



Sigma Xi

Student Research

Poster Session

15- 16 September 2016

Eldridge Commons, Swarthmore College



"Companions in Zealous Research"



Sigma Xi Student Research Poster Session

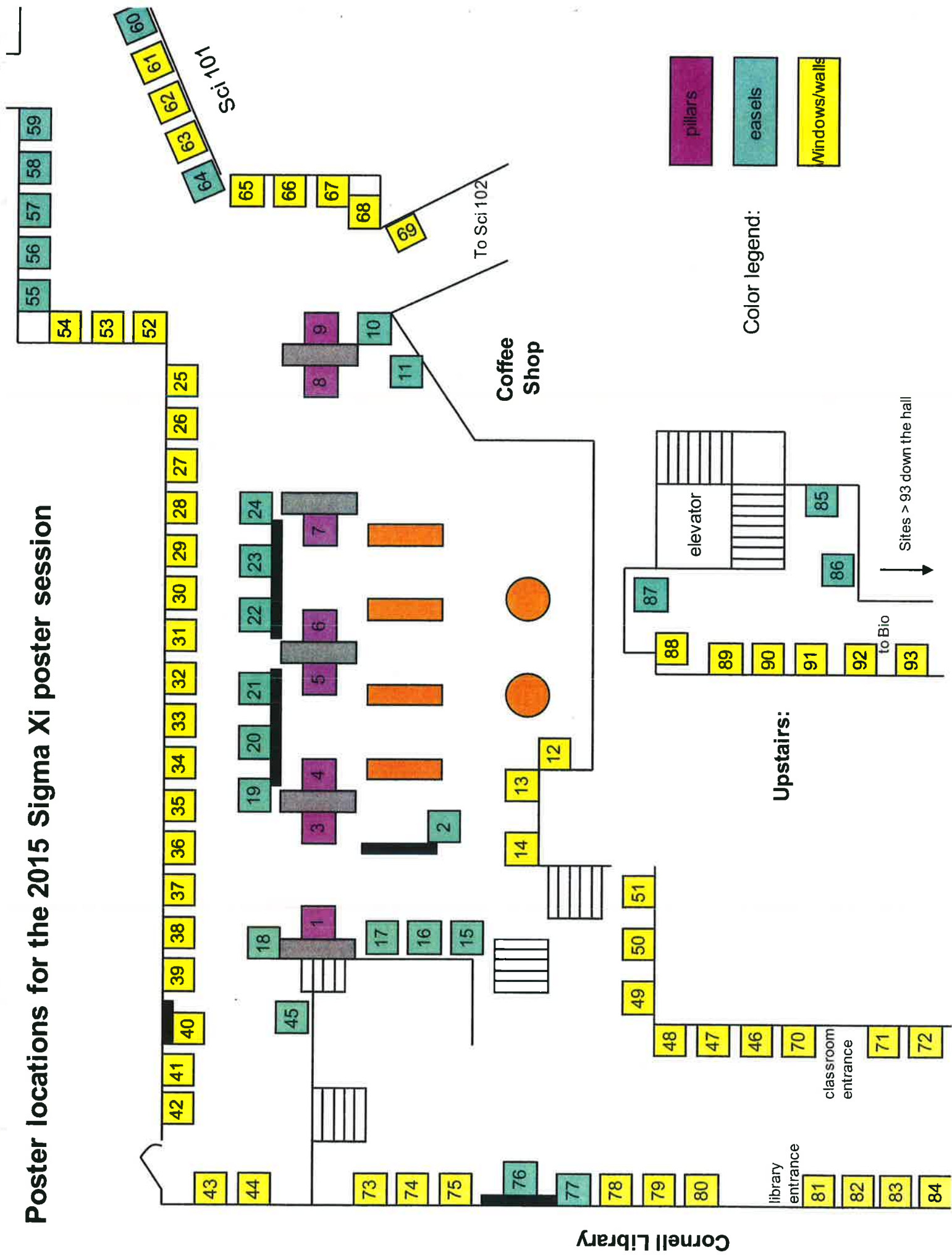
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Examination of factors relating to concussion recovery in elementary school-aged children
Robert Abishek, Gray Vargas, PhD, and Jane Crowley, PsyD
Nemours Alfred I. DuPont Hospital for Children
rabishe1@swarthmore.edu

Traumatic brain injuries (TBI) are the most common childhood injury. The majority of TBIs are classified as mild TBIs, also known as concussion. Most concussion research focuses on sports-related injuries in patients 10 and older. In 80 to 90% of sports-related concussions, symptoms resolve within two weeks. The purpose of our study was to characterize a 6 to 9-year-old clinical sample with sport and non-sports etiologies and describe their concussion recoveries. Additionally, the relationship of several demographic variables known to be correlated to recovery time in older children and adolescents were examined in this younger sample.

Data were obtained via retrospective chart review from a 2012-13 consecutive cohort of 6 to 9-year-olds (N = 81) who were seen by Psychology in a multidisciplinary Concussion Clinic at N/AIDHC. A previously collected sample of 10 to 18-year-olds from the same clinic was used for comparison (N = 278). Recovery length was defined as symptom duration, as determined by self and parent symptom report. Descriptive analyses were used to characterize the patient sample. Independent samples t-tests were used to compare group means.

Twenty-seven percent of the younger sample recovered within 2 weeks and 60% recovered in 4 weeks. No significant differences in mean recovery length were found between 6 to 9-year-olds and 10 to 18-year olds. There were no significant differences in mean recovery lengths of the younger sample considering gender, prior concussion, and pre-existing exceptionalities.

In the range of concussion etiology, 6 to 9-year-olds did not take longer to recover than 10 to 18-year-olds. In contrast to sports-related concussion literature, no factors were found to be predictive of recovery length in 6 to 9-year-olds. When examining the full range of pediatric concussion etiology, existing literature findings may not be applicable to younger children

Existence, Computation, and Stability of Breather Solutions in DNA Dynamical Model

George Abraham and Allie Longo

Adviser: Luciano Medina (NYU)

Deoxyribonucleic Acid (DNA) denaturation is the process in which temperature fluctuations cause DNA strands to unwind and separate. In order to understand this process, physicists have derived various Hamiltonian dynamical models accounting for the thermodynamical splitting of DNA. Understanding the denaturation process is helpful in understanding other DNA processes such as transcription, which incorporates denaturation as a step. It is hypothesized that DNA breathing, the formation of localized finite-amplitude oscillations, is the precursor to denaturation. Hence, our overall goal of this project is to find conditions for the existence of breathing solutions in our models, and to numerically simulate these solutions so as to gain physical insight into our system.

Most of the mathematical models of DNA stem from the Peyrard-Bishop model, which takes into account temperature when analyzing the breathers. Other models use different coordinates and factors to create a more accurate and precise representation of the DNA. For example, there are various models which take into account the helical geometry of the DNA strands, as well as other models which account for environmental factors such as external temperature sources.

We use global functional minimization and calculus of variations methods to give conditions for the existence of breather solutions. We attempt constrained minimization on a Nehari manifold, and aim to use a fibering map to give us conditions for an existence theory. Once we prove that breathers exist, we will numerically simulate them using constrained minimization tools in MATLAB. This will help us gain both mathematical and physical intuition on our various DNA models.

Verrucae on clonal anemone *A. elegantissima* are used in sediment decoration and have time-dependent, adhesive properties

Bronimir Adler-Ivanbrook, Gracie Farley, Rachel Merz

Friday Harbor Laboratory, Washington
badleri1@swarthmore.edu

Clonal anemone *Anthopleura elegantissima* exhibit a decorating behavior where they attach small pieces of sediment to the outside of their body wall. The body wall is covered in verrucae, small bumps that have a higher density of secretory cells than elsewhere on the body wall. By making time lapse video recordings of *A. elegantissima* we determined that the anemone longitudinally compresses its body wall and thus presses its verrucae into the surrounding area; particles can become immediately attached. The attachment force was measured by presenting anemones with beads for varying time intervals. These attached beads were removed with a force transducer. Beads allowed to attach to anemones for .25 and 6 days were easier to pull off, experiencing a mean of 4 ± 1.8 grams and 3.2 ± 2.7 grams of force, respectively. The attachment force peaked after anemones were allowed to attach beads for 3 days with a mean of 8.9 ± 7.3 g.

ELUCIDATING THE RELATIONSHIP BETWEEN PLIN2 AND CERS6

Maxine Esi Atta Annoh, Rotonya Carr, MD PhD

University of Pennsylvania, Pennsylvania, Philadelphia

Mannoh1@swarthmore.edu

Alcoholic Liver Disease from excessive alcohol consumption is characterized by increased lipid droplet accumulation in the liver. Fatty liver disease follows the normal progression from steatosis, to hepatosteatosis and finally, cirrhosis then cancer. There is a lack of medication and early markers to determine fatty liver disease progression. This study investigates how hepatic lipids and their associated pathways promote alcoholic steatosis and regulate Plin2, a lipid membrane protein. PLIN2 was found to increase with Ceramide Synthase production as preliminary data demonstrates. Further investigation may reveal PLIN2 and CerS6 to be adequate early genetic markers for Alcoholic Liver Disease progression.

Investigating the Structure of the LsrB LuxS⁺ Protein from *Clostridium autoethanogenum*

Judy Al, Stephen T. Miller

Department of Chemistry and Biochemistry, Swarthmore College
jal1@swarthmore.edu

Abstract

Quorum sensing is the natural phenomenon by which bacteria use cell-to-cell communication to facilitate the coordination of certain cellular behaviours. This bacterial communication is mediated by bacterial signaling molecules such as autoinducer 2 (AI-2). These signal molecules accumulate in bacterial populations, thereby facilitating the coordination of cellular behaviours such as biofilm formation, bioluminescence, and virulence. To date, two families of AI-2 receptors have been isolated: LuxP and LsrB, each of which binds to different forms of the AI-2 signal molecule. Of particular interest is evaluating the binding ability of newly-identified AI-2 receptors across a variety of bacterial strains.

This project entailed studying the putative AI-2 receptor protein *C. auto* LsrB LuxS⁺. The goal of this summer project was to crystallize the LsrB LuxS⁺ protein from *C. auto*, which has a 38.2% sequence identity with the established *Bacillus cereus* LsrB receptor protein. Crystallization of *C. auto* LsrB was accomplished; however, the crystallization process is currently being perfected, in order to yield crystals that will allow for optimal structural analysis via X-ray crystallography. It is through X-ray crystallography that we will ultimately be able to determine whether or not the *C. auto* LsrB LuxS⁺ protein is, in fact, a member of the LsrB class of proteins.

Literature Cited

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- Pereira, C. S., Regt, A. K., Brito, P. H., Miller, S. T., & Xavier, K. B. (2009). Identification of Functional LsrB-Like Autoinducer-2 Receptors. *Journal of Bacteriology*, 191(22), 6975-6987. doi:10.1128/jb.00976-09

Role of nuclear receptor *Nr4a* in long-term memory consolidation

Justine Albers, Ted Abel

University of Pennsylvania
jalbers1@swarthmore.edu

Long-term memory consolidation requires gene transcription and protein synthesis in the hippocampus. The *Nr4a* family of orphan nuclear receptors has been previously implicated in memory consolidation in mice. We investigated *Nr4a*'s involvement in consolidation by attempting to identify its downstream targets. In order to do this, we used a transgenic mouse model that has a dominant-negative (DN) form of the *Nr4a1* gene, which is selectively expressed in excitatory neurons of the forebrain and prevents the *Nr4a* family from activating other genes. By blocking the ability of *Nr4a* to activate downstream genes, we were able to use these mice to identify potential targets of the *Nr4a* family.

We used contextual fear conditioning in order to examine the effect of the dominant-negative transgene on the hippocampus at the molecular level. We found that the mRNA expression level of *Pak6*, a gene implicated in learning and memory, was significantly decreased in *Nr4aDN* mice. Quantification of protein levels in the hippocampus also revealed significant down-regulation of *Pak6* in *Nr4aDN* mice. Together, our mRNA and protein studies provide a strong indication that *Nr4a* is a regulator of *Pak6*.

Insider inhibition in Yellow Band Disease: antibacterial properties of bacteria associated with symptomatic *Orbicella faveolata*

Luella Allen-Waller and Kim B. Ritchie

Mote Marine Laboratory, Sarasota FL

lallenw1@swarthmore.edu

Coral disease rates are rising and a microbial ecology approach is increasingly essential to reef conservation efforts. This study examines antibiotic capabilities of commensal mucoid bacterial isolates from both healthy and Yellow Band diseased mountainous star corals (*Orbicella faveolata*). We screened more than 1700 native bacteria isolated from reefs in Buck Island National Monument, St. Croix, US Virgin Islands for their ability to inhibit growth of 4 coral pathogens: *Vibrio shiloi*, *V. parahaemolyticus*, *V. coralliilyticus*, and *Serratia marcescens*. We identified three consistent commensal antibiotic producers (CAPs) from diseased coral samples, including *B. marisflavi*, a novel source of antibiotics, and *Vibrio* sp. (likely known antibiotic producer *V. inhibens*). Contrary to expectations, healthy coral mucus yielded no CAPs. In all three cases, CAPs' ability to inhibit the coral pathogen *V. shiloi* varied between ambient and bleaching temperatures, although the temperature response was inconsistent across bacterial species. Some CAPs inhibited *V. shiloi* more effectively at 25° C, while the vibronic inhibitor produced antibiotic exclusively at 30° C. This study provides further evidence of commensal microbial roles in coral immunity to pathogens, and the impact of environmental temperature on these interactions.

M2 Protein Conformational Exchange is Affected by Curvature Generating Lipids

D. Stuart Arbuckle and Kathleen Howard

Department of Chemistry and Biochemistry, Swarthmore College, Swarthmore, PA

darbuck1@swarthmore.edu

M2 is a homotetrameric membrane protein of the influenza A virus. Its cytoplasmic amphipathic helix has been implicated in generation of negative Gaussian curvature (NGC), which is topologically necessary for membrane scission, a crucial step of the viral life cycle. Viral budding assays have shown the helix to be both necessary and sufficient for generation of curvature. This function has led M2 to be viewed as a promising drug target, but structural characterization of the amphipathic helix is limited. Previous work using small angle X-ray scattering (SAXS) has demonstrated that M2 induced curvature deformations in model membranes are dependent on choice of lipids. Some lipids produce greater membrane deformation and greater resultant curvature than others when in the presence of M2. Further characterization of M2's amphipathic helix by the Howard Group using EPR spectroscopy has suggested that M2 populates two low energy conformations, one of which is budding relevant. The population of each conformation has also been linked to the presence of cholesterol, which is hypothesized to stabilize the budding relevant conformation.

This study investigates the conformational dynamics of M2 in the presence of cholesterol and lipids known to allow varying generation of NGC in the presence of M2. Site directed spin label (SDSL) electron paramagnetic resonance (EPR) spectroscopy is a biophysical technique particularly well suited to the study of small membrane proteins such as M2 because it allows for measurement of protein dynamics and topology in a biochemically relevant system. A paramagnetic label is attached to a site on M2 by site directed mutagenesis. The labelled protein is reconstituted into a lipid membrane and an EPR spectrum is collected. EPR analysis can reveal the motion of the attached label and the depth of the label in the membrane.

We found that M2 preferentially occupies the budding relevant conformation in lipid known to allow generation of NGC. EPR lineshape analysis is consistent with the hypothesis that M2 populates two low energy conformations (mobile and immobile). In lipid environments linked to highly curved membranes, equilibrium favors population of the immobile, budding relevant conformation. Computational simulation of the multicomponent behavior allows extraction of the theoretical spectral components and quantification of the relative populations of each conformation in each lipid environment. Oxygen accessibility EPR data confirm that the immobile conformation is shallower in the membrane than the mobile conformation. This provides strong new evidence to the conformational exchange hypothesis and further support to the concept that attenuation of curvature generation by M2 is a viable anti-influenza strategy.

Simulating Spiral Galaxies: Trapped Orbits and Radial Migration
By Luke Barbano and Noah Lifset under the supervision of Professor Kathryn Daniel
Swarthmore College
lbarban1@swarthmore.edu and nlifset1@swarthmore.edu

An outstanding perplexity in modern astrophysics is the dynamic process known as radial mixing, a blanket term contrived to describe the apparent radial migration of stars in spiral galaxies. Previous work on the subject has established that trapped orbits in conjunction with the spiral arms' transient nature are a likely mechanism by which radial migration occurs. The purpose of this research was to investigate the effects of incorporating non-circular stellar orbits into this theoretical framework. The methodology for studying radial migration entailed designing an orbital integrator to numerically simulate the orbit of a test particle in a galactic potential, and then populating the simulation according to a realistic star distribution. Using an open source, distributed computing service called Open Science Grid (OSG), it was possible to quickly perform tens of thousands of orbit simulations and methodically examine the immense amount of resulting data. Analysis of this data has revealed a great deal about the role of trapped orbits in radial mixing, namely that migration has a clear dependence on spiral arm tightness and an unexpectedly high efficiency of mixing. This project yielded new results and provided numerous confirmations of previous theory. However, there is still more work to be done in terms of expanding the simulations to incorporate more detailed astrophysical theory.

Can Identifying Binding Partners of Novel Proteins Give Insight into Function?

Guillermo Barreto Corona, Elizabeth A. Vallen

Swarthmore College Biology Department
gbarret1@swarthmore.edu

Research on coral is essential due to the importance of coral reefs in maintaining healthy underwater ecosystems and as a food source for a large number of people from developing countries. Due to anthropogenic changes, coral reefs have been alarmingly decreasing in number. Research on coral, however, can be difficult due to the coral's exoskeleton and stringent environmental requirements. Some sea anemones fortunately can be used as a model organism for coral due to their similarities. Both types of cnidarians have many proteins of unknown function, some of which are very highly expressed. The goal of the research was to begin to investigate the function of some of these proteins. We decided that the best method to do this was through two-hybrid screening. Two-hybrid screening can identify an interaction between a protein of unknown function and a protein of known function. This could allow insights into the processes that the novel protein was involved in. Alternatively, if the protein of unknown function interacted with other proteins of unknown function, we might be able to build a new network of novel interacting proteins. We first had to select the genes that we wanted to work with from the sea anemone genome. We chose genes that expressed proteins of unknown function in high amounts. PCR was used to amplify cDNA's of our genes of interest, which were then cloned into plasmids that were transformed into bacteria. Restriction digestion and DNA sequencing were used to verify that the vectors contained the correct DNA of our genes of interest. The plasmids were then inserted into yeast to be tested for the production of our proteins of interest and for auto-activation in the two-hybrid assay. Inadequate production of our proteins of interest could lead to failure to identify binding partners. Likewise, if our proteins of interest auto-activate, these false positives would prevent us from identifying true positive interactors. During our research period we identified good candidates for two-hybrid screening, but have not yet performed the process. In the future we plan to move ahead with the candidates and screen them against our library of proteins that will interact with our proteins of interest.

Wait, don't mate (yet)! Female commitment and reproductive investment and urgency in grey tree frogs

Brandon Bastien, Jacob Malin, Desta Pulley, Casey Lu Simon-Plumb, Alexander T Baugh

Swarthmore College
jmalin1@swarthmore.edu

In many sexually reproducing organisms, the initial stages of mate attraction must be accompanied by continued commitment in order for copulation to occur. Here we examine mate choice in wild female grey treefrogs (*Hyla versicolor*) using a dynamic phonotaxis assay. By experimentally manipulating male call quality in real time during an initial phonotactic approach, we estimate individual variation in choice latency and path length. We also examine the physiological mechanisms that might influence this variation, including clutch size, reproductive urgency and concentrations of steroid hormones. This allows us to test the reproductive investment-urgency hypothesis: females with a higher reproductive investment will exhibit choosier behavior (higher choice latency) but that choosiness will decrease as they near the time horizon for oviposition in order to offset the risk of an unfertilized clutch. We demonstrate a potential endocrine basis for reproductive urgency and discuss implications for the stability of individual variation in behavioral strategies and their endocrine correlates.

