Sigma Xi Student Research Poster Session
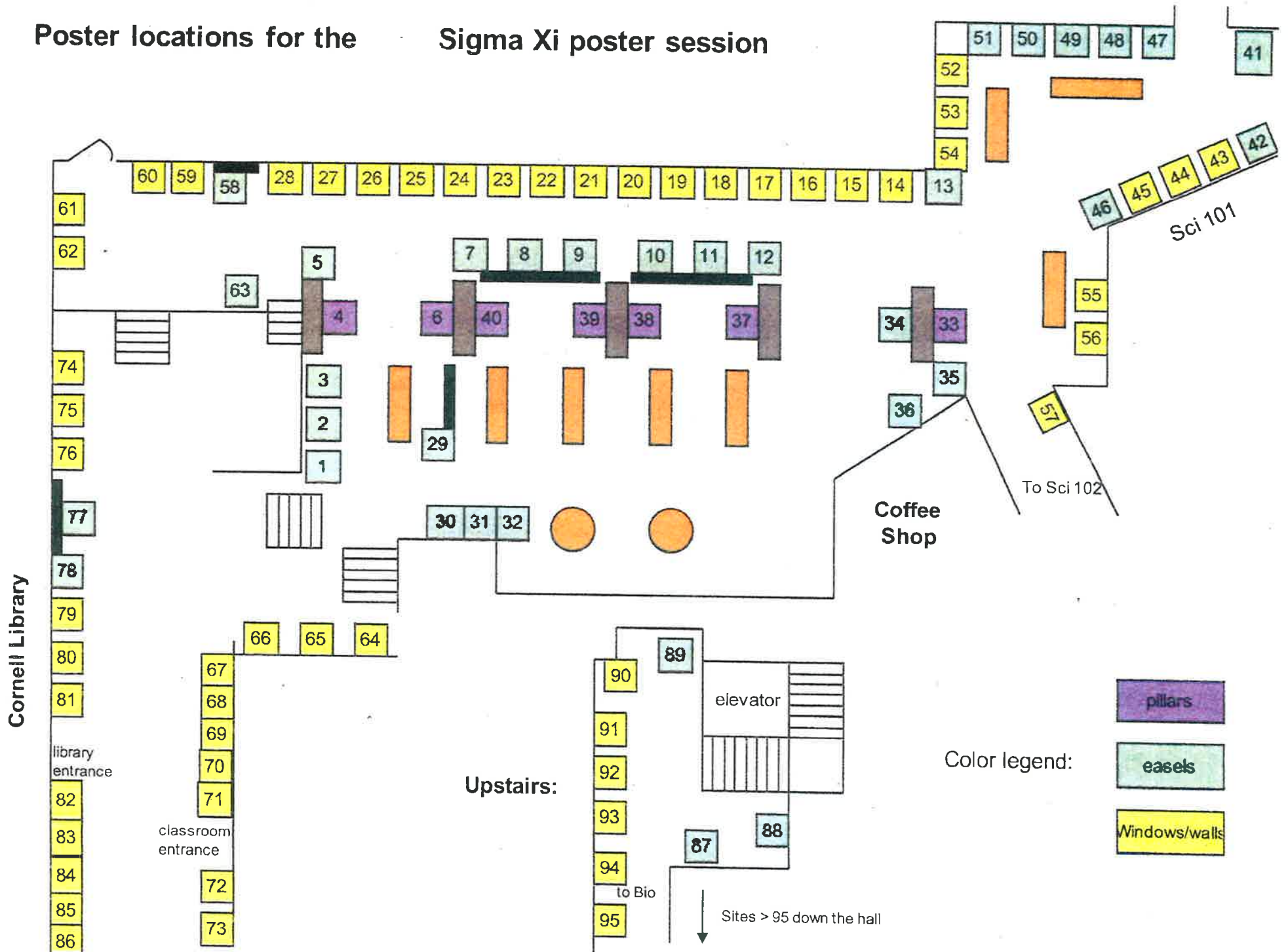
SEPTEMBER 12, SEPTEMBER 13, 2019

Eldridge Commons, Swarthmore College

Sigma Xi The Scientific Research Society
Swarthmore College Chapter

"Companions in Zealous Research"

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Reham Mahgoub	Dong Ok Kim, Elizabeth Erler, Kathleen P. Howard	Chemistry	Physical Characterization of Membrane Mimics Using DLS and EPR Spectroscopy
Elizabeth Erler	DongOk Kim, Reham Mahgoub	Biochemistry	Optimization of Influenza A Virus Matrix Protein 1 purification in order to characterize its role in viral budding
Kaitlin Gelber		Physics	Taylor State Merging Experiments at the Swarthmore Spheromak Experiment
Vinay Keefe	Jordan Ando, Mehmet Naci Inci, Lynne Molter	Engineering	Four-Core Optical Fiber Sensing
Sophie Nasrallah		Biology	Rapid assessment of mammal fauna to examine shifts in mammal diversity across time and a gradient of land use
Calla Bush St George		Biology	An analysis of the gut microbiota in migratory and non-migratory hummingbirds
Lucas Dyke		Physics	Proton Orbit Calculations in Relaxed Taylor States at SSX
Peem Lerdputtipongporn	Jae Tak Kim; Hari Srinivasulu; Joshua Brody (advisor)	Computer Science	Strong XOR Lemma
Joo Yeon Kim		Biology	cornutus)

Jonah Langlieb	Gregory Lee Professor Vasanta Chaganti	Computer Science	Applying Differential Privacy to Anonymize Mobile User Trajectories
Calla Bush St George	Amy Cheng Vollmer and Sara Hiebert Burch	Biology	An analysis of the gut microbiota in migratory and non-migratory hummingbirds
Emma Ricci - De Lucca	Keiann T. Simon, Michael P. Tobin, Charlotte R.	Engineering	Hypoosmotic Versus Hyperosmotic Microenvironments Respectively Suppress or Enhance Nuclear Rupture During Cell Migration Through Micropores
Omar Saleh	people are not additional authors of this project, but	Chemistry	Aluminum-Nitroxide Complexes Implementing Bidentate Redox-Active Nitroxide-Based Ligands
Scott Candey	Georgia de Nolfo	Physics	Enabling Technologies for Neutral Particle Detectors on Cubesats
Anna Abruzzo	Stacey J. Yu, Dr. Kristopher A. Sarosiek	Biology	BAX activation for treatment of medulloblastomas
Linda Lin	Liliya A. Yatsunyk	Biochemistry	Crystal structure and biophysical studies of G-quadruplex DNA in complex with a tightly binding porphyrin ligand
Elizabeth Stiles	Jeff Greeson	Psychology	Mindfulness-Based Stress Reduction (MBSR), Sleep Quality, & Interleukin 6
Dana Beseiso	Joanne Miao, Linda Lin, Professor Liliya Yatsunyk	Biochemistry	Studying and Solving the Structures of G-Quadruplex TET Sequences

Name	Advisor/Co-authors	Department	Title
Aqil Tarzan MacMood	Haley Gerardi, Benjamin D. Geller, Catherine H. Crouch	Physics	Enduring Attitudes of Life Science Students Towards Physics and Interdisciplinary Learning
Steven Chen		Chemistry	Design and Optimization of Nanoparticle Carrier Vaccines Targeting the Fusion Peptide of HIV-1
Naomi Bronkema		Biochemistry	Structural characterization of a HIV-1 DS SOSIP Env with an early intermediate antibody
Lia D'Alessandro	Advised by Dawn Carone Ph.D.	Biology	Determination of HSATII integration sites in transfected fibroblast cells
Lucas Heinzerling	Chris Graves	Chemistry	Aluminum complexes of nitrogen-based redox-active ligands
Maria Ingersoll	Elizabeth Vallen, Dana Novikov, Katie Barott	Biology	Visualizing a cellular pH sensor in the sea anemone Exaiptasia pallida
Victoria Overbeck	Vince Formica and Edmund Brodie III	Biology	Social Interactions predict Mating Pairs in Bolitotherus cornutus
Terrence Xiao		Engineering	Eldridge Commons Aquaponics System
Evangeline Adjei-Danquah	Amy Cheng Vollmer	Biology	Characterizing the Metabolism of Mutant Universal Stress Protein A in Escherichia Coli

Twan Sia		Biology	Mitotic Rounding Influences Cardiac Cell Fate Specification in Ciona Robusta
Lucy Decker	Professor Hillary Smith	Physics	Olivine NaFePO4 as a potential cathode material for Sodium-Ion batteries
Shelby Billups	Frank H. Durgin	Psychology	The Effect of Gender Information on Individuals‚Äô Attitudes Towards Social Groups
Gregory Lee	Jonah Langlieb	Computer Science	Applying Differential Privacy to Anonymize Mobile User Trajectories
Susannah Midla	Dawn Carone	Biology	Knocking Down RNA in vivo
Kent Chen	Nick Kaplinsky	Biology	A genetic and molecular analysis of mutants exhibiting similar heat shock responses in Arabidopsis thaliana
Shirline Wee	Jacob Brady and Mackenzie Frost	Neuroscience	Treatment of PTSD: An Animal Analogue of Exposure Therapy
Joanne Miao	Dana Beseiso, Liliya A. Yatsunyk	Chemistry	Biophysical Characterization and Crystallization of Tetrahymena thermophila Telomeric Sequences
Jack Rubien	Susannah Midla, Christina Rabeler, Liliya Yatsunyk and	Biology	The Physics of Cancer: Investigating Human Satellite II RNA structure and function

Hyun Kyung Lee	Liliya A Yatsunyk, Mamta Tahiliani	Biochemistry	Exploring Secondary Structure of SAT2 Centromeres
Emilie Morse		Biochemistry	Conformational Analysis of an HIV-1 Envelope using DEER Spectroscopy
Nora Blodgett	Megan Strachan, Yifan Yan	Engineering	Deep Learning for Optimization of Fourier Ptychography
Iris Wang		Physics	Investigation of LiFeF3 Structure Using M$\lor\eth$ssbauer Spectroscopy and X-ray Diffraction
Ariel Overdorff	Nathan Pitock	Physics	Testing Gravity on Kiloparsec Scales and Over Cosmological Times
Miriam Stein		Physics	Prussian Blue as a Cathode Material for Rechargeable Sodium Ion Batteries
Daniel Boehmler	Zachary O'Dell	Chemistry	Quantifying Silver Nanoparticle Dissolution Kinetics in Simple and Complex Biological Matrices
Sarah Weinshel	Nick Kaplinsky	Biology	Intron Retention and Regulation of the Heat Shock Response in Arabidopsis
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Ellen Adams	Tapan Goel, Sara Martin, Eva-Maria Collins	Biology	Nervous Eating: Neuronal Coordination of Hydra Mouth Opening
Veronica Bochenek	Danielle Ireland, Eva-Maria Collins	Biology	Evaluating the suitability of 3 planarian species for high-throughput toxicology screens
Daria Syskine		Biology	Repeatability of social environment in forked fungus beetles
Adam Mermelstein	Pearl Zhang, Daniela Fera	Biochemistry	Analysis of the Binding Interaction Between Antibody 133 and the Influenza Hemagglutinin Surface Glycoprotein
Kevin Choi	(ezhang4@swarthmore.edu) Steve Wang	Statistics	ESTIMATING THE DURATION OF A MASS EXTINCTION ACCOUNTING FOR SIGNOR-LIPPS EFFECT
Ayaka Yorihiro	Earl Wu	Computer Science	Analyzing Programs with Dynamic Data and Control Flow
Colin Perkins-Taylor	Proud Chanarat, Caroline A. Miller, Paulina	Biology	Body measurements of Chilean blue whales, collected non-invasively via UAS (drones), indicate morphological similarity to the pygmy blue whale
Josephine Thrasher	Kelly Finke, Nick Kaplinsky	Biology	"Understanding the genetic basis of thermotolerance in Arabidopsis using a high throughput quantitative phenotyping platform"
Lucy Atkinson		Engineering	Ultrasound in Air: Engineering with an ear toward the future

Jihye Yoon	Matthew Leslie	Biology	Molecular Systematics and Taxonomy of a Low Abundance Cryptic Lineage of Balaenopterid Whale
Edna Olvera	Cacey S. Bester	Physics	Creep and Compaction in a Granular System
Noah Cheng	N/A	Biology	Homology-directed gene repair using virus-like particles
Katherine Lima	Professor Aline Normoyle	Computer Science	Role Playing Game (RPG) Development for AI Testbed
Abby Clements	Youssef Ezzyat	Psychology	Event boundary predictability in community structure
Sarah Chang	Artur Perevalov, Ruben Rojas, Daniel P. Lathrop	Physics	Using reservoir computing to predict temperature fluctuations in turbulent Rayleigh-Bénard convection
Alexandria Rensing	Hillary Smith, Lucy Decker	Physics	The Crystal Structure and Phase Transformations of $Na(1-x)FePO4$ $0<x<1$
Janan Hui	Kathryn Riley	Chemistry	Purification of DNA Origami with Capillary Electrophoresis
Matthew Anderson		Computer Science	Conceptum: Supporting Collaborative Exam Development

Hyeyun Chae	Hector Corrada Bravo, Jayaram Kancherla	Computational Biology	Visualizing Results from Galaxy Workflows Using Epiviz
Shruthi Srivatsan		Biology	FucTA expression in lateral bipolar dendritic neurons important in regulation of Drosophila nociceptive response
Jonathan Solomon	Micah Harkins	Physics	Simulating Multiply Modulated Maps of the CMB
Geoffrey Chanenson	Alisha Bevins, Brittany Duncan	Computer Science	Exploring Design Methodologies to Create Expressive Drone Flight Paths
Adriana Knight		Computer Science	Linguistic Analyzer of SMS Texts (LAST)
Madeline Farber	Chris Chung	Chemistry	Characterizing the Behaviors of Silver Nanoparticles in Environmental Matrices
Daniel Chaiken	Sumi Onoe	Computer Science	Using Computer Vision to Automate Flatworm Image Analysis
Lillian Fornof		Biology	Examining the application and distribution of multiple anti-predatory strategies in red-tailed monkeys of Tanzania
Matthieu Chalifour		Physics	Measurement of Angular Correlation of Two Protons in Quasielastic Neutrino-Nucleus Cross-Section

Safia Bashir	Dawn Carone	Biology	Polycomb Recruitment to HSATII DNA Following DNA Demethylation
Michael Selvaggio	Andrew Danner	Computer Science	Parallel viewshed extraction on multiresolution terrains
Calvin Chan	John Todd Lawrence	Orthopaedics	ACLR Graft Preparation: Diameter Matters
Elena Do	Elise Cummings, Catherine Norris	Psychology	Pain Perception and Evaluation
Zachary O'Dell	'20 Laela Ezra '19 Professor Kathryn	Chemistry	Speciating Ag(I) and AgNPs in the Leachate of AgNP-Impregnated Fibers
Ming-Ray Xu	Akkipeddi (student), Kit Yu Karen Chan	Biology	Halogenated compound secreted by marine bacteria halts larval urchin development
Jason Jin	Kastan Day	Computer Science	Creating Causal Evidence and Measurable Health Improvement from Real World Patient Digital Wearable Data
Genji Kawakita	Jun Kitazono, Masafumi Oizumi	Mathematics	Computing Integrated Information of Consciousness Using Graph-cut Method
Graham Doskoch		Astronomy	Investigating TeV Emission from the Crab Nebula and the Flaring Active Galaxy BL Lacertae

Coleman Kilby		Astronomy	Transiting Exoplanets and KELT Follow-Up at Swarthmore
Chelsea Semper		Biology	Impact of Ecological and Social Factors on Laying Behavior in Female Forked Fungus Beetles
Ari Liloia		Physics	Jamming Thresholds of Square Pin Systems Plateau at High Densities
Veronica Chua	Lauren Holt, Professor Shannon Ballard	Biology	Examining the role of FucTA in Drosophila nociceptive behavior
Yan Cheng	Sylvanne Braganza and Edward Barbieri	Biology	Engineering the Metazoan Disaggregation System to Ameliorate Neurodegeneration
JJ Balisanyuka-Smith	Madison Shoraka, Joshua Goldwyn	Mathematics	Compare the dynamics of a detailed neuron model to a two-compartment reduced model
Alexandra Specht		Physics	Binding energy thresholds of Rhodium and Lanthanum negative ions found using a newly automated attenuator
Sophie Gray-Gaillard	Noah Lee, Stewart Silver, and Alex Baugh	Biology	Validation of water-borne androgen in t∨∫ngara frogs
Stacy Guan	Eva-Maria S. Collins	Biology	Parental Gradient Inheritance in Hydra Regeneration

Ryan Stanton	Profs. Sara M. Hiebert, Amy Cheng Vollmer	Biology	Clarifying the Differences in Migratory and Resident Hummingbird Gut Microbiota
Alyssa Davis		Physics	Determining the astrophysical 20Ne(Œ±,p)23Na reaction rate from measurements with the Notre Dame 5U accelerator
Lilia McGee-Harris	Molly Flaherty, Daniel Grodner	Psychology	"She, uh, he": Gender Pronoun Production in Young Children
Sabreen Ahmed	Professor Catherine J. Norris	Neuroscience	Emotional Responses to Gamble Outcomes
Jasiel Lopez Juarez	Dulce Ventura	Biology and Computer Science	Developmental Systems Drift Across Tunicate Species
Jean-Baptiste Robert	Amy Cheng Vollmer	Biology	Overrepresentation of Corynebacteria in the Gut Microbiota of Hummingbirds Undergoing Daily Torpor in Relation to Cold Shock
Emma Tapp		Biology	Creatinine and Corticosterone Assay Validation on the Urine of Sympatric Migratory and Resident Hummingbirds
Elizabeth Shin	Dr. Einar Sigurdsson, Dr. Hyung Don Ryoo	Biology	Pan-neuronal expression of TauR406W, scFv235, and CD8-GFP in transgenic adult Drosophila models of Alzheimer‚Äôs Disease
Jayna Jones	Jr., Chinacherem Chinaka, Lavisha Pelaez, Dr. Kirk	Public Health	Black-White Unequal Cancer Cumulative Incidence and Survival among infants in the United States, SEER (1975-2016)

Matiwos Mebratu	Michel R. Brown	Physics	MHD simulation of the merging of fully relaxed Taylor state plasma
Maria Jose Andrade	Holly Ramage, PhD, Minghua Li, PhD, Billy Truong, BA	Biology	Role of post-translational modification of West Nile Proteins
Vitor L Dos Anjos	Vince Formica	Biology	Reproductive improvement from a wild, long lived population of forked fungus beetle.
Madison Shoraka	Shoraka, Joshua Goldwyn	Mathematics	Obtaining an Accurate Reduced Model of Neural Dynamics
Stewart Silver	Noah Lee, Sophie Gray-Gaillard	Biology	Stress is Sexy, but is Sex Stressy? Glucocorticoid effects on female mate choice in Hyla chrysocelis
Samuel Sheppard	Eric Jensen	Astronomy	A Bayesian Approach to Orbit Fitting
Misha Khan		Biomechanics	Dampening Substrates affect Power Amplified Grasshopper Jumps
Moey Rojas		Biology	Tonic Immobility in Two Hummingbird Species
Mirabai Smoot	Nana Anikuabe	Computer Science	Adaptive Bayesian Learning of Playstyles

Rekha Crawford	Brian Dekleva, Robert Gaunt	Neural Computation	Effect of Intracortical Microstimulation in Somatosensory Cortex on Activity in Motor Cortex
Michael Kourakos	Sara Mathieson	Computer Science	Deep Learning and Summary Statistics to Predict Ancestral Population Size

BAX activation for treatment of medulloblastomas

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Medulloblastomas are the most common type of malignant pediatric tumor. Although the current treatment – a combination of surgery, chemotherapy, and radiation – cures over 80% of patients, it also has detrimental effects on the developing brain and off target DNA damage leads to secondary malignancies in 5-10% of childhood cancer survivors. This study determined the effects of a novel therapy that directly induces apoptosis by activating the pro-apoptosis protein BAX. Cancer cells often express high levels of BAX due to the stress of hyperactive growth and proliferation, and have been shown to be more primed for apoptosis than healthy tissues. We hypothesized that medulloblastoma cell lines would show greater sensitivity to treatment with a BAX activator compared to primary neurons. Two types of medulloblastoma cell lines, UW473 and DAOY1, and p0 primary neurons were treated with two types of previously identified small molecule BAX activators, BAXa1 and BTSA1, in combination with radiation treatment. The data indicate that treatment with BAX activators promotes medulloblastoma cell death, but sensitivity varies with the cell type and drug administered. BAXa1 induces apoptosis more efficiently than BTSA1, and UW473 cells show a greater response to treatment than DAOY1 cells. Primary neurons underwent less apoptosis than medulloblastoma cells following treatment with BAX activators, suggesting that BAX activation might effectively target medulloblastomas while sparing healthy tissues and avoiding the risk of secondary tumors associated with existing therapies.

