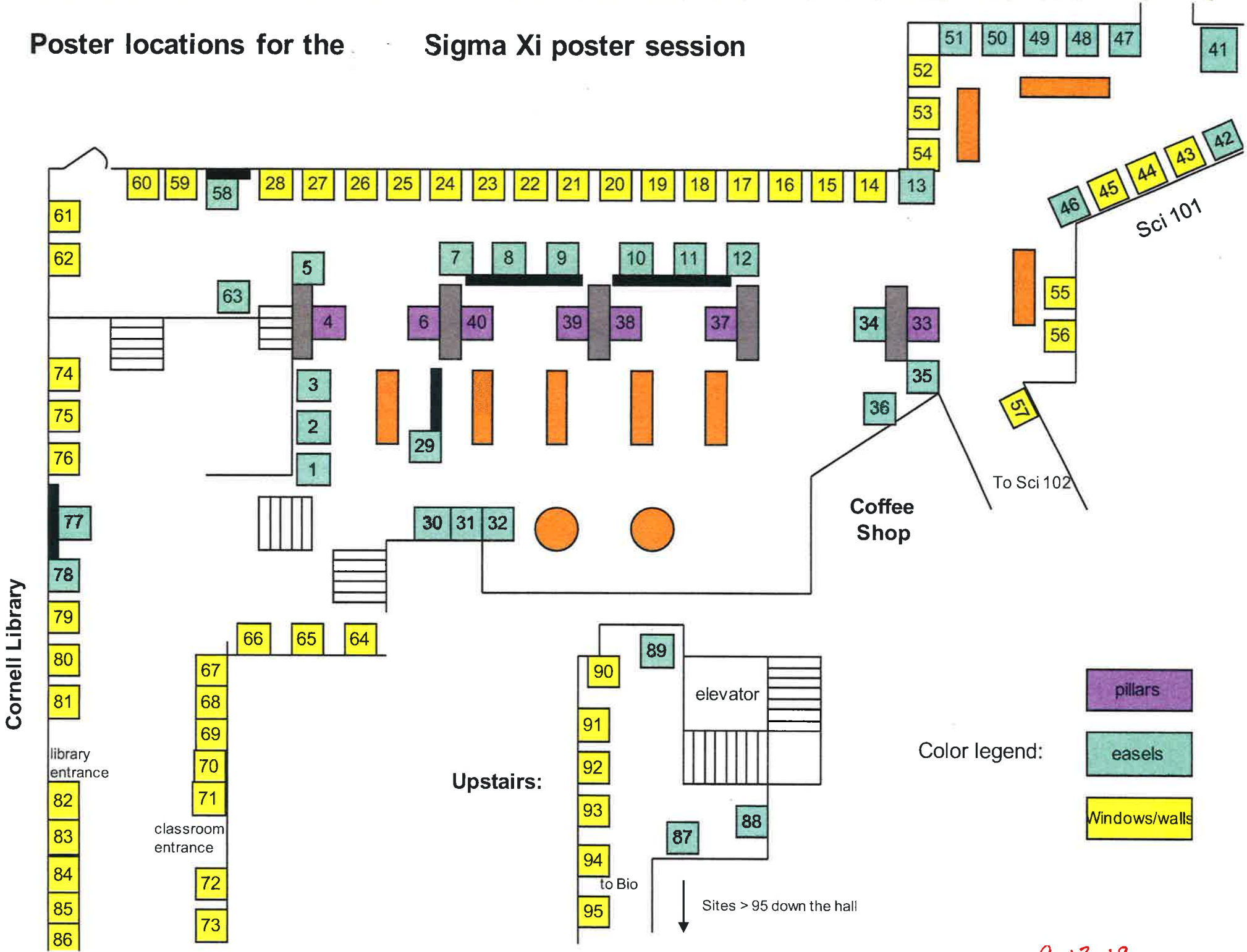
Sigma Xi Student Research Poster Session

13 – 14 September 2018

Eldridge Commons, Swarthmore College

Poster locations for the Sigma Xi poster session



9-13-18

Author(s)	Title	Field
Aaron Hersch	Characterizing the Orbital Dynamics of Protoplanetary Disks in Binary Systems	Astronomy
Erin Snoddy	The Search for Exoplanets at Peter van de Kamp Observatory Using the Transit Photometry Method	Astronomy
Vaughn Parts, Graham Doskoch	Massive Star X-Ray Analysis	Astronomy
Abigail Wong-Rolle, Reham Mahgoub	Interaction of Two Influenza A Matrix Proteins Critical to Viral Budding	Biochemistry
Ariana Yett, Samantha Nyovanie	Towards the crystal structures of VEGF and G4TERT	Biochemistry
Deondre Jordan	Biophysical efforts toward the structure of tandem DNA repeats linked to replication stress	Biochemistry
Emilie Morse	Identification of the unfavorable characteristics of 1A102R, 1AZCET, and 1AH92U antibodies against HIV	Biochemistry
Hyun Kyung Lee	Exploring Secondary Structures of SAT2 Centromeres	Biochemistry
Jeffrey Zhou	Characterizing a Quadruple Mutant in the CH103 HIV-1 bnAb Lineage	Biochemistry
Julia Morriss	An analysis of HIV antibody-virus co-evolution to guide vaccine design	Biochemistry
Linda Yingqi Lin	studies of telomeric G-quadruplex DNA in complex with a small molecule ligand as an anticancer	Biochemistry
Natalie Balbuena	Identifying Genes involved in C. Elegans Reactive Oxidative Species Stress Response	Biochemistry
Therese Ton	HIV-1 progenitor antibody mutant, and mutation of V1/V2 loops of HIV-1 Envelopes	Biochemistry

Andi Cheng, Jack Rubien	GapmeRs to Knockdown Aberrant RNA Accumulations in Prostate Cancer Cells	Biology
Calla Bush St George	E. Coli Universal Stress Protein A (UspA)	Biology
Cameron Tumey	Exploration of Asymmetrical Gene Expression within Ciona Intestinalis	Biology
Cedric Lary	Movement Among Mating Arenas Predicts Individuals,Äô Centrality In Some Social Networks	Biology
Dana Homer	Female Aggression in Bolitotherus cornutus	Biology
Elizabeth Lanphear	Linalool as a Potent and Reversible Anesthetic for Hydra	Biology
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Hanna Gutow	Predictive Factors for Forked Fungus Beetle Habitat Preference and Movement	Biology
Kathleen Carmichael	Muscles and motor neurons involved in the rolling response to nociceptive stimuli in Drosophila larvae	Biology
Lillian Fornof	Vigilance Behavior, Aggregation, and Habitat Distribution of the Red-Tailed Guenon (Cercopithecus ascanius)	Biology
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Madison Snyder Shantal Garcia	mechanisms involved in the heat shock response pathway in Arabidopsis thaliana	Biology
Moniher Deb	HSATII RNA Capture to Determine Sequence and Structure	Biology

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Ryan Stanton	Transfer of Antibiotic Resistance Genes in Swarthmore, PA	Biology
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Sophia Moody, Max Marckel	Gut Microbiome, Stress, and Fat in Rufous and Anna's Hummingbirds	Biology
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Tiara Tillis	for¬†the¬†cnidarian-Symbiodinium symbiosis: development of¬†the¬†yeast two-hybrid system to	Biology
Sumera Patel	Genetic Variation in Herbivory Resistance within *Arabidopsis* Populations	Biology
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Lucas Heinzerling, Judah Raab	Aluminum complexes of nitrogen-based redox-active ligands	Chemistry
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Caitlin Strachan	Mentoring Program for Pediatric Solid Organ Transplant Recipients	Clinical/medical research
Gabriel Meyer-Lee	Location-leaking through Network Traffic in Mobile Augmented Reality Applications	Computer Science
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Jessica Berg, Sam Shih	Dynamically Switching Transport Protocols with STRAP	Computer Science
Kei Imada, Liam Packer	Predicting Cluster Memory Usage for Adaptive Network RAM	Computer Science
Kelly Finke	Endogamous Pedigree Reconstruction using Identity by Descent	Computer Science
Kyle Richmond-Crosset	Vision Implementation of "Developing Grounded Goals through Instant Replay Learning"	Computer Science
Lizhi Guo, Effie Xu, Josh Geselowitz	Finding Equilibriums in Stochastic Games	Computer Science
Sophia (Fuhui) Lin	Distributed Private Stable Matchings	Computer Science
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Ercong Luo, Zane Meyer	Measuring 1-Axial Bend and Twist Using 4-Core Optical Fiber	Engineering

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Ke Wang	for Wearable BIS Home Monitoring Device	Engineering
Megan Strachan, Yi Fei Chang, Zachary Weiss	Deep Learning for Optimization of Fourier Ptychography	Engineering
Pemba Dorji, Temba Mateke	The Lorber Opentalk Project	Engineering
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Hao-Tong Yan	The Combinatorics of Splitting and Splittable Families	Mathematics
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Mikhal Yudien	test: Psychometric analysis and validation of the Penn Reading Assessment	Neuroscience
Alyssa Davis	Advancements and characterization of Low Energy Neutron Detector Array (Large LENDA)	Physics
David Robinson	'Dark Fluid' Cosmology	Physics
Gabriella Small	Flight mechanisms of the hawkmoth, Manduca sexta, after mass increase	Physics
Hariharan Srinivasulu	Particle Orbits in a relaxed Taylor state MHD Plasma	Physics
Jonathan Solomon	Assessing the Lasting Impact of an Introductory Physics for Life Sciences (IPLS) Course	Physics
Katie Gelber	Making a Sun in a Bottle	Physics
Nicholas Anderson	Simulating the Taylor State as an MHD Plasma	Physics
Tristan Cates, Brian Jenike	The Jamming Transition with Varying Pin Lattice Geometry	Physics
Marie Wild	Social Media and Self Completion	Psychology
Maya Smith, Jason Guadalupe, YongJoon Shin	Treatment of PTSD: An Animal Analogue of Exposure Therapy	Psychology
Sadie Camilliere , Amanda Izes	Licensing conditions of singular "they"	Psychology

Seetha Davis	Children's Understanding of Disease Contagion & Causation	Psychology
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HSATII expressing cancer cells display persistent RNA:DNA hybrids

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Human Satellite II (HSATII) is a transcriptionally silent pericentric satellite found on a number of chromosomes. However, in some cancers, the repressive methylation modifications on the HSATII DNA are lost, and HSATII RNA is expressed and accumulates in *cis* (Hall et al., 2017). Both these cancer cells and healthy human cells we have engineered to exogenously express HSATII display marks of chromosomal instability, suggesting that the presence of HSATII RNA may cause or exacerbate some of this observed instability. Building on previous results showing that satellite transcripts can form RNA:DNA hybrids, we explore the possibility that some of the observed defects may be a result of persistent RNA:DNA hybrid formation from HSATII transcripts in the nucleus. Optimizing conditions to visualize RNA:DNA hybrids and HSATII RNA in U2OS (osteosarcoma) cells using fluorescence microscopy, we show that RNA:DNA hybrid signal colocalizes with HSATII RNA in cells with high levels of HSATII transcripts, and present preliminary data suggesting a possible cell-cycle dependent expression pattern of HSATII RNA in U2OS cells. These results provide evidence of the RNA:DNA activity of HSATII RNA, and gives us a window to explore possible hybrid-mediated DNA instability in future experiments.

Solving Complete Splines: An Algorithmic Approach

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Over the course of the summer of 2018, I, under the guidance of Prof. Drellich, produced work which strongly suggests a novel, new semi-algorithmic approach to generating valid solutions to complete algebraic splines over any general ring.

We believe that this algorithm is unique in that, unlike others that have come before it, when properly applied this algorithm may produce all solutions to any complete spline, if indeed any exist. And, if not, then the absence of any solutions may also be determined with absolute certainty.

Effects of elevated glucocorticoids on female choosiness in Cope's gray treefrog

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Choosing a mate is a critical life history decision for many species. Selecting the right mate can improve the fitness characteristics of offspring and ensure the continuation of unique genetic lineages. Previous research has indicated that elevated stress hormones, or glucocorticoids (CORT) play an important role in the manifestation of behavioral phenotypes, such as in social and parental behavior (Sapolsky, 1982, Nunes et al., 2010). It has also been demonstrated that levels of stress hormones can modify selectivity of mate choice behaviors (Vitousek and Romero, 2013, Davis and Leary, 2015). Typically, females control mate choice, with males often performing some sort of behavioral display to attract females. In Cope's gray tree frogs (Hyla chrysoscelis), females prefer male vocalizations that are longer and more frequent and choose between males by performing phonotaxis (Ward et. al 2013). Using wild caught Cope's gray tree frogs, we assessed female phonotaxis behaviors after experimentally manipulating levels of circulating CORT. We assessed whether female mate choice behaviors, specifically their preferences and commitment to their initial mate choice, are influenced by circulating levels of CORT.

Simulating the Taylor State as an MHD Plasma

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Taylor state plasmas are both practically and theoretically interesting, being a strong candidate for fusion energy as well as providing the opportunity to probe the fundamental physics of plasma. Taylor state experiments, however, are expensive, time-consuming, and cumbersome. This summer I created a robust simulation of the Taylor state evolution, to provide researchers with a relatively easy and efficient way to examine the potential results of their experimental configurations without the hassle of the physical apparatus.

Identifying Genes involved in *C. Elegans* Reactive Oxidative Species Stress Response

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Membranes are found in every cell of every living organisms. The fatty acid tails of the PLs are what make them a set of incredibly diverse molecules. With methylations and desaturations, the diversity created is what gives the membrane its ability to adapt to endogenous and exogenous factors. Reactive oxygen species, such as superoxide radicals and hydrogen peroxide, are produced normally and intracellularly from normal metabolism in the mitochondria to cause oxidative stress and aging. Thus, ROS can serve as signaling agents signals to help induce the endogenous defense mechanisms membranes already have with stress including stress resistance, longevity, and mitohormesis. The concept of mitohormesis proposed that boosting ROS levels activates a response to stress that over-activates the cells own protective mechanisms. Considering the available evidence in other research, its is very much possible to suggest that ROS combined with mitohormesis can have positive roles when combined with the right ROS. However, to further analyze this process, we must begin with a fundamental understanding as to how the lipids in membrane change with stress response. Using the model organism *C.* elegans, 13C isotope labeling, lipid separation, and RNAi processes and technologies, we are able to closely look at the turnover rates and phospholipid composition of the worms' membranes. Mitohormesis suggests that the lipid turnover rate will increase as a result of the membrane replacing its damaged lipids with new ones. However, our results indicate otherwise. While the turnover rate does theoretically increase with certain fatty acid pathways, the phospholipid composition doesn't match for the RNAi knockouts related to membrane sensitivity. Thus, this suggests that rather than the membrane repairing itself, that it is remodeling itself to become more stress resistant.