Like neurons, honey bees may use explicit inhibitory feedback to flexibly allocate foragers

Talia Borofsky, Christopher Mayack, Victor Barranca
Swarthmore College

tborofsl@swarthmore.edu

Honey bees and neurons in the brain display “collective decision-making,” whereby groups of individuals together determine which external stimuli to respond to and how to respond (Couzin 2009), yet no individual is aware that a decision is taking place. Negative feedback is essential for accurate and flexible collective decision-making (Couzin 2009; Gruter 2012). We focus on how a rarely documented negative feedback signal used by honey bees, the stop signal, influences collective decision dynamics. The stop signal consists of one bee briefly making a piping noise and then butting its head into another bee waggle dancing. This behavior inhibits the waggle dance and thus dampens recruitment of other foragers to a food source. To investigate its effects on forager allocation based on nutritional quality of a foraging site, we trained a colony of *Apis mellifera* to an artificial feeder containing 2.5 M sucrose solution 50 m away from the hive. We then recorded feeder visitations and the number of stop signals produced and received per dance in the hive, before and after a decline in food quality to 0.75 M sucrose solution at the foraging site. There was a significant effect of food quality on feeder visitation ($\chi^2_{1,586} = 36.20$, $P < 0.0001$), with a decline in food quality causing an increase in visitation of both trained and recruited bees ($\chi^2_{4,586} = 32.93$, $P < 0.0001$; $\chi^2_{4,586} = 19.05$, $P < 0.0001$). Yet in the control treatment, in which the food quality remained the same, there was no significant increase in trained bee visitation, but there was an increase in the number of visits by recruited bees ($\chi^2_{4,586} = 0.01$, $P = 0.91$; $\chi^2_{4,586} = 9.78$, $P = 0.0018$). We found that visitations to the feeder increased after a decline in food quality, although this may result from increased frequency of visitation rather than increased recruitment. The increased frequency of visitations may result from the colony being more desperate for food, since during the end of July, when the experiments took place, there is a dearth in natural foraging sites. In the future, we will analyze video data and use models from theoretical neuroscience, such as the firing rate and integrate-and-fire models, to better understand if through convergent evolution both individual bees and neurons use similar regulatory feedback mechanisms to optimally make collective decisions.

Peptides as Inhibitors of Amyloid Fibril Formation

Delfin G. Buyco, Niels H. Andersen

University of Washington

dbuyco1@swarthmore.edu

Amyloid diseases are conditions in which misfolded proteins aggregate to form amyloid fibrils, which are ordered structures that are comprised of β -sheets. Small peptides (less than 20 residues) have been studied as inhibitors against amyloid formation and as potential treatments against amyloid diseases. The present study focused on inhibitors for two different amyloidogenic proteins. The inhibitors that were investigated for Islet Amyloid Polypeptide (IAPP), the aggregation of which is implicated in Type II Diabetes, were peptides that exhibited sequence homology to IAPP. For α -Synuclein (α -syn), which is implicated in Parkinson's Disease, the inhibitors that were studied were designed cyclic β -hairpins, specifically mutants of the peptide KKLTVSIpGKKITVSA. Assays utilizing Circular Dichroism spectroscopy were used to ascertain which peptides acted as effective inhibitors against amyloid fibril formation, and at what concentrations those peptides were effective. ^{15}N Heteronuclear Single Quantum Coherence NMR spectroscopy was used to determine which residues interacted with the inhibitors. Some of the peptides in this study were found to inhibit the formation of β -sheets that would result in aggregation.

**New cyclization strategies for elaboration of enantiomerically pure
N-Oxazolidinoyl Diene Iron(0) Tricarbonyl complexes**

Sooyun Choi, Professor Robert S. Paley

**Department of Chemistry and Biochemistry, Swarthmore College
500 College Ave, Swarthmore, PA 19081
schoi3@swarthmore.edu**

Multiple projects were pursued to discover new synthetic strategies to further functionalize the existing class of *N*-oxazolidinoyl diene iron(0) tricarbonyl complexes. These included: a) allylation of cyclic oxonium ions; b) ring-closing metathesis of an *N*-vinylated derivative; c) diastereoselective Pictet-Spengler reaction; d) diastereoselective Rh(I)-catalyzed C-H insertion. The most progress was made on project d), where it was shown that 1) a α -diazoester unit could be installed on a side chain of an analog of the title complex, and 2) Rh(I)-catalyzed C-H insertion of this α -diazoester into a C-H bond on an adjacent side chain proceeded with perfect diastereoselectivity. This transformation created two new stereocenters in a single step, significantly expanding the synthetic options available from the title compounds.

Spatio-Temporal Clustering of Cholera Cases: The Impact of the Density of Rivers and Streams Worldwide, During '82-'83 & '97-'98 El Nino Events

Nikhil Chopra, G. Narayanaraj

Swarthmore College
nchopra1@swarthmore.edu

This research project set out to use geographic information systems and remote sensing methods to explore the relationship between climate variability and Cholera cases on a global scale. Specifically, this study focused on the climate events caused by El Nino Southern Oscillation, a fluctuation in pressure differences between worldwide ocean currents. This cycle contributes to year-to-year variability in weather and increases the likelihood of extreme weather events such as heavy rainfall, droughts, and storms. In order to qualify as an El Nino event, sea surface temperatures (SST) must remain at or above 0.50°C greater than average for at least three months across the specific region. Since 1899, 1982-1983 and 1997-1998 have been designated as 'very strong' El Nino years due to an increase in worldwide weather anomalies during those years. These years define this study's temporal scale. Extreme weather events can affect health by a variety of mechanisms: increased rains can increase the vectors and reservoirs associated with vector-borne diseases, contaminate water and increase water-borne diseases, disrupt health services, and affect mental health. Increased dry conditions can cause malnutrition and food insecurity, decrease water quality, reduce access to health care, and cause respiratory diseases. Overall, both extremes displace populations within a specific region. There seems to be a link between a population's built habitat, interactions, and behavior in conjunction to weather. El Nino events can increase the global incidence of vector-borne diseases such as Cholera. Cholera is an acute secretory diarrhea caused by the bacterium *Vibrio cholerae*. It is a communicable disease and injects stool samples. The bacterium can contaminate drinking water supplies, resulting in transmission of Cholera. *V. cholerae* is often associated with zooplankton and shellfish in fresh water because it can use chitin as a carbon and nitrogen source. Chitin induces competence, pointing to lateral gene transfer occurring in water, especially during zooplankton blooms. For this reason, plankton can be seen as a water-based reservoir of Cholera. The presentation of Cholera is a distinct diarrheal purging after the bacteria colonize the small intestine. This direct fecal-oral transmission makes Cholera a water-borne, or water-carried, disease. In order to study the relationship between Cholera and climate variability, water availability was used as the secondary variable to the number of Cholera cases. Country-level fresh water stream and river density was used as a proxy for natural water sources.

NGF-TrkA Endosome Promotes Synapse Development and Maintenance in SCG Dendrites

William Colgan¹, Kathryn Lehigh², Katherine West³, David Ginty²

Harvard Medical School, Boston, MA
wcolgan1@swarthmore.edu

Nerve Growth Factor (NGF) is a classic neurotrophin involved in growth, survival, and synapse development. NGF binds to its receptor, a tyrosine kinase TrkA, forming a signaling endosome. Previously we discovered that the TrkA endosome is transported from the axons to the dendrites of sympathetic neurons. To study how the TrkA endosome promotes synapse development and maintenance in dendrites, we looked at the Superior Cervical Ganglion (SCG) of mice, because it had already been shown that post synaptic density (PSD) proteins in dendrites are dependent on NGF applied to the distal axon of compartmentalized sympathetic cultures. We showed that signaling competent TrkA endosomes are located near synapses throughout development by using an antibody that marks the phosphorylated tyrosine residue 785, denoted P-TrkA. We dissected the SCG out of *TH^{CreER};R26^{LSL-YFP}* mice at P7, P14, P21, and P42-56, and immunostained for P-TrkA, VACHT, and Homer. We then imaged the SCG with a confocal microscope and analyzed the puncta, asking if they were associated. Co-localization of VACHT and Homer puncta showed that synapses per μm^2 increased with age. Co-localization of P-TrkA and VACHT puncta showed overlap, which increased with age. Co-localization misses non-overlapping interactions, so we also developed and performed a nearest neighbor analysis to assess non-overlapping interactions. At all ages the median distance between a P-TrkA puncta and the nearest VACHT puncta was less than $1.5 \mu\text{m}$. This analysis confirms that TrkA endosomes promote synapse development (P7 to P21) and supports the novel hypothesis that TrkA endosomes are required for synapse maintenance (P42-56). More research is required to determine the signaling pathway by which TrkA endosomes affect PSD proteins.

¹ Swarthmore College, Swarthmore, PA

² Department of Neurobiology, Harvard Medical School, Boston, MA

³ Simmons College, Boston, MA

Pragmatic Language in the Director Role during Referential Communication in Autism Spectrum Disorder

Madeline G. Conca¹, Jane Beriont², Ashley DeMarchena³, Edward S. Brodtkin⁴, Robert T. Schultz³, & Elizabeth S. Kim³

¹Department of Neuroscience, Swarthmore College, Swarthmore, PA,

²Sidney Kimmel Medical College, Thomas Jefferson University, Philadelphia, PA,

³Center for Autism Research, Children's Hospital of Philadelphia, Philadelphia, PA,

⁴Perelman School of Medicine at the University of Pennsylvania, Philadelphia, PA

mconcal@swarthmore.edu, beriontj@email.chop.edu, deMarchenaA@email.chop.edu,
ebrodtkin@mail.med.upenn.edu, schultzrt@email.chop.edu, kime9@email.chop.edu

Abstract

Autism Spectrum Disorder is characterized by impairments in social communication, reciprocity, and restrictive, repetitive and unusual interests and behaviors.¹ One area of social communication, pragmatic language, is often investigated through Referential Communication (RefComm) tasks², and is an area of deficit for individuals with ASD.³ The RefComm paradigm is a vehicle for the controlled elicitation of both pragmatic communication and management of common ground.⁴ In the RefComm paradigm, two individuals communicate to arrange picture/shape/objects in a pre-specified order, but only one (the Director) can see the target arrangement, and the other (the Matcher) must identify and arrange the objects. In our study, each pair comprises of a participant and a confederate, who each take a turn playing both the Director and Matcher roles with each other. In our task, pairs arrange 5 permutations of a fixed set of unfamiliar objects before switching roles and completing 5 permutations of a fixed set of new unfamiliar objects; this repetition affords an opportunity to investigate how pairs form the common ground on which they refer to the objects.

Participants will include 24 adults with ASD and 24 with TD (ages 21–50 years), with diagnostic groups matched on age and full-scale IQ. Data collection is ongoing. All participants complete a series of characterizing questionnaires and standard behavioral assessments, including the Autism Diagnostic Observation Schedule, Second Edition⁵ (ADOS-2) and Wechsler Abbreviated Scale of Intelligence⁵ (WASI-II).

By examining the pragmatic aspects of language used by participants while in the Director role, we can investigate possible between-diagnostic-group differences in (1) quality of description of unfamiliar objects, (2) repair of errors or breakdowns in communication, (3) rigidity in negotiating common ground referents with the Matcher.

Pragmatic language will be manually annotated, from transcripts of utterances (themselves manually transcribed from audio recordings) and from video recordings of RefComm interactions. We will analyze the Director's role through a number of smaller variables, each aimed at evaluating a specific goal of the task: effectiveness, over or under sharing of information, errors, repair and common ground choice. Further exploratory analyses will investigate possible relationships between pragmatic language behaviors and behavioral characterizations assessed independently using questionnaires and observation-based assessments.

Group-comparison in pragmatic behaviors as Director and relationships between pragmatic behaviors and others characterized using standardized assessments will allow us to better describe the differences between TD and ASD adults, and to begin to understand what underlying behaviors, psychological, and neurological processes may contribute to the pragmatic language behaviors studied.

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Cryptogenography

Alex Crane, Joshua Brody

Swarthmore College
acrane1@swarthmore.edu

Imagine you have organized a protest against your evil government. You would like to post the location of the protest online, but your government has an agency that monitors all internet activity. If you simply publish the location, you will be arrested and your protest will have no leader. Cryptogenography tells us how you and your followers can work together to publish the location while hiding your identity. Unlike cryptography, cryptogenography concerns hiding the source of information, rather than the information itself.

We study a toy model in which two players, Alice and Bob, attempt to share a secret bit without revealing the source to an adversary, Eve. Alice and Bob speak according to a prearranged protocol, and agree on the most likely secret given their communication transcript and the protocol used. Eve, who also has access to the protocol, always chooses the most likely secret holder given the protocol and transcript. Alice and Bob win if they correctly agree on the secret value and Eve chooses the wrong player.

We can assign scores to protocols according to the probability of success that they give Alice and Bob. We are interested both in discovering new achievable scores, which we call lower bounds, and in examining the theoretical limits of protocols, or upper bounds.

Our research consists largely of experimenting with possible improvements to an algorithm called Automated Search, which generates good protocols from finite subsets of our probability space. We also use a concavity argument for functions on this space to search for new upper bounds.

We have generated new results at both ends of our research, producing improved lower and upper bounds of .3387 and .3619, respectively.

The Effects of Surface Passivation via RAFT Polymerization on the Optical Properties of Carbon Quantum Dots

Nathan W. Dow, Justin P. Cole, Erik B. Berda and Christine A. Caputo

University of New Hampshire, Durham, NH, 03824
ndow1@swarthmore.edu

Carbon quantum dots (CQDs) are carbon nanoparticles that have been the focus of numerous research projects over the last decade due to their unique photoluminescence properties, which are often enhanced via surface passivation and functionalization to obtain useful fluorescence quantum yields. RAFT polymerization, a synthetic procedure that uses a radical chain transfer agent to obtain high molecular weight and low polydispersity products, can be a facile and reliable method of developing chains from alkene-based monomer sources. These two areas of research were combined over a ten week period to carry out the synthesis of two novel CQD types, starting from a previously investigated precursor derived from a “one-pot” citric acid-based thermolytic process. The functionalization of the CQD surfaces was carried out via a series of classic organic reactions, culminating in variations on a RAFT polymerization procedure to attach unique polymers to the surfaces of the CQDs. The polymerized CQDs were characterized through spectroscopic methods, and were found via fluorometric analysis to have peak emission wavelengths that are independent of the excitation wavelength used. Because both polymer CQD types displayed useful optical behavior, they will eventually be tested as photosensitizers for use in catalyzed redox processes by attempting solar-induced hydrogen evolution from a sacrificial electron-donor solution.

Quantifying aerobic alternate electron acceptor expression in *Escherichia coli* using Lambda Red Recombineering

Luke Eppley¹, Amy C. Vollmer¹, Manuela Roggiani² and Mark Goulian²

¹Biology Department, Swarthmore College

²Biology Department, University of Pennsylvania
leppeyl@swarthmore.edu

Escherichia coli contains electron-transport chains which incorporate various dehydrogenases and terminal reductases used in respiration. While oxygen is the preferred terminal acceptor, as it offers the largest redox potential (and therefore maximizes ATP production), *E. coli* has been shown to utilize five alternate acceptors when grown anaerobically. Nitrate, nitrite, TMAO, DMSO, and fumarate, listed in descending order of energy conservation, all act as acceptors in order to maintain respiration. The reductases for these molecules are almost all regulated by two-component systems to safeguard against unnecessary energy expenditure when a better electron acceptor is present. However, previous research in the Goulian laboratory showed that expression of *torC*, the gene encoding the TMAO-specific reductase, exhibited remarkable cell-to-cell activation variation in aerobic, TMAO-induced cultures. This effect had yet to be studied in the other terminal electron acceptors. Our investigation was undertaken to determine whether this observation was specific to TMAO, or more generalizable to other alternative electron acceptors, such as the nitrate-specific *narG*, and the DMSO-specific *dmsA*. Using a fluorescent reporter (*yfp*), attempts were made to introduce promoter fusions (*narG::yfp*, *dmsA::yfp*, *torC::yfp*) into the *E. coli* chromosome. However the method for such a site specific integration were not successful. Subsequently, the *narG::yfp* construct was then placed on a single-copy plasmid, which was induced by nitrate and grown aerobically. Unlike the previous *torC* studies, fluorescent microscopy showed no significant distribution difference between aerobic and anaerobic activation. This indicates that there may be a difference between the activating mechanisms for alternative electron acceptors in anaerobic respiration, and that a difference may exist in the oxygen-dependent half of the two-component system.

Leaderless phage λ CI activity requires the coupling of transcription and translation through NusG and NusE in *E. coli*

Bolutife Fakoya, Robert Washburn, Amy Cheng Vollmer, and Max Gottesman

**Columbia University Medical Center, New York, NY
Swarthmore College, Swarthmore, PA
bfakoya1@swarthmore.edu**

Leaderless mRNA transcripts in prokaryotes lack a 5' UTR and consequently translation begins directly at the start codon of the transcript. Previous studies have elucidated the role of a 5' terminal phosphate in the initiation of translation of leaderless transcripts in *Escherichia coli*, but little has been proposed to describe the mechanism of the RNA polymerase binding to the starting AUG. The NusG/NusE(S10) protein complex has been shown previously to provide a physical linkage between RNA polymerase and the lead ribosome in *E. coli* and to couple the processes of transcription and translation.

Using *lacZ* fusions and a β -galactosidase based assay, we show that a functional NusG/NusE complex is essential for the translation of leaderless bacteriophage λ CI transcripts in *E. coli*. In *E. coli* strains with mutated NusE and NusG proteins and uncoupled transcription and translation, we see statistically significantly lower λ CI activity ($p < 0.0001$ and $p = 0.0322$ respectively). We also show that λ CI activity can be restored in NusE/NusG mutant strains through complementation with *wt* NusE and NusG expressed from plasmids. As leaderless transcripts occur frequently in many varied organisms, further studies hope to characterize this phenomenon and investigate the role of NusG and NusE in the macromolecular mechanisms of leaderless transcript translation.

Two photosynthetic symbionts differentially control light response behavior in a clonal anemone (*Anthopleura elegantissima*)

Grace M. Farley, Bronimir S.R. Adler-Ivanbrook, and Rachel A. Merz
University of Washington Friday Harbor Laboratories, Friday Harbor, WA
gfarley1@swarthmore.edu

The clonal anemone *A. elegantissima* has facultative mutualisms with two photosynthetic symbionts. Anemones predominantly hosting the unicellular green alga *Elliptochloris marina* are more light sensitive and are found in lower intertidal or shaded regions compared to brown anemones inhabited by the dinoflagellate *Symbiodinium*. *A. elegantissima* attach debris to their body, protecting their tissues from excess light exposure. Little is known about how anemones perform this decorating behavior, nor its relationship to symbiont type. We hypothesized that anemones with light sensitive *E. marina* decorate more when exposed to light than those with *Symbiodinium*. To test this, anemones in both light and dark treatments were allowed to attach pebbles for 24h. Green and white (asymbiotic) anemones increased decorating in the light compared to the dark, consistent with the idea that this behavior protects them from sunlight. However, brown anemones attached the largest number of pebbles, and this did not differ between treatments. When allowed to travel freely along a light-dark gradient, white and green anemones preferred shaded areas, while brown anemones had no preference. Pebble cover on white anemones increased their preference for light areas of the tank. These findings suggest a differential control of decorating behavior based on symbiont type, and further verifies that this behavior is related to light exposure.

Yeast Two Hybrid Screening: An Approach to Understanding Novel Cnidarian Proteins

Elizabeth M. Flores, Elizabeth A. Vallen

Swarthmore College, Swarthmore PA
eflores1@swarthmore.edu

"Coral Bleaching," a phenomenon where corals flush photosynthetic dinoflagellates out of their tissues, is a growing issue in marine ecosystems as a result of global warming and ocean acidification. Bleaching, normally a defensive behavior to rid of unproductive symbionts, is becoming harmful to coral populations and the communities they live in because of the rates at which it is occurring. *Aiptasia pallida*, a sea anemone, is a simple cnidarian that serves as a model organism to study more complex and difficult to cultivate species such as corals. Here we begin to characterize proteins of unknown function in *A. pallida* in order to gain a better understanding of cnidarians and the cnidaria-symbiont relationship that is vital to many species in this phylum.

A. pallida proteins of unknown function will be analyzed using a yeast two-hybrid system. The basic premise of this approach is to infer a protein's function by identifying its interacting partners. This is achieved by making two types of chimeric proteins: the first is known as the bait and is composed of the protein of interest and the DNA binding domain of a transcription factor. The second chimeric protein is known as the prey and is composed of a random protein encoded in the *Aiptasia* genome and the activating domain of the same transcription factor mentioned above. If the bait interacts with a prey successfully, the result will be an active transcription factor; this can be visualized by the activation of reporter genes. This project focused on constructing the chimeric bait proteins for the library screening, which will be performed in future experiments.

Four genes of interest followed the following criteria: functions are unknown, highly expressed in *Aiptasia*, does not contain a trans-membrane domain, does not go through the secretory pathway, and is expected to encode a protein smaller than 200 amino acids.

PCR was used to amplify the genes of interest from cDNA. Only one was amplified from cDNA at the expected size. Although another was amplified, it appeared to be from genomic DNA as it was larger in size than predicted for the cDNA. The other two were not amplified. The PCR products were recombined into the bait vector and transformed into competent *E. coli*. Plasmid DNA was recovered from transformants and sequenced.