Nervous Eating: Neuronal Coordination of *Hydra* Mouth Opening

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Hydra are small freshwater cnidarians famous for their regenerative abilities. Recently, they have also gotten attention for the peculiar way they feed: *Hydra* do not have a permanent mouth and must tear open a new hole in a continuous epithelial sheet each time the mouth is opened. The Collins lab has previously studied the dynamics of this unusual process and shown that the nervous system is necessary for mouth opening. However, how the nervous system controls mouth opening remains unknown. We predicted that the nervous system solely initiates mouth opening and that signal propagation is then coordinated entirely within the epithelial cells executing the process. To test this hypothesis, we took advantage of *Hydra*'s accessibility to manipulation and live imaging. It is possible to chemically generate nerve-free animals, which can fully regenerate and reproduce, but are unable to open their mouths. By grafting half of such a nerve-free animal to half of an enervated, normal *Hydra*, we generated chimeric animals. These chimeras allowed us to test whether chemically induced opening in the enervated part would initiate mouth opening in the nerve-free part. Opening of the nerve-free part would imply that epithelial coupling was sufficient for signal transduction and mouth opening once opening was triggered by the nervous system of the enervated part. Our results showed that the nerve-free half was induced to open by the enervated half, albeit with a delay and significantly slower opening rate than in enervated controls. These data support our hypothesis that the signal is propagated through epithelial coupling and that initiation by the nervous system is sufficient for mouth opening. Future work will dissect these findings in more detail using electrostimulation to initiate mouth opening in fully nerve-free animals.

Characterizing the Metabolism of Mutant Universal Stress Protein A in Escherichia Coli

Evangeline Adjei-Danquah, Amy Cheng Vollmer

Universal stress proteins are found in most bacteria and are synthesized under a wide variety of stressful conditions[1]. Activation of Universal stress protein A (UspA) is knowingly due to phosphorylation of serine and threonine residues by a tyrosine kinase[2]. However, the location at which UspA is phosphorylated is still uncertain, as are the downstream effectors of the protein. This experiment aims to examine the differing ways mutant UspA strains metabolize carbon sources. This is based on prior knowledge that under growth arrest UspA enhances the rate of cell survival and may provide a general "stress endurance" activity[3]. We hypothesize that placing a mutant UspA allele into its wild type background alters physiological stress coping responses. Mutant strains are generated by transforming serine and threonine residues to alanine and aspartic acid, which are un-phosphorylable and permanently phosphorylable states, respectively.

Emotional Responses to Gamble Outcomes

Sabreen Ahmed, Professor Catherine J. Norris

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Can people feel both happy and sad at the same time? Ambivalence is the state of holding positive and negative emotions in the mind simultaneously. In previous studies using a combination of behavioral measures and event related brain potentials (ERPs), Professor Norris has shown that yes, people can feel ambivalent. It has also been shown that personality factors affect our expectations of future events, and that they can impact feelings of ambivalence. The present study hopes to provide a more comprehensive understand of how personality affects ambivalent emotional responses. In this experiment, participants will play a gamble task designed to induce ambivalence. Participants will first be shown two cards face down on a computer screen and asked to choose one to flip over. After viewing the outcome of their decision, they will be asked if they would like to flip over the other card to see the outcome that they could have obtained. Emotional responses will be reported after each trial using an evaluative space grid (ESG), allowing us to examine overall valence and ambivalence of each response. After completing the task, participants will then complete a number of personality surveys. We will be looking at personality factors such as (but not limited to) optimism, pessimism, risk propensity, and self esteem, in the hopes that they will give us more insight into how each factor affects ambivalent emotional responses. We intend to illuminate the behavioral and neural mechanisms (using ERPs) underlying the finding that some personality factors are protective for both physical and mental health.

Halogenated compound secreted by marine bacteria halts larval urchin development

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Marine bacteria are ubiquitous and yet their ecological functions have not been fully characterized. The globally distributed *Pseudoalteromonas* genus, well known for their pervasive biofilms, produce a variety of potentially bioactive yet understudied halogenated organic products. One such secreted compound, 2,3,4,5-tetrabromopyrrole (TBP), has been found to be biocidal for several taxa of plankton while stimulating the settlement and metamorphosis of coral at nanomolar doses. Here, we tested whether the presence of TBP affects early development in sea urchins that are not in direct contact with a benthic microbial film. *Lytechinus variegatus* embryos were exposed to varying TBP concentrations for different durations of time over the first 48 hours post-fertilization. Concentrations as low as 500nM markedly reduced larval survivorship and retarded development. These deleterious effects became more pronounced as the concentration and duration of exposure to TBP were increased. Impairments in development when exposed to TBP appeared to be reversible, provided low exposure concentrations (< 500nM-1000nM) for limited exposure durations (< 1-4 hours). Immunofluorescence staining showed spindle defects in dividing embryos when exposed to TBP at high concentrations, which may contribute to mortality and impaired growth. Therefore, while TBP and other bacterial compounds like it may serve as settlement cues for corals, their cytotoxicity to single-cell algae and larval urchins could hint at the dangers of the benthos to developing embryos. If true, such compounds, along with the bacterial taxa that produce them, likely play underappreciated roles in the ecology, and potentially the evolution, of planktonic development in macroinvertebrates.

Conceptum: Supporting Collaborative Exam Development

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This summer, I took part in a project with Professor Kevin Webb to develop Conceptum, a website designed to facilitate collaborative exam development, especially in Computer Science. The website's primary focus was on concept inventories, which are exams with think-aloud, interview-style questions given at the start and end of a course that are used to identify systematic misconceptions based on students' responses. Educators can then use the results to make more objective comparisons of teaching strategies and curricula across professors and institutions, helping them implement more robust and effective teaching strategies. Concept inventories are commonly seen in several STEM disciplines, namely physics, and have played key roles in developing the pedagogy of some fields. Though only one Computer Science concept inventory existed before our project, we believe that they could have a similar impact in further evolving Computer Science education. Thus, our goals with the Conceptum project were twofold: to create a tool to facilitate and streamline concept inventory development and, by extension, encourage the advancement of Computer Science concept inventories.

Facilitating concept inventory development is so important because of how costly and intensive the process currently is. Educators, often across multiple institutions, must conduct open interviews with hundreds of students, record everything they can, then evaluate the results. Concept inventory developers must hold to a principle called exam validation, which means that if too many students misinterpret a question, that question is revised, and the entire process is repeated. This means tracking hundreds of questions, many with different versions, and hundreds of interviews, and as no serviceable tool currently exists to do this, Conceptum should serve as a robust infrastructure to store, query, and filter this data when building a final concept inventory.

After the work done this summer, Conceptum is nearly complete. All the functionality we set out to implement is done, and aside from some cosmetic touch-ups, the user interface and display is also complete. There is still room to expand upon the existing features, but Conceptum is more than functional in its current state, and should be ready for use soon.

Role of post-translational modification of West Nile Proteins

Maria Jose Andrade, Holly Ramage PhD

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West Nile virus (WNV) is a neurotropic human pathogen that is the causative agent of West Nile fever. WNV became endemic in the United States in 2004, spreading to people through the bite of infected mosquitoes. WNV is an enveloped virion containing a single-stranded, positive-sense RNA genome that encodes for the expression of 10 viral proteins. Although the WNV genome encodes only 10 proteins, it carries out its life cycle processes through hijacking and using cellular host proteins. WNV proteins required for infection need to interact with host pro-viral factors, antagonize host anti-viral factors and localize to appropriate cellular compartments. These functions can be altered by the post-translational modifications- namely phosphorylation and ubiquitylation- of West Nile virus proteins. The Cherry Lab has previously identified phosphorylation and ubiquitylation sites of WNV proteins during viral infection (Li et Al, 2019). Possible outcomes of these post-translational modifications are changes in the localization, stability, function and interactions of the viral protein (Li et Al, 2019). Of special interest is the WNV capsid protein, which localizes in the nucleolus and cytoplasm, equally, and envelops the viral genome (E.R.A. Oliveira, 2017). In this study, we generated mutations in the identified phosphorylation and ubiquitylation sites located in the WNV capsid protein to determine if these mutations alter the localization of the viral protein in the cell. We carried out site-directed mutagenesis with primers designed to generate mutations (K$\rightarrow$R, A$\rightarrow$S) in the capsid post-translational modification sites. We performed a Polymerase Chain Reaction and carried out the transformation of competent E coli, sequencing the colonies and using blast alignment to verify the presence of the desired mutations. Five mutants (phosphomutant, mutant K18, K74, K84, and K85) were acquired. We transfected the constructs into U2OS cells and used a Western blot to verify the take-in of the capsid by the cell through the expression of the protein Flag-tag in the mutated constructs. Two replicates of the constructs with Flag -ag were transfected into U2OS cells to identify the localization of the mutant proteins using immunofluorescence and the Intensity Ratio Nuclei Cytoplasm Tool, with Image J, as a method of quantitation of localization. This experiment was repeated in the context of infection to corroborate our previous replicates, by introducing a protease to cleave the anchor of the capsid. We used cellular fractionation to visualize capsid protein localization in the cytoplasm, nucleus and the membrane of U2Os through a Western Blot. Overall, our results were inconclusive. The localization quantitation data from the 2 microscopy sets were contradicting: the first set showed greater localization to nucleus in all mutants, while second set only showed less localization in mutants K18, K74, and K84. The quantitation data in the context of infection did not support the data of any of the previous 2 sets, as it showed that localization to nucleus and cytoplasm did not significantly change. Future repetition of confocal microscopy quantitation in the context of infection is needed. Furthermore, the cellular fractionation western blots showed weak expression of the phenotype, with the cytoplasmic fraction of Mt K18 and K85 showing slightly lower localization than the wild type cytoplasmic fraction. However, it is difficult to conclude, and repetition of this cellular fractionation is needed in the context of infection.

Ultrasound in Air: Engineering with an ear toward the future

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Airborne ultrasound is a growing theme of research within the field of acoustical engineering. Ultrasonic waves, which are simply sound waves at a high enough frequency so that the human ear cannot detect them, can be used in devices such as pest deterrents, motion detectors, and a variety of other applications. While the safety standards for using ultrasound are currently under revision, this research project explores a new application of airborne ultrasound, while keeping safety in mind.

The eventual goal of this research is to design a device that would allow a consumer to hold a silent telephone conversation rather than speak loudly in a public environment. The device, which would contain two ultrasonic transducers, would send ultrasonic waves into the user's mouth to reflect off of the changing shape of the surfaces in the mouth, before receiving those reflections, translating them into speech (using machine learning), and sending them to the listener on the other end of the phone.

While this is the ideal end of the research project, the current state of the project is exploratory. At the moment, the project has proof of concept: while the design is nowhere near its long-term goal, the concept of sending and receiving ultrasound using ultrasonic transducers in air, and of detecting differences in the signal based on the surface's properties or behavior, has been successfully modeled in the lab with a simple but similar representation of the set-up. This preliminary experimentation should pave the way to greater exploration and success for this project.

Compare the dynamics of a detailed neuron model to a two-compartment reduced model

JJ Balisanyuka-Smith with Madison Shoraka Supervised by Joshua Goldwyn

The neurons of the Medial Superior Olive (MSO) help the brain locate the sources of auditory inputs. Lehnert et al. (2014) created a model of such neurons that breaks the neuron's spatial structure into 45 compartments: soma, axon initial segments, internodes, and nodes of Ranvier. Our goal was to construct a minimal model that approximates the spike generation region of the 45-compartment model and incorporates soma-to-axon coupling. Using the differential equations and parameters controlling the current of the 45-compartment model as a guide, we constructed a reduced model consisting of 2-compartments; one for the soma-dendrite regions and one for the axon region. We found that our model mimics the nonlinear dynamics of the detailed 45-compartment model with high accuracy. Our analysis, which quantitatively compared the spiking current thresholds and traces of the two models, found robust agreement. These positive results for our approximation could be helpful for future researchers to efficiently and accurately model spiking dynamics of large clusters of neurons.

Polycomb Recruitment to HSATII DNA Following DNA Demethylation

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DNA methylation and Polycomb repressive complexes play a vital role in the early development of mammalian genes. The misregulation of DNA methylation and the recruitment of Polycomb repressive complexes can lead to chromatin defects. In cancer, Human Satellite II (HSATII) sequences on 1q12 is demethylated in the majority of human cancers. Demethylated HSATII sequences on chromosome 1q12 causes the recruitment of Polycomb Repressive Complex I (PRC1), which results in the formation of large PRC1 aggregate bodies. However, the mechanism for this preferential recruitment of PRC1 to HSATII on 1q12 is currently unknown. To better understand this, we examined the distribution and recruitment of PRC1 to HSATII sequences located on 1q12, in response to demethylation in normal cells. This was an initial step in distinguishing between the size, sequence, and early DNA demethylation of HSATII to determine the cause of 1q12 HSATII's preferential recruitment of PRC1. We treated human fibroblast Tig-1 cells with 5-aza-2'deoxycytidine to induce DNA demethylation, and cells were fixed every 24 hours for 5 days. To assay for global patterns of DNA demethylation, we performed an antibody stain for BMI-1 (core component of PRC1) and 1q12 HSATII DNA. While we could not determine whether PRC1 is recruiting to 1q12 HSATII DNA or whether HSATII sequences on 1q12 are demethylated earlier than other HSATII sequences in the genome, we found that the area of 1q12 and the nucleus increases when demethylated. Additionally, we found that colocalization patterns of BMI-1 and 1q12 differed between cells treated with 5-aza and the controls. To conclude, this study provides further insight on the effects of DNA demethylation of HSATII sequences on 1q12 and the preferential recruitment and distribution of PRC1.

Studying and Solving the Structures of G-Quadruplex TET Sequences

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DNA can exist in multiple conformations, including duplexes, triplexes, and even quadruplexes. This summer, I conducted research on telomeric G-quadruplex (GQ) DNA structures with and without the ligand N-Methyl mesoporphyrin (NMM).

GQs form from guanine rich sequences and are composed of stacks of G-tetrads stabilized by $\pi - \pi$ bonding. A singular tetrad is composed of four guanines, bonded together through Hoogsteen hydrogen bonding in a square planar arrangement, and further stabilized by a monovalent cation in the middle. Anticancer therapeutics could be developed by specifically targeting G-rich areas in the telomeres (short repeated G-rich DNA sequences) to induce the formation of a GQ which can act as a barrier that prevents telomerase upregulation, preventing telomeres extension, and therefore causing cell death.

I worked with seven telomeric sequences from the organism *Tetrahymena Thermophila*. The biophysical results demonstrated that all but one of our sequences fold into a GQ. We also utilized Native Polyacrylamide Gel Electrophoresis and Circular Dichroism to demonstrate that all sequences but two consist of multiple confirmations. Via Circular Dichroism melting studies we showed that all of our sequences are stable well above room temperature (>60 °C). The addition of NMM to the DNA sequences has led to an increase in stability by 7-12 °C, and a change in topology for all sequences to parallel conformation. Finally, and most excitingly, I succeeded in obtaining high quality crystals of one of the sequences called TET4B. We examined the crystals using APS synchrotron radiation and obtained excellent diffraction patterns at 1.97 Å resolution. Our end goal is to solve the GQ structure which will serve and aid in the development of anticancer therapeutics.

The Effect of Gender Information on Individuals' Attitudes Towards Social Groups

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The Stereotype Content Model and Semantic Differential are two methods of identifying individuals' attitudes towards concepts. Using five features from these two models (Warmth, Competence, Evaluation, Activity, and Potency), we can gain insight into individuals' attitudes towards particular social groups when rated along these dimensions and see how the semantic space in which they inhabit changes when additional information is added. This research explored the effects of gender information on judgments of social groups and found two possible components that account for a combined 76-88% of the ratings' variance. Using Principle Component Analysis, we find two components that we are labeling currently as "Instrumental" and "Experience/Age". We believe that these are the two main components individuals use to make their ratings along the five aforementioned dimensions. This is a facet of the precursory data that will be applied to a future project that uses this same method to understand how intersectional identities affect the location of these groups and traits within the semantic space.

Deep Learning for Optimization of Fourier Ptychography

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Fourier Ptychographic Microscopy (FPM) is a form of microscopy that maintains high resolution and high field of view, albeit at the cost of temporal resolution. An FPM reconstruction algorithm iteratively combines multiple low resolution images of a sample, illuminated by different LEDs in an array, to produce a single high resolution image. To improve temporal resolution, these low resolution and high resolution dataset pairs are used as training data for a deep learning neural network that is able to more efficiently produce high resolution images based on low resolution input. FPM, paired with a super resolution neural network, paves the way for faster and more accurate diagnosis or identification in medical or microbiological studies. This summer (2019), we further improved our laboratory's FPM technique by replacing the existing flat LED array with a dome-shaped LED array, reducing data acquisition time and producing brighter, more information-packed images in both the brightfield and darkfield range. We also improved some of the software by tailoring each image, with its corresponding LED illumination angle, to its optimized camera exposure time. This modification ensured that brighter images were not completely saturated and darker images weren't too dark to extract any visible information, thus producing a full set of valid low resolution data. As our imaging subject, we used a small aquatic organism called the hydra, provided by the Swarthmore Biology Department. The multicellular hydra is thicker and less transparent than the TIG1 cells used in summer 2018, which allowed us to test the neural network and FPM reconstruction algorithm's ability to interpret and process more challenging biological specimens. By expanding FPM and deep learning to thicker samples, medical settings will better be able to analyze samples on a slightly larger, more 3-dimensional scale, such as living tissue as opposed to individual cells.

Quantifying Silver Nanoparticle Dissolution Kinetics in Simple and Complex Biological Matrices

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The dissolution of silver nanoparticles (AgNPs) and their subsequent release of silver ions ($Ag(I)(aq)$) is a vital area of study within the field of engineered nanomaterials (ENMs) due to the relative ubiquity of AgNPs in industry and their well-characterized cytotoxic effects. Biophysiochemical surface interactions, such as protein adsorption, have the potential to modify dissolution rates of these AgNPs. To establish a simple matrix and optimized technique for monitoring AgNP dissolution in biological matrices, we report the use of Linear Sweep Stripping Voltammetry (LSSV) in determining dissolution rates of varying nanoparticle sizes (10, 20, and 40 nm) in varying concentrations (0-2 nM) of the model protein bovine serum albumin (BSA). Our data show that the presence of BSA enhanced dissolution of AgNPs at all particle sizes, and that the degree of BSA-mediated dissolution was dependent on particle size. These rate enhancements were more pronounced as particle size decreased. Dynamic light scattering, zeta potential measurements, UV-vis spectroscopy, and circular dichroism spectroscopy revealed a stronger BSA binding affinity as particle size increased. These results indicate that BSA-mediated dissolution is carried out by displacement of $Ag(I)(aq)$-loaded BSA by excess protein, and a lowered accessibility towards the AgNP surface interface due to more strongly bound BSA. However, as nanoparticle waste from industrial processes becomes more prevalent, there arises a need to move beyond simple biological matrices towards more comprehensive environmental models, such as bacterial metabolites and media. Here we also report the AgNP dissolution rate effects of peptone yeast-extract (PYE) media and its individual components, including Bactopeptone® (casein hydrolysate), yeast extract, and low concentrations of $MgSO_4$ and $CaCl_2$. In addition, we investigated the effects of "spent" PYE media used to culture *Caulobacter crescentus*, an oligotrophic alphaproteobacterium commonly isolated from aquatic environments. Our results show significant enhancement of the AgNP dissolution rate in solutions containing "spent" PYE media, as well as Bactopeptone® and yeast extract, while demonstrating slight suppression of dissolution in unaltered PYE, and no changes in the presence of low concentrations of salt. These results provide us insight into the effects of larger peptides (Bactopeptone®, yeast extract), their combinatory effects, and the influence of bacterial metabolites on AgNP dissolution rate. Further work is required to characterize the mechanisms by which these media components and metabolites interact with AgNPs.

Evaluating the suitability of 3 planarian species for high-throughput toxicology screens

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Innovative computational approaches along with high-throughput screening (HTS) using *in vitro* and alternative animal models are revolutionizing drug discovery and toxicology. Asexual freshwater planarians are a new and promising invertebrate model for neurotoxicity HTS because they possess a wide repertoire of quantifiable behaviors that can be used as readouts of neuronal function. Currently, three planarian species are used in toxicology testing - *Dugesia japonica, Schmidtea mediterranea*, and *Girardia tigrina* – but thus far only *D. japonica* has been demonstrated to be a suitable HTS system. Here, we assess the suitability of the two other species for HTS by direct comparison with *D. japonica* using a custom, robotic screening platform and semi-automated image analysis. Through quantitative assessments of morphology and multiple behaviors, we assayed the effects of 4 common solvents (DMSO, ethanol, methanol, ethyl acetate) and a negative control (sorbitol) on neurodevelopment. Each chemical was screened blind at 5 different concentrations to evaluate dose-response at two time points over a twelve-day period. Surprisingly, *G. tigrina* and *S. mediterranea* planarians showed significantly reduced movement compared to *D. japonica* under these experimental conditions, making it difficult to obtain meaningful behavioral readouts from these species. Of the solvents tested, methanol caused significant lethality [0.8mM] in *G. tigrina* and *S. mediterranea* but not in *D. japonica*, demonstrating species differences in sensitivity. Thus, these results suggest that care must be taken when extrapolating chemical effects observed in one planarian species to another. Overall, our data indicate that *D. japonica* may be best suited to HTS given the limited motility of the other species. Standardizing which planarian species is used will better allow comparisons of species in the future. Ultimately, this new system promises to fill an important gap in first tier chemical HTS, helping streamline drug discovery and toxicology testing.

