Cultivating the scientist in the next generation of women

Women are dramatically underrepresented in Science, Technology, Engineering & Math (STEM) careers. Smith College is dedicated to remedying that shortfall. Our consistently stellar students transform at graduation into an ever widening network of alumnae dedicated to fostering the generations that follow. The College itself commits an extraordinary level of physical and human resources to ensure STEM student have a rich array of opportunities and support. The accomplished Clark Science Center faculty put their students first with course-based research, hands-on laboratory experience with faculty research and Summer Undergraduate Research Fellowships (SURF).

Ever since its 1967 start, SURF has been a cornerstone of Smith's science education. Women in Science 2017 summarizes research done by Smith College's SURF Program participants during the summer of 2017. 151 students participated in SURF (144 hosted on campus and nearby field sites), supervised by 58 faculty mentor-advisors drawn from the Clark Science Center and connected to its eighteen science, mathematics, and engineering departments and programs and associated centers and units. At summer's end, SURF participants summarized their research experiences for this publication.

Smith's Approach to Science Education

We follow four principles of excellence in STEM education at Smith. For the sciences at Smith, we are guided by understanding that persistence and the best scientific thinking emerge from healthy climates that promote and value a diversity of perspectives. Smith's strategy for **ensuring access for all** is to address disparities in gender, racial, and socioeconomic representation in the sciences by pairing rigorous learning expectations with robust support and community-building for our students.

We believe that **engaging with the world** is critically important to science student success. Interactions with *bona fide* scientific problems connecting our students to the larger world facilitate the best learning. Smith connects our students with complex, real-world problems, ranging from local to global, that are often best understood through the multiple disciplinary lenses of the liberal arts.

Smith develops student mastery of the key concepts and competencies of our STEM disciplines by **developing knowledge and skills**. We integrate the work of students and cutting-edge faculty scholarship by providing widespread opportunities to apply theory learned through rigorous coursework to real life questions and problems under investigation in our labs and research centers. These best-practices pedagogies and faculty- student research collaborations result in optimal learning and future success for our students.

Persistence and success in STEM rest not only on access, opportunity, and knowledge, but also on the actions taken by individual women in particular environments using specific social understandings. By **fortifying agency and identity** among our students, we cultivate their confidence and resourcefulness in learning that will foster them becoming scientists.

Read on and celebrate "Women in Science" with us!

Thomas C. Richardson
Administrative Director,
Clark Science Center

Generous contributors who provided funding for the 2017 SURF

We extend our deep appreciation to:

Agnes Shedd Andreae 1932 Research Internship Fund

Frances Baker Holmes Internship Fund

Alumnae Gift Fund in Chemistry

Howard Hughes Medical Institute

American Chemical Society*

Margaret A. Walsh Grantham Fund

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National Institutes of Health*

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Susan M. Rambo 1905 Fund in Mathematics & Statistics

* Individual research grants to faculty members that include funds available to support SURF student research collaborations

Smith College Support

Thank you, Smith College students, faculty, staff, friends, and benefactors. It truly takes a diverse and dedicated community to sustain a program like SURF.

In particular we would like to recognize:

Center for the Environment, Ecological Design & Sustainability (CEEDS)

Committee on Faculty Compensation and Development (CFCD)

Provost's Office

Facilities Management

Some undergraduates were able to participate in summer research internships away from campus with support from the PRAXIS Internship Program.

We wish to recognize and express gratitude to the faculty members and staff who provided supervision, guidance, encouragement and support to SURF participants in the lab, doing field research, on-campus, and away from campus. SURF would not be possible without your devoted and generous contributions.

Table of Research Topics (Classified by Supervisor's Field of Study)

Biochemistry

Biological Sciences

Biological Sciences (*continued*)

Biological Sciences (*continued*)

Biological Sciences (*continued*)

Chemistry

Chemistry (*continued*)

Computer Science

Engineering

Engineering (*continued*)

Environmental Science & Policy

Geosciences

Geosciences (*continued*)

Mathematics and Statistics

Neuroscience

Neuroscience*(continued)*

Physics

Psychology

Psychology (*continued*)

Statistical and Data Sciences

The Folding and Unfolding Process of Myoglobin in Silica Gel

Hiliana Melo/2020

The folding of a protein is of great importance for its function. This process takes place when the unfolded protein assumes a compact conformation. The helices, sheets, and turns that a protein assumes determine its functional tertiary structure (1). Myoglobin is a small protein that might be expected to be able to unfold and refold. However, when unfolded in solution myoglobin often loses its heme group (an organometallic molecule that is normally bound within the folded protein) and therefore is not able to refold properly. My research focused on testing the refolding of myoglobin molecules that were held in silica cages. These cages had small volumes and were designed to keep the heme group near the unfold myoglobin. Myoglobin was chosen for this study because its structure in solution is well known and its absorbance of visible light changes when the protein unfolds. The protein was confined to pores in silica gel glass1 formed around the protein on glass microscope slides.

The silica gel was fabricated following a method published by Peterson et al. and after fabrication each silica gel sample was washed several times with buffer to ensure that all the myoglobin that was not trapped in the glass matrix had been removed. I found, however, that over a span of two weeks the concentration of myoglobin decreased with every washing. The concentration decreased at a lower rate after several washes but it still continued to decline. The drop in myoglobin concentration prevented the accurate measurement of the protein's refolding. The results did show, however, that exposure to concentrated buffer caused the myoglobin concentration to decrease more rapidly. The samples were also affected by pH, with the samples exposed to pH 2 showing the largest decrease in concentration while those exposed to pH 4 showed the smallest decrease in concentration. When the samples were returned to a pH 7 buffer solution, after around twenty minutes they regained some of their original configuration, based on their visible spectrum. Nevertheless, their myoglobin concentration continued to decrease. These results suggest that the silica gel cages, when prepared by the previously described methods, may be more porous than they have been generally assumed to be. I will be continuing this research during the semester and will focus particularly on a way to fabricate silica gel that will make a better trap for myoglobin.

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(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: David Bickar, Biochemistry

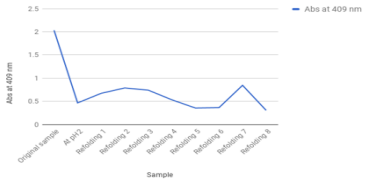

Fig.1. The absorbance of the trapped myoglobin after being exposed to pH 2 concentrated buffer.

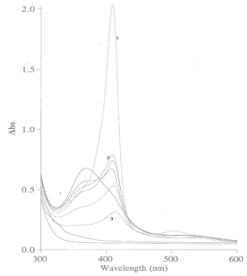

Fig.2. UV/VIS spectra for a sample exposed to pH 2 buffer. Curve 1 is the absorbance before exposure to the buffer. Curve 2 is the absorbance after five minutes. Curve 3 is the absorbance after two days.

Protein Changes with Aging and Omega-3 Supplementation in Rat Skeletal Muscle

Emily Morris/2019

Omega-3 fatty acids are a common dietary supplement that can be found naturally in fish oil1. Although often recommended as a supplement for muscle growth and anti-aging effects, the efficacy of these claims on a biochemical level has not been thoroughly explored. In a previous SURF study, high resolution 2D gel electrophoresis was used to explore rat skeletal medial gastrocnemius muscle proteins from four sample groups. These cohorts consisted of 7 young control rats (6 months), 6 aged (3 years) controls, 7 young rats supplemented with omega-3, and 6 aged rats supplemented with omega-3. These four data points yielded qualitative information on the protein expression differences between rats fed omega-3 over time versus their control diet counterparts. 2D gel spot intensity comparisons yielded a number of differentially expressed spots (± 2-fold and $p<0.05$) between the four cohorts. To determine statistical significance of these detected changes, however, quantitative data are required. This SURF project explored the quantitative changes in those proteins by quantitative immunoblot validation.

Antibodies against creatine kinase-M, parvalbumin, actin, and beta-enolase were used to more precisely quantify the changes in these proteins. Supernates and pellets were run on separate gels (8 total per protein tested) and a rat skeletal muscle extract supernatant was used as a developing control to normalize band intensity across the 8 immunoblots (Figure 1). After being scanned the blots were stripped, using Abcam's mild stripping procedure, and blotted with anti-GADPH as a loading control; it has been shown not to change significantly with age.

Initial assessment of these data supports the previous findings of the Scordilis lab, but I will be continuing this project into the fall so as to validate more proteins with detected changes. Quantitative and statistical analysis using JMP will be completed.

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(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Stylianos Scordillis, Biochemistry

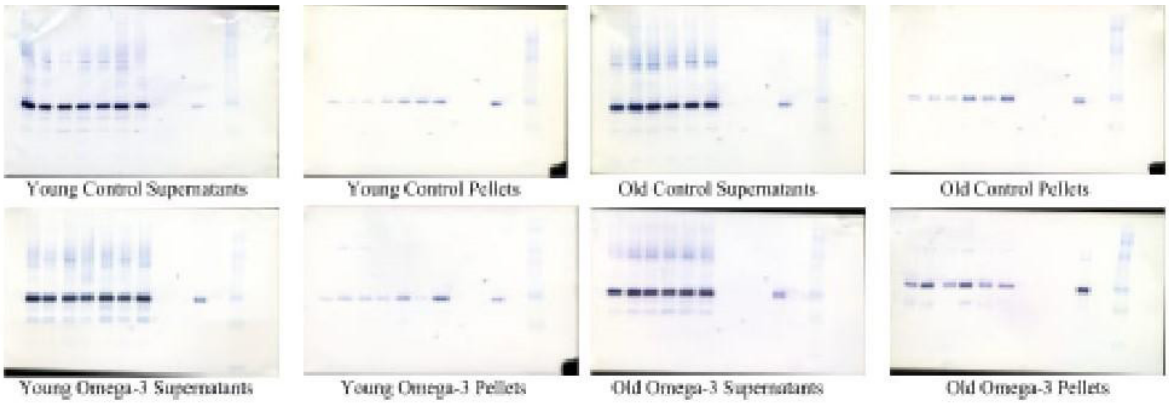


Figure 1: Western blots against Beta-Enolase across all four sample groups. Supernatants and pellets were divided into two gels, and 10ug of sample were loaded into each lane (concentrations were determined via Lowry protein estimation). 2.5ug of a normalizing control--rat supernatant extracted using the same procedure as the samples--were loaded into each gel along with a molecular weight standard. The same procedure was repeated for each protein tested.