The acquisition of self-sterility in a hermaphroditic tunicate

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Tunicates, more specifically ascidians, offer an opportunity to investigate the mechanisms underlying adaptation. Two closely related ascidians, *Corella inflata* and *Corella willmeriana* allow us to specifically explore evolutionary changes in reproductive strategies. Ascidians are usually hermaphroditic and self-infertile. Strikingly, *C. willmeriana* appears to have conserved this ancestral trail, while *C. inflata* has acquired the ability to self-fertilize. There exists a known mechanism for self-sterility in *Ciona Robusta* that involves two pairs of hyper-variable allorecognition proteins – s-Themis and v-Themis that are associated with the sperm and vitelline coat respectively. Here we show that these genes are present in both *Corellid* transcriptomes but the acquisition of self-fertility in *C. inflata* is associated with the loss and potential degeneration of some paralogs. We performed alignments between the *C. Robusta* Themis genes and orthologs from the *Correlid* transcriptomes. We found that *C. willmeriana* may possess an extra v-Themis paralog whereas *C. inflata* may have lost one. Additionally, we found a substantially lower level of sequence conservation in the *C. inflata* orthologs. The apparent conservation of self-sterility genes in *C. inflata* suggests that the Themis genes are pleiotropic. We have begun long-read sequencing of *Correlid* genomic DNA to improve genome assembly and confirm our Themis ortholog predictions. We expect that our findings will provide insight into the evolution of hyper-variable genes in association with loss of traits involving allorecognition.

Transfecting Normal Human Cells to Express Human Satellite 2

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Human Satellite 2 (HSATII) is a tandemly repeated noncoding DNA sequence found near the centromere (pericentromere) of many human chromosomes. HSATII RNA is abundantly expressed in numerous cancer types and not in normal, healthy cells. While past studies suggest that HSATII may be linked to genomic and chromosomal instability, its function remains unknown. In this study, we were interested in inducing normal cells to express HSATII by transfecting a randomly integrating HSATII expression vector into normal human fibroblast cells. We then examined the effects of HSATII expression in normal cells following lipid-mediated transfection of HSATII, alpha satellite and empty vector controls. Results indicate that while non HSATII-transfected cells displayed little to no HSATII expression, HSATII RNA accumulates in 1-2 nuclear foci in approximately 14% of HSATII transfected cells. However, higher levels of HSATII RNA expression (~12%) was present in our empty vector transfection control, requiring further analysis of the variation of HSATII expression levels upon lipid-mediated delivery.

Dynamically Switching Transport Protocols with STRAP

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Today's Internet is limited in its modern uses because it uses only two ways to access the internet from the operating system, both of which were built in the 1980's. At that time, no one could have foreseen the changing needs of modern Internet applications.

Newer transport protocols, or rules that govern communication across the Internet, have been developed to provide services that better fit the needs of today, such as optimizations for smartphones, security, video streaming, and Wifi. However, they are not widely used because to communicate in a new protocol, talking hosts must agree on the protocol a priori, which introduces significant latency. So for the past 40 years we have been entrenched in using the same two protocols.

The system we built, STRAP, allows pairs of hosts to switch to any protocol based on application preferences without adding significant latency. The mechanism we made to change protocols starts off a conversation in one of the two commonly used protocols, and simultaneously sends a small message conveying other protocols that they would want to use. If the other side agrees, the protocol switches. This mechanism relies on a small time lag because if the other side doesn't have the protocol switching mechanisms, the communication goes on as normal with a small latency and minimal overhead. But if both sides agree to change protocols, they can also do so with no significant latency because the protocol preference message acts as a substitute for the first message in the conversation.

The experiment we held to test STRAP tested the time it took for a protocol preferences message to be received and stored properly, depending on its destination. We used this information to put a delay between sending the protocol preference message and sending other messages that are dependent on the protocol preference message. We found that a delay was necessary, and that the correct delay depended on the locations of the two sides of the conversation.

Characterization of metabolism of the *E. Coli* Universal Stress Protein A (UspA)

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Universal stress proteins are found in almost all archaea, most bacteria, plants, and in schistosomes. Universal stress proteins (USPs) are expressed almost anytime an organism experiences stress, such as high heat, carbon starvation, and UV damage. They are universal due to the universality and lack of specification in their expression. UspA is found to be phosphorylated during stress and this phosphorylation occurs on at least two serines and/or theronines. (UspA is made of 144 amino acids, 18 of which are serines and threonines.) To test which serine and/or theronines are involved in phosphorylation, mutants strains of uspA in which the serines and theronies are converted to alanine and aspartic acid were created. Alanine is unable to be phosphorylated while aspartic acid is used as a surrogate of a negatively charged group resembling phosphate.These plasmids were placed inside two types of E. coli, each with a difference chromosomal background, uspA+ and Δ uspA. Previous research has shown that different mutants metabolize different carbon sources/sugars differently. To measure differences in metabolism, 96 well BiOLOG plates analyzed ability and rate of metabolism of mutant strains. So far, six mutant strains have been identified to have less than a 10 percent variance in metabolism. These strains show an inability to metabolise formic acid for the first 24 hours but not the second 48 hours after plating. This metabolic pattern is mirrors diauxic growth, a possible effect of lack of phosphorylation in uspA. All identified strains have been transformed to alanine, suggesting it is more damaging to uspA to be unable to be phosphorylated than to be permanently phosphorylated. In future experiments, I will conduct stress experiments with the mutant strains and transfer the 36 plasmids to three new backgrounds; typA, a kinase that is possibly responsible for the phosphorylation seen in uspA, and qseB and qseC, transcription factors that work together to promote uspA.

Muscles and motor neurons involved in the rolling response to nociceptive stimuli in *Drosophila* larvae

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Pain is a pervasive and negative experience that affects many organisms. Understanding the molecular and neural mechanisms underlying the perception of pain could provide much insight into what causes pain and how to treat it. The *Drosophila* (fruit fly) is easily manipulated genetically and has a larval body wall that is thoroughly mapped out. As a result, the fruit fly is an excellent model to study perception and response to pain. When touched with a heated probe (a nociceptive stimuli), fruit fly larvae display a unique and stereotypic "rolling" behavior. Although the layout of the larval body wall and the number of muscle fibers and motor neurons that innervate them are known, it is unclear which motor neurons and muscles are needed to perform the roll (and moreover, the order in which they are used). The Gal4-UAS system was used to determine which muscles and motor neurons are most important for this rolling behavior. The system drove the expression of Kir2.1, a neuronal inhibitor, in specific motor neurons. With particular motor neurons, and therefore muscles, not functioning properly, larvae were poked with a hot probe and the characteristics of their rolling response was observed. Eight Gal4 lines were crossed with UAS-Kir2.1 and produced viable and observable larvae. Of those Gal4 lines, two particular lines involve muscles that seem important for this rolling behavior. Inactivation of muscle 23 in line 43G11 and collectively muscles 6, 7, and 12 (and to a lesser extent 1 and 2) in line 22B11 each result in more than 75% and 60%, respectively, of larvae showing either a delayed roll (i.e. a roll that takes more than 1 second to complete after responding to the heated probe) or no roll at all. The muscles in these lines run perpendicular and parallel to the anterior-posterior axis of the larva, respectively, and are situated either laterally or more ventrally in the larval body wall, suggesting that there is a complex and multidirectional control of the rolling behavior. Once the exact muscles involved in the rolling response are determined, the synaptic connections of these motor neurons can be studied, potentially revealing the more general neuronal circuit involved in rolling. Elucidating the neural system underlying pain through research of responses to nociceptive stimuli in fruit flies has more general implications for understanding pain in other organisms.

ADMIT: Advanced Decision Making in Immersive Training

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Previous studies in the field of human-computer interaction (HCI) have demonstrated that virtual reality (VR) can affect empathy of participants by allowing them to take on new roles and perspectives that were previously unavailable to them in the real world. Furthermore, it has also been shown that ethical decisions can be more difficult when participants must perform a deliberate physical action, such as flipping a railroad switch to trade one life for many lives. The Advancing Decision Making in Immersive Training (ADMIT) study seeks to examine how immersive VR technologies can create realistic situations in which users can exercise moral judgment. This study is guided by theories of Presence, which pertains to how "immersed" a user is in a virtual environment and can be used to evaluate the extent, and type, of immersion a participant experiences. In the forthcoming study, we will investigate both how different levels of immersion in VR affect a participant's moral decision-making process, stress levels, and emotional reactions. This is will be accomplished by modulating various elements of the virtual environment, such as avatar fidelity, proximity to consequences, perspective, and physical effort related to a decision. To support this experiment, a virtual reality scenario was developed, replicating the trolley problem, a classic ethics thought experiment. The scenario utilizes the Unity game engine, the HTC Vive head-mounted display, and includes animated virtual characters, a physical switch lever requiring action on the part of the participant, and a moving trolley, which presents physical danger to the virtual characters and moral consequences for the participant.

Developing Methods for Tracking Sonothrombolysis Progression

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Sonothrombolysis is a process in which blood clots are dissolved using sound. To elaborate, intravenous micron-sized bubbles are manipulated using ultrasonic frequencies. This process, known as acoustic cavitation, produces violent oscillations in the bubbles to create microsecond-long periods of extreme temperature and pressure, disturbing the microbubbles in such a way that breaks down the fibrin strands of a blood clot. During the Summer of 2018, we developed methods for tracking clot dissolution progression using pressure as the indicator. We aimed to measure a noticeable pressure drop over time in the system that would indicate that the clot is being dissolved. Microbubbles in solution are flooded through a tubing system clogged with a blood clot, simulating a clogged blood vessel. An ultrasonic wave is applied to the system with the acoustic focal region encasing the blood clot. Microbubbles flowing to the clot are insonified and undergo acoustic cavitation, ripping apart the clot mesh as they oscillate through the clot strands. Pressure in the system is measured and recorded to detect improvement in flow over time. Currently, we are working on improving the system's pressure sensor sensitivity, our human plasma clot-making procedures, and the tubing system's leaks.

Finding Nothing: The Deployment of GapmeRs to Knockdown Aberrant RNA Accumulations in Prostate Cancer Cells

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Human satellite II (HSATII)—a high-copy, tandem-repeat DNA satellite sequence—exists in the pericentromeric heterochromatin of many human chromosomes. While maintained transcriptionally silent in normal cells, HSATII becomes de-repressed in many cancers, leading to HSATII RNA expression that results in the formation of large, nuclear HSATII RNA foci (Hall et al., 2017). Methyl CpG binding protein 2 (MeCP2), an intrinsically disordered protein that both activates and represses genes, has been observed to colocalize with these HSATII RNA foci as aberrantly large nuclear bodies in cancerous cells (Ausió, de Paz, & Esteller, 2014; Hall et al., 2017). As MeCP2 regulates gene expression, changes in its distribution may change the behavior or profile of a cell. In order to analyze these effects, we have performed a knockdown of endogenous HSATII RNA expression in prostate cancer (PC3) cells. HSATII expression was knocked down with antisense locked nucleic acid (LNA) GapmeRs, which behave as normal nucleic acids do but have conformationally locked ribose rings (Sarma, Levasseur, Aristarkhov, & Lee, 2010; Exiqon, 2013). This stability gives LNAs greater affinity for their base pairs (Sarma et al., 2010). When the LNA/DNA oligo binds to its complementary RNA sequence in the cell, the resulting DNA: RNA heteroduplexes recruit RNase H, an endogenous enzyme that catalyzes the cleavage of the RNA in the complex (Exiqon, 2013; QIAGEN, n.d.). We demonstrate that GapmeR-mediated knockdown of HSATII RNA results in a significant reduction of nuclear HSATII RNA in PC3 cells. Further, in order to analyze MeCP2 protein distribution upon knockdown of HSATII RNA, we optimized the procedure for RNA/antibody co-detection. Future work will analyze the levels and distribution of MeCP2 protein upon HSATII RNA knockdown and utilize qPCR as an additional quantitative method to analyze the amount of GapmeR-mediated HSATII RNA knockdown. As these twin efforts develop, they will enable us to gather a more complete picture of these protein-RNA interactions and its possible implications on cell behavior.

Group 13 Complexes of Nitroxide Ligands: Novel Redox-Active Complexes of Al, Ga, and In

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The development of aluminum complexes implementing redox-active ligands has the potential to significantly broaden the reaction chemistry of the element through expansion into redox-based chemistries. We report the synthesis and use of aluminum coordination complexes through the implementation of redox-active nitroxide based ligands. Specifically, we present our work on the $N(benylNO)_3Al$, $(^{tBu}pyNO)_2AlCl$, and $(^{tBu}pyNO_2)AlCl$ systems where the nitroxide ligand complex extends multi-electron redox chemistry to the complex. Characterization including ^1H NMR spectroscopy, X-ray diffraction, and cyclic voltammetry data will be presented in addition to our preliminary reactivity studies and first experiments of catalysis.

Advancements and characterization of Low Energy Neutron Detector Array (Large LENDA)

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The study of charge-exchange reactions is important to understand the spin and isospin structure of nuclei, which allows researchers to improve nuclear models. An upcoming experiment at the National Superconducting Cyclotron Laboratory will use the $^{12}N(p,n)^{12}O$ charge-exchange reaction to study the structure of ^{12}O. This is the first (p,n) experiment on a proton-rich unstable nucleus, and results will provide techniques to study heavier proton-rich systems, ultimately up to the region near ^{100}Sn. The reaction kinematics will be reconstructed from the energy and angle of the ejected neutron. The neutron is detected by the Low Energy Neutron Detector Array (LENDA), a set of twenty-four 30 cm-long plastic scintillators. To improve neutron detection efficiency, large 150 cm-long plastic scintillators will be added to LENDA. To ensure uniform detection capabilities across all new detectors, several characterization tests were carried out. These included light leak reduction, attenuation length measurement, optimum bias determination, gain matching, energy/position calibrations, and timing resolution measurements. Methods and results of the characterizations will be discussed.

This work is supported by the US National Science Foundation PHY-1062410, PHY-1430152 (Joint Institute for Nuclear Astrophysics Center for the Evolution of the Elements), and PHY-1565546.

Children's Understanding of Disease Causation & Contagion

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Although four-year olds have a basic understanding of sickness -- they know that germs make one sick and thus should be avoided -- their understanding is only symptom-deep and not truly causal (Solomon & Cassimatis, 1999). For example, children of that age expect all coughs to be contagious and all stomachaches to be non-contagious, regardless of the causes of those symptoms (Solomon & Cassimatis, 1999). Prior research shows that comparison helps young learners understand relational concepts, including causal relations. Here I ask two questions: Can comparison help young children learn causes of contagion? What kind of comparison -- between similar or different pieces of evidence -- works best for young children? Children (N=26) were presented with a comparison learning task, in which they either compared similar (high similarity) or different (low similarity) stories to understand how germ- and event-caused symptoms create contagion or not. During the test phase, children were asked to predict whether germ- and event-caused rashes and sneezes would be contagious. Participants in the low similarity condition performed better overall and on the rash trials than participants in the high similarity condition, but groups performed at the same level for the sneeze trials. Reported understanding of contagion is consistent with prior research without comparison learning. Causal understanding of contagion is difficult and comparison may facilitate greater understanding when that comparison is stronger.

