ES)—such as biodiversity and improved soil, water, and air quality. Yet, the degradation of ecosystems by humans has led to a depletion of ES, resulting in ecological dead zones, poorer water quality, and changes in regional climates. Conventional agriculture, characterized by monocropping, large-scale farms, and extensive use of synthetic chemicals, is a major contributor to both global warming and ES depletion. In contrast, farming methods such as regenerative and organic agriculture, show potential to mitigate climate change and ES depletion. Due to the smaller size of their farms, farmers practicing these methods commonly sell their products at farmers markets (FMs). Nevertheless, little is known about the collective ecological and environmental impact of farmers selling at FMs.

The present study investigated the ES provided by vendors selling at a Wisconsin FM. The ES of farms were evaluated over two years using a self-reported survey which quantifies the ecological and environmental impacts of farmers in six different categories: soil health, livestock, farm infrastructure and machinery, hauling to markets, biodiversity, and alternative power. In total, 36 individual farmers filled out the survey at least once, and 20 farmers filled it out both years. Typically, farmers did not use synthetic inputs like fertilizer or herbicide. In addition, farmers fostered biodiversity in several ways, such as enrolling in conservation programs, creating habitats for endangered species, using hedgerows, and using riparian buffers. Farmers enhanced carbon sequestration by following practices including reduced-till or no-till, intercropping, and cover cropping. Finally, the tool unexpectedly highlighted land access disparities among Hmong and non- Hmong vendors. These findings underscore the importance of farmers markets in sustainable food systems.

Crystal structure analysis of the non-canonical G-rich DNA TET25 in complex with PyDH2 as a potential anticancer therapeutic

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Guanine quadruplexes (GQs) are non-canonical secondary DNA structures comprised of stabilized stacks of guanine tetrads (G-tetrad). GQs are involved in various biological processes and have been implicated in human diseases, notably cancer. Small molecule ligands can change the folding and stability of GQs. The ability to control the structure of GQs can be used to develop therapeutic treatments. Here, we analyze the crystal structure of telomeric DNA from *Tetrahymena thermophila* (TET25) in complex with the highly selective GQ ligand PyDH2. Structural and spectroscopic data indicate that TET25 alone adopts a mixture of three GQ conformations: parallel, antiparallel, and hybrid. The major conformation is a hybrid four G-tetrad GQ. In the presence of PyDH2, TET25 instead adopts an antiparallel GQ conformation. Three TET25-PyDH2 antiparallel structures were crystallized and successfully solved using molecular replacement. The three structures are similar and reveal PyDH2 intercalates between the second and third G- tetrads of the antiparallel conformation. This intercalation is unique and has only been observed for the second time. Typically, ligands interact with GQs via end-stacking with the terminal G-tetrad. Compared to other antiparallel GQ structures, the TET25-PyDH2 structure has high out-of-plane deviation, resulting in a slightly more twisted structure. This study has increased our understanding of how small molecule ligands interact and affect the structure of GQ, allowing for the design of more effective GQ binders.

Evaluating CityTeam Renew with Quality of Life (QOL) Metrics

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CityTeam is a faith-based non-profit organization focusing on alleviating homelessness, poverty, addiction, and hunger. The focus of this research is on the Renew Program, run out of the Chester, PA location of CityTeam. The Renew Program is a one-year voluntary faith-based residential restorative care program for men overcoming addiction. Currently, the only way to measure success in Renew is monitoring the graduation rate of participants. This

measuring metric is limiting and does not capture the complexity of the addiction recovery process and benefits CityTeam Renew provides to participants even without graduating. In this study we aim to use quality of life (QOL) as a metric of success to evaluate the efficacy of Renew as a restorative care program. The WHOQOL-BREF survey was used to quantify participants' subjective experience in four life domains: physical, psychological, social, and environmental. The impetus for this research is to locate which aspect of Renew improves QOL, the program's pain points, and capture nuances in participants' satisfaction in different time periods in Renew. There are some conclusions that we draw from our study,

1. Environmental domain scores are highest on average, followed by the Physical Domain, Psychological Domain, and then the Social Domain. This indicate that participants are generally satisfied with the safe, drug-free, and healthy environment that CityTeam provide, but have frustrations with the social domain. There is also a high correlation among the domains, a comprehensive solution addressing social needs and other domains is advised for overall QOL increase.
2. Overall every individual's QOL has a non-linear relationship with survey number, suggesting a non-linear score trend over time in CityTeam
3. Almost all question item scores rise from survey number 1 to 2 and then drop from survey 2 to 3, indicating a slump in satisfaction.
    a. Two items have particularly low scores (money and sex).
    b. All domains of quality of life either generally improve or has minimal changes over time, there are no negative trends.
4. Relationship between interview keywords and domain scores remains inconclusive. However two initial conclusions can be drawn.
    a. Access to medical attention, transportation to services, and establishing a routine are factors important to a positive physical health experience.
    b. The high overlap between the Environmental Domain and other domains suggests that: solutions focusing on CityTeam's environmental strength can have positive effects on non-environmental QOL domains.

An Optimization Approach to EEG Feature Extraction for the Prediction of Neurological Outcome

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Under the supervision of Professor Moser, our objective was to contribute to the 2023 PhysioNet Challenge, aimed at developing a machine learning model to effectively predict neurological outcomes in comatose patients following cardiac arrest. The data for the challenge was collected from seven various hospitals, which included a precise recording of 19-channel EEG data every hour for the initial 72 hours after admitting the subjects. The goal was to achieve the highest true positive prediction rate while maintaining a false positive rate under 5%. A positive prediction implies that the patient is likely to have a poor recovery of neurological function and recovery, while a negative prediction suggests a more optimistic outcome. We utilized Matlab, a powerful high-level language, to construct the majority of our algorithms for feature selection and model construction, focusing on adaptability and accuracy.

Incorporating an AdaBoost model proved central to our methodology, wherein we leveraged this progressive ensemble method renowned for efficiently managing intricate classification tasks. The essence of the AdaBoost model lies in incrementally fitting weak learners to different versions of the data repeatedly, gradually increasing emphasis on inaccurately predicted data points. This process facilitates heightened accuracy with each iteration whilst reducing susceptibility to overfitting and easing parameter tuning complexities.

Safeguarding against overestimation of our algorithm's predicting ability necessitated a k-fold cross-validation strategy. This method partitions the original sample into 'k' subsets or 'folds'. One fold is retained as validation data for testing the model while the remaining 'k-1' folds contribute to a training set. This procedure repeats 'k' times, each time with a different fold as validation data. Cross-validation decreases bias stemming from random sampling variability and aids in robust generalization.

Translating the challenge's strict false positive threshold into our model demanded incorporating a cost matrix that heavily penalized false positives and negatives, thereby mitigating potential misclassifications. Additionally, Principal Component Analysis (PCA), a widely used technique for dimensionality reduction, was investigated as a means of reducing model overfitting. PCA transforms a large set of possibly correlated variables into a smaller set of uncorrelated variables called principal components, thereby condensing crucial information into fewer variables and easing data processing without significant loss of information. Furthermore, we found that particularly successful features came from manipulating time-domain EEG signals Fourier-transformed into frequency-domain representations. The power spectral density (PSD), a characterization of a signal's power along its frequency range, was one attribute we discovered to effectively differentiate between patients who were positively and negatively classified, by distinguishing regions of lower levels of brain activity.

We further utilized the Matlab Classification Learner toolkit to delve deeper into feature selection and refinement. Exploring various subsets within Matlab honed our understanding of feature impacts on prediction accuracy.

As we prepare for an upcoming conference, our findings, methodologies, and the journey towards the effective application of machine learning algorithms in predicting neurological outcomes will be encapsulated in a comprehensive poster presentation. This research underscores the potential of machine learning methodologies in influencing clinical decision-making and improving patient outcomes post-cardiac arrest.

Don't know: Middle-schoolers' stuckness, executive functions, and collaboration during math problem-solving in a group

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We are exploring the moments when small groups of students working together to solve open-ended mathematics problems online get stuck; our questions center on the frequency with which student groups get stuck, and its relation to whether they work to get unstuck (e.g., Did they work to resolve the questions that surfaced? Did they just give up?). We studied seven, four-five person groups of seventh grade students (15 m, 13 f; 70% Latinx) working on the same problem. We explored not only the relative frequency of group's stuckness, but also how they engaged both (a) behaviorally, their stage of collaborative problem solving (CPS; participation, cooperation, and collaboration), and (b) cognitively, their use of executive functions in practice (EFP; working memory, cognitive flexibility, and inhibitory control). Preliminary findings suggest that there is a relation among stuckness, CPS and EFP. Specifically, we find a positive association between higher frequency of stuckness and greater levels of collaboration. By focusing on mathematics in an online collaborative context, and being able to replay the students' work in the dynamic math space which provides a continuous account of their engagement, our findings contribute to and extend the existing literature on impasse, productive failure, and sensemaking. It also appears that our findings may make a contribution to practice by supporting educators to understand how they might support their students to view stuckness as a learning opportunity, and persevere to work through it.

