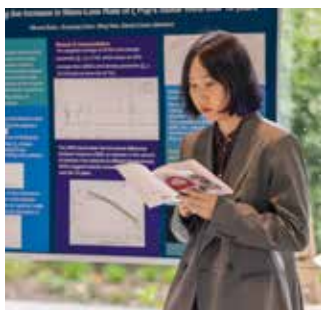
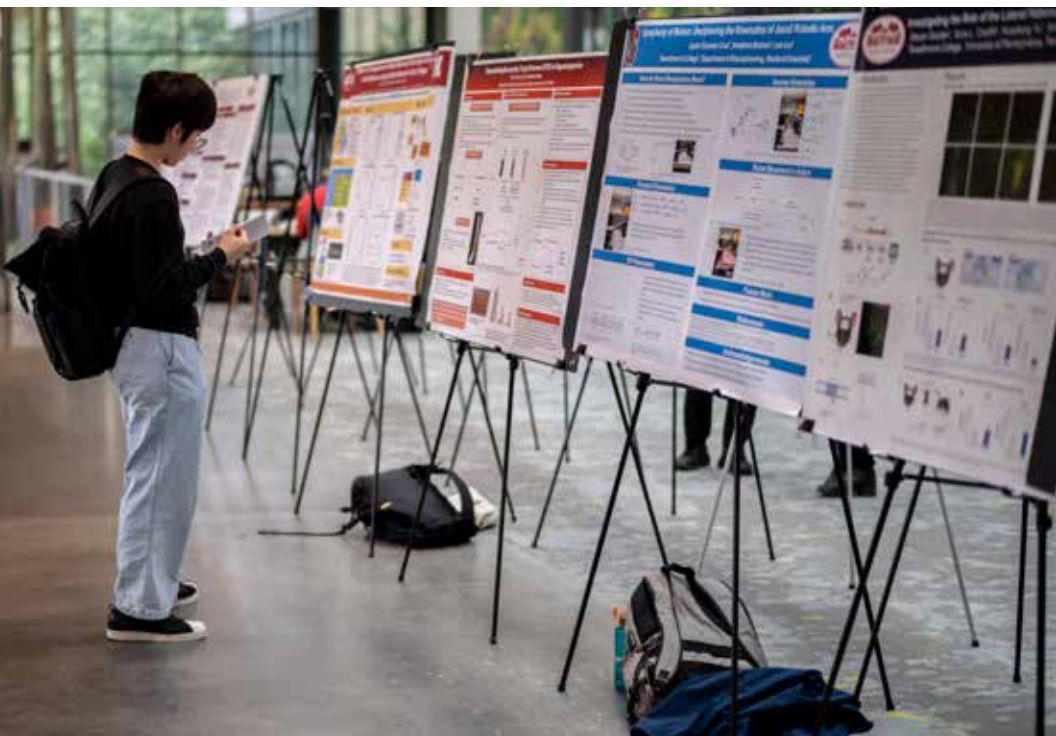


Fall Poster Session 2024



Thursday 9/26/24 • 3 PM - 5 PM
Friday 9/27/24 • 11 AM - 1:30 PM



SIGMA XI
THE SCIENTIFIC RESEARCH HONOR SOCIETY





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6	Iris Barone	2026	Christopher Chung	Using Capillary Electrophoresis to Quantify Competitive Binding of Adosrbates to Silver Nanoparticles
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19	Eliana Dellinger	2025	Niser Babiker, Grace Bancroft, Amelia J. Eisch, Sanghee Yun	In vivo neuronal activity of mouse entorhinal cortex-dentate gyrus neurons during encoding: modulation by discrimination load
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72	Sophie Rodner	2025	Senna Mieth, Liam Halstead	Validating Non-Invasive Salivary Sampling of Glucocorticoids in Couch's Spadefoots (Scaphiopus couchii)
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99	Alex Wuttig	2026		Insights into Battery Materials from Mossbauer Spectroscopy
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SIGMA XI

THE SCIENTIFIC RESEARCH HONOR SOCIETY

Fall Poster Session 2024



Singer Hall (West)



Indicates poster display areas



Finite Element Analysis of Knot Interaction in Tensile Wood

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To reduce the environmental impacts of construction, analyzing sustainable materials to broaden their use is of paramount importance. Mass timber, including Cross Laminated Timber (CLT), is a building material with lower net greenhouse gas emissions than concrete or steel, and expanding CLT's use is reliant on developing a deeper understanding of wood's structural performance. The study of CLT, as a material composed of laminated wood boards, demands further study at the board scale to inform more efficient board selection, which will decrease wasted material of functional lower grade wood while ensuring structural integrity. For lower grade wood, the interaction between nearby knots, as a major factor in the tensile strength of wood, is poorly understood. To take steps toward understanding the potential performance of lower grade wood in CLT, finite element analysis (FEA) is used to model interior knot interactions and determine the associated stress distribution, contributing to models for the performance of wood of different grades. Our models have shown that the interaction between knots is a function of the knot radius, the distance between knots, and the distance between each knot and the edge of the board. Future work may find methods to produce FEA models of boards, develop computationally cheap models for stress as a function of knot properties to improve probabilistic models of board performance, and use experimental testing with digital image correlation to confirm results. This work may inform grading procedures and expand the use cases for lower grade wood, increasing the efficiency and viability of CLT as a more sustainable construction material, thus reducing the environmental cost of our built environment.

Multipartite Entity Resolution: Motivating a K-Tuple Perspective

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Entity Resolution (ER) is the problem of algorithmically matching records, mentions, or entries that refer to the same underlying real-world entity. Traditionally, the problem assumes (at most) two datasets, between which records need to be matched. There is considerably less research in ER when $k > 2$ datasets are involved. The evaluation of such multipartite ER (M-ER) is especially complex, since the usual ER metrics assume (whether implicitly or explicitly) $k < 3$. This paper takes the first step towards motivating a k-tuple approach for evaluating M-ER. Using standard algorithms and k-tuple versions of metrics like precision and recall, our preliminary results suggest a significant difference compared to aggregated pairwise evaluation, which would first decompose the M-ER problem into independent bipartite problems and then aggregate their metrics. Hence, M-ER may be more challenging and warrant more novel approaches than current decomposition-based pairwise approaches would suggest.

There has been some research on M-ER, with the current state of the art being FAMER, a distributed clustering algorithm. However, the vast majority of ER algorithms and benchmarks are for $k < 3$ datasets.

The standard bipartite ER (B-ER) pipeline consists of both a blocking and a matching step. Given two datasets, each with N records, the naive approach compares each of the N^2 record pairs head on. To avoid quadratic complexity, the blocking step creates a reduced set of candidate pairs in linear or log-linear time. There are standard metrics for blocking that become more complicated for M-ER, but they are not the focus of this poster. The matching step then outputs probabilistic binary predictions for the candidate set and is evaluated using precision and recall.

Precision and recall are natural metrics for B-ER because a prediction that two records match is always completely true or completely untrue. However, a prediction that more than two records match can be only partially correct. Current literature only evaluates M-ER in a pairwise fashion as $(k \text{ choose } 2)$ independent bipartite problems. However, there has been no in-depth justification for pairwise as the proper metric.

In this paper, we propose a k-tuple approach for evaluating M-ER. Given k datasets, a k tuple is of the form

$(x_1, \dots, x_k)$, where x_i is a record from the i th dataset or ϵ , indicating that there is no entry from the i th dataset. In our approach, both the ground truth and the predicted matches will be sets of k -tuples. A k -tuple prediction will only be considered correct if the exact same k -tuple is present in the ground truth. Here, predictions are either right or wrong, so the standard definition of precision and recall can be used.

The goal of this project is not to propose a new method for M-ER. Instead, we demonstrate that the M-ER problem may be more difficult than previously thought and that its evaluation is more complicated than B-ER and needs to be investigated more thoroughly.

Structural Analysis of Crystal Structure TET25-TrisQ Complexes

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G-quadruplexes (GQs) are non-canonical DNA structures implicated in numerous biological processes and human diseases, particularly cancer. They are located at telomeres and oncogene promoters among other genomic regions. Telomeric sequence from *Tetrahymena thermophila* (TET25) has the propensity to form GQs, which can be targeted and stabilized by small molecule ligands. The ability to selectively stabilize GQs holds significant potential for the development of novel anticancer therapies. Herein, we investigate using biophysical and structural methods the binding interactions between the GQ-specific ligand TrisQ and TET25 to understand how ligand binding influences the conformation and stability of TET25 GQ. Circular dichroism (CD) spectroscopy reveals that TET25 alone adopts a hybrid GQ conformation but converts to a parallel GQ in the presence of TrisQ. Thermal denaturation experiments show that the binding of TrisQ to TET25 results in an increase in melting temperature by more than 30 °C. We have also measured the binding constant between TET25 and TrisQ. Excitingly, we have solved the crystal structure of the TET25-TrisQ complex at a resolution of 1.60 Å. Analysis of structural data indicate 1) TET25 GQ remains in a hybrid conformation; 2) TrisQ is oxidized to TrisQ-oxide; 3) the first guanine in the TET25 participates in tetrad within its symmetry generated GQ (a novel feature). Our studies suggest that the ligand-induced stabilization and structural transformation of TET25 could be harnessed for designing more effective GQ-binders, thereby contributing to the development of targeted anticancer therapeutics.

Steklov Eigenvalues of Nearly-Circular, Area-Normalized

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On a domain Ω in the plane, the Steklov Eigenvalues are real numbers λ such that for a harmonic function u on Ω ($\Delta u = 0$), we can solve $\partial_{\vec{\nu}}^+ u = \lambda u$ on $\partial\Omega$ where $\partial_{\vec{\nu}}^+$ denotes the directional derivative outward and perpendicular to the boundary of Ω . We see λ is an eigenvalue of the outward normal derivative operator over the exterior of a domain for a function which is harmonic across the domain's interior. This operator is known to capture the harmonics of the domain's surface: it thus has applications from medical imaging to sonar. It is of great interest for what domains of unit area Ω the Steklov Eigenvalues are maximized. We consider these values over perturbed domains in polar coordinates $\Omega_\epsilon = \{(r, \theta) \mid 0 \leq r \leq 1 + \epsilon \rho(\theta), 0 \leq \theta \leq 2\pi\}$ for some perturbation function $\rho(\theta)$, all normalized to a unit volume.

The Steklov Eigenvalues are well-known on the disk of unit volume to be an infinite set of discrete, multiplicity 2, increasing, known values. We, relying on and expanding prior analyticity results, consider our eigenvalues λ and our eigenfunction u as Taylor-expansions in ϵ around the unit-volume disk. We successfully confirmed known results at first-order in ϵ and established novel results at second-order. Specifically, we showed that for every value λ besides the first, there is some perturbation function $\rho(\theta)$ for which the eigenvalue increases in ϵ . Thus, we conclude that the disk does not optimize any area normalized Steklov Eigenvalues besides the first.

Effects of Organophosphorus Pesticides on Brain Development in Planarian—*Dugesia japonica*

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Neurodevelopmental health problems such as autism have been on the rise among children in the United States. One of the factors attributed to this trend is our daily exposure to neurotoxicants such as organophosphorus pesticides (OPs) via food products and environmental exposures. However, our knowledge on the mechanisms through which OPs may damage the developing nervous system is limited. OPs are a chemically diverse family and can affect multiple targets besides their shared primary target, acetylcholinesterase. Thus, it is difficult to extrapolate the mechanisms of one OP to another. Moreover, we do not know when the developing nervous system is most susceptible to damage by OPs.

Our research uses asexual freshwater planarians that are amenable to high-throughput screening of chemicals to understand the basic mechanisms underlying OP toxicity in neurodevelopment. To determine the window of vulnerability when developing planarian brains are most susceptible to OP exposure, we used immunohistochemistry to study effects on brain structure developing across 5 days after being exposed to 5 different OPs: Chlorpyrifos, Profenofos, Diazinon, Dichlorvos, and Malathion. We stained planarians with Synapsin and GFAP antibodies to visualize the effects of the different OPs on planarian brain neurons and glial cells, respectively, at different stages of regeneration. Qualitatively, some of the planarian brains were smaller than others on different days but we have not yet analyzed our data quantitatively to understand our results. Our research could potentially provide mechanistic insights into OP toxicity in planarian neurodevelopment. This insight may be important to serve as a guide to addressing the toxicity of different OPs used in our daily lives.

Using Capillary Electrophoresis to Quantify Competitive Binding of Adsorbates to Silver Nanoparticles

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Silver nanoparticles (AgNPs) have antimicrobial properties, which have led to their increased use in the medical and commercial industries. Because of their small size, they readily diffuse into the environment where they can interact with different biomolecules or organic matter. Once in the environment, adsorbates can bind to the AgNP surface to form coronas, which alter nanoparticle size, surface charge, and biological reactivity. Three different sized particles were studied: 10, 20, and 40 nm AgNPs. Bovine serum albumin (BSA) was used as a model protein and Suwannee River humic acid (SRHA) as the model natural organic matter. Several binding conditions were studied, including independent, competitive, and sequential adsorption of BSA and SRHA with each AgNP. The size and surface charge of the AgNPs with each corona was quantified using dynamic light scattering (DLS). Corona formation was indicated by an increase in the nanoparticle diameter and surface charge. The secondary structure of BSA was quantified using circular dichroism (CD) spectroscopy. 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. Association constants, K_a , were quantified using UV-vis spectroscopy Langmuir isotherms. The K_a values for BSA alone and SRHA alone decreased as the size of the nanoparticle increased. Current work involves a capillary electrophoresis based pull down assay to quantify the quantities of BSA and SRHA adsorbed in each corona. Data from qualitative and quantitative analyses, as well as preliminary results from the pull down assay will be presented.

Investigating Measures of Network Latency

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As Internet Service Providers continue to increase offered upload and download speeds, speed is becoming less of a barrier to end-user Quality of Experience (QoE). Attention is now moving towards other metrics of performance, including latency, latency under downstream and upstream load, jitter,

packet loss, and bufferbloat, each of which can have significant impact on end-user QoE. Such metrics are used by various parties (ISPs, policymakers, and consumers) for discrete purposes, and the way in which these metrics are measured can impact their utility in each use case. Our research, as part of a multi year initiative to expand internet access across the United States and to inform ISPs, consumers, and policymakers, aims to present and interpret data for each of these metrics based on measures collected from several different measurement platforms, and to draw conclusions regarding the reliability and proper interpretation of each measure, specifically how they relate to end-user QoE.

The platforms chosen for analysis are Google's Measurement Lab NDT, Cloudflare's speed test data, the FCC's Measure Broadband America initiative, Ookla's speed test data, RIPE Atlas router boxes, and the CAIDA ARK measuring platform. We compare variables such as location, ISP, time of day, single vs. multiple TCP connections, server point-of-presence (PoP), browser-based measurements vs. other measurement forms, broadband vs. cellular vs. satellite, and other variables. We conclude that there are meaningful distinctions between what different platforms otherwise present as the same metric. Additionally, these metrics lend themselves to easy misuse, highlighting the need for clearer labeling and interpretation guidelines. Furthermore, some datasets contain anomalies or other limitations which cast doubt upon their utility and warrant further investigation.

Minimal wordlist size for a phonological profile: New evidence from Kra-Dai languages

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Much legacy language documentation work takes the form of wordlist surveys. Given this, we must consider what generalizations can be reliably made about the phonology of languages with such limited documentation. Borin et al. described that "statistical studies are almost impossible to do in non-Western languages" due to lack of data (Borin et al. 2013). XXXXXX used 36 Australian languages in the Chirila database (Bowern 2016) with lexicons >2,000 items to show that ~400 randomly sampled words are needed to comprise a minimally complete phonological profile, defined as a wordlist where: (1) every phoneme in that language is present, and (2) distribution of phonemes is statistically comparable to the full lexicon. They conclude that many wordlists, especially Swadesh lists, are insufficient. A limitation of that work is that only one region of the world is studied.

This study replicates XXXXXXXX with new code, and extends their results to languages in the Kra-Dai language family. The methodology also extends on previous research about using statistical augmentation to analyze wordlists (Kessler 2001). We survey 54 Kra-Dai languages with lexicons >2,000 entries, and randomly sample wordlists in increments of 50, to measure the average size needed for phonemic coverage and distribution over 2,500 runs at each sample size. Furthermore, like XXXXXX, we calculate the residual sum of squares (RSS) between overall corpus phoneme frequency versus wordlist phoneme frequency, to measure a sample's fidelity of phoneme distribution. A lower RSS means a more representative distribution.

Figure 1 shows our replication of previous results, and Figure 2 shows results for Kra-Dai languages. The average wordlist size required for languages in the Chirila dataset to achieve total phoneme coverage in 95% of 2,500 runs was 307 words. This is in line with the generous 400-word recommendation by XXXXXX. Compare this to an average 398 words for the Kra-Dai dataset to hit total phoneme coverage in 95% of runs. Additionally, in both the Kra-Dai and Australian data, we observed that the largest improvements to RSS score before 400 words.

Results suggest that Kra-Dai languages require a larger wordlist on average to reliably capture every phoneme. However, increases in sample size beyond 400 words produce diminishing returns in terms of phoneme frequency distribution. In future directions we will take into account additional aspects of phonological typology, such as whether lexical tone also increases minimal wordlist size.

We conclude that a larger wordlist sample is needed for Kra-Dai languages than Australian languages to consistently reach total phoneme coverage with a faithful distribution. A better understanding of

minimal wordlists holds broad significance, given the predominance of small lexicons. Our results call into question the “one size fits all” survey-style wordlists, suggesting a need to tailor regional wordlists not only for semantic and cultural content, but for length. More nuanced understanding of these issues, with statistical testing, will help linguists designing documentation tasks make effective use of limited time and resources, so subsequent studies drawing on their data will be able to draw reliable conclusions.

Vowels Across Varieties of English

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Vowels are a group of unobstructed phonemes that are produced between consonants. In English, vowels are defined by the position of the tongue during articulation. More specifically, this position is measured in terms of tongue height and tongue backness, which can be analyzed using formant analysis. The first formant (F1) corresponds to tongue height, while the second formant (F2) corresponds to tongue backness. Through this classification, vowels are often represented in a discrete, categorical system. Experimental psycholinguistic studies have supported this system, showing evidence that steady-state vowels are perceived categorically. However, within these categories, speakers exhibit variability in vowel production. Linguists have observed that this variability is patterned according to social factors, particularly a speaker’s geographic location. Despite this, regional variation has not traditionally been used to explain differences in vowel production. Listeners are often able to resolve these variations during speech processing, but a clearer understanding of how regionality influences vowel production could enhance our comprehension of these processes. This study presents a comparative analysis of vowels produced by bilingual English speakers who have native knowledge of a Southeast Asian language. The data consists of recordings from nine speakers, taken from the Speech Accent Archive at George Mason University. Each speaker recited a 33-second script that contained thirteen English vowels, including eight monophthongs and five diphthongs. Formant values for tongue height (F1) and tongue backness (F2) were extracted using Praat software and plotted on a vowel chart. The results provide a detailed overview of vowel production in Southeast Asian varieties of English, with a particular focus on distinguishing formant characteristics. Future research should explore other regional varieties of English for comparison.

Improving Fault Localization with Heat Mapped Control Flow Graphs

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Fault localization is a critical and time-consuming aspect of debugging across various programming languages. Numerous tools, such as Jones’ TARANTULA, have been developed to address this challenge. TARANTULA uses heat mapping to color lines of code based on their likelihood of containing faults, effectively highlighting suspicious areas. However, while its heat-map visualization aids in identifying specific lines, it lacks a clear representation of the overall code structure, limiting its ability to direct the programmer to fault-prone areas.

Building upon these ideas, we present a new approach that combines TARANTULA’s heat-mapping paired with control flow graphs to visualize code execution to provide the user with a broader context. Our tool, developed in Python to analyze Java code, enhances fault localization by visualizing both the suspiciousness level of faults and the overall structure and flow of code segments. The tool parses Java source files into a series of nodes and edges, representing the code’s structure, and colors the nodes based on the suspiciousness of a line of code, i.e. the passing or failing test cases. These visualizations are output as SVG files using GraphViz. The color scheme, consisting of yellow, orange, and red, was selected based on research in heat mapping to effectively direct the user’s attention to areas of interest within the code.

Initial testing of the tool has demonstrated its effectiveness in helping users quickly identify and focus on problematic areas in the code, effectively reducing debugging time. Future work will explore extending support to other programming languages to aid as an educational tool for introductory students, as well as testing on a wider range of programs.

Fundamental Tests of Quantum Mechanics with IceCube

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Bell inequalities are an essential component of the foundation of quantum mechanics, providing a rigorous approach to testing for the presence of local hidden variables to distinguish between quantum-mechanical and classical descriptions of physical systems. Leggett-Garg Inequalities (LGI) are an analogous set of mathematical inequalities designed to test the classical principles of macroscopic realism and non-invasive measurability for any dichotomic physical system. Any physical system that provides a measured violation of an LGI furthers evidence for the quantum description of time evolution.

The quantum-mechanical phenomenon of two-flavor neutrino oscillations is a perfect candidate for an LGI test. We construct multiple LGIs using separate disappearance measurements at the IceCube neutrino observatory of different energies and trajectories. We use IceCube data to calculate flavor-conservation probabilities for mu-tau neutrino oscillations through the Earth at different zenith angles. We expect data from the IceCube experiment to provide violations of the classical bounds of the K3 and K4 violations for multiple neutrino energy-trajectory combinations. The results of this study provides evidence for the quantum-mechanical description of neutrino oscillation persisting across macroscopic distances, a valuable contribution to understanding classical emergence from quantum mechanical descriptions.