HSATII RNA Capture to Determine Sequence and Structure

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Human satellite II (HSATII) is poorly understood, but in recent years, more information has been gathered about its significance. It is often misregulated in common cancers and can further promote epigenetic changes, which compromises the rest of the genome and causes non-coding RNA to be expressed. Nuclear HSATII RNA foci have shown to amass proteins, such as MeCP2 and Sin3A, that deal with RNA-binding regulatory processes. Such protein complexes can bind to HSATII RNA foci within large nuclear bodies and in the cytoplasm during mitosis (Hall et al., 2017), termed "cancer associated satellite transcript" (CAST) bodies. Very little is known about the exact physical structure of the HSATII RNA foci, thus sequencing would allow insight about the full diversity of HSATII RNA sequences (Ting et al., 2011). Different families of HSATII RNA variants have been distinguished, but not all are expressed; thus, it is of high interest to figure out which of the variants are expressed in prostate cancer (PC3) cells. Of particular interest is the sequence on chromosome 7 that is present in Sat2 A2 and B families, but absent in Sat2 A1.

During this summer, I developed an RNA "pull down enrichment" technique with magnetic beads and successfully sequenced RNA directly using the new MinION device, which uses nanopore technology. The pull down process that I worked on involved covalently bound oligo(dT25) on a biotin bead, which hybridized to poly(A) RNA transcripts and was pulled out of a cell lysate mixture, using streptavidin (high affinity to biotin) coated metal Dynabeads. I used the metal Dynabeads' magnetic potential to separate roughly 250ng of pure polyadenylated mRNA from 25mg total *Arabidopsis* RNA (New England Biolabs, Inc.). I then prepared a library and sequenced the target RNA using the MinION device. After mapping and BLASTing the full-length reads, it was found that the sequences matched multiple well known genes in *Arabidopsis*, our organism of interest in this pilot study.

The MinION is the only device that is highly portable and offers NextGen Sequencing abilities while using nanopore technology. This is the *first time* that Swarthmore College has been able to engage in direct RNA sequencing using such high leveled technology in its own facilities. The MinION passes an ionic current through protein nanopores and measures the changes in current as biological molecules - like RNA and DNA - pass through the nanopore (Oxford Nanopore Technology). The combination and changes in current measured are used to reliably identify specific bases.

The final intent is to directly capture HSATII RNA from PC3 cells; however, due to the difficulty of direct sequencing RNA, my goal is adapt the pull down protocol I troubleshooted in the pilot study by first poly-adenylating the RNA of interest from PC3 cells in order to pull the target RNA down for sequencing. Future studies can focus on understanding the function of HSATII; additionally, by learning of its sequence, and thus its structure, we will be able to identify binding sites and understand how HSATII RNA sequesters proteins such as MeCP2, Sin3A and other transcriptional regulators.

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The Lorber Opentalk Project

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The Lorber Opentalk Project is an ongoing research project that has been carried out by students of Swarthmore College each summer since 2015. The purpose of the project is to develop a hands-free, voice-activated telephone which allows a client to communicate with specific people without the need to learn the use of the device.

The project was built around the needs of a specific client who has several disabilities including blindness and the inability to learn to do new things. The client's primary guardian is his father, and thus a system was designed to allow communication between the two. Since the client has trouble learning new instructions, the system had to be created so that it detects whatever he does when he wants to speak to his father. When he wishes to talk to his father he says "Dad?", as one would normally do if one's father was nearby. Thus a system had to be developed such that the only input from the client would be him saying "Dad?"

In the summer of 2017, a system was designed that served this purpose but it had several drawbacks. It was made of various electronic components, including three microphones, two sets of speakers, two Raspberry Pi single board computers and a wireless landline telephone put together in a shoe box. The system was delicate, massive and complex.

The goal for the summer of 2018 was to make the current system better. It had to be smaller, cheaper and easier to use. The new device, called the Beta I, had many improvements over its predecessor which stemmed from an early change in hardware. Rather than use a landline, a cellular GSM module was used. This is essentially a phone on a single PCB that can be programmed. By pairing this with a Raspberry Pi Zero, a tiny $10 microcontroller, the size and complexity of the entire system was significantly reduced.

Over several weeks, the system was eventually made small enough to be battery powered and still comfortably fit in a pocket. Additionally, the hotword detection accuracy was improved using several methods, including factoring in the frequency with which the client says "Dad?" before sending text messages. Beta I is currently running successfully and reliably at the client's house. Moving forward, we plan to make the system completely portable so the client will also be able to use the device outdoors.

Coupling particle-impact voltammetry with UV-Vis spectroscopy to monitor silver nanoparticle aggregation

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Engineered nanomaterials (ENMs) have been increasingly used over the past few years for a variety of medical and commercial applications. With their increased use, it has become more pressing to study them in detail to understand their environmental and biological effects. ENMs can undergo many transformations, including aggregation and surface adsorption of small molecules and proteins. Silver nanoparticles (AgNPs) serve as a good model ENM for the development of new analytical tools capable of studying these transformations. We are developing a voltammetric technique to monitor aggregation of AgNPs. The technique combines particle-impact voltammetry and UV-Vis detection. Particle-impact voltammetry is an emerging electrochemical technique that involves the impact of an ENM at an ultramicroelectrode, resulting in a measurable change in the current. Coupling this technique with kinetic UV-Vis studies allows us to correlate changes in particle-impact current transients to the formation of AgNP aggregates. Offline studies of particle-impact voltammetry and UV-Vis will be presented, along with preliminary data from the combined detection scheme.

HSATII integration induces RNA expression and MeCP2 aggregation in normal human cells

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The Central Dogma of Biology states that DNA is transcribed into RNA which is translated into a protein product. However, Human Satellite 2 (HSATII) is a tandemly repeated DNA sequence which does not code for protein product. HSATII has been found to be overexpressed in many cancer cell types, but never in normal human cells. In specific cancers, accumulations of HSATII form nuclear bodies, pulling regulatory proteins off their target sites. We are especially interested in the regulatory protein MeCP2 which is sequestered by the aberrant RNA. Previously, Jessica Malisa '19 and I transfected primary human fibroblast cells to ectopically express HSATII. My goal this summer, therefore, was to analyze the stably transfected cells to observe what happens to normal human cells which are made to express HSATII. Specifically, I investigated the integration site of the transfection construct into the DNA, looking for location(s) and insert copy number in addition to the proximity of aberrant accumulations of HSATII RNA. I also studied accumulations of MeCP2 in the cell nuclei. I observed that, on average, large amounts of the construct is integrated into the genome twice and that these sites are colocalized with HSATII RNA accumulations. I also observed many nuclear accumulations of MeCP2.

Modeling of mechanical interactions between echo-contrast agent microbubbles and thrombi

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We surveyed several variations and implementations of mathematical and computational models of the Rayleigh-Plesset equation for radial oscillation of echo-contrast agent microbubbles under an ultrasound wavefield. The presumed mechanism by which the microbubbles move through the thrombus is acoustic cavitation, aided by acoustic radiation force in the absence of flow. Taking into consideration radiation force, other effects proper of fluids under the action of sound waves, such as streaming, and disregarding damping and shell thickness, we were able to develop a working, simplified model of the mechanical interactions between the microbubbles and the blood clot. The authors hope for a simulation of the internal cavitation of the microbubble through the blood clot.

Endogamous Pedigree Reconstruction using Identity by Descent

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As DNA sequencing decreases in cost and increases in popularity, more and more genetic information for individuals and families becomes accessible; still, however, it is often impossible to obtain genetic information for an entire family tree, especially if the tree extends many generations back in time. Since it is often useful for biologists to examine large, complete pedigrees – such as when studying disease inheritance – a number of algorithms have been created to fill these gaps by reconstructing ancestral genotypes using estimates of the sources of known, sequenced descendants' genotypes. But many of these algorithms fail when working with complicated pedigrees, such as pedigrees that involve inbreeding, cross-generational marriages, or remarriage. When working with endogamous pedigrees – pedigrees marked by a close sharing of DNA due to the practice of marrying within the same ethnic, cultural, social, religious or tribal group – all of these complications are common. Our endogamous pedigree reconstruction algorithm, therefore, is designed to take these factors into account, allowing users to work both with typical pedigrees and more complex, endogamous pedigrees. This algorithm allows biologists to better gain insights from these genetically unique populations which can inform studies of rare traits and diseases that are disproportionately expressed in endogamous populations. Our motivation for this project comes from our collaboration with UPenn biologists Maja Búcan and Rachel Kember, who are studying inheritance patterns of bipolar disorder within an Old Order Amish pedigree.

Vigilance Behavior, Aggregation, and Habitat Distribution of the Red-Tailed Guenon (*Cercopithecus ascanius)*

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Predation risk drives the adaptations of physical and behavioral adaptations within prey species. We observed the vigilance behavior and alarm calling of a social prey species, the red-tailed guenons (*Cercopithecus ascanius*) of Issa Valey, Tanzania, in order to determine the perceived risk of predation throughout the monkeys' habitat. The purpose of this research is to develop a thesis examining the spatial distribution of predation risk as it relates to habitat utilization, habitat type, and aggregation. With preliminary data, we tested two hypotheses and began exploring how habitat utilization and anti-predatory behaviors are distributed within the guenon's habitat through spatial visualizations. We expected to find that individuals group closest together in areas of greater perceived risk and furthermore that these areas would be more open habitat types, which leave the monkeys more exposed to one of their most popular predators, birds of prey. Our results confirm our hypotheses and suggest that locations within the guenon's habitat have greater perceived predation risk which may further impact habitat utilization and aggregation within those regions.

THE COMBINATORICS OF SPLITTING AND SPLITTABLE FAMILIES

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ABSTRACT. A set A is said to *split* a finite set B if exactly half the elements of B (up to rounding) are contained in A. We study the dual notions: (1) a *splitting family*, a collection of sets such that any subset of $\{1,\dots,k\}$ is split by a set in the family, and (2) a *splittable family*, a collection of sets such that there is a single set A that splits each set in the family.

We study the minimum size of a splitting family on $\{1,\dots,k\}$, using a variety of computational and theoretical techniques to calculate new values and some theoretical bounds. We also study the structure of splitting families of minimum size, and as a result we find the exact value of the minimum size of special types of splitting families.

Next, we investigate splittable families that are in some sense just on the edge of unsplittability. First, we study splittable families that have the fewest number of splitters, giving a complete characterization in the case of two sets, and computational results in the case of three sets. Second, we define the *splitting game*, and study splittable families for which a splitter cannot be found under adversarial conditions.

Identifying the regulatory mechanisms involved in the heat shock response pathway in Arabidopsis Thaliana

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High temperatures can cause proteins to denature and unfold. This loss of structure in proteins due to heat stress consequently leads to a loss of function. Heat Shock Proteins (HSPs) are proteins that refold misfolded proteins after a heat stress in order to restore function. HSP production is controlled through a tightly regulated process known as the heat shock response (HSR). In order to better understand the various types of regulation that control the heat shock response pathway, we looked at the HSP production of mutant *Arabidopsis thaliana* plants with the hopes of cloning genes that contribute to HSR regulation. To be able to quantify the HSR in plants, we used a GFP reporter gene system that caused the plants to fluoresce in response to heat stress. A special microscope known as the Rootscope allowed us to use the fluorescence of GFP to quantitatively visualize the HSP production dynamics of hundreds of *Arabidopsis* roots over a 12 hour period after a heat shock at 37°C. Through this process we identified and individually transplanted individuals that displayed an abnormal stress response to heat out of a mutant mapping population. 50-100 individuals have been isolated for our respective mutants for Next Generation Sequencing. DNA Sequencing data will permit us to identify the causal genes which will then allow us to investigate their functions in relation to HSR regulation.

Making a Sun in a Bottle

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The Swarthmore Spheromak Experiment (SSX) lab studies hydrogen plasmas in the hopes of someday creating hydrogen fusion. Fusion, unlike nuclear fission, is the process of combining smaller elements to produce slightly heaver elements, which produces large amounts of energy as a byproduct. This process powers our sun and countless other stars, and has potential applications from powering cities to spaceships, without producing any harmful radiation in the process. However, fusion has yet to be achieved on earth, largely due to the high temperatures, high densities and relatively long lifetimes that are required for fusion to take place. The SSX lab studies such plasmas with the goal of increasing temperature and lifetimes to one day create a pellet of hydrogen plasma that could be compressed to initiate a fusion reaction.

We studied the electron temperatures in our plasma by analyzing the ultraviolet radiation emitted at two different wavelengths, C_{III} *97.7 nm* and C_{IV} *155 nm*, which are produced by carbon impurities within the hydrogen plasma. The intensities at those wavelengths are measured using a vacuum ultraviolet monochromator. We know that the C_{III} *97.7 nm* line is more likely to be present in colder plasmas, while the C_{IV} *155 nm* is more likely to be present in warmer plasmas. Thus, we average the intensity of the lines over several shots and apply a smoothing function to eliminate any high frequency noise and then take the ratio of the two lines. The ratio of the carbon lines can be related to the electron temperature using a graph produced by a prismSPECT computer simulation. The graph itself is actually a series of curves that relate the carbon line ratio and electron temperature depending on the plasma's density, which is also measured, and found to be relatively consistent between runs.

Over the course of the summer, we found that our current experimental setup was insufficient to create temperatures high enough for long lifetimes and potential hydrogen fusion. A likely theory for this result is that we recently replaced our wind tunnel with a tungsten coated copper flux conserver, in the hopes of minimizing the amount of impurities entering into the plasma. However, we suspect that our tungsten coating is actually quite porous and absorbs many impurities that are then released once the plasma enters the wind tunnel, effectively cooling electron temperatures.

Data Acquisition System for Physics-Based Robot Obstacle Traversals

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Many applications for mobile robots require robots that can traverse complex three-dimensional terrain, but the geometry-based motion planning systems commonly used for mobile robotics do not perform well in complex terrains. In contrast, animals that live in highly cluttered environments primarily use mechanical sensing to guide their movement through obstacles. Inspired by these animals, our goal is to develop a method of navigating through obstacles based on the physical interaction between the robot and the obstacle. We developed an autonomous data collection system to move a two-wheeled robot through the space of possible positions relative to a pillar and measure the forces acting on the robot at each position. Using this data, we developed a model to determine the robot's position based on the forces and torques it senses. Our model provides a fairly accurate prediction of the position of the obstacle. As we refine this model, it will form the foundation of a physics-based motion planning system.

Designing the Current Source for a Wearable Bioimpedance Spectroscopy System

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The aim of this project was to design a wearable version of Professor Delano's portable bioimpedance spectroscopy system that detects symptoms of congestive heart failure in a client. The first phase of this project involved designing a current source with maximum possible output impedance and smallest circuit size. After researching different current source topologies from scholarly articles, computer simulations were conducted to test for output impedance and shortlisted topologies were constructed on a breadboard. Two topologies were finalized to be tested in a PCB. The second phase was to build the PCB to test the current sources and assess performance for the system. A PCB was successfully designed on AltiumTM and consists of the current sources, a new microcontroller, and various other integrated components.