Treatment of Anxiety Disorders: An Animal Model

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Post-traumatic stress disorder (PTSD), a disorder characterized by persistent and intrusive negative memories of a traumatic event, affects 3 to 30% of individuals exposed to traumatic events. Although there are several FDA approved drugs on the market, none has proven entirely effective in the treatment of PTSD. Clearly then new drugs and behavioral therapies are urgently needed. Animal models are an appropriate platform for developing such therapies.

Clinical studies have shown that a behavioral procedure known as exposure therapy, in which patients recall repeatedly the original fear-eliciting memory in a safe environment, is effective in eliminating abnormal fear memories in PTSD patients. Unfortunately, the treatment is limited and the majority of patients fail to achieve clinically significant and lasting improvement.

Using an animal model of exposure therapy, known as extinction training, we conducted a series of experiments designed to enhance the effectiveness of extinction training (and by extension exposure therapy) in reducing retention of learned fear. The experiments were based on evidence indicating that fear memories upon retrieval pass through a brief state of destabilization – a state requiring protein synthesis to re-stabilize and endure.

Two experiments were conducted. Experiment 1 determined the effectiveness of administering MK 801, a protein-synthesis inhibitor, shortly after retrieval (that is, during memory destabilization) in reducing subsequent retention. Experiment 2 determined the effectiveness of a novel learning procedure introduced shortly after retrieval (that is, during memory destabilization) in updating the original fear memory with a newly acquired "safe" memory. The results indicated that both procedures were effective in reducing subsequent retention of fear 24 hours after treatment.

The clinical implications are far-reaching. If what holds for laboratory rats holds for humans---and that is to be determined---the results suggest that both the pharmacological and behavioral (updating) approaches may prove to be effective in the treatment of anxiety disorders, but with one caveat. If the pharmacological approach is to be taken seriously as a potential therapy, the results of the present experiment should be replicated using drugs that are not subject to the toxicity side effects of protein-synthesis inhibitors. On the other hand, no such constraint applies to the updating (safe memory) approach.

Structural characterization of an HIV-1 DS SOSIP Env with an early intermediate antibody

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The human immunodeficiency virus type 1 (HIV-1) Env is a glycosylated protein spike on the virion surface that is the target of neutralizing antibodies produced by an immune response. Some patients can develop broadly neutralizing antibodies (bNAbs) that can target multiple strains of HIV. A promising pathway to HIV vaccine development is through the mapping of bNAb and viral coevolution in a patient. The longitudinal study on patient CH848 provides an opportunity to fully characterize both bNAb and viral lineages to understand how this bNAb lineage was able to develop its breadth. This information will help guide vaccine design to try to elicit similar bNAbs in uninfected individuals.

There is structural data available on how late members of the bNAb lineage from the CH848 patient bind to Env. Therefore, we are focusing on an early member of the antibody lineage, an antibody called IA4. We used biolayer interferometry (BLI), together with negative stain electron microscopy (EM), to understand the interactions IA4 makes with the CH848 10.17 HIV Env, the only Env that was identified to be targeted by this antibody. We are also performing double electron-electron resonance (DEER) spectroscopy experiments to determine the conformation of the CH848 10.17 Env.

Data from BLI show that the fragment of the early intermediate antibody IA4 binds to the CH848 10.17 Env with a K_d of 9.998 x10^7 M. 2D class averages generated from EM data showed that the IA4 fragment can bind to all three lobes of the trimeric Env, but some EM images have captured only one or two copies of IA4 bound. We also obtained preliminary data using DEER spectroscopy that could give insights on the conformation of the 10.17 Env and how it compares to other Envs. Future work will be done to generate an EM 3D model of the 10.17 Env with the IA4 fragment to better understand their interactions and compare them to those of late members of the bnAb lineage with Env. Additional DEER experiments will be repeated of the 10.17 Env, to confirm the conformation of the 10.17 Env. We will compare this data to that of other Envs so that we can learn what features of the 10.17 Env allow it to bind to IA4. This information will provide insights into an immunogen that might trigger a bNAb precursor by vaccination.

An analysis of the gut microbiota in migratory and non-migratory hummingbirds

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The gut microbiome is the microbial community that lives inside an organism's gastrointestinal tract. Microbiomes have been shown to influence stress responses and changes in the weight of the organisms that they are in. Our study looks at the microbiome of two species of hummingbird, *Selasphorus rufus* and *Calypte anna*. These two species are very similar with one key distinction: *S. rufus* migrates between the pacific northwest and Mexico while C. anna mainly stays in the pacific. Hummingbirds are miniature and so migrating from the pacific northwest to Mexico requires *S. rufus* to fatten up and nearly double their body size.

Many studies of the gut microbiome have shown that body fat content plays an important role on what bacteria are part of an organism's gut microbiome. Most of these studies have been on lab mammals and so there is little know in relation to fat of wild non-mammals. The majority of studies on the gut microbiome in birds have been on chickens and lead by the agriculture industry. From 2017 to the present, we have collected fecal and urine samples from S. rufus and C. anna hummingbirds from the pacific northwest, New Orleans, and southern California. We purify DNA from the fecal samples and analysis the DNA using next generation sequencing of the 16S rRNA of the bacteria in the gut microbiome. The gut microbiomes of the hummingbirds are analyzed on a series of qualitative variables such as species, fat content, and age.

We are looking to see if there are any correlations between the known migratory patterns of these birds and other characteristics that have been previous shown in mammals to have strong influences on the make-up of an organism's gut microbiome.

Enabling Technologies for Neutral Particle Detectors on Cubesats

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Simple neutral particle detectors consisting of scintillators, sensitive photodetectors, and readout systems have been used to great effect in space- and Earth-based science for observing gamma rays and particle radiation from solar weather, astrophysical phenomena, and even lightning storms on Earth. Silicon photomultiplier-based detectors (SiPMs) are currently being tested as replacements for commonly used photomultiplier tubes (PMTs) used to detect individual photons from scintillator interactions with gamma rays. SiPMs have much lower power requirements and are much smaller than PMTs, so they fit well into Cubesat and Smallsat designs. SiPMs have been proven to be radiation hard with low energy particle beams, but lead and higher energy particles, which are dangerous for humans and cause single event resets in satellites, have not been tested. 10 Hamamatsu S13360-6050 SiPMs and 10 Hamatsu S14160-6050 SiPMs were exposed to hundreds of thousands of lead energy events in a CERN particle beam before being compared to unexposed SiPMs using current draw and resolution testing. The resolution of the exposed SiPMs from both generations worsened by 7%, though the beam exposure was much greater than any mission would receive.

In addition to radiation hardness testing, the calibration of simple gamma ray detectors was improved through Compton edge modeling and kernel density estimation. When calibrating particle detectors, the Compton edge produced by a gamma ray source such as Cesium-137 is often used to convert the raw voltage measurements histogram into a representation of the gamma ray energies interacting with the detector. The process of estimating the location of the edge on a histogram of measurements is often done by hand or with a half gaussian fit, but to simplify detector calibration using Compton edge measurements we calculated the theoretical Klein-Nashina Compton distribution, created a model of the edge with a piecewise 2nd order polynomial, and convolved the piecewise function with a Gaussian to approximate the experimental response. The response is differentiated to identify the location of the true Compton edge without estimating using a percentage of the local maximum. Using kernel density estimation (KDE), Gaussian kernels are built up to a representation of the distribution without any fitting. Numerically differentiating this plot provides the location of the true Compton edge, with much lower systematic error than the varied methods of locating Compton edges used in previous papers.

Visualizing Results from Galaxy Workflows Using Epiviz

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Galaxy is a widely used web-based open source bioinformatics platform to create scientific workflows, genomic data integration and analysis, and aims to make computational biology accessible to researchers who have less programming experience. The execution of a workflow generates results that can visualized with various genome browsers. Our goal of this project is to integrate Epiviz, an interactive visualization tool for functional genomic data, with Galaxy to analyze and explore generated datasets in the same computational environment. Epiviz can directly visualize data from indexed genomic files using the file server python library. To integrate Epiviz with Galaxy, we created a docker container, a necessary component to run custom applications within a Galaxy environment. We then implemented an interactive environment in Galaxy for Epiviz to be accessible as a visualization tool. The source code and installation instructions are available on github.

Using Computer Vision to Automate Flatworm Image Analysis

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The Collins Lab at Swarthmore College studies the neurotoxicity of various chemicals by measuring physical and behavioral changes of flatworms (*Dugesia japonica*) under chemical exposure. These flatworms model human neural architecture and are conducive to high throughput experiments. The lab collects video data of flatworms, which is currently analyzed by hand. This summer, we wrote programs to automatically analyze these images in order to allow for a greater throughput of chemicals tested. We used both convolutional neural networks and custom computer vision pipelines in order to automatically determine several categories of physical and behavioural change. One task is to determine stickiness; some chemicals cause worms to secrete mucus, sticking them in place when the plate they are in is shaken. We used computer vision techniques to automatically determine whether a worm in a given video was stuck in place. Our approaches also detect fission (a worm splitting in two) and death. In ongoing work, we use neural network architectures to classify different movement patterns exhibited by the worms.

Measurement of Angular Correlation of Two Protons in Quasielastic Neutrino-Nucleus Cross-Section

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We measure multiple proton emission in pionless, quasielastic like, charged current neutrino scattering in the MINERvA scintillator detector. The number of such observable events in MINERvA is predicted to be far greater than currently available samples. We measure the total number of such events, and study the distribution of laboratory frame angles between the multiple protons and the muon, which is sensitive to the production mechanisms for such events.

ACL Graft Preparation: Diameter Matters

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Introduction:
Over 130,000 anterior cruciate ligament reconstructions (ACLR) are performed annually in the United States (US) and are on the rise in both adult and pediatric populations. Previous studies have investigated the effect of tension and circumferential compression on the diameter of fresh-frozen allografts, but none have described its effect on ACL autografts harvested for implantation during the ACLR procedure. The purpose of this study was to elucidate how hamstring autograft diameter changes in response to tension and circumferential compression for ACLR in a pediatric population.

Methods:
100 ACLR surgeries (median age 15 [IQR 14-17] years; 53% male) were identified in one pediatric hospital. Two orthopedic surgeons dictated hamstring autograft diameters at two time-points during graft preparation. Hamstring tendons were prepared in a standardized procedure. Autografts were tensioned to 15-20 pounds and their diameters were immediately measured using cylindrical sizing blocks (time-point 1). The graft was then compressed on both the tibial and femoral aspects using sizing blocks. After 10 minutes, diameters were measured again (time-point 2) before implantation. Comparisons were made between graft diameter at each time point. Univariate linear regression models were fitted to determine associations between demographics and graft characteristics.

Results:
The median initial diameter measurement of both femoral and tibial sides of the autograft during longitudinal tension was 9.5 (IQR 9-10) mm. After tension and the addition of circumferential pressure, the median final diameters were 8.75 (IQR 8-9) mm and 8.5 (IQR 8-9) mm for the tibial and femoral aspects, respectively. The median graft diameters decreased 0.75 mm and 1 mm for the tibial and femoral aspects, respectively, after applying circumferential pressure ($p < 0.0001$ for both). Only 2% of cases did not show any decrease in diameter between time points. There was no identified common feature that could explain this group of non-responsive cases.

Conclusions:
The pediatric and adolescent population necessitates a specific skill-set to achieve the fine equilibrium between implanting a well-restored biomechanical construct while avoiding unnecessary bone loss or disruption of the physis. This study suggests that optimizing graft preparation with circumferential compression would allow for the drilling of tunnels which are two (0.5 mm) sizes smaller while providing a better fit between the graft structural content and a relatively small bony tunnel. This paradigm shift is particularly applicable to pediatric, revision, and double bundle ACL reconstruction techniques, where space for tunnel drilling is limited.

Exploring Design Methodologies to Create Expressive Drone Flight Paths

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Advances in capabilities and reduction in cost have made the existence of both hobbyist and professional unmanned aerial vehicles (UAVs) more prevalent in everyday life. In order to foster better human-drone interactions, the drones should be able to communicate with us. We are using a gesture-based approach to tackle the drone to human communication problem. Gestures, in the form of expressive flight paths, offer a natural method for drone to human communication. This approach is advantageous because these expressive flight path gestures can accommodate communication challenges such as poor visibility, bad viewing angles, or insufficient lighting. Moreover, this approach requires no additional equipment.

In previous work, the general public was unable to produce consistent flight paths. This work intends to leverage design-based thinking from students of motion to imbue their creativity into these communications. In the forthcoming study, we will conduct an elicitation study wherein our specialized group of participants will be asked to create gestures for nine distinct UAV states with the expectation that these expressive flight paths would be intuitive for a general audience. These gestures will then be replicated by the Drone Copy Cat program on a UAV. This computer-controlled gesture is recorded, confirmed by the participant as correct, and used in the process to calculate the agreement score. The UAV that we have employed in this study is a DJI Flamewheel f450 equipped with a pixhawk flight controller. The flights are facilitated by a ROS script in conjunction with a Vicon tracking system and, following take off, will be entirely autonomous. For safety purposes, there is a human backup pilot with a Futaba T16SZ 2.4G FASSTest 16CH Radio who will be ready to takeover from computer control should the need arise.

Using reservoir computing to predict temperature fluctuations in turbulent Rayleigh-Bénard convection

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Turbulent flows are ubiquitous in the fundamental processes of nature—from the Earth's mantle to its atmosphere and oceans. Among their many complexities, turbulent flows are chaotic, which makes it computationally expensive to simulate and difficult to study analytically. Thus, prediction of turbulent systems is an ongoing challenge. Machine learning methods, specifically reservoir computing, have shown promise in predicting turbulent flows. Reservoir computing is a recurrent neural network model that uses a reservoir of randomly connected and weighted nodes to process the input data and predict the output for the next time step. As a proof-of-concept, here we test the effectiveness of reservoir computing on temperature fluctuations in turbulent Rayleigh-Bénard convection because it is one of the standard means of studying turbulence in a laboratory setting and has relevant applications, like weather prediction. Rayleigh-Bénard convection is a buoyancy-driven flow, and when the temperature difference between the top and bottom of the container is large enough, turbulent convection results. We installed thermistors at multiple heights in the flow of a water-filled cylindrical convection apparatus and achieved Rayleigh numbers up to $4.5*10^{11}$. After training our reservoir computer on our experimental data, it was able to infer temperature fluctuations with more accuracy than a simple educated guess. Further study will help improve machine learning tools for predicting the properties of turbulent flows and other chaotic systems.

A genetic and molecular analysis of mutants exhibiting similar heat shock responses in Arabidopsis thaliana

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As sessile organisms on a globally warming planet, plants need to adapt to extreme temperature fluctuations and stress. At elevated temperatures, proteins denature and membrane fluidity increases, thereby inducing a heat stress response (HSR), which is a conserved transcriptional program that results in the synthesis of heat shock proteins. These proteins shield, fold, or unfold substrates to ameliorate the effects of high temperatures. Previously, to better understand the HSR pathway in Arabidopsis, we utilized EMS (ethyl methanesulfonate) Mutagenesis to create uncharacterized mutants that may have mutations within their genes. Previous attempts to understand the HSR pathways within uncharacterized mutants consisted of using the Rootscope, an automated fluorescence microscope with a heated plant growth chamber for imaging Arabidopsis roots; the RootScope identified eg6 (RUXF) and HG11-60—mutants with similar altered heat shock kinetics. While former studies have cloned eg6, we have yet to learn about the molecular basis of HG11-60.

As HG11-60 and eg6 both are mutants with delayed, overexpressed HSRs, this experiment hopes to answer the question whether HG11-60 is an allele of eg6 through genetic complementation and molecular sequencing approaches. However, a complementation test failed to fully show complementation nor failure of complementation. Still, results indicate that there is some mutation as there is a delayed HSR. As per molecular sequencing, primers were designed to amplify the entirety of the RUXF gene in HG11-60. PCR reactions using different combinations of the primers all showed DNA amplification and were sequenced. Yet, after aligning the molecular sequence of RUXF in HG11-60 onto the reference genomic sequence on Geneious, there was no indication of mutations within the gene in HG11-60. Questions still remain regarding where the mutation that leads to an altered HSR lies within HG11-60. A potential reason that we do not see a mutation in the molecular sequencing is that the mutation that leads to an altered HSR does not lie in the actual RUXF gene, but rather HG11-60 could be a RUXF regulatory mutation that lies outside of the region we sequenced out.

Design and Optimization of Nanoparticle Carrier Vaccines Targeting the Fusion Peptide of HIV-1

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Virus-like particles (VLPs) are special molecules that closely resemble viruses, but lack genetic material. Their highly repetitive structure allows them to function as antigen-presenting scaffolds to elicit strong B cell and T cell responses. In HIV-1 vaccine research, a central goal has been the envelope (Env) trimer located on the membrane. The fusion peptide (FP) epitope, located within the Env trimer, mediates virus-cell membrane fusion and is our current design target. Herein, we present the design and optimization of a stabilized nanoparticle system using Encapsulin derived from *Thermotoga maritima*. While nanoparticles isolated from several different bacteria have shown promise in development, the stability of the construct was not optimal. In designing our Encapuslin-based vaccine, we mutated two residues in the subunit to cysteine in order to promote the formation of stabilizing disulfide bonds. Through optimization of expression and downstream purification procedures, we demonstrate that Encapsulin nanoparticle is durable –disulfide bonds allow the nanoparticle to withstand high temperatures and ammonium sulfate precipitating conditions. In addition, the prepared nanoparticle is antigenic, which gives potential for Encapsulin to be a universal vaccine design platform. We recently began preclinical trials in mice to test the ability of this nanoparticle platform to eliciting FP-directed antibody titers.

Homology-directed gene repair in human cells using virus-like particles

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CRISPR-Cas9 genome editing tools have the potential to transform the treatment of human genetic-based diseases. For CRISPR-Cas9 tools to be used as clinical therapeutics, delivery methods must be developed that provide tissue specificity, limit off-target effects, and avoid adaptive immune responses. Virus-like particles (VLPs) harness viral packaging and targeting mechanisms to address the challenges of delivering genome editing tools for both *ex vivo* and *in vivo* gene editing. In addition to generating gene knockouts, CRISPR-Cas9 editing tools have the potential to promote gene correction through homology directed repair (HDR), a DNA repair mechanism. Here we investigated the potential for VLPs to direct gene repair via HDR.

To measure HDR frequency, we used a blue fluorescent protein (BFP) to green fluorescent protein (GFP) reporter human cell line, in which the cells that have undergone HDR express GFP. We tested several methods of introducing a specific DNA template into the cells using VLPs. Firstly, we transfected the ssDNA donor template into the nucleus of the cells, a procedure called nucleofection, and then treated cells with VLPs carrying Cas9-sgRNA ribonucleoprotein complexes (RNPs) targeting the BFP gene. Secondly, ssDNA templates were electroporated into the same VLPs, and these particles carrying the template were used to treat cells. In the other methods, an integrase defective VLP encoding the HDR template in its lentiviral genome presented the template in an extrachromosomal episome. Through nucleofection, HDR frequency reached 40%, while electroporation to load VLPs with the template resulted in 0.3% HDR efficiency. Using integrase-defective VLPs carrying both the RNP complex and the lentiviral genome encoding the HDR template, we obtained 0.03% HDR frequency. Finally, co-transducing cells with a constant amount of a VLP carrying just the RNP complex and increasing concentrations of a VLP carrying the lentiviral genome-encoded HDR template, we recorded 0.8% HDR efficiency with the highest concentration of the later VLP.

Virus-like particles are able to mediate homology directed repair where the donor template is provided in numerous methods. Nucleofection of the HDR template into cells and subsequent treatment with VLPs was most efficient. However, electroporation of the donor template into the VLP and presenting the template as an episome are both sufficient to stimulate HDR events. Further work must be done to optimize HDR using VLPs, as HDR is a promising strategy for correcting disease-causing genetic mutations.

Engineering the Metazoan Disaggregation System to Ameliorate Neurodegeneration

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Heat shock proteins (HSPs) are essential for cellular stress response and play crucial roles in refolding insoluble aggregates. Hsp104 is a powerful member of the family, but its homolog is not found in metazoans. Instead, mammals have three classes of HSPs (i.e. 110s, 70s, 40s) that form complexes to disaggregate the misfolded proteins (Nillegoda and Bukau, 2015). Unfortunately, their efficiency is much lower than the Hsp104, and the accumulation of abnormal protein structures is implicated in neurodegenerative diseases.

Under the guidance of Dr. Barbieri, I attempted to conduct a directed evolution experiment in established *S. cerevisiae* FUS and TDP43 disease models, using CRISPR-dCas9-AID to mutagenize target genes of the canonical APG2-Hsc70-DNAJB1complex. *S. cerevisiae* with beneficial mutations will be rescued against the induced protein stress and divide to form healthy colonies.