This poster provides an overview of LGI functions, a discussion of their physical properties and limitations, and the implementation of data from IceCube into our experimental design.

Discovery and Synthesis of Novel, Porous Organic Cages via Dynamic Imine Chemistry Enabled in Continuous Flow

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The recent development of dynamic covalent chemistry (DCvC) has enabled systematic studies on complex chemical systems involving readily reversible covalent bonds. Yet, it remains a challenge how we can navigate the energy landscape of a reaction, such that we could favour certain products over the others in a resulting dynamic combinatorial library, in an effective and sustainable fashion. While the design of monomers plays a crucial role in determining reaction pathways through proper sizing and orientation, this project explores alternative reaction methods. It hypothesises that continuous flow chemistry has the potential to efficiently navigate energy landscapes owing to its capability to precisely tune reaction parameters, including temperature, pressure, retention time, and feed composition.

Trialdehyde building block 1,3,5-Tris(4-formylphenylmethyl)-2,4,6-triethylbenzene was designed that could favourably form either a [4+6] and a [2+3] porous organic cage with *p* phenylenediamine, confirmed through preliminary Gaussian Hartree-Fock/STO-3G optimisation. Striking similarity was observed between their electronic energies per molecular mass, indicating that they correspond to two comparable energy wells on the energy landscape. The trialdehyde monomer was successfully synthesised through a one-step Grignard reaction, purified, and characterised using nuclear magnetic resonance. Moreover, an elementary flow system has been assembled using commercially available components, featuring an 8 mL temperature-adjustable coil reactor, a back pressure regulator, and two pumps: one for the trialdehyde and the other for the diamine monomers.

For future directions, cage synthesis will be first carried out both in batch to test to optimise solubility conditions, then rapidly screened in flow to observe cage selectivity under different reaction conditions. The flow synthesis approach is anticipated to yield enhanced selectivity over cage formation, in addition to its significant sustainability benefits.

Investigation of the C-Terminal Domain of the trans-editing protein ProXp-ala

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The genetic flow of information from DNA to RNA to protein is essential because it allows cells to translate the genetic instructions stored in DNA into functional proteins. During this process, it is critical that no errors occur, as mistakes in protein synthesis can compromise cell viability. Aminoacyl-tRNA synthetases (aaRSs) are proteins that attach specific amino acids to their corresponding tRNAs, which is crucial for the translation process. However, some aaRSs can mistakenly attach noncognate amino acids to its cognate tRNA, which may result in the production of nonfunctional proteins. To mitigate such mistranslation, aaRSs use two main editing functions, namely pre- and post-transfer editing. One such method of post-transfer editing is the use of *trans*-editing proteins such as ProXp-ala. Our research focuses on the protein ProXp-ala, a *trans*-editing factor of prolyl-tRNA synthetases (ProRSs). ProXp-ala can edit Ala-tRNA^{Pro} made by ProRS's occasional mischarge of noncognate Alanine onto tRNA^{Pro}. In the plant *Arabidopsis thaliana*, ProXp-ala contains an extra C-terminal domain (CTD) that is absent in other kingdoms of life. This plant exclusive CTD has been previously found to confer dimerization of ProXp-ala as well as enhanced tRNA binding. The goal of our research was to investigate the functional and structural benefits or drawbacks of CTD and determine whether it provides better binding of tRNA for effective ProXp-ala editing. The project started with various DNA plasmids containing genes of Wild Type ProXp-ala (WT), CTD truncated ProXp-ala (Δ CTD), CTD alone (CTD), tRNA^{Pro}, and tRNA^{Ala}. Using these plasmids, we successfully transformed each DNA into two different *Escherichia coli* competent cell lines, BL21 (DE3) and DH5 α , with the goal of purifying the proteins and DNAs, respectively. Following an induction of our three ProXp-ala variants (WT, Δ CTD, and CTD), we used Ni-Resin column chromatography to isolate these proteins and then performed a Bradford Assay to obtain their final concentrations. We noticed some anomalies in the SDS-PAGE gels of our CTD protein, which indicated significant oligomerization. These findings could hint at the possibility that CTD plays a larger structural role than previously believed and is thus a direction we hope to explore in the future.

Combinatorial Approaches to the Word Problem on p-groups

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Letter braiding functions on a presented group are defined by counting (not necessarily contiguous) substrings of letters. Starting with homomorphisms as degree one functions, letter braiding functions realize a notion of polynomial functions on groups. We explore how letter braiding functions can encode the structure of groups, and build on previous work connecting them to the augmentation ideal filtration of group rings. We prove that mod- p letter braiding invariants give a linear-time (with regard to word length) solution to the word problem for p -groups, improving on the general quadratic-time algorithm for finite groups.

Children's (Mis)Understanding of (Mis)Representation in the Media

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TV shows are a cornerstone of the media children consume. However, television programs geared towards children often contain unequal representation of racial/ethnic and gender groups. In the current study, we examine how children's own explanations for unequal racial and gender representations in the media might be a key mechanism through which this increasingly ubiquitous form of cultural input fosters the development of social biases during childhood. In particular, we will test the hypothesis that children tend to assume that unequal patterns of representation must be the result of intentional choice, and that these explanations are a key mechanism through which children internalize the inequalities they observe in the media. Participants aged 6-10 will be assigned to either a low-diversity condition or a high-diversity condition. Participants will then respond to an online survey that asks how they are thinking about representation in the media, including the intentions and fairness of non-representative

samples, the prototypicality of certain racial/ethnic and gender groups over others, the internal innate attributes of samples, and the malleability of those attributes. We predict that children are aware of the rates of representation in the media they consume, assume that non-representative samples are chosen intentionally, and generate their own causal explanations for non-representative samples, like inferring group-based differences in innate attributes, that may change across childhood.

Generation of an antiviral reporter gene in erythroid progenitor cells

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Erythroid progenitors, the precursors to red blood cells, derive from stem cells in the bone marrow. Upon generation, erythroid progenitors have organelles. However, in healthy individuals, erythroid progenitors lose their organelles before entering a person's bloodstream. In sick adults, healthy neonates, and fetuses, however, erythroid progenitors circulate throughout the body. It is unclear as to why erythroid progenitors are circulating in the bloodstream of these populations.

Previously, research from our lab has shown that erythroid progenitors in humans express immune machinery, but their immunological role is unknown. We want to understand the immunological function of erythroid progenitor cells.

After an immune cell detects viral nucleic acid, the cell initiates a signaling cascade that results in the movement of transcription factors into the nucleus. In the nucleus, these transcription factors bind to a promoter sequence called the interferon stimulated response element (ISRE), which induces the transcription of antiviral genes. My goal for the summer was to create a tool that would assess whether antiviral immunity is activated or inactivated in erythroid progenitors. To accomplish this goal, I built a reporter plasmid that has the ISRE sequence upstream of GFP. This tool will allow me to visually monitor and quantify activation of the antiviral immune response in different contexts. Using synthetic DNA oligos, I prepared an insert containing three ISRE sequences, then ligated the insert into a plasmid backbone upstream of a minimal promoter and GFP. After assembling the plasmid, I confirmed that I constructed the desired plasmid via sequencing.

Now that I have successfully assembled this reporter plasmid, I will utilize this tool to understand more about the immune function of erythroid progenitor cells.

Immersive Reality for Indigenous Language Revitalization

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Our research focuses on developing immersive reality/virtual reality technology as a tool for revitalizing an endangered Iroquois language called Onondaga. By integrating Onondaga's complex grammatical systems into a virtual learning environment, we aimed to create a more engaging and effective means of educating Onondaga community members.

Previous researchers developed a private educational website for the Onondaga community, containing various cultural and language-learning resources. Our project aimed to build upon this foundation by creating proof-of-concept IR lessons that could be web-integrated and used by learners with a high school education level. The push for utilizing IR specifically in the context of learning Onondaga is because of the language's unique grammar system. Onondaga's complex pronoun system (with variations based on the number of people involved, who is included, and the speaker's point of view), presented a compelling opportunity for exploration with IR: Learners could interact with virtual characters representing various first, second, and third-person scenarios. Additionally, Onondaga's aspect system, which focuses on how events relate to each other in time and space, aligns well with the cinematic nature of VR, where scenes unfold in 3D environments.

As such, our main goal was to explore IR web technologies and determine their efficacy in language-learning, guided by preexisting resources made over the years (storyboards, short videos). For instance,

simple conversational scenes were filmed using a 360° camera to allow users to explore the environment and visualize the aspects through 3D space manipulation. Our most impactful work was in programming generated 3D scenes within a modeling engine called A-Frame, a web framework built on the WebVR API used for building VR experiences. By manipulating the properties of our asset models (usually people, animals, and plants), we made simple animations allowing for user-interactivity with the mouse and arrow keys, as well as controller + headset functionality with Meta Quest headsets.

Overall, in exploring different IR mediums, we produced various playable media using the 360 camera and in AFrame, and fully housed our work online

(<https://vr.greatlatwteachings.com/>). In testing the interactive capabilities of A-Frame, we

developed a short dialogue-based scene with user-controlled animations (onscreen text, 3D assets made from scratch) and a pronoun/aspect quiz was developed to test interactive capabilities. These results support the idea that immersive technologies can be harnessed to create language-learning environments, while laying the groundwork for future development of comprehensive IR learning experiences.

Mice susceptible to chronic social defeat stress hypothesized to express more mu-opioid receptors and cFOS in the PVT than resilient counterparts

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The opioid epidemic has become increasingly prevalent since the late twentieth century with a consistent rise in overdoses per year. A potential risk factor for opioid abuse, and substance abuse disorders in general, is social, emotional, and psychological stress. Particularly in the year 2020, the onset of the COVID-19 pandemic was preceded by an increase in the amount of opioid-related deaths, exemplifying this trend. To study the impact of this type of stress in mouse models, we utilized chronic social defeat stress (CSDS). In this paradigm, a B6 test mouse is exposed to a CD1 aggressor mouse for five minutes over ten consecutive days, during which the test mouse will often experience physical defeat from the aggressor. Following this, the two mice are separated by a perforated divider to ensure 24 hour sensory stress. After the completion of CSDS, a social interaction (SI) test is performed in which a B6 test is placed in a cage with a CD1 aggressor that is restrained in a small, transparent, perforated box. Results from the SI test allow us to classify mice as either “resilient” if it interacts with the aggressor for more than half the duration of the test, or “susceptible” if otherwise. Additional behavioral paradigms, such as tail suspension test (TST), elevated zero maze (EZM), and marble burying were used to assess the phenotypes obtained from the SI test. Overall, though these additional assays did not substantiate the obtained phenotypes, 62% of mice were classified as susceptible, which is congruous to the expected SI ratios following CSDS. Future projects seek to examine the drug-associated molecular changes that occur after CSDS by considering the mu-opioid receptor (MOR). Pharmacologically, both endogenous and exogenous opioids exert their analgesic effects via MORs, which are highly concentrated in the paraventricular thalamus (PVT) as well as mesolimbic reward regions. Furthermore, the B6 mouse line expresses the *Sun1* gene which allows for the visualization of MORs. In short, test mice will be sacrificed and perfused 90 minutes following acute defeat, and immunohistochemistry targeting MORs and cFOS, an immediate early gene that serves as a protein correlate for neuronal activity, will be performed. In this way, it is hypothesized that susceptible mice will display a greater concentration of MORs and cFOS in the PVT when compared to resilient counterparts.

In vivo neuronal activity of mouse entorhinal cortex-dentate gyrus neurons during encoding: modulation by discrimination load

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Behavioral pattern separation (BPS) is the ability to discriminate between similar stimuli that is presented. Deficits in pattern separation tasks, often are symptoms of cognitive decline (Alzheimer's disease, depression, age-related memory issues). Previous research has shown the underlying neural circuitry of behavioral pattern separation consists of the hippocampal input from the lateral entorhinal cortex (LEC) of the brain. Specifics of this circuitry that underlie the encoding phase of BPS are unclear. This study observes LEC fan cell activity during differing memory loads of the encoding stage in BPS tasks. Female and male SIM-1 cre lox-p mice aged 8 weeks, underwent brain surgery to attach a miniscope for brain activity recording and LEC injection of an adeno-associated virus to express green fluorescent protein on active cells. They participated in a form of BPS task: spontaneous location recognition. Mice are acclimated to an arena with 3 artifacts in different locations. After encoding the locations of these items, two items are left, a familiarly located item and one located in a novel position. The amount of time the mice spend around artifacts indicates whether they have successfully separated patterns or not (mice are drawn to novel objects rather than familiar ones by nature). The implanted miniscope takes videos of the fluorescent activity within the LEC neurons. Following testing, videos are analyzed and converted into quantitative data. The cell activity from these videos is then compared to mouse's location in the arena during cell activation to determine when LEC fan cells activate during BPS tasks. Results show that during the encoding stage of memory LEC fan cells fire more frequently when extra-similar stimuli is presented versus similar and dissimilar stimuli. There is more cell activity when the patterns presented are more similar than less similar, indicating that these cells are necessary for discriminating between similar stimuli. In future stages of this project, it would be beneficial to test older mice and mice with depressive symptoms, further relating the study to age-related cognitive decline and diseases. It would also be beneficial to test the retrieval stages of the mice in BPS tasks to determine any differences in the phases of memory.

Coin Cell Battery Chamber Design for Low Temperature Operando Experiments

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Exploring cycling performance of batteries at low temperatures is essential for verifying the viability of battery materials to be used in applications in which they would be exposed to low temperature environments. However, low temperature battery cycling equipment is either expensive (>\$10,000 USD) or ineffective at preventing battery corrosion, straining lab budgets and preventing low temperature cycling in labs that do not focus on such experiments. A design is proposed that is cost effective (<\$1,000 USD) and fast to implement, allowing more research to be conducted on batteries at low temperatures.

This design's main objectives are to limit condensation, achieve a constant desired temperature, allow battery cycling, and maintain an affordable price point. Limiting condensation is essential to prevent corrosion of the battery samples and is the reason a typical fridge cannot be used in this application.

The design's main chamber is airtight and was machined from Delrin, a plastic material. The sealed chamber prevents additional air (and thus, moisture) from interfering with the experiment. The chamber is also designed to be barely larger than the samples, so there is not enough moisture in the chamber to cause significant condensation.

Stable cooling is achieved using an on-off controller that controls two thermoelectric modules. This controller along with the small chamber size allows the temperature to be more precise than most commercial fridges. However, the whole chamber is placed in a commercial mini fridge to ensure the dissipation of enough heat.

The design also includes a custom lid that has connections to the batteries which enables battery cycling. 3D printed parts are used for circuitry mounts, battery alignment guides, and wiring organization.

The current design has been at $0 \pm 0.5^\circ\text{C}$ at its center while closed for 3 months. The temperature can be lowered to -10°C , and small modifications would allow for significantly lower temperatures. Other small modifications would allow for other types of batteries or samples to be used.

Characterization of interactions between five tetrad G-quadruplex LM7 and small molecule ligands

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DNA G-quadruplexes (GQs) are non canonical secondary DNA structures that form in guanine-rich sequences of the genome, often in telomeric DNA sequences. Prior studies have indicated that GQs play a role in affecting epigenetics, safeguarding telomeres, and acting as barriers to hinder the activity of telomerase. This telomerase activity is associated with preventing cell proliferation, a process implicated in 85-90% of cancers. In this study, we investigate the structure of a novel putative five-tetrad G-quadruplex formed by the LM7 DNA sequence and its interactions with several small-molecule ligands. Six GQ ligands were characterized: TrisQ, NMM, BRACO-19, PyDH2, RHPS4, and PhenDC3. Circular dichroism was used to investigate the effect of ligand on the folding of LM7 as well as the effect of ligand on the stability of LM7. UV-vis titration was used to evaluate binding affinity and binding model of LM7 to ligand. LM7 was found to have antiparallel topology. PhenDC3 stabilizes LM7 the most by 31°C at three equivalents and NMM destabilizes LM7 by 1°C at five equivalents. TrisQ has a much stronger binding affinity to LM7 than NMM, which is likely due to NMMs preference for parallel GQs. No crystals of the LM7 G-quadruplex were obtained. However, the biophysical data indicate promising prospects for solving the structure of this unique five-tetrad GQ. These results contribute to our understanding of G-quadruplex structures and their interactions with small molecules, highlighting potential therapeutic strategies for targeting GQs in cancer treatment.

Automatic Music Transcription for Balinese Gamelan Music

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Automatic music transcription (AMT) is the process of converting music signals into some notation systems without human intervention. AMT would empower musicians and listeners in a variety of ways such as music education, production, and musicological research. Despite current progresses in AMT for Western music, transcribing complex polyphonic music from non-Western traditions remains a significant challenge. This project focuses on developing an automatic music transcription system, initially targeting general music signals, but later narrowing to Balinese Gamelan, a traditional Indonesian musical genre. Gamelan music is inherently polyphonic with complex layers, making it particularly challenging for listeners unfamiliar with non-Western music. The aim of the project is to create an interface capable of extracting key features from Gamelan music, including different tempo layers, scales, and the identification of specific instruments within the ensemble.

The current phase of development emphasizes scale recognition and beat-tracking. Balinese Gamelan music often utilizes scales with five or seven notes, occasionally modulating between them. For scale recognition, a Power Spectral Density (PSD) plot is generated from the input signal to identify the most prominent peaks, which likely correspond to the melodic instruments. By removing harmonics and merging close frequencies, the top five or seven frequencies within an octave are identified, representing the scale. Further refinement of this approach through noise cancellation and filtering will be necessary to handle various signal inputs effectively.

Beat-tracking for Gamelan presents another challenge due to the genre's complexity. Existing beat-tracking algorithms struggle with polyphonic music, necessitating innovative solutions. One method being explored involves filtering the signal to preserve the beat profile while reducing irrelevant noise. Another approach focuses on analyzing the PSD plots of tempo-setting instruments, which are distinct from melodic instruments. We recorded each note of each instrument from the Swarthmore Gamelan ensemble and analyzed their PSD plots. By recording and analyzing each instrument's notes, the project seeks to develop a method to filter out beat signals from recordings.

Small Scale Energy Harvesting Using Wind Induced Oscillations

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When an object is subjected to a moving fluid, it periodically sheds vortices that induce an oscillatory motion in the object, a phenomenon explained by the interplay between the natural frequency of the object and the frequency of vortex shedding. This research aims to develop a system where a flexibly-mounted circular cylinder exhibits such vortex-induced oscillations for the purpose of studying Many engineering structures are designed to minimize these oscillations in order to prevent structural damage. While many scientific studies on this topic focus on suppressing these oscillations, our approach seeks to amplify them to harness the resulting kinetic energy. Basic theoretical calculations suggest that maximum oscillation amplitude occurs when the cylinder's natural frequency (k/m), where (k) is the spring constant and (m) is the mass, aligns with the vortex shedding frequency.

Key challenges addressed include creating a durable and adjustable setup that allows for the isolation and testing of various parameters affecting vortex-induced oscillations. Critical design considerations involved calculating the optimal cylinder density ratio (m^*) to balance between ease of lifting and structural fragility, designing a non-intrusive support mechanism, and selecting appropriate springs.

Initial designs for spring attachment involved welded or glued hooks, which proved inadequate. The final design incorporates a top and bottom plate, both screwed into two 80/20 rods, allowing precise adjustment of the cylinder's height. These plates feature cutouts to accommodate different spring sizes while maintaining structural integrity. This design enables the cylinder to be suspended horizontally in mid-air, facilitating the study of vortex-induced oscillations under controlled conditions. Maybe add something about how the design fits in with the Swarthmore wind tunnel

This setup provides a robust framework for exploring the mechanics of vortex shedding and optimizing conditions for effective kinetic energy harvesting. The project has shown promising results in generating oscillations, but the electricity generation component remains to be tested. Future work will involve utilizing an electro-mechanical system to complete the energy harvesting process.

A Combination of Darker Skin Tone and Lower Perfusion Negatively Affect the Quality of Photoplethysmography Data Used for Pulse Oximeter Readings

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Pulse oximeters are medical devices commonly used in hospitals to non-invasively estimate blood oxygenation (SpO_2) levels. Blood oxygenation is an important marker for someone's health, allowing doctors to identify how well their organs are functioning. During the COVID-19 global emergency, pulse oximeter readings were a determining factor for an infected individual's hospitalization. Initial studies have shown that devices currently on the market are more likely to produce overestimated SpO_2 readings for patients with more melanin in their skin, as the red light is more absorbed by melanin than infrared light, both of which are used in pulse oximeters. Previous research has shown that both darker skin tones and low perfusion lead to SpO_2 overestimation. The effect from a combination of the two variables is unclear, along with a quantification of the overestimation. We measured the impact of low perfusion and darker skin tones together to attempt to learn more about the effects. We used one reflectance and two transmissive pulse oximeters to record raw photoplethysmography (PPG) data from the inner wrist, outer wrist, and finger. The measurements were taken on a racially diverse pool of 18 volunteers. The diversity of skin tones was ensured by quantitative measurement using a Konica Minolta CM-700d spectrophotometer, along with qualitative measurement using Monk and Fitzpatrick skin tone scales. To alter perfusion in the hand, participants were asked to keep one hand in the cold ($15^\circ C$) and warm ($43^\circ C$) water for two minutes. We continuously took SpO_2 measurements during and after temperature treatment with the transmissive devices. Preliminary analysis revealed a significant decrease

in the pulsatile portion of the PPG signal in individuals with low perfusion and dark skin tone. Graphing pulse amplitudes with respect to the conditions of the hand (cold, warm, or at rest) additionally revealed a trend where individuals with darker skin tones had low pulse amplitudes that decreased proportionally with decreasing perfusion. This correlation might be one of the contributing factors to the instances of faulty PPG signals in consumer pulse oximeters. Everything considered, the collected data supports our initial claims of racial bias in pulse oximetry. The initial findings and the continuation of this research could inform the creation of a pulse oximeter prototype that minimizes the inaccuracy of SpO2 readings and reduces racial inequities in healthcare.