Treatment of PTSD: An Animal Analogue of Exposure Therapy

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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 to treat PTSD, none has proven entirely effective in the treatment of PTSD. Thus, new drugs and behavioral therapies are 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 abnormal fear memories return. In an earlier study using an animal model of exposure therapy, known as extinction training, we found that returning the animals to the conditioning apparatus in the absence of shock for a brief 30 sec period was effective in reducing short-term retention of fear and, most importantly, preventing long-term recovery of the memory. These results are particularly noteworthy when compared to the standard extinction procedure, which consists of a lengthy exposure (10 min) to the conditioning apparatus in the absence of shock and results in recovery of retention. Surprisingly, an exposure as brief as 30 seconds was better at preventing fear recovery than the longer exposure.

The present experiment focused on the physiological mechanism underlying the brief-exposure extinction effect. It is well established that when stored fear memories are recalled they often enter a brief state of destabilization that requires protein synthesis to restabilize and endure. Using drugs to manipulate protein synthesis, results indicated that D-cycloserine, a drug that enhances protein synthesis, rendered the brief exposure procedure ineffective in reducing subsequent retention of fear. Conversely, MK 801, a drug that inhibits protein synthesis, enhanced the effectiveness of the brief exposure procedure in reducing subsequent retention. These data indicate that the brief exposure procedure had two effects: 1) it triggered recall of previously stored fear memory and 2) it blocked the protein synthesis normally required for the restabilization and subsequent retention of fear.

Next-step research will be directed at determining the longevity of the brief exposure effect in preventing recovery of fear, and then – given that the effect is an enduring one – the extent to which it applies in the form of a novel exposure therapy to the treatment of anxiety disorders including PTSD.

Predictive Factors for Forked Fungus Beetle Habitat Preference and Movement

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Habitat plays an important role in the fitness of most organisms. Therefore, the process of choosing a habitat is often critical. When choosing habitats, some species exhibit site fidelity meaning they return to the same location year after year (Hoover 2003, Wiklund 1996, Clark 1999). Prior research has shown site fidelity is often related to the reproductive success of the individual at the location (Switzer 1997, Hoover 2003, Wiklund 1996) and available foraging opportunities (Courbin 2018, Knox 2018). One aspect of site fidelity that has not been studied in great depth is the loyalty organisms have toward small sites on a day-to-day basis. A good model organism for such an investigation is *Bolitotherus cornutus*, the forked fungus beetle. Forked fungus beetles live, mate, and forage on the fruiting bodies of various fungi ("brackets") on dead logs. Forked fungus beetles have the ability to move between these brackets, and are observed doing so on a daily basis. However, the reason behind this movement is unknown and some beetles appear to be much more loyal to certain brackets than others. This study will investigate if the observed behavior of a beetle can predict whether or not that beetle will be on the same bracket the next time it is observed. I hypothesized that the probability of beetles staying on the same bracket would be higher if the beetle was observed performing a mating behavior on that bracket or if the bracket was of high foraging quality. The results of this study indicate female beetles are more likely to leave a bracket if they are observed laying on the bracket, while there was no significant difference in the probability of a male beetle staying regardless of their behavior. Additionally, both male and female beetles were significantly more likely to stay on a bracket if they had more social partners or if the bracket was of the species *Ganoderma applanatum*. These results suggest there are both social and environmental factors at play in patterns of beetle movement and also suggest *G. applanatum* may be a preferred food source of *B. cornutus*.

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 tool-box 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 will be discussed.

Diastereomerically Selective Rh^{II} Catalyzed C-H Insertions Directed by Planar Chiral Iron(0) Tricarbonyl Diene Complexes

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New methodology is presented for the synthesis of 5-membered rings bearing two adjacent stereocenters by means of Rh^{II} catalyzed C-H insertion, generating both stereocenters with 100:0 diastereomeric selectivity. Attachment of a chiral oxazolidinone generates a diene, which is then complexed with an $Fe(CO)_3$ moiety with planar diastereomeric selectivity up to 22:1. This iron-centered moiety provides significant steric bulk which is responsible for the diastereomeric selectivity of the C-H insertion. Multiple examples of this chemistry have been generated and analyzed.

Further exploration of the generated cyclopentene has consisted of oxidative removal of the $Fe(CO)_3$ moiety, intramolecular Diels-Alder reaction and hydrolytic removal of the oxazolidinone. Current research is focused on generating further examples of selective C-H insertion as well as continued exploration of the potential chemistry of the insertion product.

Characterizing the Orbital Dynamics of Protoplanetary Disks in Binary Systems

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Many of the known planetary systems are quite unlike the Solar System. Some contain multiple "hot Jupiters" or planets orbiting the host star on highly eccentric or inclined orbits. Although already formed planets orbit most stars, hot disks of matter orbit many young stars. These swirling disks are often known as protoplanetary disks, as they usually form into planets eventually. Understanding the spatial orientations of protoplanetary disks in a binary system, or a system containing two central stars orbiting each other, provides significant insight into the formation of many previously discovered strange planetary systems.

We analyzed the orbital orientations of 28 protoplanetary disks in 14 binary systems using the ALMA array. We measured the position angle of each disk, or the angle from the north side to the redshifted side of the disk, or the side of the disk containing material moving at least partially towards us in our line of sight. Our primary quantity of interest was the position angle difference between two disks in the same binary system, allowing us to deduce whether or not the disks may be aligned with the binary orbit, posing interesting applications to planet formation theory. Out of the 8 disk systems that had strong enough emission for both to be detected, 5 have position angle differences within 30 degrees while 3 have position angle differences greater than 40 degrees, implying that many of the disks are rather aligned. We achieved p-values in the range of 0.0037 to 0.085 for the Kolmogorov-Smirnov, Kuiper, and Anderson-Darling Tests, which we used to test the null hypothesis that the degree of misalignment of protoplanetary disks in binary systems is randomly distributed. These p-values allowed us to reject the null hypothesis with at least 90% confidence, likely demonstrating that protoplanetary disks within binary systems tend to be aligned with the binary orbit.

Brain network interactions to polysemy during the viewing of naturalistic stimuli

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Lexical ambiguity occurs when there are multiple possible interpretations of a lexeme. The processing of lexical ambiguities is aided by contextual information such as gestures, facial expressions, intonation and other paralinguistic features. The extent to which speech comprehension depends on context, and the stage of comprehension in which context is accounted for, differs between models. In the reordered access model (Duffy et al., 2001), both the activation of all possible meanings of a word and the final selection of a candidate is modulated by contextual factors and dominance. In contrast, a predictive model of language processing posits that the process is largely top-down, and a candidate word or 'hypothesis' is selected before sensory input is received. The bulk of the cognitive processing involved used to compare the hypothesis to the actual perceived sensory information. This study looked at the neural networks involved in the processing of high and low polysemy in the presence of high or low emotional context during the free viewing of a movie under fMRI scan. The results showed a main effect of polysemy on the left pars orbitalis, anterior temporal pole and posterior medial temporal gyrus, and an interaction effect in the right prefrontal cortex and inferior parietal lobe. These findings validate naturalistic stimuli under fMRI as a method for studying language processing. The activation in the left inferior frontal gyrus to high polysemy is consistent with past research showing the LIFG as responsible for lexical disambiguation, yet also lends support to a predictive model which anticipates that greater polysemy and lower predictability requires more activity in language processing regions.

Female Aggression in *Bolitotherus cornutus*

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Forked fungus beetles (*Bolitotherus cornutus*) have been studied because of their social interactions, but many studies have focused on the behaviors of males. This study analyzed interactions between females to assess whether females are aggressive and how their aggression compares to males. Females were paired randomly in the lab and allowed to interact in a small cell for four hours. Interactions were then scored using video software and categorized into different set behaviors. Ethogram analysis revealed that males and females share very similar pathways between behaviors. ANOVA tests and linear regression models showed that of the behaviors displayed in both males and females, only the mounting behavior occurred more frequently for males. Linear regression models also showed a positive relationship between mounting and body size for males and females. Models also found a negative relationship between chasing and body size for females but a positive relationship between chasing and body size for males. These preliminary results imply that females display aggression very similarly to males, an important aspect of their social interactions previously missing from the literature. Future studies will continue analyzing interactions to further establish patterns of behavior and test the repeatability of aggression.

Modeling Decision-Making with Different Network Structures

Bill Huang, Genji Kawakita. Instructor: Victor Barranca

In this study, we developed and analyzed a new dynamical system neural network modeling framework for decision-making in tasks involving a large number of alternatives. After carefully comparing various choices for our model and selecting the most ideal candidate, we conducted a comprehensive analysis on the most canonical network generalization - the all-to-all network. We analyzed the existence, uniqueness and stability of equilibrium points, corresponding to different decisions, as well as the reaction time necessary to make a decision. We also determined an ideal parameter regime for accurate decision-making, which is biologically desirable, since it is physiologically realistic and yields reasonably good performance, and mathematically appealing, in the sense that it persists even as the number of choices tends toward infinity. Furthermore, having more than two alternatives in the model allows for a choice in network structure. To understand the impact of different structures, we explored three additional types of topologies, including regular, random, and small-world connectivity. Through extensive investigation, we concluded that regular and small-world networks excelled in achieving high accuracy in decision-making tasks, which echoed existent results suggesting a correlation between network clustering coefficient and effectiveness in information integration. In addition, we studied the characteristics of two different gain functions, sigmoid and binary, which represent the different ways exogenous information is integrated. We showed via asymptotic analysis and numerical simulation that more gradual gain functions yield faster response times at the price of depreciation in accuracy. However, in the presence of noise or degradation of connections, a sigmoidal transfer function garners accurate decision-making significantly more robustly than binary gain. Our findings thus explain the advantage of more gradually integrating information and corroborate with the experimental studies.

Licensing Conditions of Singular *They*

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Singular *they* has a long history of use in English, specifically in instances such as in (1) when used with quantified antecedents or antecedents of unknown or unspecified gender (Balhorn 2004).

(1) a. Everyone should know their own phone number.
b. (*Seeing an unidentified distant figure*) They're waving at us.
c. Someone left their sweater.

More recently, a new use of singular *they* has emerged as the personal pronoun of reference for individuals who identify as gender non-binary. This new use seems to have led to a variation in distributions of the use of singular *they*, with some people finding its use acceptable in certain contexts that others find unacceptable. Bjorkman (2017) claims that speakers can be categorized as either innovative or non-innovative speakers based on their use of singular *they*; those who accept *they* with singular, definite, specific antecedents (e.g. as in "My friend forgot *their* jacket") are considered innovative while those who reject *they* in that context are considered non-innovative. Konnelly and Cowper (Submitted) propose a theory that includes a third stage of singular *they* use in which gender features are completely optional and non-contrastive, allowing for use even with gendered antecedents.

The current study utilizes an empirical approach to determining the accuracy of these linguistic theories. Specifically, we ask (1) whether multiple populations of singular *they* speakers exist, and (2) to what extent do grammatical gender and social distance (how close the speaker is to the antecedent) mediate how the pronoun is accepted and used on a regular basis. We were also investigating whether acceptance of singular *they* was influenced by personal differences between individual speakers, such as age or acceptance of non-binary people. We presented 160 participants from Mechanical Turk and Prolific with sentences that used a variation of the pronoun *they* (i.e. *they*, *them*, *their*, *themselves*) and one of nine antecedent conditions, and asked them to rate how naturally the pronoun referred to the antecedent. A survey following the judgment task recorded information on demographic information, such as age and gender identity, as well as measures of familiarity with and openness to non-binary individuals.

At this point in our data collection and analysis, we have found trends which suggest that both grammatical gender and social distance factor into people's acceptability judgments of singular *they*. Specifically, as social distance increases between the antecedent and the reader, acceptability of singular *they* also appears to increase. There is correlatory evidence that age, acceptance of non-binary and transgenderism, and non-binary gender identity of the participant mediates the effects of grammaticality and social closeness. While these early patterns do not support Bjorkman's theory of multiple grammars among the population, they do suggest some level of grammatical gradation among the English speaking population that may align closely with the Stage II and Stage III speakers described by Konnelly and Cowper (Submitted).

The Jamming Transition with Varying Pin Lattice Geometry

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Jamming is a transition that takes a disordered material from a fluid-like to a solid-like state. We study, via computer simulation, the effect of introducing lattices of pins (i.e. fixed particles) with varying geometric structure on jamming in a 2-dimensional system with periodic boundary conditions. Over hundreds of simulations, we arrange soft, mobile, bidisperse disks with harmonic repulsive potentials in randomized initial configurations. We use the FIRE algorithm to minimize the system's energy to see how many of the simulations jam for different densities of mobile disks. This allows us to trace out a "jamming threshold" curve. We show that the presence of a pin lattice lowers the jamming threshold of a system. Importantly, we find that a triangular lattice of immobile pins has the greatest power to facilitate jamming, for each pin density studied.

Evaluation of Spectral Coherence in Large Clinical Dataset

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An EEG or electroencephalogram, is a method of detecting electrical activity in the brain using electrodes attached to the head. Previously, the FDA has done work with EEG in measuring the variability of different EEG features, and determining what features could be used as baseline EEG metrics. The purpose of this project was to determine if a relationship between signals from different electrodes exists for different patient populations. One feature not examined in previous works is the spectral coherence, which can be used to measure the causality between two signals. This work develops a methodology to calculate the specific feature coherence, and explores how the feature differs across different groups. We use EEG data for over 12,000 patients from the Temple University Hospital Neural Engineering Data Consortium database. For each patient, voltage vs. time session data of 19 EEG electrodes were available. The data were preprocessed so that all of the samples used were at least 16 minutes in length, downsampled to 100 Hz, and filtered through a 0.5 Hz to 50 Hz band pass filter. Using clinical notes accompanied with each patient recording, patient data were classified according to gender, approximate age, and certain medications taken by the patient.

Using a balanced sample of patients, we calculated the coherence between each pair of electrodes for a commonly used range of frequency bands. The bands are defined as: ℓ (lower) : < 1 Hz, δ(delta) : $1 - 4$ Hz, θ(theta) : $4 - 8$ Hz, α(alpha) : $8 - 12$ Hz, μ(mu) : $12 - 16$ Hz, β(beta) : $16 - 25$ Hz, and γ(gamma) : $25 - 40$ Hz. In this exploratory analysis, we hypothesized that the level of spectral coherence between two electrodes would be spatially dependent (i.e. electrodes closer to each other would have high spectral coherence). Using tools from PyMVPA, we were able to view topological plots of the coherence between each combination of two electrodes, and histograms showing the coherence for each of the known EEG frequency bands. A GUI was also developed to easily view a topological plot of electrode coherence for a chosen EEG electrode and frequency. Finally, we analyzed the coherence across classified populations, including: male vs. female, "normal" vs. "abnormal", and older (age > 60) vs. younger (age < 10) to see if there was a significant difference in coherence between populations. Understanding these relationships gives us better insight as to whether coherence is a useful metric in qualitative EEG.