Plasmids encoding the correct chimeric protein were transformed into yeast. The expression of the protein was confirmed through Western blots. The bait proteins were tested to ensure that they did not activate reporter genes on their own to confirm that they are good candidates for use in future yeast two hybrid screenings.

Traditional Physics vs. IPLS: Comparing Student Experiences

Haley Gerardi, Catherine Crouch, and Benjamin Geller

Swarthmore College

`hgerard1@swarthmore.edu`

At Swarthmore College, a first-semester Introductory Physics for the Life Sciences (IPLS) course was recently introduced that draws on authentic biological examples relating to kinematics, Newtonian mechanics, and thermodynamics. Because the course is offered only every other year, we are uniquely situated to compare the experiences of those students who take the IPLS course to a similar set of students who take a traditional first-semester introductory physics course that covers the same topics but does not foreground biological connections. Researchers drew upon conceptual and attitudinal survey data, as well as a series of case-study interviews, to describe the conceptual, epistemological, and affective differences that we observed between the two student populations. Features that were most salient to the IPLS students' experience were identified, and suggest how particular course structures may have been especially important in supporting students' ability to do well in the IPLS environment.

Volumes of Polytopes

Joshua Goldstein, Ben Goodman, Joshua Mundinger, Thomas Hunter

Swarthmore College

jgoldst1@swarthmore.edu, bgoodma1@swarthmore.edu, jmundin1@swarthmore.edu

We explored the mathematical field of Ehrhart theory, which studies the connections between the volumes of polygons, polyhedra, and their higher-dimensional analogues (polytopes) and the number of integer points contained within them. We focused to a large extent on the question of what makes two polytopes “the same” from the perspective of Ehrhart theory. The most promising notion we found, *lattice scissors congruence*, states that two polytopes are the same if they can be divided into smaller polytopes such that the pieces of one may be mapped by lattice-preserving transformations to the pieces of the other. We examined different notions of lattice scissors congruence and, drawing heavily on existing literature, determined which essential properties of Ehrhart theory they preserve.

***Bmal1* expression in the muscle not brain alters sleep phenotypes**

Azikiwea Green, Dr. Christopher Ehlen and Dr. Ketema Paul

Morehouse School of Medicine, Atlanta GA

agreen1@swarthmore.edu

Studies have shown that sleep loss stresses the body and specifically impairs cognitive processes and executive functioning. Sleep Recovery is critical in preventing these effects. However, the mechanisms which facilitate this recovery are not well understood. Genetic deletion of the circadian transcription factor *bmal1* in mice reduces their ability to recover from sleep. *Bmal1* whole-body knockout also causes a variety of physical abnormalities that are unrelated to sleep. Using tissue-specific *bmal1* rescue and knockout models, this study sought to isolate effects on sleep from these ancillary phenotypes. In addition, we looked to find the mechanism which mediated these effects on sleep phenotypes.

Using tissue-specific *bmal1* transgenic models, *bmal1* was rescued in whole-body knockout mice selectively in both the brain and the skeletal muscle. In addition, *bmal1* transgenes on a wild-type background selectively overexpressed *bmal1* in the brain and skeletal muscle. The study also used an inducible muscle-specific *bmal1* knockout. EEG recordings, used to measure sleep phenotypes, revealed that during baseline *bmal1* rescue in the brain did not restore NREM sleep to wild-type levels. Surprisingly, *bmal1* rescue in skeletal muscle did restore NREM sleep.

After 6 hours of forced wakefulness, there was no significant difference in NREM sleep between wild-type and brain-overexpressed mice. However, muscle over-expressed mice exhibited significantly less NREM sleep when compared to wild-type. Whereas brain-rescue mice gained sleep during recovery, muscle-rescue mice were more vigilant after sleep deprivation than during baseline. During 24 hours of forced wakefulness, overexpressing *bmal1* in the muscle significantly reduced NREM sleep. Also, *bmal1* muscle-overexpressed mice slept less intensely than wild type during all protocols. Selective knockout of *bmal1* in the muscle increased NREM sleep identical to observations of whole-body *bmal1* knockout mice during baseline.

Overall, data from this study suggests that *bmal1* expression in the skeletal muscle is more important for sleep regulation and recovery than *bmal1* expression in the brain, a novel finding given that sleep was thought to be exclusively regulated in the brain. Recently, research has classified a group of muscle-derived factors named myokines. We assume that at least some of these factors facilitate the pathway by which skeletal muscle alters sleep. Subsequently, we have identified a primary myokine of interest, irisin, that may be a part of this pathway using a combination of research on exercise, sleep deprivation and depression.

Molecular characterization of a new coenzyme Q10 deficiency

Jennifer Guo, Dr. Thierry Vilboux, Dr. May C.V. Malicdan

National Human Genome Research Institute, Bethesda MD
jguo1@swarthmore.edu

Abstract

Coenzyme Q10 (CoQ₁₀) is a lipid present in virtually all eukaryotic membranes, where it participates in several biochemical pathways as an electron carrier and protein cofactor. Primary CoQ₁₀ deficiencies are rare genetically heterogeneous disorders caused by mutations in genes required for the biosynthesis of CoQ₁₀. Over a dozen genes are involved in the biosynthesis of CoQ₁₀, and mutations in several of these have been associated with human disease. Here we report a new primary CoQ₁₀ deficiency involving three patients with defects in *COQ5*, a gene with previously no related clinical manifestation. The patients present symptoms that are consistent with those of other documented CoQ₁₀ deficiencies, including encephalopathy, cerebellar ataxia, myoclonus, nystagmus, and developmental delay of variable onset. Through homozygosity mapping and copy number analysis of whole genome sequencing analysis of a patient genome, we identified a mutation in *COQ5* involving a tandem duplication of the last four exons. This duplication induces a nearly complete loss of COQ5 enzyme by producing an mRNA with an abnormal 3' UTR.

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Boundary Condition Effects on Taylor States in SSX

Jeremy Han, Professor Michael Brown

Swarthmore College
jhan2@swarthmore.edu

Three different boundary conditions are applied to the SSX 0.15 meter diameter plasma wind tunnel and the resultant Taylor states* are characterized. The glass walls of the wind tunnel act as an insulating boundary condition. For the second condition, a flux conserver is wrapped around the tunnel to trap magnetic field lines inside the SSX. For the last condition, the flux conserver is segmented to add theta pinch coils, which will accelerate the plasma. We used resistive stainless steel and copper mesh for the flux conservers, which have soak times of 3 microseconds and 250 microseconds, respectively. The goal is to increase the speed, temperature, and density of the plasma plume by adding magnetic energy into the system using the coils and compressing the plasma into small volumes by stagnation. The time of flight is measured by using a linear array of magnetic pick-up loops, which track the plasma plume's location as a function of time. The density is measured by precision quadrature He-Ne laser interferometry, and the temperature is measured by ion Doppler spectroscopy. Speeds and density without the coils are 30 km/s and 10^{15} cm^{-3} . We will reach a speed of 100 km/s and density of 10^{16} cm^{-3} by adding the coil.

*Gray, et al, PRL **110**, 085002 (2013)

Is Less More? Pediatric Intractable Migraine and Botox Treatment
Sarah Hancock, Tara Pezzuto, APRN, Liya Beyderman, MD, Li Xie, Diane Chugani, PhD
Nemours Alfred I. duPont Hospital for Children
shancoc1@swarthmore.edu

Chronic migraine occurs in approximately 1.75% of adolescents in the United States. Preventive and abortive medication with a combination of integrative therapy is standard practice in headache programs. This approach is ineffective or limited by adverse responses in some patients. OnabotulinumtoxinA (Botox) 155-200 unit dose was approved by the FDA for treatment of Chronic Daily Headache in adults in 2010. Botox is used off-label in refractory pediatric and adolescent patients but no standard dose has been established.

A retrospective chart analysis was performed in all patients who received Botox between February 2014 and March 2016 at the Nemours Pediatric Headache Clinic to assess age, headache type and effectiveness of dose administered. Forty-four patients (35 females, 9 males, and age range 11-20 at time of treatment) received Botox using a modified dose approach based on location and tolerance, with parent and patient consent. The location of pain reported determined the location of injections provided.

Significant improvement in migraine intensity and frequency was reported in 73% of patients who received Botox. Significant improvement is defined as a decrease of intensity or frequency of 50% or more. Of those that responded, 6% responded to 115-155 units, 66% responded to 80-110 units, 12% percent responded to 55-75 units and 16% responded to 35-50 units. Soreness at the injection sites was the only reported side effect. The data support prospective studies of optimal dosing in medically refractory pediatric migraine patients, and, if projectable to the general population, suggest a greater efficacy in lower doses for children compared to adults.

Effects of N-terminal acetylation on alpha-synuclein membrane binding

Zain Hannan, Jessica Sarver

**Swarthmore College
zhannan1@swarthmore.edu**

Alpha-synuclein, a 140-residue protein, is an important protein in the pathogenesis of Parkinson's disease. Alpha synuclein is a naturally disordered protein, but becomes ordered in the presence of lipid vesicles. Research has identified a certain conformational shift of alpha-synuclein that leads to the aggregation of secondary structure beta-sheets. The beta-sheet conformation is associated with the pathogenesis of Parkinson's. On the other hand, the formation of alpha helices increases lipid binding tendency. Recent studies have found that the post-translational modification, N-terminal acetylation, is a key step in aiding alpha-synuclein to form alpha helices. It is also evident that the formation of alpha-helices allows the protein to be more resistant to beta-sheet aggregation. These literature findings imply that N-terminal acetylation of alpha-synuclein limits the beta-sheet aggregation, and also increases lipid binding propensity.

The recent alpha-synuclein studies on N-terminal acetylation mainly use circular dichroism (CD). As useful as CD might be for determining the overall structure of proteins, we were also interested in looking at site-specific folding. To accomplish this goal, our project utilized Electron Spin Resonance spectroscopy (ESR). The objective was to determine any differences in lipid vesicle binding between alpha-synuclein mutants and their n-terminal acetylated counterparts. Using biochemistry techniques, we prepared multiple samples of protein mutants. We utilized the NatB complex to synthesize N-terminal acetylated proteins. The lipid vesicles were extruded to certain diameters and finally these components were prepared for the ESR experiments. We collected spectra from each of our samples and were able to determine differences between the samples. This research will aid our understanding of alpha-synuclein, and is also very important for us to increase our understanding of Parkinson's.

The Genome and Embryonic Transcriptome of *Corella Inflata*

Lincoln Harris and Brad Davidson

Swarthmore College

lharris1@swarthmore.edu

Demystifying the developmental underpinnings of cardiac disease remains an active area of research with potential to benefit a great number of lives. Essential to proper heart development are highly conserved GRNs – gene regulatory networks – that coordinate suites of molecular activity during embryogenesis. Here we present the assembled and annotated genome of *Corella inflata*, with hopes that it can be used in comparative genomic investigations of early heart development GRNs. *Corella* is a member of the subphylum *tunicate*, and is a close relative of *Ciona intestinalis*, the model system for early development research. The genomes of six *tunicate* species have been sequenced and assembled, with four more currently in the works, all of which will soon be available on the ANISEED public database. When uploaded to ANISEED, our genome and transcriptome will represent an additional resource for comparative genomics investigations of early heart GRNs.

Infection characteristics of four potential therapeutic coliphages targeting Shiga toxin-producing *Escherichia coli* O157:H7

**Alice Herneisen, Cristina Howard-Varona, Natalie Solonenko,
Dean Vik, Lauren Chittick, and Matthew Sullivan**

**Department of Microbiology and Department Civil, Environmental, and Geodetic Engineering,
The Ohio State University**

ahernei1@swarthmore.edu, howard.1264@osu.edu, and mbsulli@gmail.com

The overuse and misuse of antibiotics has driven the proliferation of multidrug resistant bacteria, prompting concerns that common infections may again become untreatable. One alternative to such broad-range, nonspecific antibacterial agents is phage therapy, which uses bacteria-targeting viruses (bacteriophages) to specifically kill pathogenic bacteria.

Shiga-toxin producing *Escherichia coli* (STEC), such as the O157:H7 serotype, is a major cause of foodborne illness in both developed and developing nations. Complications associated with STEC infections include hemorrhagic colitis and hemolytic-uremic syndrome, which is the primary cause of kidney failure in children in the United States. STEC strains are frequently resistant to common antibiotics, and antibiotic treatment may exacerbate the condition by inducing the release of toxins. The treatment of STEC infections, therefore, may benefit from the development of alternative therapeutic strategies such as phage therapy.

Here, we study the infection characteristics of four coliphages against a Shiga toxin-producing *E. coli* O157:H7 (ATCC43895) host. After determining growth dynamics of the ATCC43895 strain, we experienced difficulties propagating the phages to high and stable titers. Adsorption kinetics and one-step growth curves revealed that the phages appeared to inefficiently infect the host. The four phages were propagated to high titer on the original host of isolation (b000z), suggesting that the two genetically and physiologically similar host strains experienced widely different infection outcomes. To investigate how pathogens evolve resistance to phages, we also measured the growth dynamics and susceptibility to infection of bacteriophage-insensitive mutants belonging to the ATCC43895 strain. The mutants did not exhibit cross-resistance or altered growth compared to the wild type. This study underscores the need for more informed therapeutic phage selection and additional tools for the investigation of inefficient phage-host interactions.

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Solar Feasibility Report for Swarthmore College

Report submitted by: Ye Linn Htun
Mentors: Melissa Tier, Carr Everbach
Office of Sustainability, Swarthmore College
yhtun1@swarthmore.edu

With a commitment to be carbon neutral by 2035, Swarthmore currently purchases Wind Energy Credits (WRECs) to offset 100% of its electricity consumption. However, the manner in which these WRECs were purchased means we cannot know where in US these WRECs come from. This results in an inability to calculate how much fossil fuels these WRECs offset, uncertainties as to the additionality of these wind projects and Swarthmore's surroundings not receiving benefits of renewable energy projects (e.g. jobs and cleaner air).

A Solar Pathfinder was used in conjunction with the accompanying PV Studio Software to establish upper bounds for electricity production potential of Swarthmore's roofs, parking lots and open ground spaces. For each site, three readings - best, center of site, and worst - were taken for roofs and open ground spaces, and five readings - four corners of the site and the center - were taken for parking lots.

The Solar Pathfinder readings were analyzed with the PV Studio Software to determine the year-round insolation of a site. This result takes into account shading, obstacles (e.g. HVAC units on roofs), access paths left uncovered by solar modules and system losses from multiple sources including soiling of panels. Sites receiving less than 60% of the available, year-round insolation were discarded. The results are shown below in Table 1.

	Expected Output (kWh)
Roofs	9.42×10^5
Parking Lots	1.52×10^6
Open ground space	7.03×10^5
Total Expected Use	1.8×10^7
Total Output	3.16×10^6 (17.5% of total)

Table 1. Total expected output from on-campus arrays. PV Studio takes the shading analysis and local weather data to simulate an array designed by the user in the aforementioned conditions. Schüco International KG SPV 220 SMAU-1 (220 Watts) solar module and SolarEdge Technologies Inc, SE9KUS (120V) inverter was used in these simulations.

Evidence of social niche construction in *Bolitotherus cornutus*

Robert Hwang, Vince Formica

Mountain Lake Biological Station, Pembroke VA
rhwang1@swarthmore.edu

Social niche construction is a phenomenon that occurs when an organism actively shapes their current social niche to improve its fitness. Forked fungus beetles (*Bolitotherus cornutus*) are a species of darkling beetle that construct complex social networks. The social network position of an individual has been shown to correlate with its individual fitness. Using network data calculated from joint-sex networks, we took the next step to examine if forked fungus beetles are changing their social network position over the course of a field season to positive or negative effect. Although the network data was joint, statistical analysis was run separately for the sexes. A change in strength and betweenness from July to August was shown to be none significant in increasing individual fitness for both males and females. However, a negative change in clustering coefficient during the same time period was shown to be significant in increasing individual fitness for males. This level of significance was not observed among females. Male individuals who were becoming less “cliquish” were found to have more mate partners in the latter half of the field season. This finding points to possible evidence of social niche construction among forked fungus beetles.

The effect of the social network position on female fitness in *Bolitotherus cornutus* (forked fungus beetle)

Zhazira Irgebay¹, Vince A. Formica¹

1 Department of Biology, Swarthmore College, Swarthmore, PA

zirgeba1@swarthmore.edu

The social environment of an individual has a major impact on the fitness of individuals. The majority of the current literature focuses on the characteristics of males, few studies explore the social characteristics of the females and the influence of their social phenotype on their reproductive success. This study evaluated the effects of social network position of females on their fitness. We also explored whether the fitness effects of network position were mediated through the reproductive behavior that precedes egg laying using a path model framework.

The social environment (strength, betweenness and clustering coefficient) and female fitness (the number of eggs laid) was studied in wild populations of *Bolitotherus cornutus* (forked fungus beetle) in the Pond Drain metapopulations in the Appalachian Mountains in southwest Virginia. We recorded the activity and social interactions of individuals by daily scan sampling twice a day during July and August. The relationship between the social network metrics, reproductive behaviors, and fitness was estimated using general linear model and piecewise structural equation modeling (SEM) in R.

We found a significant negative relationship between strength and female fitness, such that females with greater number of social partners laid fewer eggs. Betweenness and clustering coefficient, did not show a significant correlation with female fitness. Furthermore, the results of the piecewise SEM showed that strength was not significantly correlated with reproductive behavior, suggesting that strength is directly influencing female fitness. The mechanisms that drive the relationship between strength and fitness remain unknown, but possible causes include aggression among social partners and energy allocation trade-offs. Our results confirm the presence of selection on female network position, suggesting that the females are influenced by the characteristics of their social environment.

The Neural Correlates of Selective Attention

Maneepunnarai Jiwjinda

Advisor: Dr. Lisa Payne

Psychology Department, Swarthmore College

mjiwjin1@swarthmore.edu

Paying attention not only helps us to better perceive, remember and later recall new information, but also enables us to work more effectively on the task at hand. However, our attentional capacity is limited, and in order to effectively focus on something, we have to withdraw ourselves from other stimuli competing for our attention. Amplitude increases in the electroencephalogram (EEG) alpha frequency band (8 - 14 Hz) are thought to represent the suppression of extraneous sensory processing that allows us to concentrate on task-relevant information [1]. Recently, researchers have also linked fluctuations in alpha activity, occurring over language-related brain regions, to the suppression of verbal, semantic information [2]. The goal of the current study was to replicate this novel result in a modified version of the experiment.

Our study had participants alternate between attending to and ignoring visual and auditory stimuli. Participants were first presented with a word either in italics or normal print, and then heard it spoken by either a man or woman. Depending on the trial, they were instructed to attend to only the visual or auditory presentation. When instructed to ignore the printed word, participants exhibited increased neural activity in left frontotemporal regions (such as Broca's region) thought to be involved in language processing. These results serve as reliable, preliminary evidence that these fluctuations in alpha activity could be correlated with the inhibition of semantic information. They are also in agreement with newly emerging data that alpha-related suppression plays a role in higher cognitive processes such as memory encoding [3] and retrieval of meaningful information from long-term storage [4].

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Interactions between non-canonical DNA structures and small molecule ligands and ions

Deondre Jordan, Sayed Malawi, and Liliya Yatsunyk

Swarthmore College

djordan1@swarthmore.edu

smalawi1@swarthmore.edu

Although the canonical secondary structure of DNA as a double helix has been known for decades, other structures have come to light only recently. Segments of DNA rich in guanine bases are known to form G-quadruplexes (GQs) – non-canonical structures characterized by a multi-layered planar arrangement of four guanine bases (G-tetrads) held together by hydrogen bonds and π - π stacking. GQs have become a focus in anti-cancer research, as oncogene promoters and telomeres are rich in guanines, and the formation of GQs has been hypothesized to inhibit the operation of enzymes like telomerase.

Our lab is interested in studying GQs and other non-canonical secondary structures of DNA, and how they interact with various ligands. CA5-5, a variant of d(CAGAGG)_n, is a secondary structure we seek to determine. We are collaborating with Dr. Brad Chaires' lab at the University of Louisville on a biophysical characterization of a specific ligand-GQ pairing. Molecules such as NMM, RHPS4, and methylene blue have shown promise in our various projects.

Probing the unexplored structure of tungsten-172

Charles Kacir, Carol J. Guess

Swarthmore College
Charles Kacir1@swarthmore.edu

High resolution gamma coincidence data from $^{50}\text{Ti}(^{128}\text{Te}, ^{172}\text{W})6n$ reaction has been used to more accurately construct the level scheme of tungsten-172 than has previously been done. Most known energy bands were extended, and several new bands were discovered, consisting of a significant improvement to the known level scheme. Rough DCO ratios have been calculated, but have yet to be properly analyzed.