Engineering tightly regulated *S. cerevisiae* promoter is an active area of research, and currently, very few are available as biochemical tools. During the initial trials of the experiment, the CRISPR and the disease protein genes were cloned into separate vectors with the GAL promoter. However, i. CRISPR mutagenesis is rendered by DNA damage and ii. the presence of FUS/TDP43 leads to protein aggregation stress. Unleashing both simultaneously may have led to extreme toxicity that selected for escapers. Improving on this system, we cloned FUS/TDP43 into an available GAL-aTc promoter and characterized the expression profile with Western blots. This system is not leaky and allows i. and ii. to be induced at different times. One challenge was that the CRISPR mutagenesis is inherently toxic to the cells, so successful rescue can be masked by this growth impairment when comparing to the vector controls with inactive CRISPR. We are currently working to clone the CRISPR system into the GAL-aTc instead to allow for better control of this protein to reduce its toxicity.

Estimating the duration of a mass extinction accounting for Signor-Lipps Effect

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A key question in studies of mass extinctions is whether the extinction was a sudden or gradual event. This question may be addressed by examining the locations of fossil occurrences in a stratigraphic section. However, due to the Signor-Lipps effect, the fossil record can be consistent with both sudden and gradual extinctions. Rather than being limited to rejecting or not rejecting a particular scenario, ideally we should estimate the *range* of extinction scenarios that is consistent with the fossil record. In other words, rather than testing the simplified distinction of "sudden versus gradual," we should be asking, "How gradual?"

Wang et al (2012) described a method for answering the question "How gradual could the extinction have been?" by developing a confidence interval for the duration of a mass extinction. For example, the method can be used to estimate with 90% confidence that an extinction took place over a duration of 0.3 to 1.1 million years, or 24 to 57 meters of stratigraphic thickness. However, their method assumed uniform preservation and recovery, which is unrealistic. Here we describe a new method for estimating the duration of an extinction event that does not assume uniform recovery. We also implement a binary search algorithm to speed up the computation time by an order of magnitude. The method incorporates the Adaptive Beta Method of Wang et al (2016) to allow for increasing or decreasing fossil recovery potential. We illustrate its use with data from Late Cretaceous ammonites from Seymour Island, Antarctica.

Examining the role of *FucTA* in Drosophila nociceptive behavior

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An animal's nervous system plays a major role in regulating many of its behaviors. Pain sensing (nociception) in eukaryotic organisms is an evolutionary trait necessary to survival. Biologists who research the mechanisms behind nociception commonly use the powerful genetic model of Drosophila (fruit flies) as a model due to stereotypic nociceptive response. Drosophila larvae display an escape behavior that involves initiating a roll, C-bending, and completing said roll. The genes that regulate nociceptive behavior, however, have yet to be identified. Thus, we examined the role of *FucTA* (α-1,3-Fucosyltransferase A) in Drosophila nociception.

S89 is a mutated fly line known to exhibit impaired rolling behavior. We have determined through deficiency screening and subsequent sequencing that the S89 fly line maps to the *FucTA* gene and contains a 125 bp. Using mid- to late-third instar larvae, we found that $FucTA^{S89}$ mutants display a slight delay in the time to initiate rolling behavior, a moderate decrease in percentage of larvae that committed a C-bend, and a severe delay in time to complete the roll in comparison to control larvae.

These results suggest that *FucTA* function is required in the neuronal circuit that regulates the rolling behavior and that it most likely functions between the interneurons of the central nervous system and the motor neurons.

In addition, expression analysis suggests that *FucTA* is expressed in the lateral bipolar dendritic (lbd) neuron in the peripheral nervous system. We generated the stocks necessary to examine the role of the lbd in pain-sensing rolling behavior, as well as to determine the role of *FucTA* in the lbd.

Temporal community structure shapes behavioral responses to events by modulating expectation

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People's ability to rapidly parse a continuous stream of experiences into discrete, meaningful events is essential to encoding and storing episodic memories. This process, which is known as event segmentation, has been hypothesized to work based on predictability, such that event boundaries are created when the near future becomes uncertain (Zacks et al., 2007). While evidence has been found to support this hypothesis, other research in network theory and statistical learning has suggested that event representations can also form around clusters, or "communities," of mutually predicting stimuli. Schapiro et al. (2013) found that when subjects were presented with sequences of abstract stimuli in a community structure (that is, when each stimulus could only be followed by specific other stimuli), participants were able to group stimuli into events as a result of the statistical community structure. This experiment was notable because predictability was held constant at all times, so the only possible basis for event discrimination was the similar temporal contexts of the stimuli.

The current study extends Schapiro et al.'s work by manipulating the predictability of the transitions from one community to another and by recording EEG data to examine the neural activity surrounding each transition. During the study, participants were first exposed to a sequence of stimuli created by random "walks" through the community structure. They performed a cover task that required them to determine the orientation of each stimulus. In the second phase, participants were shown a stream of stimuli created by a combination of random walks and Hamiltonian walks, wherein each stimulus was presented exactly once. They were told to press a key when they believed there was a natural breaking point in the sequence. The transitions of interest in the parsing phase occurred when the sequence moved from one community to a another. Under the community structure, such a transition could only occur at two of five stimuli (the "outer" stimuli). In the current experiment, some of these transitions—the controls—occurred in a valid way, such that the transition went from one outer stimulus to a corresponding outer stimulus in a different community. Other transitions were manipulated such that the transition went from an inner stimulus to an outer stimulus in another community. Thus, they were invalid according to the statistical pattern the participants had previously been exposed to. We then analyzed the proportion of times the participants pressed the key for control transitions, manipulated transitions, and non-transitions, as well as reaction time data for all keypresses.

Preliminary results show that participants are more likely to press the key during transitions (both control and manipulated) as opposed to non-transitions, thus replicating the results of Schapiro et al. (2013). Data from the exposure phase showed that participants tended to react more slowly on the cover task after a community transition, demonstrating rapid unconscious learning of the community structure. The proportion of keypresses was not significantly different between the manipulated and non-manipulated transition; however, a difference was observed in the reaction time data, such that participants tended to react more slowly on manipulated transitions. Future analysis will focus on analyzing scalp EEG recordings of the parsing phase to determine how learned community structure modulates the brain's response to expected and unexpected events.

Determination of HSATII integration sites in transfected fibroblast cells

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Human Satellite 2 (HSATII) is a tandemly repeated, 26bp monomer sequence present in the heterochromatin on a subset of chromosomes that does not code for protein product. Former findings indicate that HSATII RNA is overexpressed in many cancer types, yet never in normal human cells. In an effort to understand the effect of HSATII RNA expression, primary human cells were transfected with lipid-mediated reagent FuGENE HD and antibiotic selection to aberrantly express HSATII. In these stably transfected cells, the construct is randomly integrated into the genome. This is supported by varying signal location on different sized chromosomes and different chromosome types, such as acrocentric and sub-metacentric. We found that 62.7% of cells scored contain a single site of integration.

Determining the astrophysical ^{20}Ne(α,p)^{23}Na reaction rate from measurements with the Notre Dame 5U accelerator

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In binary star systems including at least one white dwarf, the companion star may accrete mass onto the white dwarf until electron degeneracy pressure can no longer support the additional mass. A threshold is surpassed at high accretion rates, causing a stellar explosion categorized as a type Ia supernova. The system undergoes nucleosynthesis throughout the mass transfer and supernova process, producing heavier elements. Uncertainties in the Ne(a,p) Na reaction rate have been shown to significantly affect the final abundances of a number of nuclei produced in type Ia supernovae. Although previous inverse kinematic measurements have been conducted to model this reaction rate, the explored beam energies were not of astrophysical significance. Utilizing the 5U vertical pelletron accelerator and the Rhinoceros extended gas target at the University of Notre Dame, new direct kinematic cross section measurements were conducted using beam energies as low as 3.5 MeV. Experimental methods and results will be discussed.

NaFePO$_4$ as a Potential Cathode Material for Sodium Ion Batteries

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Lithium-Ion rechargeable batteries are found in many common applications, such as cell phones, laptops, and electric vehicles, but there are existing limitations on their sustainability and production. We are investigating the properties of a potential cathode material, NaFePO$_4$, for Sodium-Ion batteries that can perform as well as classic Li-ion batteries in capacity and cyclability. Sodium is an especially desirable replacement for Lithium because it is similarly reactive and far more abundant in nature, causing it to be a cheaper and safer alternative.

Some rechargeable batteries operate through reversible intercalation reactions, in which ions move in and out of a lattice as a battery charges and discharges. The material that we are interested in as a potential cathode material is olivine structure NaFePO$_4$, which does not occur in nature but is electrochemically active due to its ability to intercalate. Another structure, Maricite NaFePO$_4$, occurs in nature, but is not thermodynamically active because it does not have diffusion pathways for ions to intercalate.

Olivine NaFePO$_4$ is difficult to obtain because of this reason, so this summer we synthesized our own sample of olivine NaFePO4 by delithiating a sample of LiFePO4 and subsequently sodiating it. We also spent a great deal of time synthesizing desolated samples of Na$_{(1-x)}$FePO$_4$ for $0 < x < 1$, at values of $x = 0.1$, 0.2, 0.5, 0.7, and 0.9. These samples are valuable because they represent the cathode material at different stages within the charging and discharging processes, and we can run experiments on them to see what is structurally happening within the battery.

On these prepared samples, we took powder X-Ray Diffraction data, from which we can extract a lot of information regarding the crystal structure and lattice parameters. When we compare the XRD data from all of our samples, patterns emerge that tell us about the phase of the sample at various levels of sodiation. In the future we will be using Mossbauer Spectroscopy and Differential Scanning Calorimetry to learn more about the temperature dependent behavior of our samples. We will also be constructing battery cells using our materials to conduct in-situ tests.

Pain Perception and Evaluation

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Currently, across the United States there are great disparities in pain treatment due to individual differences in pain empathy. Differences in pain empathy can affect pain perception, evaluation, and treatment of others. We used an oddball paradigm to investigate differences in the P300 event-related potential (ERP) responses to patients' faces in 100% pain, 50% pain, or neutral expressions. Differences in the P300 ERP response to pain, pain evaluation, and prescribed treatment were moderated by the participant's degree of empathetic concern. This study has important implications in the healthcare system and paves the way for future interventions.

Investigating TeV Emission from the Crab Nebula and the Flaring Active Galaxy BL Lacertae

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Since 2012, the VERITAS gamma ray observatory has seen a substantial decrease in flux across its observations. Numerical correction factors have been developed to compensate for this effect. Here, we test out these correction factors on the Crab Nebula, a common calibration source used by VERITAS, and also apply the factors to BL Lacertae, an active galactic nucleus and blazar that has exhibited several TeV flares. Our analysis shows that the correction factors fail to adequately correct for the decrease in flux, and lead to some unphysical results.

Proton Orbit Calculations in Relaxed Taylor States at SSX

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We aim to analyze the dynamical properties of plasma particles within the cylindrical, helical Taylor state magnetic field structure. We also wish to study the potential confinement properties of the Taylor state to assess if it is a viable fusion energy configuration. We simulate the motions of particles in the Taylor state through simulation of a total of 2×10^5 orbits of particles with a set distribution of initial positions and velocities. The field structure itself is calculated by first solving the eigenvalue equation $\nabla \times B = \lambda B$ using the program PSI-Tet. Then, the Boris algorithm is implemented to solve the equations of motion for the particle orbits. Particles are simulated for a predetermined number of orbits, and their velocity and position data are saved for each step. The results of the simulation show that the majority of escaped particles escape either at the ends of the Taylor state or at points along the surface of the cylinder containing the state that have a weak field. In addition, we found that the particles that remain confined within the state for an extended period of time exhibit general trends for the distribution both radially and along the z-axis. The data also shows that particles initialized with greater initial velocities were generally more likely to escape the Taylor state during the duration of the simulation, and vice versa. Overall, the percentage of particles that stayed confined for the duration of the simulation was asymptotic at approximately 55%.

Optimization of Influenza A Virus Matrix Protein 1 purification in order to characterize its role in viral budding

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Influenza remains a serious global health threat and further characterization of key viral proteins is necessary in order to develop novel drugs and vaccines. Matrix Protein 1 (M1) and Matrix Protein 2 (M2) play key roles in the viral life cycle of Influenza A Virus. M2 has been shown to be critical for budding of new viral particles from infected cells and M1 has multiple roles, including packaging viral RNA and recruiting it to the budozone through interactions with M2 and other viral membrane proteins. M1 oligomerizes through interactions with other M1 monomers to form a sheet inside the emerging virion. Studies have found that the M1-M1 interaction as well as interactions between M1 and other viral proteins which likely occur at the C-terminal of M1 are influenced by the M1-membrane interaction at the N-terminal region. As a result, it is important to use full-length M1 in order to characterize how different domains of the protein affect the M1-M2 interaction. In this study, we are working to optimize a purification protocol for full-length M1. We successfully expressed M1 and optimized a lysis protocol using sonication. M1 was formed inclusion bodies during expression and can be purified from inclusion bodies using a series of washes followed by denaturing and renaturing the protein.

Characterization of the Binding Behaviors of Biological and Environmental Adsorbates to Silver Nanoparticles

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In recent years, the use of nanotechnology has dramatically increased in a variety of industries due to the antimicrobial and antibacterial properties of the nanomaterials. Because of their widespread commercial use, there is an unprecedented level of silver nanoparticles (AgNPs) leaking into the water systems, with unknown implications and effects on the environment and its diverse inhabitants. For this reason, it is crucial to understand how AgNPs interact with various environmental matrices, for example, with proteins or natural organic matter. UV-Vis spectroscopy and dynamic light scattering (DLS) assays were developed and applied to understand these complicated systems. The localized surface plasmon resonance (LSPR) of AgNPs can be monitored by UV-Vis and shifts in its wavelength maximum caused by adsorption of bio- and eco-molecules can be used to quantify binding kinetics and affinity. DLS and zeta potential measurements can be used as secondary confirmation of binding interactions and to understand how adsorption affects particle diameter and surface charge. These techniques were applied to two independent analyses; (1) to quantify the protein coating, or "corona", formed on AgNPs in the presence of proteins, and (2) to evaluate the influence of sequential bio- and eco-corona formation on binding characteristics. In the first study, three model proteins were examined including bovine serum albumin (BSA), human serum albumin (HSA), and glycated HSA (g-HSA). BSA is an affordable model protein that was used for optimization of UV-vis and DLS methods. Then, the binding characteristics of HSA and g-HSA were compared to see what affect posttranslational protein modifications (like glycation) have on protein corona formation. Interestingly, all three proteins exhibited remarkably similar binding characteristics. In the second study, the binding characteristics of humic acid (HA), a model environmental adsorbate, and BSA were evaluated. Then, experiments were conducted to see how the binding of BSA changed if the AgNPs were first coated with HA. The binding of BSA to AgNPs was greatly reduced when the particles were first coated with AgNPs.

Examining the application and distribution of multiple anti-predatory strategies in red-tailed monkeys of Tanzania

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Although individuals spend much of their life foraging and exploring areas for high resources, they will abandon prime locations if they pose a risk of predation. As a result, many species have developed a spatial distribution which is driven by the trade-off between habitat use and predation risk. This work aims to better understand how anti-predatory behaviors may be also be influenced by the habitat, the group, and explore the interaction of multiple behavioral strategies to comprehend a more exhaustive measure of predation risk as perceived by prey. I have measured three anti-predatory behaviors in the red-tailed monkeys (Cercopithecus ascanius) of Issa Valley in Mahale, Tanzania from June 2018-April 2019. Using these data, I compare the application of multiple measures of perceived predation to ask how these behaviors vary as a function of their distinct trade-offs. I expect that monkeys will employ each anti-predatory behavior to different degrees given the resource availability, social context, and habitat type, reflecting varying relationships with my measured factors.

Taylor State Merging at SSX

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We are studying plasma with the hopes of someday being able to use Magneto-Inertial Fusion (MIF) energy to power the earth in a clean, safe way. Fusion is the process that powers the sun, and thus producing fusion on earth requires extreme temperatures and densities, like those found in the center of the sun. To achieve such high temperatures and densities, we are studying the merging and magnetic reconnection between two Taylor states (twisted blobs of plasma). We record the ion temperature with ion Doppler spectroscopy, and electron density with a Helium-Neon interferometer. We also record the magnetic field vectors. We time the Taylor states so that both arrive at the center of our diagnostics within a microsecond. We have examined both co-helicity and counter-helicity merging, where the Taylor states have both left-handed twists, or one left-handed and one right-handed twist, respectively. Preliminary results show an increase in the magnetic field strength and electron density at the midplane, followed by an increase in ion temperature. We observe a heating event of about 20 eV (230,000 °C), likely driven by magnetic reconnection. We also find that while there appears to be more heating in the counter-helicity merging, the co-helicity merged state holds together better, and thus is a better target for MIF. Work supported by DOE ARPA-E ALPHA, Velay Foundation, and NSF-DOE programs.

Validation of water-borne androgen in túngara frogs

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Most methods to estimate hormone concentrations in wild vertebrates are invasive and can be fatal for the individuals being studied. Minimally invasive techniques offer the opportunity to repeatedly study behavior and measure hormone concentrations without interference. Over the course of a two-phase project, we have examined circulating testosterone concentrations in túngara frogs (*Physalaemus pustulosus*) using a non-invasive water-borne method, aiming to validate the technique. Phase 1 tested the efficacy of water-borne testosterone extraction in both male and female frogs. A human chorionic gonadotropin (hCG) pharmacological challenge significantly elevated testosterone levels in male frogs over a 24-hour period, while female frogs did not show a significant increase in testosterone concentrations. We concluded water-borne assays can be used to accurately measure biologically informative levels of testosterone in both adult male and female túngara frogs. In phase 2, we again experimentally elevated circulating testosterone by injecting male frogs with hCG or gonadotropin releasing-hormone (GnRH). We measured the circulating testosterone levels over a nine-day timeframe to explore how water-borne hormone validation functions over multiple timepoints. We tasked male frogs with two rounds of phototaxis trials using synthetic male advertisement calls to correlate testosterone concentrations to phonotactic behavior and male sexual behavior. Data collection for this phase is underway and predictions will be discussed.

Parental Gradient Inheritance in *Hydra* Regeneration

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Hydra is a freshwater cnidarian polyp with a simple anatomy. It consists largely of an outer ectoderm and an inner endoderm that form a hollow tubular body column with a head on one end and a foot on the other. *Hydra* is famous for its regenerative capabilities and an attractive model to study pattern formation. When *Hydra*'s body column is cut into small tissue pieces, each piece can regenerate into a fully functioning *Hydra*. If sufficiently small, the piece first rounds up into a seemingly homogeneous sphere, then elongates to form a new body axis and regenerates head and foot. A recent study has shown that the body axis of regenerating tissue pieces is inherited from the parent, but it is unknown how this information is passed down. The body axis can be defined by two main criteria: 1) a network of extracellular actin filaments called myonemes that run parallel to the body axis in the ectoderm, and 2) a biochemical gradient that defines the head and foot ends. We hypothesized that the inherited biochemical gradient determines the body axis rather than the ectodermal myoneme structure, as previously proposed. To test this experimentally, we perturbed the biochemical gradient of parental *Hydra* with drugs to manipulate Wnt signaling, which acts as the key morphogen in axial patterning. In addition, we performed grafting experiments to further modify the biochemical gradient and then excised tissue pieces from these manipulated animals. Our data show that the head-foot polarity of the regenerated tissue pieces follows the modified biochemical gradient. The results suggest that the morphogen gradient is crucial in deciding the head-foot polarity and body axis formation in regenerating *Hydra* tissue pieces.

Aluminum complexes of nitrogen-based redox-active ligands

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The development of aluminum complexes supporting non-innocent, redox-active ligands aims to expand the toolbox of aluminum-based chemistry through the introduction of new reactivity profiles and/or the stabilization of novel functional groups. We have been investigating the chemistry of aluminum complexes coordinated to redox-active ligands containing nitrogen heteroatoms, including diimine ligands, and will present our newest results in this area. The full characterization (small-molecule X-ray diffraction, multinuclear NMR spectroscopy, UV-vis spectroscopy, cyclic voltammetry) of complexes of various ligands will be presented and their initial reactivity profiles, including their propensity for oxidation reactions, will be discussed.

Purification of DNA Origami with Capillary Electrophoresis

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The selectivity of base pairing and programmable sequencing of DNA as a construction material allows for the controlled nanoscale folding of two- and three-dimensional shapes, with enormous potential in applications such as drug-delivery and bio-sensing. However, current techniques to purify DNA origami from precursors and other impurities have shown low yields, low scalability, and generally lack optimization for automation. Herein, the development of capillary electrophoresis (CE) as a purification technique for DNA origami is described and shown to be a potential alternative to current methods. DNA origami with various morphology such as a tetrahedron, notched rectangle and thermostat were separated from excess staple and scaffold DNA used in synthesis of the nanostructures. Capillary zone electrophoresis (CZE) and capillary transient isotachophoresis (*ct*ITP) were two modes of CE employed for the purification of DNA origami, where the origami were labelled with intercalating dye and separated based on differences of size and charge. Buffer composition, pH, and concentration, as well as sample injection volume, and separation voltage were manipulated to obtain a high quality and reproducible separation of formed structures and precursors. Three different non-covalent intercalating dyes were characterized by fluorescence spectroscopy to determine binding effects. Fraction collection procedures were also optimized to yield purified origami samples for offline characterization.