Data Visualization: AI Incidents and their Impacts

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Recent advances in artificial intelligence (AI) have taken the world by storm through industry leaders such as OpenAI, DeepMind, and Google, among many others. This has led to popular interfaces used daily such as ChatGPT, Bing, and Bard, not to mention the thousands of AI processes working in the background of industries across the globe. Underneath these developments is a deep concern about potential dangers ushered in by this new technology. There are reports in the global media of incidents in which AI has harmed or near-harmed the real world in its deployments, but these incidents are just beginning to be cataloged and analyzed to find structure, patterns, and trends to guide future strategies for the safety of societies. The project utilized statistical and machine learning tools such as the Naïve Bayes classifier to explore important characteristics of AI-related incidents reported in the AI Incident Database (AIID), an open-source initiative of the Responsible AI Collaborative. Incident reports include information such as location and date of incident report, alleged deployer, harmed parties, and taxonomy of the incident type; it can be related to chatbot, autonomous driving, and deepfake video generation, among many others. The project intends to further direct machine learning techniques back on the system to identify potential risk factors associated with these incidents by addressing research questions such as: "What types of AI incidents are the most prevalent?" and "Who are the worst alleged offenders of these incidents?" The first reported AI incident from the AIID occurred in September 1983, corresponding to the Soviet nuclear false alarm incident from the Oko early warning system. Recently, there has been a gradual increase in deepfake-related incidents, especially during political elections and celebrity news. The United States and the United Kingdom had the most reported incidents in the areas of face recognition, autonomous vehicles, and automatic systems. These are examples of the findings that were unraveled from the AI Incident Database. Ultimately, the project aims to contribute to a more informed approach to AI development, ensuring that as AI continues to evolve, industries can carefully consider potential risks and mitigations to build trust and confidence in such systems.

Probing antibody binding to a potential target for a universal influenza vaccine

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Influenza is the result of an infection of the respiratory tract by influenza viruses. Its epidemics cause 3-5 million cases of severe illness and several hundred thousand deaths in the US every year. Current influenza vaccines reduce the risk of the illness in roughly 40-60% of the overall population at its most effectiveness. Seasonal flu vaccines are based on the most prevalent strains predicted for the upcoming year. Frequent mutations make the prediction of future strains for the upcoming year very challenging. In search of a possible universal vaccine, our lab studies a protein called matrix protein 2 (M2) found on the Influenza A virus. M2 is a 97-amino acid length homotetrameric membrane protein that acts as a pH-gated proton channel within the host cell and is implicated in the budding process of new viruses. It consists of four main sections: the ectodomain, transmembrane, amphipathic helix, and the cytoplasmic tail. M2 is highly conserved which has been attributed to its overlapping genetic reading frame with another matrix protein and its low natural immune response. The amino acid sequence for the

ectodomain (M2e) is especially known for its high conservation between strains, making it an attractive candidate for a universal influenza vaccine. To understand conformational changes M2 may experience when exposed to an antibody, our lab chose to study its binding to an antibody named 1C2. 1C2 is the first ever monoclonal antibody for M2 and is often used as a standard for antibody binding. We received samples of this antibody from collaborators in the Tompkins Lab at the University of Georgia. I used biolayer interferometry to study the binding constants of the antibody to the M2e on the full-length protein only and in nanodiscs. There is continued collaboration with UGA to observe the binding. Once binding properties are established, electron microscopy work will be used to examine the complex of 14C2 to M2-nanodiscs.

Effect of Carboxyl-terminated Polystyrene Nanoparticles on larval sea urchin

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Plastic Pollution has become an increasing threat to marine biodiversity. Nanoplastics (NPs) and microplastics (MPs), which can be directly manufactured or the product of the degradation of larger plastic materials, have been a subject of a growing interest. Multiple effects have been reported, such as growth inhibition and other developmental impairments. However, few studies have examined how the physical-chemical interactions between NPs and ions in seawater alter the ecological impact of NPs. We described the aggregation process of NPs in seawater and conducted experiments to examine both the lethal and sublethal effects of carboxyl-terminated polystyrene NPs. The LD₅₀ for early development of the urchin *Lytechinus variegatus* was 8.6 mg*m⁻³. Such concentration is not exceeded the current environmental concentration of NPs at 4.2mg*m⁻³, implying there was no immediate mortality risk. However, at lower concentrations, we observed morphological abnormality. Therefore, we exposed larval *L. variegatus* to a sublethal concentration of Carboxyl-terminated NPs of 1 mg*m⁻³ for 7 days. Not only did we observed a significant reduction in survivorship, elevated level of arms asymmetry was recorded in larvae exposed to NPs. Congruent with the whole organism observational, reactive oxygen species (ROS), normalized per amount of protein, were higher in the NP-exposed group, suggesting cellular damage. Our work highlights the risk of NPs as emergent pollutant and contribute towards determining its adverse outcome pathway.

In Search of Soil Health Bioindicators in Suburban Gardens

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Soil health depends on the abundance and diversity of soil organisms, as well as on the optimal physical and chemical properties of the soil, which support diverse soil communities. Together, these contribute to highly productive agricultural systems. Recently, there has been a surge of interest in the establishment of urban agriculture for local food production. Yet identifying specific health indicators in urban soils remains a challenging task. Our work began the process of identifying bioindicators of soil health in the context of suburban and urban multipurpose gardens and farms. Specifically, we selected three sites around Swarthmore's campus: an experimental potato farm prototype that was established earlier in the spring, the student-run Good Food garden, established 30 years ago, and the Swarthmore Garden Collective.

Our goal was to investigate the abundance and diversity of macro- and meso- invertebrates at these three sites. We placed a particular emphasis on nematodes, vastly abundant meso-invertebrates that are usually less than 1mm long. Nematodes occupy many levels of the soil food web, and can play important roles in ecosystems including cycling nutrients and controlling pest populations, making them excellent

bioindicators. Furthermore, previous literature suggests that their trophic level proportions can indicate particular soil conditions. To extract nematodes from soil samples, we used the Whitehead-Hemming tray. We then counted the number of nematodes and measured their length, as well as identified a subset of them to their trophic level (herbivore, fungivore, bacterivore, predator, or omnivore) by examining their mouth-parts.

In addition, we sampled a variety of additional invertebrates using Berlese funnels and pitfall traps. We counted and identified the invertebrates to their taxonomic order, and calculated Shannon-Wiener indexes to evaluate the biodiversity of the soil. We found that the biodiversity and invertebrates present differed among the three sites. We also tested for different soil properties (pH, soil organic matter, bulk density, and water capacity) in order to determine if there were correlations between soil health and our invertebrate results. We found a positive correlation between nematode abundance and soil organic matter, supporting the argument that nematodes positively influence the health of soil. As our project is in its beginning stage, our results are predominantly inconclusive. In the future, we hope to use a wider variety of methods to sample invertebrates in order to more accurately represent the variety and abundance of species present. Furthermore, we hope to expand our research to a greater number of sites, in hopes of better understanding the correlation between gardening practices and soil invertebrates.

Yohimbine- and Pellet-Priming-Induced Reinstatement of Palatable Food Seeking Behavior in Mice

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The increasing prevalence of disordered eating is linked to the widespread availability of palatable foods (i.e. foods rich in fat and sugar) that possess addictive properties. Recent literature suggests that compulsive eating and various addictive behaviors share similar traits, including a pronounced tendency to relapse. Many individuals attempt to control their food consumption through dieting; however, long-term success is low. In humans, relapse to maladaptive eating patterns can occur after brief exposure to palatable foods, food-associated cues, and stress. Here, we used an adapted reinstatement model (commonly used to study relapse to drugs of abuse) to determine whether food priming or a pharmacological stressor triggers the reinstatement of palatable food seeking behavior in male and female mice. Mice were food restricted to 90% of their free-feeding body weight and trained to self administer palatable food pellets (calorically dense and rich in sugar) on a fixed-ratio 1 (20-sec timeout) reinforcement schedule during 3 hour sessions 6 days per week for 2.5 weeks. After self-administration training, mice underwent extinction training (during which nose pokes were not reinforced). We then assessed the reinstatement of food-seeking behavior following pellet-priming (i.e. non-contingent pre-session delivery of food pellets) or the administration of yohimbine (an α_2 -adrenoceptor antagonist that promotes anxiety in humans and anxiety-like behavior in animals). Mice quickly learned to nose poke for palatable food pellets during self-administration training and displayed a marked reduction in nose pokes during extinction training. Both pellet-priming and, to a lesser extent, yohimbine injection led to a significant increase in active port nose pokes, suggesting the reinstatement of palatable food seeking behavior. Next, we will examine Fos-protein expression following yohimbine-induced reinstatement of palatable food seeking. Specifically, we will examine Fos induction in the lateral hypothalamus, which has been implicated in stress-induced reinstatement of alcohol and sucrose seeking.

Chronic Consumption of Palatable Diets Differentially Induced Anxiety-Like Behavior in Female Mice

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The long-term overconsumption of palatable diets (i.e. “comfort foods” rich in fat, sugar, and/or carbs) have been associated with weight gain and obesity as well as other attendant psychological changes such as anxiety-like behavior. However, while previous studies indicate this general link, differences surrounding specific types of high-calorie diet, time-points of exposure, and modes of anxiety measurement still remain to be elucidated. Our experiment therefore sought out to investigate and compare the effects of two of these such palatable diets, High Fat Diet (HFD) and Western Diet (WD, a high-fat/high-sugar diet), on weight gain and anxiety-like behavior in female mice. Though many rodent studies have been conducted using HFD (enabling causal claims about consumption and anxiety), human studies have predominantly been conducted using WD, leaving certain questions about overall directionality. We thus used two cohorts of mice ($n=32$) – a WD cohort and a HFD cohort – each with their own control ($n=8$) and experimental ($n=8$) groups, which had ad-libitum access to their respective diets. The first effect of consumption of these palatable diets on the mice was their considerable weight gain (obesity phenotype). While the HFD cohort’s average weight increased to a greater degree than did the WD cohort, both were significantly higher than the chow controls. The second effect of consumption of these palatable diets was the development of anxiety-like behavior, measured using the OFT (open-field test), EZM (elevated-zero maze), and the LDT (light-dark box) at weeks 6, 16, and 20. Although the results were somewhat mixed, we found that generally while the WD mice did not display anxiety-like behavior, the HFD mice did display anxiety-like behavior across weeks. These findings begin to suggest the direct role of chronic consumption of palatable foods in both weight gain and anxiety-like behavior, and future research using these and other more specific diets in both male and female mice will be needed to further explore such trends.

Eliciting Privacy Values and Tensions in Regulating Generative AI

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Audiovisual generative AI has begun to impact every aspect of our personal and professional lives. This includes negative impacts such as advertising scams with video deepfakes of celebrities, extortion schemes that mimic the voices of loved ones or coworkers, and disinformation campaigns that seek to influence elections. In this work, we created eight privacy-related scenarios involving a common use of multimodal generative AI: deepfakes. Using the scenarios in 14 focus groups across 40 participants, we sought to communicate to everyday people the potential harms of deepfakes and develop a contextual understanding of (in)appropriate use and regulation. We found that participants all agreed on the need to obtain consent and increase transparency, but disagreed on whether and how lawmakers or software developers should regulate deepfake use and who to hold accountable for resultant harms. Participants were also overwhelmingly pessimistic about their ability to maintain privacy online. We discuss how these scenarios surfaced more contextual understandings of privacy values (trust, consent, and accountability) and the implications of our findings for technology and policy design.

Force Structures Signal Creep Motion in Granular Media: Can We Predict When a System Will Fail

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Granular media include a broad spectrum of materials, such as sand, soil, cereals, and Saturn’s rings. Despite exhibiting a disordered structure at the granular scale, granular media can behave like solids, fluids, or gases on the macroscopic level (Andreotti et al., 2013).

Due to this nature, granular materials can slowly deform through subtle creep motions or collapse into sudden avalanches, transitioning from solid to fluid. In this project, we investigate the creep behavior of granular piles composed of solid granular particles in response to external disturbances. We aim to identify the conditions under which a granular pile fails, leading to an avalanche, by characterizing

changes in particle positions, the evolution of force chains, and the changes in voids over time.

In our lab, we experimentally simulate creep behavior by disturbing a 2D pile of photoelastic grains. Using a motor-controlled tapping mechanism, we disturb the pile at precise locations with consistent frequency. All experimental runs are recorded with a dual-camera setup: one captures white light images, while the other, equipped with a polarizer, captures polarized light images. This dual-camera setup allows us to simultaneously gather information about both the particles and the underlying force chains. The cameras are mounted vertically to ensure that the images can be accurately mapped onto each other, enabling a straightforward comparison of the evolution of particle arrangements and force chain structures.

With our data processing pipeline, we mark and track the position of each particle to study particle movement over time. We study force chain evolution by subtraction of images taken by the camera with a polarizer in front. We take the first polarized light image and subtract all subsequent images from it to create a series of images containing black and white pixels. Black pixels denote regions that are missing in subsequent images compared to the original image, while white pixels represent areas where subsequent images add to the original image. Therefore, the black or white pixels indicate the disappearance or emergence of force chains as creep motion happens in the pile. By analyzing these changes in pixels, we can use them as a proxy to study the changes in the force chains.

A unique aspect of our research is our ability to monitor and describe the granular pile using two distinct approaches: macro changes in the pile, such as creep and avalanche behaviors, and more nuanced information about the grains at the microscopic level, such as the force chain structures deep within the bulk of the pile.

Our current results indicate that significant changes in the rearrangement of grains are often preceded by changes in the force chain structures. We are in the process of acquiring more data to further corroborate this finding and to determine if force chain information can be used to predict the future evolution and potential failure of the pile.

Semaglutide restores leptin receptor (pSTAT3) signaling in leptin-insensitive DIO mice

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Leptin is a hormone that is produced by fat and activates a satiety pathway in the brain that inhibits hunger in humans and animals. Leptin resistance occurs when a human or animal has high levels of leptin in their bloodstream, however, the brain no longer responds with a signal to stop eating, leading to obesity. Research has identified that semaglutide-induced weight loss plateaus around 12 months, and unfortunately, the majority of patients regain weight after stopping treatment. Previous studies suggest that combination treatment with leptin and semaglutide leads to weight loss and a decrease in food intake. The goal of this project is to confirm the synergy of the previous research as well as determine the mechanism behind these findings. Additionally, the research question was do Glp1 receptor agonists like semaglutide restore leptin sensitivity in diet-induced obese (DIO) mice? Our hypotheses were that DIO mice will change from leptin insensitive to leptin sensitive when given semaglutide and mice will lose more weight with combined semaglutide and leptin than with either therapy alone. The methodology included DIO mice implanted with pumps to deliver leptin or PBS and were given daily subcutaneous injections of either semaglutide or vehicle for 21-days; Bodyweight, food intake and temperature were measured daily; Body composition was measured at baseline and post-treatment; Plasma leptin was measured at the end of the treatment period via ELISA assay; Leptin sensitivity was assayed by measuring pSTAT3 expression in the hypothalamus 30 minutes after intraperitoneal injection of leptin. The results showed increased pSTAT3 staining in the hypothalamus of PBS+Semaglutide treated mice suggesting semaglutide has restored sensitivity to leptin in DIO mice, however, semaglutide combined with leptin does not increase weight loss or leptin signaling. In conclusion, semaglutide restores leptin sensitivity in leptin-insensitive DIO mice.

Investigation of Intramolecular Left-Handed G-Quadruplexes

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G-quadruplexes are DNA structures composed of 4 interacting strands (compared to 2 in B-DNA) in guanine-rich regions. Guanine bases interact via Hoogsteen bonds in lateral fashion, forming a planar tetrad that is further supported by π - π orbital stacking and interactions with monovalent cations integrated in an ion channel. Different topologies of strand 5'-3' end orientation, loops, and handedness are possible depending on the glycosidic conformation of guanines, solvent, co-solute, etc. Guanine tracts can stack to form intermolecular GQs or be directly conjoined by non-guanine base linkers to form intramolecular GQs. Sequences with the potential to form GQs are commonly found in telomeric and promoter - especially proto-oncogene - regions, and GQs that form in these regions have been found to inhibit the extension of telomeres by blocking the access of telomerase to the strand. GQs are also able to be targeted by small-molecule ligands, potentially acting as therapeutic targets for cancer and other diseases.

Handedness is the direction in which the guanine tract of the GQ progresses, also described as a helical twist: a right-handed structure (RHGQ) will twist in a counterclockwise direction, while a left-handed structure (LHGQ) will twist in a clockwise direction. Intramolecular GQs can be fully left-handed, fully right-handed, or form LH/RH hybrid structures, with two subunits of differing helical twists. Using biophysical assays (e.g. circular dichroism and UV-Vis spectroscopy) and X-ray crystallography, we are characterizing the formation of fully left-handed, intramolecular GQs. LHGQs are extremely sequence-dependent - only two sequences, composed of GGT repeats, have been found to form LHGQs, known as Motif1 (GTGGTGGTGGTG) and Motif2 (GGTGGTGGTGTG). They are often disrupted by nucleotide additions, so most GQs are right-handed. However, there are several proto-oncogenes known to us to contain Motif1 and/or Motif2, with the potential to form LH/RHGQs or fully left-handed GQs. These sites could serve as very specific targets for therapeutics, so understanding the formation of intramolecular LHGQs and their interactions with small-molecule ligands would start the way to treatments that target RH/LHGQ and LHGQ proto-oncogenes.

Artificial Intelligence Toolkit

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The Artificial Intelligence Toolkit (AITK) is an open-source project aimed at providing resources for non-experts to learn about and get hands-on with AI technologies such as deep learning, data manipulation, and generative AI; with a particular focus on highlighting the ethical and real-world impacts of these technologies. The project comprises a set of accessible Python tools and a collection of interactive computational essays (Jupyter notebooks). It is designed for use both by independent learners and also as material for classroom educators.

This summer, we reorganized our Github repository and ReadMes. Since this is how most users will access our toolkit, we wanted to make it navigable even for those unfamiliar with Github, and also provide guidance on which notebooks would be appropriate for users of different levels and needs. There were also many notebooks that were works in progress, or were outdated due to new package releases, that we have now brought up to date.

Our main focus was on developing new computational essays to cover contemporary and emerging topics in AI, especially relating to new AI technologies like ChatGPT and Midjourney which have taken the world by storm. Our Word Embedding notebook is an introduction to language modeling, discussing how LMs absorb problematic associations from texts. Our Data Manipulation notebook lets users

adjust class imbalance in a dataset before training a classifier on it, to show how that differentially affects the classifier's performance and introduces bias. Our NanoGPT notebook is a high-level tour through building and training a tiny GPT-style generative language model that generates Shakespeare. We are working on two notebooks to follow this one; a more technical notebook on transformers in general, as well as a notebook focused specifically on the attention mechanism. And our Image Generation notebook is a notebook introducing the broad concepts – diffusion, and CLIP embeddings – powering modern image generation models like Dall-E.

Finally, we performed some user testing on existing and new AITK material – and the redesigned Github repo – to assess its accessibility and educational value. From the results of our testing, students from various demographics generally think this notebook is quite effective and usable.

The Explorer-Director Game on Graphs

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The Explorer-Director game, first introduced by Nedev and Muthukrishnan, is a game that considers movement of a token to different locations as determined by two players. One player, the Explorer, desires to have the token visit as many locations as possible, and contributes to the movement of the token by saying a distance for the token to move. The Director—who wants to minimize the number of locations visited—then gets to decide based on the required distance, what specific location the token visits. In the consideration of the game on graphs, these locations are the vertices, and distance is defined as the shortest path between two vertices.

We considered the number of vertices visited on different graphs and starting vertices when both players play optimally. Additionally, we considered the existence of closed sets of vertices on the graphs, which are defined as sets where for every vertex in the set, for every distance the Explorer could say, there is another vertex in the set at that distance. Once the Explorer enters one of these sets, the Director is able to keep them inside of it. We also considered certain types of graphs, specifically Dutch Windmill graphs and Hypercube graphs. For Dutch Windmill graphs, we found a pattern that suggests the number of vertices visited depends on the size of the largest two cycles in the graph, as well as the size of the cycle started in, if it was separate from the two largest. For Hypercube graphs, we found that, due to the symmetry of the graphs, the solution depended on the smallest closed set of vertices. We found a minimum size for these sets and two patterns that suggest maximums for these sizes, all depending on the dimension of the graph.