Exploring AI-2 binding interactions in an LsrB-type receptor

Meghann Kasal, Dr. Stephen T. Miller

Swarthmore College
mkasal1@swarthmore.edu

Although bacteria are single celled organisms, they have developed mechanisms to communicate with each other and coordinate certain community-wide behaviors. This process, known as quorum sensing, relies on small molecules to transmit signals between the organisms, allowing the community to behave much like a multicellular entity. Quorum sensing results in mutually beneficial behaviors for the bacterial community such as bioluminescence, virulence, and antibiotic production.^{1,2} By exploiting this phenomenon, we hope to develop methods to regulate the communication between the bacteria and manipulate their behaviors.

Most signaling molecules, known as autoinducers, are species specific and facilitate intraspecies communication, but autoinducer-2 (AI-2) is produced and recognized by a variety of bacteria,³ enabling interspecies communication.⁴ The AI-2 signal is a family of interconverting molecules that exist in equilibrium depending on the environment. To date, two types of AI-2 receptors have been identified that bind chemically distinct forms of DPD. The receptor protein of interest in these studies, LsrB, a component of the LuxS-regulated (*lsr*) operon, directly binds one known form of AI-2.⁵

In *Thermobacillus composti*, we discovered a novel AI-2 receptor protein has a 30.1% sequence identity with the reporter strain and a 33% conservation of the active site residues. This relatively low sequence homology could indicate that an alternative form of the AI-2 signal is binding to the receptor or that a novel receptor is involved in binding. Intrinsic fluorescence studies are being conducted to assay the binding of AI-2 to the receptor protein in *T. composti*, which can elucidate its dissociation constant and lead to further characterization of the AI-2 binding to this LsrB-type receptor.

GIS based terrain analysis with GPU and CPU strategies

Charles W. Kazer, Dr. Arthur Lembo

Salisbury University

ckazer1@swarthmore.edu

Geographic Information Systems (GIS) are used in many different fields to analyze spatial data and plan accordingly. Geographic data has been growing in size exponentially in recent years as measurement tools become more precise, and while some GIS tools to analyze this data have been created, usage and efficiency have been lagging behind since many geographers have little to no technical background. The advent of massively parallel computing, specifically the availability of GPU programming where thousands of cores can be utilized simultaneously, have made a more efficient solution possible since most GIS calculations are embarrassingly parallel. QGIS is an open source GIS platform that has gained much traction in the computational geography community. We created a QGIS plugin that leverages GPUs to increase calculation speed of simple terrain analysis on large data sets. We developed this plugin with the geography community in mind, using Python to make code easy to read, portable, and modifiable.

Functionalizing single-walled carbon nanotubes with $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$ as a potential mode of drug delivery

Elise Kim, Bo Lim Lee and Dr. Silvia Porello

Department of Biochemistry, Swarthmore College, Swarthmore, PA
ekim4@swarthmore.edu, blee2@swarthmore.edu

Recent studies have demonstrated the considerable potential of carbon nanotubes for applications in a wide array of fields due to their unique structural, thermal, mechanical and electronic properties. Single-walled carbon nanotubes (SWCNTs) are a broad category of such nanoparticles, describing nanotubes made of a single layer of graphene sheet rolled into a cylindrical structure. Their wide surface areas and delocalized electron system allow for non-covalent adsorption of therapeutically active molecules with extended π systems onto the nanotube surface, making them promising candidates as drug carriers for targeted drug delivery¹. Evidence suggests that loading therapeutics onto SWCNTs can protect the drug from degradation, reduce side effects and localize the effects to intended regions. In addition, SWCNTs have been shown to exhibit low toxicity in cells following cellular uptake². In this research, we worked with SWCNTs and the metal complex $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$, a DNA intercalator considered useful as a possible therapeutic agent³. The goal of our work is to study the drug-delivering capabilities of SWCNTs by functionalizing them with $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$ and transporting them to cells.

Modification of SWCNT surfaces was achieved through successive rounds of sonication and centrifugation of an aqueous solution of SWCNTs and $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$, which dispersed the SWCNTs from their aggregated states enough so that π - π interactions could occur between anchor groups on the metal complex and the nanotube surface. Evidence for the formation of the Ru-SWCNT composites was provided by UV/Visible and emission spectroscopy, which, when compared to the spectra of pristine SWCNTs, revealed the appearance of an MLCT band characteristic of the Ru(II) complex⁴ and enhanced fluorescence, respectively. Successful binding of $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$ to pUC19 DNA was also monitored using a minimum intercalation gel shift assay and fluorescence spectroscopy. Our findings suggest that it is possible to “load” SWCNTs with $[\text{Ru}(\text{bpy})_2\text{dppz}]^{2+}$, expanding the possibility that they may be used to transport and release the complex and similar drugs to target cells.

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Conformation of the Domain of the Influenza M2 Protein that is Critical to Viral Budding

Grace Kim and Kathleen P. Howard
Swarthmore College, Swarthmore PA 19081
gkim2@swarthmore.edu

The M2 protein is a 97-residue multifunctional transmembrane homotetrameric protein. It is found in the viral coat of the Influenza A virus, which is responsible approximately 250,000 to 500,000 annually worldwide. Extensive research has elucidated M2's role as a ion channel, which plays a critical role in the uncoating of the viron once it has entered the host cell. Recently however, it has been implicated that C-terminal tail of M2 plays a crucial role in generating curvature in the cell membrane to mediate viral budding. Additionally, it has been shown that deletions in the C-terminal tail of the M2 protein lead to impaired viral infectivity. While the early portion of the C-terminal tail (46-60) has been extensively studied, high resolution structural detail is limited in the regions following (61-70) though it has been shown that these regions also play a role in viral budding. This study uses site-directed spin-label electron paramagnetic resonance (SDSL-EPR) to look at the region following the membrane proximal region of the C-terminal tail (61-70) in the absence and presence of cholesterol. Continuous wave EPR line shapes suggest that this region is more mobile than the previous region suggesting that its movement is not restricted the lipid bilayer. This assertion is also confirmed by power saturation EPR which demonstrate low $\Delta P_{1/2}$ values, which demonstrate that this region is not as oxygen accessible. Interestingly, a novel finding from this study is that this region may confer a helical structural which contrast previous predictions that suggest that this region may be disordered. While further investigation is necessary, the experiments presented in this study provide a preliminary characterization to the later C-terminal domain (61-70) of the Influenza M2 protein.

Optimizing Protocol for Electron Paramagnetic Resonance (EPR) Spectroscopy

Jacob Kirsh, Jessica Sarver

Swarthmore College
jkirsh1@swarthmore.edu

Alpha-synuclein (α Syn) is a small 14.5 kDa protein that has been implicated in Parkinson's Disease (PD) since around the year 2000. The binding interaction of α Syn and lipid membranes is of particular interest because improper protein-lipid interaction may play a role in the neuronal fibril formation characteristic of PD. Varying the size and charge of the lipid membranes may impact α Syn-lipid binding, and these binding events can be probed through EPR. Specifically, differences in EPR spectra can elucidate details of the binding interaction. As such, it was required that a protocol be optimized to express and purify α Syn and its mutants from the DH5 α cell line. The goal was to grow α Syn at a suitable concentration and purity for EPR use. By the conclusion of the Spring semester of 2016, the protocol was optimized such that a high quality EPR spectrum was obtained.

Neutrophil Cathepsin G Induces Hapten-Presenting Dendritic Cell Production of IL-12 to Skew Hapten-Reactive CD4 T Cell Development to IFN- γ - and IL-17-Producing Effector Cells in Allergic Contact Sensitivity

Susie Min, Danielle Kish, Robert L. Fairchild

Department of Immunology, Cleveland Clinic, Cleveland, OH 44195
smin1@swarthmore.edu

Contact hypersensitivity (CHS) is a CD8 T cell-mediated response to skin sensitization and challenge with hapten. Contact hypersensitivity (CHS) is a hapten-induced skin inflammation mediated by hapten-reactive CD8 T cells that produce IFN- γ and IL-17. CHS responses are further regulated by hapten-reactive CD4⁺ T cells that produce IL-4. We have previously reported that CXCR2-dependent neutrophil recruitment into the skin challenge site is required to direct subsequent infiltration of the effector CD8 T cells into the site to elicit CHS. Surprisingly, CHS responses are observed when sensitized CXCR2^{-/-} mice are challenged with the hapten. This study investigated the role of neutrophils during hapten-priming of T cells to mediate CHS. Consistent with our previous results neutrophil-depleting antibody given at the time of challenge, but not sensitization, eliminated T cell infiltration into the challenge site and the CHS response. Unlike sensitized wild type mice, however, hapten sensitization of CXCR2^{-/-} mice and WT mice depleted of neutrophils generated both reactive CD4 and CD8 T cells producing IFN- γ and IL-17 and either population of hapten-primed T cells was capable of mediating a response to skin challenge. Sensitized mice lacking the neutrophil serine protease cathepsin G had elevated and elongated CHS responses to challenge and both reactive CD4 and CD8 T cells producing IFN- γ and IL-17. The hapten-reactive CD4 cells producing IFN- γ and IL-17 were not generated following sensitization of IL-12^{-/-} mice or wild type mice treated with anti-IL-12 in the absence of neutrophils. Neutrophil depletion in wild type mice at the time of hapten sensitization resulted in increased numbers of IL-12-producing dendritic cells in the skin draining lymph nodes. Overall, these results suggest that following hapten sensitization of the skin neutrophil-derived cathepsin G inhibits the activation of hapten-presenting dendritic cells to produce IL-12 needed for the development of hapten-reactive CD4 cells to IFN- γ and IL-17 producing effector cells in the CHS response.

Fluorescence Studies on the Quorum Sensing transcriptional regulator LsrR from *Salmonella typhimurium*

Elijah N. Kissman, Emily Gale, and Stephen T. Miller

Swarthmore College, 500 College Avenue, Swarthmore, PA 19081

ekissma1@swarthmore.edu

Quorum sensing is a signal molecule dependent cell-cell communications system in bacteria responsible for modulating growth rates, biofilm formation, and the secretion of virulence factors most notably in cell co-culture. Autoinducer-2 (AI-2) is a unique quorum sensing signal molecule because it is involved in interspecies communication between both gram-positive and gram-negative species. The transcriptional repressor protein LsrR is responsible for regulating the *lsr* operon, which controls the import and subsequent processing of AI-2. Previous results suggest LsrR may be regulated directly by the glycolytic intermediate dihydroxyacetone phosphate (DHAP) by way of its ligand binding domain. Fluorescence assays on an N-terminally truncated construct of LsrR from *Salmonella enterica serovar Typhimurium* tagged with a hexahistidine affinity tag and a Maltose Binding Protein solubility tag were used to assay the binding of DHAP to the protein. The assay was inconclusive in that it showed an increase in measured DHAP levels in solution following incubation with LsrR compared to the standard. This result is unlikely to lead to a conclusion about the binding because no increase in fluorescence should be seen since all control and experimental samples contained the same concentration of DHAP. Future directions include further optimization of the fluorescence assay, electrophoretic mobility assays, protein crystallization in complex with the ligand, and potentially ^{31}P NMR studies.

ESR studies of alpha-synuclein binding to membranes of varying charge and curvature

Aditi Kulkarni, Jessica Sarver

Swarthmore College
akulkar1@swarthmore.edu

Alpha-synuclein (α S) is a small 140-residue protein that has risen to prominence in recent research as a result of its implications in Parkinson's disease. It is a major component of Lewy bodies, which are the aggregates of protein that reside inside nerve cells of Parkinson's patients. With a molecular weight of around 14.5 kDa, α S is a small, soluble protein that is inherently disordered in solution. However, in the presence of lipid membranes, it experiences a conformational shift to a primarily α -helix structure. The protein-membrane interactions and associations of alpha-synuclein can be modulated by curvature and electrostatics of both lipid charge and charge on the membrane-associated protein. In this work, we are looking at the binding properties of alpha-synuclein, by varying lipid curvature and electrostatics.

To date, much of the studies done on alpha-synuclein involve fluorescence correlation spectroscopy (FCS). While a useful technique, FCS does not provide insight into the depth of the binding. However, it has established that alpha-synuclein preferentially binds to smaller vesicles with more curvature and more charged vesicles. To further understand these interactions, this work will use electron spin resonance (ESR) spectroscopy to probe the binding of alpha-synuclein when varying both the charge of the membrane vesicles and the C-terminus of alpha-synuclein. The ESR experiments will probe membrane accessibility, which will allow us to more fully understand the orientation of the protein, and the depth of the binding. This work will provide more site-specific details into the effects of electrostatics on the membrane binding of alpha-synuclein. This feature of alpha-synuclein is thought to play a role in both the normal function of the protein and the diseased function with Parkinson's. In order to more fully understand α S's function in Parkinson's, it is imperative to understand its conformational shift as the lipid conditions change.

When can children recognize imitation as third-party observers?

Sona Kumar, Narges Afshordi

Harvard Lab for Developmental Studies

skumar1@swarthmore.edu

When can children recognize imitation as third party observers? If children recognize when one person imitates another, do they also infer an affiliation between those people? Are these abilities influenced by the type of action that is imitated? In this study, 118 three-, four-, and five-year olds saw three imitation sequences: vocalizations, bodily movements, and instrumental actions. Each sequence involved three roles: target, and non-target, and copier. Children watched an introductory sequence and two warmup trials that acted as memory checks. They then watched five imitation trials in which the target and non-target performed an action and then the copier performed the same action as the target character. In the test trial, the target and non-target characters acted, but the animation stopped before the copier acted. Experimenters then asked an imitation question, *Do you think [copier's name] will do [target's action] like [target's name] or [non-target's action] like [non-target's name]?* and an affiliation question, *Do you think [copier's name] likes [target's name] best or [non-target's name] best?*

For bodily movements, all three age groups chose the target of imitation significantly more than the non-target. For the vocalization sequence, three-year-olds answered the imitation and affiliation questions at chance, while four- and five-year-olds succeeded. Only five-year-olds correctly answered the test questions significantly above chance on the instrumental action sequence. Pattern of success for affiliation was identical to imitation. The ability to recognize imitation is present at age three and improves with age. Children performed better on the bodily movements sequence than on the vocalization sequence, and better on both of those sequences than on the instrumental actions sequence. Future studies should explore these distinctions further. Follow-ups should examine whether children are perseverating when asked the affiliation test question, or if they are indeed making the inference.

Generation of UCP1 and EBF2 Reporter Lines for human iPSC Differentiation via CRISPR-Cas mediated gene-editing

Daniel Lai, Kate Slovik, Wenli Yang

UPenn iPSC Core

dlai2@swarthmore.edu

In recent years, brown adipose tissue (BAT) has garnered attention as a therapeutic intervention for obesity and certain metabolic diseases like type 2 diabetes. Unlike white adipose tissue, which serves as an energy deposit for the body via lipid storage, brown adipocytes can dissipate energy by burning glucose and fat to generate heat. This thermogenic process is mediated by Uncoupling Protein 1 (UCP1), a transmembrane polypeptide residing in the inner mitochondrial membrane of brown adipocytes. When activated, UCP1 dissipates the proton gradient generated by the electron transport chain, thereby reducing mitochondrial membrane potential, driving substrate phosphorylation, and generating heat.

In addition to its essential role in brown adipocyte function, UCP1 also serves as a marker for fully differentiated and activated brown adipocytes. Developing robust protocols for the differentiation of brown adipocytes from a pluripotent state is necessary for studying these cells both *in vivo* and *in vitro*, and UCP1 expression provides a means to measure the effectiveness of such protocols. To this end, we generated a UCP1 Luc2-Katushka (TurboLuc) reporter line in human induced pluripotent stem cells (human iPSCs) via CRISPR-Cas mediated gene editing. In addition, we generated an EBF2-CherryPicker reporter line using CRISPR-Cas editing, as EBF2 both serves as a marker for brown adipocyte precursor cells and drives a brown-adipocyte-specific program.

Cells transfected with the donor and Cas9 plasmids for each experiment were plated at clonal density and screened via PCR for homologous recombination at the UCP1/EBF2 locus. Junctions of both the UCP1 reporter and wild-type alleles were sequenced to ensure no novel mutations were introduced. Seven UCP1 clones were generated, two of which were homozygous for the reporter construct. 28 clones were positive for homologous recombination at the EBF2 locus, and junctions will need to be sequenced to ensure no novel mutations occurred.

Inequality and Mobility in Spain (1372-1932)

Kevin Lai, José-Antonio Espín-Sánchez

This project aims to provide a more comprehensive analysis on inequality and social mobility in Spain from 1372-1932. While this is our long term goal, we have started to analyze this data with our preliminary analysis (1754-1786).

The preliminary analysis done will cover all people (men and women) from all classes (rich and poor) in two years 1754 and 1786. Family trees are constructed from matching the 1754 Census, 1786 Census, Baptism Record, and Marriage Record to track mobility in one generation.

From our preliminary analysis, we see two main things:

- (1) There is a significant linear association between number of household members and income. As income increases, we expect an increase in number of household members. Similarly, Don families had more household members than Non-Don families. This was only found in 1786.
- (2) Murcia City in 1754 was closer to perfect equality than Murcia City in 1786.

Influence of Sodium Cationization versus Protonation on the Gas-Phase Conformations and Glycosidic Bond Stabilities of 2'-Deoxyadenosine and Adenosine

Justin Lee, Paul Rablen

Wayne State University
Jlee5@swarthmore.edu

The influence of noncovalent interactions with a sodium cation on the gas-phase structures and N-glycosidic bond stabilities of 2'-deoxyadenosine (dAdo) and adenosine (Ado), $[\text{dAdo}+\text{Na}]^+$ and $[\text{Ado}+\text{Na}]^+$, are probed via infrared multiple photon dissociation (IRMPD) action spectroscopy and energy-resolved collision-induced dissociation (ER-CID) experiments. ER-CID experiments are also performed on the protonated forms of these nucleosides, $[\text{dAdo}+\text{H}]^+$ and $[\text{Ado}+\text{H}]^+$, for comparison purposes. Complementary electronic structure calculations are performed to determine the structures and relative stabilities of the stable low-energy conformations of the sodium cationized nucleoside complexes and to predict their IR spectra. Comparison between the measured IRMPD action spectra and calculated IR spectra enables the conformations of the sodium cationized nucleosides present in the experiments to be elucidated. The influence of sodium cationization versus protonation on the structures and IR spectra is elucidated by comparison to IRMPD and theoretical results previously reported for the protonated forms of these nucleosides. The influence of sodium cationization versus protonation on the glycosidic bond stability of the adenine nucleosides is determined by comparison of the ER-CID behavior of these systems. All structures present in the experiments are found to involve tridentate binding of Na^+ to the N3, O4' and O5' atoms forming favorable 5- and 6-membered chelation rings, which requires that adenine rotate to a syn configuration, and leads to O4'-endo sugar puckering. Sodium cationization is found to be less effective towards activating the N-glycosidic bond than protonation for both dAdo and Ado. Both the IRMPD yields and ER-CID behavior indicate that the 2'-hydroxyl substituent of Ado stabilizes the N-glycosidic bond relative to that of dAdo.

USee Project: A Self-Refraction Study

Alice Liu and David S. Friedman

Baltimore, MD

Aliu1@swarthmore.edu

David S. Friedman at the Wilmer Eye Institute at Johns Hopkins Hospital conducted a pilot study on the USee device, a new self-refraction device aimed at reducing uncorrected refractive error in the developing world. A total of 68 participants, of which 61 were deemed eligible, partook in the study to determine how accurately patients could self-refract themselves with the USee device. A comparison of the proportion of patients who corrected to 20/30 or better using USee refraction measurements and clinical manifestation refractions was deemed statistically significant. Factors including age and high cylindrical power were associated with the failure of participants to correct to 20/30 or better. Future plans entail making modifications to the USee device and the protocol to improve the accuracy of self-refraction when using the device.

Whose Preferences Do Children Generalize to the Population

Rongzhi Liu, Prof. Stella Christie

Swarthmore College
rliu3@swarthmore.edu

We make generalization based on limited data. How far we generalize is constrained by the goodness of the sample. A diverse sample is more informative than a narrow sample for drawing broader generalizations¹. For example, to find out the level of difficulty for all courses at Swarthmore College, it is more informative to generalize based on a sample of an intro level physics class and an advanced level literature class (diverse), than based on a sample of two intro level psychology classes (narrow). Prior research showed that within the social domain, even 5-year-olds could evaluate that a diverse set of evidence is more generalizable than a narrow set of evidence². To find out about a toy preference of all children, 5-year-olds preferred to query the preferences of a diverse rather than a narrow group.