Applied Philology and Indigenous Language Revitalization

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Out of more than 7,000 languages spoken on Earth, about half are considered endangered. This is the case for many Indigenous languages of North America. There are, however, efforts throughout Indigenous communities on this continent to revitalize the use of these languages. One of these efforts has been hosted by Swarthmore College for the past five summers. As part of this project, Tri-Co students aided an anonymous Indigenous linguist in his decades-long effort to create resources for his community's language. While previous language revitalization efforts, for this language and others, have focused largely on grammar lessons, the focus of this summer's work was classic Indigenous literature. The project now has a new direction, centering around texts, and learning that is immediately applicable to culturally relevant narratives.

Taking this new direction meant that our work mainly consisted of bringing stories in the language back to the community through a community-facing website. These stories, originally transmitted orally, were recorded and held under copyright by non-Indigenous linguists. Adding them to the website makes them available to their original community, and out of colonial hands. The stories are now available at various language skill levels, from beginner vocabulary and grammar breakdowns to full texts to read. In addition, we expanded the existing grammar lessons to contain more examples from stories, with the aim of creating links between the language lessons and central elements of the culture. Going forward, we want to be of use to Indigenous linguists in reclaiming pieces of language that have been taken from their community, and continue to shape language lessons around meaningful narratives, leading toward a socially-conscious linguistics.

Using Alpha Absolute and Alpha Relative as Biomarkers for Depression and Anxiety

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Mental disorders, namely depression and anxiety, are highly debilitating and detrimental to the quality of life of many. Neurological biomarkers have the potential to improve the accuracy and efficiency of diagnosis, help monitor treatment outcomes, as well as provide insights into the mechanisms of mental disorders. An extensively studied biomarker for depression and anxiety using electrophysiology (EEG) is alpha power abnormalities.

However, given the inconsistencies in the literature, we investigated alpha power in an online dataset using more novel analytical techniques to reexamine this phenomenon. A resting state EEG dataset consisted of eyes-open and eyes-closed state recordings from a subclinical college student population available to the public on *openneuro.com*. Trait anxiety (STAI) and depression scores (BDI) of the subjects were provided, allowing us to contrast pathological and healthy activity. Before analysis, raw EEG data was processed using the recently developed *Reduction of Electroencephalographic Artifacts* (RELAX), which is an automated EEG pre-processing and cleaning pipeline. Next, absolute and relative alpha power values were calculated and stored for every open or closed segment for every subject. Subject-level outliers, taking into account channel and state, were removed based on thresholds of 2 z-scores away from the mean. Finally, topography and statistical results were generated based on these values. Wilcoxon rank sum tests were used to contrast depressed or anxious versus healthy individuals at each electrode. EEG topographical maps showed control and depressed or anxious trends across states. As expected, posterior electrodes in the closed state exhibited higher alpha absolute and relative values than in the open state in both control and anxious or depressed individuals. Ranksum comparisons of depressed or anxious vs. controls at individual electrodes within each state showed limited significant differences. Linear mixed-effects models (LMM) were further used to assess the predictability of alpha absolute and relative in relation to BDI and STAI behavioral scores while taking into account variation due to sex, channel, and individual subject differences. Fits based on the inclusion of BDI, STAI, or both in LMM were assessed using AIC. Across most regions of interest, BDI in the LMM showed slight significance for alpha absolute in eyes-open and eyes-closed states. AIC demonstrated the best models for alpha absolute were those that include BDI or both BDI and STAI (full model). LMM for alpha relative were non-significant. Subdivision of electrodes into regions, such as posterior right electrodes in the closed state, showed more significance and slightly higher AICc weights. In conclusion, our confirmation analysis found some significant differences in alpha power between healthy and depressed or anxious individuals at specific electrodes (e.g., CP4) dependent on eye-open or closed states.

Understanding the Neural Circuits for Aggression: Drosophila Wing Threat Behavior

Mina Mandic

Mentors: David Anderson, Shuo Cao

Innate social behaviors involve complex and functionally relevant movements. However, it remains unclear how these actions are coordinated by the brain. Drosophila display “wing threat” behavior - a complex, multi-motor aggressive behavior, composed of four different actions: wing elevation, pump, turn, and charge. The Anderson lab has identified genetically labeled “AIP neurons” that specifically control wing threat display. To understand the aggression circuitry in the Drosophila brain, it is crucial to identify other connectome-derived neurons that are involved in wing threat and elucidate their connection to AIP neurons. Our methodology entails identifying split-gal4 drivers to label each downstream neuron of interest, followed by gain-of-function and epistasis behavior experiments. Gain-of-function results tell us which behaviors are caused by activation of the neuron of interest. Epistasis results determine whether the effects of AIP neurons are mediated by the inhibited neuron. Our preliminary findings indicate that the neuron CL139 plays a role in wing elevation, CL176 is an inhibitory neuron for locomotion, and DNp45 induces an augmented velocity response to optogenetic stimulation. Future investigations involve epistasis tests to discern which wing threat behavior DNp45 and CL176 are responsible for.

How Does Acetylation Impact Emotional Memory Consolidation?

Lauren Martindale, Marcel Elkouri, Jacklyn Staffeld, Francesca Czesak, Sara Aton PhD, Jonathan Morrow MD, PhD

Sleep is essential for memory consolidation, and sleep deprivation is associated with impaired *spatial* memory performance and decreased histone acetylation. Previous studies have shown that this effect can be reversed by inhibiting histone deacetylase enzymes (HDAC), thus increasing acetylation. It is unknown if HDAC inhibition could similarly improve *emotional* memory performance following sleep deprivation. We sought to confirm this impact in mice in preparation for a study investigating individual differences in emotional memory consolidation in rats. Mice underwent a contextual fear conditioning (CFC) paradigm and following training were immediately injected with either saline or sodium butyrate, an HDAC inhibitor. Mice were then allowed to sleep or were sleep deprived for 6 hours. We hypothesized that sleep deprivation would impair emotional memory consolidation, and administration of sodium butyrate would reverse this. All groups exhibited an increase in freezing following CFC training, suggesting that all groups learned an association between the context and the shock. Sleep deprivation was not observed to have any effect on emotional memory consolidation, and there was a trend towards decreased freezing in mice that were given sodium butyrate – suggesting impaired memory consolidation.

Following the mice pilot study, a preliminary cohort of rats underwent Pavlovian Conditioned Approach (PCA) and developed one of three behavioral phenotypes: sign tracking, goal tracking, or intermediate responding. After PCA, the rats underwent CFC training and received saline or sodium butyrate injections followed by sleep deprivation or sleep, like the mice. During CFC testing, rats of all behavioral phenotypes displayed increased freezing, suggesting that all groups learned an association between the shock and the context. Conclusions could not be drawn about the effect of individual differences on emotional memory consolidation due to the small number of sign trackers. Rats that were allowed to sleep and given saline demonstrated the least freezing, and there was no significant difference in freezing between the other three groups. This study did not assess the effect of non-specific freezing following training due to stress from sleep deprivation, so future studies may introduce a second neutral context and explore less stressful methods of sleep deprivation.

Adrenergic signaling in *Ciona robusta* is required for maintenance of a cardiac stem cell population

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Innervation is important for heart function. Neural inputs appear to also impact heart growth, but the exact mechanism is not yet well characterized. We aim to address this question by studying the impact of neuronal signals on heart stem cell populations in the invertebrate chordate *Ciona robusta*. Our previous work indicates that stem cells form a single file line in the developing *Ciona* heart, referred to as the 'undifferentiated line.' The

Ciona heart is innervated by both extrinsic neurons outside of the heart and intrinsic neurons within the heart. We have also found that knockout of the neuropeptide tachykinin in extrinsic heart neurons severely disrupts heart growth. According to our current model, secretion of tachykinin from extrinsic neurons stimulates intrinsic cardiac neurons which then produce a signal that promotes proliferation of stem cells within the 'undifferentiated line.' We have not yet identified this intrinsic signal, but single-celled RNA sequencing data indicates that adrenergic signaling from the intrinsic neurons promotes 'undifferentiated line' proliferation. In particular our scRNA data suggests that this receptor is expressed in the 'undifferentiated line.' Here we show that inhibition of adrenergic signaling results in a reduction of undifferentiated line cells. To characterize 'undifferentiated line' growth, we counted the number of cells within the 'undifferentiated line' for a control group and a group treated with doxazosin mesylate, a competitive antagonist of alpha1-adrenergic receptors. Juveniles were cultured until 3 days post fertilization (dpf) and then one group was treated with doxazosin mesylate and the control group with DMSO until 7dpf. As predicted by our hypothesis, treatment with doxazosin mesylate led to a consistent and significant reduction in undifferentiated line cells. However, there was only an average of ~1 less 'undifferentiated line' cell in experimental samples vs. controls across three trials. Our prior quantification of UL growth indicates that 3 ULs are added during the treatment period. Thus, our data suggests that adrenergic signaling is not the only factor impacting UL growth. These results serve as a starting point to discover and characterize how neuronal signaling coordinates heart growth.