The role of temperature in regulating virulence and stress response in commensal and Uropathogenic *Escherichia coli*

Isidora Stankovic/2020

Escherichia coli are a mastermind amongst bacteria that are able sense environmental changes and regulate their gene expression accordingly. Temperature is one environmental cue this bacterium uses to modulate its changing environments, both external (23˚C) and within the human host (37˚C). Previous studies in the White-Ziegler lab have demonstrated that around 10% of all E. coli genes in a non-pathogenic commensal strain are temperature regulated (1). Thus, temperature is thought of as one of the major forces that drives gene regulation in this bacterium. The aims of my research project were to further explore the effect of temperature in regulating expression of virulence and stress response genes along with its impact on the small associated small regulatory RNAs (sRNAs) important for control of mRNA and protein levels. These studies were conducted in commensal and in uropathogenic E. coli (UPEC) strains. While commensal strains are beneficial, uropathogenic strains are responsible for over 80% of UTIs in the world today (2).

To assess the impact of temperature on gene expression, bacterial cells for these experiments were grown at 23°C, then shifted to 37°C and harvested at various time points after the shift, and RNA was isolated. This temperature shift mimics the pathway bacteria undergo when transferring from room (23°C) to human body temperature (37°C). Using previous studies and bioinformatics software such as sRNATarBase, candidate genes and small regulatory RNAs were identified and their relative expression was measured using qRT-PCR.

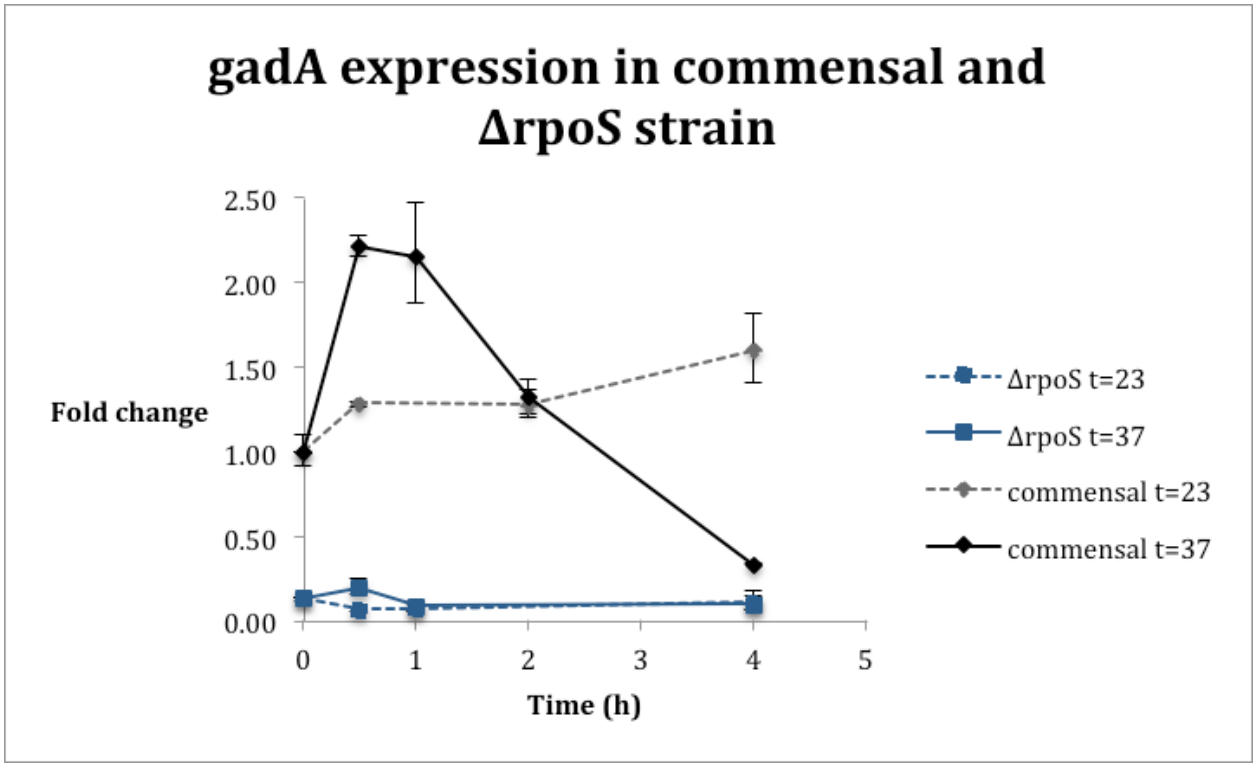
My research showed that in commensal E. coli strain, expression of virulence genes was highly regulated by temperature. Four genes (ompT, ompW, flu, ivy) demonstrated ≥ 3-fold increase in mRNA levels by 30 min after the upshift to 37°C with flu and ompW showing further 12 times-fold increases by 2 hours. As these are all genes significant in initial attachment of bacteria and resistance to the host's immune system, this supports a model in which temperature is a cue that helps bacteria respond to the host environment.

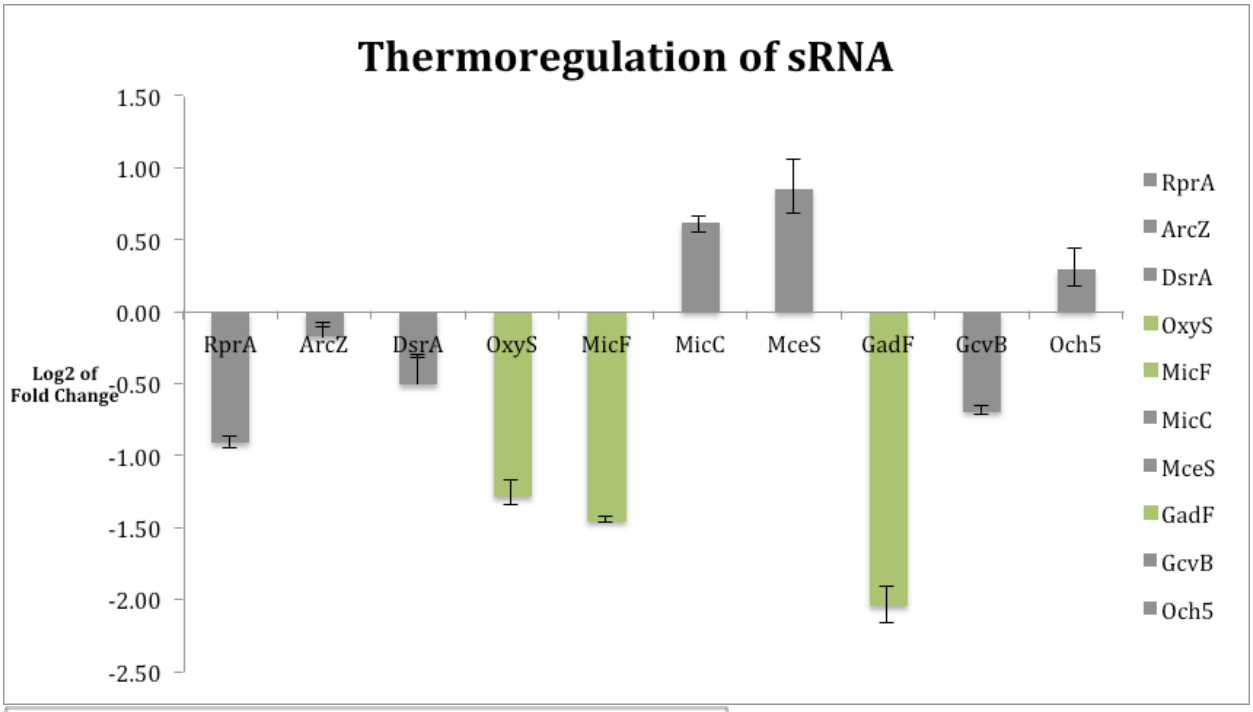
As the environment of the host imposes significant stress on bacteria, additional experiments assessed how temperature regulates stress response genes. A central transcriptional regulator of the stress response in E. coli is the sigma factor RpoS. Many thermo-regulated genes that regulate osmotic and acid stress response (gadA, osmY, dps) are under the regulation of RpoS. My hypothesis was that RpoS was required for the low temperature activation of these genes, a model which this project proved to be true. When assessing expression of these three genes (gadA, osmY, dps) in ΔrpoS mutant cells, it was observed that transcript levels of all three were over 99% decreased when compared to their expression at 23°C in commensal, non-mutant cells. This proves that one of the important ways in which these genes are thermo-regulated is through their interaction with RpoS.

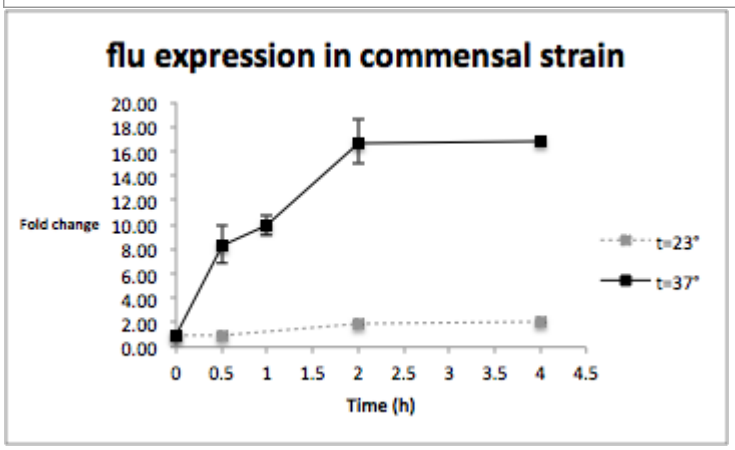
Since RpoS was discovered as a major factor in thermoregulation, my studies were focused on identifying additional molecules that might control gene regulation in response to temperature. In previous studies from the lab, small regulatory RNAs (sRNA) were identified to both affect gene regulation by binding to mRNA3 and to be thermo-regulated in UPEC.4 In this project, three more sRNAs were discovered in UPEC that are thermo-regulated. These include sRNAs previously identified to repress RpoS (OxyS), as well as sRNAs known to regulate genes involved in acid response (GadF) and high osmolarity conditions (MicF). These results further confirm the potential importance of sRNAs as regulators of gene expression and that this function may be controlled by the temperature regulation of the sRNA itself. Taken together, these studies support the importance of temperature in regulating gene expression that may be important to bacterial survival in the host and external environments.