Here we explored how children employed this rational inductive inference when the group's preference was known. Children were told that the diverse group liked X while the narrow group liked Y. The question is whether children extended X—the preference of the diverse group—to the rest (majority) of the group.

In Study 1, children had to choose to generalize either the diverse group's preference X or the narrow group's preference Y to the majority of the group. Diversity is created by race and gender. In contrast to our prediction, children overall selected the narrow group's preference for generalization, in both race and gender trials.

We hypothesized that children chose the narrow race group, which is their own race group because they assumed that they were generalizing to their typical environment—where the majority are Caucasian children. To examine this in study 2, we gave a new group of 5-year-olds a picture that explicitly shows that the to-be-generalized population consists of mixed race and gender children. Now we found that 5-year-olds favored the diverse group's preference for generalization, suggesting that children's representation of the to-be-generalized group dictates their inductive reasoning.

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Behavioral changes in *Bolitotherus cornutus* after copulation

Marianne Lotter-Jones, Vince Formica

Mountain Lake Biological Station, Pembroke, VA
mlotter1@swarthmore.edu

Many insects exhibit behavioural changes before and after copulation. Behavioural changes can occur in both sexes and include changes in their social environments, increasing their remating interval, and their circadian rhythms. However, few studies have looked at behavioural changes in the wild. This study focuses on five changes in the forked fungus beetle's (*Bolitotherus cornutus*) behaviour 48 hours before and after guarding (guarding acts as confirmation of a successful copulation): 1) number of times observed 2) number of courtships 3) number of unique bracket transitions 4) number of female partners and 5) number of male partners. The data was collected by field observations during the *B. cornutus*' mating season and analyzed using multiple regression statistical models. The number of times a beetle was observed significantly decreased after guarding for both males and females. Surprisingly, males significantly increase the number of their female associations after guarding while females also significantly increase the number of their male associations after guarding. Though both sexes increase their number of associations with the opposite sex, there is no significant difference between the number of courtship events for both sexes. These results show that the behavioural changes that *B. cornutus* reduces its activity levels after guarding. Further study is required to determine why males and females increase their associations of the opposite sex though there is no correlation with increased mating behaviour.

Investigating female sexual receptivity modulators in *Drosophila melanogaster* using behavioral assays

Gurrein Madan and Prof. Kathleen K. Siwicki

Swarthmore College, Department of Biology

gmadan1@swarthmore.edu, ksiwick1@swarthmore.edu

The sexually dimorphic courtship behavior of *Drosophila melanogaster* has contributed to our understanding of learning and memory, sexual selection and evolution. Unlike *Drosophila* males, whose active behavior before copulation has been intensely studied, females decide whether to copulate by assessing both their environmental cues, including their suitor's courtship display, and their developmental sexual readiness (i.e. receptivity). Our yearlong goal is to characterize some of the interactions between the behavioral and the genetic & neural components of female receptivity. This summer, we specifically investigated two potential receptivity modulators: early exposure to male courtship and male/female circadian clock activity.

We hypothesized that early exposure to male courtship will increase female receptivity, measured by their copulation rates, and as suggested by previous research in the Siwicki lab. We introduced a more controlled manipulation of critical variables that involved collecting subject females as pupae and using ken males, which are incapable of copulation, to provide courtship experience. We also hypothesized that receptivity follows a similar pattern to individual fly circadian clock activity: peak copulation rates would be observed after dawn and during dusk in a 12 hr light: 12 hr darkness cycle, whereas significantly lower rates would be observed mid day during the *Drosophila* siesta time.

Surprisingly, the baseline receptivities of the females were extremely low to assay for an effect of male courtship. Females used in these assays belonged to a recently acquired wildtype stock, Canton S-64349 (Cs) that has not been previously tested in the Siwicki Lab. On eliminating the possibility of external artifacts, we suspected a defect intrinsic to the stock that may affect female receptivity directly, or indirectly via low male courtship behavior. We compared these behaviors in the Cs stock with those in the w1118 stock, another wildtype stock with a different eye color. Females from the w1118 stock (n=52) had significantly higher copulation rates than Cs (n=101) females ($p<0.001$). However, male courtship behavior was more vigorous in the Cs stock than in the w1118 stock ($p=0.02$), suggesting that the low Cs copulation rates are not due to a lack of male courtship activity. Finally, receptivity levels of females through the day did not necessarily follow fluctuations in activity levels usually observed in individual flies: high copulation rates were found at the middle and the end of the day and unexpectedly low rates at the beginning of the day.

In conclusion, our work provides strong evidence for an intrinsic abnormality in the Cs-64349 stock that substantially represses female receptivity. In upcoming months we will use the w1118 stock to further our efforts in assaying the effect of receptivity modulators.

Effects of aging on oncogene and tumor-suppressor gene expression

Cameron Marsh, Joseph N. Paulson

Center for Cancer Computational Biology, Dana Farber Cancer Institute
cmarsh1@swarthmore.edu

While it is well known that patients are more susceptible to cancerous disease as they grow older, there is no clear understanding of the effect of age on the development of cancer. In order to provide an explanation of this relationship on the molecular level, we investigate the effect of age on tissue-specific gene expression, utilizing RNA sequencing data from the Genotype-Tissue Expression (GTEx) dataset, focusing on protein encoding genes. By investigating the activity of genes and their associated functions, we can better speculate how age-related changes in gene activity contribute to cancer susceptibility. Our goal is to understand the genetic changes over time and how they relate to the development of tissue-specific cancerous diseases.

Throughout this study, we model the expression of genes using linear models. The linear model accounts for the age and gender of a sample to understand their influence on gene expression levels. We investigate the relationship of gene expression and age through four separate analyses. Our first analysis involves the interpretation of significant cancer-related genes within specific tissues and their relationship with age. Understanding this relationship provides greater insight into the molecular processes involved in the development of cancer in older patients. We then eliminated the term accounting for gender in our linear model and investigated differences in expression profiles between men and women. However, we found no major differences as the expression of genes were essentially the same for both genders. Our third analysis involved finding the ages at which the expression of certain genes begin to change. By finding the points of inflection on polynomial models of expression over time, we can gain insight into the age ranges when patients become more at risk to cancerous diseases. We also investigated expression in colon tissue as a special case due to known associations with age and cancer development. Our investigation of age-associated molecular changes in specific tissues can provide a potential explanation for the increased risk of cancer development with age.

The Combinatorial Nullstellensatz in Higher Dimensions

Jake Mundo, Alperen Ergur, J. Maurice Rojas

Texas A&M University
jmundol@swarthmore.edu

The celebrated Combinatorial Nullstellensatz of Alon describes the form of a polynomial which vanishes entirely on a Cartesian product of sets in one dimension. Alon's theorem gives circumstances under which a polynomial must be expressible as a linear combination of polynomials in one variable each and in which the coefficient of a particular monomial term of the polynomial must be zero. We explore analogues of the Combinatorial Nullstellensatz in higher dimensions, that is, we give restrictions on the form of polynomials which vanish entirely on Cartesian products of arbitrary dimensional sets, giving two generalizations of the original theorem. For the special case where all the sets are in two dimensions, we also give another generalization. Finally, we discuss possible applications of these results to generalizing the famous Schwartz-Zippel lemma.

Triclosan in Toothpaste and Oral Health Outcomes: A Population Analysis

Kate H. Musen, Catherine K. Su and Jay Bhattacharya

Center for Primary Care and Outcomes Research, Stanford University, Stanford, CA

kmusen1@swarthmore.edu

Abstract

Although the antimicrobial agent triclosan has been used in a variety of hygiene and cosmetic products since the 1960s, only recently has the additive been seriously questioned. In December 2013, the FDA declared that soap manufacturers would have to demonstrate that triclosan-based soaps are more effective than regular soaps and that they are safe for long-term use [1]. After soap manufacturers failed to provide convincing evidence that the benefits of triclosan outweigh the risks, the FDA banned triclosan in soaps in September of this year [1]. Despite increasing concerns over triclosan in soap, triclosan-based toothpastes have not received the same level of scrutiny, largely due to the substantial evidence from randomized controlled trials that triclosan toothpaste improves oral health [2].

This study aimed to determine whether the positive effect of triclosan on oral health found in randomized control trials could also be found in the general United States population.

We analyzed National Health and Nutrition Examination Survey (NHANES) data from 2003-2008 and conducted a factor analysis of seven important oral health variables to create a composite index of dental hygiene. We then employed multivariate regression to measure the relationship between this index and urinary triclosan concentration, controlling for patient demographics and proxy variables to account for differences in hand washing. We also conducted a power analysis to measure our ability to find clinically meaningful effects given our sample.

We found no statistically significant association between urinary triclosan concentration and oral health (95% C.I.: -0.000045 to 0.00017), and the regression coefficient on triclosan remained small throughout our estimations. Our power analysis indicated that we had the ability to detect a relatively small effect size. Our study suggests that the positive effect of triclosan on oral health found in randomized controlled trials is not detectable via NHANES data in the general United States population with typical use of triclosan toothpaste.

Given the potential health risks of triclosan absorption, our findings suggest that health researchers need to evaluate further the benefits of triclosan toothpaste within the community setting. If practical usage of triclosan toothpaste does not improve oral health, health policy makers should exercise more caution in their approval of this product.

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Accounting For The Signor-Lipps Effect In Estimating The Duration And Number Of Pulses In The Cambrian Explosion

Jason Z. Lin, Katrina M. Midgley, Tuan A. Nguyen, Steve Wang

Swarthmore College, PA

Zlin2@swarthmore.edu, Kmidgle1@swarthmore.edu, Tnguyen4@swarthmore.edu,

Although the Signor-Lipps effect is most often associated with mass extinctions, it also plays a role in “mass origination” events. The Cambrian explosion is arguably the most important such example and a pivotal event in the history of life. The general timeline of the Cambrian explosion is well established, but details about the duration and pattern of origination events 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 attempt to provide a statistically rigorous estimate for the duration and number of pulses in 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 origination event, we construct a confidence interval for the time span between the earliest and latest originations, by inverting a hypothesis test for whether a given duration is consistent with the observed fossil record. To estimate the number of pulses, we use a k-Nearest Neighbor classifier, which takes in a vector of Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) weights and outputs a vector indicating the posterior probability for each possible number of pulses.

Protoplanetary Disk Survey: Binaries in Taurus

Natasha Nogueira and Stefan Laos, Professor Eric Jensen

Swarthmore College

nnoguei1@swarthmore.edu, slaos1@swarthmore.edu

From a survey of young binary systems in Taurus, taken with the Atacama Large Millimeter Array (ALMA), we analyzed disk structures surrounding the sources. By determining certain properties of the disks, such as the size, position angle, and total flux density, we can better understand how multiplicity effects star and planet formation. Six of the systems captured images of both the primary source and the secondary source which allowed for analysis, specifically relating to the presence of protoplanetary disks and their sizes. Three of the binary sources, XZ Tau, GH Tau, and IS Tau, were able to undergo further analysis of the binary separation and binary position angle due to previously recorded data. It was determined that each of these sources demonstrated continuation of trends set by previous data. Further analysis regarding these young binary star systems in Taurus and how planet formation will be effected will be conducted as this research continues.

Machine Interpretation of American Sign Language

Darbus Oldham

Advised by Professor Carr Everbach

Los Gatos, California

doldham1@swarthmore.edu

Abstract

American Sign Language (ASL) is commonly used in the United States and Canada in the Deaf community, in families with Deaf and hard of hearing individuals, and by others who do not use spoken language. ASL is independent from spoken English and has complex grammar like any other language. Accordingly, like words in spoken language, signs in ASL can be broken up into phonemes, with signs consisting of five components: palm orientation, location, movement, non-manual markers, and handshape. Machine interpretation of ASL has the potential to be a communication tool in the absence of an interpreter, as well as providing the means for an ASL to English dictionary. However, there are numerous limitations on the effectiveness of such a system, including limits in technology and the understanding of sign language, as well as the myriad factors which hinder computerised translation of spoken languages.

My research this summer consisted of extensive reading on prior work in and limitations of this field and developing the beginnings of a system for sign language recognition. I used the Leap Motion Controller (LMC), a device designed to detect hand and finger movement with a high degree of precision, and programmed in Python. My system is designed to recognise phonemes and identify signs from them, as this can be effectively scaled up in a way that whole sign recognition cannot. Based on the capabilities of the LMC and the focus of prior work on this topic, I chose to limit the scope of my work to palm orientation and local movements.

Synthesis of π -Conjugated Polymers for the Dispersion of Single Walled Carbon Nanotubes

Kyrstyn Ong, Catherine Kanimozhi, Professor Padma Gopalan

University of Wisconsin-Madison
kong1@swarthmore.edu

Semiconducting single-walled carbon nanotubes (s-SWNTs) are seamless cylinders of carbon atoms packed into a honeycomb lattice that have the potential to revolutionize nanoelectronics due to their high conductivity [1]. However, the propensity for raw semiconducting nanotubes to conglomerate with undesirable metallic nanotubes (m-SWNTs) makes the widespread application of s-SWNTs in field effect transistors difficult. It is therefore essential to be able to disperse these nanotubes while maintaining their excellent electronic properties and to be able to select particular chiralities, lengths, and diameters of the nanotubes for use in specific applications.

Although there are many methods of nanotube dispersion, wrapping with conjugated polymers has demonstrated a particularly exceptional ability to disperse and to preserve the conductivity of s-SWNTs through noncovalent interaction with the sp^2 hybridized surface [2]. However, it is not well understood why certain conjugated polymers, such as those that are fluorene based, are much better dispersants than other polymers.

To that end, we synthesized different molecular weights of poly[(9,9-dioctylfluorenyl-2,7-diyl)-alt-co-(6,60-(2,20-bipyridine))] (PFO-BPy) via a Suzuki coupling carbon-carbon reaction in order to compare its thermal and photophysical properties with commercially available polymers. We determined that the properties were consistent, indicating the successful synthesis of PFO-BPy with this method. The fact that the low molecular weight fraction dispersed carbon nanotubes demonstrates the selective sorting strength of this conjugated polymer.

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Ion flux controls heart and gut asymmetry in *Ciona intestinalis*

Karl Palmquist, Brad Davidson

Swarthmore College, USA
Kpalmqu1@swarthmore.edu

During development, bilaterian organisms are patterned along the left-right axis. While the TGF β -family member, Nodal, is thought to play a highly conserved role in this process, the impact of other signaling mechanisms on this process is poorly characterized. To better understand what other signaling pathways contribute to asymmetric organogenesis, we employ the tunicate *Ciona intestinalis*. We have found that the *Ciona* heart and gut-tube are positioned on the right side of developing juveniles. Asymmetric positioning of these organs is first observed during larval stages. Intriguingly, we show that while nodal signaling is crucial for proper gut asymmetry, it is dispensable for heart asymmetry in larva. Through inhibitor experiments, we have found that H⁺/K⁺-ATPase dependent ion flux is necessary for proper heart and gut positioning in both larvae and juveniles. Based on our findings, we hypothesize a model where ion flux and ciliary flow act through a feed-forward mechanism to direct heart and gut asymmetries. These results provide the groundwork for future studies pinpointing the mechanisms underlying left-right patterning in vertebrates.

Developing a Game Model of a Multi-Agent Environment with Varying Degrees of Agent Competitiveness

Joon Sung Park, Bryce Wiedenbeck

Swarthmore College, Department of Computer Science
jpark3@swarthmore.edu

Some people are competitive, some are not. As vague as its definition in colloquial settings may be, the concept of competitiveness is not foreign to us. We can roughly imagine how a competitive person would act, pick out those who are relatively more competitive, and ponder whether our society encourages competitive behavior. But if we can more precisely understand competitiveness beyond our colloquial understandings and map out its consequences, we may be able to provide a richer context to our study of competitions. Given a game, would a competitive agent thrive over those who are less competitive? How would the utilities distribute when some agents are more competitive than the others? Would an environment with more competitive agents incur a better equilibrium than an environment with less competitive agents?

To answer the above questions, our study here offers an agent-utility model that attempts to encapsulate varying degrees of competitiveness in a given agent. Agent-utility model, actively studied in the field of economics game theory, attempts to express an agent's decision making in a mathematical expression. Our current model, which is inspired by previous studies that describes a competitive agent's tendency to feel pain by being outperformed, takes into account the agent's relative performance determined by overall rankings where the agent's potential gain in utility sharply drops by the loss against another agent.

While our model here is a work in progress, by studying its Nash equilibria (the solution concept to the model in which no agent can gain greater utility by unilaterally changing his or her strategy), we report some noteworthy results. As a preliminary step of exploring our model, we observed agent behaviors in an environment where all agents are hyper competitive, and also in an environment where all agents are only mildly competitive. In both environments, we observed that agents who lack talent give up before others when the cost of effort rises.

Spectral Energy Distributions and Eddington Ratios of Luminous, Dust-Reddened Quasars

Nathaniel Peters
Advisor: Eilat Glikman

Middlebury College
npeters3@swarthmore.edu

Quasars are a subset of active galactic nuclei (AGN) by the accretion of matter onto supermassive black holes. Young quasars, thought to be triggered by galactic interactions, are reddened by the disturbed dust of the merger. Using archival and new photometry across wavelengths of $\lambda = 0.36\text{--}500\mu\text{m}$, we compiled spectral energy distributions, which model the electromagnetic flux within this range of wavelengths. These models allow us to disentangle galactic light from AGN emission. We compared the estimated AGN luminosity to their black hole mass estimates and found that most of these AGN have bolometric luminosities between 10% and 100% of their Eddington luminosities, the maximum stable emission rate.

Initial Attempt at Crystallization and Observation of the Impact of LsrE on the Lsr Quorum Sensing Pathway

Nicholas E. Petty, Stephen T. Miller

Swarthmore College
npetty1@swarthmore.edu

Bacteria are generally considered primitive organisms, however they have developed systems of communicating between organisms and between species that mimics the communication seen in multicellular organisms, quorum sensing. One such quorum sensing pathway is found in the *Lsr* operon, which is present in *Escherichia coli* and *Salmonella typhi*, along with a host of other bacterial species. The majority of proteins coded for by the *Lsr* operon have had their functions determined however one protein, LsrE, remains a mystery in the quorum sensing pathway. I attempted to purify and crystalize a truncated construct of LsrE through expression in *E. coli* to examine its structure, and began initial attempts to introduce purified LsrE into known Lsr pathways to observe any impact that LsrE might have. Truncated LsrE was obtained and purified enough for initial attempts at NADH consumption assays, however crystallization purity was not reached. Moving forward, further attempts at purification to reach crystallization-ready levels of purity will be a priority. Additionally, with initial functionality assays underway, the next step will be to introduce metal catalysts to observe if LsrE requires a metal cofactor for functionality.

Determining properties of halo dust for the Herschel EDGE-on galaxy Survey (HEDGES)

Jacklyn M. Pezzato, Eric J. Murphy

National Radio Astronomy Observatory (NRAO)
jpezzat1@swarthmore.edu

The Herschel EDGE-on galaxy Survey (HEDGES) aims to study the distribution of dust in the halos of nearby spiral galaxies. More specifically, its goals are to determine the physical characteristics of this dust, what relationship there might be between halo dust content and star formation activity, how halo dust might expose information about the far-infrared (FIR)-Radio correlation, and how the physical distribution of this dust might relate to that of other gas tracers. The work presented here aims to investigate the physical characteristics of this halo dust and how they change with height above and below the plane of the six galaxies in the HEDGES sample: NGC 0891, NGC 3628, NGC 4244, NGC 4517, NGC 4565 and NGC 4631. To achieve this goal, code has been written that, for each galaxy, can extract vertical profiles and photometric data from nine different bands (taken using the Herschel Space Observatory and the Spitzer Space Telescope) in the FIR part of the electromagnetic spectrum. These photometric data are then fit to a suite of Silicate-Graphite-Polycyclic Aromatic Hydrocarbon (PAH) dust models produced by Bruce Draine and Aigen Li in 2007. With the completion of a few final tests of this code's functionality, it will be ready to produce final results as soon as the entire suite of the Draine/Li dust models is available.