Visualizing a cellular pH sensor in the sea anemone *Exaiptasia pallida*

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The coral reef is one of the most biodiverse as well as one of the most vulnerable ecosystems on the planet. Flush with life, reefs support countless other species. The trophic basis of the reef ecosystem depends on endosymbiotic dinoflagellates of the genus *Symbiodinium* which inhabit the cells of the corals and provide the host with fixed carbon (sugar) by photosynthesizing. In exchange, the corals give the *Symbiodinium* shelter and nitrogen. In a healthy ecosystem, this relationship benefits the symbiotic partners, the many species that inhabit the coral reefs, and humans, as we depend on the reefs for their coastal protection and as a habitat for commercial fish. Unfortunately, with global increases in CO_2 concentration and water temperature, the *Symbiodinium* frequently leave or are evicted from their host in a process known as "bleaching," which eventually leads to the death of the coral. The molecular pathways through which these two species interact are key to understanding the biochemical mechanisms behind bleaching events.

The sea anemone *Exaiptasia pallida* (Aiptasia) is an excellent model system to study interactions between a cnidarian host and *Symbiodinium* as it is easily grown in the lab and may be manipulated with ease. Because these organisms live in the ocean, which has a pH of 7.9-8.3, coral, anemones, and many other sea-dwelling animals must have a manner to carefully regulate their internal pH. In symbiotic species, such as the coral and anemones that I study, this becomes even more important; the symbiosome, the domain of the cnidarian cells in which the *Symbiodinium* reside, must be able to maintain a pH of 4 – a difficult feat when considered alongside the proton gradients for the photosynthesis of the dinoflagellates and nutrient exchange between host and symbiont. All of these factors become even more pressing because of the current status of our oceans, which are acidifying and warming due to anthropogenic climate change.

One molecule that has been shown to play a key role in cellular pH maintenance in many species, including the coral *Pocillopora damicornis*, is soluble adenylyl cyclase (sAC). This enzyme, when stimulated by bicarbonate ions (HCO_3 is produced in the hydration of CO_2 to H^+ and HCO_3 by carbonic anhydrases), converts ATP to cyclic AMP (cAMP), which may then modulate cellular processes by the activation of other proteins. Thus, sAC activation provides a means for the cell to produce a homeostatic response when under acid/base stress.

This research undertook the visualization of sAC across a variety of conditions in Aiptasia using immunohistochemistry. We qualitatively analyzed the differences in sAC expression between symbiotic and aposymbiotic (bleached) adult anemones, as well as in symbiotic and aposymbiotic (naïve) Aiptasia larvae. This study suggested that sAC expression is higher in cells exposed to seawater in both symbiotic and aposymbiotic adults and larvae, but that symbiotic adults also present higher and more homogenous sAC expression across almost all cell types. In larvae, there is high sAC expression in the outer tissue layer, which becomes even more concentrated around the mouth. What role this plays in the cellular internalization of the symbionts is yet to be determined.

Creating Causal Evidence and Driving Measurable Health Improvement from Real World Patient Digital Wearable Data

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Research Advisors: Maggie Delano

We present Memento Labs, an online platform to facilitate guided individualized and randomized self-experiments for health. An increasing amount of health data is being produced from wearable health monitors, many of which are accessible to consumers, including the Apple Watch (for activity), Oura Ring (for sleep), and more. However, there have only been few and limited applications of actionable insights derived from this data. The goals of our research study was to deriving unique, personalized insights from n-of-1 experimentation, and delivering them in an actionable, implementable manner to users with wearable devices. Memento Labs is developed to streamline the process of experimentation, collecting experimental data, and clear visualizations of effects for individuals by automatically collecting wearables data and generating personalized, data-driven self-experiments, and more based on a collection of template recommendations such as meditation, magnesium supplementation and more, created with from clinicians and sleep scientists. The platform was launched to 120 users recruited from online forums and groups, with 70 consenting research participants. We evaluate Memento Labs in this study, measuring the effect of the interventions, and population-level changes in health outcomes from using the platform.

Black-White Unequal Cancer Cumulative Incidence and Survival among infants in the United States, SEER 1975-2016

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Objective: Cancer remains the leading cause of disease-related mortality among children, 0-14 years in the United States. While incidence continues to increase, survival has substantially improved due to advances in cytogenetics and precision medicine initiatives. The current study aimed to assess subpopulation differences in infant cancer mortality and survival. **Materials and Methods:** Retrospective cohort design was used to assess the temporal trends by race and sex as well as mortality and survival in infant mortality. The Surveillance Epidemiology and End Results (SEER) population-based dataset (1975-2016) was used for the assessment. Binomial regression and Cox proportional hazard model were used to assess the predictors of mortality and survival, respectively. **Results:** Of the 6,870 infants diagnosed with cancer, 1,829 experienced mortality, (26.6%) which was highest among black/AA infants. Compared to whites, black infants with malignant neoplasm were 8% more likely to die; risk ratio (RR) = 1.08, 95% CI, 0.96-1.12. Blacks/AA infants experienced a survival disadvantage relative to whites and other. Compared to white infants, there was a 7% increased risk of dying among blacks/AA, Hazard Ratio (HR) =1.07, 95% CI, 0.93-1.24. There were sex differences in infant cancer survival, with a 5% increased risk of dying among males relative to females, HR=1.05, 95%CI, 0.95-1.15. After adjustment for confounding, racial disparities persisted, although imprecise, adjusted HR (aHR) = 1.06, 99% CI, 0.90-1.26. **Conclusions:** Whereas cumulative incidence in infant cancer mortality was highest among whites, blacks/AA experienced survival disadvantage, which persisted after controlling for tumor prognostic factors and social determinants of health outcomes.

Computing Integrated Information of Consciousness Using Graph-cut Method

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Integrated Information Theory (IIT) of Consciousness is one of the most promising mathematical theory of consciousness, which hypothesizes that the level of consciousness is related to "Integrated Information (Φ)," the information-theoretic measure quantifying the information loss caused by splitting a system into parts. While calculating Φ in real neural data has been computational expensive, an efficient algorithm was recently proposed, which allows us to compute Φ in large datasets within a practical amount of time. In this study, we developed a pipeline for computing integrated information based on graph-cut method, an approximate method to compute Φ. We applied our pipeline to Electrocorticography (ECoG) datasets of marmosets (N=4) at different states of consciousness (awake eyes-opened, awake eyes-closed, and anesthetized). We converted the neural time-series data into vector-autoregressive (VAR) model and calculated Granger Causality between ECoG signals following the procedure from previous studies. We then computed Φ utilizing graph-cut method to examine whether and to what extent our method could distinguish the qualitatively different states. Our algorithm was able to distinguish the different states of consciousness of a single marmoset to a certain degree; however, it was not so robust as to extract the global trends across the four marmosets.

Four-Core Optical Fiber Sensing

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Four-core optical fibers are specialty fibers where each core acts as a separate waveguide within a single cladding. Light emerging from these cores has an interference pattern, or interferogram, that is a 2D grid of nearly circular bright spots. Sensing is accomplished by deforming the fiber to induce path-length differences between the cores, which results in phase shifts of the interferograms. Consequently, a four-core fiber can be used to sense bending, twisting, or other properties such as pressure or temperature. In this research, a four-core fiber's ability to detect three-point bending while embedded in an aluminum beam was investigated. A repeatable, linear relationship between beam deflection and interferogram phase shifts was demonstrated. In addition, the behavior of four-core fiber was modeled using COMSOL Multiphysics. The modes and their coupling in the fiber were simulated as part of the work toward a full model of a sensor that produces the interferograms observed experimentally. Finally, future applications of four-core fiber as a sensor for magnetic field or radiation pressure were examined.

Transiting Exoplanets and KELT Follow-Up

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This summer, I was a part of the KELT Follow-up Network (KELT-FUN) which is a scientific collaboration that makes use of the data from the Kilodegree Extremely Little Telescope (KELT) survey telescopes. The main goal of KELT is to discover transiting exoplanets orbiting their host stars. As a member of the follow-up collaboration this summer, my purpose was to observe potential transit events as frequently as possible using the Peter van de Kamp observatory at Swarthmore College which has a smaller field of view but higher resolution than KELT. Using the AstroImageJ (AIJ) package for data reduction, the images from a given night could then be crafted into light curves which would illustrate the brightness of a given star with time. Seeing a dip in this data would suggest a planetary transit or eclipsing binary star system. One of KELT-FUN's primary objectives is to eliminate false positives such as an eclipsing binary (EB) or a near eclipsing binary (NEB). These false positives arise when stars are blended in the KELT aperture. Using this method of gathering and analyzing data, I made 38 submissions to KELT (none confirmed exoplanet discoveries to date) and began to learn and work with the submission process for the Transiting Exoplanet Survey Satellite (TESS).

Title: Strong XOR Lemma

Advisor: Professor Joshua Brody

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Given a computation task, one natural question a researcher can ask is how difficult it is or how much resource is required to perform such computation. Query Complexity is a field in Theoretical Computer Science that explores these questions. Our research group researches on Strong Direct Sum problem – a subfield in Query Complexity that studies how the computational resources (e.g. time, space, energy) and error scale with the instances of computation. More specifically, our research group works on Strong XOR lemma as defined below:

Let f be a Boolean function (a function that takes n-bit inputs and outputs 0 or 1) with some very low error. Suppose we want to compute multiple copies of f and XOR them (i.e. count if there are odd or even number of output 1) altogether, how much resource do we need to compute those XOR with a low error?

Because XOR is itself a Boolean function, this Strong XOR lemma lends itself to several interesting mathematical properties.

Characterization of site fidelity in forked fungus beetles
(*Bolitotherus cornutus*)

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Based on previous knowledge on how social behavior among animal species adapt and change depending on different resources, environments, and social interactions, we realized there was an avenue to explore what such factors imply for animal behavior. For this, we studied site fidelity which is the combination of site allegiance, recognition, and preferential bias towards previously visited locations (Richardson et al., 2017). The study organism was forked fungus beetles (*Bolitotherus cornutus*) and specifically in regard to how site fidelity may impact their social interactions and how site fidelity itself may be altered depending on differing physical traits. Previous studies pointed to site fidelity as being an indicator for successful resource capture and usage and, as a result, would be reasonable to hypothesize that perhaps more mating potential may correlate with increased site fidelity (Mair and Rutheer, 2018). Forked Fungus Beetles (*Bolitotherus cornutus*) are found east of the Appalachian Mountains and inhabit polyporoid fungi in forested areas. Since they breed during the summer season, these organisms provided a simple system to sample from in Mountain Lake Biological Station, of which we noted their location, social partners, and behavior. Using collected data from previous years (2016-2018), site fidelity was be measured by calculating occurrence (IO), permanence (IT), and periodicity (It) to account for recursive movement (Tschopp et al., 2018). Ultimately, we found larger males saw more site fidelity, but larger females saw the opposite trend of less site fidelity. Additionally, more site fidelity yielded more social interactions for both sexes with only the periodicity component displaying contradictory trends for the sexes. Here, we drew to elements of territoriality and laying behavior for possibly explaining the trends deduced from body size. Nonetheless, these findings provide ample evidence for site fidelity being a significant element of animal behavior and potential for explaining differing degrees of social behavior. Future questions can look into whether site fidelity can predict fitness and social network metrics as well as whether site fidelity can undergo evolution as a phenotypic trait.

Anonymizing SMS Data for Analysis of Interpersonal Relationships through NLP

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Among psychologists who research interpersonal processes, cell phone usage (and texting in particular) has emerged as a topic of keen interest. Generally speaking, however, those studies rely on self-reported data about cell phone usage. Detailed analysis of interpersonal relationships requires finer grained information than that which can be obtained from individuals' retrospective reflection. Natural Language Processing (NLP) provides a promising avenue for *automatically* extracting communication patterns and behaviors that study participants might not be aware of themselves.

Currently, in the field of NLP, the majority of work relating to text messaging has focused on simple text processing for creating SMS bots. However, these tools and bots make use of models trained on more formal text. We hypothesize that models built for formal text registers will not match the register of communication between close friends and family members over SMS. However, due to the personal nature of the data and scarcity of research in this area, there is presently a lack of training data that can be used to create NLP tools better suited for these contexts. One of our overarching goals is to make it easier for social scientists to collect SMS data that could then be used to train NLP models on this genre of text.

Our approach to this problem is called the Linguistic Analyzer of SMS Texts (LAST), an anonymizing tool for researchers looking to work with text conversations. LAST prioritizes the need for *interpretable* anonymity: participants in data collection studies can be included in the processes of anonymization such that they are confident that their data has been successfully anonymized. LAST is a GUI that imports SMS data, generates classification predictions based off of an NLP model via the NLP library spaCy, and allows for quick manual correction of incorrect or insufficient automatic anonymization. LAST also logs any manual corrections made by the user. This logging creates hand-labeled data as a side effect, allowing for iterative training and evaluation of NLP models for SMS data.

Deep Learning and Summary Statistics to Predict Ancestral Population Size

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Our DNA is a mosaic of the DNA of our ancestors, containing encoded information passed down from generations past. Our goal is to use deep learning to analyze modern genotypes in order to predict the ancestral population size of any given group of individuals. Nearly all human populations experience bottlenecks; the population starts off high, then drops, and then rises again. One commonly studied cause of population bottlenecks is the migration from Africa, where all human populations originated. If we look at any single population that experienced a migration event from Africa, we can see that the history of their population can be modeled using 3 numbers. N3 describes the high population size when all humans were part of a single population in Africa, N2 describes the low bottleneck size when the population split off from the others and left Africa, and N1 describes the population size after the new population settles down in a new land, and the population rises again. We would like to be able to accurately predict N1, N2, and N3 from a dataset of SNP arrays.

We will use CNNs, fully connected networks, summary statistics, and transfer learning to accomplish our task, with all training performed on data simulated by MSprime. CNN stands for Convolutional Neural Network. This involves a window, or "kernel," sliding across the data and performing some mathematical operation. This process creates filters that are used to find significant groupings of data. Fully connected networks are used in conjunction with summary statistics as another attempt to predict ancestral population sizes. First, summary statistics are calculated from the input SNP arrays, and these statistics are passed into a fully connected network that tries to create a regression formula mapping the summary statistics to N1, N2, and N3. Lastly, transfer learning is used to allow a model fully trained on one population's parameters to be quickly retrained to work on another population's parameters.

Applying Differential Privacy to Anonymize Mobile User Trajectories

Gregory Lee, Jonah Langlieb advised by Professor Chaganti

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The ubiquitous collection of real-world, fine-grained user mobility data from Wi-Fi access points (APs) has the potential to revolutionize the development and evaluation of mobile network research. However, releasing Wi-Fi Syslogs with simple anonymization schemes, can result in a profound breach of user privacy. Releasing such data has the potential to reveal the number of devices a user has, user's visit locations, network usage patterns, and even reveal co-traveller identities. The nascent field of differential privacy offers solutions by assuring quantifiable guarantees of user privacy, while still providing demonstrably high data utility. In this work, we apply differentially private algorithms to provide the first, publicly available release of 802.11 WiFi Network traces of a large-scale campus network with more than 4000 Access Points and nearly 40,000 daily users. To provide the best trade-off between privacy gained and data utility for network researchers, we evaluated a variety of privatizing algorithms (MWEM, DAWA, Hb, GreedyH, Identity, Uniform), aided by an open source differential privacy framework, Ektelo (Zhang et al. 2018). Through our evaluation, we found the optimal input parameters and algorithms to release noisy histograms for campus-arrival rates, service times, and inter-AP transitions. Additionally, we built privatized user-trajectories using a recently developed variable length n-gram algorithm (Chen et al. 2012). Finally, we show that there still exist challenges in privatizing time-series data, especially trajectories of users travelling across campus. We highlight open questions and the potential for a rich set of questions leading on from this work, including, (1) how do we embed timing information in a differentially-private dataset release while still providing high utility? (2) the variable length n-gram algorithm performs well for trajectories with up to three hops, how do we reduce the error-rate for trajectories longer than three hops? (3) can we establish a threshold of network utility performance, and provide a range of DP algorithms that meet this requirement?

Optimization of Gold Nanoparticle Release from Polymer Microbead Template for Sensitive Colorimetric Detection of DNA

Maura Dresner-Pfau, Elise Layne '23, Joy Sigurdson, Siddharth Naidu, Jeunghoon Lee

Boise State University

Gold nanoparticles (AuNP) change color based on the oscillation of free electrons known as surface plasmon resonance. AuNPs are good optical markers due to their high surface to volume ratio and their large extinction coefficients. Unlike other metal nanoparticles such as silver, the color change caused by aggregation of AuNPs is easier to observe, allowing the fabrication of a colorimetric sensor to be efficient and inexpensive. Using an autocatalytic DNA network and AuNPs, the colorimetric sensing signal can be significantly amplified to create a sensitive DNA sensor. In order to prepare the AuNP disassembly-based colorimetric sensor, thiolated DNA was attached to AuNPs. After the functionalization, the DNA AuNPs were then assembled onto polymer beads by the hybridization of DNA and biotin-streptavidin interaction. Sensitivity of this network was tested in the presence of DNA fuel strands and varying amounts of catalyst strands. In addition, the network operation was optimized based on the design of DNA reaction networks and active DNA strand density on the nanoparticles. The resulting nanoscopic assemblies will be used for applications such as biological imaging, chemical sensing, and optoelectronic devices.

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Radii Distribution Effects on Jamming Thresholds at High Densities

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Jamming is a phenomenon often observed in systems of disordered, macroscopic particles, where the system transitions from a flowing liquid-like state to a solid-like jammed state. In Summer 2018, the Graves research group studied how the jamming thresholds of two-dimensional systems of mobile soft disks were affected by pin lattice geometry, pins being immobile particles with negligible size. We found that at higher particle densities, the effects of different geometries created thresholds which diverged from one another. Even more interestingly, in the case of the square lattice, as the ratio of pins to mobile disks (n_f) was increased past a certain value, the system's jamming threshold had tentative evidence of a plateau. In our research in Summer 2019, we sought to determine whether or not this result was robust. My individual contributions to our research utilized a "polydisperse" model for mobile particle sizes, which, rather than large and small particles, featured a continuous range of radii. The end goal was to determine the threshold density at which the system jammed for these two models. We employed and modified a C++ computer simulation, a collaboration with Andrea Liu's soft matter group at U. Penn, of a system with a fixed pin distribution and number of mobile particles. In my experiments, I determined the probability that a system starting from a random configuration of mobile particles would jam after being "cooled" down to a minimum energy. (Note that the polydispersity, in the form of the size ratio between the largest and smallest particle, was held constant.) I fit the jamming probability to a sigmoid to determine the small radius for which it was closest to 0.5, an accepted criterion for the jamming threshold. From the threshold, we were able to calculate the critical packing fraction, ϕ_j, at jamming. Our goal was to understand the behavior, via a simple scatter plot, of ϕ_j as a function of n_f. In repeating this experiment with different numbers of mobile soft disks and pins, using both polydisperse and bidisperse simulations, we confirmed that the plateau appeared in the bidisperse case; in the polydisperse case, the threshold still diverges, but no plateau is visible. For random lattices, we saw no diverging thresholds in either case, ϕ_j decreased linearly with n_f. This result is exciting because it shows that the distribution of radii is not a negligible characteristic of soft matter systems, and must be taken into account when setting up and running simulations. Further research is needed to trace the source of the bidisperse plateau and describe the trend in ϕ_j vs n_f for the square lattice in the polydisperse case.

Exploring Structures of SAT2 Centromeres

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Satellite 2 (SAT2) consists of tandem repeats and is located near the center of chromosome 1. SAT2 is a non-perfect repeat similar to that found in SAT3. SAT3, on the other had, consists of (GGAAT)n perfect repeats. Here S2 is a four repeat sequence, (GGAAT)4. This sequence is proposed to form a stable loop-stem-loop structure. Based the similarities between SAT2 and SAT3 we proposed that SAT2 variants will fold into a similar loop-stem-loop model. In order to elucidate the structure of SAT2, a variety of 2 aminopurine (2AP) modified sequences were created. The focus of the study was to gain structural information using the 2AP probes. Because 2AP has a similar structure to Adenine, it can be inserted into the DNA sequence in place of Adenine. By conducting biophysical studies and fluorescence studies, we were able to gain an idea of the secondary structure of the modified SAT2 sequences. Although the study shows that 2AP may cause a disruption in the native structure based on its decreased in stability and shifted peaks in CD spectra for some of 2AP modified sequences, we were able to deduce some ideas of the secondary structure from the results of biophysical studies and the fluorescence studies.

Radii Distribution Effects on Jamming Thresholds at High Densities

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Role Playing Game (RPG) Development for AI Testbed

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Our main goal this summer is to create a custom RPG game that will allow for the basis

for testing artificial intelligence companions for future research. Games have been a

popular method for testing AI algorithms. Naturally games have been a popular domain

for AI development because of their non-trivial decision making environments. They

provide rich human-computer interactions where AI cooperate with humans to win game

objectives. The research and advancements that come out of this kind of work can go

from helping game designers come up with new and more engaging games for the public,

where the AI can help by fulfilling roles such as design assistant, data analyst, play tester,

game critic, team member and even game director. Our approach is to develop a player

versus player, capture the flag game that would allow the user to set up matches, use

custom abilities and fight other players. We used an open source medieval fantasy role

playing game called Flare. It contains many of the basic features that we would need for

the game, such as fighting abilities, weapons, Health/Mana points and ability to die and

respawn, graphics, user interface, animation system and path-planning. However, to turn

Flare into the testbed we need, there has to be a lot of custom work done. Flare is a

single-player quest-based adventure game, that needed to turn into a multiplayer capture

the flag game.