Biophysical efforts toward the structure of tandem DNA repeats linked to replication stress

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DNA replication is a process essential to every living organism. Replication stress can lead to double strand breaks and replication fork collapse, ultimately promoting cancer. The (CAGAGG)n DNA repeat (where n is 80-100) has been identified in a bioinformatics study of the mouse genome as heavily associated with DNA breaks. We hypothesize that this repeat form a stable secondary structure, capable of blocking DNA replication enzymes. Based on our earlier biophysical data we proposed that (CAGAGG)n repeat forms a tetrastranded, antiparallel structure with two GCGC tetrads stacked on top of each other and connected by AGAG loops. In order to test this model and gain further structural details, we have designed 24 N-to-T single point mutants of the shortest sequence capable of forming stable secondary structure, 5'-AGG(CAGAGG)3CAG-3' (also termed 1Core). The folding and thermal stability of mutants were analyzed via Circular Dichroism (CD) and UV-vis spectroscopies, and PAGE. Our results show that mutating any nucleotide in the GCGC core destabilizes the structure by > 15°C and is detrimental to its stability. Mutating AGAG loops changes the stability of the structure only mildly, by no more than 5 °C. Our mutagenesis study strongly supports the model described above.

In order to understand how 1Core structural units combine into a longer, more biologically relevant higher order structure, we have studied a 2Core sequence, 5'-AGG(CAGAGG)7CAG-3'. We proposed two possible arrangements of 1Core units into 2Core structure. We complement our extensive CD and UV-vis studies of 2Core with the use of 2 amino-purine (2AP) fluorescence to differentiate between the two models The environment of some adenines occupying the same position in the 2Core sequence, differs significantly in the contending models. We make use of the ability of 2AP to fluoresce while exposed to solvent; the florescence is quenched, however, in crowded environments (such as when 2AP is stacked).

Combined our data shed light on the secondary structure of (CAGAGG)n repeat and, more generally, have great utility for understanding the secondary structures of intrinsically difficult-to-replicate repeat sequences. Such information can lead to the development of future anticancer therapeutics.

Developing A Calf Volume Monitoring Device to Be Used with A Portable Bio Impedance Spectroscopy Measurement System for Congestive Heart Failure (CHF) Management

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Bio-impedance spectroscopy is a measurement method used mainly for body composition measurements in a clinical setting. The data can be used to determine the amount of fluids in the body as well as estimate body composition. I worked with Professor Maggie Delano to develop her portable bio-impedance measurement device into a wearable one. The overall significance of this project was in preventive/predictive monitoring capabilities in the treatment of patients diagnosed with congestive heart failure (CHF).

My part of the project dealt with the need to monitor volumetric changes in patient's lower limbs (specifically the calf region) and took on the task of devising accurate and reliable ways to track such changes in volume and circumference. This consisted of developing two different methods and taking measurements and conducting tests. The two methods developed were **the strain gauge method** and **the magnetic sensor method**. The final results were that the strain gauge method worked well and was good for measuring and monitoring changes greater than 3mm. The magnetic sensor method was functioning however the transfer of data to the computer was not robust enough or at a reliable stage for measurements of calf circumferences to be made. The steps forward would be to refine the magnetic sensor method with the goal of consistency and then to compare the precision to the strain gauge method.

Exploring the Ovarian Cancer Odor Signature

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With indistinct symptoms and no recommended screening test, ovarian cancer (OVCA) often goes unnoticed until late stages when prognosis is poor. Using trained canines, we have confirmed that there is a unique odor signature caused by disease-mediated alterations in cellular metabolism, and ultimately this odor can be used for earlier diagnosis for OVCA. Previous research suggested that micro-preparative gas chromatography (MPGC) collection of SPME-collected plasma volatile organic compounds (VOCs) could contain the VOCs that canines recognize as "OVCA." The results of bioassays suggested that cancer VOCs collected this way have a detectable odor that varies slightly from or is weaker than the odor of cancerous blood plasma. Our goal is to use canines trained on diluted cancer blood plasma to confirm the presence of OVCA odor in samples collected using MPGC. This technique employs a gradient-cooled glass tube connected to the GC outlet which traps the VOCs and then is presented to the canines. Using glass wool to cap the tubes, we were able to collect enough recognizable odor for the dogs to know it as the OVCA odor. The next steps in this research are to confirm the dog's sensitivity and specificity to the odor prepared in this way and then present specific isolated parts of the odor to the dogs. After the specific VOC biomarkers are identified, a vapor sensor device can be created as a practical diagnostic technique for early stage OVCA.

Linalool as a Potent and Reversible Anesthetic for Hydra

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The ability to make transgenic Hydra lines has opened the door for quantitative in vivo studies of Hydra regeneration and physiology. An anesthetic with the ability to reliably and innocuously relax Hydra tissue or whole animals would provide researchers with improved control over their experiments and enable in vivo imaging with sub-cellular resolution. Urethane is frequently used as a pre-fixative to relax and immobilize Hydra. However, live animals in urethane are not sufficiently immobilized for live imaging at high magnifications. Linalool, a monoterpene alcohol derived from different plant extracts, is a reversible anesthetic previously studied in rats, mice, and humans. It operates in these systems cytostatically through competitive inhibition of glutamate. Behaviorally, Hydra react to linalool with a full extension of the body column, tentacles splayed outwards, a posture that is particularly useful for fine manipulations. As the animals are sufficiently immobilized in linalool, it is possible to take fluorescent multi-channel z-stacks at high magnification. Using the pinch test as a readout, we found that Hydra incubated in 1mM linalool are fully anesthetized in under 10 minutes and become responsive again in less than 20 minutes after being returned to Hydra medium. While long-term incubation in 1mM impairs head regeneration, at lower concentrations of linalool (≤0.25 mM), head regeneration is not impacted. The linalool concentrations that were deemed effective in the absence of overt toxicity for short and long-term applications, respectively, are now being evaluated for possible side-effects on the cell cycle, cell death, and build-up of tolerance. Our studies suggest that linalool is a promising agent for use in Hydra as it acts quickly, reversibly, and innocuously, allowing for unprecedented precision in manipulation and live imaging.

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Movement Among Mating Arenas Predicts Individuals' Centrality In Some Social Networks

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Because social interactions depend strongly on the positions of the interacting individuals, studying how movement affects those social interactions could give us a better understanding of where individuals fit within their societies. While previous work has shown that centrality metrics like strength and betweenness are significantly influenced by morphological traits, little is known about how these centrality metrics are affected by movement. We performed a general linear mixed model analysis to determine whether movement among mating arenas predicted strength and betweenness within forked fungus beetle (*Bolitotherus cornutus*) populations. In the analysis, sex, elytra size, and number of observations were used as fixed effects while population was used as a random effect. Our results showed that despite being highly correlated, strength and betweenness are affected by movement differently. Sex-specific social networks proved to be the most significant source of variation among the results with male-only social networks yielding consistent results across both centrality metrics. Additionally, although the effects of movement on strength in all social networks fell within our expectations, the effects of movement on male-only betweenness highlights a unique feature of male-only social interactions.

An HMM-CNN Method for Inferring Natural Selection Strengths in Evolutionary History

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Advances in genetic sequencing technology have given way to an abundance of accessible genetic data. Recent work on inferring populations' evolutionary histories using genetics has turned to machine learning to take advantage of such data. We propose a Hidden Markov Model (HMM) to Convolutional Neural Network (CNN) pipeline that retrieves global and local information about a population sample to predict where and how strongly natural selection has affected that population. HMMs have been an effective unsupervised method for capturing general trends across the entire genome. We predict that CNNs – one successful model of deep learning – can learn to detect local patterns within a genomic region, with the help of global information via HMMs. Our objective is to develop an integrated method to identify regions of natural selection from raw genetic data. Our goal is to improve upon traditional methods, which use summary statistics to capture measurable information about a population's evolutionary events. Summary statistics reduce the dimension of the information drastically, and the results are often affected by confounding variables. The model trains on population genetic data generated by coalescent simulators. Results prove that the integrated model, where deep learning takes advantage of the global information learned by HMM, performs more accurately and reliably than a CNN with only original sequence information. The model is used to infer natural selection strengths in regions of chromosome 2 of Mexican ancestry population from the 1000 Genomes Project (http://www.internationalgenome.org/).

Exploring Structures of Satellite 2 Centromeres

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Satellite 2 (SAT2) sequences are located in the centromere of chromosome 1 and play an important role in replication. Specifically, it was hypothesized by Tahiliani's lab that SAT2, when single-stranded, could form non-canonical loop-stem-loop secondary structure which blocks replication fork leading to chromosomal rearrangement and double strand breaks – both causes of cancer. Importantly, SAT2 sequences contain multiple CpG islands whose cytosine are commonly methylated. This process is an important part of gene regulation, and either hypomethylation and hypermethylation of DNA can lead to cancer. Due to this strong link to cancer, it is of great importance to understand the secondary structure formed by DNA from SAT2. Specifically, we are trying to understand, how the secondary structure of SAT2 may signal DNA methylation or demethylation or block the replication machinery.

To address our goal we are working on crystallization of DNA sequences from SAT2 as well as characterization of the selected sequences and their variants via biophysical methods. We designed a variety of constructs, all of biological importance, as well as a range of loop mutants which disrupt the CpG island or nucleotides in the vicinity. We characterize all of the sequences (about 40) using Circular Dichroism (CD) spectroscopy. The CD spectra provide characteristic signature for each DNA fold and indicate changes caused by the introduced mutations. We learned that loop mutants that maintained the CpG island presented similar signature as the native sequences while the ones where CpG island was disrupted (by replacing either C or G) showed different CD signature. Gel electrophoresis studies were conducted to test the folding, molecularity and homogeneity of the samples. Finally, we have determined the effect of mutations on DNA stability using UV-vis melting experiments. Sequences without CpG island were significantly destabilized posing a connection between CpG island and stability of the DNA.

To test the validity of proposed model, we also designed a variety of 2AP mutants. It is commonly known that 2AP fluoresces strongly when free or part of a flexible region of DNA but its fluorescence is quenched when 2AP is basepaired or stacked. Thus, we hypothesized that modifications placed in the loop will show high fluorescence signals while those placed in the stem of the loop-stem-loop structure will show diminished signal. In general, our data support the proposed model.

Lastly, we have attempted the crystallization of nine different variants of SAT2 sequences as well as three mutants. We obtained diffraction quality crystals for S10nt-GGA mutant and S32 variant. The former diffracted with an impressive resolution of 1.8 Å. Progress toward structure solution will be discussed.

Put together our data suggest that SAT2 sequences fold into stable loop-stem-loop structure which plays regulatory role in cancer and during replication. Understanding the details of this structure and its stability can inspire novel cancer treatments.

Crystal structure and biophysical studies of telomeric G-quadruplex DNA in complex with a small molecule ligand as an anticancer strategy

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The G-quadruplex (GQ) is a non-canonical DNA secondary structure formed by G-rich DNA sequences found throughout human genome. Stable GQ structures 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', with a water-soluble porphyrin ligand, *N*-methyl mesoporphyrin IX (NMM). UV-vis and fluorescence titrations revealed a 1:1 binding stoichiometry with a tight binding constant, K_a, of $50 \pm 30\ \mu M^{-1}$. Isothermal titration calorimetry demonstrated that the binding interaction is enthalpically-driven and thermodynamically favorable ($\Delta H = -17 \pm 3$ kcal/mol, $\Delta G = -10 \pm 3$ kcal/mol). We solved the crystal structure of the DNA-NMM complex at 2.34 Å. The crystal structure reveals that the DNA forms a dimer of parallel GQs bound at both ends with NMM via end-stacking interactions, supporting the 1:1 binding stoichiometry observed in our biophysical studies. Our studies provide biophysical and atomic-resolution details of the NMM-parallel GQ complex, which can inform the design of novel, highly-selective anticancer drugs targeting G-rich DNA sequences.

Distributed Private Stable Matchings

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The stable matching problem can be solved in quadratic time by the famous Gale-Shapley algorithm. Running Gale-Shapley requires the existence of a central authority that holds all the preference lists. However, agents might prefer to keep their preferences private. We designed a non-cryptographic protocol that helps agents on a synchronous distributed network find a stable matching without revealing their preference lists to an external authority or to each other. The protocol is based on Shamir's secret sharing, and has a rounds complexity of O(nlogn). We are still working to find a lower bound on the rounds complexity of the problem.

Transformative experience in a physics course designed to facilitate connections to biology

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We examine the trajectory of biology student ("Bryn") who entered an Introductory Physics for Life Science (IPLS) course with a negative view about the relevance of physics to her primary interests, and with a strong disciplinary identity as a biologist. After the IPLS course, Bryn's perspective on physics had evolved in profound ways. We leverage the idea of "transformative experience" (Pugh, 2010) to understand Bryn's evolution, and suggest how one might expand Pugh's definition to account for the experiences of students as they move between disciplinary classrooms. We argue that transformation is not just about seeing physics in the everyday world, but about seeing physics in other disciplines. By the end of the IPLS semester, Bryn has a set of "wonderful ideas: not only about physics, but about the relationship of physics to her primary biological interests.

Measuring 1-Axial Bend and Twist Using 4-Core Optical Fiber

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Abstract: A four-core optical fiber is introduced as a 1-axial bend and twist sensor to explore phase shifts corresponding to micrometers of force-induced deflection or degrees of twist. Phase shift is witnessed by the change in 2D interferograms of a four-core fiber and calculated with MATLAB programs. Repeatable plots of linear phase shift vs 0-100 micrometers of deflection and 0-40 degrees of twist were demonstrated.

A MATLAB Simulation of a Probabilistic Colorectal Cancer Model

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Colorectal cancer (CRC) is one of the deadliest forms of cancer that can develop and, according to the American Cancer Society, will approximately account for 50,000 deaths in 2018. To prevent these cancers deaths, it is imperative to develop intervention strategies that can identify the disease in its earliest stages when it is most treatable. Because of this, there has been significant research in developing mathematical models that can predict the incidence rates and progression of CRC across multiple populations. Various validated mathematical models accomplish the task of predicting cancer onset and development, but these models can also be used to predict outcomes if one changes specific parameters. One parameter of interest is the overall screening rate of the population. Proper and frequent screening is a necessary aspect of finding an early onset of colon cancer, and while there has been a significant push to get the US population to reach an 80% colorectal cancer screening rate by 2020, a clear majority of screening tests being done are colonoscopies or sigmoidoscopies. An American Cancer Society research survey estimates that in 2015 approximately 60% of adults took at least one colonoscopy in the past ten years, but only approximately 6% of adults took fecal tests. Fecal tests can provide a cost-effective and non-invasive way to test for CRCs. These tests can be taken at home and mailed into a lab and have a specificity of upwards of 94%. Compared to invasive tests which require a medical professional and thorough preparation beforehand, fecal tests can provide an accessible way to screen for CRC, increasing the overall screening rate, especially in communities with low income. For this summer research, we created a MATLAB simulation incorporating a probabilistic CRC progression model and once implementing the model, changing the population screening rates with an emphasis on non-invasive fecal tests. Increasing fecal screening could provide a cost effective way to reach the 80% goal by 2020 which according to the American Cancer Association may save as many as 200,000 lives by 2030.