Intrinsically Difficult to Replicate Sequences: Pursuing the Structure of (CAGAGG)_n Repeats

Barrett Powell and Dr. Liliya Yatsunyk

Swarthmore College

bpowell1@swarthmore.edu

The mouse genome has been identified to have several regions that are challenging to replicate, resulting in frequent breaks and mutations. Upon bioinformatics analysis by the Brown lab at the University of Pennsylvania, these regions are composed of highly repetitive sequences; one such example is d(CAGAGG)_n, where n averages about 80 repeats. The d(CAGAGG) repeats were hypothesized to form a GQ-like structure, but analysis via a variety of biophysical methods indicated that the structure was uniquely different from expectations. Our lab is attempting to crystallize this repeat sequence to determine its structure via x-ray crystallography. Previous crystallization attempts produced crystals that diffracted to 6 Å resolution, which is not sufficient to provide useful structural information. Further crystallization was pursued using three approaches: variations in length and frame shift of CAGAGG repeats, brominated CAGAGG repeats, and ligand bound CAGAGG repeats. Each approach began with a commercial crystallization screen before optimizing any suitable hits. Mediocre hits were identified for all three brominated sequences and for the methylene blue + CA5-5 setup. Small crystals were observed for CA2core under a variety of conditions. Excellent crystals were formed with CA5-5; upon optimization, it became clear that the crystallization conditions were closely related to a previously identified hit.

Investigation of the therapeutic potential of combining PARP and CDK12/13 inhibitor strategies in SCLC

Alexandra R. Rabin and Camilla L. Christensen Ross
Dana Farber Cancer Institute
arabin1@swarthmore.edu

Small cell lung cancer (SCLC) is a particularly aggressive subtype of lung cancer that comprises 10-15% of lung cancer patients. The five-year survival rate for this disease is about 6%, necessitating novel treatment strategies beyond standard chemotherapy. A number of targeted therapies, which act to inhibit aspects of cancer cells' DNA replication and uncontrolled cellular division, are currently being studied. Among these, drugs targeting cyclin-dependent kinases (CDKs) have been found to be effective in many subtypes of cancer, including small cell lung cancer. Of particular interest are potential opportunities for synergy between these CDK inhibitors, certain subtypes of which have downstream effects on DNA repair and replication, and drugs that specifically modulate DNA replication, including PARP (poly-ADP ribose polymerase) inhibitors. Previous research has found that disabling CDK12 in ovarian cancer sensitizes cells to PARP inhibition¹. Here, we investigate whether PARP inhibitors, which restrain the activity of DNA-repair proteins, can synergize with CDK12/13 inhibitors in SCLC.

Previous research by Carnell *et al.* identified a series of SCLC tumor cell lines responsive to PARP inhibition alone, all with IC50 values below 15 nmol/L, suggesting a particularly strong response to these drugs². Using many of the same cell lines, the same 5- and 8- day cell viability assay was carried out with resulting IC50 values between 10 and 1000 nmol/L, calling into question the efficacy of the same PARP inhibitors in SCLC. We then assessed the effect of combining PARP inhibition with CDK12/13 inhibition using a similar cell viability assay, and found a tremendous response (measured in terms of tumor cell death) regardless of PARPi concentration. This suggests that the novel CDK12/13 inhibitor is exceptionally effective alone. cDNA analysis using quantitative PCR demonstrated that treatment with this new inhibitor upregulates the expression of certain DNA repair genes in a subset of cell lines. Future directions include investigating downstream effects of treatment with this CDK12/13 inhibitor to further determine both its impact in cells and potential opportunities for synergy with other protein inhibitors, as well as treating mice with the inhibitor to assess its efficacy *in vivo*.

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Removing Spurious Associations in Microbiome Analysis

Vivek Ramanan^{1,2}, Rajita Menon³, Kirill S. Korolev³

¹**Department of Biology and Computer Science, Swarthmore College, 500 College Avenue, Swarthmore PA, 19081.**

²**Boston University BRITE Bioinformatics REU Program, Summer 2016, 24 Cummington Mall, Boston MA 02215**

³**Department of Physics and Bioinformatics, Boston University, 590 Commonwealth Avenue, Boston MA 02215.**

Vramanal@swarthmore.edu

Microbes play many essential roles in the human body, ranging from digestion to protection from harmful antigens. Imbalances in bacterial abundances are associated with many diseases from inflammatory bowel disease to cancer. Recently, several large-scale efforts have been undertaken to characterize microbial dysbiosis and detect disease-causing taxa. Current statistical methods however do not account for microbial interactions and are likely to produce spurious correlations. Indeed, if microbe A suppresses microbe B, then changes in A's abundance due to disease will affect B's abundance even if B is not directly involved in the disease. To circumvent this problem, we developed an inference approach based on maximum entropy models in statistical physics. In synthetic data, our method successfully identifies direct associations with the disease and removes spurious associations due to microbial interactions. We applied this novel analytical tool to RISK, the largest pediatric cohort (700 samples) of controls and patients with Crohn's disease. The number of detected associations was reduced by about ten fold, but the strength of associations increased. Thus, our approach can help clinicians sieve through the large number of taxa correlated with Crohn's disease by narrowing the search for disease-causing microbes.

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Modeling Patient Flow in Emergency Departments

Meghana Ranganathan, David Yao, Yuan Zhong

Department of Industrial Engineering and Operations Research, Columbia University

mrangan1@swarthmore.edu

Emergency departments are known nationwide for being slow, inefficient processes. These delays can have disastrous consequences for patients' health, and fixing the process has been the focus of a lot of research. This project focused on Columbia University's hospital with the intention of submitting to them a report detailing the most efficient allocation of resources (i.e. physicians, nurses, beds, ambulances). The goal of the project is to develop a model of the patient flow of the emergency department using simulation software ARENA and then test the model with different capacity of resources to see which maximizes efficiency of patient flow. I cleaned and analyzed hospital and patient wait time data provided by the hospital, fitting distributions for arrival rates and departure rates, boarding time, and patient wait time for the purposes of building the model. Then, I focused on developing models of the intake area of the emergency department to test data collection techniques in ARENA and collect initial data on simulation runs. We have determined thus far that primary bottlenecks in the process are during medical evaluation and nurse triage. Additionally, the most demanding hours are between 2PM and 4PM, and so increased physicians especially during that time could remedy these problems. For the future, more simulations need to be run on the larger model, both for accuracy and to test different resource allocations.

Developing a DSL for Pushdown System Specification

Charlotte Raty, advised by Zachary Palmer

Swarthmore College

craty1@swarthmore.edu

Demand-Driven Program Analysis, or DDPA, is a model of program analysis that traces backwards through a program, unfolding the control-flow graph on an as-needed basis. DDPA is specified in terms of reachability on a complex pushdown system (PDS). This research project developed a domain-specific programming language (DSL) to abstractly describe pushdown systems. This DSL eases the development of DDPA-style analyses.

Because a program can have many branches but a program analysis cannot determine which branch will be taken without running it, program analyses are necessarily nondeterministic. Therefore, the nondeterminism of pushdown systems makes them well-suited to program analysis. However, creating a pushdown system for program analysis is difficult, largely due to this inherent nondeterminism. To avoid manually writing error-prone PDS construction code, my project attempted to develop a DSL for specifying pushdown systems. This DSL is implemented as an OCaml metaprogram.

The program analysis operates by pushing values to be analyzed onto the stack, and then popping them as needed. At points in the program analysis at which a pop from the pushdown system's stack is needed, the analysis needs to be able to pause until the appropriate input is received. Therefore, the code needs to be broken up different linked functions, called continuations, which can be called as the stack pops happen. Because the program analysis is nondeterministic, this means that each piece of code can be run as many times as necessary to choose every path possible with each stack pop. Much of my work this summer had to do with the construction of this function, which is integral to the DSL and which can also be used as a general metaprogramming tool in other projects.

In addition to developing a continuation transform function that breaks up OCaml code based on the structure of its Abstract Syntax Tree (AST), I also created an A-Translator, another metaprogramming tool, to flatten the ASTs and make them simpler for the continuation transform to process. These tools, along with a few other small tools I developed, will help create an environment that makes development of PDS much easier. Additionally, these metaprogramming tools can be used in other OCaml code transformation projects, and the DSL for PDS specification, which will be dependent on these tools and which I will assist in building as part of my future work, will be able to be used to encode or approximate other problems using pushdown systems.

Cholesterol Decreases Depth and Mobility of Full-Length Membrane-Bound Influenza A M2 Protein

Hayley Raymond and Kathleen P. Howard

Department of Chemistry and Biochemistry, Swarthmore College, Swarthmore, PA 19081
hraymon1@swarthmore.edu

The C-terminal region of the M2 membrane protein is crucial for viral budding in the life cycle of influenza A, making it a drug target. In order to link the protein's structure to its function, site-directed spin label electron paramagnetic resonance data was collected for full-length M2 reconstituted into POPC:POPG (1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine:1-palmitoyl-2-oleoyl-sn-glycero-3-phospho-1-rac-glycerol) 4:1 lipid bilayers in the absence or presence of 30% cholesterol, as cholesterol is necessary for viral budding. Continuous wavelength spectra revealed that residues 55 and 58 have a larger population of the immobile component and a lower population of the mobile component in the presence of cholesterol than in the absence of cholesterol. Results of residue 55 were consistent with previous findings of studies of an M2 truncated construct. Differences observed in residue 58 in the presence and absence of cholesterol were not as pronounced as those in residue 55, and residue 58 revealed a larger population of the immobile component in POPC:POPG than previous Howard Lab work on full-length M2. Power saturation data of residue 55 revealed that in the presence of cholesterol, residue 55 is less deeply embedded in the membrane, also consistent with previous findings on the M2 truncated construct. Results suggest that data collected on the M2 truncated construct lacked artifacts and are physiologically relevant.

Chick provisioning in Common Terns on Great Gull Island, NY

Indiana Reid-Shaw, Kalaina Thorne, Pam Loring, Curtice Griffin and Paul Sievert

Department of Environmental Conservation, University of Massachusetts Amherst

ireidsh1@swarthmore.edu, kthorne@brynmawr.edu, cgriffin@eco.umass.edu,
psievert1@eco.umass.edu,

Abstract

There is much interest in the ecological implications of proposed offshore wind energy sites. More information is needed at the species level to understand the potential risks to migratory seabirds posed by future wind turbines. This project aims to inform policy that supports 'smart from the start' initiatives that can mitigate ecological externalities while promoting vital renewable energy in the United States. I am analyzing data from my two weeks of fieldwork on Great Gull Island in Long Island Sound, NY. Great Gull Island hosts the largest breeding colony of Common Terns, *Sterna hirundo*, worldwide. My fieldwork team conducted two-hour observations of nano-tagged bird nests from blinds three times a day. We recorded prey composition, nest attendance, and delivery rate for 10 nests of Common Terns. Our study suggests that time of day, day in breeding cycle, and sex of parent have the potential to affect chick provisioning for common terns on Great Gull Island. Any variation in feeding is noteworthy as fledgling success hinges largely on prey base during the breeding period. This project will also help to inform future prey delivery study designs as well as potential fishing laws related to fish species common terns rely upon.

The role of microtubules in *Ciona intestinalis* heart progenitor induction

Elijah Reische, Bradley Davidson

Swarthmore College

ereisch1@swarthmore.edu

It has been found that induction of heart progenitor cells in *Ciona intestinalis*, a tunicate chordate, is determined by enrichment of the fibroblast growth factor receptor (FGFR) on the ventral side of the dividing cardiac founder cell (Cota and Davidson 2015). What is not known is how this process occurs. It seems likely that microtubules, which are long, slender polymers essential to many types of intracellular transport, are involved. I attempted to uncover the role of microtubules in the process of FGFR trafficking and heart progenitor induction in *Ciona* by using nocodazole, a drug that destabilizes microtubules.

I found that embryos treated with nocodazole showed no heart progenitor induction as well as abnormal cardiac founder cell formation and unusual morphology. Furthermore, the ventral polarization of FGFR that occurred in control embryos was not observed in the nocodazole-treated embryos, whose FGFR distribution was more uniform.

The lack of heart progenitor induction could have been directly caused by disruption of microtubule activity, but it is also possible that nocodazole treatment arrested embryo development, preventing new genes from being translated, including the reporter constructs used for the induction assay. Additionally, the difference in FGFR distribution also may have been due to microtubule disruption, but it also could be that microtubules are important for matrix adhesion, which has been found to be necessary for FGFR polarization.

Creating Learning Tools for the Language Wooi

Emma Remy, advisor: Professor Emily Gasser

Manokwari, West Papua, Indonesia

eremy1@swarthmore.edu

West Papua, Indonesia is home to hundreds of languages that are increasingly being forgotten in favor of Indonesian. In affiliation with the Center for Endangered Languages Documentation (CELD), housed at the Universitas Negeri Papua in Manokwari, vocabulary and grammatical data was collected from native Wooi speaker Jimmi Karter Kirihio to use in a website teaching the basics of the language. Wooi is spoken by approximately 200 people on Yapen Island. The consultant was met with every day, Monday through Friday, for around three weeks. He was asked for translations into Wooi of vocabulary, sentences, and grammatical structures. The elicitation was conducted in a combination of standard Indonesian and Papuan Malay, the local dialect of Indonesian. He provided several hundred Wooi words, verbs in various conjugations, question words, adjectives, inalienable and alienable possessives, a short story in Wooi, and information about orthography and history. This data was recorded, analyzed for understanding of morphological and syntactic structure, and used to create a simple website outlining the basics of the language. This data allows for further linguistic analysis of Wooi and other languages of the region and contributes to the preservation of the Wooi language and culture as Indonesian becomes increasingly dominant in Papua.

**Investigating a new social behavior in
satin bowerbirds, *Ptilonorhynchus violaceus***
Tessa Rhinehart, Sara Hiebert Burch
Swarthmore College
trhineh1@swarthmore.edu

Male satin bowerbirds (*Ptilonorhynchus violaceus*) clear and decorate a display court on the forest floor and build a structure out of fine sticks called a bower, where females crouch to watch the male's energetic dance.¹ The purpose of multiple components in complex courtship displays has been the subject of much debate by evolutionary biologists. Multi-component displays have been shown to accommodate varying female preferences in the satin bowerbird. While older females make mate-choice decisions based on the quality and vigor of the male's dance, younger females are sometimes startled by the vigorousness of this display, and instead make mate-choice decisions based on the decorations present at the bower.²

We studied a previously undescribed component of the male display termed the "hunched walk," in which the male satin bowerbird crouches and walks several steps forward, repeatedly opening and closing his bill in a gape reminiscent of begging avian fledglings. Because female birds are predisposed to respond to begging fledglings, we hypothesized that this fledgling-like posture may entice a startled female to return to the bower. While previous studies have focused on the modulation of aggressive behaviors in the satin bowerbird courtship display,³ our study tests the idea that males may also attempt to attract the attention of adult females by including behaviors that mimic the qualities of younger birds. We also proposed two additional hypotheses: that the behavior is aggressive; or that it is a "frustrated" behavior without an intended audience.

From video clips recorded at males' bowers, we identified approximately 40 interactions involving hunched walks. We found that compared to recordings without hunched walks, this behavior was significantly more frequently associated with social situations. Additionally, we noted that observers' positions tended to be farther away directly following a male's hunched walk compared with directly before a baby walk. We found a marginally significant association between number of hunched walks by a male in an interaction, age/sex class of the observer, and difference in position after a hunched walk. These results do not confirm that the hunched walk entices observers to return to the bower, but do indicate that the behavior is associated with startling. Future research must seek to provide more conclusive evidence for one of the proposed hypotheses.

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Bird-Window Collision Prevention

Alex Robey, Carr Everbach

Swarthmore College
arobey1@swarthmore.edu

Every year nearly a billion birds are killed or wounded following collisions with glass windows in the United States. This makes bird-window collisions the second leading cause of bird death after habitat destruction. It has been shown that birds of different species die with equal probability when colliding with windows. These windows become particularly dangerous at higher altitudes and when they reflect images of surrounding flora. A method to prevent such collisions is to place specially designed UV-reflecting screens over window panels to deter birds from flying toward them.

Following the University of Chicago's construction of the William Eckhardt Research Center, there has been an effort to dissuade birds from flying into the large class windows of this building. However, the University decided that it wanted a way to monitor which windows birds were flying into before implementing the UV-reflecting deterrent screens. I designed a device that selectively records video footage of a window frame based on a window's vibration pattern. The vibration pattern is caused by external impact. This video is stored in a database and sent to a website that keeps track of all the sensors in a given location and maintains a running collision counter. The goal is to optimize the location of UV-reflecting screens to save the maximum number of birds.

“Therapeutic restoration of glutamate homeostasis after mild traumatic brain injury attenuates alcohol drinking and anxiety-like behavior in rats”

Peter F. Sayde^{a,b}, Jacques Mayeux^b Patricia Molina^b

^a Swarthmore College, Swarthmore, Pennsylvania

^b Department of Physiology and Alcohol and Drug Abuse Center of Excellence: LSUHSC
psayde1@swarthmore.edu

The Center for Disease Control and Prevention recognizes traumatic brain injury (TBI) as a major public health concern in the United States, resulting in over 2.5 million hospitalizations and 52,000 deaths per year. The most common form of TBI present in the United States is a mild TBI (concussion) caused by blunt trauma or rotational forces to the head. TBI mainly affects young and otherwise healthy individuals such as athletes and military personnel. Common behavioral consequences of mild TBI are increased anxiety, depression, and alcohol misuse. Alcohol use following TBI is harmful because it exacerbates neuroinflammation (the main cellular pathology following TBI) and can cause excitotoxicity and synaptic dyshomeostasis. Currently the only treatments for TBI are palliative, indicating a need for further therapeutic research in the mechanisms of TBI-induced behavioral changes.

Mild TBI results in neuroinflammation and a reduction of glutamate transporter proteins in astrocytes (GLT-1 in rats; EAAT-2 in humans), ultimately resulting in increased extracellular glutamate, altered neuronal signaling and, potentially, behavioral changes. Previous research has shown that ceftriaxone, a β -lactam antibiotic, helps combat excitotoxicity by restoring glial transporter protein action within the astrocyte. Ceftriaxone has also been shown to reduce alcohol consumption in genetically bred alcohol preferring P-rats. Because of this we hypothesize that IP injection of ceftriaxone post-TBI will restore normal behavior and attenuate escalated alcohol drinking in rats.

Male Wistar rats (n=15) were trained to operantly self-administer alcohol four weeks prior to TBI on a fixed ratio schedule until drinking stabilized (baseline). Rats were counterbalanced based on baseline alcohol drinking into three treatment groups: sham surgery (with sterile water injection), TBI-Vehicle (sterile water), or TBI-ceftriaxone. During the two-weeks post-TBI, motor behavior, cognition, and anxiety were assed via NSS and NBS, Y-maze and Open Field tests, respectively. Alcohol drinking was evaluated via a fixed-ratio schedule for ten days post-TBI and motivation to consume alcohol was determined by a progressive-ratio schedule nine days post-TBI.

Mild-TBI via lateral fluid percussion resulted in increased apnea duration, increased righting reflex, and decreased respiratory rate. Y-maze (48-hrs post-TBI) outcomes showed TBI negatively affects spatial cognition: only sham-rats performed significantly better than random chance. Our results indicate a significant impairment in motor behavior (NSS and NBS), as well as a significant attenuation of anxiety-like behavior from ceftriaxone treatment. No significant difference in alcohol consumption was observed between treatment groups; however, ceftriaxone treated rats tended to consume the least amount of alcohol. Due to the exploratory nature of this project, sample sizes were relatively low. However, encouraging trends with our data demonstrate further research ceftriaxone's effect on post-TBI behavior and drinking with larger sample sizes could be beneficial.

Using honey bee (*Apis mellifera*) pathogen screening to develop a streamlined colony health assessment tool for beekeepers

Sassicaia Schick '17, Elizabeth Eppley '19, Robert Broadrup, Helen White, Anthony Macherone, and Christopher Mayack

Swarthmore College Biology, Haverford College Chemistry, Johns Hopkins University, Agilent Technologies

Sschick1@swarthmore.edu, eeppley2@swarthmore.edu, cmayack@gmail.com

The western honeybee (*Apis mellifera*) plays an invaluable role in both maintenance of biodiversity and agricultural production as a general pollinator. Recently the health and general population has been deteriorating due to a number of stressors including parasitic infections, pesticide exposure, and loss of foraging habitat. As part of a larger collaborative effort, 32 hives from 6 distinct geographic locations around Southeastern Pennsylvania were sampled for disease screening and exposomic analysis. Swarthmore students screened for two fungal pathogens (*Nosema apis* and *Nosema ceranae*) using semi-quantitative PCR, and plan to detect and quantify the ten most common viruses associated with bee declines in one reaction using Reverse Transcriptase Multiplex Ligation-dependent Probe Amplification (RT-MLPA). We found that of the 32 beehives sampled, 12 were infected with *N. ceranae*, while three had relative infection loads greater than 15. We did not detect *N. apis* infection in any of the hives.