(Supported by Blakeslee Fund)

Advisor: Christine White-Ziegler, Biochemistry


gadA expression in commensal and ΔrpoS strain
Fold change
2.50
2.00
1.50
1.00
0.50
0.00
0
1
2
3
4
5
Time (h)
ΔrpoS t=23
ΔrpoS t=37
commensal t=23
commensal t=37


Thermoregulation of sRNA
Log2 of Fold Change
1.50
1.00
0.50
0.00
-0.50
-1.00
-1.50
-2.00
-2.50
RprA
ArcZ
DsrA
OxyS
MicF
MicC
MceS
GadF
GcvB
Och5


flu expression in commensal strain
Fold change
20.00
18.00
16.00
14.00
12.00
10.00
8.00
6.00
4.00
2.00
0.00
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
Time (h)
t=23°
t=37°

Analysis of the Structure and Kinetics of a Mismatched DNA Duplex Using NMR Spectroscopy

Leigh Tanji/2018

Mismatched base pairs in DNA duplexes occur for many reasons, such as replication errors, mutagenic chemicals, and ionizing radiation. These non-complementary pairs are often found and corrected by DNA polymerase and postreplicative mismatch repair systems. If the error is neglected, it may cause mutations that significantly distort genetic information. To understand how mismatches are detected before repair, the structure and kinetic differences between a control 11-mer DNA duplex (Figure 1) and the same duplex with a G-G mismatch in the G6/G17 position were compared using 1D proton NMR Spectroscopy and 2D Nuclear Overhauser Effect Spectroscopy (NOESY).

NOESY spectra were obtained on a Bruker 500 NMR spectrometer at pH 7 and 8 °C. Most of the resulting data were analyzed using the NMR peak assignment program SPARKY. The 1D proton NMR spectra were also obtained on a Bruker 500 NMR at pH 7 from 8-45 °C (Figure 2). Contrary to literature findings, temperature studies done in previous years found all imino peaks except for the G-G mismatch imino peaks expected to appear around 10.5 ppm. The peaks were found this year, at temperatures 10 °C and lower, confirming that the intended 11-mer with a G-G base pair was synthesized.

Moving forward, a new 11-mer duplex sample at pH 8 will be made to conduct a temperature study. Additionally, proton NMR imino peaks must be completely assigned in order to conduct base-pair opening kinetic studies and learn more about how this mismatch affects the dynamics of the DNA helix.

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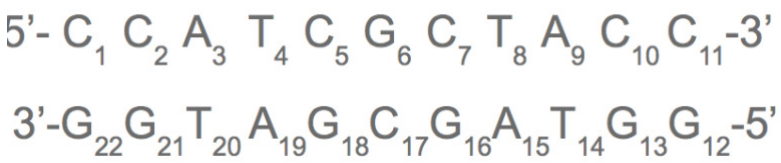
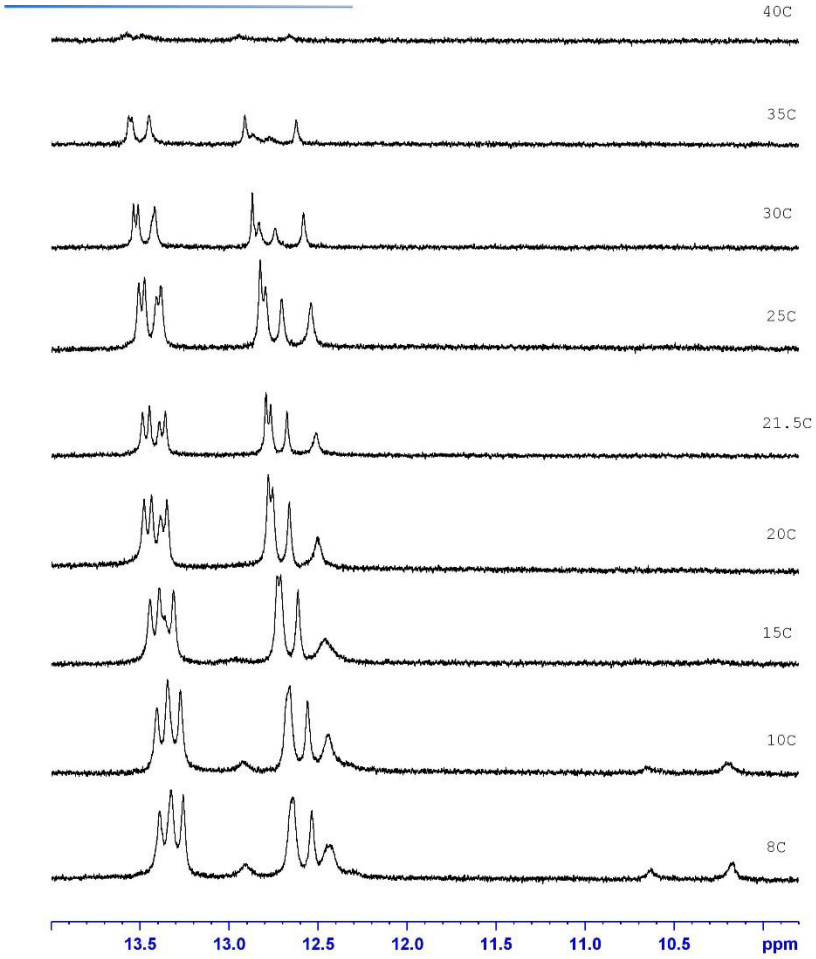
(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Elizabeth Jamieson, Biochemistry

Figure 1. Control 11-mer DNA duplex.




40C
35C
30C
25C
21.5C
20C
15C
10C
8C
13.5
13.0
12.5
12.0
11.5
11.0
10.5
ppm

Hair and Odor Molecules

Jinyi Yang/2018

Odors, functioning as chemical cues, are important tools animals use to detect surroundings, mates, etc. Humans nowadays do not depend on such chemical cues to sense the environment; however, people are willing to invest in perfumes and hair products to smell good. These actions support a huge industry, suggesting that a pleasant body odor is part of a person's natural needs. Occasionally, however, it is unavoidable to pick up smells from the environment. Hair is a versatile carrier of numerous types of molecules, including volatile odor molecules. It is susceptible to odors from the environment: all kinds of smells from ocean, coffee, pets, etc., can readily stick to hair. Which odor molecule does hair interact most with? This information can be obtained using the headspace gas chromatography (GC). This method is extremely sensitive, picking up all volatile molecules that are potentially interacting with hair. We found that, while hair is an almost universal acceptor, its highest affinity appears to be for hydrophobic molecules, particularly cyclic terpenoids, such as pinene and limonene. Odors that have been tested on the headspace include citral, geranial, neral, terpinene, citronellol, carveol, and dramascones.

Cyclodextrins are cyclic compounds made up of sugar molecules and have a hydrophobic interior which can trap small, hydrophobic organic molecules. This feature of cyclodextrin allows its prevalent use in the hygiene industry, for example, in Febreze©'s products. Inspired by this, we proposed to coat hair with cyclodextrin to modify its ability to bind and release odor molecules, which are generally small and hydrophobic. Via an azlactone-functionalized polymer, PVDMA, we were able to attach β-cyclodextrin on to hair. The modified polymer was confirmed using infrared spectroscopy (IR). The presence of the polymer on hair was confirmed by fluorescence microscopy using amino-fluorescein as the fluorophore. The surface structure of hair did not change significantly, which was demonstrated by SEM (Scanning Electron Microscope) images. Due to the inefficient reaction between the polymer and cyclodextrin, and the possibility that the polymer could occupy the interior hydrophobic core of the cyclodextrin, thereby decreasing the capturing efficiency of the cyclic oligosaccharides, we modified β-cyclodextrin further by attaching an amine functional group, which is most reactive with the polymer. The synthesis of the amino-β-cyclodextrin was not very efficient: multiple functional groups were introduced and attached to β-cyclodextrin, causing great difficulties for the final identification of the molecule.