Gut Microbiome, Stress, and Fat in Rufous and Anna's Hummingbirds

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Extensive research has shown that the diversity and makeup of the gut microbiome has correlations with the host organism's fat deposition, stress behaviors, and stress hormone levels in mammals, but there has been much less research on these correlations in birds. Hummingbirds offer a useful model of study for these questions because of their rapid metabolism, nectarivory, and high sucrase activity. In terms of fat deposition, some species, such as the *Selasphorus rufus* (Rufous Hummingbird), undergo annual cycles of fattening in preparation for southern migration, while others, such as *Calypte anna* (Anna's Hummingbird) remain relatively constant fat stores throughout the year. Thus, we sought out to investigate whether the seasonal migratory fat increase shown by Rufous birds is elicited by change in their gut microbiome. Furthermore, we are interested in possible correlations between the birds' gut microbiome, stress hormone levels, and stress behaviors. We collected feces for gut microbe analysis and cloacal fluids for stress hormone (corticosterone) analysis from Rufous and Anna's hummingbirds in the San Juan Islands (WA, USA). Fat levels of the birds were categorized and the length of their tonic immobility (TI) was measured as a potential indicator of stress behavior. Rufous birds collected in earlier summer months (May-June) showed lower levels of fat than the birds measured in later months (July-August). In addition, juvenile Rufous were more prevalent in the later summer months. Anna's hummingbirds measured low fat levels throughout the entire summer. Anna's hummingbirds also had significantly longer lengths of TI than Rufous birds, and adult Anna's showed significantly longer TI lengths than juvenile Anna's. We plan to further examine correlations between the diversity and makeup of the gut microbiome, fat levels, stress hormone levels, and length of TI in order to determine if established interactions between stress, fat and gut microbiota in mammals also occur in hummingbirds.

Location-leaking through Network Traffic in Mobile Augmented Reality Applications

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Mobile Augmented Reality (AR) applications allow the user to interact with virtual objects positioned within the real world via a smart phone, tablet or smart glasses. As the popularity of these applications grows, recent researchers have identified several security and privacy issues pertaining to the collection and storage of sensitive data from device sensors. Location-based AR applications typically not only collect user location data, but transmit it to a remote server in order to download nearby virtual content. In this paper we show that the pattern of network traffic generated by this process alone can be used to infer the user's location. We demonstrate a side-channel attack against a widely available Mobile AR application inspired by Website Fingerprinting methods. Through the strategic placement of virtual content and prerecording of the network traffic produced by interacting with this content, we are able to identify the location of a user within the target area with an accuracy of 94%. We are able to extra the location information from the structure of the network traffic data using a novel method based around a 1D Convolutional Neural Network. This finding reveals a previously unexplored vulnerability in the implementation of Mobile AR applications and we offer several recommendations to mitigate this threat.

An analysis of HIV antibody-virus co-evolution to guide vaccine design

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Worldwide, more than 35 million people are infected with human immunodeficiency virus type 1 (HIV-1). Infected individuals develop antibodies to the envelope glycoprotein (Env) expressed by HIV-1, and HIV rapidly mutates its envelope to evade neutralization by antibodies. After several years, 10 to 20% of patients develop broadly neutralizing antibodies (bnAbs) capable of binding and neutralizing the majority of viral lineages, rather than a single variant of the antigen. The DH270 lineage of bnAbs was isolated from patient CH848, who was followed for approximately five years after initial infection. The structures and binding modes of bnAbs from late in the lineage have been determined, but the binding of earlier intermediates and the unmutated common ancestor are unknown. I sought to determine the structure of an early intermediate, IA4, and characterize its binding to Env. I obtained preliminary crystals of the unliganded IA4 for structure determination by X-ray crystallography. I also analyzed negative stain electron microscopy (EM) data of IA4 in complex with the wild type Env to generate a low-resolution model of the binding and found that Env is not fully saturated with antibody, potentially due to weak interactions. Thus, I generated mutants of an Env that lack some glycosylation sites. Preliminary kinetic data with these mutants suggest that they bind more tightly to the antibody, and so these constructs will be used for future EM studies. Knowledge of the evolution of bnAbs and the binding modes of bnAb precursors is crucial for developing an HIV vaccine to elicit bnAbs in uninfected patients to guard against infection.

Identification of the unfavorable characteristics of 1A102R, 1AZCET, and 1AH92U antibodies against HIV

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The role of antibodies in the human body is to neutralize infection by blocking the antigen from binding to the target cell. Broadly neutralizing antibodies (bnAbs) are elicited in up to 20% of HIV-infected individuals and neutralize more than one strain of HIV (*human immunodeficiency virus*) making them a prominent topic of study in the development of a successful HIV vaccine. 1A102R, 1AZCET, and 1AH92U are three antibodies that derive from the same unmutated common ancestor (UCA) as the CH103 lineage, a well-known HIV bnAb lineage. The purpose of this project is to identify the unfavorable characteristics of 1A102R, 1AZCET, and 1AH92U that give them a lower binding affinity to the virus envelope ("Env"), the spikes found on the virus surface. The gene of the Fab region, the part of the antibody that binds to Env, was cut from a bacterial plasmid and placed into a new plasmid that was suitable for introduction into mammalian cells. This DNA was then purified and introduced into mammalian cells in order to produce protein. The cells were harvested and the protein produced was purified. Low yields of properly folded protein were obtained and the results of a series of binding experiments showed that the antibody fragments could not bind well to Env. It is hypothesized that these particular antibodies are not stable in Fab form. Thus, the next step in this project is to produce the full-length antibodies, known as IgGs, by inserting the genes of the Fab fragments into a new vector containing the rest of the antibody molecule. This will allow us to more accurately assess the interaction between antibody and virus Env.

The effect of body size, activity level, and sex on vulnerability to predation in the forked fungus beetle

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As one of the largest drivers of natural selection, predation is a determining factor in the morphological and behavioral traits of populations of prey. Certain phenotypes like male ornamentation tend to be more susceptible to predators and can lead to biased predatory patterns which may drive the evolution of traits that are selected against in sexual selection. Studies of the predation of model organisms like forked fungus beetles (*Bolitotherus cornutus)* provide great insight into their evolutionary history and the development of their current morphological and behavioral characteristics. It is reasonable to assume that beetles with high activity levels (and so frequently expose themselves) are more susceptible to predation. Previous studies have shown that predation also selects against extensive male ornamentation and large body size. This project explores whether activity level, body size, and sex in forked fungus beetles affects their vulnerability to predation. Beetles in the Appalachian mountain range in the southwest of Virginia were scan sampled three times a day to determine their activity levels, and their morphological traits were scanned and measured. Morphological properties and behaviors of living beetles were compared to those of beetles that became deceased after a week-long period of high predation in the same population. Though there was a suggestion of significance in the contribution of male ornamentation to beetle death, neither sex, nor body size, nor activity level had a significant effect. These results suggest that a forked fungus beetle's susceptibility to predation is not dependent upon the beetle's behavioral or morphological features. These results, however, only encompassed predation in 2017, and show potential for evidence of sex-biased predation. Larger amounts of beetles were predated in 2018, and future work comparing predation patterns between the two years may yield more accurate results.

Electrochemical Monitoring of Protein-Driven Silver Nanoparticle Dissolution

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Over recent years, engineered nanomaterials (ENMs) have been increasingly used in a variety of fields, including medicine and commerce. The increased use of ENMs warrants more research into the properties of ENMs and how their fate and transport affects environmental and biological systems. Silver nanoparticles (AgNPs) are widely used in nanomaterial-containing products, making them an excellent model to study the properties of ENMs. Metal ENM dissolution is an important mechanism in evaluating ENM reactivity and evidence in the literature suggests that proteins can facilitate AgNP dissolution. Our research group aims to provide real-time analysis of the dissolution kinetics of AgNPs in a variety of matrices using anodic stripping voltammetry (ASV). Inductively coupled mass spectrometry (ICP-MS), a current method to analyze ENM dissolution, is both very expensive and requires intensive sample preparation. Not only is an electrochemical system much cheaper, but ASV requires very little sample preparation. In this work, ASV was applied to monitor protein-driven AgNP dissolution. Using model protein bovine serum albumin (BSA), changes in the total concentration of Ag^+ released and in the dissolution rate were evaluated and compared to AgNP dissolution in the absence of protein. ASV was also used to evaluate AgNP dissolution of different sized nanoparticles. Ultra-violet visible spectroscopy (UV-Vis) data and circular dichroism spectroscopy (CD) data will be presented in order to provide information on how AgNPs and BSA are individually affected when bound together.

Predicting Cluster Memory Usage for Adaptive Network RAM

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The increasing popularity of big data in the modern era of high performing computers entails the increase in demand for larger memory pools to process massive amounts of information. A cluster computer — a collection of computers, or nodes, connected by a fast network — is one way to provide such vast memory pools. Although cluster computers are less expensive than most kinds of parallel computers, they usually have imbalances in resource usage, often causing significant slowdowns of parallel programs. Network RAM (NRAM) ameliorates this problem by abstracting a collective memory pool of the cluster computer, allowing applications on one node to access memory on other nodes with little additional overhead.

Many NRAM implementations reserve parts of node memory spaces to store data from remote nodes, but this fixed reservation mechanism leads to system slowdowns when node workloads become memory intensive.

To solve this problem, we investigated whether we could make memory intensive programs run faster on a cluster with a dynamic memory reservation implementation of NRAM that grows and shrinks in response to memory needs of node workloads.

Our approach was a multi-step process. We first identified important system characteristics for predicting high and low node memory usage, and then used them in an adaptive NRAM system that would solve the problem of fixed memory reservations.

We found that a statistical model was a promising and fruitful approach to our problem. Our results show that it is possible to take countermeasures and ameliorate slowdowns of the system during periods of high memory usage.

Massive Star X-Ray Analysis

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Massive stars have strong stellar winds, which produce x-rays through the formation of shock waves. X-ray spectra of these stars can yield information about the composition of the winds, the mass-loss rates of the stars, and temperature distributions of wind material. Here, we fit the x-ray spectra of six stars using a new method that takes into account absorption within the wind. We found mass-loss rates in agreement with those found by other modern techniques, which are lower than those predicted by theory. Additionally, our results suggest post-shock temperature distributions consistent with predictions.

Genetic Variation in Herbivory Resistance within *Arabidopsis* Populations

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Arabidopsis, the model organism, has been the subject of many plant-herbivore interaction studies. The studies are based on the observations that there exists genetic variation within Arabidopsis populations and that herbivores exhibit preferences in feeding between different plant genotypes. The objective of our study was to investigate if different *Arabidopsis* genotypes within a population vary in resistance to a plethora of ecologically relevant herbivores and pathogens by carrying out a genome-wide association study (GWAS) to uncover genetic polymorphisms (SNPs) in *Arabidopsis* accessions relating to variation in herbivory resistance. As of now only two high-throughput assays were conducted. Using a generalist, *Arion subfuscus* (slugs), and a specialist, p*hyllotreta cruciferae* (flea beetles), traits such as plant area removed and number of leaves removed were dependent on plant genotype.

Whole Building Life Cycle Assessment of New PPR and Danawell Connector

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Incorporating life cycle assessments (LCAs) of building designs into the planning process for new projects enables the College to apply its carbon charge to building decisions, allowing the social cost of carbon and its environmental impacts to be considered in cost-benefit analyses.

Life cycle assessment, which is a method that reports the environmental effects of a product over its lifetime, can be used to quantify the impact of materials used in building and look at its total cost, not just monetary up-front or operational costs. Considering the environmental cost of the building project will aid future decision making in regards to the design and construction. Tally® is best suited for performing LCA at Swarthmore, based on the previously given files from the architects. This software generates reports that show the environmental impacts based on lifecycle stage and material divisions. Through the use of these reports and hot spot analysis, the areas of greatest environmental impact can be identified and work can be done to reduce these contributors. Based on the Danawell and NPPR, concrete and the operation energy stage were found to be the greatest contributors.

Based on these findings, the College will begin to develop a process for future buildings that will incorporate LCA into the project scope. This will bring more awareness to the College on the environmental impact of buildings and materials in addition to being able to more accurately apply the carbon charge to projects.

Vision Implementation of "Developing Grounded Goals through Instant Replay Learning"

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Developmental robotics, sometimes referred to as epigenetic robotics, is a subfield of robotics that studies developmental mechanisms and architectures that allow for open-ended lifelong learning and often mimic human development. In 2017, Professor Lisa Meeden and Douglas S. Blank published *Developing Grounded Goals through Instant Replay Learning*, which describes a developmental robotic architecture that prioritizes dramatic changes in sensory information during basic exploration and then "remembers" the moments leading up to those states so as to make them repeatable and achievable as goals. The interest and vision components of the previous implementation was redesigned so the architecture could incorporate camera readings effectively. Several convolutional autoencoders were developed, including types of variational autoencoders, which condense camera data into high-level abstractions that replace the sensor data in a low-level neural network. Preliminary results found that the standard autoencoder produces more effective abstractions than variational autoencoders, which often produce disentangled representations but condense the camera data to such an extent as to make the encoded representation difficult to interpret.

'Dark Fluid' Cosmology

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In this project, we utilize two generalized dark matter (GDM) parameters (the equation of state parameter $w(a)$, and the effective sound speed $c_{\text{eff}}^2(a,k)$) to model the behavior of the standard cosmological dark sector (cold dark matter, massless neutrinos, and dark energy) as a single GDM component. We construct generalized equations to describe two non-interacting GDM component as a single GDM species, and calculate these quantities for the full dark sector considered as a single 'dark fluid'. We then implement the evolution equations for GDM into CLASS. The effective sound speed for the full dark sector is non-analytic, so we must analytically approximate it. We then run CLASS with cold dark matter, dark energy, and neutrinos replaced with 'dark fluid' GDM and compare the resulting power spectra to the standard cosmology results. We successfully reproduce the qualitative bumps and wiggles of these power spectra, but more work is necessary to get quantitative agreement and ensure that the GDM equations of motion capture the full dynamics of each dark sector component.

Predicting Transcription Factor Binding Activity with Deep Neural Networks

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Transcription factors are proteins that play an essential role in the regulatory processes of organic systems. Therefore understanding their binding behavior has become an important research goal in the genetics community. In the past decade new lab techniques have been developed to collect data on the binding activity of transcription factors on a larger scale than previously possible. This has led to the creation of large binding site datasets for numerous transcription factors across several varied cell types in the human body. This has motivated an examination into the different statistical models that can be trained on this data to predict binding sites. Such models could help improve our understanding of transcription factor activity without requiring any expensive lab work.

Previously attempts have used this data to identify small DNA motifs (5-10 nucleotides long) that are informative to the binding behavior of a chosen transcription factor. More recent methods have begun to explore the possibility of training convolutional neural networks for this task. This family of models has seen a wave of success across several different problem domains in the past five years, driven by the creation of datasets large enough to allow for their effective training. They work by scanning for many different small patterns in the data and combining them into a hierarchical representation for classification. Their application to transcription factor binding site prediction has proven fruitful, becoming state of the art for the task. However, these approaches have for the most part used shallow networks, examining only small sequential dna segments for their classification. In this research we examine the application of deep networks for this task, with the expectation that they will be able to learn a deeper hierarchy that captures more long range interactions in the binding behavior. In addition, these networks have proven very effective at incorporating additional data into their prediction, allowing us to use information like chromatin accessibility to further improve classification accuracy. We show that increasing model depth has a positive effect on performance, motivating further investigation into deep architectures for this task.