Crystal structure and biophysical studies of G-quadruplex DNA in complex with a tightly binding porphyrin ligand

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The G-quadruplex (GQ) is a non-canonical DNA structure formed by G-rich DNA sequences found throughout the human genome. Stable GQs at telomeres are suggested to inhibit telomerase activity and disrupt telomeric structure, leading to cancer cell apoptosis. In this work, we investigate the interaction of a G-rich sequence from the *Tetrahymena thermophila* telomere, 5'-GGGTTGGGTTGGGTTGGG-3' (T1), with a water-soluble porphyrin, N-methyl mesoporphyrin IX (NMM). UV-vis and fluorescence titrations revealed a 1:1 binding stoichiometry with an impressively tight binding constant, K_a, of 50 ± 20 μM^{-1} ($K_d \approx 20$ nM). Isothermal titration calorimetry demonstrated that the binding interaction is enthalpically-driven and thermodynamically favorable ($\Delta H = -17 \pm 3$ kcal/mol and $\Delta G = -10 \pm 3$ kcal/mol). Job plot confirmed the 1:1 binding stoichiometry in a model-independent manner. We present the crystal structure of the DNA-NMM complex solved at 2.34 Å. The structure reveals that the DNA forms a dimer of parallel GQs bound at both ends to NMM via end-stacking interactions, supporting the 1:1 binding stoichiometry observed in biophysical studies. Our work provides invaluable details of GQ-ligand interactions, thereby informing the design of novel, highly-selective anticancer drugs targeting G-rich DNA sequences.

Developmental Systems Drift Across Tunicate Species

Students: Jasiel Lopez and Dulce Ventura
Advisor: Bradley Davidson

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As organisms evolve, their genetic regulatory networks can drift. Often, this drift involves mutations of regulatory elements that do not impact regulatory network outputs or phenotypes. This is known as Developmental Systems Drift and can be detected by reduced cross-compatibility between closely related species. Our intent is to discover how gene regulation has evolved over time and how this has changed their role within the organism. This past summer, we conducted experiments to determine how the regulatory elements of Ets-regulated neural genes have evolved between tunicate species *Ciona robusta* and *Corella inflata*. We determined that the *Corella* orthologs are still capable of driving full neural expression in *Ciona* embryos. We are also working to identify exactly how the protein binding sites within the gene regulatory elements have evolved between the two species. Analyzing how these binding sites have evolved will further our understanding of how gene regulatory elements evolve over time and how gene regulatory networks as a whole evolve over time.

Enduring Attitudes of Life Science Students Towards Physics and Interdisciplinary Learning

Student researchers: Aqil Tarzan MacMood, Haley Gerardi '17
Faculty researchers: Benjamin D. Geller, Catherine H. Crouch

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We explored the longitudinal impact of Introductory Physics for Life Science (IPLS) by examining whether and how student experiences in an upper level Neurobiology course were impacted by students' prior exposure to relevant physics; in particular, we analyzed attitudinal data to address this question. While there was evidence that life science students enrolled in Introductory Physics for Life Science (IPLS) courses find physics to be more engaging and relevant to their primary interests than do their counterparts in more traditional introductory physics environments, we did not yet know whether those attitudes and affective responses persist. By studying the attitudes toward physics and interdisciplinary learning of life science students both during *and after* their IPLS experience, we began to unpack how enduring these attitudes actually are. We find that positive sentiments to interdisciplinary science learning, that is the relevance of physics and math to biology, increase over the course of the second semester IPLS class and persist a year after. Additionally, over the course of the intermediate Neurobiology course, IPLS students maintain strong positive sentiments while non-IPLS students have more positive sentiments. In this poster we describe the results of preliminary efforts to assess this durability. We report on data obtained from surveys, journaling prompts, and interviews conducted with students in both the IPLS course and in subsequent upper level biology courses.

Physical Characterization of Membrane Mimic Using DLS and EPR Spectroscopy

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The Influenza A virus causes a contagious respiratory infection. Most adults and healthy individuals with strong immune systems are able to fight off the virus and recover. However, the virus can be fatal for young children and older people with underlying illnesses and weakened immune systems.

Studying influenza proteins essential for the viral life cycle offers an opportunity to design new antiviral drugs. The Influenza A M1 and M2 proteins play key roles in the viral life cycle. Direct physical interaction between soluble M1 and membrane-bound M2 at the inner surface of the viral membrane has been proposed to be essential for the formation of new viral particles. Research in the Howard Lab has shown that the M2 protein contributes to viral budding by inducing curvature in the cell membrane making it possible for the virus to bud out and spread. In order to be able to study M2 and its binding interactions with other proteins, we need to be able to access the C-terminal domain of the protein when it is in a membrane structure. Unfortunately, when M2 proteins are reconstituted in a liposome, they can insert in two different orientations. One of the orientations inserts the C-terminal domain facing the lumen of the vesicle which can make it inaccessible to other proteins and surfaces which as a consequence makes studying M1-M2 binding interactions difficult. The research conducted over the summer aimed to study different membrane mimics (bicelles and SMALPs) that give accessibility to both sides of the protein 100% of the time. The project aims to understand which membrane mimic is the most uniformly formed, gives accessibility to both sides of M2 and gives data close to data collected from the protein in a lipid bilayer (most physiologically relevant model of cell membrane).

Our primary tools are the uses of site-directed spin-label electron paramagnetic resonance spectroscopy (SDSL-EPR) as well as Dynamic Light Scattering (DLS). SDSL-EPR has proven to be a powerful method to study proteins associated with membranes and our research group has used this method to study M2 protein in membranes. EPR spectroscopy was used to study the effects that different membrane mimics can have on M2. DLS was used to physically characterize the diameters of the different membrane mimics and to optimize their formation. By comparing dynamic parameters from EPR as well as consideration of size data from DLS, we have shown that we are not forming a homogenous species of either membrane mimic and that the formation of SMALPs immobilizes M2. Our next steps are to optimize the protocols to form a more homogenous species of SMALPs and bicelles and use them to study M1-M2 binding.

The Developmental Trajectory of Gendered Pronoun Production in Children

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The developmental trajectory of gendered pronoun usage in young children is currently undocumented in psycholinguistic literature. The purpose of this experiment was to investigate errors in gendered pronoun production in children's speech and document how these errors change throughout the course of language acquisition. Specifically, we examined how children use the pronouns *he* and *she* in response to simple questions that are meant to elicit sentences that contain a pronominal subject and a verb that describe the action of a character on screen. We hypothesized that there would be an overall increase in adult-like responses as children aged, as well as that children in our age range will make gender errors in their pronoun usage, despite being able to correct identify the gender in humans in their daily life.

In the experiment, children aged 2 years 6 months to 4 years 4 months viewed short videos, about three seconds in length, in which an actor—a boy, girl, or ball—complete a simple action. After each trial, the child's response to the elicitation question, "Can you tell me what just happened?" was recorded. Preliminary results of the experiment show two different patterns. First, responses to the elicitation question become more adult-like as children develop, meaning the gendered pronoun correctly matches the presented actor's gender and the verb phrase describes the action presented in the video. Second, as children develop knowledge of the English gender pronoun system, they seem to make systematic errors that are variable across individuals. For example, some children have overgeneralized the pronoun *he* to both inanimate objects and actors of another gender, while others show the same pattern with the pronoun *she*. There seems to be a general developmental trajectory where children at the youngest end of our age range perform most poorly at the production task, with a middle phase of children making systematic pronoun errors that indicate that the child is nearing the cusp of mastering the English gender pronoun system, and an end phase where children nearly always produce the correct gender pronoun in the given experimental setting.

"MHD simulation of Taylor state merging at SSX"

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We present results of a resistive MHD simulation of the evolution and merging of two Taylor state plasmas. The simulation models merging experiments at SSX, where we have characterized the magnetic structure, velocity ($40\ km/s$), density ($0.5 \times 10^{16}\ cm^{-3}$), proton temperature ($20\ eV$), and magnetic field ($0.4\ T$) of relaxed helical Taylor states (see K. Gelber, *et al*, this session). We simulated the merging of both co- and counter-helicity Talyor states. We are using the Dedalus framework, and run simulations on the Bridges Supercomputer. Dedalus solves differential equations using spectral methods, written with a Python wrapper in an open-source, MPI-parallelized environment (http://dedalus-project.org/). Simulations are run on a rectangular grid (NxMxP=28x24x180). Initially we have a 2x2x10 rectangular box with two spheromaks and dense plasma regions at each end and low density regions in the middle. Perturbation is added to the structure of the spheromaks to break axisymmetry. At the boundaries we have free slip and perfectly conducting walls. The code has been verified by solving the Hartmann problem (vertical magnetic field, uniform pressure gradient) on a rectangular grid of same size with no-slip and perfectly conducting boundary conditions. Here we found the results to be nearly identical to the analytical solution as can be shown with many statistical measures.

Analysis of the Binding Interaction Between Antibody 133 and the Influenza Hemagglutinin Surface Glycoprotein

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Influenza (flu) is a virus that causes pervasive infectious disease. The flu represents an urgent health concern, as public health officials estimate that up to 20% of the global population gets infected by the virus annually. One of the reasons the flu is difficult to combat is because of the antigenic variability of its viral surface glycoproteins, primarily hemagglutinin (HA). Due to antigenic drift that occurs in the globular "head" region of HA (HA1), this glycoprotein has become a premier target of researchers engaging in anti-influenza vaccine design. One method of targeting a variety of antigenically diverse influenza strains is through the elicitation of broadly neutralizing antibodies (bnAbs). Triggering the development of bnAbs is a goal of universal vaccine design.

We examined the binding of a new anti-influenza HA antibody called "133." Antibody 133 was elicited in response to immunization of mice with a modified influenza HA that contained extra glycans around HA1. This hyper-glycosylated HA was designed to induce antibodies against the *conserved* receptor-binding site (RBS), the site that binds to host cells for entry. The goal of our work was to determine if 133 binds to the RBS, which would suggest 133 could be a bnAb precursor and the designed HA would be a useful vaccine component. To examine how 133 interacted with HA, we performed bio-layer interferometry (BLI), co-elution studies, and negative stain electron microscopy (nsEM). We imaged an HA-133 complex using the microscope at the University of Pennsylvania's Electron Microscopy Resource Lab. We also examined HA-133 interactions with another published antibody called FI6, which targets a stem-region epitope for comparison.

BLI and co-elution experiments suggested that the interaction between 133 and HA was not very strong, which required us to change our approach for preparing nsEM grids. Once optimized, we collected nsEM data and analyzed images using a software called EMAN2. By comparison to the ternary HA-133-FI6 complex, we could tell that 133 binds to the head-region of HA, away from FI6. We also observed both top- and side-views of the HA-133 complex, with different complexes containing one, two, or three copies of 133. These results provide evidence that 133 is an anti-HA1 head antibody. We will work towards getting a 3D model to see if 133 binds to the RBS. If so, the antibody may carry broadly neutralizing potential, thus making the hyper-glycosylated HA an ideal candidate for implementation in a universal flu vaccine.

Biophysical Characterization and Crystallization of *Tetrahymena thermophila* Telomeric Sequences

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Stabilizing G-quadruplexes (GQ) in the telomeric region with small molecule ligands is being explored as an anticancer strategy. In this project, the G-rich telomeric sequences (TTGGGG repeat) of Tetrahymena thermophila are studied alone and in complex with the ligand N-methyl mesoporphyrin IX (NMM). The presence of 295 nm inverse peaks on the thermal difference spectra shows that the sequences fold into GQ. CD scans and native PAGE results have revealed the sequences' GQ conformation, which were mostly mixed conformation with 1 parallel conformation. CD melts provided information on the stability of the sequences. Using these same methods, the effect of NMM on the sequences were studied. The sequences in complex with NMM, except for Tel14+NMM, still fold into GQ, but all the complexes adopted parallel conformation. Additionally, NMM increases the stability of the sequences. Crystallization efforts have yielded crystals for the sequences TET4+NMM, TET4B+NMM, and Tel26 whose best diffraction patterns have resolution of 11.0 Å, 2.2 Å, and 2.4 Å respectively.

HSATII GapmeR

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Human satellite II (HSATII) is a tandemly repeated DNA sequence found in the pericentromeric region of select human chromosomes. HSATII is silenced in normal human cells however, in cancer cells HSATII is expressed as a noncoding RNA that accumulates in the nucleus[1]. HSATII nuclear RNA accumulations recruit MeCP2, a protein involved with activating or inactivating methylated DNA, and this recruitment may affect the genome-wide distribution of MeCP2 in cancer cells[2].

To begin to investigate the function of these foci in cancer cells, we set out to investigate the effects of knocking down HSATII RNA. Because HSATII RNA is restricted to the nucleus we chose to use GapmeRs, antisense oligonucleotides with a combination of DNA and LNA bases, which recruit RNase H in order to degrade HSATII RNA. Because RNase H only degrades the RNA component of GapmeR/RNA hybrids, the GapmeR is able to target more RNA in the nucleus leading to a potent and long-term knockdown. We carried out GapmeR transfections in both human osteosarcoma (U2OS) cells and human prostate cancer (PC3) cells, two cell lines previously demonstrated to harbor different amounts of accumulated HSATII RNA. We show that GapmeRs targeting HSATII is very effective at knocking down HSATII RNA in both cell types, eliciting a 60 and 50 percent knockdown, respectively. Because we now know that GapmeRs work to knock down HSATII RNA we would like to investigate the effects this has on global MeCP2 distribution, the cell cycle, and how long the GapmeRs are effective at knocking down HSATII RNA.

Conformational Analysis of an HIV-1 Envelope using DEER Spectroscopy

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The HIV-1 envelope (Env) is the spike found on the outer surface of the virus that is necessary for host cell entry and is the target of antibodies produced by an immune response. Env conformation is an important consideration for vaccine design due to its co-evolutionary relationship with the antibodies that it elicits. Throughout infection, the Env mutates to avoid neutralizing actions taken by antibodies. The mutations change surface features of Env, which leads to the elicitation of altered antibodies. These antibodies can be either non-neutralizing or broadly neutralizing. The production of broadly neutralizing antibodies and its precursors is key to vaccine design.

The purpose of this study is to determine the Env conformation of the initial infecting virus (called the "transmitted founder" or "T/F") of CH505, a patient that produced broadly neutralizing antibodies. We are doing this using double electron-electron spectroscopy (DEER), in which we measure the distance between added spin labels on Env. The spin label we used requires a cysteine residue at the site of interest. Thus, a mutation was added to the CH505 T/F SOSIP Env to create the N173C DEER mutant. This resulted in a change from an asparagine residue to a cysteine residue at position 173. This mutation was located on a loop on Env that is known to undergo drastic changes when Env changes between "open" and "closed" conformations. A spin coupling agent was added to the cysteines, and electron paramagnetic resonance (EPR) was used to confirm successful spin coupling.

When compared to results of an M2 FL protein sample produced by the Howard Lab, EPR results showed a lower intensity for our N173C DEER mutant protein. DEER spectroscopy of the same N173C DEER mutant showed a low signal, perhaps a result of protein loss at numerous points of the experimental procedure. Future studies will involve increasing the volume of cells used during protein production, in addition to altering the spin coupling procedure to reduce protein loss. The long term goal of this study involves analyzing the conformation of CH505 virus Envs from different time points of infection, so that specific Env conformations that trigger the production of broadly neutralizing antibodies can be examined and used for vaccine design.

Rapid assessment of mammal fauna to examine shifts in mammal diversity across time and a gradient of land use

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Mammals provide far-reaching ecological functions and ecosystem services, including top-down ecosystem regulation, seed dispersal, and insect control. Furthermore, the presence of mammals can reflect the levels of human impact and climate change on natural systems, and mammal diversity serves as a proxy for ecosystem health. Despite its importance, a thorough assessment of mammal diversity is lacking in the Crum Woods ecosystem (CW), a semi-natural temperate forest that includes the Crum Creek and is part of the Delaware River watershed. The CW features a mosaic of management activity and presents a natural experiment for the examination of diversity across a human-use gradient as it encompasses unmanaged forest to restored habitat to manicured arboretum. In the scientific literature, the most recent systematic mammal survey in Delaware County occurred in 1952. Though the 1952 survey did not include the CW directly, it can provide a baseline for historical levels of species diversity in the area. Using live traps, trail cameras, and passive ultrasonic acoustic recording devices, we documented the current mammal assemblage in the CW and contrasted today's diversity with the 1952 Delaware Country survey in order to examine changes over the past 67 years. Preliminary results provide insight into the response of this mammal assemblage to suburban spread and yield useful information for the responsible management of this managed and semi-natural setting.

Speciating Ag(I) and AgNPs in the Leachate of AgNP-Impregnated Fibers

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Due to silver's antimicrobial and antibacterial properties, the use of silver nanoparticles (AgNPs) in consumer products has increased exponentially over the past few decades. This increase has occurred despite the lack of environmental studies on AgNP waste products. AgNPs themselves can undergo numerous transformations such as dissolution of ionic silver (Ag(I)), aggregation, protein corona formation, and adsorption of natural organic matter. The transformation of AgNPs when they are eventually discarded in the environment (through wastewater runoff for example) ultimately affects their toxicity to that environment and thus requires further study. Current techniques to analyze AgNPs are often expensive, time consuming, and requires intensive sample preparation. Furthermore, many techniques used by researchers in the field only allow for measurement of AgNPs or Ag(I) and are unable to speciate the two forms of silver simultaneously. Thus, in our study we attempt to create an efficient, inexpensive technique that is able to simultaneously measure the release of AgNPs and Ag(I) into the leachate of AgNP-impregnated fibers.

Due to silver's redox activity, we are able to use electrochemical techniques to quantify the amount of Ag(I) and AgNPs in solution. In previous work, our lab has demonstrated that an electrochemical technique known as linear sweep stripping voltammetry (LSSV) can accurately determine the amount and rate of dissolution that AgNPs undergo in solution by measuring the amount of Ag(I) over a 4-hour period. In other work, our lab has demonstrated that by coupling an electrochemical technique known as particle-impact voltammetry (PIV) and ultraviolet-visible (UV-Vis) spectroscopy we can accurately quantify the rate of AgNP aggregation in various solution conditions. Thus, in order to simultaneous detect Ag(I) and AgNPs in the leachate of AgNP-impregnated fibers, we have coupled these two existing techniques into one technique capable of speciating between the two types of silver.

Creep and Compaction in a Granular System

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Creep is the subsurface, slow movement, of constituents in a granular packing, such as sand or sediments, due to the disordered nature of its grain-scale interactions. The phenomena of creep in granular systems is relatively new and understudied, leaving many open questions. This summer we explored creep through experiments in which we observed the influence of a controlled disturbance on creeping motion in a granular packing. Our granular system consists of disks that are made from a birefringent material; this allows us to use image acquisition to observe both the movement of the grains and the force distribution of the system as grains experience stress. In the experiment, we deliver disturbances via taps of a pendulum to one side of the chamber that contains the granular packing. The tapping strength is then measured using an accelerometer. During the taps, we tilt the chamber to varying slopes to observe changes in system response as we approach the critical slope for more rapid granular flow. Using image analysis, we examine grain rearrangements, changes in packing density, and force redistribution as the grains creep due to disturbances.

Social Interactions predict Mating Pairs in *Bolitotherus cornutus*

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Forked fungus beetles (*Bolitotherus cornutus*) eat, live, and socially interact on fungi of dead trees. Mating behavior consists of three stages: courtship, copulation, and guarding. We know that Male *B. cornutus* prefer larger females and a male's size does not influence his preference for female size. We know that male horn size (specifically, larger horn size) is selected for in *B.cornutus*, but I was interested in digging deeper: are there other reasons that a pair of beetles mate? Are they more likely to mate if they have socially interacted before? Does mate choice have to do with size, familiarity, or both? In this study, we examined if the number of social interactions between a pair can predict the number of mating interactions – courtship, copulation, and guards – between that same pair. We used observational scan sampling data from 18 populations of forked fungus beetles near Mountain Lake Biological Station in Giles County, VA. Populations were surveyed three times daily throughout June and July in 2016 and 2017 at approximately 06:30, 14:30, and 22:30. We performed a generalized linear mixed model regression with a Poisson distribution and used the number of social interactions to predict the number of mating behaviors (courtship, copulation, and guard). We found that pairs of beetles often socially interact before they mate. We also found that pairs of beetles that spent more time together socially are more likely to mate. Future work can further examine these interactions to determine if there is evidence of mate-choice copying in *B. cornutus*. Mate-choice copying has been observed in vertebrates to influence the mating success of the males. Despite significant research on mate-choice copying in vertebrates, there has been little research of mate-choice copying in invertebrates.