The next step of the project would be to first purify the amino-β-cyclodextrin as much as possible to gain better control over the polymer and subsequent hair modification. Second, we would test whether the modified hair, coated with either cyclodextrin or amino cyclodextrin, has a different affinity to various odor molecules using the headspace GC. We hypothesize that the β-cyclodextrin on hair will trap the odor molecules, thereby decreasing the number of volatile odor molecules that escape and generate the unpleasant smell people have after cooking, for example.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: David Bickar, Biochemistry

Thermoregulation of genes related to virulence in Escherichia Coli

Ka Aminata/2018

For my summer research, I worked in the Christine White-Ziegler lab. In this lab, we focus on the gene expression of Escherichia Coli under temperature changes. E .coli is a known commensal strain that is naturally part of the microflora of the human gut (3). However, it has a lot of deadly strains such as Enterotoxigenic E. coli (ETEC) Enteropathogenic E. coli (EPEC), Enteroinvasive E. coli (EIEC), Enterohemorrhagic E. coli (EHEC), and Uropathogenic E. coli (UPEC) which are known to cause catastrophe diseases; for example diarrhea in third world countries from Enteropathogenic E .coli (EPEC) (4). Our project focused especially on Uropathogenic E. coli (UPEC) which is responsible of 70-90% of urinary tract infections and 40% of UTIs in women (2). This strain's virulence increases based on several factors such as the ability to grow and survive in the human gut; the caecum. Thus, to understand better which virulence factors make it possible for UPEC to survive in the caecum, we looked at several genes such as ompT, ompW, fliC, flU, ivY, csgA, and csgD to see how their expression changes from 23˚C to 37˚C (the human body temperature that the bacteria has to overcome in order to survive and colonize the host) using RNA isolation of the transcriptome and quantitative RT-PCR to measure the change in gene expression in a given strain from the initial time (t=0). The gene's expression is associated with foreign protein degradation (ompT), cell wall hydrolysis (ivy), biofilm formation (flu), flagellin coding (fliC), curli formation (csgD and csgA) (1). Results in our lab from the commensal strain K-12 shows that these gene's expression significantly increases as temperature increases from 23˚ C to 37˚C (1). Based on that, we hypothesized that we would see the same results in the UPEC strain as these genes are associated with virulence and survival in the host. Our preliminary results on one isolate of UPEC CFT073 (UPEC 567 T) shows that ompT, ompW, flu, csgA, and csgD have an increased in expression as temperature increases from 23˚ C and 37˚C, however ivy and fliC have decreased in expression. We are working on an another isolate UPEC 567 Y to confirm these results.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Christine White-Ziegler, Biological Sciences

Investigating the essential role of reelin-disabled signaling during neural development in zebrafish

Katrina Anderson/2018

Understanding the way that our brains are built, from stem cells to neurons to glia, is an immensely complex and substantial task given to our generation of scientists. It will be through the comprehension of the minute processes that occur in our developing brains, that we will be able to solve the complex problems that plague one of our most dynamic organs. Through SURF in the laboratory of Dr. Michael Barresi, I have explored molecular cues that are involved in the proper patterning of the vertebrate central nervous system.

I am specifically interested in understanding how neural development is affected by the perturbation of cell signaling mediated by reelin. RELN is a secreted glycoprotein that regulates microtubules and actin, the cytoskeletal elements that enable cell motility and migration, through its network of transmembrane receptors (ApoER2, VLDLR) and intracellular mediators (Disabled1) (reviewed in Vaswani and Blaess, 2016). Reelin signaling machinery is present in mouse radial glia, a main neural progenitor cell type in the central nervous system, and it is clear that these neural progenitor cells interact with the secreted protein throughout development (Luque et al., 2003). Although reelin has been extensively studied in mouse over the last 60 years, little is known about its normal functioning in zebrafish neurogenesis. Our research would greatly contribute to the understanding of reelin signaling across species and strengthen the comprehension of its role in vertebrate neural development.

Previously in the Barresi Laboratory, I developed a 17 base-pair deletion mutant in the reelin gene through CRISPR-Cas9 mediated mutagenesis. My main goal is to now begin work on the characterization of that reelin mutant. The first step in that analysis was gaining the ability to visualize RELN in our desired tissues. With the use of antigen retrieval and an extended immunohistochemistry protocol, I was able to successfully label the RELN protein in the zebrafish embryo (Inoue and Wittbrodt, 2011). Upon close analysis of the data found in the mouse mutant, I then began looking at the location and migration patterns of Islet-1 positive cells (motor neurons and Rohon-Beard neurons) in the zebrafish spinal cord. In the mouse mutant, there is a distinct over migration defect of Islet-1 positive cells in the spinal cord. In this system, Reln is thought to act as a stop signal for migrating motor neurons in the spinal cord and inhibit their ability to migrate ventrally back towards their origin (Yip et al., 2000). Although the analysis of this data in zebrafish is not yet complete, it appears that there may also be a disorganization of Islet-1 positive cells in the zebrafish reelin mutant.

There is much more work to be done on the analysis of the reelin signaling pathway in zebrafish and in the coming year our team plans to develop a complete model of reelin signaling expression, investigate possible neural and behavior phenotypes and begin to construct an understanding of the role of reelin signaling in the neural development of zebrafish.

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(Supported by NIH: National Institute of Health)

Advisor: Michael Baressi, Biological Sciences

To eat or to be eaten. . . that is the question: interactions of grazers *Littorina litorea* and *L. obtusta* and the invasive predators, *Hemigrapsus sanguineus* and *Carcinus maenas*

Sarah Chin/2019, Giovanna Noe-Wilson/AC, and Anastasia Konefal/2017

A key component shaping community structure in any ecosystem is the functioning of balanced trophic interactions. When effective biological invaders, such as non-native species, are introduced into otherwise stable communities, they can have negative impacts on vulnerable native species. We examined the effects of two invasive predator crab species introduced to the New England area, *Carcinus maenas* (Green Crab) and *Hemigrapsus sanguineus* (Asian Shore Crab), on distribution and grazing patterns of the herbivorous gastropods, native *Littorea obtusata* and its congener *L. littorea*. Both crab species have been reported as predators of *Littorina spp.* While Green Crabs were introduced into the area >200 years ago, Asian Shore Crabs are more recent invasives.

In the field, we found that *L. obtusata* densities were 2-3X higher in the high-intertidal than mid-intertidal zone in Rhode Island (RI). In contrast, L. littorea showed no consistent pattern in abundance or shell size with tidal height. Predator-choice experiments indicated a preference for L. obtusata by both Green Crab and Asian Shore Crab. Further, both invasive crabs were able to consume larger *L. obtusata* than *L. littorea*, likely due to thinner shell thickness of the former species. In both Rhode Island and Maine, greater than 95% of the L. obtusata populations are less than 13 mm length (Putnam 2016), indicating limited escape in size from either crab predator. In contrast, more than 50% of L. littorea are larger than 17 mm and most Asian Shore Crabs are too small to crack the shells of L. littorea in RI. Even large Green Crabs (56-90 mm carapace) collected in subtidal areas preferred L. littorea less than 15 mm. Thus, this snail species has a clear escape in size in RI.

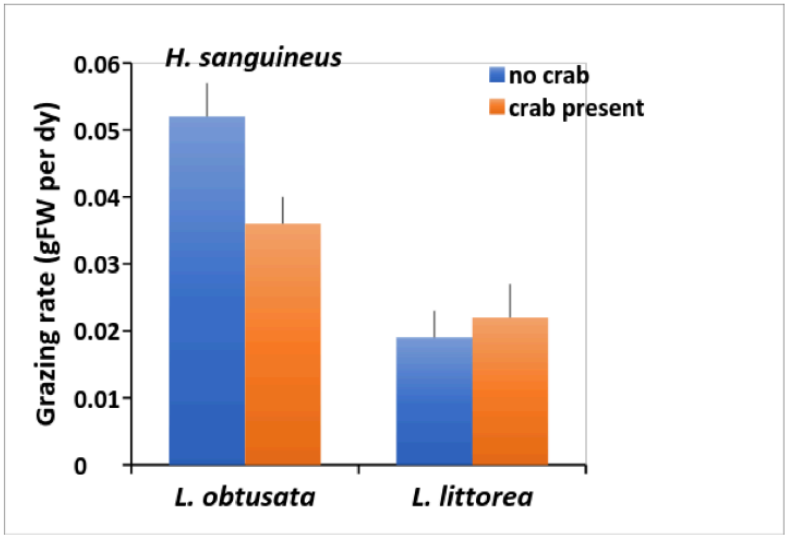
Using laboratory experiments, we examined grazing rates of L. littorea and L. obtusata in the presence of either C. maenas or H. sanguineus, or when held in water in which Littorina had been consumed by the crab species (snail-mortality water). In the presence of live crabs, grazing rates of L. littorea decreased only in the presence of C. maenas, whereas herbivory of L. obtusata decreased significantly in the presence of both C. maenas and H. sanguineus (Figs. 1 & 2). Similarly, L. obtusata showed reduced grazing rates when held in water in which its conspecies had been consumed by either predatory crab, while herbivory of L. littorea was similar in ambient and snail-mortality water. We conclude that predation pressures from both invasive crab species place L. obtusata in a continuous state of vulnerability, and thus might contribute to the limited distribution and herbivory of this herbivorous gastropod in rocky intertidal areas.

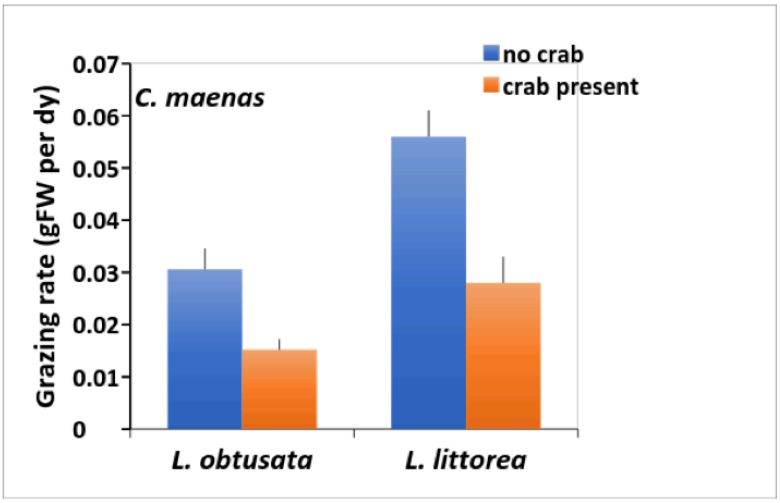
Fig. 1. Mean (+SE) grazing rate (g FW per day) of Littorina obtusata and L. littorea in the presence and absence of the crab Hemigrapsus sanguineus. L. obtusata showed a significant ($t = 2.33$, $P = 0.02$) reduction in herbivory in the presence of the crab.

Fig. 2. Mean (+SE) grazing rate (g FW per day) of Littorina obtusata and L. littorea in the presence and absence of the crab Carcinus maenas. Both gastropod species had significantly (t tests, $P < 0.002$) lower herbivory in the presence of the crab.