Investigating the Effect of Centriculum Structure on Microtubule Organization in *C. elegans*

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Errors in mitosis cause myriad diseases, from cancers to developmental disorders. In order for chromosomes to properly segregate, the nuclear envelope breaks down and microtubules pull the duplicated chromosomes apart. Central to this process is the newly described centriculum, a porous membrane surrounding the centrosome and constituted of endoplasmic reticulum (ER) proteins. It is hypothesized that the centriculum transmits force from the separating centrosomes to the nuclear membranes, pulling them apart and allowing proper mixing of chromosomes. Furthermore, the porous structure of the centriculum suggests it functions as a microtubule "filter," ensuring properly-oriented microtubules pass through.

The goal of my project was to determine the effect of centriculum structure on microtubule localization during mitosis using embryos of *C. elegans*, a transparent worm. To affect centriculum structure, I downregulated atlastin, a protein which forms junctions between ER proteins. Since the centriculum is constituted of ER, lower levels of atlastin should disrupt the membrane, forming larger gaps. Indeed, downregulation of atlastin increases centriculum size, confirming that the structure is changed.

As centricula increase in size, they contain a lower concentration of tubulin, consistent with the hypothesis that centricula with undisrupted structure more effectively filter microtubule exit from the centrosomes. However, as centriculum size increased, I did not observe a corresponding increase in tubulin concentration outside the centriculum. I found these results in both my strain and in a separate strain with overexpressed tubulin tagged with a different fluorescent marker. These results may occur because the vast majority (>95%) of tubulin is in the cytoplasm, so any increase in tubulin there is too small to be detected.

Finally, blocked microtubules impact the centriculum membrane, so disrupted (larger) centricula show decreased tubulin fluorescence in the membrane, indicating fewer microtubules have impacted.

3D Magnetic Reconnection in SSX: Statistical Study

S. R. Murdock, K. Butterfield, Ayla Cimen, and M. R. Brown

We present statistical data on a large number of shots ($N \approx 1000$) at SSX. The experiment generates two fully ionized relaxed MHD plasmas which move towards each other with approximate velocity $v = 30\ km/s$. Each plasma is enclosed in a flux conserving cylinder which makes it evolve into a twisted rope structure as it moves. The magnetic field in the reconnection region is measured with a planar 4x4 array of B-dot probes. The line averaged electron density in the center of the reconnection region is measured using Mach-Zehnder interferometry. Ion temperature is measured using ion Doppler spectroscopy. Typical SSX plasmas have $B = 0.4\ T$, $n_e = 3 \times 10^{15}\ \mathrm{cm}^{-3}$, and $T_i = 10\ eV$. Current density is calculated in the plane of the probe array using the curl of the magnetic field. Each shot was examined for evidence of magnetic reconnection, a large density peak followed by significant ion heating as a well as oppositely directed magnetic fields around the same time. We report average n_e, T_i , and magnetic energy across observed reconnection events. Trends in the number of anti-parallel adjacient probes as well as current density around the time of the reconnection are reported. The aggregate data is compared to existing models of reconnection.

Exploring Math Moments: Middle-schoolers' Phases of Problem-Solving, Executive Functions in Practice, and Collaborative Problem-solving

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Collaborative problem solving (CPS) has been shown to both engage and benefit students' learning of mathematics. However, there is evidence that group work is not always easy to facilitate, in part because educators lack details about learners' engagement during group work: the processes of problem solving involved, and how these are engaged. In this exploratory study, we focused on these processes in the moments of related math activity, or math moments, engaged by two groups of urban, middle-school aged students during four sessions of work in the online Virtual Math Teams (VMT) environment. We examined three phases of their problem solving: Exploring, Constructing, and Checking. In addition, to further describe the students' cognitive and behavioral engagement, we considered both the process of students' use of executive functions (EF), during problem solving, termed executive functions in practice (EFP), as well as the stage of their CPS, during phases of problem solving. We learned that the relation between each phase of problem solving, categories of EFP, and stages of CPS vary; for example, the problem solving phase of Exploring was found to have a more positive effect on EFP and CPS than either Constructing

or Checking. Implications for educational practice, and next steps for related research are described. There were no significant differences between the number of math moments in each problem solving session of each group.

Mathematically Modeling HIV in the Lymph Nodes

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Recent research suggests the existence of latent-infected cells,cells that contain HIV DNA transcriptionally silent until activation after which they are able to produce the virus. Previous investigations have identified the lymph nodes as sanctuary sites where these latent-infected target cells can lie dormant for up to decades before being activated and Previous have used the compartmental model of the lymph nodes to create nonlinear differential equations modeling the T-cells, infected cells, and virus as it spreads in the lymph nodes, based on several parameters including: the generation rate and death rate of the T-cells, the rate of infection, a given drug's efficacy, the death rate of infected cells, the rate at which virus produces infected cells, the death rate, and the contribution of infected cell reservoirs to the total amount of infected cells. We further investigated these parameter values by utilizing differential equation solvers to create a Matlab script with the ability to test parameter value guesses – and the predicted data they produced – against real patient data. We then utilized Monte-Carlo Markov-Chain (MCMC) analysis to accept and reject predicted values based on the sum of squared errors they produced and randomly altered our parameter value guesses. This process produced a set of accepted values that followed log normal statistical distribution and provided us with a set of best parameter values for the generation rate of T-cells, the death rate of infected cells, the rate of infection, and the death rate of T-cells (lambda, alpha, beta, and d respectively). We were able to find a mean and 95% confidence interval for each of these values. Ultimately, we hope that these findings will improve models of HIV to be used in testing for drug efficiency and optimizing drug cycles.

Dietary impacts on larval sand dollar performance under marine heatwave conditions

Ruby Novogrodsky, Dr. Karen Chan

Marine heatwaves are a growing ecological threat. In addition to putting physiological stress on individual organisms, marine heatwaves can disrupt energy transfer by changing primary producer communities and affecting feeding at higher trophic levels. In this study, we investigate the relationship between the planktotrophic larvae of the Pacific sand dollar *Dendraster excentricus* and their algal prey in the context of simulated marine heatwaves. We hypothesized that elevated temperature and/or altered diet resulting from marine heatwaves would reduce larval performance due to increased metabolic costs and/or reduction in food quality. We found that neither larval rearing temperature nor algal culturing temperature alone significantly decreased larval survivorship, but the two had a significant interactive effect. Larvae reared under marine heatwave conditions and fed algae cultured under those same conditions exhibited significantly lower survivorship than control larvae, highlighting the importance of considering ecological interactions when determining the impact of climate change stressors.

Membrane Scaling in Industrial Wastewater Filtration: An experimental Investigation

Lucas Oberdiek

The goal of this research was to experimentally look at how scaling, or salt deposition, affects the performance of zero liquid discharge (ZLD) water recovery systems. This would be done by building a bench-scale ZLD system and operating it under different conditions to find when scaling occurs, how much it reduces efficiency, and to find the mechanism by which scaling occurs. The experimental system would work by using a pump to pressurize a salt solution. Once a great enough pressure is reached the water in the solution would be pushed through a semipermeable membrane which allows water to pass through but rejects almost all dissolved particles.

The power sector is the single largest consumer of water in the United states, and the vast majority of this goes to cooling water for nuclear and fossil fuel powered plants. Zero liquid discharge systems are used in power plants to desalinate then recycle the cooling water being used. This allows for less water to be taken in by the power plant, and prevents harmful discharge from the powerplant back into the environment. One of the major drawbacks to ZLD systems is their high costs. Knowing how scaling occurs would allow for ZLD systems to be designed and operated with greater efficiency, saving more water, and reducing costs.

After setting up our experiments and running initial tests it was evident that the system was not desalinating the water as expected. The research then shifted to systematically testing parts of the system to find what was going wrong and potentially a fix to it. Though the system ultimately did not work, the research that went into understanding how the experimental system works and finding a solution to the problem led to a much more in depth understanding of how ZLD systems work. The detailed knowledge has the potential to be useful for further research for our group in designing experiments and looking for ways to make ZLD systems as efficient as possible.