Testing Gravity on Kiloparsec Scales and Over Cosmological Times

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This summer, we have developed a code that can be used to explore how the post-Newtonian parameter γ affects our understanding of gravity. We are working on using this code in order to explore how γ changes over large distance scales and cosmological time scales, as well as how it is intrinsically related to other parameters that describe the contents and behavior of the universe. Understanding γ can help us test Einstein's General Relativity as well as more recent modified theories of gravity, which predict a dependence of γ on some specific parameters.

Body measurements of Chilean blue whales, collected non-invasively via UAS (drones), indicate morphological similarity to the pygmy blue whale

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Blue whales (*Balaenoptera musculus*) were heavily targeted during the commercial whaling period in the 20th century, leaving many populations endangered or critically endangered. Currently, there are two named blue whale subspecies in the Southern Hemisphere, Antarctic blue whales (*B. m. intermedia*) and pygmy blue whales (*B. m. brevicauda*), which have distinct morphologies, genetics, and acoustics. However, a small data set from historical whaling records suggests that a third blue whale subspecies, the Chilean blue whale, may exist because their body lengths are intermediate between pygmy and Antarctic blue whales. This is supported by contemporary genetic and acoustic data. We measured blue whales in Chile (n = 24) during the austral summer in 2015 and 2017 using an unmanned aerial system (UAS, a.k.a. drone) to test the Chilean blue whale subspecies hypothesis with contemporary morphological data. Unlike the historical records, we found that the contemporary Chilean blue whale is morphologically similar to the pygmy blue whale, indicating that the population may have experienced a decline in body size most likely due to commercial whaling. Future UAS studies of pygmy and Antarctic blue whales would help explain if blue whale stocks decreasing in size is a trend, or a unique aspect of the Chilean population. Although our measurements are contradictory to the whaling records, the contemporary genetic and acoustic data do strongly suggest that Chilean blue whales should be considered their own subspecies.

Investigating the Crystal Structure and Phase Transformations of $Na_{(1-x)}FePO_4$ 0<x<1

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Sodium is a major component of the earth's crust and is both environmentally abundant and affordable. As a result, the development of sodium ion batteries come as a more sustainable and affordable alternative to lithium ion batteries. Triphylite phase $NaFePO_4$ (also known as olivine phase) has demonstrated similar electrochemical capabilities to LiFePO4, a cathode material that has been commercialized in rechargeable lithium ion batteries. We are investigating the different phases, structure, and stability of $Na_{(1-x)}FePO_4$ for 0<x<1. When a sodium ion battery is cycle, the concentration of sodium in changes as the battery charges and discharges. It is important to observe any major changes in NaFePO4 through these stages in order to evaluate its potential as a battery cathode material

We prepared $NaFePO_4$ in the olivine phase by delithiating LiFePO4 to form $FePO_4$, then sodiating to form $NaFePO_4$. The fully sodiated material was then desodiated to form intermediate compositions ranging from 0<x<1.The phases and crystal structure of our materials were investigated with X-ray Diffraction (XRD). The X-ray diffraction patterns were analyzed through a process called Rietveld Analysis performed with the software GSAS II and using Jupyter notebooks. Rietveld analysis was used to determine lattice parameters during different sodiation periods and any other structural changes.

In addition to analyzing the materials prepared at Swarthmore, Rietveld Analysis was also used to analyze operando neutron diffraction data collected on NaFePO4 batteries at the Australian Center for Neutron Scattering. This data gives the diffraction pattern measured with neutron (instead of x-rays) of NaFePO4 as a cathode material in a functioning battery that is being charged and discharged while the diffraction pattern is collected. These results in combination with the x-ray diffraction work performed here will help give a more complete picture of the crystal structure and phase transformations of $Na_{(1-x)}FePO_4$ 0<x<1.

Hypoosmotic Versus Hyperosmotic Microenvironments Respectively Suppress or Enhance Nuclear Rupture During Cell Migration Through Micropores

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Introduction: During tumor growth and metastasis, cancer cells squeeze through interstitial pores, across basement membrane barriers, and into micron-sized blood capillaries. Along with these and other solid stresses, cancer cells also endure fluid stresses due to tumor microenvironments that can be dysregulated in terms of pH, osmolarity, and more. Constricted migration severely deforms the cell and its nucleus—even causing rupture of the nuclear lamina and envelope as well as mis-localization of key nuclear factors and excess DNA damage—but cancer cells also undergo osmotically-induced swelling or shrinkage due to dysregulation of ion homeostasis. Cancer cells regulate their osmolality in response to compressive forces, and osmolality impacts the treatment of cancer, as uptake of chemotherapeutic agents into tumor cells increases when drugs are administered *via* hypotonic solutions but decreases in hypertonic solutions. How osmolality influences a cancer cell's migration through a constricting pore, or how the combination of constriction and osmotic stress impacts the integrity of the nucleus, are poorly understood issues.

Materials and Methods: U2OS human osteosarcoma and A549 human lung cancer epithelial cells were seeded on top of either 3 μm or 8 μm pore membranes at high density and allowed to migrate to the bottom of the membranes for ~24 hours. During migration, cells were incubated in hypoosmotic (~120 mOsm/kg), hyperosmotic (~650 mOsm/), or normal (~300 mOsm/kg) culture medium: DMEM high-glucose medium for U2OS and Ham's F-12 medium for A549, supplemented with 10% fetal bovine serum and 1% penicillin/streptomycin. After migration, the pore membranes were formaldehyde-fixed, stained for DNA, lamin-A/C, and lamin-B1, and imaged using a Leica TCS SP8 confocal microscope.

Results and Discussion: For both cancer cell lines tested, hypoosmotic stress causes elevated cell death on a pore membrane—or possibly failure to adhere to the membrane—as well as reduced migration rate through both constricting 3 μm and larger 8 μm pores. Importantly, hypoosmotic stress also reduces the frequency of nuclear envelope rupture during constricted migration, as indicated by a ~25-30% decrease in nuclear bleb formation. These results are consistent with previous studies suggesting that slower migration protects nuclear envelope integrity, with myosin II inhibition *via* blebbistatin eliminating nuclear blebs while severely decreasing migration rate. On the other hand, for A549 cells, hypertonic medium also enhances cell death and slows migration, yet hyperosmotic stress was found to increase nuclear blebbing after migration through 3 μm pores. Upregulation and remodeling of cytoskeletal components under hyperosmotic stress, as has been reported in a variety of cell types, might lead to extra force on the nucleus, thus counteracting the rescue effects of reduced migration rate.

Conclusions: Tumor growth and metastasis depend on cell migration, and cancer cells that squeeze through stiffer tissues—and therefore smaller interstitial pores—experience greater mechanical stress. Mechanical stress can also be induced by varying the osmolalities of the solutions in which cells migrate. Whereas hypotonic and hypertonic solutions both cause elevated cell death and reduced migration rate, they have opposite effects on nuclear envelope rupture: hypotonic medium decreases rupture frequency, while hypertonic medium increases it. Cytoskeletal organization might be altered and could provide insight into these differential effects.

Overrepresentation of Corynebacteria in the Gut Microbiota of Hummingbirds Undergoing Daily Torpor in Relation to Cold Shock

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Hummingbirds living on the west coast of the North American continent, *Selasphorus rufus* and *Calypte anna*, were found to have radically different gut microbiome populations than other animals, including other birds. They have up to 60% of *Corynebacteria* species composing their microbiota, as opposed to negligible amounts in other surveyed animals. We attempted to determine the reason for this, and preliminary results have shown a correlation between the process of torpor and the repartition of bacteria in these birds' intestinal fauna. Both undergo nightly torpor, wherein they decelerate various metabolic processes, but more importantly lower they body temperature from about 39°C to 12°C overnight. Our findings so far have shown that *Corynebacteria* species survive better when submitted to periodic drops in temperature from 37°C to 10°C than when simply incubated at 37°C. Most other bacterial species we surveyed followed the opposite pattern. The phylum *Actinobacteria*, to which the *Corynebacteria* belong, has been found to frequently be overrepresented in very cold environments, such as Antarctica. The *Corynebacteria's* survival during cold shock may be attributed to the genus' cold shock proteins which could be different from other genera's. Cold shock proteins fold into different conformations depending on the temperature of the environment, preventing the formation of secondary structures due to the cold, which harms the bacterium, as well as having other functions related to cold shock survival. The former's cold shock proteins have been found to be able to fold near-instantly, which means a near instant reaction to cold shock. The exact difference between *Corynebacteria's* and other genera's cold shock protein refolding speeds remains to be explored.

The Physics of Cancer: Investigating Human Satellite II RNA structure and function

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Almost 20 years since the Human Genome Project, there remain large patches of DNA on each of your chromosomes (up to 10 *million* bases on a single chromosome) which have not been sequenced. One type of this un-sequenced DNA, Human Satellite II (HSATII), is thought to contribute to the development of human cancers. In healthy cells, HSATII DNA is not expressed, but in many types of cancer cells, HSATII DNA is transcribed into HSATII RNA, which is hypothesized to cause healthy cells to develop cancerous traits. I investigate the physical properties of HSATII RNA to uncover its function inside of cancer cells. Here, I show that HSATII RNA phase separates into spherical droplets, and that this phase separation is dependent on the size and sequence of the HSATII RNA. HSATII RNA is known to form spherical bodies inside cell nuclei, suggesting that this is a result of RNA phase separation. Further, these spherical bodies are known to interact with proteins that are important for genome regulation. I hypothesize that phase separated droplets of HSATII RNA sequester key genome regulation proteins, providing a mechanism for HSATII RNA's role in cancer. In support of this hypothesis, I show that short fragments of HSATII RNA fold into particular structures which could bind specifically to proteins. With further testing to determine the exact structure, we could predict which proteins bind HSATII RNA, creating a substantiated model for HSATII-RNA droplet-mediated protein sequestration, a huge step forward in unraveling the function of HSATII RNA in cancer. Here, the physics of HSATII RNA (its ability to form droplets and fold into ordered structures) has proven to be key to understanding its function, creating new and promising future avenues for understanding the genetic basis of human cancers.

Aluminum-Nitroxide Complexes Implementing Bidentate Redox-Active Nitroxide-Based Ligands

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The chemical field is heavily dependent on different catalysts that involve precious and toxic elements such platinum and palladium. However, Aluminum, which is the main focus of the Grave's lab, is abundant, cheap, and environmentally friendly.

This summer, I worked on developing a series of redox active pyridine-based aluminum complexes from bidentate ligand precursors, to be used as cheap and sustainable catalysts. The reactive, spectroscopic, and structural aspects of those compounds were investigated. The aluminum complexes were characterized by ^{1}H and ^{13}C Nuclear Magnetic Resonance spectroscopy, X-Ray Crystallography, and Elemental Analysis.

Aluminum mainly exists in one stable +3 oxidation state, which prevents it from undergoing redox chemical reactions like other metals such as copper. The nitroxide $N-O$ group exists over three different oxidation states. Therefore, the aluminum complex will also have multiple oxidation states, hence expanding its catalytic abilities. The long term goal of this project is to make an important catalyst out of one of Earth's most abundant metals.

A series of aluminum-nitroxide complexes of the form $[^RpyNOAl(CH_3)_2]_2$ (R = H, OCH$_3$) were prepared by a deprotonation-complexation reaction of the bidentate ligand (^RpyNOH) with trimethyl aluminum (AlMe$_3$). After characterization, a series of reactions of those compounds were ran with various Lewis acids and bases. Those reactions showed that the substituents of the ligands and the nature of the Lewis acid or base might have an effect on those reactions. The ultimate goal of those reactions is to study the effect of Lewis acids and bases on the electronic structure of the aluminum compound-Lewis acid/base complex.

In order to synthesize new complexes, I also experimented with using Aluminum tert-butoxide and dimethyl aluminum chloride as the starting material. Those reactions indicated that the aluminum starting material affects the manner by which the ligand coordinates to the aluminum. The reaction of $^{OMe}pyNOH$ with Al(t-buO)$_3$ resulted in the substitution of the three tert-butoxide groups by the ligand, yielding Al($^{OMe}pyNO$)$_3$. However, with Me$_2$AlCl, the ligand replaced the two methyl groups to produce (^RpyNO)$_2$AlCl.

Parallel viewshed extraction on multiresolution terrains

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The viewshed is the set of all points visible on a 2D grid of elevations T from a given viewpoint. We worked to parallelize existing viewshed algorithms by exploiting the processing power of the GPU using CUDA. We focused on modifying the multiresolution horizon-based viewshed algorithm so that it would work in parallel in the hopes of reducing runtime. Horizon based viewshed algorithms work by scanning the horizon in layers outward around the viewpoint, saving a copy of the horizon in *totalHorizon* which is continually updated. The multiresolution algorithm uses this algorithm, but adds an additional layer of abstraction: Given a block size b, it creates a grid T' containing blocks that each represent b^2 points on T. The algorithm then generates a viewshed for T', marking each block in T as visible or invisible. Each point in a block marked invisible is guaranteed to be invisible in the viewshed of T. Thus, when computing the high resolution viewshed, the algorithm skips checking the visibility of any point guaranteed to be invisible, saving significant computation time.

We analyzed the most costly parts of this algorithm and chose to parallelize the functions COMPUTEVISIBILITY() and MERGEHORIZONS(). COMPUTEVISIBILITY() computes the visibility of each point in a layer. We modified this function such that the visibility of each point in a layer could be computed simultaneously, without depending on the results of the other points in the layer. Furthermore, we restructured MERGEHORIZONS(), the function that combines new horizons with *totalHorizon*, to divvy up its work among different threads on the GPU. Our version of COMPUTEVISIBILITY() is about 4 times faster than the previous version, but our version of MERGEHORIZONS() is about 5 times slower.

Overall, our algorithm is slower than the pre-existing algorithm, but we are still working to further optimize our work. Overhead communicating between the CPU and GPU has been costly, and we are developing workarounds for some of the inconvenient intricacies of CUDA. We have created an environment useful for future research and will continue work on speeding up this algorithm.

Impact of Ecological and Social Factors on Laying Behavior in Female Forked Fungus Beetles

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The Optimal Oviposition Theory suggests that females are influenced by strong selective pressures to choose oviposition sites that will be best for their offspring's performance and fitness. Specifically, females prefer to oviposit at locations with ample resources and minimal competitors for their offspring. Using behavioral observational data collected during the previous four years by the Formica lab, data analysis was completed to investigate how the ecology and social location of the fungal brackets on which females lay their offspring impact the laying behavior of female forked fungus beetles, *Bolitotherus cornutus*. Studies conducted on other insect species found that females were choosier towards resource quality than conspecific egg density when deciding where to lay their offspring. In general, females were most deterred from laying at sites with high conspecific egg densities, or at locations with unknown or low-quality nutrition sources. Based off of these studies, we predicted that female forked fungus beetles would prefer to lay on brackets with higher quality resources, even if other females were observed on those same brackets.

Using the ecological factors of fungal bracket age and size and the social factors of total number of females observed on a bracket, total number of males observed on a bracket, and the localized sex ratio, we analyzed data of observed female lays to see if any of these factors significantly impact female oviposition behavior and choice. Ecologically, females prefer larger sized and younger brackets for oviposition, whereas as socially, females preferred to lay on brackets where greater numbers of females had been observed. Local sex ratio and number of observed males did not significantly impact egg laying behavior. These results suggest that female beetles prioritize resource quality when laying eggs, even at the cost of exposing their offspring to increased competition by laying in areas where other laying females are present. Another potential reason for this result would be social learning occurring between female beetles, where females use the presence of other laying females on specific brackets as a cue that those locations are preferable for oviposition.

Pan-neuronal expression of Tau^R406W, scFv235, and CD8-GFP in transgenic adult *Drosophila* models of Alzheimer's Disease

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Alzheimer's Disease (AD) is a chronic neurodegenerative disease that eventually leads to memory loss and cognitive decline. Current knowledge of AD reveals that in the preclinical stage, abnormal deposits of amyloid plaques (aggregates of beta-amyloid proteins) and neurofibrillary tangles (formed of hyperphosphorylated tau protein) are present in the brain even before symptoms appear (Schneider & Tarshis, 1995). Current research of animal models studying tau protein pathology have shown much potential, revealing that tau lesions correlate more highly with the degree of dementia observed than do Aβ deposits (Pedersen & Sigurdsson, 2015). Thus, it is reasonable to predict based off the research into animal models that eliminating tau lesions in the brain may prove more effective than clearing Aβ plaques in terms of treating the various symptoms of AD. There are currently clinical trials being conducted that investigate the efficacy of the antibody-mediated removal of tau deposits. Other studies have developed immunostaining methods to probe tau pathology to study other factors of tau antibodies, such as deciding which epitopes to target, the mechanism of uptake of tau antibodies into neurons, and potential pathological effects (Sigurdsson, 2016).

This project builds on existing research that has shown certain short chain variable fragment (scFv) antibodies interacting with pathological tau. This project specifically investigates (1) whether scFv antibody 235 and co-localizes with mutant tau^R406W protein and transmembrane CD8-GFP protein and (2) optimizing a protocol to lead to clear and consistent immunostaining. Citing a widely-used *Drosophila* AD model originating from the Feany lab, we established a transgenic cross expressing scFv235, tau^R406W, and CD8-GFP in all neurons and used various brain dissection and immunostaining techniques to produce confocal images (Wittmann *et al.*, 2001). The results suggested that most tau^R406W and scFv occur intracellularly in flies at both younger (week 1) and older (week 3) ages. However, there was also evidence of non-neuronal staining of scFv-tau interaction that did not co-localize with CD8-GFP, which may be due to the nature of the signal peptide in scFv235. These findings provide insight on the binding mechanism of mutant tau protein and scFv235, which could aid in renewing clinical trials investigating tau antibodies for AD.

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Mitotic Rounding Influences Cardiac Cell Fate Specification in *Ciona Robusta*

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Mitotic rounding occurs during cell division entry in which cells become more spherical, allowing for proper chromosome and spindle alignment. Even though mitotic rounding is a critical part of most cell divisions, it is still unclear how rounding may impact cell signaling and fate specification during asymmetric divisions. During the development of *Ciona robusta*, the embryo's four pre-cardiac founder cells each undergo an asymmetric division, giving rise to a tail muscle progenitor and a heart progenitor. Previous research has shown that the induction of the heart progenitor is caused by the polarized distribution of fibroblast growth factor receptors (FGFR) onto the adherent ventral membrane. Through several pharmacological inhibition experiments, we show that both primary processes of mitotic rounding, osmotic pressure and actomyosin cortex contraction, play a critical role in this mitotic protein redistribution and resulting cell fate specification. We propose that the osmotic pressure generated by the influx of water during cell cycle entry geometrically reduces adhesions to the ventral epidermal layer, while the actomyosin cortex contraction localizes matrix adhesions, allowing for the ventral polarization of FGFR. Our results suggest a way biomechanics can play highly influential roles in cell signaling and fate specification. Furthermore, this study highlights previously undocumented connections between fate specification and several cellular pathways, including ion channel activity and cell cycle regulation.

Obtaining an Accurate Reduced Model of Neural Dynamics

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The neurons of the Medial Superior Olive (MSO) help the brain locate the sources of auditory inputs. Lehnert et al. (2014) created a model of such neurons that breaks the neuron's spatial structure into 45 compartments: soma, axon initial segments, internodes, and nodes of Ranvier. Our goal was to construct a minimal model that approximates the spike generation region of the 45-compartment model and incorporates soma-to-axon coupling. Using the differential equations and parameters controlling the current of the 45-compartment model as a guide, we constructed a reduced model consisting of 2-compartments; one for the soma-dendrite regions and one for the axon region. We found that our model mimics the nonlinear dynamics of the detailed 45-compartment model with high accuracy. Our analysis, which quantitatively compared the spiking current thresholds and traces of the two models, found robust agreement. These positive results for our approximation could be helpful for future researchers to efficiently and accurately model spiking dynamics of large clusters of neurons.

Simulating Multiply Modulated Maps of the CMB

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Our research is a new way to study the Cosmic Microwave Background (CMB), which is radiation left over from the Big Bang. Perturbations in the CMB as it was released from the Big Bang can give significant insight into the structure and evolution of the early universe. Our goal is to simulate maps of this radiation as we might see it from Earth, in order to isolate different distortions that may impact our understanding of the early universe. To do this, we wrote a computer program that can simulate unaffected maps, the fields that contribute to the distortions, and the final product. All three of these are used by our collaborators at the University of Chicago to train a machine learning algorithm that will in the future be able to deconstruct our real measurements of the CMB into the component parts. With these findings we hope to learn more about the development of the early universe.

Binding energy thresholds of Rhodium and Lanthanum negative ions found using a newly automated attenuator

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Negative ions, atoms or molecules with at least one extra electron, have several applications in physics. This summer, we studied the Rhodium ion, which has a valence shell ideal for studying electron interactions, and the Lanthanum ion, which is a good candidate for improved laser cooling. We are measuring the binding energies of various excited states of these ions so that they can be used in their respective applications. We make this measurement by crossing a beam of negative ions with a laser, which photodetaches electrons from their ions if the wavelength of the laser is short enough. We vary the wavelength until we see thresholds where significantly more electrons are photodetached, which indicates that we have found a binding energy for an electron transition. This summer, my main project was to automate an attenuator, which allows us to keep the laser power roughly constant during the experiment, decreasing uncertainty and allowing us to do longer scans of the laser. I wrote a program that decides whether to increase or decrease laser power based on the data being collected, which then controls a motor attached to the attenuator. Two attenuator systems were necessary for different wavelength ranges. We ran the system in the final week, and it successfully decreased the variation of the laser power. With some of the data aided by the attenuator system, we found one definitive threshold for Rhodium with several more that will require further analysis to characterize. We were also able to precisely measure a previously detected resonance structure of Lanthanum.