(Supported by B. Elizabeth Horner Fund)

Advisor: Paulette Peckol, Biological Sciences


H. sanguineus
no crab
crab present
Grazing rate (gFW per dy)
0.06
0.05
0.04
0.03
0.02
0.01
0
L. obtusata
L. littorea


C. maenas
no crab
crab present
Grazing rate (gFW per dy)
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
L. obtusata
L. littorea

Third Year of Paradise Pond Project: Macroinvertebrates as Bioindicators of River Health

Sasha Clapp/2019, Lisa Mena/2019, and Lyric Williams/2019

A proud landmark and integral ecological component of Smith College's campus, Paradise Pond is an impoundment of the Mill River. Like most impoundments, its very presence possesses the potential to negatively alter the physiochemistry downriver and damage its precious ecosystems [1]. In order to mitigate ecological catastrophe in the Mill River, state regulations require that Smith College approaches any management of Paradise Pond with ecological sensitivity. Caution not to disrupt ecosystems downriver of the pond during and after the redistribution of the ever-accumulating sediment is pertinent.

In order to assess Smith College's impact on the Mill River, the Before-After-Control-Impact (BACI) design was utilized to compare diversity indices of macroinvertebrates upriver and downriver of Paradise Pond [2]. Aquatic macroinvertebrates function as critical bioindicators because many are incredibly intolerant of pollution. Comparisons of upriver and downriver sites provide essential information about how, if at all, Paradise Pond is impacting the Mill River. Using kicknet sampling, macroinvertebrates were collected and identified at upriver and downriver riffle sites during the months of June and July - approximately one year after the last sediment redistribution.

A healthier river is typically more diverse. One of the ways to compare diversity between the upriver and downriver sites is to compare species rank abundance curves from each site using a pairwise Kolmogorov-Smirnov test. Species (or lowest taxa the organism was identified to) were ranked from most abundant to least abundant. Relative abundance was calculated as the number of an organism found divided by the total number of all the organisms in the sample, and then multiplied by one hundred. Based on our species rank abundance curves, there was no significant difference in diversity sampled between the upriver site and the downriver site during the summer months (Figure 1). This suggests that sediment redistribution is not impacting the level of diversity in the downriver site. This preliminary data indicates that we are not negatively affecting the health of the Mill River.

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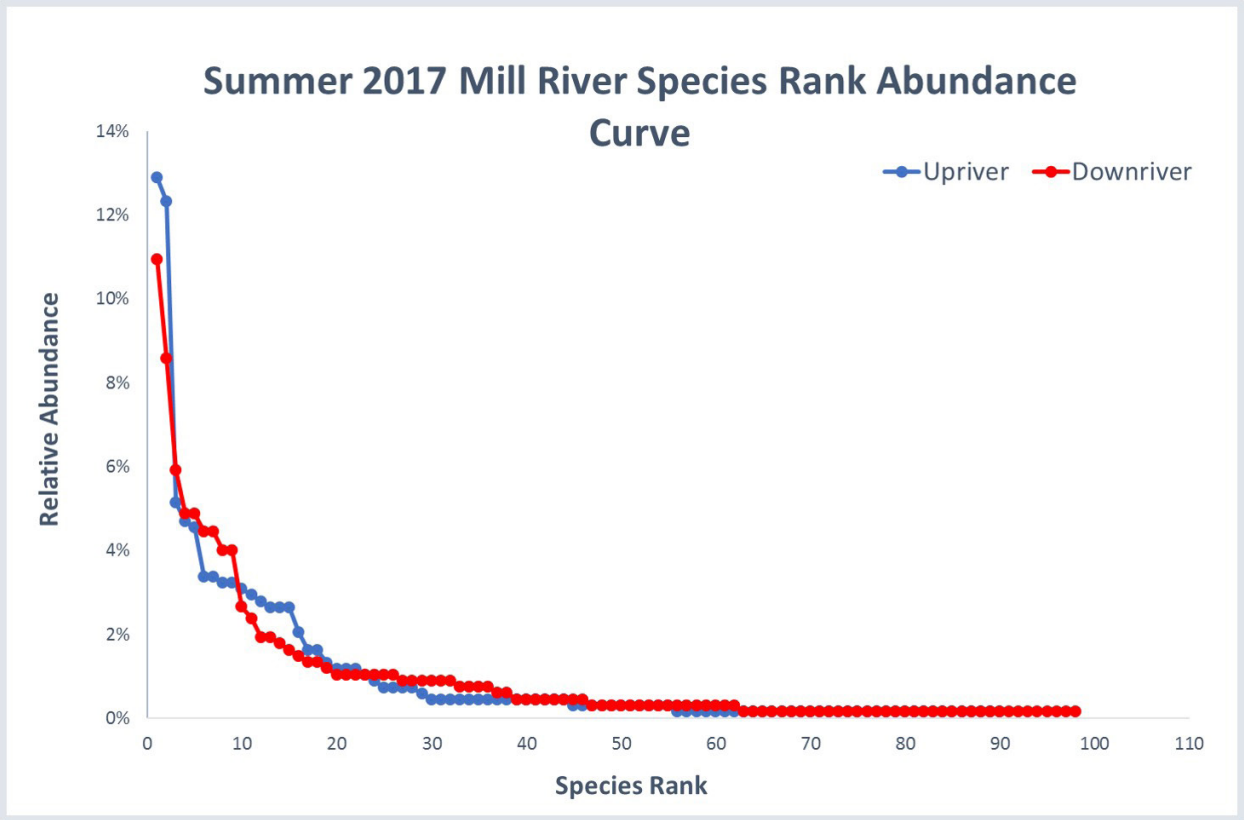
2. Strayer, D. L., and D. R. Smith. 2003. A guide to sampling freshwater mussel populations. American Fisheries Society, Monograph 8, Bethesda, Maryland.

(Supported by Pond Project)

Advisor: Marney Pratt, Biological Sciences


Summer 2017 Mill River Species Rank Abundance Curve
Upriver
Downriver
Relative Abundance
14%
12%
10%
8%
6%
4%
2%
0%
0
10
20
30
40
50
60
70
80
90
100
110
Species Rank

Revisiting Bergmann's Rule Using Museum Study Skins for Sciurus carolinensis

Isabella Fielding/2017

Many specimens of the eastern gray squirrel, Sciurus carolinensis, have been collected and preserved in museums across the United States over the past 150 years. One goal of this investigation was to determine how museum data can and cannot be used to conduct investigations of body size of well-studied organisms. Since data have been collected for this species over the past century and a half, this study also sought to study the effects of year as a proxy for climate change on body size in S. carolinensis. Lastly, the effects of latitude on body size were examined in S. carolinensis to evaluate the validity of Bergmann's Rule within this species and taking subspecies into consideration as a confounding variable. Information from 1928 study skins was collected from 27 museums and used to calculate General Linear Models in Minitab 18 that showed the relationships of head and body length with the variables of latitude, subspecies, and year. Study skins were assigned to subspecies based upon their recorded localities of origin and the subspecies distribution map by Edwards et al. (2003). The results suggest that body size of S. carolinensis increases with latitude, in accordance with Bergmann's Rule, and that subspecies plays a lesser role than does latitude in body size determination. Year also has a negative effect on body size in S. carolinensis, with a stronger effect in the south than in the north. Considering the correlation between year and climate change, these results suggest that temperature may be influencing size in S. carolinensis according to Bergmann's Rule, but that body size changes are a reaction to increases in warmer temperatures rather than colder temperatures.

(Supported by B. Elizabeth Horner Fund)

Advisor: Virginia Hayssen, Biological Sciences

A Biochemical Approach to Understand Gene Expression in Filarial Parasites

Nicole Frumento/2018

Filariasis is a tropical disease caused by parasitic helminths, nematodes that have been extremely successful in surviving in the host environment. Gene expression of parasitic genome undergoes dramatic changes when the parasite is transmitted from the mosquito into the human host. It has been recognized that transcription factors play a significant role in causing alterations in gene expression, but even though we know the parasite's entire genome sequence, determining what promoters look like in these parasites is still unknown. Identifying transcription factors unique to Brugia malayi, our model organism, could lead to an explanation of how parasites regulate their genes, and to the discovery of new drug targets to help combat infectious diseases.

Bioinformatics tools were used to perform a comparative analysis of whole genome data sets in order to screen for targetable genes in B. malayi. Once the gene coding for the transcription factor of interest was selected, the cDNA copy of the gene was amplified by PCR using RNA isolated from adult male worms as template. The accuracy of the amplification was confirmed by agarose gel electrophoresis. Because of high homology with C. elegans, the putative transcription factor UNC-86 was selected as the best candidate for our project.

UNC-86 is a transcription factor involved in specifying the identities of neuronal cells by regulating the expression of other genes (1). UNC-86 has been shown to bind to the promoter of the mec-3 gene in C. elegans at six different binding sites (2,3). Alignment of the upstream region of the B. malayi mec-3 gene with the six UNC-86 binding sequences showed high homology (Fig 1). By aligning the mec-3 promoter regions of B. malayi with that of two closely related nematodes, B. pahangi and O. volvulus, the UNC-86 binding sites showed great similarities between the different species both in the location relative to the start codon and in the base-pair sequence. These results convinced us that UNC-86 in B. malayi could behave similarly to UNC-86 in C. elegans. In the future, we hope to sequence and clone the gene encoding the putative transcription factor UNC-86 and produce large quantities of the protein in an expression vector. We will later perform binding assays to illustrate the specific binding of UNC-86 to its target. I intend to complete an honors thesis project during my senior year where I will be able to expand upon the current results of this project.