Wind Turbine Aerodynamics and Wind Farm Modeling

Chisom Obiora-Egbuziem

This report delves into the crucial areas of wind turbine aeroacoustics and wind farm modeling, examining their significance in the context of wind energy development. The study on Aeroacoustics focuses on understanding and mitigating noise emissions from wind turbines, which can have considerable impacts on nearby communities and wildlife. The investigation of wind farm modeling utilizes advanced computational tools to analyze the complex dynamics of wind farms, optimizing layout design and assessing energy yield. The report also explores the concept of wake loss, which affects wind turbine performance and overall farm efficiency. By integrating insights from Aeroacoustics, wind farm modeling, and wake loss analysis, this research contributes to the development of efficient, environmentally responsible, and economically viable wind energy projects.

Elucidating the mechanism of biomolecule- mediated silver nanoparticle dissolution

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Silver nanoparticles (AgNPs) are widely used in commercial and medical products, yet their fate and reactivity in biological systems is poorly understood. Here, we describe the kinetics of AgNP dissolution, which is important to AgNP toxicity mechanisms. Specifically, we studied the impact of spherical nanoparticle sizes and the presence of biomolecules on AgNP dissolution. Our experimental studies will contribute to our understanding of AgNP reactivity. Linear Sweep Stripping Voltammetry (LSSV), an electrochemistry technique, was used to measure the amount of silver ions released into solution from dissolved silver nanoparticles at five minute intervals over two-hour periods. The dissolution rate constants of silver nanoparticles were then calculated. It was found that dissolution rate constants decreased as nanoparticle size increased. Preliminary studies have also shown that dissolution rate constants of silver nanoparticles increase in the presence of low concentrations of Glutathione (GSH), a biomolecule of environmental and biological importance.

Robotic Model Barnacle Nauplii

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Like most crustaceans, barnacles have a naupliar form that has three pairs of limbs, which are used in both feeding and swimming. Furthermore, they all have the taxon-defining pair of frontal horns. Body extensions, as such, can influence the hydrodynamics of the larvae by acting as sea anchors. To better understand the role of body extensions and their interactions with limb motion in larval function, we set forth to develop a robotic system to analyze the swimming pattern of barnacle nauplii. To ensure the robot was lightweight and compact, Nitinol springs were used as a substitution for conventional motors. Springs were controlled with a microcontroller that could either enable the flow of electrical current through the springs, causing them to heat up and contract, or halt the current flow, allowing the springs to cool down and expand. Utilizing a series of springs, microcontrollers, and 3D-printed components, the cyclic motion of the nauplius's power and recovery stroke within their swimming pattern was successfully replicated. In future, this robotic model will undergo testing in a viscous fluid, and particle image velocimetry will be used to analyze the flow patterns during the robot's free swimming. The development of this robotic system helps inform the role of body extensions in low to intermediate Re swimmers and, more broadly, the evolution of planktonic larval form.

Contextual cues potentiate sated consumption of palatable foods

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Binge Eating Disorder (BED) is characterized by consumption of unusually large amounts of food in a short period of time (binge eating) and feelings of loss of control during binge episodes. Individuals with BED report that binge episodes are triggered by many variables, including access to palatable foods, times of day, or exposure to cues. Specifically, contextual cues, such as one's environment, are thought to gain control over binge eating through the process of associative learning - cues repeatedly paired with food reward while hungry eventually gain the ability to trigger overconsumption while sated. Stern et al. (2020) developed a feeding paradigm to model cue-potentiated feeding in male mice using contextual cues (context-potentiated feeding), but we have previously tried to replicate the findings and failed. Therefore, the goal of this study was to optimize the paradigm for use in our lab, to replicate the findings in male *and female* mice, and to collect neural tissue for future analysis. After refining the procedure, we were able to replicate the paradigm and observe robust context-potentiated feeding in male and female mice. Further, the revisions we made to the procedure revealed that the paradigm is extremely sensitive to the stress of the animals and that factors such as acclimation to the experimentation room, reduced number of handlers, and better distinctions between contexts can facilitate success. In the future, we are planning to collect additional cohorts of mice and use their neural tissue to analyze the neural circuitry involved in this form of non-homeostatic feeding. Specifically, we hypothesize that protein markers of neural activity (c-Fos) will reveal elevated activity in the striatum, hypothalamus, and amygdala during context-potentiated feeding.

Developing FPGA Test Procedures for Memory controller

Xezel Peshlakai

The University of Tennessee, Knoxville, Integrated Circuits and Systems Laboratory (ICASL) produces integrated circuits to withstand high TID (total ionizing dose) and cryogenic temperatures for NASA's mission to Europa. It is critical for the produced circuits to operate without failure to achieve successful travel, so developing comprehensive testing procedures are important to validate performance. This project aimed to program an synchronous dynamic random-access memory (SDRAM) fixed field-programmable gate array (FGPA) with a memory controller based on the novel ECL standard cell library to validate ICASL's integrated circuits' memory operations. ICASL's integrated circuit is designed with reduced pin count to support system requirements. A 64MB Intel FPGA development board with embedded switches, buttons, and LEDs is used to display results. The memory controller is developed upon Jet Propulsion Laboratory's novel design and manages data between the CPU and main memory storage. The SDRAM is the main storage needed to be accessed to receive and return data. It balances access rate, cost, and capacity. A successful synthesis on the FPGA should confirm reading and writing commands. The SDRAM and FPGA achieved reading and writing results through simulation and implementation utilizing buttons for writing memory and LEDs when reading memory. Further work includes testing FPGA against ICASL's integrated circuit to validate the circuit. Additionally testing in NASA's lab to recreate extreme environments will need to take place to validate the integrated circuit design. In conclusion the project has led to the exploration of FPGA to validate integrated circuits design specific to ICASL's collaboration with NASA's mission to Europa.

Characterization of Dihydrochalcones in Apple: Identifying Differentially Expressed Genes

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Dihydrochalcones (DHCs) are a class of flavonoids known for their diverse potential health benefits including anti-diabetic, cancer fighting properties. The study explores the presence and expression patterns of DHC-related genes in interspecific apple (*Malus*) hybrids using RNA sequencing technology. The study involved the collection of young leaves from thirteen samples, followed by RNA extraction and sequencing. The study employed bioinformatic tools and statistical analyses to process the RNA-seq data, quantify gene expression, and identify differentially expressed genes associated with dihydrochalcone biosynthesis, specifically the DHCs sieboldin, phloridzin, and trilobatin. The findings reveal significant variations in the expression of genes involved in the dihydrochalcone biosynthetic pathway across the sampled apple leaves. By correlating the gene expression patterns with the concentration of DHCs in apple tissues, we establish potential gene candidates responsible for DHC production. Additionally, the study provides insights into the regulatory networks and genetic factors influencing DHC accumulation in *Malus domestica*. Overall, this research contributes to a deeper understanding of DHC biosynthesis in apples and lays the groundwork for further investigations into the functional roles of these compounds in apple physiology and their potential applications in the food and pharmaceutical industries. The identified genes may also serve as valuable targets for genetic engineering efforts aimed at enhancing DHC content in apples and other related fruit crops.

Catching Clusters: Optimizing a membrane nanodisc system to studyan influenza protein

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Nanodiscs are a biomimetic membrane system that consists of a lipid bilayer disc surrounded by scaffold proteins. Our project involves biophysical studies of matrix protein 2 (M2) of the Influenza A virus embedded in nanodiscs. M2 performs various functions crucial for the viral life cycle, such as channel functions and inducing membrane curvature for budding. Our goal is to study single functional units of M2 surrounded by lipids. However, our lab has found evidence through dynamic light scattering and size-exclusion chromatography that the M2 protein can form non-specific protein rich clusters when embedded in nanodiscs. Clusters of M2 complicate the interpretation of conformational studies and prevent using our method of choice, pulsed electron paramagnetic resonance spectroscopy (DEER-EPR) experiments. DEER is a powerful biophysical tool that can provide distances between two spin-labels attached to a protein. We optimized the nanodisc system using a combination of nickel affinity and size exclusion chromatographies to remove nanodiscs containing M2 clusters from our samples. We are currently using these optimized nanodiscs to prepare samples for DEER- EPR studies. Our plan is to measure distance variation across various conformational states of the M2 protein, which can inform drug-development or vaccine research.

Developing lipid membrane models to elucidate silver nanoparticle toxicity mechanisms

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In the last decade, the usage of silver nanoparticles has increased exponentially, due to their antimicrobial and antibacterial properties. Their large surface area to volume ratio allows these nanoparticles to easily dissolve and release toxic Ag^+ ions. Silver nanoparticles can be found in numerous industrial and commercial products, from health and fitness equipment to water filters. Silver nanoparticles are inevitably released into the environment through washing and incorrect disposal. While their non-specific toxicity towards bacteria allows for a wide range of applications, the silver nanoparticles can be detrimental to the environment after release. Although research is underway, silver nanoparticle's mechanism of toxicity is poorly characterized. A comprehensive understanding of silver nanoparticles' interactions with bacterial lipid membranes is crucial to determining their effects on the environment. To study these interactions, this project takes an *in vitro* and *in vivo* approach. The *in vivo* approach examines interactions between silver nanoparticles and *Caulobacter crescentus*, a commonly found bacteria in nutrient-poor environments, such as wastewater treatments and sewage systems. Silver nanoparticles are mostly released into these environments, allowing us to use *C. crescentus* as a model organism. The *in vitro* studies determine the mechanism of interactions using a model membrane that resembles *C. crescentus*. Liposomes, the type of model membrane created, can be used to probe different interactions such as lipid extraction, changes in liposome size, leakage of cellular contents, and changes in the fluidity of the membrane. A fluorescence anisotropy assay is being used to measure how the behavior of silver nanoparticles impacts the fluidity of the lipid membrane. Further work with a dye leakage and pull-down assay will characterize other interactions in this nanoparticle-liposome system.