Structural Analysis of Alloys of Chromium Thiophosphate with Indium and Aluminum

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There is currently a need in quantum computing, and especially in information storage, for materials that can be precisely controlled at the atomic level. 2d Van-der-Waals (VdW) materials are a particularly good candidate for this purpose, being composed of atomically thin layers held together by VDW forces, and can thus be facily separated into single layers. Of these materials, chromium thiophosphate (CrPS4) is of particular interest due to being air stable and easy to synthesize. CrPS4 also has unique magnetic and optical properties; it is an A-type antiferromagnet and displays unusual magnetic and temperature dependent photoluminescence. However, there is still debate within the literature regarding the origin and mechanism of these phenomena. In order to better understand the nature of CrPS4, in this project we alloyed CrPS4 with aluminum and indium in varying ratios using vapor transport synthesis. Preliminary results suggest that we successfully synthesized a chromium thiophosphate lattice with alloying ratios of up to 20-30%. Inserting In and Al in place of Cr systematically perturbs the lattice, and so comparing the properties of the alloyed versus un-alloyed samples may provide a pathway towards better understanding CrPS4.

Trafficking of Fibroblast Growth Factor Receptors via CDK1-mediated phosphorylation of Rab7 GTPase throughout the cell cycle

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Rab GTPases are key regulators of endosomal trafficking through coordination of intracellular movement, localization, and fusion of vesicles. In particular, the rab7-dependent pathway regulates fusion of mature endosomes with the lysosome, where membrane proteins are degraded. Recent studies indicate that the cell cycle regulator cyclin dependent kinase 1 (CDK1) suppresses degradation of the membrane protein fibroblast growth factor receptor (FGFR). However, membrane trafficking during mitosis via regulation of rab GTPases remains poorly understood. C terminal sites (serine 201, 204, 206) in rab7 match a consensus for CDK1 phosphorylation. Motivated by these findings, we investigated the hypothesis that CDK1 phosphorylates rab7 to suppress lysosomal trafficking of FGFR during mitosis. We used mass spectrometry to examine rab7 phosphorylation in mitotically enriched cultured mouse keratinocytes, and will examine the effect of CDK1 inhibition on phosphorylation patterns of rab7. Our results aim to contribute towards understanding how membrane proteins are trafficked throughout the cell cycle via rab7 GTPase activity.

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

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Rechargeable lithium-based coin cells are now commercially available offering an eco-friendly alternative, but their use is not as widespread. Its major concern is safety: batteries of small size are more susceptible to rapid heat conduction, and physical impacts are more likely to be caused by falling and puncturing. Using in a nonambient temperature environment could cause thermal

runaway or surge in impedance, significantly degrading their performance. Detailed performance tests for the coin cells are an urgent matter. We report on a non-destructive, temperature-dependent performance comparison of six different commercially available, rechargeable 2032 coin cell models through galvanostatic cycling: LIR2032 (CT-Energy), LIR2032H (CT-Energy), LIR2032 (EEMB), LIR2032H (EEMB), LIR2032 (LoopaCell) and ML2032 (Maxell). The batteries were cycled over 100 cycles at three different temperatures: 60°C, 24°C, and 0°C. In situ data collection was performed using temperature-controlled test chambers. Performances at room temperature were consistent with the manufacturer's datasheet. At hot temperature, all cells performed in a stable manner but experienced faster degradation, mainly because of their electrolyte decomposition or the formation of SEI. At cold temperature, all LIR2032 showed stable performance, yet LIR2032H cells performed poorly. At initial hot and room-temperature cycling, we also observed an increase in initial capacity, which may be due to an increase in lithium inventory from electrolyte salt dissolution, as identified from dQ/dV analysis and EIS. Most cells showed an initial ohmic resistance decrease, then loss of both electrode's active material and faradaic rate decrease of cathode at mid- and end-cycles. Both XRD results and dQ/dV analysis allowed prediction of electrode composition, where LIR cells were identified as LCO/GIC, and ML2032 (Maxell) being LMO/Mg2Si.

Determining whether deposition of histone marks over olfactory receptor genes is altered in the absence of Testis expressed gene 15

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A critical process for a mammal's perception of smell is the detection of chemical odorants by olfactory

sensory neurons (OSNs) in the main olfactory epithelium (MOE). Olfactory receptors (ORs), expressed by OSNs, are the proteins responsible for the direct detection of these odorants. OSNs have been observed to be highly selective in that each OSN only expresses one allele of one OR gene out of about 1400 OR genes. However, the exact mechanism regulating this monoallelic OR expression remains unclear. We have confirmed that a protein linked to gene silencing and heterochromatin deposition, testis expressed gene 15 (Tex15), is localized in the nucleus of OSNs during differentiation. Previous research indicates OR expression is distorted by a loss of Tex15, with a few OR genes being markedly upregulated. Thus, we hypothesize Tex15 has a role in heterochromatic silencing over OR genes. The aim of my research is to determine whether a loss of the Tex15 gene alters histone mark deposition on OR genes. I conducted native ChIP-seq experiments to map the deposition of heterochromatic marks and active marks to regions of the genome, comparing the histone modifications between Tex15 knockout (KO) and control OSNs in whole MOE tissue. We hypothesize to observe a reduced signal of heterochromatic marks in the Tex15KO over OR genes. Indeed, preliminary results show reduced heterochromatic H3K9me3 signals over OR clusters and OR genes in the Tex15KO. Thus, by mapping the deposition of histone modifications, we can begin to decipher the gene regulatory networks that support monoallelic OR expression.

Compression of pinned granular systems II: Simulation

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Granular systems are complex systems made of constituents that interact through contact forces. These constituents can vary widely, ranging from hard particles like sand grains to soft materials such as soap bubbles, and can measure anywhere from microns to meters. A key feature of granular systems is the "jamming" phase transition, where the system transitions from a fluid-like state to a disordered solid state due to changes in density or applied stress. Previous research by our group and others has shown that the introduction of pinned particles (fixed degrees of freedom) near the jamming threshold changes both microscopic and macroscopic properties. The current work investigates the effects of fixed pins on properties of granular materials under uniaxial compression.

Using LAMMPS (Large-scale Atomic/Molecular Massively Parallel Simulator), a powerful molecular dynamics program, we analyze the dynamical behavior of a jammed two-dimensional, bidisperse granular system with pin numbers ranging from 0 to 225, amid 4096 particles.

Visualization with OVITO software reveals interesting dynamical features, such as the propagation, oscillation, and eventual breakup of the vertical velocity front as the simulation progresses. Additionally, we track the development of the force chain network during compression. The stress-strain analysis shows that the system experiences extended transient noisy periods with occasional linear responses, typical of many materials. The packing fraction as a function of pressure shows a linear relationship as predicted by theory. The y-intercept of a linear fit corresponds to the critical jamming threshold, which decreases as pin density increases, consistent with previous findings. The slope of the fit line, proportional to the bulk elastic modulus, does not change significantly across different pin densities. This could be due to the limited range of pin densities explored in the study. Future research is necessary to resolve the discrepancy between the slope of this fit and the expected value from the force network, which currently differs by half an order of magnitude.

Some of the results of this research are corroborated by compression experiments conducted by the Bester group at Swarthmore. Their single pin experiments on bidisperse discs in two dimensions have roughly the same pin density as our systems which contain four pins.

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A Robust, Third-Order Accurate Solver for the 1D1V Vlasov-Poisson

Equation

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The 1D1V (one dimension in both physical and velocity space) Vlasov-Poisson (VP) equation is a kinetic model used to describe collisionless plasmas via a probability density function. To numerically compute the solution to the VP system, we discretize the function over a phase space mesh, and then update in time the solution over this grid. In particular, we use high-order weighted essentially non-oscillatory (WENO) for spatial reconstruction, combined with a third-order strong stability-preserving Runge-Kutta (SSP-RK) method for the time stepping. At each RK stage, we first solve a Poisson equation using the Fourier transform to compute the electrical field from the particle number density. We then use fifth-order accurate WENO to reconstruct from the centered nodes the fluxes at the cell boundaries in both physical and velocity space. It is generally challenging to accurately resolve solutions with sharp discontinuities and high filamentation, and spurious oscillations can occur if spatial reconstruction is not handled properly. However, WENO maintains high-order accuracy while resolving sharp discontinuities and smoothing out spurious oscillations.

We evaluate the proposed solver's accuracy and robustness on several classic plasma problems, including weak Landau damping, strong Landau damping, and two-stream instability. These tests also demonstrate that the numerically computed electrical fields evolve with the correct theoretical decay rates. Currently, we are working on extending this solver to the 1D2V Vlasov-Fokker-Planck model, which accounts for plasma particle collisions and requires both implicit and explicit time stepping methods, ideally of high-order accuracy. Moreover, we are developing a low-rank extension to reduce the storage complexity of the solution.

Using Large Language Models (LLMs) and Machine Learning to Characterize Chemical Vapor Deposition (CVD) Synthesized MoS₂

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Two-dimensional (2D) materials, such as transition metal dichalcogenides (TMDCs), have attracted significant attention due to their unique atomic thickness. These materials exhibit a range of characteristics, including high carrier mobilities, mechanical flexibility, high optical absorption, and photothermal effects. Consequently, 2D materials hold promise for a wide array of applications, including electronics, soft robotics, catalysis, and biosensing.

Synthesis and analysis are pivotal areas of research for 2D materials. In our lab, we synthesized monolayer molybdenum disulfide (MoS₂) flakes using chemical vapor deposition (CVD). By optimizing the growth parameters, we achieved various sizes and structures of MoS₂ flakes, with the largest flake measuring approximately 100 μm .

Image processing and identification techniques powered by machine learning were employed to distinguish the domain and layer numbers. To achieve more automation of optical microscopy and accelerate the identification process, I use large language models (LLMs) to assist with unsupervised learning to quickly identify the features of MoS₂.

Advanced Neutron Scattering Techniques for Operando Characterization of Phase Change Materials

Y. Jin, H.L. Smith

The reversible amorphous to crystalline phase transition in Ge-Se glasses has led to their critical use in

applications ranging from heat sensors for real time temperature monitoring to optical media storage. Despite these important applications, our understanding of the dynamical changes occurring across this phase transition remains incomplete. This work describes the development of an operando inelastic neutron scattering technique as an advanced thermal and material characterization tool to study the phase transition in bulk Ge-Se glasses. The operando inelastic neutron scattering technique produces time-resolved information about the phonon vibrational dynamics in these materials transition from amorphous solid to undercooled liquid and crystalline solid. This new technique allows us to capture a phonon density of states in as little as 90 seconds, providing real-time quantitative evaluation of the vibrational entropy in the glass, liquid, and crystalline phases. Aspects of operando neutron scattering data collection and analysis will be discussed alongside new insights into the vibrational dynamics in Ge-Se glasses. Potential for application of this technique to additional phase change materials will also be discussed.

Modeling Transmission Dynamics of SARS-CoV-2 in Wildlife

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Following the global COVID pandemic, our society continues to grapple with a virus that infected millions of people and many species of animals. Conceptual frameworks of SARS-CoV-2 transmission dynamics in ecological communities allow us to account for wildlife host interactions, community prevalence, and spillover transmission. Coupling dispersal and joint species distribution with disease transmission models allows us to investigate the transmission of pathogens across dynamic and complex landscapes. It is imperative to know the distribution of different species to quantify the likelihood of interactions between species to better predict and describe disease transmission dynamics. With this rationale, a machine learning model, MaxEnt (Maximum Entropy), was employed to describe the probability of suitability for land cover in the eastern United States for eighteen native mammal species. Using numerous packages in R, we efficiently wrote code to break down and extract relevant values from large data repositories, such as the Global Biodiversity Information Facility and WorldClim. With the necessary data, we trained a model to predict the probability of suitability for the entire extent of continental America (North America and Mexico). After training the model, we tested the model only on the eastern region of the United States and collected AUC (Area Under Receiver-Operating-Characteristic Curve) scores to evaluate the accuracy of the model. For the 18 species, the average AUC was 0.879 (standard deviation = 0.07), above the generally accepted field standard of 0.8.

There is an immense amount of data on SARS-CoV-2 prevalence in a variety of animal species. This is unique across zoonotic pathogens, and this theoretical work is necessary to better understand and contextualize that biological data. Building on species distribution models, future studies could dive deeper into the intricacies of species-species interactions and species-habitat interactions, such as the prevalence of species and viral transmissions in urban hotspots.

Compression of pinned granular systems I: Experiment

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Granular materials are aggregates of solid particles, usually larger than 100 micrometers, such as sand, rocks, piles of candy, and snow. Granular systems can behave as different phases of matter, and exhibit a phase transition of 'jamming', above which they behave like solids. This study investigates the role of fixed pins in altering the stress distributions and jamming behavior of granular materials under uniaxial compression. We conducted experiments in a semi-two-dimensional system to explore the effects of different pin configurations on force chains, particle stress, and contact number. By varying the position and number of fixed pins, we aimed to understand how these obstacles influence local stress environments and the onset of jamming. To indirectly measure the stresses between grains, the gradient-squared (G^2) method was used for polarized images. We analyzed force chain networks through photoelastic imaging and the distribution of G^2 within the system.

Results show that the presence of pins significantly increases the stress borne by particles beneath them, with force chains often extending from the pin to the compressing bottom wall. The pins cause a shielding effect, decreasing G^2 for grains above them by terminating force chains originating from the bottom wall. Pins positioned at the vertical center of the system exhibited the most pronounced effect, particularly in raising the G^2 of particles below the pin. This effect diminished as horizontal distance from the pin increased, suggesting a localized influence of the pin on stress distribution. Double-pin configurations displayed an increase in G^2 throughout the system, however the shielding effect only occurred in the arrangement with the largest distance between the pins. In addition to stress analysis, we examined the average contact number (Z) across various pin arrangements. Heat maps of Z reflected trends similar to those found in G^2 , with the pin arrangements creating a distinct contrast between the top and bottom halves of the system.

Our findings indicate that fixed pins influence the jamming behavior of granular materials by increasing particle contacts and enhancing force chain formation for grains between the pins and the compressing wall, while in some circumstances shielding grains on the opposite side from compression stresses. Future research should include a larger apparatus to contain the grains, higher density pin configurations, and an incorporation of particle-pin contacts in the calculation of average contact number to more accurately capture the system's behavior.

This research is related to compression simulations conducted by the Graves research group at Swarthmore. Results such as the reduction in the jamming threshold thanks to pins are supported. Results on increased stress at pin densities equivalent to ours, and the anisotropic geometry of the force network are currently being generated.

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Characterizing the canonical DNA/RNA-sensing pathways for erythroid progenitor antiviral immunity through genetic knockout

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Red blood cells are primarily recognized as oxygen transporters. However, recent studies by the Clements lab have indicated that nucleated erythroid progenitor cells (red blood cell precursors) also play an active role in the immune response of neonates and critically ill adults. Single-cell transcriptional analyses revealed the expression of nucleic acid-sensing pattern recognition receptors in erythroid progenitors. In classical immune cells, upon viral infection, pattern recognition receptors detect viral DNA or RNA and initiate a signaling cascade that activates the upregulation of type I interferon transcription that activates the transcription of antiviral genes. My goal in the Clements lab was to determine which (if any) components of the DNA/RNA-sensing pathways contribute to innate antiviral immunity in erythroid progenitors through CRISPR-Cas-9-mediated gene knockout. This summer I successfully designed and constructed plasmids containing the machinery required to knock out genes important for the canonical DNA-sensing pathway (cGAS and STING), RNA-sensing pathway (MDA5 and MAVS), or both pathways (IRF3). Next, my constructed plasmids will be transfected into human erythroid progenitor cells and further investigations will analyze how antiviral immunity changes in the absence of canonical DNA/RNA-sensing genes. Our research on the antiviral immune response in erythroid progenitors will provide insight into the development of targeted therapies for viral infections, autoimmune, and inflammatory disorders in neonatal health and severely immunocompromised adults.

Learning-enabled Safety-Guaranteed Navigation Algorithm for Communication-Free, Heterogeneous Multi-Mobile Robot Systems Using Voronoi Tessellation

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In this paper, we propose a safety-guaranteed navigation algorithm for heterogeneous, communication-free multi-agent systems (MAS) that addresses the challenge of maneuvering in an unknown environment without prior knowledge of non-ego agents.

Voronoi tessellation-based methods are a popular choice for partitioning the state space of multi-agent systems (MAS) to ensure the safe navigation of agents. This is because they not only offer strong mathematical guarantees for safety but also impose minimal restrictions on individual agent's controllers. When applied to communication-free MAS, Voronoi tessellations often assume that all agents maintain a consistent, real-time map of the environment, ensuring agreement on the partitioning. This assumption becomes problematic in heterogeneous systems, where each agent reacts differently to the same environment—represented by the safety notion parameters in this work—making it impossible for all agents to share a consistent map, thus losing safety guarantee.

Due to this limitation, many existing approaches allow local communication between agents or assume that safety notion parameters are provided as prior information. However, such assumptions may not be realistic in dynamic, outdoor environments, where communication can be unreliable or unavailable, and prior knowledge of other agents' safety parameters is unlikely. As a result, there is a critical need for a novel solution that allows agents to operate without relying on prior information or guaranteed communication, enabling them to learn and adapt to their environment online.

To address these challenges, we introduce a Bayesian inference-based online learning navigation algorithm that offers three key contributions. First, through Bayesian inference, each agent learns the safety parameters of other agents by observing their movements, achieving an error margin of less than 10% in 90% of cases. Second, although the full convergence between agents' safety parameter estimation and the true parameter values is not guaranteed, we provide a rigorous mathematical proof proving that all agents will converge to a consistent map. This ensures that the system always creates a safe map, guaranteeing safety 100% of the time, while accurately reflecting agents' true safety parameters in 90% of cases. Finally, we validate the algorithm's efficiency and effectiveness through comprehensive simulations in diverse environments, demonstrating its practical applicability in real-world scenarios.

Computing Homotopies Using Homotopy Fixed Point Spectral Sequences

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Topology is the study of properties of topological spaces which are invariant under continuous reversible deformations. A common problem is the ability to differentiate between various topological spaces. One method of differentiation associates a sequence of algebraic structures to a topological space using generalized homology theories. We are particularly interested in the generalized homology theory $E_2^{hC_6}$ and wish to compute the $E_2^{hC_6}$ -homology of RP^2 and $RP^2 \wedge CP^2$. To do this, we use Homotopy Fixed Point Spectral Sequences (HFSS), which are a means of computing homology groups by taking successive approximations of the associated graded. This means that the spectral sequence computes extension problems for each homology group, which can then be resolved to find the homology groups through additional topological data. In our poster, we discuss our process of computing $E_2^{hC_6} * RP^2$ and $E_2^{hC_6} * (RP^2 \wedge CP^2)$. In particular, we delve into detail on the process of importing differentials from one HFSS into another by constructing commutative maps of algebraic structures.

Hydrodynamics of larval urchins: ontogenetic changes and tracer influence

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Many marine plankters are suspension feeders, relying on efficient particle collection to survive in environments with low food concentrations. Understanding how suspension feeders collect food in dilute

environments is crucial to understanding their physical form and ecological function. Echinoderms have a planktonic larval stage that uses ciliated bands for swimming and feeding. Using the pluteus of the urchin *Lytechinus variegatus*, we examined changes in larval hydrodynamics through ontogeny utilizing micro-Particle Image Velocimetry (μ PIV). Additionally, we tested the effect of tracer type on larval velocity and flux by using the alga *Isochrysis galbana* and 6.62 μ m polystyrene beads as tracers in independent trials. We observed Stokeslet-like flow around larvae, for which the streamline velocity increased as the larvae developed. We did not observe vortex arrays nor ciliary tangles as previously observed around larval seastars. The estimated flux towards the oral region of the larvae increased with age and using *Isochrysis galbana* as tracers led to higher flux estimates compared to polystyrene beads. Larvae in algal tracers were observed swimming in more convoluted paths compared to beads. Comparison between flux estimates and clearance rates can further shed light onto particle selection during feeding. Our work demonstrates an important caveat of μ PIV: tracer type may influence larval behaviors. Mindful experimental design and reporting can further our understanding of the hydrodynamics of small ciliated swimmers, and ultimately larval form.

Interannual Variability of River Discharge and Winds: Implications for Residence Time in Beaufort Sea Lagoons

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Nutrient availability in arctic coastal lagoons impacts primary production, food webs, and subsistence hunting for local communities. Estuarine circulation modulates nutrient availability, impacting how long riverine nutrients remain in coastal lagoons versus being exported to the ocean. The objective of this study is to characterize long-term trends and interannual variability of wind velocity and river discharge, both of which impact the residence time of nutrients, specifically near Arey and Jago Lagoons on the Alaskan Beaufort Sea coast. Daily mean wind data between 2010-2023 and daily river discharge data between 1984-2018 were analyzed to identify interannual trends during May through October, which roughly corresponds to the open water season. During these months, winds blow predominantly towards the west. High wind days, defined as days where daily mean windspeeds exceed the May-October 95th percentile ($>11.82 \text{ m s}^{-1}$), occurred 8.0 ± 4.42 days per summer between 2010-2023. No trends were found in the number of high wind days per year ($p = .38$). There were $+2.85 \pm 4.34$ more days of high winds towards the west than towards the east per summer. Mean river discharge into Arey and Jago Lagoons was found to increase between 1984-2018, although not significantly, with $+0.25 \text{ m}^3 \text{ s}^{-1} \text{ y}^{-1}$ into Arey Lagoon ($p = .09$) and $+0.12 \text{ m}^3 \text{ s}^{-1} \text{ y}^{-1}$ into Jago Lagoon ($p = 0.17$). The timing of high wind events to river discharge is also being analyzed. Our results imply that increases in river discharge may shorten the residence time of freshwater in lagoons. Variability in wind direction during events may impact the fate of freshwater and nutrients from individual rivers.