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3) Xue D, Finney M, Ruvkun G and Chalfie M. (1992). Regulation of the mec-3 gene by the C. elegans homeoproteins UNC-86 and MEC-3. The EMBO Journal, 11 no. 13, 4969 – 4979

(Supported by Blakeslee Fund)

Advisor: Steven Williams, Biological Sciences

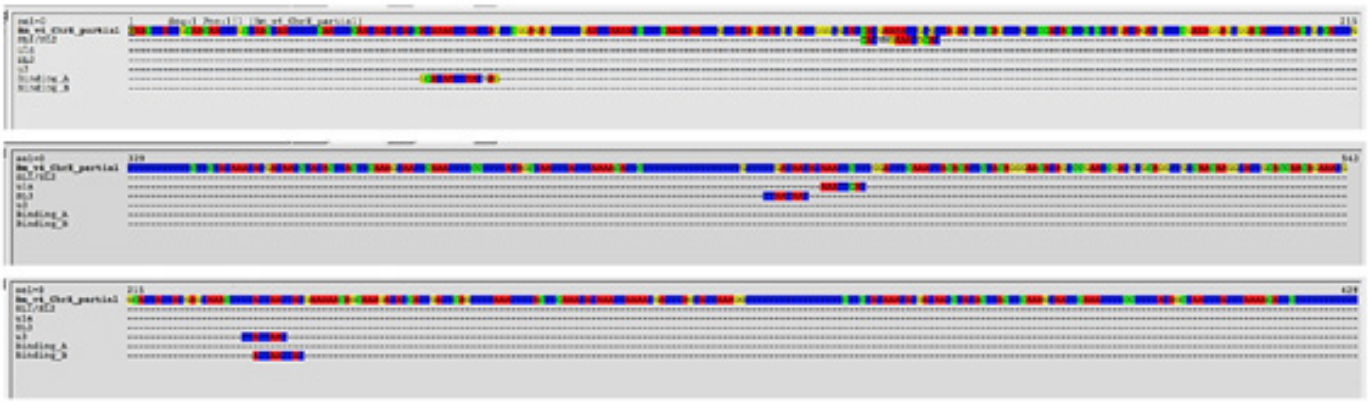


Figure 1. Alignment of the upstream region of the *B. malayi* mec-3 gene with the six UNC-86 binding sites. All six show either complete or partial complementarity with sequences on the mec-3 promoter region.

The distribution and diversity of endemic forest plants in the eastern United States reflects impacts of past climate change and influence of ecological traits

Anna George/2017

Small-ranged endemic species are a key component of biodiversity and their conservation will be significant challenge in the face of modern climate change. By comparing the biogeography and ecological traits of small-ranged endemics to wider ranging forest plant species, I aim to improve our understanding of the historical and contemporary environmental factors that influence the distribution and diversity of these important species.

I assessed patterns of county-level species richness, mean climate, glacial history, and distance to the Last Glacial Maximum for 206 small-ranged endemic plants associated with Temperate Deciduous Forests habitats in the Easter United States. I compared ecological traits, including height and diaspore dispersal mode, between the small-ranged endemic species and 285 wider-ranging forest plant species.

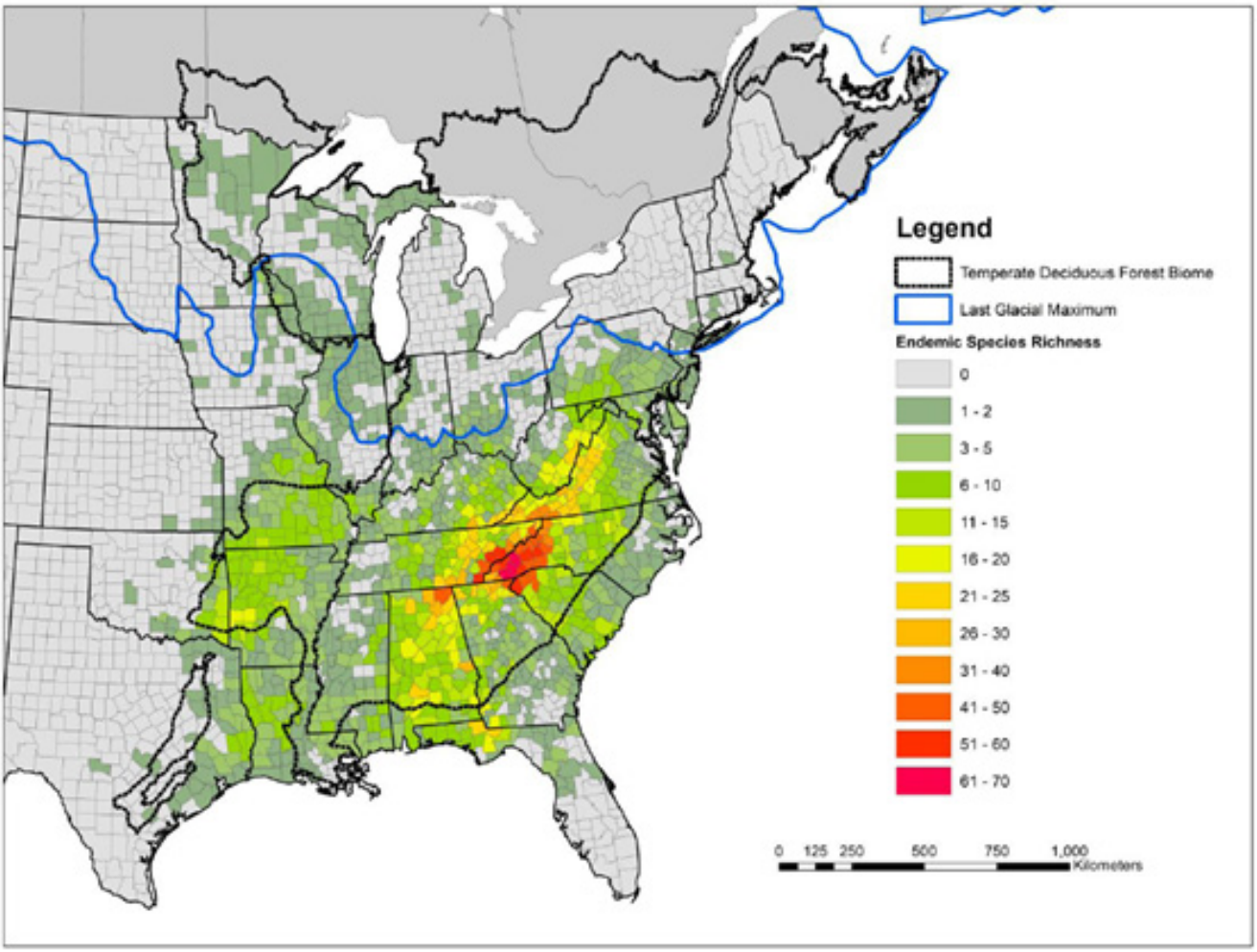
Endemic forest plants were rare or absent north of the Last Glacial Maximum boundary in the study area, but common to abundant in the southeastern US. Present-day environmental factors correlated with endemic richness in divergent ways between unglaciated and formerly-glaciated regions. In unglaciated areas, endemic forest plant richness was negatively correlated with increased mean annual temperature, but positively correlated with elevational range. Endemic forest herbs were distributed closer to the LGM boundary than endemic woody species. Compared to wider-ranging species, endemic herbs were significantly less likely to produce diaspores dispersed by vertebrates.

The distribution and diversity of endemic forest plants in the eastern United States suggests a persistent imprint of glacial history. The long-term persistence of these biogeographic patterns is likely influenced by dispersal limitation of small-ranged forest plants. These small-ranged endemics could face significant challenges with modern climate change, as their current distributions are often confined to southern areas, their richness tends to decline with warmer temperatures, and future dispersal appears unlikely. Thus, some endemic species threatened by climate change might become candidates for assisted colonization in the future.

(Supported by DOD/Brown-Bellemare, J."Plants")

Advisor: Non-Smith Advisor, Biological Sciences

Total Endemic Richness August 2017



Genome Architecture of Foraminifera

Elly Goetz/2019

Foraminifera (forams) are single-cellular, eukaryotic organisms belonging to the protist super-group Rhizaria. They are primarily marine and amoeboid with pseudopodia emerging from one or many apertures of their shell or 'test' (Lee and Anderson, 1991).

Cells used in this study were collected from salt marshes at three locations: Sapelo Island, GA, Sippewissett, MA, and Stonington, CT. The top few millimeters of sediment was scraped from the mudflat and sieved to sort for appropriately sized particles. Individual cells were then picked under a microscope, and placed in culture dishes. Morphospecies were generally similar between the sample sites but differed greatly in their abundance. Common genera between the sites include: Ammonia, Haynesina, Textularia, Trochammina, Miliammina and Quinqueloculina.

DAPI staining and close observation of nuclei were used to study and map the lifecycles of these morphospecies. Active cells (those with pseudopodia present) were fixed in paraformaldehyde and placed on a slide with DAPI, a fluorescent, nuclear stain, using Weber and Pawlowski's (2013) protocol. Nuclear location and size were imaged on the Leica confocal microscope and based on these observations, the lifecycle stage was inferred.

Molecular techniques were also used to study foraminiferan genome dynamics. Whole genome amplifications (WGAs) were used to amplify the DNA of the cell, and whole transcriptomes amplifications (WTAs) were used to amplify the RNA, giving us the genes being expressed at the time of lysis. These techniques could later give us insight into lifecycle specific genes, and foram evolution.

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Weber, A.A-T., 2013 Pawlowski, J. Can Abundance of Protists be Inferred from Sequence Data: A Case in Foraminifera. PLoS ONE. 8(2): 2.

(Supported by NSF: National Science Foundation)

Advisor: Laura Katz, Biological Sciences

Monitoring Oyster aquaculture and eelgrass habitats

Emily Goss/2018

This summer, I worked on a project begun this year, comparing fish and invertebrate habitat utilization of natural eelgrass beds with bivalve aquaculture gear beds on estuary flats in the Puget Sound. The newness of this project offered me the opportunity to help design the study and develop methods for field and lab protocols. Bivalve aquaculture (oyster, clam and geoduck cultivation) beds contain plastic or metal nets, frames and long lines, referred to as "gear," that hold the shellfish in place on or off bottom. Bivalve aquaculture displaces natural eelgrass beds and modifies adjacent eelgrass beds. We set GoPro cameras at several oyster farms in the following layout: in the center of a gear type area, in a natural eelgrass patch for reference, and at the edge where the two habitat types (gear and natural) meet. Our research design included different aquaculture gear types in different areas of Puget Sound. The cameras were set to capture footage at high tide to document what species are making use of these habitats. At each camera setup we laid a transect and used a .5 x .5 m quadrat for eelgrass presence and density surveys, making note of both the wide and longer native (Zostera marina) and narrower, smaller non-native (Z. japonica) eelgrass. We also sampled eelgrass for biomass estimates and sediment cores for composition assessments. Analysis of eelgrass shoot length and biomass, along with sediment composition provides insight into vegetation and soil characteristics at these habitats and what species might be attracted to in them.