Our disease data will be correlated with both exposomic and ambient-air chemical profiles to establish reliable and robust volatile chemical biomarkers of bee health. Currently, absorbent silicone wristbands are being placed inside beehives by beekeepers for 24 hours to determine if previously established chemical biomarkers, indicative of hive health status, can be detected using this passive sampling method.

Rule vs. Object: Language Acquisition

Jordan Sciascia and Stella Christie

Swarthmore College

Jsciasc1@swarthmore.edu

Languages are governed by complex rules. It is enough to think about your experience learning a foreign language to understand the challenge of learning a new grammar. How do young children learn these complex rules of language? Cognitive research shows infants as young as 7 months of age can abstract simple rules. After hearing strings of sounds such as “ga-ti-ti; gi-la-la, ta-ni-ni” infants recognize a new string of sound that exhibit the ABB pattern (Marcus et al., 1999). But later in development, research with visual (non language) rules showed that three-year-olds ignored rules in favor of matching objects. For example, given [oo] and a choice between [xx] and [ox], children matched the look-alike [ox] than the same-rule [xx] (Christie & Gentner, 2007). My study is the first to ask whether three-year-olds and six-year-olds prefer the same rule or the same objects in the language domain, charting the learning trajectory of rule learning and abstraction in language acquisition.

Probabilistic Analysis of Pedestrian Dynamics

Jimmy Shah, advised by Amy Graves

Swarthmore College Department of Physics and Astronomy

jshah1@swarthmore.edu, abug1@swarthmore.edu

In the study of jamming phenomena, one specific subject of interest is the application of traffic patterns to pedestrians. Pedestrians complicate common jamming setups, since simple physical forces are not enough to capture the entirety of the scene. We must also include psychological forces such as follow factors and collision avoidance routines, among other factors. Using Easy Java Simulations, bi-dispersed particle flow was modeled through a corridor with a narrow opening in the middle. To fully capture the simulation and properly analyze the results, a program was created to observe and model the output file.

The analysis routine first worked to find the steady state time so that statistical anomalies would minimally interfere with the analysis. This value was constructed through averaging the entropy and current for time periods of fixed size, and then plots were generated for the valid data. Some of these outputs included pedestrians transited, entropy of each group, current density, and histograms. Furthermore, probability distribution functions were generated for the size of a cluster of particles for each of the opposing groups. Complimentary cumulative distribution functions also displayed behavior for the size of a lag, during which no particles from the opposing groups crossed the opening. The cCDF was then tested as a power-law distribution, and fitted on a loglog plot if applicable through a newer statistical method.

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Characterization of Diabetic Autonomic Neuropathy via Pupillometry in Pediatric Diabetes Mellitus Patients

Christina Shincovich, Mentor: Dr. Julia Finkel, MD

Children's National Medical Center

cshinco1@swarthmore.edu

Diabetic autonomic neuropathy (DAN) is a serious complication for those afflicted with diabetes mellitus. Despite its severe consequences to several organ systems through damage to the autonomic nervous system, DAN is very infrequently recognized and poorly understood. Diabetic neuropathy is very rarely diagnosed in children, though it may be the underlying cause of dysautonomia in pediatric diabetics.

The goal of the study was to utilize pupillometry to compare the pupillary responses of pediatric diabetes mellitus Type 1 patients at baseline and under orthostatic stress. Eight pupillary light reflex (PLR) parameters were assessed and compared to both healthy controls and postural orthostatic tachycardia syndrome (POTS) patients to compare DAN to a dysautonomia. Previous pupillometry studies in POTS patients and in subjects with other forms of dysautonomia suggest there is an increased latency to constrict and decreased constriction velocity, as expected in patients who are beginning to show clinical symptoms of DAN. Pupillary parameters were analyzed relative to the duration of the diabetes, in years since diagnosis, and severity as defined by the hemoglobin A1C score. Additionally, this study measured the sensory detection and tolerance threshold data to ascertain the integrity of each sensory nerve fiber, as is used to diagnose neuropathies. This sensory data was expected to relate to pupillary changes.

The Neuroptics PLR-2000 pupillometer was used. Patients were dark adapted and in the supine position for 5 minutes, then a baseline reading was taken. Patients were directed to stand, and pupillary measurements were repeated at 5 and 10 minutes of standing. The NEUROMETER® CPT neurostimulator was used to measure sensory threshold and perception at each of the intervals.

A significant difference was observed in constriction amplitudes for diabetes mellitus type 1 patients between baseline and 5 and 10 minutes after orthostatic stress. These patients have significantly different constriction amplitudes than POTS patients and healthy controls. The total time taken by the pupil to recover to 75% of resting size after peak constriction (T75) in diabetic patients was significantly lower than both POTS patients and healthy controls when measured at baseline. The T75 of diabetic patients was also significantly lower than POTS patients for the readings at 5 and 10 minutes. There was no correlation between pupillary measures and duration of the disease or A1C scores. However, both years since diagnosis and A1C score were strongly correlated with sensory threshold and moderately with sensory detection.

It remains unknown why the T75 and constriction amplitude are affected in the diabetes mellitus patients. Since latency to constrict (LAT) and constriction velocity were not significantly affected, these results could indicate that DAN is causative for degeneration of nerves. Demonstrated correlations exist between the threshold and perception from the neurostimulator and the duration of the disease and Hb A1C score. This affects pupillary parameters, such as the constriction amplitude. The T75 may be lower in diabetes patients due to reduced impact of the stimulus, supported by the reduced pupillary amplitude among diabetes patients. Alternatively, glycosylation of small nerve fiber types may lead to diminished reactivity to the given stimulus, and effect decreased conduction velocity and other parameters.

Future studies will increase the cohort of diabetes mellitus type 1 patients, and additionally compare to diabetes Type 2 patients, normal controls, and other patient data. The results could be applied towards a diagnostic tool to indicate early signs of DAN.

Amateur Radio on the International Space Station Assistant (ARISSA)

Alexander Siegel, Ken McCaughey

NASA Goddard Space Flight Center Greenbelt, MD
asiegell@swarthmore.edu

Amateur Radio on the International Space Station Assistant (ARISSA) is a computer program which takes into account the trajectory of the International Space Station (ISS) and determines when it will pass over HAM radio ground stations on Earth in order to make radio contacts with astronauts aboard or bounce radio packets off of the ISS repeater. Over the summer 2016 period, the program was written based on a backbone of FORTRAN programs which leveraged third party satellite tracking software to follow the ISS and compute “best passes” trajectories—taking into account the length of time of each pass, the angle relative to the Earth, the time of day, and the ground station location in order to print out a list of where optimal contacts could be made. The project involved taking a mostly manual, FORTRAN process which could only be run on DOS computers and updating the software to work on Windows 7, 64-bit computers (currently the NASA standard). New software was written in Python and more processes were automated—FORTRAN programs which were difficult to re-write in Python were drawn upon by the Python programs. This resulted in a portable program which could be easily updated to run on future 128-bit systems and used by any employee at NASA to plan ISS contacts for educational, recreational, or backup purposes. The time to plan passes was reduced from hours of manual entry to several minutes. Lastly, several additional features were added to ARISSA, including Daylight Savings Time (DST) being updated without user input and incorporating an automatic check for USNO leap seconds that are added periodically every few years.

Constraining Compensated Isocurvature Perturbations using the Cosmic Microwave Background

Rhiannon Smith, Kyle Yee, Tristan Smith

Swarthmore College

rsmith2@swarthmore.edu, kyee1@swarthmore.edu

We can model the universe as a dynamical system whose evolution is determined by a set of linearly-coupled differential equations described by Linear Perturbation Theory. In this model, the initial conditions of Linear Perturbation Theory determine the eventual properties and structure of the universe we see today. These conditions take the form of perturbations, which describe variations in the densities, velocities, and energies of various materials throughout space.

Compensated isocurvature perturbations, or CIPs, are a proposed modification to Linear Perturbation Theory. CIPs are a type of density perturbation where the baryonic (ordinary matter composed of protons and neutrons) and cold dark matter densities in a region of space vary relative to one another while the sum of these two quantities, the total mass density, remains unaltered.

The standard model has a CIP amplitude of zero. The preliminary runs of our programs show that if we allow the CIP amplitude to vary, current data prefer a non-zero value, with a best fit value ranging from 0.007 to 0.0137. Additionally, in the standard model, the lensing amplitude, A_{lens} , is defined to be 1; however, the Planck data are not consistent with this value. If we allow A_{lens} to vary with no CIPs, the data prefer higher values of A_{lens} , ranging from 1.145 to 1.22. However, the effects of CIPs and A_{lens} on the power spectrum are partially degenerate, so when we allow both to vary we get best fit values that are more consistent with the standard values.

All of the values for the CIP and lensing amplitudes we found using the MCMC analysis are consistent with previous work done using Fisher analysis, a less rigorous way of approximating the best fit values. Our results so far confirm the tension between the standard model and the Planck 2015 CMB data, as we would expect the data to prefer a CIP amplitude of 0 and a lensing amplitude of 1 in order to be consistent with theory.

Bridging qualitative and quantitative methods: A study of perceived influence of childhood cancer on the parents' marital/partner relationship

Sarah Solomon; Marina Noronha Ferraz de Arruda Colli, M.S.; Sima Zadeh, Psy.D. & Lori Wiener, Ph.D.

National Institutes of Health
ssolomo1@swarthmore.edu

When a child is diagnosed with cancer, parents face numerous stressors which may place strain on a parental relationship. Depending on how parents cope with stress, these added stressors can strengthen or weaken the relationship. If the parental relationship is weakened then the entire family can be negatively impacted. However, the fact remains that marital and partner relationships are often not addressed when providing care to children with cancer. There are currently no evidence-based interventions for couples designed to decrease stress and improve coping skills related to managing the challenges posed by the childhood cancer experience.

This was a multi-center study that used both quantitative and qualitative methods. The quantitative method consisted of a 51 item self-administered questionnaire that included the Revised Dyadic Adjustment Scale (RDAS) and other open and closed items designed by the research team. Participants who scored 1 sd above or below the norm on the RDAS were invited to participate in the qualitative piece of the study, which was an in-depth interview that further explored which components of parenting a child with cancer were most stressful to the relationship.

Significant results emerged. The study found that parents felt most emotionally connected with each other at the time of diagnosis. That suggests that this may be an appropriate time for initiating an intervention, with 'booster' sessions offered during hospitalization and some other times identified as high stress. Specific stressors included not having time to spend with other children, being away from work, and lack of emotional intimacy. Educating parents about these stressors at the time of the cancer diagnosis and then checking in on a regular basis has the potential to mediate the stressors' harmful impact on parental relationships.

Study findings also highlight the benefit of utilizing both quantitative and qualitative analysis. The quantitative data identified time points that are most stressful to couples while the qualitative information described what takes place during these time points and will be used to inform the content of an intervention. The combined data gathered from this study will help inform the development and method of delivery for a couple's intervention. The intervention will be tested at the Pediatric Oncology Branch at the National Cancer Institute, National Institutes of Health.

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Low-Flow Showerheads' Impact on Residents' Shower Water Usage

Sierra Spencer, Carr Everbach, Melissa Tier

Swarthmore College
Sspence1@swarthmore.edu

In conjunction with Swarthmore College's emphasis on conservation and sustainability, I worked over the summer to conserve resources on campus. Showers in dormitories are a major consumer of water and energy, and I investigated whether low-flow showerheads could actually conserve water on campus. I wanted to know if students take significantly longer showers with the low-flow showerheads, so I collected data on the shower times of both the regular and low-flow showerheads of students living in summer housing in Willets. I determined that there was not a significant difference in the shower times between the two types of showerheads. Therefore, I can infer that lower-flow showerheads do not hinder students' showering efficiency, and recommend that these showerheads be installed in dorms throughout campus. I also measured the actual flow rates of the different showerhead types to be able to, along with information on average student shower times, more accurately estimate shower water usage and savings. I found that at least roughly 98,214 gallons of water will be saved in Willets dormitory per semester by switching to low-flow showerheads.

200 showerheads installed

PROPRANOLOL AS AN ADJUNCT TO EXPOSURE THERAPY IN THE TREATMENT OF PATHOLOGICAL FEAR MEMORY: AN ANIMAL MODEL

Jasmine Sun, Christine Yao, Abigail Wild, Allen Schneider

Swarthmore College, Department of Psychology

jsun2@swarthmore.edu, cyao1@swarthmore.edu, awild1@swarthmore.edu

Clinical studies have shown that a therapeutic procedure known as exposure therapy—the gradual exposure to a feared object in the absence of actual harm—is effective in reducing abnormal fear memory. The treatment, however, is limited: many patients benefit from the therapy but only about half experience a lasting reduction in the abnormal fear memory.

Using an analogue of exposure therapy in laboratory animals—referred to as the brief exposure procedure—we investigated the extent to which the effectiveness of the brief exposure procedure in reducing retention of fear (and by inference the effectiveness of exposure therapy in the treatment of pathological fear memory) could be augmented by 1) varying the duration of exposure and 2) administering the β -adrenergic blocker propranolol prior to the exposure.

Male Long Evans rats underwent fear conditioning—a single mild foot-shock (0.5 sec) in a dimly lighted compartment—followed 24 hours later by the brief exposure procedure—exposure to the compartment for 30 or 60 seconds in the absence of shock. Propranolol (10 mg/kg) or saline was injected 20 minutes prior to the brief exposure procedure—the time interval required for the drug or saline to reach the brain. Control animals received propranolol or saline in the absence of exposure. A retention test was administered the next day, after the drug wore off, and fear was measured in terms of freezing behavior.

The results indicated that the effect of propranolol on retention of fear was bidirectional and depended on the duration of exposure: administration of propranolol prior to the 60 second exposure increased its effectiveness in reducing subsequent retention of fear 24 hours later; administration prior to the 30 second exposure decreased its effectiveness in reducing subsequent retention of fear 24 hours later.

Thus, while supporting the efficacy of propranolol as an adjunct to exposure therapy in the treatment of pathological fear memories, the present results caution that the duration of exposure therapy may be just as important as the drug dose itself in determining propranolol's therapeutic effectiveness.

Synthetic beta-peptides as a potential clinical supplement for antibiotics

Serena Sung-Clarke, Yunn Hwen Gan

National University of Singapore – Yong Loo Lin School of Medicine

ssungcl1@swarthmore.edu

Antibiotic resistance is a growing global problem. Frequent use (and overuse) of antibiotics drive antibiotic resistance and conventional antibiotics are slowly becoming weaker against increasingly resistant strains. Many cells produce antimicrobial peptides, proteins that combat pathogens, but the use of antimicrobial peptides for clinical purposes has not been yet fully explored. The purpose of this experiment was to see if synthetic antimicrobial peptides, specifically beta-peptides, have the ability lower the minimum inhibitory concentration of antibiotics against opportunistic pathogens.

A laboratory at the Nanyang Technological University engineered synthetic peptides and sent us two types of beta-peptide to test (denoted A and B). Alongside with these peptides, we used three antibiotics: amikacin, ceftriaxone, and ciprofloxacin. These were both tested on two species of bacteria, *Klebsiella pneumoniae* and *Acinetobacter baumannii*. In a 96-well plate, one of the beta-peptides was serially diluted down the wells and one of the antibiotics was serially diluted across the wells, creating a lattice of varying concentrations of antibiotic and beta-peptide. The bacteria were then put into each well and the plate was incubated. The optical densities of the wells were read 24 hours later to determine bacterial growth. This was repeated for each combination of beta-peptide, antibiotic, and bacterial strain.

The beta-peptides alone, even at the highest concentration tested, had no inhibitory effect on bacterial growth. When used with antibiotic, however, it sometimes decreased the minimum inhibitory concentration (MIC) of the antibiotic by up to 6-fold. Beta-peptide B had little inhibitory effect, even when used in conjunction with antibiotics, but beta-peptide A decreased the MIC of ciprofloxacin against the *K. pneumoniae* strain and decreased the MIC of ceftriaxone against both bacterial species. It did not, however, decrease the MIC of ampicillin against either bacteria. Because of lack of time and beta-peptides, this experiment could not be repeated, but synthetic beta-peptides still show potential to diminish our reliance on antibiotics, and should be explored further.

Linking genotype to phenotype: Using CRISPR/Cas9 to alter the wing pattern coloration of *Heliconius* butterflies

David Tian¹, Carolina Concha², and W. Owen McMillan²

¹Department of Biology, Swarthmore College, Swarthmore, PA

²Smithsonian Tropical Research Institute, Panama City, Panama
dtian1@swarthmore.edu, carolacmcl@yahoo.com, mcmillano@si.edu

Abstract

Elucidating the links between genotype and phenotype remains a fundamental biological challenge. We understand genotype and how DNA is replicated, transcribed into mRNA, and translated into amino acids to form a protein. On the other end, we can observe and categorize different phenotypes. However, how proteins interact with each other under the influences of development and environment to create phenotypes remains an unclear process that represents a great challenge for modern biology. Understanding these interactions on a micro-evolutionary level is key for us to understand how natural selection results in phenotypic variation and the generation of biological diversification. In order for us to discover these complex relationships between proteins and begin mapping them, we require functional tools to probe and manipulate the genome.

The specificity, power, and ease of CRISPR/Cas9 along with the phenotypic diversity of *Heliconius* butterflies were leveraged to gain insight into the links between genotype and phenotype. Based on previous genetic mapping and association tests, a list of candidate genes involved in wing color patterning was generated. We specifically focused on *optix*, which controls for the color red, along with *wntA*, *cortex*, and *domeless*, which control for melanin production and as a result the color black. Our first objective was to provide functional genomic evidence that the roles of these genes were accurate, which is the gold standard for assigning functions to genes. We used CRISPR/Cas9 to knock out these genes and see if a significant phenotypic difference could be seen in the wings.

Our results indicate that *wntA* does control for melanin production, and that we are capable of successfully running CRISPR/Cas9 experiments in butterflies with our current protocol and setup. *Optix*, *cortex*, and *domeless* mutants did not exhibit strong phenotypic differences. However, we are hopeful that by improving our injection methods and using different guide RNAs that we will be able to significantly different phenotypes in our mutants. Moving forward, our work will focus on knocking in certain regulatory regions upstream of our wing pattern coloration genes to generate predicted phenotypes and enhance our network view of protein interactions.

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Assortative Mating for Social Behaviors in Forked Fungus Beetles

Soumba Traore, Vincent A. Formica

Mountain Lake Biological Station, Pembroke, VA

Straore1@swarthmore.edu

Assortative mating has been widely observed in nature and is known to have consequences on sexual selection. Most studies assessing assortative mating mainly concentrate on phenotypic traits such as body size of mated partners. Few have documented assortative mating for social behavior. The goal of this study was to determine if assortative mating for social behavior occurs in wild populations of *Bolitotherus cornutus*, the forked fungus beetle. We constructed male-male social networks and female-female social networks from nine wild populations and examined whether mated pairs correlated in their position within these social networks. We examined both courtship and mate guarding pairs because they represent different decision periods in the mating process. Position in social network was measured by three metrics: degree, betweenness and clustering coefficient. We found that in both guarding and courting pairs, for males or females there was no assortative mating for clustering coefficient and for the majority of the analysis done with degree. However both males and females tend to perform mating behaviors with other individuals with a similar betweenness to their own. The assortative mating for betweenness is surprising because betweenness is truly an emergent trait that can only be measured in the presence of an entire network, suggesting that either *B. cornutus* use social behaviors in choosing mates, or other underlying behaviors that drive an individual's betweenness score also influence mating opportunities.

Identification of Proliferating Cells Involved in Cortical Bone Stem Cell-Mediated Cardiac Repair and Scar Formation After Myocardial Infarction

Sarah Tupchong, Steven Houser, Ph.D.

Lewis Katz School of Medicine, Cardiovascular Research Center
stupcho1@swarthmore.edu

Objective: Ischemic heart disease, known as coronary artery disease (CAD) is the leading cause of death in the world. Since cardiomyocytes have limited proliferative capacity, an ischemic injury such as a myocardial infarction (MI) results in irreversible damage to the heart. Because of the up-regulation of immune response immediately after ischemic injury, reliably identifying alterations in cell growth post-MI could lend insight into the remodeling process. Additionally, previous studies have demonstrated the potential of transplanted exogenous cortical bone-derived stem cells (CBSC) to improve cardiac function through the secretion of paracrine factors, which promote cardiac cell proliferation and differentiation. The objective of this study was to identify proliferative cells involved in cardiac repair and scar formation in the mouse heart and compare the difference in cell quantity between vehicle and CBSC-treated hearts one-week post-MI.