Progress towards the synthesis of orthogonal porous organic cages with multiple pore sizes

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Porous organic cages (POCs) are molecular cages which have used for molecular sensing, gas adsorption, and drug delivery. POCs are typically constructed using dynamic covalent bonds, which undergo reversible formation and cleavage. POCs containing these reversible bonds can be constructed using simple monomers, which then assemble into the most thermodynamically stable structure. The use of multiple, orthogonal dynamic bonds introduces new properties and responsiveness for POCs. Specifically, the use of orthogonal bonds can result in POCs with multiple pore sizes. Previously-synthesized orthogonal cages have used alkynes with imine and boronic esters with imines. Recent work

on a dynamic S_NAr mechanism has enabled reversible ether formation.

The present study describes current progress in the Yang Lab towards synthesizing POCs containing orthogonal ether and imine bonds. First, computational simulations were used to guide the design of monomers for the construction of the orthogonal POC. Next, monomers were synthesized based on the results of the computational analysis. S_NAr reactions were then performed on various monomers to produce macrocyclic building blocks for future imine bond formation. During reaction optimization, an unusual product distribution emerged. Investigation of this product distribution revealed that the ether bonds were hydrolyzed at increased temperatures, resulting in the hydrolyzed monomers being removed from thermodynamic equilibrium. This result stands in contrast to imine bonds, which hydrolyze under acidic conditions. Future work will investigate the formation of an orthogonal POC with pH-responsive disassembly into macrocycles.

Large-Scale Horizontal-Vertical Bias

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The horizontal-vertical bias is the tendency for observers to overestimate the length of a vertical object relative to a horizontal one. In previous literature, the bias has been reported as a 5-10% overestimation, and a more sizable effect of 15-25% has been observed for large objects in the real world. Our experiment sought to replicate previous findings from an experiment in virtual reality, whereby the magnitude of the bias is larger if the two objects are separated in depth compared to when they are presented in the same depth plane. We explored other nuances in how characteristics of the viewing scene affect the horizontal-vertical bias, and we sought to explore angle distortions as an underlying factor of the bias.

We conducted two experiments to investigate these questions. In the first, 48 participants were tasked with adjusting the horizontal gap between two balls until the length of the gap was equal to the vertical height of the pole. Participants were randomly assigned to one of four conditions defined by viewing posture (upright or supine) and depth order of the objects (aligned or separated). One azimuthal angle judgment collected in Experiment 1 led us to explore angle judgements more robustly in Experiment 2, where 24 participants were asked to give verbal reports of multiple azimuthal angles. Similarly, they were randomly assigned to a condition based on viewing posture (upright or supine) and direction of angle (right or left).

Our results did replicate the findings first observed in VR; judgments made in the separated condition were significantly larger than those made in the aligned condition. We did not find a significant effect of viewing posture on the horizontal/vertical matching task, but in the follow up experiment we did find a significant effect of viewing posture for azimuthal angle judgments. Our results contribute to the ongoing theories working to explain this sizable distortion in our perceptual experience of the world. Furthermore, they inform the use of fMRI in the study of space perception since those undergoing fMRI are supine, and their experience of the world could differ accordingly.

Effect of maternal water restriction on offspring water balance physiology in *Octodon degus*

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Octodon degus is a caviomorph rodent species endemic to the Chilean matorral. In this habitat, degus experience predictable seasonal variation in precipitation, where most of the year's rainfall occurs during the winter when degus are pregnant. However, annual rainfall is highly variable, and is currently becoming more so due to climate change-induced aridification. Because winter rainfall is the main predictor of annual food availability, water cues during gestation likely have important impacts on offspring development and future fitness. We hypothesized that degu pups which developed under water-restricted maternal conditions would express more conservative water balance physiology. Throughout gestation and lactation, captive-bred pregnant females were given either 80% of their average daily water

intake or *ad libitum* water. Pups were weighed regularly until 28 days post-parturition. On postnatal day (PND) 28–34, we used open-flow respirometry to evaluate basal metabolic rate and evaporative water loss, and collected water-deprived urine samples to assess urine concentrations via osmometry. We found that pups with water-restricted mothers (WRM) had significantly higher urine osmolality than control pups. Water restricted pups gained significantly more body weight per day from PND0–3 compared to control pups. However, this trend reversed over the course of development, as water restricted pups gained significantly less weight per day from PND 24–27, approximately the time of weaning. Finally, we repeated metabolic trials and osmometry for the mature pups to assess the long-term effects of developmental water restriction, and mated female offspring at 4 months of age to assess whether this impacted reproductive output.

Intermittent limited access to palatable food reveals individual variability in binge eating consumption patterns

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Binge eating behavior impacts the lives of many individuals as it is common across a variety of eating disorders, such as binge eating disorder. Binge eating disorder is characterized by binge eating that occurs frequently over time- at least once a week for three or more months. Moreover, binge eating appears to be triggered by palatable foods, foods high in fat and/or sugar; but not all individuals who consume those foods binge on them and/or develop binge eating disorders. Currently, the neural mechanisms underlying persistent binge eating behavior and binge eating disorder are not well understood, and well-characterized animal models are needed to study them further. To that end, we set out to characterize a diet-induced binge eating model in female mice. Specifically, we described the behavior of two cohorts of mice exposed to an Intermittent Limited Access (ILA) schedule, during which they had access to a palatable food source for a discrete time period, one or three times per week. In the first cohort, the binge eating (BE) group had access to a high fat diet (HFD) for two hours three times per week for ten weeks and then once a week for seven weeks (2h ILA). The BE group developed a consistent binge eating pattern over ten weeks (consuming significantly more food during the three weekly binge sessions compared to the continuous access controls), and then they continued to binge eat at comparable levels when the frequency of access to HFD was switched to once per week. The second cohort was run using a similar paradigm, but instead with a one-hour binge session three times per week and Western Diet (a high-fat/high-sugar diet) as the palatable food. Like the 2hr ILA schedule, this schedule was effective in establishing binge eating behavior within the BE group, such that the BE group consumed significantly more calories during each binge session than the control group. Despite all the mice in the BE groups experiencing the same paradigm, they did not all display the same magnitude of consumption during binge sessions. This result informed an analysis of the individual differences in bingeing patterns of the BE group from the second cohort. Of the 10 BE mice, 3 were binge eating prone (consistently bingeing in the top tertile) and 3 were binge eating resistant (consistently bingeing in the bottom tertile). This result raises curiosities about what neurological differences exist between binge eating prone (BEP) and binge eating resistant (BER) individuals. Thus, we plan to follow up on these analyses with neural analyses of BEP and BER mice in order to reveal information about the neurobiological risk factors for binge eating disorder.

Tensor Decompositions for Computationally Efficient Many Body System Energy Calculations

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Tensors are a common tool to computationally represent multivariable functions used in simulation algorithms such as modeling quantum many-body systems. However, this convenient representation comes at a cost; the operational cost of accessing and modifying elements of a tensor grows exponentially

with the number of functional parameters. Tensor decompositions aid us in reducing the dimensionality of and finding patterns in large data sets. A tensor network is a collection of tensors which are tied through some series of linear and multilinear algebra. In modeling algorithms, researchers often seek to decompose individual tensors within a network to reduce the computational complexity of computing the tensor network. Unfortunately, this process introduces a degree of error which is propagated through the network. The degree of error in the network then may grow without mitigation and can be intensified. To tackle this issue, we developed a method to decompose the exact tensor network in a matrix-free manner. In this work, we focus on utilizing the canonical polyadic (CP) decomposition to represent the order-four particle-particle ladder (PPL) tensor diagram, which is commonly encountered in the coupled cluster (CC) family of methods in electronic structure theory. In general, this approach is not limited to a single family of tensor decompositions or tensor networks. Using this approach we compute the coupled-cluster energy of small water clusters and find with relatively modest CP rank that grows linearly with the molecular system size, we can recover the PPL with over 98% accuracy and compute relevant energy values within the margin of chemical accuracy (1 kcal/mol). This approach allows for controllable accuracy in the approximation of high-cost tensor contractions.

Investigating palatable diet-induced alterations in motivation to consume healthy foods

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Our modern food environment contains an array of foods with high percentages of fats and sugars. The palatability and availability of these calorie dense foods often perpetuate overconsumption and disordered eating. Diet-based approaches to treating compulsive overconsumption consistently show high rates of relapse, and this resistance to treatment may be attributable to altered motivation to consume healthier, less palatable foods. Previously, we found that three-day palatable food access in the homecage reliably induced overconsumption and led to subsequent undereating of a less palatable chow in mice fed on a fixed ratio one schedule. We hypothesize that this undereating and decreased food seeking was driven by a decrease in motivation to earn standard chow due to their exposure to the high fat, high sugar palatable diet. Thus, we are now investigating the effect of three-day palatable food access on subsequent motivation to earn chow using a resetting progressive ratio task. In this task, mice are able to earn food by performing an operant nosepoke behavior. The number of pokes required to earn each food pellet increases over the course of the meal and resets following a period of inactivity. Motivation can be quantified both by a mouse's average number of pokes per pellet and by the maximum ratio the mouse completes (ie: their breakpoint). In this iteration, the mice underwent two periods of palatable diet exposure. As before, mice overate the palatable food and then underate the chow for one day following both palatable diet exposures. Our initial analyses suggest that the mice exhibited decreased motivation to earn chow following their second exposure to palatable diet as indicated by a decrease in pokes per pellet. This semester we will analyze the breakpoints and consumption patterns throughout the 24 hour period to gain more insight about their motivated behavior. This study will increase our understanding of the effects of high sugar, high fat diets on motivation to consume healthier options and aid in the development of effective treatments for compulsive overconsumption.

Computational Tools For Studying The Geometry Of The Hyperbolic Plane

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In a metric space, a quasi-geodesic is a parameterized path γ where the distance between $\gamma(a)$ and $\gamma(b)$ is within a multiplicative and additive factor of $|a - b|$. Thus, quasi-geodesics appear coarsely like geodesics at large enough scale. Uniquely for hyperbolic spaces, it has been shown that a geodesic and a quasi-geodesic with the same endpoints can be bounded in distance, as measured by the Hausdorff distance metric, by a constant which is independent of the geodesic's length.

To study the optimality of previously proven bounding constants—and to facilitate further study of quasi-

geodesics—we develop computational tools for generating arbitrary collections of quasi-geodesics in the hyperbolic plane. We also describe and implement an algorithm for calculating the Hausdorff distance between two piecewise-geodesic curves by adapting previous techniques to hyperbolic settings.

We first generate a quasi-geodesic via a random walk procedure, where we calculate the range of allowed directions of travel at each step so that our generated curve remains quasi-geodesic. We terminate once a certain distance away from the starting point has been reached, and then use our second algorithm to calculate the Hausdorff distance between our generated quasi-geodesic and the geodesic between its end points. We run this across hundreds of trials to collect many measurements for the Hausdorff distance.

From our data, we show that increasing both the distance between endpoints and the chance for discontinuous jumps both significantly increased the observed Hausdorff distances. However, all of our measurements fall one to two orders of magnitude below the predicted theoretical bounds, suggesting potentially nonoptimality. Based on these results, we discuss further experimental avenues for the use of these computational tools and identify how theoretical and computational limitations of our approaches may be mitigated in future work. For example, we show how computational precision issues caused by the exponential growth of hyperbolic space can be addressed via an implementation of multi-component floating point numbers.

Airborne Wind Energy Kite Research and Testing

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Airborne wind energy (AWE) kites offer a source of renewable electricity generation by harnessing wind energy at higher altitudes than can be reached by conventional wind turbines. As the kite, tethered to a ground-based generator, rises from its lowest position, it generates electricity by turning the generator. Once it reaches apogee, it is reeled in so that the relative wind speeds are lower – allowing a net energy gain. However, having to reel in the kite while the tether is under tension still represents a significant energy loss.

With this project, we are working to develop a novel way to increase power generation. By using a kite with an inverting wing, we can control its lift characteristics. During the power-generation phase of the cycle, the kite's wings have a positive camber, generating lift. However, during the reel-in phase, inversion of the wing shape will instead create “negative lift”, allowing the kite to “fly itself back” to a starting point with minimal reel in energy required.

Past research on this project focused on finding an optimal airfoil shape and arrangement. Through computer modeling and wind tunnel testing, the following characteristics were settled on: a NACA 6412 airfoil with a circular leading edge centered at 10% of the original chord, a 10° dihedral angle, a 20° sweep angle, and an ideal angle of attack between 10° and 15°. With these parameters in mind, we constructed a 7 kg kite with a wingspan of 5 m, consisting of 3D-printed frames and wheels, carbon fiber spars, and aluminum rods that connect the two wings to a central spar. To implement and test the concept of inverting airfoils, we covered each skeletal wing in ripstop nylon fabric and used an air pump to inflate both wings while locking them at maximum camber.

With this prototype kite, we conducted multiple flight tests. In these tests, the kite, tethered to a vehicle moving at up to 11 m/s, sustained flight for a maximum of 6 m. The central spar of the kite was repeatedly redesigned.

Identification of Centrosome Localization Domains in the Novel CAPture-Identified Protein EDC4

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Centrosomes are small, membraneless organelles consisting of a pair of centrioles surrounded by pericentriolar material. As the primary microtubule-organizing centers in animal cells, they are crucial

for mitotic spindle assembly, cell division, migration, and polarity.

The Gergely lab developed a single-step affinity purification method called CAPture, offering improved centrosome isolation over traditional sucrose density gradient centrifugation. CAPture combined with mass spectrometry (CAPture-MS) identified over 50 new centrosomal components and revealed cell type-specific differences.

One notable protein identified was EDC4, an mRNA decapping protein usually found in ribonucleoprotein granules called P-bodies. EDC4 was unexpectedly found in centrosomes across multiple cell lines, raising questions about its function there.

EDC4 has an N-terminal WD40 domain, a serine-rich region, and a C-terminal region with two alpha-helical domains (proximal and distal). Previous experiments showed full-length EDC4 and its C-terminal domain localize to centrosomes and P-bodies, with the proximal domain necessary for centrosome localization and the distal domain co-localizing with P-bodies.

The goal of my project was to identify the smallest domain responsible for centrosome localization and to separate it from the P-body association domain. When I joined the lab, the minimal centrosome localization domain was mapped to exons 25-29. Individual exons seemed too short to properly fold so I designed a strategy to eliminate one exon individually or in combination from the full-length EDC4. All constructs were tagged with GFP and after sequencing validation, were transfected into retinal pigment epithelial (RPE1) cells to study their cellular localization.

The first construct made, lacking exons 25-29 (EDC4 1-24), localized to P-bodies but not centrosomes, confirming exons 25-29 are crucial for centrosome localization. This result was unexpected, since from previous data, we expected the P-body localization domain to be in exons 27-29. This experiment suggested the presence of a distinct P-body localization domain within exons 1-24. Colocalization studies with the P-body markers DCP1a, DCP2, and DDX6 confirmed these findings. While I write this abstract, further constructs have been validated. If successful, I will present data for these constructs.

This work successfully separated EDC4's functions at the centrosome and P-bodies. Next, this construct will be used in rescue experiments in EDC4 knockout cells to elucidate the centrosomal roles of EDC4.

Understanding perceptual multistability and autism using a neuronal network model with image inputs

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Binocular rivalry refers to a phenomenon that occurs when very different images are presented to each eye and the monocular stimuli compete for dominance, resulting in irregular switching between the two percepts. We created a neuronal network model with two competing pools corresponding to the two percepts in order to replicate the switching behavior, and then we applied a compressed sensing approach to reconstruct the dynamic percept at different time points. We created a fusion-based approach for the visual reconstructions, where the percepts were recovered at fixed time intervals using a mixture of two monocular stimulus reconstructions weighted by the relative firing rates of their corresponding pools. This approach used data collected over a short time horizon comparable to human reaction time and yielded improved reconstructions if instead the two stimuli are identical as in visual fusion. Previous research had shown that individuals with autism experience longer dominance durations, and our model demonstrated how this behavior could be replicated by scaling the inhibitory connections to be smaller or excitatory connections to be larger, which is consistent with leading theories on the cause of autism. Finally, we extended our modeling framework to perceptual multistability in the case of three or more competing percepts, such as in trinocular rivalry where the brain interprets the stimuli in three separate ways over time. The model showed that the percept reconstructions were of the same quality as in the binocular rivalry case, but they had shorter dominance durations as often seen in experiment. Based on this, we hypothesize that similar organizing principles may underlie most forms of visual multistability.

The Relationship Between Gastroesophageal Disorders and Lung Allograft Outcomes

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Lung transplant recipients (txp) suffer from a low 5-year survival rate. There is growing evidence that gastroesophageal reflux disease (GERD) increases the risk of allograft dysfunction defined by lower early lung function and chronic lung allograft dysfunction development in addition to comorbidity of esophageal dysmotility (DYS). We hypothesized that patients presenting GERD and DYS would have lower median FEV1 and change in FEV1.

Using Machine Learning to Predict Pathogenicity of Transcription Factor Binding Motif SNVs in Congenital Heart Disease

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Congenital heart defects (CHDs) are structural defects of the heart that are present at birth. CHDs are the most prevalent type of birth defect, yet despite extensive studies, most cases cannot be conclusively linked to genetic or environmental factors. This research aims to deepen our understanding of CHDs by analyzing mutations located in regions of DNA to which transcription factors bind. Transcription factors are proteins that bind to DNA and are essential for translating genetic information into proteins. These factors typically bind to specific DNA sequences known as transcription factor binding motifs (TFBMs), thus involving these regions in gene expression. Previous research has linked mutations in TFBMs to developmental issues of other organs, likely because breaking these motifs prevents expression of genes crucial for organ development. Using a machine learning (ML) classifier, we hope to first predict the pathogenicity of single nucleotide variants (SNVs) found in heart-related TFBMs based on their likelihood of being in the gnomAD database. Using these predictions and a variety of other annotations of each variant, we hope to demonstrate that certain SNVs are implicated in CHDs. Our results indicate that SNVs predicted to be pathogenic are observed in higher frequencies in CHD patients at Nationwide Children's Hospital than in the control group. Some of these pathogenic SNVs were present in the gnomAD database yet were implicated in CHD cases by the model if they occurred as homozygotes. Other predicted pathogenic SNVs that were not present in the gnomAD database occurred as heterozygotes. Further research is needed as they do not elucidate a definitive mechanism for CHDs. Nonetheless, these results implicate TFBM variants in the etiology of CHDs and reinforce their vital role in proper organ in general.

Generating synthetic pulsar timing array data sets

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One cutting-edge field in Gravitational Wave detection is the Pulsar Timing Array (PTA). A PTA has three key components: Supermassive Black Hole Binaries (SMBHBs), Millisecond Pulsars, and Earth-based telescopes. SMBHBs, located far outside our galaxy, emit gravitational waves as they orbit each other. Within our galaxy, Millisecond Pulsars emit radiation beams from their magnetic poles, which carry the influence of these gravitational waves. When these beams cross Earth's line of sight, our Earth-based telescopes detect them as pulses. This data is analyzed to extract gravitational wave signatures using a timing model, which accounts for various parameters of the pulsars and our telescopes. We categorize many of these parameters as Noise, which need to be managed to detect gravitational wave signatures. Over the past 15 years, the North American Nanohertz Observatory for Gravitational Waves (NANOGrav) has collected pulses from these Millisecond Pulsars and publicly shared their findings for researchers in Gravitational Wave detection and related fields. Currently, the project is in the early stages of generating synthetic data sets that streamline this process, requiring fewer parameters than the existing

15-year dataset. The focus has been on producing data that accurately reflects what the time of arrivals (TOAs) will look like for a set number of Millisecond Pulsars over a period exceeding 15 years.

Planning, Design, and Synthesis of a Peptoid Water Filtration Membrane

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With the growing demand and increasing scarcity of freshwater, new and improved methods of water purification are needed to continue to support global needs. Increasingly, this is being done by use of membrane technology, which is more energy efficient and environmentally friendly than older processes such as thermal distillation. However, membrane technology is still largely in its infancy and a number of key areas in which it needs to be improved to be a more practical and effective means of producing clean water. The principal problems of current membrane technology include general performance, fouling (essentially clogging of the membrane), lifespan and maintenance, and ability to operate under a wide range of chemical and physical conditions.

It has been shown that by changing the surface chemistry and structure of membranes more effectively, fouling resistant, long-lasting membranes can be produced. The problem that remains is finding an easy way to create membranes with these properties. Ideal surface chemistries have super hydrophilic, especially zwitterionic, characteristics and are smooth on the molecular level. It is believed that a material possessing these properties can be found by using highly stable and chemically tunable peptoid oligomers. Peptoids, often called N-substituted glycines, are a type of biomimetic polymer similar in structure and properties to peptides but with functional groups branching from backbone nitrogen instead of the α -carbon. Peptoids offer a few key advantages. Peptoids are resistant to proteases, have a simple and high-yield synthesis, and have a type of monomer sequence shown to be able to self-assemble into bilayer-nanosheets, or β -sheets, a few nanometers in width and hundreds of microns in length and depth.