Native eelgrass is a species of concern in Puget Sound in part due to its role as an important habitat in early life history of several Pacific salmon species. Bivalve aquaculture, cultivating mostly shellfish non-native to the Pacific Northwest, often occurs in former eelgrass beds, and modification and loss of eelgrass habitats may hamper recovery efforts for salmon, which are culturally and economically important species in the Puget Sound. However, bivalve aquaculture is an increasingly important industry, with Washington state leading US production of farmed bivalves. The structure of aquaculture gear has also been found to provide the same services as eelgrass to certain benthic invertebrates [1]. Our research adds to understanding how various species use both bivalve aquaculture and eelgrass habitats, and will provide farmers, legislators, and scientists a more informed means for evaluating trade-offs and developing management plans for these estuary flats.

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(Supported by Agnes Shedd Andreae '32 Research Fund)

Advisor: Non-Smith Advisor, Biological Sciences

The Effect of DEET on Human GABAA and Glycine Receptors

Gariel Grant/2019

N, N-Diethyl-meta-toluamide (DEET) is an insect repellent that has been widely used beginning in the 1950s. Since then, exposure to DEET has been associated with the onset of seizures, particularly in young children. Convulsants such as DEET, often induce such activity by acting as either antagonists to GABAA and glycine receptors, the major inhibitory receptors of the nervous system, or conversely, acting as agonists to glutamate receptors, which usually play an excitatory role within the nervous system. Firstly, the aim of this project is to investigate the mechanism of action by which exposure to DEET causes convulsions. This is done by examining the effects of the chemical on human GABAA and glycine receptors. Secondly, this project aims to aid in identifying potential chemical substitutes to DEET, which are as effective in repelling insects, without the harmful effects to the nervous system. Throughout the project, the two-electrode voltage clamp technique is used to record GABAA and glycine currents through receptors expressed in Xenopus laevis oocytes.

Research that we have carried out thus far supports the theory that DEET acts as an antagonist to the human glycine receptors, resulting in an inhibition of glycine currents when DEET is co-applied with the receptor's natural ligand, the glycine neurotransmitter (Figure 1). Furthermore, the data suggest that DEET acts as a competitive antagonist to glycine receptors, thereby shifting the glycine dose-response rightward. Future research will investigate the effect of DEET on GABAA receptors. Additionally, in order to aid in finding a viable substitute to DEET, 17 novel compounds will be screened on GABAA and glycine receptors, and their effects compared to that of DEET.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Adam Hall, Biological Sciences

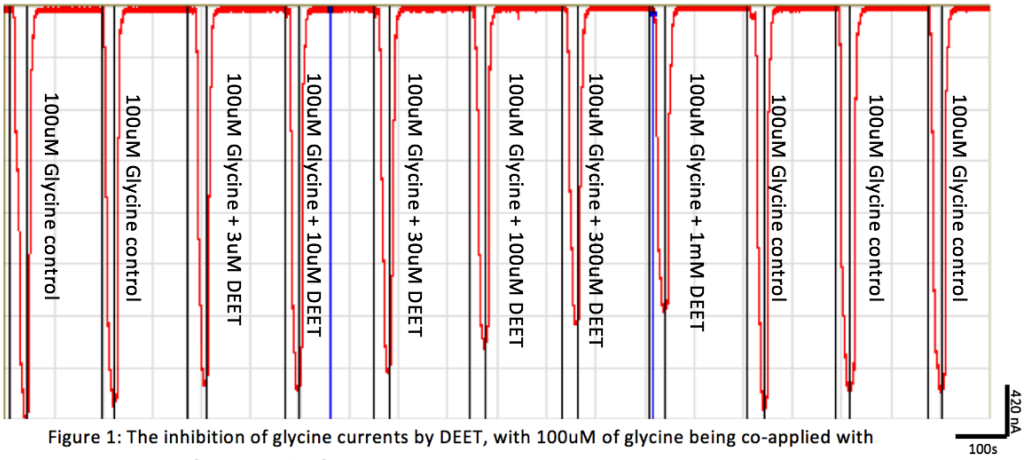


Figure 1: The inhibition of glycine currents by DEET, with 100uM of glycine being co-applied with concentrations of DEET varying from 3uM to 1mM

Intertidal Invertebrate Population Dynamics: The Role of Phenotypic Plasticity in Evading Novel Predation

Renee Halloran/2018

Phenotypic plasticity is the range of phenotypic variation expressed by a single genotype in response to an environmental influence. Numerous previous studies have illustrated the ability of molluscan prey to express adaptive plasticity (e.g., increased shell thickness) in the presence of predatory cues as a defensive measure to evade predation.

The Asian shore crab Hemigrapsus sanguineus is a relatively new invasive species to the Gulf of Maine. The crab was found on the coast on New Jersey in 1988 and since has established populations moving northward in the Gulf of Maine. H. sanguineus presents a novel predatory cue to intertidal snails Littorina littorea and Littorina obtusata in the Gulf of Maine, the effects of which have not been studied. The aim of this study was to investigate the plasticity potential of L. littorea and L. obtusata when exposed to the novel predator, and energetic tradeoffs, such as reduced linear shell growth and tissue growth, associated with defensive morphology in the presence of predator cue.

In May 2017, L. littorea and L. obtusata were collected north of the H. sanguineus invasion front in Lubec, Maine, where snails were expected to have not encountered H. sanguineus. The snails were reared in control water (clean seawater) or cue water (water containing H. sanguineus cue). Shell growth, internal architecture, tissue growth, and reproductive effort were measured over the course of the summer. Preliminary results show that the Littorina species recognize H. sanguineus cue, as evidenced by differences in shell growth between the two treatments. This laboratory experiment highlights the complexity of intertidal predator-prey interactions.

(Supported by B. Elizabeth Horner Fund)

Advisor: L.David Smith, Biological Sciences

Fear and loathing in Carcinus maenas: a biogeographic study of behaviors associated with invasion success in European green crab

Nicholas Hathaway/2018

With the expansion of international trade and development of coastal ecosystems, marine invasions are a major conservation priority. Exotic species must pass through sequential filters (i.e. transport, establishment, spread) to invade ecosystems, with each presenting novel ecological interactions that may be mediated through behavioral plasticity. Because success is generally low for each introduction stage, invasions can levy strong selection pressure for traits that predict high invasibility (e.g., aggression, boldness), yielding invasive populations that are behaviorally distinct from native sources and may change over time since establishment. To investigate the dynamics of invasion-related behaviors and potential behavioral syndromes (i.e., sets of correlated behaviors), I conducted a series of laboratory assays on European green crabs (Carcinus maenas) collected from three regions of invaded range in the northwestern Atlantic (i.e., southern Gulf of Maine, northern Nova Scotia, western Newfoundland,) that have been respectively established for approximately 200, 30, and <5 years. Assays include an open-field test to quantify boldness and activity via EthoVision XT motion-tracking software, dyadic trials to quantify aggression via an ethogrammatic scoring system, and predator-cue experiments to assess plasticity in foraging patterns. Specimens will be dissected for evidence of parasite infection, and genotyped to compare target behaviors between haplotypes and confirm population origins in respect to mtDNA data collected in recent years. These independent and genetically distinct invasions from Europe offer a fortuitous opportunity to compare behavioral patterns in invasive populations of different age and origin. If behavioral syndromes facilitate invasions and eventually wane (in sensu founder effect), I expect a higher prevalence of invasion syndrome correlates in crab populations from the more recent invasions versus the older invasion. Such behavioral differences would suggest an important role of behavioral plasticity in invasion success and help to predict competitive outcomes where earlier and more recent invasion fronts co-occur. A greater understanding of the behavioral patterns exhibited by this globally important invader will provide useful mechanistic insights into the factors that influence marine invasions.

(Supported by Blakeslee Fund)

Advisor: L.David Smith, Biological Sciences

Coral Reef Ed-Ventures Summer 2017

Emily Hitchcock/2019, Mandy Castro/2017, Abby Onos/2017, Sabrina Cordero/2019, Dana Vera/2019, and Jasmine Pacheco-Ramos/2019

This summer, six Smith students participated in the eighteenth year of the Coral Reef Ed-Ventures Program, in partnership with the Hol Chan Marine Reserve. Coral Reef Ed-Ventures is based in the town of San Pedro on the island of Ambergris Caye, Belize. Beginning in the year 2000, Coral Ed was designed as a way to support environmental education and conservation in the San Pedro community. In addition to providing two free summer camps for the children on the island, Smith students and their faculty advisers work together to conduct research on the local mangrove and coral patch-reef ecosystems. The team also began an investigation of beach erosion issues on Ambergris, focusing on seawall construction issues.