Introducing Urban Heat Island Data to Improve Simulations of Building Electricity Use in Austin, Texas

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The urban heat island (UHI) effect causes urban areas to experience higher temperatures than surrounding rural areas due to differences in land cover. This creates spatially varying microclimates. As a result, urban heat islands can alter electricity consumption in buildings and potentially exacerbate energy burdens on vulnerable populations. Understanding the impact of UHIs on electricity consumption can inform energy policy and energy assistance. Research in this area also sets a foundation for understanding how future climate change will impact building energy consumption. Currently, yearly electricity use in buildings can be simulated using ResStock software from the National Renewable Energy Laboratory. This simulation takes as input a file containing weather data. However, the weather data used to simulate buildings in Austin is collected from a single weather station in the city. Therefore, this data does not reflect microclimate variations across the region. This research explores methods of modifying a weather file to more accurately reflect varying climate conditions across the city. We found that, of the weather parameters most influenced by the UHI effect, dry bulb temperature has the greatest impact on a building's net electricity consumption. Thus, we modified the original weather file such that it reflects variations in dry bulb temperature across the city. After running simulations of building electricity use with modified weather files, we found that electricity consumption differed across the city due to variations in local temperature. Our results suggest that the UHI effect impacts building electricity use in Austin. Future research will include incorporating projected climate change data into building simulations to analyze the effects on building electricity consumption.

Dimension-Preserving Functions

Emmi Rivkin, advised by Neil Lutz

Many familiar types of numbers, such as integers, fractions, or even irrational fundamental constants like π, can be fully and succinctly described to a computer and therefore stored as data. This convenient property, *computability*, is statistically rare; vastly more numbers are *uncomputable*, meaning that a computer with a finite amount of memory can only approximate them. *Effective dimension* is a mathematical way to quantify the level of uncomputability of any given number by describing the relationship between the precision of the approximations and the amount of memory required.

Studying the effective dimensions of individual numbers, or of points in higher-dimensional spaces, is a central pursuit in the field of algorithmic information theory and has applications in other fields such as geometric measure theory and computational complexity. One topic of specific interest is which functions *preserve* the effective dimension of all points. It was shown by Jan Reimann that effective dimension is preserved by any function that (1) can be algorithmically implemented and (2) is *bi-Lipschitz continuous*, meaning that its graph is never too steep or too flat.

In this work, I show that the bi-Lipschitz continuity condition can be weakened, meaning that a larger class of functions preserve effective dimension. This weaker condition permits functions whose graphs may be arbitrarily steep or flat in some locations, as long as the slope does not change too abruptly as these locations are approached. Given such a function f and an approximation of any point x up to some number r bits of precision, we can algorithmically approximate $f(x)$ or $f^{-1}(x)$ to the same level of precision using a number of additional bits of data that is sublinear in r, which is sufficient to prove that x and $f(x)$ have the same effective dimension.

Thinking Outside the Membrane: Investigating the Structure of Influenza A M2 Ectodomain

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Viral membrane proteins play a critical role in viral replication and infection, making them prime candidates for combating diseases. However, evolutionary mutations often cause drug resistance. This constant evolution poses a challenge to scientists who aim to treat influenza infections, and takes up time and resources to continually be looking for novel drug methods and vaccines. As such, there has been an increased interest in developing universal vaccines, which would target a wide range of viruses in the same family and would not be as affected by constant mutations (improving disease *prevention*), as well as nanobody drugs that can target hidden, non-mutating parts of the protein (improving disease *treatment*).

Our protein of interest, matrix protein 2 (M2), comes from the Influenza A virus. Influenza leads to annual epidemics that result in 3-to-5 million cases of severe illness each year and occasional devastating pandemics. M2 plays several roles in the viral life cycle, including acting as a channel and inducing membrane curvature in the presence of cholesterol during viral budding. The M2 extracellular domain, or M2e, is an understudied 22-residue stretch of M2 that extends out from the viral coat. M2e is highly conserved across Influenza A viruses, making it a strong candidate for study.

This research project studies the conformation and dynamics of M2e embedded in a biomimetic model. Attaching reporter groups to residues along M2e allows the use of electron paramagnetic resonance (EPR) to measure the topology of the residues with respect to the membrane surface. Previous lab studies on different regions of the M2 protein have shown that patterns in EPR measurements can create a picture of how the protein folds and moves. Our ultimate goal is to apply these findings to this new stretch of M2 and identify the secondary structures in M2e.

Modeling of Protein and Peptide Assemblies

Christopher Ostaszewski and Walter Ben Rosin, Computational/Physical Chemistry

Long, threadlike proteins fill numerous roles in vitro and comprise many textiles and biomaterials, but are difficult to manufacture in lab. Small, 29 residue sequences can self-assemble into tetrameric coiled-coil quaternary structures which can combine into threads via covalent click chemistry. These coiled-coils become monomers in a new library of threadlike polymers comprised of discrete coiled-coil protein segments, facilitating an easier method of synthesis for threadlike proteins. We gain control over the sequence of protein monomers in a thread if each coiled-coil consists of two chemically distinct pairs of identical alpha helices which combine in an alternating, antiparallel heterotetrameric coiled-coil[2] . We design peptide sequences capable of self-assembling into such a specific structure using a CMA-ES energy minimization optimization algorithm. We test the likelihood of designed peptide sequences to form the desired coiled-coil structure using AlphaFold, a machine-learning protein structure prediction software. We then ascertain the peptides' ability to retain their structure in an aqueous salt solution via Nanoscale Molecular Dynamics (NAMD), a molecular dynamics simulation software. We find that our peptide sequences consistently form the designed structure, which endures in solution for the entirety of a 50 nanosecond simulation. Our prediction and simulation of our protein structure prove that our peptides reliably assemble into coiled-coils durable enough to bind together in multi-protein threads. Future revisions of our peptide sequences would limit the likelihood of the peptides assembling into unintended quaternary structures predicted by AlphaFold, and minimize deviations from the intended structure which were observed over the course of the simulation.

The Late Positive Potential as a Biomarker of Depression

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Depression and related mood disorders are the most common disability among adults in the United States, with a lifetime prevalence of 20.6% (Hasin, 2018). This crisis is deepened by the lack of access to scientific diagnosis and treatment, as many mainstream treatments for depression require a long period of trial and error. Electroencephalography, or EEG, has the potential to identify differences in electrical activity that could constitute biomarkers of depression and related disorders. One signal that can be read from EEG is the late positive potential, or the LPP, which is a signal generated by the parietal region of the brain shortly after a subject is presented with a photo. The LPP has been shown in previous research to respond to differences in the emotional valence of affective images, that is, to have a greater amplitude in response to negative images compared to positive images. The goal of this research is to replicate this finding and to determine behavioral correlates between depressed mood and LPP (Fedorenko, 2023).

The EEG and behavioral data used in this pilot analysis was obtained from the NIH NIMH archive (Phan, 2015). Subjects participated in a passive viewing task in which they were presented with images with positive, negative, and neutral emotional valances. A processing pipeline was constructed using MATLAB's EEGLab extension to filter the data, re-reference to remove noise, and remove outliers in the data. A grand average of Event Related Potentials (ERP) data was created, and a linear mixed effects model was analyzed to determine if there were significant differences in the LPP depending on a picture's emotional valence.

It was found that the differences in amplitude in the LPP were significantly different, with the amplitude being the greatest for negative images, followed by neutral and positive images. This data suggests that more emotional attention is paid to negative images than positive images in the general population. Further, it suggests the LPP as an attractive potential biomarker of depression as depression is associated with negative bias, or increased attention towards negative emotions or realities.