Typical design of membrane starts by modifying a polyethersulfone (PES) membrane support. This is done by dipping the PES in a dopamine solution which coats the membrane and polymerizes. From this an acid chloride containing an azide functional group will be added to react with the dopamine, allowing for the membrane to be able to undergo a copper catalyzed azide-alkyne click (CuAAC) reaction. Lastly, a number of layers of CuAAC capable peptoid nanosheets will be deposited onto and “clicked” to the modified membrane support to create the active layer of the membrane. Herein, this work will describe the use of peptoids to modify the surface chemistry of a PES membrane support as well as the reasoning behind why certain chemical reactions and groups were chosen.

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 contribute to our understanding of AgNP reactivity. Linear sweep stripping voltammetry (LSSV), an electrochemistry technique, was used to measure silver nanoparticle dissolution kinetics based on the amount of silver ions released into solution. 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. Results describing size-dependent and biomolecule-mediated AgNP dissolution kinetics will be presented, as well as results from nanoparticle characterization

experiments.

A conserved toolkit between the germline and the brain: Investigating the role of *oskar* in the *Drosophila* central nervous system

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Animals across various phyla encode experiences through long-term memory, a core neurological process essential for learning and survival. However, we have not identified all the components necessary for memory formation, even in well-studied model organisms. Previous studies have suggested a key player for this process: disrupting *oskar*, a gene with a well-established role in germline specification, leads to defective memory in fruit flies. However, these experiments used a mutant allele that may have disrupted the neighboring gene *polychaetoid* (*pyd*) rather than *oskar*. Here, we aim to directly test the role of *oskar* and *pyd* in the *Drosophila melanogaster* central nervous system. First, we are revealing where *oskar* and *pyd* are present in the nervous system, using immunostaining, *in-situ* hybridization, and reverse transcriptase polymerase chain reaction. Then we are analyzing the neurodevelopmental effects of *oskar* and *pyd* loss of function. These investigations will provide a basis for behavioral and mechanistic studies, including olfactory learning assays and neuromorphological phenotyping experiments of *oskar* and *pyd* alleles, to determine whether *oskar* or *pyd* play a role in encoding long term memory in fruit flies. Our research addresses one of the fundamental mysteries of life—how living things utilize the same tools to accomplish vastly different phenomena.

Design for Deconstruction and Reuse of Cross Laminated Timber: Recommendations and Guidelines for North American Implementation

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This research identifies the barriers, challenges, and requirements to standardize practices for Design for Deconstruction and Reuse (DfDR) of Cross Laminated Timber (CLT) structures in North America, aiming to increase circularity in the built environment. In the United States of America (USA), construction and demolition produce high volumes of timber waste. To enable the recovery and reuse of structural elements from CLT and mass timber buildings, DfDR philosophies need to be applied in the initial design phase. After reviewing current literature, interviews were conducted with industry stakeholders in DfDR work to gain insight into their perspectives and attitudes. This is an initial step toward the development of new guidelines and additional research thrusts to promote DfDR of large structural CLT elements.

Barriers to DfDR of structural materials include inflexible regulations and policy, inadequate information and standards for design, a lack of a market for recovered components, and challenges to developing a business case for DfDR. While guidelines and standards for recertification of CLT do not exist, several organizations in the USA have developed recertification programs for grading or reuse of recovered lumber. This work begins to address challenges of implementing DfDR for mass timber and CLT, developing guidelines for DfDR of mass timber structures, and providing design approaches to support the circularity of CLT elements in the emerging North American Market.

How Closely Related are Different Measures of Reward Sensitivity?

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Impaired reward sensitivity (RS), manifesting as hypo- or hypersensitivity to rewarding stimuli, is a feature of many mental disorders. Given its clinical significance, numerous measures have been developed to assess RS, each probing different aspects of the construct. Examples include the Behavioral Activation System scale (BAS), Temporal Experience of Pleasure Scale (TEPS), Reward Probability

Index (RPI), and Positive Valence Systems Scale (PVSS). Given the diversity of measures assessing RS, a crucial question remains: To what extent are existing measures correlated with one another? Understanding the magnitude of these associations will illuminate the homogeneity of the RS construct and the defensibility of grouping different facets of reward responding within a single domain, as seen in the Research Domain Criteria (RDoC) framework. A mixed sample of 177 community-dwelling adults with generalized anxiety disorder ($n = 47$), major depressive disorder ($n = 22$), comorbid GAD-MDD ($n = 58$), or no lifetime psychopathology ($n = 50$) participated in the study. Participants completed the BAS, TEPS, and RPI, yielding subscale scores: Drive, Reward Responsiveness, Fun-Seeking, Anticipatory Pleasure, Consummatory Pleasure, Reward Probability, and Environmental Suppressors (the latter of which was reverse-scored). A subset of participants ($n = 69$) also completed the PVSS, which yields a total score covering multiple RDoC reward related constructs. Consistent with the notion that these measures assess different dimensions of a broader RS construct, the eight scale/subscale scores shared mostly moderate to high correlations with each other (median $r = .38$, with nearly two-thirds of r values $> .30$). The eight scores also formed an internally consistent scale (Cronbach's $\alpha = .83$), indicating that they hang together statistically. At the same time, the wide range of correlation magnitudes ($.03 < r < .66$) suggested that the scores are not interchangeable and, in some cases, not at all related. BAS Fun-Seeking and TEPS Consummatory Pleasure, in particular, shared much weaker associations with scores on other scales ($.03 < r < .36$) and had a negligible impact on Cronbach's alpha when excluded. Our results suggest that existing measures assess related yet distinct facets of RS. This supports the grouping of reward sensitivity constructs under a single Positive Valence System domain in the RDoC framework, while at the same time underscoring the heterogeneity of the RS construct. In particular, weaker connections of fun-seeking and consummatory pleasure with other facets suggest they may be more distantly related or even fall outside the RS construct. Future research should further examine the role of fun-seeking and consummatory pleasure in the broader reward system.

Fluorescence lifetime imaging to assess amyloid β 42 peptide polymorphism

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Amyloids are protein aggregates with fibrillar structure that is rich in beta sheets. Our research will investigate the physical and chemical factors that influence the simultaneous formation of different amyloid structures (polymorphs) for the same protein. Understanding amyloid assembly is important as amyloids have been implicated in several neurodegenerative diseases. This research will investigate the polymorphic nature of amyloid structures using Fluorescence Lifetime Imaging Microscopy (FLIM). FLIM enables quantitative lifetime analysis of amyloids, facilitating analysis of the impact that different variables have on their assembly. Manipulating solution conditions will be the primary method of investigating the chemicophysical driving forces of polymorphic amyloid formation. This project will explore how NaCl concentrations and Hofmeister ions impact fibril polymorphism of the amyloid- β (A β) 42 peptide which is associated with Alzheimer's Disease. The group hypothesis is that fewer polymorphs will form at higher NaCl concentrations. NaCl inhibits interactions between charged amino acid side chains, therefore, at higher NaCl concentrations, some protein-protein interactions will be inaccessible and there will be fewer possible fibril structures. FLIM will be utilized to capture lifetime images of the amyloid fibrils and analyze the data and images that are collected to test this hypothesis. Fluorescent dye that binds specifically to amyloid fibrils will be used, and quantitative lifetime analysis of the dye's fluorescence enables assessment of the presence of fibrils with different lifetimes. This analysis will be indicative of the different fibril polymorphs present. After imaging various fibrils, the group can formulate ideas about the quantity and populations of distinct polymorphs formed under variable conditions.

Analyzing changes in groundwater level resulting from rainfall at an infiltration site in Mitchells Plain

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Cape Town, South Africa is a water-scarce region, as demonstrated by the 'Day Zero' water crisis between 2015 and 2018. In 2019, the City of Cape Town developed a new Water Strategy in which the City committed to become a water-sensitive city and diversify its water supply. Most of the city's water comes from surface water sources, but the city also has options for groundwater, including the Cape Flats Aquifer (CFA) which lies beneath the city. Rainfall, currently an underutilized water resource, can be leveraged through stormwater harvesting (SWH) and managed aquifer recharge (MAR) into the CFA. A stormwater detention pond in Mitchells Plain, Cape Town was recently retrofitted with an infiltration swale to enhance the pond's infiltration capacity, which serves to recharge the CFA below. This research explores the relationship between rainfall and groundwater level (GWL) at various locations across the detention pond. It investigates trends in rainfall datasets and GWL measurements to identify how long it takes for GWL to respond to rainfall, and at what quantity GWL responds to rainfall at different points across the pond. Results show that locations close to the infiltration swale experience greater and more immediate changes in GWL in response to rainfall events. This provides insight into small-scale groundwater level dynamics at the Mitchells Plain site and indicates that the process of retrofitting the detention pond enhanced its infiltration capacity. An opportunity is presented to retrofit other ponds around the City to develop blue-green infrastructures, and to utilize stormwater to recharge the CFA as a part of the City's Water Strategy. Data for this research was associated with the 'Pathways to water resilient South African cities (PaWS)' project – a collaboration between the University of Cape Town and the University of Copenhagen, and funded by the Danish Ministry of Foreign Affairs (DANIDA MFA).

Validating Non-Invasive Salivary Sampling of Glucocorticoids in Couch's Spadefoots (*Scaphiopus couchii*)

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The current gold standard to measure anuran hormones is blood sampling, however, this method is incredibly invasive, resulting in stress in the animal that potentially confounds hormone measurement, and the sample cannot be taken simultaneously with behavior. In amphibian populations experiencing environmental stresses such as climate change or various other challenges, measuring glucocorticoids, namely corticosterone (CORT), is essential to understanding the environmental impact of such stressors. Thus, establishing non-invasive hormone sampling techniques in frogs is of critical importance when studying the hormone-behavior relationship. Our lab has previously established water-borne hormone sampling as a valid non-invasive method of measuring CORT levels in Couch's spadefoots (*Scaphiopus couchii*). However, a disadvantage of water-borne hormone sampling is the need for a one hour sampling period, limiting temporal clarity. The animal's submersion in water can also prevent behavioral sampling. Thus, we aimed to explore whether salivary hormone sampling is a valid non-invasive technique of CORT sampling in *S. couchii*, as it could improve temporal specificity and occur in close proximity to behavior sampling to better elucidate hormone-behavior relationships. First, using pooled saliva samples, we determined the dilution factor and validated the parallelism of our new matrix. By using an adrenocorticotrophic hormone (ACTH) challenge to artificially raise the CORT levels, we examined whether salivary CORT levels correlated with the established matrices of plasma and water-borne hormones. Two and four hours after the pharmacological challenge, there was a positive correlation between plasma-borne CORT and salivary CORT. In the absence of exogenous ACTH, there was no significant correlation between plasma CORT and salivary CORT. Considering the fact that a correlation between salivary and plasma CORT only exists at artificially elevated levels of CORT, it is difficult to determine whether salivary CORT would reliably detect individual differences in the field. However, in populations that are experiencing major environmental stressors, salivary CORT sampling has the advantage of improved temporal clarity, sampling capacity, and proximity to behavior, therefore allowing for stronger inferences about hormone-behavior relationships. These attributes would be especially useful

in field research and conservation studies.

Talking Tech: Parents' decision-making and communication about screen time rules

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Screen-based devices are becoming more and more ubiquitous in children's daily lives, leading to conflict in many families over how many hours of screen time parents allow their children to have. What kinds of information do parents use to set these rules and how do they communicate their reasoning to their children? In an online survey, parents of children ages 3-11 ($N = 155$) answered questions about their family's screen time habits and estimated how much screen time they think is typical and ideal for children like theirs. Parents in general thought that other children like theirs typically used screen-based technologies much more often than what they thought was ideal, and also more than what they reported for their own child. Parents also answered questions about their child's problematic internalizing and externalizing behaviors and the frequency of family conflicts about screen time; conflicts about screen time rules more strongly predicted problematic behaviors in children than screen time itself. Finally, parents rated how often they used different types of explanations with their kids about screen time rules. Parents who reported using more "stick" explanations (e.g., "you can't have screen time because you broke the rules") also reported that their children used screens more. It is possible that these explanations are more effective for children who are more motivated by screen time, or that they lead children to want to use screens more. In ongoing research, we are examining how children reason about responsible technology use and how parents and children navigate the co-construction of social norms around technology use and screen time in daily life.

In Search of Soil Health Bioindicators in Suburban Gardens. Part 1: Nematodes

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Soil health depends on the abundance and diversity of soil organisms, as well as on the optimal physical and chemical properties of the soil, which support diverse soil communities. Together, these contribute to highly productive agricultural systems. Recently, there has been a surge of interest in the establishment of urban agriculture for local food production. Yet identifying specific health indicators in urban soils remains a challenging task. Our work began the process of identifying bioindicators of soil health in the context of suburban and urban multipurpose gardens and farms. Specifically, we selected three sites around Swarthmore's campus: an experimental potato farm prototype that was established earlier in the spring, the student-run Good Food garden, established 30 years ago, and the Swarthmore Garden Collective, established in 2021.

Our goal was to investigate the abundance and diversity of macro- and meso- invertebrates with particular emphasis on nematodes, a vastly abundant group of meso-invertebrates that are usually less than 1mm long. Nematodes occupy many trophic levels (i.e., herbivores, predators, omnivores, bacterivores, and fungivores), and can play important roles in ecosystems including nutrient cycling and control of pest populations, making suitable bioindicators. Furthermore, previous literature suggests that their trophic level proportions can indicate particular soil chemical and physical conditions. Nematodes were extracted using the Whitehead-Hemming tray method. We counted the number of nematodes, measured their length, and classified them based on their trophic level by examining their mouth-parts. We also tested for different soil properties (pH, soil organic matter, bulk density, and water capacity) in order to determine if there were correlations between soil health and our invertebrate results.

In addition, we sampled a variety of additional invertebrates using Berlese funnels and pitfall traps. We counted and identified the invertebrates to their taxonomic order, and calculated Shannon-Wiener

indexes to evaluate the biodiversity of the soil.

We found that the abundance and diversity of nematodes varied among the three sites. there was a positive correlation between nematode abundance and soil organic matter, indicating that nematodes positively influence the health of soil. As our project is in its beginning stage, our results are predominantly inconclusive. In the future, we hope to use a wider variety of methods to sample invertebrates in order to more accurately represent the variety and abundance of species present. Furthermore, we hope to expand our research to a greater number of sites, in hopes of better understanding the correlation between gardening practices and soil invertebrates.

Effects of aging on cortisol regulation in *Octodon degus*

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The hypothalamic-pituitary-adrenal (HPA) axis controls the body's endocrine stress response by regulating the release of cortisol. The hypothalamus releases corticotropin-releasing hormone (CRH), which then stimulates the pituitary gland to release adrenocorticotrophic hormone (ACTH) into the bloodstream. ACTH then stimulates the adrenal cortex to release cortisol into circulation. Appropriate levels of cortisol are maintained via negative feedback: for example, when cortisol levels are high, plasma cortisol inhibits the release of CRH and ACTH, ultimately reducing cortisol production by the adrenal gland. This successful regulation of cortisol is fundamental for an organism's fitness, as prolonged exposure to high stress hormone concentrations can weaken the immune system, disrupt metabolic activity, suppress reproduction, and increase the risk of cardiovascular issues. To understand how common degus (*Octodon degus*) respond to stress over their lifespan, we repeatedly quantified plasma cortisol levels from these same individual rodents in a laboratory population at 1, 4, 7, 10, 13, 16, 23, 29, and 42 months of age. At each age, blood samples were collected under three conditions: under baseline (non-stressful) conditions, after exposure to stressful stimuli, and after administering dexamethasone, a cortisol agonist that stimulates negative feedback. Cortisol levels were then measured via enzyme immunoassay. We hypothesized that the ability of degus to suppress cortisol production would decline with age. Specifically, we predicted that both baseline cortisol and stress-induced cortisol levels would increase with age, while negative feedback strength would decrease with age. Our predictions were generally supported, as compared to older degus, younger degus exhibited lower baseline cortisol levels, lower stress-induced cortisol levels, and stronger cortisol suppression through negative feedback. These results add to a growing literature on how the HPA-axis changes with age, and how these changes may impact health and fitness parameters.

Diel variation in baseline testosterone levels in a diurnal rodent (*Octodon degus*)

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Testosterone is correlated with various social and reproductive behaviors such as aggression and territory acquisition. However, testosterone tends to vary over a 24-hour cycle, with most species showing peaks during their inactive period. For the common degu (*Octodon degus*), researchers have found low concentrations and low inter-individual variability of testosterone in both the field and laboratory, however, these samples have exclusively been collected during the active period (daytime). We hypothesized that baseline testosterone levels peak during the inactive period (nighttime) in degus, and also show greater inter-individual variation during the inactive period. Therefore, we measured testosterone levels of captive degus at six different time points across a 24-hour cycle with three samples during the lights-on period (10:00, 14:00, or 18:00) and three samples during the lights-off period (22:00, 02:00, or 06:00). Gonadotropin-releasing hormone (GnRH) challenges were also performed during the daytime sampling periods to see if peak nighttime baseline testosterone levels could be simulated during the daytime. As expected, baseline testosterone was highest during the inactive period,

with a peak 2 hours before lights turned on. The GnRH challenges significantly increased the baseline testosterone levels two hours after injection, however, these levels were still much higher than peak baseline testosterone levels. We also found a positive correlation between daytime testosterone levels and post-GnRH levels. The overall peak in testosterone during the degu's inactive period expands on existing research regarding diel testosterone rhythms in mammals. High testosterone levels after a GnRH injection could represent increases in testosterone in male mammals after social and reproductive behaviors, and simulating those surges in testosterone can offer strategies for examining relationships between testosterone and androgen-mediated behaviors.

Key Words: androgen, circadian rhythms, GnRH, mammal, sex steroid

Effects of Annealing in Pt-Cu-P Metallic Glass

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Ultra-fragile Pt-Cu-P metallic glasses and their thermodynamic properties have been systematically investigated using differential scanning calorimetry. The thermodynamic functions of excess enthalpy, entropy, and Gibbs free energy between the liquid and crystal phases were calculated. New calorimetry results, coupled with statistical analysis, suggest a high likelihood of insufficiency of the Kubaschewski equation in accommodating heat capacity in the supercooled liquid phase for some metallic glasses. In particular the difference between annealed and unannealed samples has been analyzed. Additionally quasi-elastic neutron scattering techniques have been used to analyze the dynamics underlying above T_g annealing. Using this QENS data diffusion methods of annealing have been investigated.

Predicting Arctic Stonefly Responses to Climate Change

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Climate change is one of the drivers of a global insect decline. Stoneflies (Insecta: Plecoptera) have one of the highest local extinction rates among insects, in part due to their requirements for cold, highly oxygenated, unpolluted water. Investigating the population structure of stonefly species is integral to their conservation as it has the ability to identify populations at risk of localized extinction. In this study, we extracted DNA from *Nemoura arctica*, *Nemoura cinerea*, and *Nemurella pictetii* specimens collected across Arctic Alaska, Sweden, and Finland. We sequenced the mitochondrial COI gene and the nuclear 28S gene of 96 specimens from 9 locations. We constructed haplotype networks for these three species by combining our sequences with publicly available data from the Barcode of Life Database (BOLD) and NCBI Genbank. We then modeled past, present, and future habitat suitability using species distribution models in the program Wallace. Haplotype networks suggest that *Nemoura arctica* and *Nemoura cinerea* have higher COI genetic diversity than *Nemurella pictetii*, with potential evidence for the description of new species. Species distribution models (SDMs) predict that all three species will lose most or all of their current suitable habitat by 2070, no matter the climate scenario. Arctic stoneflies with low COI genetic diversity like *Nemurella pictetii* may be less suited to adapting to rapidly changing environments and should be a focus of conservation efforts.

Using Neutrinos to Investigate the Interior Structure of the Moon

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Although the Moon's mass and volume have been precisely measured, much is still uncertain about its precise matter distribution. Seismic data suggests that the Moon possesses a dense core, although its precise size and density remains uncertain. Fortunately, though, neutrinos may provide insight into this unknown matter distribution.

Neutrinos are fundamental particles that are extremely difficult to detect, as they rarely interact with other particles. However, this makes them very enticing to study, as a neutrino can travel through the Moon (or across a galaxy) without hitting anything.

As neutrinos travel, they oscillate between states called “flavors.” This flavor oscillation occurs differently when neutrinos travel through matter of higher densities. This means that, depending on how matter is distributed throughout the Moon, neutrinos that pass through it would oscillate differently. Furthermore, once we have detected these neutrinos, we could potentially use their flavor to make inferences about the Moon’s matter distribution.

We have simulated neutrino oscillation through the Moon for different models of lunar matter distribution, in order to learn whether data from the IceCube Neutrino Observatory could provide insight into which of these models is most accurate. We found that, with enough data, it is likely possible to constrain the density and radius of the moon’s core.

However, because neutrinos interact with matter so weakly, current detectors may not detect enough neutrinos to place strong constraints on lunar matter distribution. Many upgraded neutrino detectors will be implemented in the coming years, so we also will consider whether these detectors will be sufficiently large.

Characterizing Vortex-Induced Vibrations of a 3D Printed Circular Cylinder in a Wind Tunnel

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Vortex shedding is a natural phenomenon that occurs when rotating fluid structures (known as vortices) form downstream of an object in a moving fluid. When a cylinder is placed in a fluid where the elements of the flow such as velocity, viscosity, and density allow the formation of vortices, vortex-induced vibrations (VIV) will appear when the frequency at which the vortices are shed in the wake (f_s) approaches the natural frequency of the structure (f_N). Since vortices impart a fluctuating lift force on the cylinder as they are formed and move downstream, the synchronization between f_s and f_N will induce the structure to respond. This results in oscillations of the cylinder, with the response amplitude being highly dependent on characteristics of both the structure and the fluid. Vortex-induced vibrations are well-known to cause material wear on structures immersed in a moving fluid (underwater pipelines, chimney stacks, etc.), so most fundamental research on VIV is motivated by the need to suppress vibration in such structures. However, recent work has also explored VIV as a form of small-scale energy harvesting, and therefore focuses on enhancing the vibration resulting from vortices.