FucTA expression in lateral bipolar dendritic neurons important in regulation of *Drosophila* nociceptive response

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Organismal behavior can be better understood by examining the genes and neuronal circuits involved in its regulation. This research focuses on nociceptive, or pain-sensing, behavior. *Alpha-1, 3-Fucosyltransferase A (FucTA)* is a gene that has been implicated in the regulation of the nociceptive response of *Drosophila melanogaster*. The S89 deletion within the *FucTA* coding region results in an increase in the time that *D. melanogaster* larvae take to complete a roll and a lower likelihood of performing a C-bend in response to a heated stimulus, the stereotypic responses to pain. This research focused on identifying the neurons in which *FucTA* expression is required for *D. melanogaster* larvae to elicit a normal response to this noxious stimulus. Using the Gal4-UAS system, the expression pattern of different FucTA-Gal4 constructs, which vary in the FucTA regulatory regions that drive their expression, were examined on larval central and peripheral nervous systems. Confocal imaging revealed that in the ventral nerve cord, *FucTA*-Gal4-0396 was expressed in a subset of interneurons, as well as lateral bipolar dendritic (LBD) neurons. *FucTA*-Gal4-0391 expression was present solely in the LBD neurons. Phenotypic study of these larval crosses revealed that reduced *FucTA* expression in cells with *FucTA*-Gal4-0396 expression resulted in an increase in the time necessary to initiate and complete rolling behaviors. These delays were also exhibited when *FucTA* expression was reduced in cells with *FucTA*-Gal4-0391 expression. Increasing expression of wild-type *FucTA* in *FucTA*-S89/*FucTA-Gal4-0396* mutants enabled a rescue of normal phenotypic behavior. Evidence suggests that the expression of *FucTA* in the LBD neurons, as well as a subset of interneurons, appears to be essential in the regulation of nociceptive behavior of *D. melanogaster*, which is significant because the LBD neurons have never before been implicated in the pain-response. Future research will focus on isolating *FucTA* expression in the LBD neurons to further support the importance of *FucTA* expression in these cells. The molecular function of *FucTA* in the neurons in which it is expressed has yet to be addressed, as well.

Clarifying the Differences in Migratory and Resident Hummingbird Gut Microbiota

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Microbial communities that animals host maintain health and physiology in organisms and populations. Studies of microbiomes have demonstrated that changes in the proportions of symbionts within the gut alter the weight of organisms. Migratory populations of hummingbirds gain a large amount of weight prior to each of their journeys while their local counterparts do not undergo weight change. Investigations into local *Calypte anna* and migratory *Selasphorus rufus* hummingbirds have demonstrated both birds experience changes in the proportions of their symbiont populations over the late spring and summer months. However, different symbiont populations in each bird are affected to different degrees. Questions remain over how communities change in a year, how the microbiomes within populations of *S. rufus* might change as they migrate to different regions, how different species of symbionts are affected by conditions like temperature change, and how the microbiota change with the physiology of their respective host birds. DNA purification was performed on hummingbird feces collected from Spring 2018 until Spring 2019 from the two species from Riverside, California; New Orleans, Louisiana; and the San Juan Islands in British Columbia. This poster presents the future directions of this laboratory work. Beginning with 16S rRNA gene Next Generation Sequencing, the microbiota in sampled hummingbirds will be identified and compared to their closest related studied taxa. These communities will then be related to the physiological characteristics of the host birds, particularly fat score, stage and type of molt, and number of ectoparasites. These parameters will inform our understanding of the bird's ecocycle of fattening, feather renewal, and migration and how the functional profiles of the microbiota affect these physiological processes.

Prussian Blue as a Cathode Material for Rechargeable Sodium Ion Batteries

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Prussian Blue is most commonly known for being the first modern synthetic pigment used in paints. However, it also has properties that make it promising as a cathode material for rechargeable sodium ion batteries. Prussian blue and its derivatives are gaining attention for electrochemical energy storage applications due to its high theoretical specific capacity, non-toxic nature, and relatively straightforward procedure for synthesis. Prussian Blue samples ($Na_{1-x}FeFe[CN]_6$) were synthesized using different concentrations of NaCl to control the amount of sodium ions in the synthesized products. Seven samples were synthesized with varying sodium content, providing materials that are analogous to a cathode material at varying states of charge. These samples were characterized using X-ray diffraction to confirm the structure of the material. Lattice parameters and particle size were determined as a function of sodium concentration by analysis of the diffraction patterns. By examining the differences between samples with varying amounts of sodium, we are able to gain a better understanding of what happens when the material charges and discharges as the cathode of a battery. We found the lattice parameters increase with increasing sodium content indicating that the unit cell expands when sodium intercalates into the material. We also found variation in the values of the different lattice parameters in materials with higher concentrations of sodium, suggesting the lattice begins in cubic structure but begins to cant over time as more sodium ions are added to the material.

Mindfulness-Based Stress Reduction (MBSR), Sleep Quality, & Interleukin 6

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The application of 'omics' technologies to study genes, proteins, metabolites, inflammation, and other complex biological systems signifies a marked advance in scientific discovery, with enormous potential for improving medicine and healthcare. Concurrently, mindfulness-based interventions have been shown to reduce stress and improve well-being, while also inducing changes in the brain and immune system. However, less is known about the molecular biology and functional genomics that likely underlie the mental and physical health benefits of mindfulness. This study investigates the intersection of Mindfulness Based-Stress Reduction (MBSR), the immune system, and sleep. It has been shown that MBSR reduces stress, stress directly correlates to pro-inflammatory cytokine interleukin 6 (IL-6) levels, and IL-6 elevation lowers sleep quality. Thus, it was hypothesized that lower IL-6 levels are a biomarker of individuals whose sleep and stress improved after MBSR, called sleep responders and stress responders respectively. Thirty healthy, stressed adults attended an 8-week MBSR program. IL-6 levels were determined from blood samples taken before, during, and after stress induced by the Anger Recall Task both before and after MBSR. It was found that sleep responders' and non-responders' average IL-6 levels were the same at baseline. Sleep non-responders' average IL-6 levels were significantly greater than that of sleep responders' after MBSR. Most stress responders were also found to be sleep responders. Most stress non-responders were also sleep non-responders. These correlations were not statistically significant (p=.06). Stress responders' and non-responders' average IL-6 levels were the same at baseline and after MBSR. It was concluded that MBSR may not lower IL-6 levels in healthy adult stress and sleep responders. Rather, non-responders IL-6 levels may simply appear greater after MBSR, perhaps due to unexpectedly higher cortisol reactivity from greater engagement and coping. More intensely stressed samples should be tested in the future to determine whether MBSR acts as a protective buffer against stress.

Repeatability of social environment in forked fungus beetles

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Repeatability compares an individual's variation in behavior to population variation. Highly repeatable behaviors depend mostly on properties of the individual, and suggest a heritable, genetic basis; behaviors with low repeatability, on the other hand, depend on outside factors. Repeatability has been found in many different behaviors – including aggression, exploratory behavior, and copulation – in many different organisms. Like these behaviors, the social environment of individual organisms is known to have strong effects on their fitness. Forked fungus beetles *(Bolitotherus cornutus)* form relatively stable social networks, but is their social environment stable and repeatable?

Forked fungus beetles live in distinct, stable populations on logs within the Mountain Lake Biological Station metapopulation. These logs were scanned daily in summer 2016 and summer 2017; the behavior and ID of each beetle observed was recorded. From these data, I calculated 5 measures of social environment for every individual beetle, for the first and second half of either summer 2016 or 2017. The 5 measures of social environment used were focal degree, total social interactions, mean social partner elytra (split by sex), and mean thoracic horn size (of male social partners). I then used the 'MCMCglmm' package in R to estimate repeatability values for every measure. Repeatability estimates with a 95% confidence interval bounded above 0 were considered significant. The repeatability estimates suggested that focal degree, mean social partner elytra, mean social partner thoracic horn, and number of social interactions were all repeatable, with the exception of the number of social interactions in summer 2017. Mean social partner elytra and thoracic horn were both more repeatable than focal degree or number of social interactions.

The repeatability of all these measures of social environment suggests that they depend more on properties of the individual than on environmental factors. The higher repeatability of partner and thoracic horn size may have been due to the strong effects of beetle size on fitness – an individual's size relative to its social partners may be just as important as its absolute size. The number of social partners and focal degree, however, may depend more on the size of an individual's population. To further clarify the nature of repeatability in forked fungus beetles, I will better control for the effects of population variation when calculating repeatability, will use internal stability statistics to determine if sex or size determine repeatability, and will attempt to determine whether individual beetles' social environments are repeatable across years as well as summers.

Creatinine and Corticosterone Assay Validation on the Urine of Sympatric Migratory and Resident Hummingbirds

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This project focused on analyzing urine samples from two hummingbird species (Rufous and Anna's hummingbird). The purpose was to validate and run assays on previously collected urine samples for corticosterone, the principal glucocorticoid stress hormone in birds, and creatinine, a reference substance that is used to adjust for the dilution of the urine. Having an accurate and reliable assay for creatinine levels is an important first step for measuring other hormone concentrations in urine. Hummingbird urine creates a unique problem due to the urine's small volume and extreme dilution. The extreme dilution, which has been equated to the dilute urine of a freshwater frog, of hummingbird urine is in large part due to the nectar-based diet of the birds. These birds must ingest a large amount of nectar in order to maintain their high metabolic rate and the sugars from the nectar is retained as fuel while the water is released in urine.

In total, three different creatinine assay kits were tested using pooled urine samples and analyzed for parallelism. Parallelism is an indication that changing the concentration of the samples affects optical density readings proportionally to changing the concentration of the standards by the same amount as well as insuring against matrix effects. After testing all three kits, it was determined that the Thermo Fisher Scientific kit would be the best kit moving forward because of the consistency of results and ease of procedure. Consistency was illustrated by the low CV values between duplicates of samples and the reproducibility of results. This procedure included only one reagent and one set of standards contributing to minimal time for preparation. This kit was also validated and found to be effective when using half the volume of reagents and urine, allowing samples to be tested individually rather than requiring them to be pooled together. Testing individual samples expands the analysis possibilities and the number of questions that we can attempt to answer with these urine samples.

Future work on this project will begin to focus on validating assays for corticosterone. This is valuable because most of what is in urine is actually metabolites of corticosterone and therefore we need to find an assay kit that has an antibody for the non-modified corticosterone or one with an antibody specific to one of the metabolites. There are many questions that we can begin to delve into with future results, but the ultimate goal is to attempt to connect corticosterone levels to the gut microbiome, which has previously been shown to affect stress and anxiety response.

Understanding the genetic basis of thermotolerance in *Arabidopsis* using a high throughput quantitative phenotyping platform

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One of the observable phenotypes that plants exhibit after experiencing elevated temperatures is a depression in growth rate. For this project, our goal was to create an imaging pipeline that could accurately and efficiently track the growth rate of roots before and after heat stress affects a plant. By using high resolution document scanners, we can image 800 *Arabidopsis thaliana* seedlings every 18 minutes over a 24-hour period. After allowing the scanners to image the roots for a baseline period, the plates are submerged in a water bath and then placed back on the scanner to track the root growth rates after heat stress. By using H.A.R.G.I.S. software that can compute the root growth rates, we found that after a heat shock the roots of wild type *Arabidopsis* plants grow at ~10% of their normal growth rate and recover to a steady growth rate after about 10 hours. However, in thermotolerance mutants like *eg6* the growth rate goes down to zero and takes almost 20 hours to recover. These data correspond to previous findings that *eg6* mutants are more sensitive to heat stress. In addition to *eg6*, we have used this imaging pipeline to image other mutants with mutations in genes without documented heat response phenotypes. Preliminary results show that several of those mutants have heat shock phenotypes.

Investigation of LiFeF₃ Structure Using Mössbauer Spectroscopy and X-ray Diffraction

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Rechargeable lithium ion batteries have long been the subject of materials science, physics, and chemistry research. The need for electrode materials that can perform with high capacity and cycling stability has driven our research to explore the structural mechanisms underlying the behavior and performance of lithium ion batteries with FeF_3 cathodes. Through cycling, the battery cathode undergoes a conversion reaction that produces $LiFeF_3$ in its intermediate stages. This electrochemical reaction is of particular interest to us because FeF_3 offers high theoretical capacity and is cheaply and widely available but has low electronic conductivity which limits its practical use as a battery cathode. We hope to distill how the characteristics of $LiFeF_3$ impact the usage of the material as a cathode. Our ultimate goal is to determine whether it is possible to fabricate a cell that begins cycling with fully formed $LiFeF_3$, thus bypassing the lithium insertion and conversion reaction altogether. Consequently, we could achieve the high cycling capacity of a conversion-type cathode without requiring a conversion reaction.

In analyzing Mössbauer spectra and x-ray diffraction patterns of $LiFeF_3$ at different temperatures, we are one step closer to fully understanding the material properties of $LiFeF_3$. From the *in situ* Mössbauer, we observed that the iron atoms exhibited ferromagnetic behavior below the Curie transition temperature of around 90°C. Above the Curie transition temperature there was no ferromagnetic contribution. These results suggest a significant phase transition and structural changes that occur across the Curie transition temperature. Our analysis of XRD patterns also supports the observation of structural changes at higher temperatures. The XRD patterns showed that the contribution of pure FeF_3 increased with the temperature, while the contribution of $LiFeF_3$ decreased. These observations indicate that lithium ions begin to leave the FeF_3 structure at higher temperatures, producing irreversible structural changes. Once the material reached a certain temperature however, the changes stabilized, suggesting that LiFeF3 has decent structural stability at higher temperatures and could feasibly be stable enough for voltage cycling.

Intron Retention and Regulation of the Heat Shock Response in *Arabidopsis*

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As temperatures continue to rise around the world, understanding the molecular basis of how plants respond to high temperatures is crucial. Organisms react to external stressors with changes in gene expression that are regulated at the level of transcription, translation, or RNA processing. In the case of exposure to high temperature, organisms express heat shock proteins (HSPs) that function in the heat shock response (HSR).

We used RNA-seq data to identify genes that are induced by high temperature and exhibit intron retention (IR). These genes are enriched for functions in the HSR. At 24° these genes have low expression levels, at 37° they are expressed and spliced, and at 40° they exhibit IR. I confirmed this pattern for a few representative genes using RT-PCR. The *eg6* mutant, caused by a mutation in a spliceosome subunit, exhibits similar splicing patterns as wild type plants but at lower temperatures. While wild type plants exhibit IR for these genes only after a 40° heat shock, *eg6* plants show a similar pattern of IR at 37°. Data from our collaborator Yee-Yung Charng shows that *eg6* mutants have a delay in production of heat shock proteins after a heat shock of 37°, the temperature at which the mRNA for these proteins exhibit IR.

These data led to the development of our hypothesis that IR serves as a mechanism for delaying heat shock protein production at high temperatures. Specifically, IR transcripts are retained in the nuclei of heat shock cells. Once the temperature has gone down sufficiently so that proteins can function productively, the IR transcripts are post-transcriptionally spliced, exported from the nuclei, translated, and function in the heat shock response. To test this hypothesis, I isolated nuclear and cytoplasmic transcripts from heat shocked plants. I found that that IR transcripts for several genes are retained in the nuclei of 40° heat shocked cells while fully spliced transcripts are found in both cytoplasmic and nuclear fractions.

Eldridge Commons Aquaponics System

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The goal of my research project was to design and construct an aquaponics system in Eldridge Commons. Aquaponics combines hydroponics, which consists of growing plants without using soil, and RAS-aquaculture, which refers to the cultivation of fish in a closed, recirculating system. The wastewater produced by the fish provides nutrients to the plants, and at the same time, the plants help filter and clean the wastewater so that it is safe for the fish to inhabit. Aquaponics has great potential as a form of sustainable agriculture. It is a highly efficient system that produces both plants and fish, while consuming less resources – water, energy, and land – than industrial agriculture.

My research focused on designing a functional and balanced aquaponics system, which would also act as an aesthetic display. In order to create a system that could operate perennially and with minimal management, careful consideration and testing was used to determine the appropriate flow rates, volumes, and surface areas of the various components. From an ecological perspective, the system also required careful management of the primary functional biotic groups in aquaponics – the bacteria, fish, and plants – particularly when the system was first set up. Construction of the system took about six weeks, with most materials consisting of consumer-grade hardware. The Engineering and Physics & Astronomy workshops were used to construct the various components of the system, with final assembly occurring where the system is currently on display: an indoor terrace overlooking Eldridge Commons. The main components of the system are a glass aquarium for the fish, equipped with a solids lift overflow, two media grow-beds for the plants, each equipped with a bell siphon, and a sump tank containing an electric pump. The total volume of the system is around 250 gallons, and it has a footprint of about 22 square feet. After the system has fully matured, operational management will largely consist of feeding the fish, occasional cleaning and harvesting, and adding water to compensate for evaporative loss.

While the system isn't optimized or intended for food production, it does demonstrate how aquaponics can be used for sustainable agriculture. Through this, I hope the aquaponics system can become a functional greenspace for Eldridge Commons, and catalyze community awareness, critical conversations, and engagement with broader social and environmental issues surrounding the current global food system. This research project was funded by the Halpern Engineering Design Fund and the Academic Division Summer Opportunity Awards.

Molecular Systematics and Taxonomy of a Low Abundance Cryptic Lineage of Balaenopterid Whale

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The taxonomy and evolutionary relationships among large baleen whales are a work in progress. Ambiguity in the evolutionary relationships among balaenopteroid whales (genera *Balaenoptera* + *Megaptera* + *Eschrichtius*), including rorquals (traditionally grouped in the clade Balaenopteridae), creates confusion for taxonomy. This is especially the case for medium-sized balaenopteroid whales, the Eden's whales (*B. e. edeni*), Bryde's whales (*Balaenoptera edeni brydei*), and a possible new taxon, the Gulf of Mexico (GoMx) Bryde's whale (*Balaenoptera* cf. *B. edeni*). Genomic tools are often used to resolve these relationships and provide clarity for improving taxonomy. However, previous genome-scale studies have had poor taxon sampling, particularly for medium-sized balaenopteroid whales. In this study, we used a novel method to isolate >3000 ultra-conserved elements from throughout the nuclear genome of all balaenopteroid taxa. We then used high-throughput methods to sequences these genome-wide regions. For my summer internship, I conducted phylogenetic analyses of these data. We found that Gulf of Mexico Bryde's whales represent a distinct lineage outside of the clade that includes the subspecies Eden's whales and Bryde's whales. This pattern supports previous findings based on mitochondrial data that showed Gulf of Mexico Bryde's whales as an independent lineage. Our results also show humpback whales (*Megaptera novaeangliae*) and gray whales (*Eschrichtius robustus*) are nested within a clade that includes all members of *Balaenoptera*. This indicates the genera *Megaptera* and *Eschrichtius* are not valid and should thus be renamed as species within the genus *Balaenoptera*. Furthermore, our results add evidence to support the clear paraphyly of Balaenopteridae (Eschrichtiidae is within Balaenopteridae). These issues in taxonomy must be resolved because accurate naming is a critical prerequisite for conservation strategies for endangered species.

Analyzing Programs with Dynamic Data and Control Flow

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Let's be honest—even the most skilled programmer makes mistakes, and nobody likes debugging. This is where program analysis comes to the rescue: it's a type of program that aims to analyze properties of other programs and predict their behaviors without running them. While it is provably impossible to have a perfectly precise analysis, a relatively robust and efficient analysis can contribute greatly to the creation of reliable, bug-free programs.

Our summer research focused on program analyses for higher-order functional programs. This type of program contain lots of dynamic data flow (what values affect each other?) and control flow (which line of code gets executed next?) that are deeply intertwined. It is commonly known that a program analysis that targets higher-order functional programs should consider the two in tandem.

However, in *Context-, Flow-, and Field-Sensitive Data-Flow Analysis using Synchronized Pushdown Systems*, a paper published in POPL 2019 (Principles of Programming Languages), the authors presented Boomerang SPDS, an analysis that analyzed data and control flow separately. They claimed that this separation would not affect their analysis' precision on functional-style programs. Since they didn't provide enough evidence to support this claim in the paper, we sought to assess the validity of their argument.

We designed a series of programs that exemplified common functional code and Object-oriented design patterns. To test whether the separation of data and control flow has an impact on analysis precision, we experimented on three pairs of analyses: Boomerang SPDS and Boomerang (Java alias analyses), kPlume and SetPlume (demand-driven functional analyses), and kADI and SetADI (forward-running functional analyses). Within each pair, one analysis has a higher level of separation between flow than the other. The results depicted that in general, the analysis with a higher level of separation has a lower precision on these programs. Thus, we concluded that the connection between data and control flow should be preserved in order to yield precise results when analyzing programs that contain highly dynamic data and control flow.