Integrating Space Use with Social Network Analysis Using Vectors

Caleb Scott-Joseph

We propose a novel method for incorporating space usage into social network analysis. An organism's place in a social network should be at least in part determined by where it tends to be located in physical space. However, very little research has been done to investigate this link which is largely because there are not good techniques to quantify an individual's space usage over a long period of time. We propose filling this gap by representing an organism's space usage as a vector and using cosine similarity to measure how similar two individuals space usage habits are. We then looked at association index, as a measure of how often two individuals interact, and saw that pairs with higher similarity in space usage also tended to interact more. However, this was not constant across all demographic factors with significant differences in both the absolute magnitude of association index and the strength of the relationship between space usage similarity and association index across sex and age. We also made a similar vector that quantified an organism's social position which takes into account how similar two beetle's social partners are, essentially measuring their social habits. We found similar age and demographic differences in the social vector similarities as we did with association index. We also found that similarity in space usage vectors was correlated with similarity in social vectors. However, this relationship was constant across all age and sex categories. We argue that these new measurements provide researchers with a novel way to investigate questions of environmental effects in social network analysis.

Simulating Random Walks on the Hyperbolic Plane

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We simulated random walks on the hyperbolic plane to examine its properties. We focused on quasi-geodesic paths that don't double back on themselves. We are interested in quantitative estimates of the quasi-geodesic constants of such paths, how these constants may vary, and by how much. We want to get a good quantitative read on what effect the constants have by examining the statistics of the random walks.

Since hyperbolic space expands exponentially, we expect that small local differences between some paths in hyperbolic space should lead to those paths having necessarily different endpoints. Thus while two walkers on the Euclidean plane can always meet with each other without doubling back on their path, there are many paths where two walkers on the hyperbolic plane can no longer reach each other without doubling back. Therefore at extreme length, two paths with the same endpoint must remain within some distance D of each other that does not depend on the choice of paths. We simulated random walks with a straight path interspersed with "upward" jumps, i.e. a sort of stair pattern. Using a simulation based on the Poincaré half-plane model written in MATLAB, we varied the total length of the path, the number of jumps, and the minimum length of each step of the random walks to create quasi-geodesic paths in the Hyperbolic plane.

We observed that the ratio between the geodesic and "walking" distance appears to be approximately between 80% and 90% no matter the conditions. This suggests the endpoint of the walks can be used as a decent (although not exact) proxy to calculate the number of jumps. We hypothesize that the variation in the first step leads to a large variance initially, but as the number of jumps increases, the variation gets averaged out. Also, each jump appears to add a constant amount of distortion from being geodesic while long straight segments make the path closer to being geodesic. We can see that as the individual parts of the paths get longer (walk length or jump length), the distance between the start and end points of the path also gets longer.

Engineering a Low-Cost UV Nanoimprint Set-Up for Diffraction Grating Replication

Zoe Sperduto

In this work, a low-cost UV-nanoimprint procedure was developed to imprint a commercial diffraction grating onto the surface of silicon substrates. Other options for etching a diffraction grating directly onto the surface (such as electron beam lithography) are timely and expensive and require access to a Cleanroom laboratory. Diffraction gratings are used to separate light into individual wavelengths and are made up of a pattern of transparent slits on an opaque screen. Applications of diffraction gratings include spectroscopy, laser tuning, astronomical measurements, and optical couplers.

It is important that the nanoimprint procedure is cheap and easily replicable in ordinary lab settings (i.e. not a Cleanroom). We were able to establish a baseline procedure which proves that cheap nanoimprint of a diffraction grating onto silicone is possible. A master diffraction grating stamp was first silanized on the surface, then imprinted into SU-8 photoresist on a D263 wafer substrate. Pressure and ultraviolet light were then used to cure the photoresist, and then the stamp was removed from the substrate. The diffraction grating was successfully transferred to the substrate, though the removal process often led to the grating stamp and nanoimprinted grating being damaged. Further work needs to be done to fine-tune the stamp removal process to ensure a clean imprint of the diffraction grating.

Geographical distribution and differences in disease burden caused by ticks in Ile de France

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Ticks, as vectors of many pathogens for humans and animals, are responsible for high burden and high economic loss. In Europe, the species *Ixodes ricinus* remains a leading actor in the high frequency of vector-borne pathogens. Facing changes in climate as well as an increase in outdoor activities and more contact of humans with the environment (with both hosts and vectors), we assessed in this study the distribution of tick-borne pathogens in forest, urban, and peri-urban areas in the Ile de France region in France. We aim to provide recommendations based on risk maps of tick bites and pathogens spp. transmissions in these various green spaces. After RNA extraction of ticks (nymphs and adults), we determined disease burden by detecting six groups of pathogens using polymerase chain reaction detection. We tested 350 ticks previously collected in the Spring and Autumn of 2022 in the Ile de France region. Although some tick species carried bacteria that are endosymbionts, we found *Borrelia burgdorferi* to be the dominant pathogen in ticks across forests (~6.43%), peri-urban (~25.8%), and urban (~4.76%) regions. We found the prevalence rate of *Rickettsia sp*. to be 9.9%, 3.52%, and 4.76% for the forest, peri-urban and urban areas, respectively. Results from *Babesia sp*. and *Bartonella sp*. showed prevalence rates of 0.99% and 2.47% within forest only. *Francisella tularensis* wasn't detected in any of these areas. *Anaplasma sp.* showed a higher-than-normal prevalence rate. However, this has been attributed to the primer used, which also detects symbiont found in previous studies: *Midichloria sp.* These findings are consistent with previous research that characterized ticks as vectors of public health concern for pathogens in other suburban areas in France. Moreover, these data validate the need for risk maps to prevent people from tick bites and aid the diagnosis of tick-borne diseases.

Development of a Tunable Redox-Active Aluminum Catalyst

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The goal of this project is to prepare redox-active aluminum complexes featuring tris- pyrazolylborate (Tp) and α-diimine ligands. It is predicted that this highly reducing

Tp- Al-α-diimine complex will allow for the polymerization of electron rich olefins. I specifically focused on preparing a series of Tp-Al-α-diimine complexes featuring variations of the Tp and α-diimine ligands.

My partner and I created a chart including various Tp ligands and Diimine ligands we could derive in the lab. We derived these two ligands as well as sublimating AlCl3 and preparing KC8. All these compounds are precursors to the Tp-Al-α-diimine complex. KTp salt was prepared from the reaction of pyrazole with potassium borohydride. α-diimine ligands were derived through the condensation of 2,3-Butanedione with anilines. Each of these reactions were done on a multi-gram scale to provide sufficient material for further study.

To prepare the Tp-Al-α-diimine complexes the KTp salts were first reacted with $AlCl_3$ to make $TpAlCl_2$ complexes. To add the α-diimine ligand (L_R^{2-}) it was first reduced with two equivilants of KC_8 from L_R to L_R^{2-} and then reacted with the $TpAlCl_2$ complex. This process yielded red/orange powders. At each step I used HNMR spectroscopy to determine the structure and purity of each sample. I also recrystallized samples to obtain crystals which I took to Penn's crystallographers to be analyzed.

Over the course of the summer, I was able to synthesize and recrystallize relatively pure samples of the plain Tp ligand and the $Tp^{3,5\text{-}Me}$ ligand. I also synthesized L_{ph}, L_{dipp}, L_{mes}, $L_{t\text{-}butyl}$, L_{NMe2}, L_{tol}, and L_{ome} ligands. Through analysis, I found the L_{ome} and L_{NMe2} α-diimine ligands to be the most promising because they had the cleanest NMR results. In my last week of research, our group hypothesized that one of the methyl groups on the α-diimine ligand was being deprotonated with the R-group. I began synthesizing α-diimine ligands that didn't include the methyl group. I did this using glyoxal instead of 2,3-Butanedione. I plan to investigate this type of α-diimine ligand in the coming semester which will hopefully clean up my HNMR results.

Expected Number of Turns and Win Probability of Combinatorial Games Played Randomly

Pat Devlin & Paulina Trifonova

In this project, we investigated combinatorial games where both players move randomly (each turn, independently selecting a legal move uniformly at random). Most of this project focused on a game called Chomp. The research process involved coding a simulation for the combinatorial games and then extracting patterns from the generated data. Using this model, we analyzed and proved closed form expressions for the expected number of turns of a game of Chomp with any starting condition. We also proved and analyzed and proved the probability each player wins for a game of Chomp with starting conditions of a top row of any length and a second row with 0, 1, or 2 cells. Additionally, we were able to find the expected number of turns and the probability of each player winning for a game of Nim of any size.

Imitator Homomorphisms from Strong Special cube Complexes and Homotopic Paths in 1-Skeletons

James Wang, Professor Teddy Einstein

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When studying an algebraic structure, a good strategy is constructing a homomorphism from it to another of the same type. This summer, I worked with Professor Einstein on basic Geometric Group Theory. We were especially interested in building interesting homomorphisms with cube complexes. Some additional tools are hyperplanes, the fundamental group, and a walker-imitator game proposed by Sam Shepherd.

Suppose there are two topological spaces X and Y, with Y embedded in X. There is always an inclusion homomorphism from the fundamental group of Y to that of X, but can we construct a retraction homomorphism from the fundamental group of X to that of Y collapsing all of X on Y? It turns out this is only possible when Y is local isometrically embedded in X. Sam Shepherd proposed a walker-imitator game that re-interprets this retraction homomorphism from a different perspective.