In this work, we analyze the vortex-induced oscillations of a 3D printed circular cylinder of high structure-to-fluid mass ratio (m^*) in Swarthmore’s open circuit wind tunnel. The cylinder is mounted horizontally with four springs that can be replaced to change the spring constant (k). Experimental results are obtained using MATLAB’s image processing toolbox to track the location of the cylinder’s circular cross-section. We consider a mass ratio of 108 and a moderate Reynolds number range of 10^3 - 10^4 to determine the range of nondimensional flow velocities that cause a VIV response (known as “lock-in”) for different values of k . In addition, we look for the presence of hysteresis, which has been found in previous studies on vortex-induced vibrations. The relation between the natural frequency and the frequency of oscillation in the wind tunnel is also explored.

Results indicate a peak non-dimensional response (A^*) of 0.8 at a reduced velocity ($V_r = U/(f_N D)$) of 6.7. Future work will include testing setups with different spring constant values to optimize VIV response for small-scale energy harvesting. Results from this study will be used to inform the design of a larger and more robust version of our system.

Influenza Induced c-fos Activity

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New evidence suggests a connection between the central nervous and peripheral immune systems. When the body undergoes an infection, the peripheral immune system responds by sending immune cells to the area of infection. These cells can then send nerve signals to the brain, alerting it to an ongoing infection. The brain then processes this information and elicits a larger immune response, which can entail physiological and emotional changes such as altered eating habits, fatigue, an increased body temperature, and feelings of isolation. While working at the Choi Lab at the Picower Institute of Learning and Memory at the Massachusetts Institute of Technology, I researched under the guidance of Yire Jeong, a post-doctoral researcher. I contributed to his research, searched for regions of mouse brain activity during influenza infection, and imaged the brain using c-fos staining and confocal microscopy. I discovered that the prefrontal cortex, hypothalamus, amygdala, and auditory cortex exhibit increased c-fos expression. These findings suggest that these regions are potentially responsible for some of the aforementioned physiological and emotional immune responses. My research serves as a preliminary screening for future research in neuroimmunological responses to influenza infections. It enables other scientists to investigate how each region, such as the hypothalamus, may contribute to an immune response. For instance, the hypothalamus is responsible for maintaining homeostasis, and future research could reveal that it is responsible for altered eating habits and fatigue.

Using Machine Learning to Speed Up the Analysis of Cosmological Models

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Many cosmological models remain untested or under-tested due to computational limitations. In order to compare a theoretical model to observed data, codes which calculate these models have to be called upwards of 10^5 to 10^6 times in a Monte Carlo Markoff Chain (MCMC) algorithm. Furthermore, a complete analysis consists of not just one of these MCMC algorithms but multiple, utilizing different datasets. One of these computationally intensive cosmological models is KMIX, a model which through incorporating two kinetically-mixed scalar fields shows promise of resolving both the Hubble and S8 tensions. Though there have been efforts to optimize the ten free parameters of this model, there has not yet been a full analysis. This is primarily because of how computationally intensive it is—the model is calculated by a modified version of CLASS that takes anywhere from two minutes to over an hour per run. This can be sped up with multiprocessing, but even so an MCMC would still take months to run. And so, in order to conduct an analysis of KMIX and constrain its parameters against the data, we utilize machine learning. Emulators, neural networks trained with machine learning to precisely imitate cosmological codes, are a promising solution to the issue of computational limitations. In previous research, emulators have been shown to provide incredible speed-ups in analyzing cosmological models. We utilize CONNECT, a code for generating cosmological emulators, to produce emulators for KMIX and conduct an analysis of the model. CONNECT utilizes a new type of sampling for the training set, which allows the size of the training set to be reduced by excluding any points in parameter space which are ruled out by observed data. This is particularly important as the generation of the training set is by far the rate limiting step in the creation of an emulator. While we have not produced a full analysis of the model yet, we have produced emulators, with which we have run initial MCMC algorithms.

Effect of chronic inflammation via IFN- γ on the cellular plasticity of human erythroid progenitor (HUDEP-2) cells

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Hematopoiesis gives rise to both erythrocytes and myeloid cells. Erythrocytes have traditionally been viewed as immunologically inactive, but have recently been proven to have immunomodulatory abilities. Myeloid cells are crucial to innate immune function. Chronic inflammation, particularly mediated

by IFN- γ , has been implicated in skewing hematopoiesis towards the production of myeloid cells, contributing to conditions like Anemia of Chronic Disease (ACD), which is characterized by a deficiency in healthy red blood cells in chronically or terminally ill persons. This study explores the cellular plasticity of human erythroid progenitor (HUDEP-2) cells in response to chronic inflammation via IFN- γ . HUDEP-2 cells, an immortalized cell line derived from umbilical cord blood, were exposed to IFN- γ over a 22 day period. Cell viability, density, and genetic expression of key transcription factors in myeloid differentiation and function were assessed. Additionally, phenotypic changes suggestive of myeloid cell differentiation were examined through cell staining and microscopy. While chronic exposure to IFN- γ negatively impacted cell viability and density, the qPCR analysis of Day 16 samples revealed no significant up-regulation of myeloid-associated transcription factors, PU.1 and CEBPa, nor down-regulation of erythropoiesis factor GATA1. Qualitative phenotypic assessment of cell morphology identified an abnormal appearing subset of cells from a Day 22 sample, but further quantification is needed to validate such observations. The results of this experiment do not support the hypothesis that chronic IFN- γ exposure induces myeloid-like properties in HUDEP-2 cells. Limitations of this experiment include variability in cell culture conditions and technical challenges during qPCR. Further research will involve comprehensive phenotypic quantification, a repeated qPCR and testing the effect of IFN- γ exposure on erythropoiesis. Understanding the mechanisms governing erythroid plasticity and hematopoiesis in the context of chronic inflammation holds promise for advancing therapeutic strategies for ACD and provides insights into the broader immune implications of anemia.

Computational Visualization of Influenza Spike Protein Binding with Antibody

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A universal flu vaccine will offer protection against different variants of the virus. To design such a vaccine, it is necessary to understand the structural features of the viral spike, called haemagglutinin (HA), and its interaction with antibodies that prevent infection. We are studying two antibodies, called 133 and 144, which were produced by mice immunized by a modified HA. We previously determined a high resolution crystal structure of antibody 144 and a low resolution model of antibody 133 bound to an HA using negative stain electron microscopy. We are now using computational approaches, including homology modeling and docking, to generate a model of antibody 144 bound to HA. This model will allow us to visualize atomic contacts at the antibody-HA interface and better understand what features of HA were important for eliciting this antibody response. This will further guide the design of HA that can be used in a vaccine to elicit an antibody response that can target a wide range of flu variants.

TET25 G-Quadruplex in complex with small molecule ligand TrisQ

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Guanine-Quadruplexes (GQs) are non-canonical DNA secondary structures that arise from the non-Watson Crick bonding of guanines in guanine rich sequences. These structures can have genomic consequences; Their formation and stabilization, as it is related to telomeric regions of DNA, can aid in the prevention of cancerous diseases. In this poster, we are looking at binding of small molecule ligand TrisQ, a known GQ binder, to TET25, a sequence of telomeric DNA originating in protozoa *Tetrahymena thermophila*. The sequence has very similar repeats to human telomeric DNA sequences that have already been extensively studied. We also look at the binding of TET25 and TrisQ-Oxide. During crystallization, the ligand was oxidized but still found to bind with the TET25 GQ. Biophysical characterization revealed that for both TrisQ and TrisQO, TET25 topology changes from hybrid to parallel and increases in thermal stability. Titration revealed a 1DNA:1Ligand ratio is the best fit for TET25 and TrisQ, but that binding for TET25 and TrisQO may be tighter and thus less simple to uncover through previous

methods.

Characterization of a *Dugesia japonica* homologue of Neuropathy Target Esterase

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Neuropathy target esterase (NTE) is a well conserved, ER-membrane bound phospholipase proposed to play roles in nervous system development and upkeep in humans. NTE was discovered while searching for an initiating target of organophosphate (OP)-induced delayed neuropathy (OPIDN); irreversible NTE inhibition by neuropathic OPs was shown to be necessary for OPIDN. However, the physiological function of NTE and its mechanistic link to OPIDN remain poorly understood. Despite having greatest abundance neuronally, human NTE is found in a variety of non-neuronal tissues and thought to be active in membrane phospholipid homeostasis and the constitutive secretory pathway, suggesting multifaceted uncharacterized roles. Understanding NTE function therefore has potentially broad physiological implications.

This study aims to establish the activity, expression, and physiological function of an NTE homologue in the freshwater planarian *Dugesia japonica*. We believe that planarians are a useful invertebrate *in vivo* model system for NTE studies because planarians are sensitive to OPs and have a putative NTE gene (*Djnte*) with high sequence similarity to human *nte*, including all catalytically relevant residues.

To confirm enzymatic activity of DjNTE, we adapted a biochemical assay originally developed in hen brain; we have detected esterase activity but more work is needed to confirm *Djnte* as responsible. To study DjNTE expression, we performed immunohistochemistry experiments using two commercially available NTE antibodies. The specificity of these antibodies remains to be demonstrated using RNA interference (RNAi). We conducted functional studies of DjNTE using RNAi by comparing head regeneration in decapitated *Djnte* RNAi and control worms. We did not find any differences in head regeneration rate, suggesting that there may be compensatory mechanisms, a lack of NTE involvement in head regeneration, or that the reduction of *Djnte* expression (75% as confirmed by qPCR) was insufficient to cause phenotypic changes. Our results provide first insights into NTE's physiological role in planarians, whose unique ability to regenerate all organs, including the complete nervous system, make it a potential model to study NTE throughout development to understand new aspects of NTE function.

Automorphism Groups of Rank Metric Codes

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In a post quantum world, most current cryptographic methods will become insecure. One method to create secure post-quantum cryptography relies on error correcting codes to generate encryption keys. However, while classical error correcting codes are secure, they generate very large and inefficient keys. On the other hand, rank metric error correcting codes generate more efficient and smaller keys while remaining secure. To determine if a rank metric code is useful for secure cryptography, it is important to analyze its automorphism group, which describes the symmetries of an error correcting code.

We worked with the rank metric error correcting code introduced in "An Exponential Bound on the Number of Non-Isotopic Commutative Semifields" by Faruk Göloğlu and Lukas Kölsch. This code is semilinear, so unlike linear rank metric codes, most common techniques used to determine the automorphism group of rank metric error correcting codes are not applicable to this code. Moreover, the automorphism groups of rank metric codes similar to this code are largely unknown, so this problem is generally novel.

We analyzed the automorphism group by expressing automorphisms of the code as collections of linearized polynomials. We considered subcases with restrictions on these polynomials and determined

that in each subcase, all automorphisms could be expressed as a collection of monomials. With similar methods, we showed that all automorphisms of the code fell into one of those subcases and used that structure to compute the automorphism group entirely. Our computation of the automorphism group for this code will enable a variety of cryptographic applications.

Activity and Structure Across MEK and ERK Kinase Variants

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The mitogen-activated protein kinase pathway (MAPK) pathway is a signal transduction pathway involved in cell proliferation, differentiation, apoptosis, and other cellular processes. The pathway consists of the RAS-RAF-MEK-ERK signal cascade with abnormal activity of the pathway heavily implicated in tumorigenesis. Allosteric modulation of downstream members of the pathway has emerged as an attractive therapeutic approach due to issues including paradoxical activation and drug resistance when targeting the active site of oncogenic mutants. This work centers on elucidating the interaction between MEK and ERK kinases since a complete structure of their complex is unavailable.

Ciona intestinalis is a commonly used model organism to study embryonic development, heart tissue regeneration, etc. due to its close evolutionary relationship to humans. The MAPK pathway is highly conserved in *C. intestinalis* which this work takes advantage of to investigate the interaction between MEK and ERK kinases. This study uses a combination of computational and experimental methods to identify conserved residues between human and *C. intestinalis* MEK constructs and determine whether they are involved in ERK binding. Several MEK residues were identified and tested via biolayer interferometry (BLI). BLI results indicated that mutating some of these residues led to a decrease in ERK binding affinity compared to unmutated MEK. Future work will focus on computational modeling of possible MEK-ERK complexes and examination of potential sites of interaction on ERK kinase.

The Effect of NaCl Concentration on Functional Amyloid Formation Studied Using Fluorescence Lifetime Imaging

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My research looks at the factors that affect the structural heterogeneity of functional amyloid fibrils, which are beta-sheet rich insoluble fibers that result from the nucleation elongation polymerization of soluble, disordered protein. In our research, we use a molecular dye that is fluorescent only when bound to amyloid fibrils. Using Fluorescence Lifetime Imaging Microscopy, we can measure the fluorescent lifetime of the fibril-bound dye, which is the average amount of time that the molecular dye stays in the excited state before releasing a photon. This lifetime will vary based on the interaction between the dye and the fibril, which means that different fibril structures will result in different measured lifetimes. By varying the conditions under which amyloid fibrils are formed, we can assess the factors that affect fibril heterogeneity. Using Fourier transforms on the Fluorescence Lifetime Imaging Microscopy data, we produce phasor plots, which allow us to qualitatively compare the various lifetimes seen in a sample.

If the molecular dye is added before amyloids have formed – when the proteins are still monomers – the kinetics of amyloid formation can be examined by plotting fluorescent intensity as a function of time. When an amyloidogenic protein starts as monomer, the kinetics follow a sigmoidal curve: a lag phase as monomers begin to nucleate, a growth phase as protofibrils form, and then a plateau as the amyloids form.

One of the main goals that we have accomplished thus far is identifying a method that reliably causes a growth phase in the kinetics. This is important because units that are smaller than complete amyloids will be most affected by environmental conditions. We have also begun to look at the effect of pH on amyloid formation, finding that at extreme pHs, amyloid formation is inhibited, and the fluorescence of our molecular dye is severely diminished. The next step in our research is to establish a procedure that

reliably results in a lag phase in the kinetics. Once this has been achieved, we will be able to thoroughly study the impact of environmental conditions – specifically NaCl concentration – on amyloid structural heterogeneity.

On the metal-ligand cooperative reactivity of group 13 metal complexes

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The development of metal coordination complexes designed to undergo the metal-ligand cooperative (MLC) activation of small molecules is an exciting area of research. Development of a system to split polar H-X (X=heteroatom) bonds is particularly important because it introduces these reagents into catalytic processes without formal metal-based oxidative addition. We have been investigating the coordination chemistry of group 13 metal complexes supporting non-innocent ligand frameworks and have most recently been working on the coordination chemistry of the tripodal, tris(nitroxide) ligand system TriNOx^{3-} . In this contribution we will discuss our continuing work on the reactivity of the full set of $(\text{TriNOx}^{3-})\text{M}$ (M = B, Al, Ga) complexes with O-H bonds. We will also discuss the reactivity of $(\text{TriNOx}^{3-})\text{M}$ (M = Al, Ga) with CH_2Cl_2 .

Large sample study and modeling of three-dimensional magnetic reconnection at SSX

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We have recently been performing large sample statistical studies of magnetic reconnection at SSX. We have over 600 merging events so far. Our most recent analysis focuses on energy of the merging plasma. The experiment generates two fully ionized relaxed MHD hydrogen plasmas which move towards each other with approximate velocity $v = 30$ km/s. 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 $B = 0.3$ T, $n_e = 4 \times 10^{15} \text{ cm}^{-3}$, and $T_i = 40$ eV. Current density is calculated in the plane of the probe array using the curl of the magnetic field. In addition, we have added a heterodyne interferometer to compare with our Mach-Zehnder measurement. We are using the Dedalus framework, an open-source flexible spectral method Python framework, to simulate MHD time evolution of two spheromaks merging in a cylindrical 1:10 chamber. We use CFL dynamic timestepping in a $64 \times 64 \times 320$ resolution Cartesian grid, with periodic boundary conditions. Temperature is initialized proportionally to density under ideal gas assumptions. Typical magnetic Reynolds number $R_m \approx 1000$ and mechanical Reynolds number $Re \approx 200$. The vector potential is initialized from the force-free equation $\nabla \times \mathbf{B} = \lambda \mathbf{B}$ and given a perturbation to break axial symmetry. The simulation runs for ~ 20 Alfvén times during the reconnection event, with the spheromaks merging in the midplane at ~ 5 Alfvén times.

Towards a Typology of Harm Caused by Deepfakes

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Scholars, politicians, and journalists have raised alarm over the potential for AI-generated photos, video, and audio — often referred to as deepfakes — to reduce trust in one another and our institutions. Despite these clarion calls, little empirical work exists on how deepfakes are being used to harm individuals outside of non-consensual intimate imagery (NCII). This research provides a preliminary analysis of 50 wide-ranging incidents of deepfake harm. We find that the most common types of harm are relational, systemic, financial, and emotional. Apart from AI-generated NCII, the most prevalent uses of deepfakes to cause harm were instances of mis- and disinformation, fraud, and misrepresentation of or stereotyping

about marginalized groups (e.g., women and racial minorities). We concluded with recommendations for future work and discuss potential challenges in identifying, quantifying, and preventing harm caused by deepfakes both online and off.

The N-terminus of mitotic spindle-associated Nek9 may mediate its cell cycle dependent degradation by ubiquitin-conjugating enzyme UBE2H

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The ubiquitin-proteasome pathway (UPP) is a highly conserved eukaryotic pathway that regulates the degradation of proteins. By linking proteins with a 76-residue peptide chain termed ubiquitin, the UPP may direct the ubiquitin-tagged protein to the proteasome for degradation. Such degradation is essential for maintaining proper concentrations of proteins. The UPP's role in regulating cell division, however, is incompletely understood. Preliminary data from our lab indicate that the ubiquitin-conjugating enzyme UBE2H is active in interphase but not mitosis. We performed proteomic analysis on human retinal pigment epithelial-1 (RPE-1) cells with wildtype or constitutively active, overexpressed UBE2H. We identified NIMA-like kinase 9 (Nek9), a mitosis-active serine/threonine kinase involved in proper centrosome separation and spindle formation, as a protein highly downregulated during mitosis in cells with constitutively active UBE2H compared to cells with wildtype, mitosis-inactivated UBE2H. Proteomic data also revealed that Nek9 levels are similar in interphase cells with wildtype or overexpressed UBE2H, suggesting low levels of UPP-mediated Nek9 degradation in interphase. Given that Nek9 is active during mitosis, we then investigated whether Nek9's active conformation leaves it susceptible to degradation by UBE2H, while its inactive state protects it from degradation. We cloned N-terminal fluorescent protein-tagged Nek9 constructs and performed site-directed mutagenesis to introduce activating or inactivating Nek9 mutations. After exogenously overexpressing Nek9 mutants in RPE1 cells, we performed immunoblot analysis. Contrary to our expectation that constitutively active Nek9 would be degraded more in interphase cells, wildtype, active and inactive exogenous Nek9 all demonstrated similar degradation patterns in interphase. Further, while exogenous Nek9 degraded in cell lines with overexpressed UBE2H compared to wildtype levels, endogenous Nek9 did not show similar degradation. Our results indicate that the N terminal fluorescent-tag may direct UPP-mediated degradation of Nek9, suggesting, instead of activity status, a role of Nek9's N-terminus in its degradation.

Developmental Differences in EEG Frequency Domain Patterns During Object Recognition

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This study investigates developmental differences in EEG patterns between infants and adults during object recognition tasks, focusing on frequency domain analysis. Utilizing EEG data from Ashton et al.'s 2022 study, we achieved a highest classification accuracy of 96.60% by applying the Fast Fourier Transform to convert time-domain data to frequency-domain and using Support Vector Machines (SVM). We analyzed EEG data from infants and adults during object-viewing tasks, examining 18 features, including individual band powers, power ratios, and spectral slopes across 18 electrodes located in the frontal, occipital, posterior, and parietal regions. We normalized band powers and utilized periodogram analysis to verify the comparability of infant and adult data before running the SVM models. Combining all frequency bands yielded an accuracy of 93.55%, with the theta/(alpha+beta) ratio showing the highest individual accuracy of 94.38%. Posterior regions, particularly occipital and parietal areas, provided the most informative data. Frequency band permutation analysis revealed optimal ranges for differentiation: theta [4-9 Hz], alpha [9-12 Hz], and beta [12-30 Hz], achieving the highest accuracy of 96.60%. Our findings indicate significant developmental differences in EEG frequency patterns during object recognition, with the prominence of theta/alpha and theta/(alpha+beta) ratios and the importance of posterior regions suggesting ongoing maturation of visual processing networks from infancy to adulthood (Ashton 2022).