Estimating the Duration of the Cambrian Explosion

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The Signor-Lipps effect is most often associated with mass extinctions, but it also affects "mass origination" events. The most important example is the Cambrian explosion, in which representatives of most modern phyla first appear. The general timeline of this pivotal event is well established, but details about the duration and pattern of originations remain unclear. Maloof et al. (2010) found that a dataset of small shelly fossils through the earliest Cambrian showed three pulses of fossil appearances over approximately 16 million years. Here we give a statistically rigorous estimate for the duration of the Cambrian explosion using novel methods that account for Signor-Lipps-type effects. We used a revised dataset of fossil occurrences of 166 genera of small shelly fossils from Mongolia, Siberia, and China, dating from the earliest part of the Cambrian (Nemakit-Daldynian and Tommotian, or Terreneuvian). To estimate the duration of the Cambrian explosion, we construct a confidence interval for the time span between the earliest and latest originations. We used trellis plots to visualize our results and investigate their sensitivity to uncertainty in radiometric dating, stratigraphic correlation, and sedimentation rate.

Flight mechanisms of the hawkmoth, *Manduca sexta,* after mass increase

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This experiment investigated what information encoded in the muscles of the *Manduca sexta* hawkmoth allowed it to retain its impressive flying abilities after its mass increased dramatically. We studied what mechanisms the nervous system implemented in the hawkmoth that allow it to maintain its maneuverability after increasing its mass by up to 50 percent while feeding. While tracking oscillating flowers, the hawkmoth maintained a consistent and near perfect positional gain in both the low and high mass conditions across multiple tracking frequencies. A rigid body model acted on by aerodynamic forces showed that the moth produced a 70 percent increase in the gain of its nervous system from the unfed to the fed conditions in order to remain in flight. The nervous system accomplished this dramatic increase in gain by adjusting the signals sent to the muscles to change the power output and force generated by the muscles. Specifically, the number of spikes of the upper 3rd axillary steering muscle had additional modulation in the fed moth than the unfed moth and the 3AX spiked later than the dorsoventral muscles at the extrema of the moth's turning maneuver.

Conducting Exoplanet Follow-Up Observations at Peter van de Kamp Observatory using the Transit Photometry Method

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One topic of interest to astronomers is the search for planets and life beyond our Solar System. This topic includes exoplanets. The passage of a planet between the Earth and its host star is called a transit. The transit photometry method detects exoplanets by measuring differences in brightness of a potential host star over a set period of time. Our research is done in collaboration with the KELT (Kilodegree Extremely Little Telescope) team; we perform follow-up observations based on the discovery images taken by them. KELT discovery images have a wide field of view, but correspondingly low-resolution. This allows for candidate stars to be blended with nearby stars. The telescope at PvdK allows us to observe the same stars and obtain images that are better resolved. We then generate light curves of these potential host stars to determine if "dips" in brightness are indeed caused by transiting exoplanets.

Assessing the Lasting Impact of an Introductory Physics for Life Sciences (IPLS) Course

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Introductory Physics for Life Science (IPLS) courses seek to equip life science students with skills and reasoning strategies that will be important for their later work in upper level biology courses and biology research environments. To assess whether IPLS courses are actually meeting this goal, we assess the written work of students in biology courses taken after the IPLS experience. In examining these data, we look for evidence of (1) quantitative reasoning, (2) facility coordinating between biological systems and simple physical models, and (3) mechanistic reasoning. We compare these results to results from the work of students who had not experienced the IPLS environment.

Particle Orbits in a relaxed Taylor state MHD Plasma

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Confinement is one of the main challenges in nuclear fusion. Current approaches to controlling the high-temperature gases involved in fusion include inertial confinement fusion (containment using light) and magnetic confinement fusion (containment using external magnetic fields, e.g: tokamak). Both of these approaches are expensive and impractical.

A Taylor state is a plasma equilibrium involving a twisted magnetic field structure that closes on itself. It has been long studied as a target for fusion since they are self-organized, meaning that external magnets are not used to impose the structure, and they are force-free, meaning that some instabilities are naturally absent.

The objective of our project was to begin to explore the confinement properties of the Taylor state. This was investigated by simulating particle orbits using Python and tracking if and when particles leave a specific structure. Our final simulation tracked the orbits of 0.6 million protons with velocities drawn from a Maxwellian distribution in a cylinder spread throughout the volume of a 10:1 Taylor state.

Preliminary results indicate that roughly 65% of all protons remain confined within the structure. Future directions for research include analyzing the relationship between confinement and parameters such as initial velocity of a given particle, pitch angles, position within the structure etc., identifying classes of particle trajectories, and determining the confinement properties of Taylor States of different aspect ratios.

Transfer of Antibiotic Resistance Genes in Swarthmore, PA

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Ubiquitous use of antimicrobials introduce a strong selective pressure for genes that produce resistance phenotypes in bacteria. The prevalence of these genes in wild strains local to Swarthmore, PA has not been surveyed. Further, some of these genes are held on bacterial plasmids, which can be horizontally transferred. The frequency at which these strains engage in horizontal gene transfer is unknown. Antimicrobial screens and replica plating were utilized in order to quantify the resistant phenotypes of 97 unique strains collected from around the College's campus. These procedures, however, left the question of where within a cell of a strain the resistance gene is held. Conjugation and transformation assays were employed in the attempt to transfer resistance genes from seven isolated wild strains to a known laboratory recipient strains. What qualified these seven strains was their lack of nalidixic acid resistance, due to the recipient holding that resistance gene, and the presence of resistant phenotypes against multiple antimicrobial agents. The results of these assays were used to identify whether genes lie in the chromosome, one or more small plasmids, a large plasmid, or some combination of those locations. As the use of antimicrobials has grown, selection for pathogenic bacteria that can survive these substances has strengthened, and other chemicals are often applied to our environment. Therefore, research into the population dynamics of bacteria with these resistances is a reasonable for applications in public health and environmental ecology.

Stakeholder Perspectives in Peer Mentoring Program for Pediatric Solid Organ Transplant Recipients

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Peers4PATH is a peer mentoring program aimed to improve medical adherence and heath related quality of life (HRQOL) in solid organ transplant (SOT) recipient adolescents and young adults (AYA). A randomized control trial compared peer mentor + standard of care (SOC) to SOC patients. Peers4PATH was designed based on Social Cognitive Theory (SCT) which promotes positive health behaviors in AYA through social modeling, social support and increased self-efficacy (SE). However, after primary data analysis, there was no significant difference in medical adherence, HRQOL or (SE) in the peer mentoring + SOC compared to SOC.

This sub-study analyzed qualitative feedback surveys completed by mentors and mentees documenting their experiences. Survey data was utilized to detect emergent themes, determine areas for program improvement and identify derived benefits from participation. Mentee survey responses were matched with their respective mentor's responses to evaluate concordance or disparity among pairs. Analysis showed mentees reported personal growth in several areas, namely social support (68%) and empowerment (58%). These reports suggest the program goal to provide social support and role modeling was achieved. Mentors and mentees tended to share concordant positive perspectives. However, when perspectives differed, the mentor was the less satisfied party.

Rather than focusing on medical adherence, future studies should explore innovative ways through which peer mentors might be used to provide social support and role modeling in both daily life experiences and future aspirations of AYA who suffer from chronic illnesses.

Deep Learning for Optimization of Fourier Ptychography

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Computationally improving image resolution is a priority of microscopy research because optically enhancing resolution by choosing a lens of higher numerical aperture requires sacrificing field of view. Super resolution microscopy techniques artificially increase the numerical aperture in post-processing, increasing resolution while preserving the full field of view. Fourier ptychographic microscopy is a time-intensive super resolution technique that iterates through the Fourier space of dozens of variably illuminated images to construct a single high resolution composite. By modifying microscope hardware to illuminate the sample in an optimized pattern, it is possible to enhance the quality of information encoded in a single image and reduce the size of the input dataset necessary for reconstruction. This study uses example-based deep learning to simultaneously identify the ideal illumination pattern and optimize the reconstruction algorithm for a fixed sample type to achieve super resolution reconstruction from a single low resolution image. The light source of a phase-contrast microscope was replaced with a programmable LED array. Low resolution images of TIG1 cells were collected under sequentially varying single LED illumination for Fourier ptychographic reconstruction, then again using the ideal illumination pattern generated by the neural network. Comparison of the two results demonstrates the efficacy of the two-pronged technique in improving both temporal resolution and reconstruction quality.

AprilNav: An Indoor Navigation and Localization System for Autonomous Testing of Electrostatic Sail Dynamics

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An electrostatic sail (E-sail) is a new type of propulsion which harnesses the Sun's solar wind to propel a spacecraft. Voyager I took about 40 years to reach interstellar space using solid rocket propellant, whereas electrostatic sails can travel the same distance in 6-10 years by using small but constant acceleration. As part of Marshall Space Flight Center's (MSFC) Space Systems Department and Advanced Concepts Office, research was continued for the Heliopause Electrostatic Rapid Transit System(HERTS) E-sail project.

MSFC's Flight Robotics Lab (Flat Floor) allows for 2-dimensional simulations of spacecraft dynamics using air-bearings to "float" a system. Previous researchers developed a Nano Air-bearing Simulator (NAS) for initial testing of E-sail tether deployment dynamics on the Flat Floor. An indoor navigation system, AprilNav, was developed and has been implemented on the ceiling of the Flat Floor for localization and autonomous testing of the bearing-equipped NAS; AprilNav is accurate to 5cm in x and y and 1° in yaw. With two NAS, tether deployment dynamics between the two simulators as well as steering control algorithms are being tested on the Flat Floor using AprilNav.

Aiptasia pallida as a model for the cnidarian-*Symbiodinium* symbiosis: development of the yeast two-hybrid system to probe protein-protein interactions

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Coral reefs are described as these beautiful ecosystems home to a vast collection of organisms. In addition to being pleasing to the eyes, coral reefs are important for economic and cultural stability through trade, tourism, and vaccines. However, coral reefs are undergoing a process known as bleaching at alarming rates. This bleaching epidemic is associated with environmental stresses such increased temperature and results in the degradation of reefs.

The pigmentation loss known as coral bleaching is associated with the expulsion of essential microbes known as Symbiodinium. Symbiodinium and coral have a mutualistic symbiotic relationship in which the coral provides the Symbiodinium with a source of nitrogen and shelter while the symbionts provide sugar from photosynthesis to the coral. In the face of stressors, this symbiotic relationship is disrupted, but can potentially be recovered through the re-taking up of symbionts from the environment. This potential recovery process intrigued us in terms of understanding how coral can distinguish between their symbionts and other, possibly harmful microbes.

With this question in mind, we used the sea anemone, Aiptasia pallida, as our model organism to examine the innate immune system responsible for distinguishing between pathogenic and commensal microbes. Within this immune system, cnidarians like corals and sea anemones contain a pathway known as the NF-kappa B pathway which aids in immune defense in both vertebrates and invertebrates. However, this pathway is not well characterized in cnidarians. Based on the sequencfes present in the genome of Aiptasia, we and others have constructed a hypothesized pathway and are utilizing a protein-protein analysis known as a Yeast2Hybrid (Y2H) assay to potentially fill in the missing pieces. My research focuses on the protein-protein interactions that are taking place between dimerizing TIR domains and the protein MyD88 in the upper portion of our hypothesized pathway. In other systems, some TIR-domain containing proteins bind to microbes and then interact with MyD88 to activate the NF-kappa B pathway. The Y2H assay allows us to test protein-protein interactions through the formation of a functional transcription factor that can turn on reporter genes. Through successful interactions, we are taking steps towards identifying important genes and proteins in the Aiptasia genome that can be translated into understanding their symbiotic relationship, their innate immune system, and the NF-kappa B pathway.

Purification of a fragment of an Anti HIV-1 progenitor antibody mutant, and mutation of V1/V2 loops of HIV-1 Envelopes

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HIV-1 is a difficult pathogen to neutralize via vaccine-induced antibodies because of its rapid mutation rate. Understanding the co-evolutionary pathways that result in broadly neutralizing antibodies (bnAbs), which target many viral variants, may provide insights into vaccine development. I analyzed virus sequences from the infected patient CH505 who produced the CH103 bnAb clonal lineage tree. To further our understanding of affinity maturation, we are seeking a high-resolution structure of a complex between the HIV envelope (Env) and the progenitor antibody from this lineage (termed the "UCA"). This requires us to produce a well-behaved virus envelope that can be used for structural studies. Another goal is to investigate how Env changes over the course of infection, something that has not been studied structurally before.

Towards these goals, I purified and analyzed the binding of a single chain variable fragment (scFv) of the CH103 UCA S56E mutant, and found that it binds tighter to the CH505 virus envelope than the wild-type UCA. Unfortunately, the CH505 trimer is not conformationally homogenous, a feature needed for structural determination. For this reason, I have begun introducing mutations into the first and second variable (V1/V2) loops, an important domain located at the apex of Env that influences Env conformation. Mutated V1/V2 loops correspond to the most frequent V1/V2 loops found in viruses during infection weeks 72, 96, 137, and 157, time points that span timeframes before and after antibodies in the patient became "broad". Once the four CH505 SOSIP Envs with the mutant V1/V2 loops (from week 72, 96, 137, and 157) are purified, binding studies with the UCA mutant will be conducted to determine whether the complex is stable enough to undergo structural studies. These studies will contribute to understanding the co-evolution between the CH103 antibodies and Envs throughout the course of infection and identify Env features that could be used for a vaccine.

Exploration of Asymmetrical Gene Expression within *Ciona Intestinalis*

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The processes underlying left- right asymmetry are highly conserved across a wide range of species. Nodal signaling, H+/K+ ATPase dependent ion flux and ciliary flow are required for lateral asymmetry in both protostome and deuterostome clades yet details regarding how these initial processes lateralize organ morphogenesis remain poorly characterized. We use the invertebrate chordate *Ciona intestinalis* to investigate asymmetric organ development along the left-right axis. In *Ciona,* the heart and endoderm are positioned to the right and this asymmetry arises simultaneously. Surprisingly, previous research indicates that *Ciona* heart asymmetry is dependent on ion flux but does not require Nodal signaling. To understand the link between ion flux and lateralized organ morphogenesis, we have begun to characterize laterally asymmetric gene expression in *Ciona* embryos. By sequencing RNA in thin sections spanning the left-right axis, we have established a list of 19 candidate genes displaying strongly lateralized expression including orthologs to *Cspp1, Gpr161, Taf9, Nup155, Lars2, FoxC, Siah1B*, and *Prmt9* that are strongly expressed on the right side of the embryo and *Tor1B, Sept9, Klhl4, Mef2, Pitx, Nodal, sFzd(Crd), Dnah8, Crkl, Lrrc46,* and *Kat2a* that are strongly expressed on the left side. We have confirmed six of these predicted expression patterns through in-situ hybridization. These studies have revealed that many of the candidate genes are expressed in the trunk lateral cell lineage, a group of mesodermal cells that migrate extensively in the larval head and differentiate into blood and muscle. We have also begun to characterize the dependence of these candidate genes on ion flux using the H+/K+ ATPase inhibitor omeprazole. The further characterization of asymmetrically expressed genes should provide critical insights into the molecular mechanisms driving heart and endoderm asymmetry within *Ciona* and vertebrate embryos.