Methods: Myocardial infarction was induced by permanently occluding the left anterior descending coronary artery (LAD) via ligation. CBSC-treated and phosphate-buffered saline (PBS) treated hearts were exposed to 5-ethynyl-2'-deoxyuridine (EdU), a novel thymidine analog used to identify and measure newly synthesized DNA, for 1 week via

osmotic mini pump implantation. Immunohistochemistry staining was performed to examine the immune response infiltration and endothelial cell proliferation using antibodies against CD45 (protein tyrosine phosphatase, which is present on all immune cells) and vWBF (Von Willebrand factor, a blood glycoprotein involved in platelet adhesion found on mature endothelial cells).

Results and Conclusions: There was no significant difference in the border, infarct, or remote zones in the amount of EdU⁺ cells or vWBF⁺ EdU⁺ cells between PBS and CBSC-treated hearts. In the remote zone only, there was a significant difference in the amount of CD45⁺ EdU⁺ cells in CBSC-treated hearts compared to those treated with PBS. These results suggest that at 1-week post MI, CBSC administration after MI modulates the immune response, with the immune cells being localized at the site of injury and away from the viable tissues in the remote zone. Further experiments are needed to investigate the mechanism and effect behind these results.

Prevalence of *Salmonella* and *Vibrio* in Chesapeake Bay Oysters (*Crassostrea virginica*)

Linda Vu, Ar'Quette Grant, Joan Meredith, and Salina Parveen

University of Maryland Eastern Shore, Princess Anne, MD 21853

lvu1@swarthmore.edu

Foodborne illnesses annually impact millions of consumers and cause symptoms ranging from fever and diarrhea to necrosis and death. Raw oyster consumption is a particular risk to a consumer's health because oysters are filter feeders and intake environmental pathogens, such as *Vibrio* and *Salmonella*. The purpose of this study was to investigate the prevalence of *Vibrio* and *Salmonella* in American oysters (*Crassostrea virginica*) from the Chesapeake Bay. Samples of oysters and surface water were collected from five locations in the Chesapeake Bay from June to July, 2016. For *Vibrio* prevalence, water and oyster samples were diluted with buffered peptone water with 0.1% NaCl and a Colony Overlay Procedure for Peptidases (COPP) assay was performed. To determine *Salmonella* prevalence, most probable number (MPN) was used by inoculating water samples in tryptic soy broth and oyster samples in buffered peptone water. For water, turbid samples were applied to rappaport-vassiliadis (RV) and tetrathionate (TT) broths. For oyster samples, modified semi-solid rappaport-vassiliadis (MSRV) agar and xylose-lysine-tergitol 4 (XLT4) agar were used to determine preliminary positives. PCR amplifying the *invA* gene was used for final *Salmonella* verification on positive samples. *Vibrio* levels varied ranging from 12 to 320 cfu/mL in water samples and 3.1×10^3 to 1.3×10^5 cfu/g in oyster samples. Some sites decreased in *Vibrio* prevalence over time whereas other sites maintained increased prevalence. For *Salmonella*, out of the five oyster and water samples collected, only one water sample was found to be positive with *Salmonella* at a level of 1.3 MPN/ml. The low *Salmonella* prevalence rate found supported the findings of previous studies on *Salmonella* in *C. virginica*. These results suggest that oysters may be a potential source of *Vibrio* spp. but not *Salmonella*.

A novel *S. pombe* mitochondria-associated gene retards contractile ring constriction rate

Nhu Vu, Phong Tran

University of Pennsylvania
nvu1@swarthmore.edu

Mitochondria produce cellular energy in the form of ATP. Mitochondria are dynamic organelles that undergo normal fusion and fission. Defects in fusion and fission lead to defects in mitochondria morphology, which can result in mitochondria malfunction.

The fission yeast *Schizosaccharomyces pombe* (*S. pombe*) has ~5000 genes, of which ~10% showed protein localization to the mitochondria [1]. We hypothesized that deletion of the mitochondria-localized genes may reveal their cellular function. We have a collection of individual gene-deletion strains [2], referred to as DC strains. We examined 6 previously uncharacterized DC strains for potential defects in mitochondria morphology and cell division. We created the 6 DC strains expressing Cox4-mCherry (mitochondria marker) to visualize mitochondria, and Rlc1-GFP (contractile ring marker) to visualize cell division. We found that the 6 DC strains have defective mitochondria morphology compared to wild-type cells. Interestingly, only 1 DC strain (DC.668) showed specific slow contractile ring constriction rate compared to wild-type cells.

Of particular interest is the uniquely slow contractile ring constriction rate of DC.668 compared to wild-type. As mitochondria generate ATP and regulate reactive oxygen species (ROS), it is possible that DC.668 may have less ATP (which is needed for ring constriction) or more ROS (which damages subcellular structures such as contractile rings), which may explain the phenotype observed. Future work will focus on DC.668/SPBC146.02 and its specific role in mitochondria morphology and cell division.

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Could neuroscientists be incorrectly interpreting classical short-term memory tasks? The role of visual attention in short-term memory

Richard Vu, Lisa Payne, PhD

Swarthmore College
500 College Ave, Swarthmore, PA 19081
rvu1@swarthmore.edu

Many neuroscientists rely heavily on the classical Sternberg paradigm to examine the neural correlates of short-term memory and the effects of medical treatments or drugs of abuse. In the Sternberg task, a sequence of digits is presented, and then, following a brief retention interval participants indicate whether a probe digit had been a member of the sequence. Finally, they are asked to recall the sequence in order. A primary assumption is that the Sternberg task tests for verbal working memory. However, the original Sternberg paradigm has many parameters that are modified in later studies such as the removal of the final step in which participants recall the sequence of digits presented to them. Previous research by Corbin and Marquer (2013) show that removal of the recall task appears to shift the Sternberg task from testing verbal working memory to testing visuospatial memory. This finding led us to question how we might induce this shift in the type of memory and cognitive processes utilized through modification of the Sternberg task. Specifically, we tested whether expectancy—in our case, the ability to predict the number of stimuli on the next trial—could also affect whether verbal or visuospatial memory is the primary underlying memory subsystem. In addition, we tested expectancy using letters instead of digits, another common modification of the Sternberg task believed to increase the reliance on verbal working memory. When the number of letters randomly varied between trials (intermixed, no expectancy condition), performance in the modified Sternberg task correlated with visuospatial memory, but not verbal working memory. In contrast, when the number of letters remained constant within a block of trials (blocked with expectancy), task performance correlated with verbal working memory, but not visuospatial memory. These results suggest that simple modifications to the Sternberg task can influence cognitive processes and the type(s) of memory used in the task. Furthermore, as manipulating expectancy involves manipulation of predictability, our results suggest that visual attention plays a stronger role in situations that involve dynamic changes compared to predictable situations.

Telomere attrition induced senescence in fission yeast

Erika Weiskopf, Dr. Megan King

Department of Cell Biology, Yale School of Medicine
eweisko1@swarthmore.edu

During senescence, individual cells permanently exit the mitotic cycle. Such senescent cells remain alive but do not undergo mitotic division. Stresses which challenge the genomic integrity of a cell, and thus limit its potential for accurate division, can induce the senescence decision, highlighting the protective role of senescence against conditions linked to genomic instability, such as cancer. One such stress is the attrition of protective telomeric repeat sequences. We assessed the effect of telomere length on the senescence decision in *Schizosaccharomyces pombe* (fission yeast) cells primed to exit the cell cycle via nutrient deprivation. Results suggest that arrested cells use telomere length as a cue for entering and exiting the cell cycle; cells without functional telomerase have greater difficulty reentering the cell cycle than cells with functional telomerase.

Jamming in the Presence of Obstacles
Prairie Wentworth-Nice, Professor Amy Graves
Swarthmore College
pwentwo1@swarthmore.edu

We investigated the effects of different configurations of obstacles on the jamming of soft-spheres in a unit box with periodic boundary conditions. Jamming is when particles in motion interact closely with one another, and can eventually become stuck, so that few or none of the particles can move without the aid of an external force. I placed different lattices—specifically square, triangular, honeycomb, and kagome—in the box to create obstacles, affecting the particles’ “movement” as they equilibrated down to a state of minimum energy. The goal was to compare the effects of different lattice properties on properties of jamming. I found that the pins lowered the “jamming threshold”. That is, the systems with pin lattices began jamming but also showed jamming virtually 100% of the time, at lower particle fractions than when the simulation was run without any lattice.

Interaction of mitochondrial DNA with RHPS4

Irene Xiang, Brett Kaufmann, and Liliya Yatsunyk

Swarthmore College, 500 College Ave, Swarthmore, PA 19081

Vascular Medicine Institute, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15261

Quadruplexes (GQ) are non-canonical tetra-stranded DNA structures implicated in cancer and aging. Recent evidence indicates that mitochondrial DNA can fold into GQ structures [1], suggesting that GQs can affect mitochondrial genome stability. We have investigated the interactions between the well-known quadruplex ligand, RHPS4, with two different mitochondrial G-rich DNA sequences, oligo A and B, through CD melting and UV-vis titration experiments. 10 μ M RHPS4 is found to stabilize these oligonucleotides by 7.9 ± 1.0 °C and 14.6 ± 0.8 °C. In the case of oligonucleotide A, RHPS4 decreases observed hysteresis from 32.4 to 19.5 °C suggesting that folding process for oligonucleotide A is kinetically slow and the presence of ligand speeds up this slow kinetics. Upon titration of RHPS4 with GQs formed by each Oligo A and by Oligo B, similar red shifts and hypochromicities are observed. At 510 nm, Oligo A had a red shift of 11.5 ± 0.2 with a % hypochromaticity of 22 ± 2 while Oligo B had a red shift of 11.6 ± 0.5 and % hypochromaticity of 23 ± 2 . These rather high values suggest significant overlap between the π -systems of RHPS4 and the G-tetrad, and thus indicate close interactions, most probably end-stacking. Our data suggest that RHPS4 binds Oligo A with a 3:1 stoichiometry and a binding constant of $(0.5 \pm 0.3) \times 10^6 \text{ M}^{-1}$. In contrast, RHPS4 binds with Oligo B with a 2:1 stoichiometry and very similar binding constant, $(0.5 \pm 0.1) \times 10^6 \text{ M}^{-1}$. The ability of RHPS4 to bind and stabilize Oligo A and B has biological importance in mitochondrial anti-cancer agents.

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Truss Analysis Software Research

Bilige Yang, Professor Faruq Siddiqui

Swarthmore College
byang1@swarthmore.edu

The goal of the research is to create a structural analysis software that is easier to use than the industry-standard structural engineering software, Multi-frame. During the summer of 2016, we focused on the part of 2-D truss analysis. We analyzed the drawbacks of Multi-frame and addressed them in our software.

We made our software a web application, instead of a desktop software like Multi-frame. This design decision is made by recognizing a general trend in software development industry. The software market is making an elusive but far-reaching and impactful shift: More and more things can be done on a single webpage and people download less and less softwares onto their computers. A web application can satisfy all the goals we are trying to reach: cross-platform, no downloading nor installing, and easy-to-use-ness. To ensure stability, safety, and easy maintenance, this web app is a static front-end webpage, purely done in HTML, CSS, and Javascript.

A fully functional truss analysis web application is finished. By going to the site biligeyang.github.io/truss-analysis, any user across the globe is able to use it. The user can easily draw a truss, add member properties, loads and supports, and get calculated results, including internal force, stress, joint deflections. The source code can be accessed through <https://github.com/BiligeYang/truss-analysis>.

Fabricating and 3D printing fibrin clots to gain insight into sonothrombolysis

Chung Yuen Brandon Yeung, E. Carr Everbach

Swarthmore College
cyeung2@swarthmore.edu

Blood clots, or thrombi, forming inside the body impede blood flow and can lead to dangerous conditions such as ischemic stroke. Traditional pharmacologic therapy affects the body systemically and may lead to hemorrhage if the patient has benign blood clots. Such risk is reduced with sonothrombolysis—high-amplitude pulsed ultrasound that drives micron-sized bubbles—called microbubbles—into violent oscillations. Ultrasound mechanically pushes and pulls on the tissue it passes through. The effect of ultrasound is amplified when microbubbles are driven into violent oscillations and destroy the fibrin mesh-like structure of a thrombus.

Previous research has studied the interactions of ultrasonic microbubbles with thrombi, but made assumptions about the detailed structure of a real thrombus. The purpose of this research was to fabricate fibrin clots *in vitro* using varying concentrations of the reagent thrombin, image them using a confocal microscope, analyze images and 3D print plastic models.

For each of three clots, 240 confocal micrographs were taken, each covering an area approximately 200-by-200 microns, and together spanning a depth of approximately 50 microns. The image analysis software Fiji was used to compensate for fluorescent bleaching, reduce noise and separate fibrin ropes from the background. A 3D representation was reconstructed for each clot. To reduce computer memory requirements, a 50-by-50-micron sized area was strategically chosen from each clot that contained as much of the heterogeneity in structure as possible. The resulting 50-by-50-by-50-micron cubes were 3D printed, giving realistic and visually comprehensible models that clearly delineated the variations in clot structure as thrombin concentration varied.

Image analysis of micrographs showed that the mean pore size of clots made from 0.1 units/mL, 0.5 units/mL and 1.0 units/mL thrombin concentrations were 61.49 microns², 44.39 microns² and 12.74 microns² respectively. Each clot demonstrated significant variations in pore size, though the majority of pores in each clot were clustered around the mean size. 3D printed plastic models suggested the same distinct reduction in porosity as thrombin concentration increased. Plastic models additionally indicated that fibrin structure was isotropic—pore size was approximately equal in every spatial direction. This research concluded that artificially fabricated fibrin clots can be realistically reconstructed into 3-dimensional models, and that increasing the concentration of thrombin decreases the average pore size and increases the density of the fibrin mesh produced.

Mitotic Kinases Regulate Polarised Movement of FGFRs

Dong Shin You, Christina D. Cota, Bradley J. Davidson

Swarthmore College
dyoul@swarthmore.edu

During mitosis of asymmetrically dividing cells, cell signalling components are distributed in a polarised manner. The biased movement of Fibroblast Growth Factor Receptors (FGFRs) in heart founder cells of *Ciona intestinalis* is essential for proper induction of the heart progenitor cell (HPC), and the eventual development of the heart. In these heart founder cells, FGFRs are enriched on the ventral half of the dividing cell, which allows the future HPC to inherit a large proportion of the FGFRs. The mechanism behind this polarised movement, however, is currently unknown. Here, we demonstrate that mitotic kinases are necessary for proper ventral enrichment of FGFRs in dividing *Ciona intestinalis* heart founder cells. By quantitating FGFR distribution, we found that disruption of cyclin-dependent kinase 1 (CDK1) activity during prophase increased ventral enrichment of FGFRs. Prolonging the activity of CDK1 and inhibiting Polo-kinase during metaphase both decreased ventral enrichment of FGFRs. Finally, inhibiting Aurora-kinase during prophase increased membrane localisation of FGFRs. Our results show that mitotic kinases orchestrate mitotic trafficking of FGFRs in spatially and temporally precise manner. Our study into mitotic trafficking sheds light into a critical feature of asymmetric cell division, which in combination with other studies, such as endocytic path taken by these FGFRs, will provide us with a greater insight into this fundamental cell process. Deeper understanding of asymmetric trafficking of cell signalling factors will also allow us to better appreciate how cells can incorrectly activate cell signalling as they do in cancer.

Optimizing HIV Treatment Times with Neural Networks and Cluster Computing

Terry Yu, Mike Piovoso

Swarthmore College
tyul@swarthmore.edu

HIV treatment is still very difficult on account of its high mutability, which means that immune strains quickly develop once a patient is exposed to antiviral drugs. My research looked into developing mathematical models for HIV and using these networks to determine optimal treatment times.

Our first task was adapting the model laid out in a research paper into Matlab code, so we could do useful computation with it. This was a fairly straightforward task of writing equations into a Matlab script. As I run into some trouble with the built in differential equation solver, I had to rewrite my own implementation of the Runge-Kutta 4th order solver.

Once I had developed code that represented the differential equations, I needed to generate some very large datasets that would simulate a large number of patients, so our end algorithm could be used with any generic patient. To do this, we used datasets generated with a Monte Carlo simulation, to represent 200,000 virtual patients with traits statistically similar to 200,000 real patients. Our simulation was then run on these virtual datasets.

In order to execute our solver on such a large dataset, my side project was to put together a computing cluster with 8 spare desktop computers that the engineering department no longer needed. There were quite a few networking and imaging issues to deal with, but I successfully networked the computers together and created a computing cluster with around a teraflop of computing power. This cluster aided significantly in the computations, and writing some of the code to put it together was a very educational experience in networking and data management.

The final portion of the project was to train a neural network with the generated data and then use the neural network to determine the optimal treatment time. I looked into the theoretical basis of creating a neural network. Unfortunately, our data was not of sufficient quality to generate training sets for our neural network. However, I did still manage to learn a lot about setting up a cluster and much of the theoretical basis for neural networks and parallel computing.

Cyclizations of η^4 - Iron(0) Tricarbonyl Diene Complexes

Mason Yu, Professor Robert S. Paley

Swarthmore College, Swarthmore, PA, 19081
myu1@swarthmore.edu

Natural products that are pharmaceutically useful are often specific enantiomers of heavily functionalized chemical compounds. Because of this, asymmetric synthesis is critical to creating these natural products. One common approach towards asymmetric synthesis uses chiral scaffolds, which can be manipulated later in the synthetic pathway, to direct the formation of new chiral centers. We study the viability of using the planar chiral iron(0) tricarbonyl diene complex as a chiral scaffold. To this end, we are currently exploring the versatility of the complex by exposing the complex to a variety of reactions not previously explored on these systems. This summer we worked towards functionalizing the complex to form enynes and using either enyne metathesis or gold(I) catalysis to cyclize the complex. We find that the iron complex is compatible with the Seyferth-Gilbert homologation in order to successfully synthesize an enyne with promise for performing an enyne metathesis; this reaction is also included in our approach for the gold-catalyzed cyclization.

Photon Collection's Efficiency and Fidelity for a Potential Loophole-Free Test of Bell's Inequality using Trapped Ions

Zechen Zhang, Prof. Boris Blinov

University of Washington, Seattle
zzhang2@swarthmore.edu

A violation of Bell's inequality is an important test for quantum entanglement. Till recently there has only been experiments showing a loophole-free Bell violation using photon-photon entanglement. Motivated by a potential using Ion-Ion entanglement for the test as well as fundamental block of quantum computing, we propose a new paradigm for Bell's test through trapped ions located in two separate traps. The success of entanglement and Bell's test rely highly on fidelity and the entanglement rate generated by the trap. Nevertheless, there is usually a trade-off between these two factors in the light collection process. In this research project, we have calculated the fidelity and entanglement rate as functions of solid angle we will collect from the parabolic mirror in the trap, and we propose an optimum for the solid angle used in the experiment theoretically.

Cdc42: A potential therapeutic target in acute myelogenous leukemia (AML)

Anne Zhang, Dr. Deepak Sahasrabudhe, MD, Dr. Jane Liesveld, MD

University of Rochester Wilmot Cancer Center

Azhang1@swarthmore.edu

Autonomous and unregulated growth is one of the hallmarks of cancer. Constitutive activation of signal transduction pathways can result in autonomous and unregulated growth. Cdc42 (cell division control protein), a Rho GTPase, which initiates signaling cascade, is one example of such a signaling. Preliminary data suggested that Cdc42 is activated in acute myelogenous leukemia (AML). We hypothesized that inhibition of signaling via Cdc42 will affect cell proliferation in AML.

We studied human AML cell lines, THP-1, MV4-11, and K562. Cdc42 was constitutively phosphorylated in these cells grown in complete media. We measured the effect of inhibitor of Cdc42, AZA1, on proliferation using the MTT assay on the three cell lines. AZA1 inhibited cell growth in a dose dependent and time dependent manner on the three cell lines. The cells were exposed to increasing concentrations of AZA1 and progression through the cell cycle was measured by flow cytometry. The percentage of cells in the G2/M phase increased in a dose-dependent manner. These results provide proof of concept for targeting the Cdc42 pathway in AML.

Integrate-and-Fire Model in Hermann Grid Illusion

George Zhu, Victor Barranca

Swarthmore College, PA
xzhul@swarthmore.edu

Previous research has suggested that the illusory effect of Hermann Grid Illusion is due to the receptive field structures in the visual system. We speculate that the illusory effect can be explained by the difference in strength of neuron signals. We use an Integrate-and-Fire network to model the On-center/Off-surround receptive field structure and reconstruct the perceived image. By simulating the network with the grid as stimulus, we demonstrate that the accuracy of the reconstruction diminishes as we further enforce the assumptions of On-center/Off-surround receptive field structure. We suggest that the reconstructed illusory effect is related to the sampling mechanism for the On-center/Off-surround receptive field structure.