Histone Methyltransferases GLP and G9a are Essential for the Development of Neural Crest Derivatives

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GLP and G9a are crucial methyltransferases promoting dimethylation on the 9th lysine residue on the H3 histone protein (H3K9me2). Previous research has shown that decreased GLP and G9a activity can lead to prominent cardiac defects when GLP is knocked out in cardiomyocytes. In this study, we present the first complete knockout of both GLP and G9a using a reliable Cre-Lox recombination system and investigate its effect on selected neural crest-derived tissues. Through histological analysis, we identified the prominent phenotypes of a cleft palate and patent ductus arteriosus (PDA) in GLP and G9a knockout craniofacial mesenchyme and cardiac outflow tracts respectively. These phenotypes likely contribute directly to the newborn's inability to feed and increased potential of cardiac failure. These findings provide insights into how histone modifications, specifically H3K9me2, can impact neural crest development. Further mechanistic investigation into the etiology of these defects and the gene expression regulated by H3K9me2 will be conducted to achieve a deeper understanding of the role of GLP and G9a in the context of neural crest development.

Investigating a neurological imbalance of excitation and inhibition in Kabuki Syndrome Type 1

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Kabuki Syndrome is a rare neurodevelopmental disorder that causes facial deformation, developmental delay, and intellectual disability. 50-70% of cases are caused by a mutation in *KMT2D* and are considered to be Kabuki Syndrome Type 1 (KS1). *KMT2D* codes for a lysine-specific methyltransferase that operates as part of the ASCOM complex to promote open chromatin states. The Patzke lab has shown that neurons from a KS1 mouse model have increased synapse counts and higher amounts of the vesicular GABA transporter. We hypothesize that the KS1 genotype leads to an imbalance of excitation and inhibition as well as changes in presynaptic and postsynaptic terminal counts in mouse neurons.

In order to investigate this hypothesis, we infected KS1 mouse neurons with a lentivirus to express a fluorescent calcium reporter protein. We then used calcium imaging of these neurons to examine their electrical network activity. These results show an increase in asynchronous calcium transients, but do not allow for parsing inhibitory and excitatory signaling specifically. In order to address this, we decided to employ iGluSnFR and iGABASnFR, proteins whose fluorescence is dependent upon detection of glutamate and GABA, respectively.

The genes coding for these proteins were cloned into plasmids with a strong promoter taken from the expression cassette of Ubiquitin. These genes were also cloned into plasmids containing a Tetracycline On expression system. These plasmids were then made into lentiviruses with HEK293 cells and stored for future use. These lentiviruses will allow us to isolate and examine excitatory and inhibitory signaling in the heterogeneous mixtures of neurons that result from KS1 mouse primary neuronal cultures.

By characterizing the KS1 phenotype in neuronal cell culture, we are contributing to the knowledge base surrounding this disease and eventual development of therapies to rescue the phenotypes observed. This information also provides insight into the impacts of disruption of the ASCOM complex, whose elements are associated with Kabuki Syndrome Types 1 and 2, Spastic Paraplegia, Retinoblastoma, AIDS Dementia, and Rubenstein Taybi syndrome.

Evaluating the Impact of AI-Generated Visual Explanations for Image Matching

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In recent years, intelligent systems have grown increasingly complex and harder to understand. To address this, prior work has attempted to shed light into these complex systems by providing the user with explanations of how such systems operate. These explanation methods can provide the user with more context or clarity when interacting with intelligent systems. Although various explanation methods, such as text-based and visual aids, have been proposed, their usefulness and interpretability to users remain uncertain. Effective explanations are expected to improve users' ability to predict outcomes and enhance their task performance. This work investigates the impact of AI generated visual explanations on the performance of novice users in an AI-assisted image retrieval task, focusing on their ability to accurately identify a hotel from query images. We incorporated a visual explanation feature which highlights regions of similarity into an existing image retrieval system to evaluate the explanation's effectiveness. Our human evaluation aimed to determine if this added explanation improves users' ability to accurately identify the correct hotel compared to a baseline without such explanations. Our results showed that the explanations had no significant impact on user performance, however familiarity and AI-background played an important role in this task. Participants who had more familiarity with AI performed significantly better than those who were less familiar. Despite their higher performance, their confidence dropped significantly, which may suggest that the explanations introduced unnecessary complexity to the task. These findings highlight the importance of designing explanations that users can easily understand and apply in real-world scenarios.

Insights into Battery Materials from Mossbauer Spectroscopy

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The motion of active ions in a battery is critical to all major issues facing electrochemical battery systems. A battery's energy density, operating potential, and charge/discharge rate are determined by the ionic conductivity in the cathode. This work uses Mossbauer spectroscopy to assess the activation energy and electron dynamics in sodium-based Prussian blue analogs. The onset of polaron motion in each material is assessed through Mossbauer measurements at increasing temperatures and indicated by spectral distortions that occur when Na atoms become mobile and the iron atoms experience a fluctuating local environment. The critical role of Mossbauer spectroscopy in completing our understanding of conductivity in battery materials will be discussed alongside results for a series of sodium-iron Prussian blue analogs.

Structural Analysis of a Left-Handed G-Quadruplex

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Left-handed G-quadruplexes are a non-canonical DNA structure discovered in 2015, distinguished from their right-handed counterparts in their helical twist, from which they derive their names [1]. Formation of left-handed G-Quadruplexes has been found to be highly sequence dependent, with only variations of two minimal sequences, Motif1 ($G(TGG)_3TG$) and Motif2 ($((GGT)_3GTG)$), forming this secondary structure [2]. All discovered DNA Left-Handed G-Quadruplexes form a distinct four-layered structure, with 2 subunits (each formed by a single minimal sequence) containing 2 tetrads each [3]. We used X-ray crystallography to determine the structure of a sequence consisting of Motif1 and Motif2 connected by a TT-linker. Crystals were obtained in two different space groups yielding two different conformations: fully left-handed and left-right hybrid. In both conformations, the Motif1 subunit folds left-handed. The conformations differ in the fold of the Motif2 subunit, which is left-handed in one structure and right-handed in the other. The differing fold of the Motif2 subunit produces differences in crystal packing between the two structures. The fully left-handed conformation interacts with other copies through

thymine stacking interactions, while the left-right hybrid conformation dimerizes through its Motif2 subunit.

Quantifying the Aggregation Behavior of Polystyrene Nanoparticles in the Marine Environment

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Globally, plastic production has been increasing. It is estimated that the amount will reach 710 million metric tons by 2040. Due to improper disposal, 4.8 to 12.7 million tonnes of them were estimated to disperse into the environment. Once plastic products are exposed to the environment, they undergo biotic and abiotic degradation (e.g. mechanical wear, heat, UV degradation, or biological factors), producing nano-scale plastics spread broadly in the soil, air, and oceans. Nanoplastic particles (NPs) have small sizes (1 nm-1 μ m) and behave uniquely compared to macro- or micro- scale plastics due to their high surface-to-volume ratio. In particular, their aggregation behavior, transportation fate, and influence of the eco-corona are unique. The eco-corona is a biofilm on the surface of NPs as a result of attachment of biomolecules, such as proteins. It has been reported that the eco-corona changes NPs' aggregation, distribution, and toxicity. Consequently, the eco-corona has a lot of impact on the marine biota and thus is a key to understanding the influence of NPs.

Based on the urgency to reveal the possible adverse effects of and measures for NPs pollution, our lab (Dr. Riley's lab) collaborates with Dr. Chan's lab at Swarthmore biology department to investigate the interactions between sea urchins and NPs. The study presented in the poster is a part of this project, which aims at studying the bioavailable form of plastic particles in the marine environment. More precisely, the homoaggregation behavior of polystyrene particles (PSPs) in seawater were quantified using an analytical tool. The tool used was dynamic light scattering (DLS), which enables to track the particles' size changes based on their Brownian motion. To quantify the aggregation behavior, the value of critical coagulation concentration (CCC) was determined. The CCC value can be obtained by the calculation based on colloidal aggregation theory (i.e. DLVO theory), and is a useful parameter to characterize the aggregation behavior of plastic particles.

The experiment was designed as such: PSPs and simulated seawater with/without biomolecules were used as the model of NPs and natural seawater, respectively. To investigate the influence of surface chemistry, either amino- or carboxyl-surface coated PSPs were used (noted as PS-NH₂ or PS-COOH, respectively). Two types of seawater were prepared to see the influence of biomolecules, one of them was prepared from salts (simulated seawater, SW) and the other contained biomolecules that were excreted from sea urchins (sea urchin spent media seawater, SM-SW). As a result of the experiment, the CCC value of PS-NH₂ in SW and that of PS-COOH in SW and SM-SW were obtained. Also, the impact of biomolecules was estimated. In the future direction, we are going to investigate the influence of dominant ions present in seawater (i.e. Na⁺, K⁺, Mg²⁺, or Ca²⁺) and natural organic molecules (NOMs) such as alginate.

α -Diimine aluminum complexes as tunable catalysts for atom transfer radical polymerization

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Aluminum is an attractive metal in developing novel homogeneous catalysts due to its natural abundance, low cost, and benign environmental impact. Thus, derivatives of our previous (L_{Ar}^{2-}) AlX(THF) (L_{Ar}^{2-} = doubly reduced diimine ligand; X = Cl, Br, I) will be presented with emphasis on Ar = -Mes (C₉H₁₁). The -Mes ligand was also modified to include substituents with different Hammond parameters to probe the effect of electronics on this catalytic system. Characterization of Al- α -diimine complexes was conducted using NMR spectroscopies, X-ray Diffraction, and electrochemical techniques. Redox activity was further investigated using oxidative halogenation with metal and inorganic oxidants.

The redox tunability of this system was leveraged in the catalysis of atom transfer radical polymerization (ATRP). This controlled radical polymerization technique is compatible with olefin monomers, resulting in high control of dispersity and molecular weight as opposed to uncontrolled free radical polymerization. During ATRP initiation, the metal ligand system is oxidatively halogenated by 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 compatible with common ATRP initiators and led to successful polymerization of methyl methacrylate, as demonstrated by 1H NMR spectra and Gel Permeation Chromatography.

Future directions include altering polymerization experimental conditions including initiators, solvent and catalyst loading to understand the potential effects of each on polymerization activity. In addition, it has historically been very difficult to subject electron-rich monomers to ATRP and has only recently been reported for the most-active

Cu-based catalytic systems. Thus, the electron-rich monomers, vinyl acetate and N vinylpyrrolidone, will be screened.

Planar Turán Number for Theta-graphs and Friendship Graphs

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For the past year, I have been working on a research project on extremal planar graphs. In mathematics, a graph consists of a vertex set and an edge set, where every element in the edge set is a pair of vertices. In 1941, Pál Turán initiated the study of extremal graph theory by his famous Turán's theorem. It has since become the central research area of graph theory, and people started to investigate numerous analogous problems, such as the ones with an additional requirement of planarity. The formal statement of an extremal planar graph problem is the following. Given a (planar) graph G and a natural number n , what is the maximum number of edges in an n -vertex planar graph that does not contain G as a subgraph? This maximum number is called the planar Turán number, denoted by $ex_P(n, G)$.

Previous research has calculated the planar Turán number for simple graphs such as cycles and complete graphs. We focused on Theta₆ graphs and friendship graphs. Here, a Theta₆ graph is a hexagon with a single diagonal, and there are two possible Theta₆ graphs. A friendship graph F_k consists of k triangles sharing a common vertex. Utilizing and modifying the notion of triangular blocks, that is, maximal sets of triangular faces connected through sharing edges, we proved upper bounds of planar Turán number for Theta₆ graphs and friendship graphs. We verified their sharpness by providing extremal constructions for infinitely many n . We also made conjectures and created possible extremal constructions for Theta₇, Theta₈, and generalizations of friendship graphs, which consist of multiple cycles sharing a common vertex.

Recursive Majority

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Query Complexity, also known as decision tree complexity, investigates the cost associated with determining the output of a Boolean function $f: \{0, 1\}^n \rightarrow \{0, 1\}$. The recursive majority function is a specific problem within Query Complexity, where the problem is represented by a height- h complete ternary tree with 3^h inputs of either 0 or 1 at the leaves, and each internal node functions as a majority gate. The objective is to determine the output of this tree with the minimum number of bit queries.

In this paper, we aimed to improve algorithms for solving this problem by combining traditional theoretical analysis with modern optimization techniques, specifically simulated annealing. We implemented the simulated annealing optimization in C++, defining the search space as all possible

algorithms on a finite depth tree and using neighbor selection through the reconstruction of decision tree branches. In addition, we evaluated its performance in relation to existing algorithms.

Moreover, we classified the algorithm design into three main subroutines: Eval(v), Comp($v, v1$), and Comp*($v, x1$), and explored various implementations of these subroutines, including combinations involving mixed depths. Using Matlab and Python, we solved recurrence formulas, achieving the best upper bound of $(1.06776 \times 2.6497^h)$. Furthermore, we extended the Comp($v, v1$) function to a depth- k algorithm, which facilitated the derivation of a recurrence formula for the lower bound.

Long-term effects of psilocybin on dendritic spine dynamics

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Dendritic spines are critical for synaptic transmission and plasticity, serving as key sites for the formation, strengthening, and elimination of synapses, which enable the communication and integration of information within neural circuits. These micron-scale protrusions experience structural changes that are most pronounced during early postnatal development and progressively decrease with age. Both internal genetic factors and external influences shape this process. Psychedelic substances like psilocybin have recently been shown to modify dendritic spine structure in adult mice, leading to rapid and lasting increases in spine formation. This suggests that psilocybin might trigger functional changes in the mature brain and potentially reactivate periods of plasticity. However, human data on psilocybin's effects on cognition are mixed, and direct correlations between psilocybin's effects on spine structure and cognitive function are lacking. Emerging findings from our experiments reveal that psilocybin accelerates the acquisition of motivated behavior components in a sensory evidence accumulation task. In this project, we test the hypothesis that psilocybin-induced cognitive improvements in mice are associated with changes in cortical spine density and morphology. Since the manual nature of spine identification and categorization remains prohibitively slow and variable when performed by humans, consuming significant time and labor and imposing limitations on sample size, statistical power, and reproducibility, we are utilizing the state-of-the-art, deep learning-based framework, DeepD3, to quantify spine density and size in basal and apical dendrites of cortical pyramidal neurons across three distinct brain regions in mice following intraperitoneal administration of a single dose of psilocybin (2 mg/kg) after employing confocal microscopy and DiOlistic labeling. We are testing mice with psilocybin, with evidence accumulation training, and with both psilocybin and evidence accumulation (3 conditions; $n = 8$ mice per group, 180 dendrites per mouse). Effects at both early and final stages of behavioral shaping are being investigated. The results could provide new understandings of the processes behind the therapeutic potential of psilocybin.

Berglund-Hübsch Transpose and Einstein five-folds

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Our research aims to explore the relation of five-dimensional manifold pairs via the Berglund-Hübsch Transpose, which constructs manifold pairs based on zero sets of invertible polynomials. We have discovered interesting geometric properties that are preserved under the Berglund-Hübsch Transpose and we have shown how certain numerical data gets transformed under the Berglund-Hübsch transpose.

For example, the Berglund-Hübsch Transpose allows us to construct pairs of manifolds with the same useful numerical data, namely, the Betti number, Milnor number, weights, degree, and Fano Index. At the same time, we have also discovered that the preservation of the Einstein condition over the Berglund-Hübsch Transpose cannot be proven on five-dimensional Einstein manifolds using known methods. The approach involved translating polynomials into matrices, whose numerical data satisfy a specific Einstein condition, and taking the transpose of this matrix to arrive at the transpose polynomial, which yields a new manifold with a new set of weights, Betti number, and Milnor number. Our research has shown that

the Berglund-Hübsch transpose can preserve, under certain conditions, geometric properties such as the Betti and Milnor numbers, while failing to preserve Einstein conditions proposed in existing literature.

Our research attempts to borrow ideas from classical mirror symmetry. Roughly speaking, mirror symmetry states that it is always possible to find pairs of Ricci-flat (zero curvature) six-dimensional manifolds that share similar geometries, with a notable symmetry among special numbers called Hodge numbers. Mirror symmetry was first discovered by theoretical physicists in the 1990s in the context of string theory. As a result, its scope has so far been limited to Ricci-flat or Calabi-Yau spaces which are even dimensional. Our work aims to expand the scope of mirror symmetry to five-dimensional Einstein spaces, using Berglund-Hübsch Transpose to construct pairs of manifolds that, like in the original version of mirror symmetry, share similar geometries.

Local-Global Conjecture Within Circle Packings

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Circle packings are fractal arrangements of mutually tangent circles, often with integer curvatures. The Local-Global Conjecture is a 21 year old statement about the integers which appear in circle packings. It predicts that every sufficiently large integer satisfying certain modular restrictions will appear within a packing. Last year, this conjecture was disproven for the Apollonian, or tetrahedral circle packing, using classic ideas from number theory including quadratic reciprocity. Tetrahedral circle packings fall under a class of circle packings known as polyhedral packings. These packings have circle configurations whose tangency relationships are based on a polyhedron. Other polyhedral circle packings include the cubic and octahedral packings. Another class of packings have infinite circle configurations whose tangency relationships are based on tilings of a plane using polygons. Some examples include triangle, square, and hexagonal packings. We disprove the Local-Global Conjecture in certain cases of each of the cubic, octahedral, triangle, square, and hexagonal packings. We do so using methods mimicking the strategies from the tetrahedral case. This includes first separating each individual case into subcases through their modular restrictions, then creating an invariant using an expanded form of quadratic reciprocity. This allows us to determine that certain sets of integers, of the form a constant times a perfect square, cannot exist within certain packings, disproving the Local-Global Conjecture in these specific cases. Additionally, we collect data to support our findings, and give evidence that the obstructions to the Local-Global Conjecture we find are in fact the only ones.

Thermodynamic Properties of Pt-Cu-P Bulk Metallic Glasses

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Ultra-fragile Pt-Cu-P metallic glasses and their thermodynamic properties have been systematically investigated using differential scanning calorimetry. The thermodynamic functions of excess enthalpy, entropy, and Gibbs free energy between the liquid and crystal phases were calculated as a function of Cu content from the isobaric specific heat capacity measurements of the glass, crystal and liquid phase. The glass transition, crystallization, and liquidus temperatures, and the enthalpies of crystallization and melting were also assessed. New calorimetry results, coupled with statistical analysis, suggest a high likelihood of insufficiency of the Kubaschewski equation in accommodating heat capacity in the supercooled liquid phase for some metallic glasses. These results will be discussed in the context of previous work on these glasses which introduced a more general empirical form for the liquid configurational enthalpy [1].

Age effects on cognitive function and glucose tolerance in *Octodon degus*

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Similar to humans with Alzheimer's disease, degus (*Octodon degus*, a Chilean rodent related to guinea

pigs) naturally undergo cognitive declines and develop amyloid- β plaques as they age. Degus also spontaneously develop diabetes, and past research has shown a correlation between type 2 diabetes and Alzheimer's disease. This led us to examine the relationship between age, cognitive function, and glucose tolerance in captive 3- and 4-year-old degus, where we hypothesized that cognitive function would decline with age while diabetes-like symptoms would increase with age. For cognitive function, we subjected degus to burrowing tests that have been successfully used in a variety of rodent models including degus, where larger volumes of material burrowed are associated with higher cognitive function. To assess symptoms of diabetes, we employed glucose tolerance challenges, which are performed by taking baseline (fasted) blood glucose readings, and then additional readings 15, 30, and 60 minutes after a bolus glucose injection. Degus with higher integrated blood glucose levels (calculated as the area under the curve [AUC]) are considered to have worse glucose tolerance and thus more diabetic-like symptoms. We found that our prediction regarding cognitive function was not met, as the amount of burrowed material was similar between 3- and 4-year-old degus. Additionally, we found no correlation between the amount of bedding burrowed and glucose tolerance, whereas we had predicted a negative correlation between the two variables. However, our prediction regarding glucose tolerance was met, as 4-year-old degus had significantly higher glucose AUCs compared to 3-year-old degus, and this was driven by 4-year-olds having higher glucose peaks and reduced abilities to decrease glucose levels after reaching these peaks. We also found that female degus had significantly higher glucose AUCs compared to male degus. These findings suggest that age has major impacts on glucose regulation in degus but less so on cognitive function. Future studies will continue the same glucose tolerance and cognitive testing on degus of different age groups, as the results may be more pronounced with larger age differences.

The Impact of Generative AI on Artists

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Generative AI is profoundly reshaping the creative industries, providing both new opportunities and challenges for artists. This paper explores the multifaceted impact of generative AI on artists by conducting a thematic analysis of social media posts. While some artists embrace generative AI as a tool to enhance their creative processes, many express concerns about its detrimental effects on their profession. A major issue is the unethical use of artists' work in training datasets for AI models without consent, which raises legal and moral questions. Furthermore, artists report increasing anxiety over job displacement as employers opt for AI-generated content to cut costs. These concerns have led some artists to shift their career paths toward fields less impacted by AI or to develop new skills in anticipation of reduced demand for their services. The rise of generative AI has also influenced the public's perception of artists. Many artists face accusations of using AI in their work, leading to emotional distress and a decline in trust between artists and the public. This distrust can even affect artists' employment opportunities, as some clients and collaborators question the authenticity of their work. Despite these challenges, certain segments of the artistic community remain largely unaffected. Experienced artists with established reputations and those working in mediums not easily replicated by AI, such as traditional painting or ceramics, have reported minimal impact. However, there are concerns that future advancements in AI may eventually affect even these artists. This study highlights the need for protective measures, including regulatory interventions and consent-based data collection practices, to safeguard artists' intellectual property and livelihoods. The findings suggest that while generative AI holds potential for creative innovation, its unchecked growth poses significant risks to the artistic community. Further research is needed to explore how policies can mitigate these risks and ensure that AI is used in ways that support, rather than undermine, human creativity.

NOTES



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