Pseudomonas aeruginosa biofilm formation after cultivation in simulated microgravity

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Pseudomonas aeruginosa can attach to surfaces and form aggregates known as biofilms. It has been found that *P. aeruginosa* cultivated in space form thicker and structurally different biofilms than those grown in Earth gravity. The purpose of this experiment was to see how microgravity simulated in a lab would influence the biofilm formation abilities of *P. aeruginosa* mutants *flgK* and *pelA*. *Flg k* is defective in the initialization of biofilm formation, while *pelA* is hindered in biofilm growth and maintenance. The bacteria were cultivated in a High Aspect Ratio Vessel (HARV) bioreactor that was used to simulate microgravity and inside vials in a shaking incubation as an Earth gravity control. At the end of the incubation time, the bacteria were extracted and grown on a 24-well plate under the identical conditions in Earth gravity. After 24 hours, their biofilm formation abilities were compared by emptying the culture from the 24-well plate, staining and solubilizing the remaining biofilm in the wells, and then reading the solutions in a spectrophotometer. This experiment is still ongoing, so a conclusion cannot be made at this time, but the preliminary results suggest that wild type *P. aeruginosa* grown in simulated microgravity for at least nine days may form biofilms with higher biomass than those grown in Earth gravity. The experiment will be repeated with the mutant strains this fall.

Are we entering a sixth mass extinction? Age selectivity of modern extinctions

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There is growing debate on whether the earth has entered a sixth mass extinction. Most previous research has focused on the rate of modern extinctions compared to that known from the fossil record. Here we compare the age selectivity of modern extinctions with mass extinctions and background extinctions in the fossil record. We evaluate age selectivity using logistic regression to quantify the relationship between extinction risk and genus age. While genus age is measured similarly in all time intervals, extinction risk is a binary outcome for fossil groups and an estimated probability for modern groups, with the latter calculated to make fossil and modern analyses as comparable as possible. To estimate extinction risk for modern data, we used assessments of threatened species from the International Union for Conservation of Nature (IUCN) Red List. For Phanerozoic background and mass extinctions, we compiled data from the Paleobiology Database supplemented with the Sepkoski Compendium. We find that with respect to genus age selectivity, modern extinctions are significantly more similar to mass extinctions in the fossil record than to background extinctions.

Characterization of Textile Electrodes for Wearable BIS Home Monitoring Device

Ke Wang, Professor Maggie Delano

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My summer research project aims to help patients with **Congestive Heart Failure (CHF)** by designing a wearable home monitoring system. CHF affects more than 5.7 million American people and is very common among people of old age. It is a condition where the patient's heart's function as a pump is impaired, resulting in fluid overload.

Bioimpedance spectroscopy (BIS) can be used to determine human body composition in order to monitor body fluid volume to help patients with CHF. BIS is a painless, non-invasive and relatively simple measurement method that involves driving small, painless current of a wide range of frequencies through the human body. The measured data can be used to determine the amount of fluids in the body as well as estimate body composition.

We are developing wearable monitoring device based on a portable device developed previously. The benefits of a wearable device over a portable one includes long-term continuous monitoring, comfort of usage and repeated uses. The industrial and clinical standards use Silver/Silver Chloride (Ag/AgCl) electrodes that cannot be used repeatedly, can cause skin irritation, and dry out over time. The aim of this summer project is to find suitable replacements, namely textile electrodes, that could rival the electrical properties of Ag/AgCl electrodes but also enable long term and repeated usage.

Detailed Objectives:

1. Design and setup experiments to investigate properties of different textile materials compared to Ag/AgCl electrodes.
2. Choose acceptable materials according to electrical properties and practicality.
3. Investigate the reason why textile materials in general do not perform as well as Ag/AgCl for receiving biological signals.

In this poster session, I will introduce background knowledge on how our device would work. I will also provide experimental methods and results from preliminary testing conducted this summer. Future research directions will also be discussed.

Social Media and Self Completion

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Background: More than 70 percent of people between 18-24 years old use social media platforms like Facebook, Snapchat, and Instagram in the United States (Smith & Anderson 2018). Psychologists since the nineteenth century have been researching the self, and research in this realm has highlighted the fact that people achieve self definition by using indicators of attainment which to attempt to influence others, and provide self-descriptions of one's own performances and interests in order that others will be exposed to those descriptions (James 1890 Wicklund & Gollwitzer 1981), . While social media platforms appear to be a suitable arena for these types of displays, the literature has not yet extended these theories to online applications on social media platforms.
Method: Here I sought to examine the extent to which research on the self and self-completion has been applied to online or social media settings by conducting keyword searches on PSYCInfo, and analyzing the published studies in a combination of meta-analyses, experimental, and correlational studies.
Results: In the number of studies examining the self and/or social media, no studies were found in which causal methods were implemented to investigate psychological motivations for self-completion online. While some studies examine effects of using social media, or evaluate correlations between level of social media use and metrics of success, no studies were found to experimentally manipulate these conditions.
Conclusion: Research examining the relationship between self-completion and social media appears lacking. Corrective action by conducting causal experiments to investigate social media and motivations is needed in this field of study, because it would shed light on important aspects of self-discovery and self-definition, which is important on theoretical and practical levels.

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Interaction of Two Influenza A Matrix Proteins Critical to Viral Budding

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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. Although there have been in vitro biophysical studies of M1 and M2 individually, to our knowledge there is no published work on atomic level details of how these two proteins interact at the surface of a membrane. The overall goal of our research is to elucidate the molecular interaction of these two key players in viral budding.

Our primary tool is the use of site-directed spin-label electron paramagnetic resonance spectroscopy (SDSL-EPR). 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. A new direction of our lab is the characterization of binding of M1 protein to membrane-bound M2 protein in liposomes. We have overexpressed a construct of M1 protein and characterized the protein both alone and in the presence of membrane liposomes. We have also laid the groundwork for using spin-labeled probes to analyze the impact of both M2 and M1 proteins on the dynamics of membrane lipids. Spectral simulation techniques using the microscopic-order-disorder (MOMD) model have been used to fit spin-label spectra to extract order parameters. By comparing the dynamic parameters extracted from our fits we have shown that the M2 protein changes the dynamic properties of spin-labeled lipids incorporated into liposomes. Our next steps are to determine how M1 alone impacts the membrane, and finally how the presence of both M1 and M2 impacts membrane properties.

Finding Equilibriums in Stochastic Games

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Stochastic games are situations in which multiple agents make decisions in random environments. This research attempts to find optimal strategies for this type of game. Early research combines standard reinforcement learning with Nash-equilibrium calculations, resulting in an algorithm called Nash-Q learning. Though Nash-Q learning can solve simple games, it performs poorly in highly random games or games with many players. Inspired by the recent advancements in machine learning, this research uses neural nets to evaluate potential strategies. The resulting algorithm exhibits improved ability to generalize across scenarios as well as faster performance in finding optimal strategies. To test the algorithm, we created a variety of stochastic games. We found that our algorithm performed better in solving larger games, but it was slow or at times unable to solve some more complex games. Many real-world situations, ranging from border patrol to international tariffs, could be better modeled by using stochastic algorithms. Thus, our improved algorithm represents an early step in putting theoretical models to practical use.

Large Actuation Network with Pneumatic Multiplexing

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In the field of soft robotics, researchers are looking at the ability of finer controls on an increasing number of outputs for smarter and more dexterous robots. Currently, most pneumatic soft robots are actuated with less than ten independent actuators. There is a gap in the literature for an affordable and scalable solution to actuating many (50+) pneumatic actuators in a soft robot. My project this summer involved proposing and validating a potential solution to address this.

A similar problem (controlling many fluidic outputs) occurs in the field of microfluidics, where researchers do chemical mixing, sampling, and reaction processes on the size of a computer chip. They have developed a method to facilitate the control of a high number of reactants and product outputs, using a structure called Quake valves. Quake valves are analogous to transistors in a computer. And with a process like multiplexing in computer, which can control more outputs with less inputs, a typical microfluidic chip can control thousands of outputs with only a dozen inputs.

Our solution adapts Quake valves and fluidic multiplexing to the field of soft robotics, with significant improvements on scalability and pressure rating. The typical fabrication method in microfluidics involves PDMS molding and multilayer lithography. The PDMS material is too soft to take the high pressure needed for soft robotic applications and multilayer lithography is a complex process requiring specially trained lab workers. With digital fabrication method, we designed our Quake valves in computer CAD programs (Solidworks) and 3D-printed them with a multi-material 3D-printer (Connex Objet 350). This process is highly scalable due to modularity of the design. And the valves printed are with both hard and soft materials thus they can take much higher pressure in the channels.

The concepts were proved with a demonstration device, which controls 64 pneumatic output at 20 psi pressure with only 12 pneumatic inputs. The device is easily scalable to significantly higher outputs with a minimal addition of inputs. A display board with 60 pneumatic pixels was also manufactured to show the capacity of the controls.

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Splines: Algebraic and Analytical

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The dictionary definition of a spline is a thin piece of wood. This was also the definition originally used by engineers in fields such as shipbuilding and other designs. Mathematicians use various definitions for splines with the most common being: a function defined continuously by piecewise polynomials. This research project was conducted making use of two more nuanced definitions of splines in the fields of algebra and analysis. From this, we developed some basic theorems and propositions in regards to the algebraic definition while exploring further into the field of applicable splines in analysis, specifically a phenomenon known as supersmoothness.

Towards the crystal structures of VEGF and G4TERT

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A G-quadruplex DNA (GQ) is a non-canonical DNA structure formed by the $\pi-\pi$ stacking of multiple G-tetrads, in which guanines are held together by Hoogsteen hydrogen-bonding. DNA sequences with GQ-forming potential are overly abundant in telomeres and in promoters of oncogenes, which establishes GQs as a promising anticancer target. My research is aimed towards solving crystal structures of representative GQ DNA and exploring their interactions with selective small molecule ligands. Specifically, I focus on two G-rich DNA sequences, VEGF and G4TERT. VEGF is found in the proximal promoter region of the vascular endothelial growth factor gene. This gene is upregulated in a variety of cancers and promotes the growth of cancer cells. G4TERT is found in the promoter region of hHERT gene, which encodes for the catalytic domain of human telomerase, and promotes cancer cell survival. Both DNA sequences form parallel stranded GQ structures. My study investigates the interactions of VEGF, G4TERT, and their variants with N-methylmesoporphyrin IX (NMM), a porphyrin characterized by our lab and others to have exceptionally high selectively and stabilizing ability for parallel GQ structures. I have examined these sequences and their variants using circular dichroism (CD) and UV-vis spectroscopies. I have determined ideal crystallization conditions using PAGE gels and Analytical Ultracentrifugation (AUC). Binding parameters and energetics of NMM-GQ interactions were investigated using isothermal titration calorimetry (ITC) and UV-vis titrations. Currently I am working on crystallization trials of VEGF and G4TERT in complex with NMM. My results and results of my lab-mates will further our knowledge of what contributes to NMM's exceptional binding ability and selectivity toward GQ DNA. Such knowledge is invaluable for improving the design of anticancer therapeutics.

Development of a new premorbid IQ test: Psychometric analysis and validation of the Penn Reading Assessment

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Philadelphia Neurodevelopmental Cohort (PNC) is a collaborative research initiative that focuses on researching the interaction between the brain, behavior, and genetics. The sample consists of over 9,500 adolescents (ages 8-21) who were genotyped and completed clinical psychiatric assessment, neurocognitive testing, and neuroimaging in order to study the impact of genetics on cognitive development and vulnerability to psychiatric illnesses.

A critically important component of such a neuropsychological evaluation consists of an assessment of premorbid intelligence in order to estimate a patient's general cognitive capability independent of any neurological impairment. Premorbid IQ tests gauge abilities that remain relatively unaffected by neurological insult such as neurodegenerative diseases, traumatic brain injury, or other neurological impairments. The most commonly used method consists of measuring performance on achievement test reading sections such as the reading subtest of the Wide Range Achievement Test (WRAT), which has been shown to be a reliable predictor of general intelligence across various populations. However, the WRAT, albeit the predominant test utilized in the field of neurocognitive assessment, is not without its flaws: it has been shown to underestimate the intelligence of those in the higher intelligence range, it is proprietary and expensive to purchase, it is longer than it need be, and it remains a pencil-and-paper task despite the field's shift toward computerized adaptive testing (CAT).

The BBL developed two forms of an alternative reading test, the Penn Reading Assessment (PRA), and administered them to a subset (n = 3,185) of the PNC along with the WRAT. This study aimed to psychometrically analyze and validate the PRA in order to justify its use as a reliable, valid, and publically available alternative reading test. Statistical tests (i.e., factor analysis, internal consistency analysis, item analysis, correlational validation, predictive validation) were performed in order to primarily determine: a) if the PRA measures only one factor (i.e., reading ability as a proxy for IQ), b) how closely related the items of each test are, c) how much information each test gives about differing ability levels, and d) how well the PRA correlates with neurocognitive, fMRI volumetric, environmental, and clinical predictors.

Results indicate that the PRA is an equally valid and reliable measure of reading ability as a proxy for IQ as the WRAT, the gold standard in the field of neurocognitive assessment. This finding supports the use of the PRA as the first free, computerized, adaptive, and sound measure of premorbid IQ for future neuropsychological research.

Characterizing a Quadruple Mutant in the HIV-Induced CH103 Broadly Neutralizing Antibody Clonal Lineage

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Human immunodeficiency virus (HIV) remains a difficult pathogen to neutralize via vaccine-induced antibodies due to the speed at which it mutates. The Fera laboratory has access to longitudinal sequence data of both viruses and antibodies from patient CH505, a chronically HIV infected individual. I worked with a lineage of antibodies called CH103, a lineage that resulted in a broadly neutralizing antibody (bnAb), which is able to bind to a variety of HIV-1 viruses. Throughout the evolution of this lineage the antibody shifted its variable loops away from each other in order to accommodate for an insertion mutation in the virus. Therefore, we wanted to see if we could identify the amino acid mutations responsible for this shift. Towards this goal, I expressed and characterized a quadruple mutant of the CH103 unmutated common ancestor (UCA) antibody, which was based off of a triple mutant that was previously expressed. I introduced a glutamine to glutamic acid mutation at position 50 in the light chain (Q50E). This mutation occurs during the natural antibody evolution of this lineage. As such, I hypothesized that it would affect the interaction between the heavy and light variable chains. I crystallized and determined the structure of the quadruple mutant to 2.33 Å resolution and revealed that the Q50E mutation interacted with an asparagine residue in the heavy chain, altering the antibody to be more like the CH103 bnAb. This mutation pulls two loops between the heavy and light chains closer together, making it notably different from its predecessor triple mutant. Initial binding experiments confirm that the quadruple mutant binds to the transmitted founder virus envelope. Understanding the regions of the antibody that evolved in response to the virus will help guide preventative vaccine design.