Now suppose X and Y are both cube complexes, with hyperplanes. While the walker can travel within all of X including Y, the imitator must always stay in Y. The algorithm is as follows: every time the walker travels from one vertex to another through a hyperplane, the imitator travels if and only if it is adjacent to the same hyperplane. With five strong special conditions on the hyperplanes, we get a well-defined group action of the fundamental group of X acting on the vertices within Y.

The fundamental group gives an interesting way to distinguish spaces, because it determines a homotopy class of loops at any vertex in X. The iterated algorithm on any vertex in Y determines the endpoint of the imitator's trajectory based on the class. Moreover, the definition of group actions gives a natural homomorphism from the fundamental group of X to the symmetric group of Y, which we can always quotient by the kernel to invoke the First Isomorphism Theorem. Finally, pick some classes that generate the kernel of this homomorphism, there is always another homomorphism from the kernel to the fundamental group of Y where we map each class to the associated imitator loop.

I presented this subject at the math department's summer research showcase at the end of July. As of this semester, I am doing a directed reading with Professor Einstein in which we seek to generalize situations when a group acts "very nicely" on a cube complex.

Cross-cultural adaptation of statistical learning tasks reflects strong measurement reliability and task validity

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Infants acquire language patterns through statistical learning (SL), which is a learning mechanism for segmenting continuous input into smaller units, like breaking words into syllables. In SL, linguistic units are emphasized through co-occurrence probabilities which help build language proficiency. Moreover, correlations between SL and literacy suggest that children also learn print language patterns based on statistical regularities. Zinszer et al. (2023) examined this relationship in Cote d'Ivoire, finding evidence of children using familiar transitional probabilities to gradually decrease their response times to complex stimuli. However, their post-test discrimination accuracy did not reflect this improvement, leaving many limitations to be addressed.

As a result, the current study emphasizes cross-cultural validation, improved measurement reliability, and elimination of potential confounding variables in SL tasks. Our goal was to validate Zinszer et al.'s visual and auditory SL tasks with adults in the U.S. For comparison, we added a visual spatial SL task, which we hypothesized would improve the intuitiveness of the task through spatial co-occurrence. Furthermore, measures for procedural (Serial Response Time) and visual working (Dot Memory) memory were added as control tests for confounds.

Additionally, in the initial pilot data collection, the ASRS-v1.1 inventory was used to measure ADHD symptoms and their possible relationships to SL performance. We found high internal reliabilities (split-half) for all the SL-related measures (> 0.70). These tasks also showed high mean performance, with most scores indicating performance greater than chance. Even after controlling for differences in visual working memory, participants' performance in auditory and visual SL were significantly correlated, reflecting strong convergent validity. Moreover, procedural memory (SRT) had weak correlations with all SL measures. In contrast, dot memory was strongly correlated to auditory performance, suggesting that working memory capacity may still play a role in SL performance across sensory modalities.

Measurements of thumb-tip movement produced by muscles

Howard Wang

Understanding the unique joint angular trajectories produced by individual extrinsic and intrinsic thumb muscles is key for biomechanics and rehabilitation. Our project developed an arm fixation device with a motion tracking system and actuation device. We manipulated extrinsic muscles, the Extensor Pollicis Longus (EPL), Extensor Pollicis Brevis (EPB), and Abductor Pollicis Longus (APL), and the intrinsic Flexor Pollicis Longus (FPL). We then measured the resulting thumb movements, focusing on the angles at the carpometacarpal (CMC), interphalangeal (IP), metacarpophalangeal (MP) joints, and the hand's torsion. The project involved camera accuracy testing, motor systems and data consolidation discussions, T-shaped marker construction, video data analysis, and actuation system. The results of our project provide advancements in thumb-tip motion measurement and actuation system development and set a foundation for future research. By providing a better understanding of the thumb-tip movements, our approach has the potential to refine rehabilitation strategies and training programs, improving patient outcomes in hand function recovery.

Online Processing of and Adaptation to Nonbinary Pronouns

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Introduction. With the growing salience of nonbinary gender identities comes increased usage of nonbinary personal pronouns – *they/them* in reference to a definite, specific antecedent of known gender, as well as neologistic pronouns such as *xe/hir* and *ze/zem*. Prior work indicate that the grammaticality of these pronouns is in transition. Online processing experiments on they revealed a processing difficulty relative to s/he which was smaller than that elicited by gender mismatches (Shenkar 2022). Similarly, studies on neopronouns has shown that they were perceived as less acceptable than s/he or they, but more so than errors in case or animacy (Rose 2023). The present research continues this line of work by investigating how people adapt to the nonbinary pronouns *they* and *ze* over the course of the experiment through a Web-based maze task.

Experiment. 32 participants were trained on the usage of either they or ze, then asked to read sentences about named individuals "who would be referred to with their pronouns." The names were biased toward male, female, or either gender (established via a web-based survey on a separate group of participants). Sentences contained a critical pronoun (*s/he*, *they*, *ze*) that to different extents agrees with the stereotypical (most common) gender and number features associated with the subject. 100 stimuli were developed and divided among four presentation lists using a Latin square design and pseudorandomly interspersed with 25 filler items. At each word position in the sentence, participants had to select which of two words could continue the unfolding sentence grammatically. Reaction times and error rates at the pronoun were recorded to assess processing difficulty.

Results. Preliminary data suggest accuracy was at ceiling. Average reaction times were greater for *ze* than *they*, and greater for *they* than for *s/he*, suggesting some difficult was elicited by *ze* and, to a lesser extent, *they*. Reaction time decrease over the course of the experiment was greatest for *ze* and least for *they*; this difference in adaptation may have resulted from *they*'s inherent referential and pragmatic ambiguity. Analyses will be performed on processing difficulty and adaptation effects pending further data collection.

Studying Crystallization and Structural Relaxation through changes in the electrochemical properties of Li2O 3 B2O3 glass

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Typically, crystal growth is measured and observed through ex situ techniques, such as electron microscopy or x-ray diffraction. In this work, we propose that changes in the electrical property of the sample can be used to measure crystal growth. To test this hypothesis, the electrical properties of lithium triborate glasses under different heat-treatments was observed using Electrochemical Impedance Spectroscopy (EIS). Glasses experience relaxation after long periods of heat treatment close to T_g, where the structure of the glass and the angles between the molecules shift slightly to release stress, and if they are annealed for long times at relatively high temperatures, the crystallization process takes place. Using a specially designed furnace and an EIS system, electrical properties of samples were collected as they were undergoing structural relaxation and crystallization. Preliminary results are in agreement with data from the literature, indicating the methodology can be used to measure relaxation and crystallization parameters accurately. The authors would like to acknowledge NSF for their continuous support (Research Experiences for Undergraduates REU–1950330 and Research in primarily Undergraduate Institutions RUI–2203142).

Astrocytic and Behavioral Changes in Rodents Following Chronic Stress

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Affective disorders are a major cause of disability, with 1 in 5 US adults developing a mental illness over the course of their lifetime. It has been shown that prolonged stress can lead to impairments such as poor emotion regulation and hindered cognitive function, increasing the risk for and severity of such disorders. There is an abundance of research on the effect of stress on neuronal function in the medial prefrontal cortex (mPFC), as this is one of the key targets of stress in the brain, but there is also emerging research on the role of glial cells in neuronal and behavioral responses to stress. Still, little is known about how the activity of astrocytes changes in response to chronic stress. In this pilot study we aimed to determine changes in mPFC astrocyte gene expression in a rodent model following repeated restraint stress. Our rodent model consisted of 24 male and 24 female Long-Evans rats split into 3 different groups: 1) chronic stress-14 day restraint 2) acute stress-1 day restraint and 3) No stress controls. Chronic stress animals were restrained in a plastic restrainer bag for 2 hours for 14 consecutive days, with tissue collection occurring on day 15. Recordings were taken of the animals' behavior on day 1, day 7, and day 14 during restraint. Acute stress animals were restrained for 2 hours on the day before tissue collection and recorded. During tissue collection we obtained mPFC tissue along with adrenal and thymus tissue. We then used Fluorescence Activated Cell Sorting (FACS) to isolate astrocytes in the collected brain tissue, which would then be used to analyze gene expression using qRT-PCR. Although much of our collected data is still in the process of being analyzed and PCR is still being run, we have found that the behavioral data proved to be promising. After analyzing the recordings of the chronic stress group we found that percent time struggling over the first 30 minutes of restraint stress decreased from Day 1 to Day 7 and that these animals weighed significantly less than the no stress controls in both the males and females when compared to animals of the same sex. We also found that over the course of the 14 day restraint, male subjects gained significantly less weight than female subjects. The forward scatter plots produced by our cell sort also showed that we were successfully able to sort astrocytes from the other brain tissue contained in our collected mPFC sample. These findings will provide a basis for further research on astrocyte's functioning in stress responses and allow for new developments in the field.

An Investigation of Mycorrhizal Fungi and Invertebrates of Crum Woods

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Last summer, the Machado lab performed research on ecological concepts that were new, but interesting, to both the students and Professor Machado. We sought to investigate the connection between various soil-based organisms, specifically soil-dwelling invertebrates and plant-associating fungi–namely arbuscular mycorrhizae. The main goal of our study was to look into the relationship between these groups of organisms and to see if we could use them to characterize various locations within the Crum Woods in an attempt to gauge concepts such as soil health and soil quality through biological means. After which, we had hoped to compare using the same metrics upon other sites such as urban green spaces, differing forested settings, and various local gardens.

Unfortunately, due to the constraints put on by the limited amount of time we had, we were unable to fully explore our research; however, we did gain much insight into how to conduct it. Given that this was a field that had no progress within it before we started, we made significant effort to set up the foundation for future studies.

Our introductory work mainly focused on literature studies to gain new techniques as well as the testing execution and refinement of said techniques. Through these tests, we collected a basic survey of various species of the Crum, allowing us a glimpse into various potential test organisms in the future through basic sampling. Afterwards, learning how to adapt to our specific circumstances was also a priority, us having worked with other parties such as Sam Scoma to construct custom equipment as well as the recognition of flaws and adjustments to correct for such of various techniques which were more applicable in other conditions. In the future, we hope for the opportunity to explore more experimental procedures as well as to refine our identification skills and see exactly what the Crum Woods has to offer.

Investigation of a Hybrid RH-LH G-Quadruplex

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Left-handed G-quadruplexes are a non-canonical DNA structure discovered in 2015. Within the context of G-quadruplexes, left-handed g-quadruplexes are distinguished from their right-handed counterparts in their helical twist, from which they derive their names. We tested SLC, a sequence from an oncogene promoter region which forms a right-left hybrid g-quadruplex, in regards to its ability to tolerate 5′ and 3′ additions according to its genomic context and its interactions with NMM, a ligand known to selectively bind right-handed G-quadruplexes. It was determined that SLC could not tolerate 5′ addition, and that NMM selectively bound and stabilized the right-handed subunit of SLC, eliminating intermediate species observed in the SLC melting process.

Rational Approximation of Bidirectional Reflectance Distribution Function

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In computer graphics, Bidirectional Reflectance Distribution Function (BRDF) has been widely studied as a model to render surface appearance of objects with various materials. Since BRDF calculation in real-time can be challenging due to its complexity and large size, we explored rational functions to approximate the model for more efficient representation. Our work mainly investigates methods to effectively fit a rational function through quadratic optimization that 1) implements as pole-free function to avoid asymptotic curves, 2) identifies appropriate size of degrees of the function, and 3) constructs a set of polynomial bases with stability. The algorithm sets a boundary condition along the true value curve driven by the minimization of the magnitude of the coefficients. The condition restricts the fitted function from undefined solution and the minimization function searches for the most stable rational function. With the analytical BRDF model, we compared the rendered image with a public dataset of real-world material to see if approximated version visually resembles the BRDF model. For our future work, we need to explore an approximation method that can handle drastic slopes of objects with specular peaks.

Development of a tunable redox-active aluminum catalyst system for the atom transfer radical polymerization of olefins

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Aluminum (Al) is a relatively earth abundant and cheap metal with benign human and environmental effects. However, compared to transition metals, its catalytic chemistry has not been explored as thoroughly. Thus, an aluminum catalytic system with tunable redox energetics was developed using α-diimine ligands, whose phenyl substituents can be changed to modify electronic properties. Specifically, $[L_{mes}{}^{2-}]AlCl(THF)$ complex was synthesized using metathesis between the reduced α-diimine ligand $[L_{mes}{}^{2-}]$ and $AlCl_3$. Optoelectronic and chemical properties were investigated using NMR spectroscopy, X- ray

crystallography, and electrochemical techniques. Specifically, we report the redox activity of the $[L_{mes}{}^{2-}]AlCl(THF)$ complex through cyclic voltammetry, showing reversible two-electron redox activity and a highly negative redox potential.

The catalytic application of the complex's redox activity was explored through Atom Transfer Radical Polymerization (ATRP) of methyl methacrylate. This controlled radical polymerization technique is compatible with olefin monomers with high control of dispersity and molecular weight as opposed to uncontrolled free radical polymerization. In ATRP initiation, a metal ligand system undergoes oxidative halogenation with an alkyl halide initiator, creating radical alkyl species, whose amount is subsequently controlled through redox reactions with the metal catalyst. With its negative redox potential and reversible two-electron redox activity, our catalytic system, $[L_{mes}{}^{2-}]AlCl(THF)$, was shown to be compatible with common ATRP initiators and led to polymerization of methyl methacrylate, as demonstrated by ^1H NMR spectra.

Moreover, the common ATRP catalytic system of Cu(I)Br and nitrogen-based ligands has only recently been used in combination with other techniques for the polymerization of electron-rich olefins such as N-vinylpyrrolidone and vinyl acetate. In the future, the $[L_{mes}{}^{2-}]AlCl(THF)$ complex with its negative redox potential will be screened for its applications in the polymerizations of these electron-rich olefins which are not typically compatible with ATRP.

Investigating the Presence of GlycoRNA in *Arabidopsis Thaliana*

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The recent discovery of glycosylated RNA (glycoRNA) on the surface of mammalian cells has posed new questions about its properties and potential function/s while reinforcing the importance of RNA modifications in understanding the complex processes of the biological world. Therefore, we asked ourselves if these same RNA modifications exist in other organisms, namely plants. We hypothesized that glycoRNA is present in plants since glycosylation is highly conserved throughout different kingdoms. Additionally, both RNA and glycan modifications are crucial in plant stress response and development. We began our experiments by labeling glycans through established methods such as metabolic labeling. The RNA was then extracted, purified, and analyzed through dot and northern blotting. After metabolically labeling glycans and performing a Cu-free click reaction, imaged RNA samples from *arabidopsis thaliana* presented positive signals which preliminarily suggest the presence of glycoRNA. Additionally, initial trials of enzymatic, digestive treatment seem to demonstrate an exclusive and significant RNAse sensitivity, in turn further supporting the existence of plant glycoRNA. Therefore, the preliminary results from our study suggest that the presence and significance of glycoRNA is not exclusive to mammals. This is a very exciting finding as it opens up a new field of research that could be used to help plants withstand extreme changes in environment.

Evaluating Differentially-Private Algorithms on Mobility Data: A Comparative Study

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Mobility data, such as information collected by access points (APs) to help devices connect to the network, can provide insights into users' interactions with their environment. With the widespread use of mobile devices and the granular geo-location data they gather, such data often reveals fine-grained sequences of users' visit locations. This type of information is crucial for network resource optimization and capacity planning. However, due to the sensitive nature of the data, there exists a pressing need to release it in a privatized manner to safeguard individual privacy. One promising solution is the use of Differential Privacy (DP), a mechanism that provides mathematical guarantees of privacy by infusing noise to original data entries, such as value counts, coordinates, and trajectories.

In our research, we examined the efficiency of various DP algorithms in privatizing mobility data without compromising its utility. We utilized a public dataset from the KTH campus in Sweden, which captured AP connection data from January 2014 to January 2015. While the ngram algorithm was our primary focus, we also evaluated the DPT, AdaTrace, and DP-loc algorithms. Comprehensive error analyses indicated that the ngram model was suboptimal, particularly in retaining sequence patterns inherent to our dataset. Our future research will further explore and contrast the errors generated by the DPT, AdaTrace, and DP-loc algorithms.

Interactive Exercises for Dive into Systems

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This project sets out to create interactive exercises for the free online computer systems textbook, Dive into Systems (DIS). Originally a non-interactive text, DIS is now extended with a highly visualized and interactive exercise book that aims to enhance educational effectiveness by providing top-quality resources to students from all backgrounds nationwide.

The overall target of our project is to introduce various facets of interactivity. To achieve this goal, we use Runestone Academy, an open-source platform for building interactive textbooks, as our exercise book host. We are allowed to create various types of exercises with some pre-built functionalities. However, in order to satisfy the specific pedagogical needs of computer system topics, we further modified Runestone.

Compared to the vanilla Runestone release, our improved version can further support infinite randomly generated exercises based on crafted algorithms. We also extended our efforts to research question quality and content visualization, so that every generated question best aids understanding.

Pedagogically, we empirically discovered fundamental characteristics of interactive exercises that best support students' learning. We concluded that our question bank needs to cover as many circumstances and concept subtleties as possible and that we need consistent and color-coding instruction for students' learning experiences.

NOTES

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