The theme of this year's youth camp was "Protecting our Communities." The students learned about a different marine protected ecosystem each day (including mangroves, seagrass, shallow sea/coral reef, and deep sea) and discussed the importance of protecting each. They also learned about how marine reserves help to protect these habitats as well as about potential actions they can take to spread awareness about protection. For the older schoolchildren, this year's R.E.E.F. (Research in Ecology and the Environment is Fun) Program, also explored the theme of protection with a focus on teaching the students research methods. The students learned how to conduct social surveys, carrying out interviews in the community about protection of the island and reef. They expanded their research skills through an investigation of the composition of the island's beach sand. Lastly, during field trips to the mangrove and reef ecosystems, the students conducted biodiversity surveys. With a greater understanding of how research is conducted, the students gained an appreciation for the value of marine protected areas in their community. Smith students participated in three research projects with professors David Smith, Denise Lello, Camille Washington-Ottombre, and Al Curran, including assessing coral patch reef health, mangrove propagule survival, and shoreline reinforcement locations. This included drone flights with Scott Gilman from the Spatial Analysis Lab to generate aerial images of the mangroves and coastal sea walls. Coral research was conducted using scuba and snorkel at Mexico Rocks, a site that recently received protected status in the Hol Chan Marine Reserve system. The goals of the long-term surveys at Mexico Rocks are to quantify live coral cover and soft coral abundance and diversity and track changes over time. This project is also studying the impact of Hurricane Earl (2016) on the coral mounds at Mexico Rocks. The second project tracks mangrove propagule survival in an area of high environmental stress and development pressure. Data collected in the field will help to ground-truth drone aerial imagery of propagule location and survival. Using kayaks, students also collected underwater images of organisms associated with prop roots and assessed breakage and herbivory of the propagules. In the third project, students examined seawalls, beach erosion, and property-owner attitudes about coastal protection measures. Methods included interviews with coastal property owners, drone imaging, and GPS data collection. This is part of a long-term study of adaptation to climate change on Ambergris Caye.

(Supported by the Environmental Science and Policy Program (ES&P) and Agnes Shedd Andreae Fund, Biological Sciences' B. Elizabeth Horner Fund and Margaret W. Grantham Fund, and a gift from Linda Salisbury '78)

Advisors: L. David Smith, Denise Lello, Biological Sciences, Al Curran, Geosciences, Camille Washington-Ottombre, Environmental Science and Policy, and Miguel Alamilla, Jr., Hol Chan Marine Reserve, with help from Shannon Audley (Education and Child Studies), Carol Berner (Education and Child Studies), Scott Gilman and Jon Caris (Spatial Analysis Lab), and Anne Wibiralske (ES&P).


06 14 2017 10 03

Polycyclic Aromatic Hydrocarbon Teratogenesis Effects Craniofacial Development Through Disruption of Pharyngeal Pouch Morphogenesis

Emilie Jones/2018

Polycyclic aromatic hydrocarbons (PAH's) such as Naphthalene (naph), are hazardous compounds which could be found at high concentrations in crude oil released during the Deepwater Horizon Disaster. PAH encounters are almost impossible to avoid as variations can be found in cigarette smoke, car exhaust and even mothballs. By using zebrafish as a vertebrate model system for PAH induced teratogenesis, we investigated the developmental mechanisms by which naph impairs craniofacial development. The craniofacial skeleton is derived in part from cranial neural crest cells (NCCs) which migrate through transient structures known as the pharyngeal pouches and arches. We postulated that naph could be targeting its effect on three possible cell types: the cranial NCCs, cells of the developing pharyngeal pouches, or epibranchial placodal cells that interact with pouch/arch growth. Using antibody and transgenic reporters for both arches and pouches, we demonstrate that naph causes specific malformations in the posterior most region of the pharyngeal system. Using in situ hybridization on embryos treated at 10hpf with a 200 uM naph dose, we characterized the expression of dlx2a, hoxa2b, hoxb2a, and jag1b at 30, 36, and 42hpf. Although naphthalene treated embryos labeled for hoxb2a and jag1b showed no difference in expression from the control embryos at any of the time-points, dlx2a and hoxa2b expressions were reduced at all time-points. Dlx2a is known to promote the formation of arches and NCCs, while hoxa2b is thought to assist in the formation of the pouches. The specific molecular mechanisms that naph is operating upon are still unknown, but we are continuing to narrow in on the involvement of these specific cell types most affected by naph. We are currently assessing the involvement of placodal cells and the dynamics of the interactions between the arches, pouches and placodes following naph treatment. It is our prediction that naph operates through the Aryl hydrocarbon receptor pathway to influence the molecular regulation of posterior pouch migration.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Michael Baressi, Biological Sciences

The investigation of design and directed evolution of novel antimicrobials that reduce the emergence of antibiotic resistance.

Nancy Jung/2020 and Lizette Vargas/2018

Microbes produce defense mechanisms such as antibiotics, lytic agents, protein exotoxins, metabolic by-products, and bacteriocins. Bacteriocins, proteinaceous toxins released by bacteria, have a narrow killing spectrum unlike classic antibiotics. This narrow killing spectrum enables cells to target only close relatives of the producing strain. Colicins, bacteriocins specific to Escherichia Coli, are typically composed of three genes: a colicin gene, an immunity gene, and a lysis gene. The colicin gene encodes the toxin. The immunity gene encodes a protein, which binds to and inactivates the toxic protein, thus conferring specific immunity to the producer cell. In turn, the lysis gene encodes a protein that lyses the producer cell and releases the colicin. If the genetic code of the killing domain is successfully altered, the anticompetitive measures may be harnessed and later used to treat infections. This project is part of a continuing Special Studies during the 2017 fall semester.

The colicins' killing domains were isolated and inserted into pFLAG plasmids after PCR, double digestion, ligation and transformation. To check if the colicin gene was inserted and accepted by the pFlag plasmid and the plasmid closed, the samples were grown on LB ampicillin plates.

Over the course of 10 weeks, there was one successful transformation. However, upon further examination, it was found that the growth was most likely due to contamination of the sample. Colicins E7 and E8 exhibited more consistent results and thus were chosen as the selected colicins for the project. The PCR, double digestion, and ligations were found to be very effective and produced positive results, however gel electrophoresis results suggested that the plasmid was not ligating to the inserted colicin genes but rather to a primer dimer.

The novelty of the project suggests that there need to be various trials and alterations made. There were a variety of variables throughout the experiment which made it difficult to isolate, which is why there was no growth was exhibited. Further experimentation is required to achieve more conclusive results.

(Supported by NSF: National Science Foundation)

Advisor: Robert Dorit, Biological Sciences

Research Method Development in Microscopy and Molecular Biology

Esther Kerns/2020

The foraminiferan is an amoeba that is characterized by the presence of a test and a pseudopodial network (1). Foraminifera have shells composed of CaCO3 or agglutinated particles (2) The tests often have multiple chambers that are often assembled in elaborate patterns (1).

Originally, I planned to image the pseudopods of the foraminifera using the Scanning Electron Microscope (SEM). A challenge that I encountered was finding alive foraminifera and getting them to stay attached during the cacodylate and glutaraldehyde washes to image the pseudopods on the SEM. Because of the difficulties surrounding the methods associated with imaging the pseudopods, I changed direction and used the SEM to image to characterize the test morphology of foraminifera seen commonly in lab. One of the challenges associated with this method was that the salt water crystalizes onto the test and obstructs the view of the test. I developed a procedure to wash the residual salt off the foraminifera prior to mounting that greatly improved the image quality.

Previously, the Katzlab has encountered a roadblock in isolating DNA from soil samples because foraminifera would not lyse in an old version of the lysis buffer. I planned and carried out an experiment to show that foraminifera lyse when exposed to the newer lysis buffer. Though PCR, and other procedures carried out by Chip Sission, foraminifera DNA was obtained from environmental samples. The particular samples obtained were destroyed in a freezer malfunction in lab. Despite this unfortunate incident, this research opens doors to more community research on foraminifera.

In addition, I worked with testate amoeba, single-celled organisms that are classified by the morphology of their tests and pseudopods (3). I worked to update various the protocols that will be used during the academic year. One of my most exciting accomplishments was a successful COX1 PCR on testate amoeba, a PCR that has not worked in many years.

During my research, I learned more about techniques for microscopy and molecular work. Throughout the summer, I gained competence in the laboratory techniques required for SEM, PCR, Sanger sequencing, WGAs, WTAs, and the BioAnalyzer. One of my additional focuses was to create resources to help those new to the lab learn laboratory practices faster. I developed various microscope manuals, comparison tables, and video tutorials in lab in order to assist those new to Katzlab.

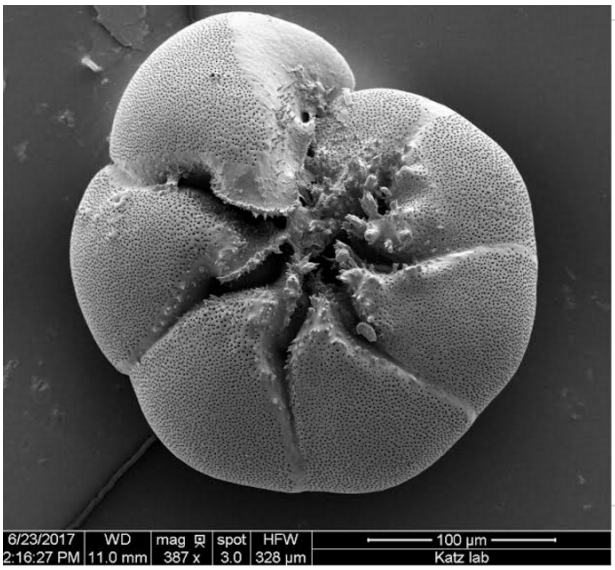
1. Pawlowski, et al. "Next-Generation Environmental Diversity Surveys of Foraminifera: Preparing the Future." The Biological Bulletin, The University of Chicago Press Journals, July 2014, www.journals.uchicago.edu/doi/full/10.1086/BBLv227n2p93.

2. Lipps, Jere R. "Test Structure in Foraminifera." Test Structure in Foraminifera | Annual Review of Microbiology, UC Davis Department of Geology, 1973, www.annualreviews.org/doi/pdf/10.1146/annurev.mi.27.100173.002351.

3. Kosakyan, Anush, et al. "Current and Future Perspectives on the Systematics, Taxonomy and Nomenclature of Testate Amoebae." Current and Future Perspectives on the Systematics, Taxonomy and Nomenclature of Testate Amoebae - ScienceDirect, www.sciencedirect.com/science/article/pii/S0932473916300013.

Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Laura Katz, Biological Sciences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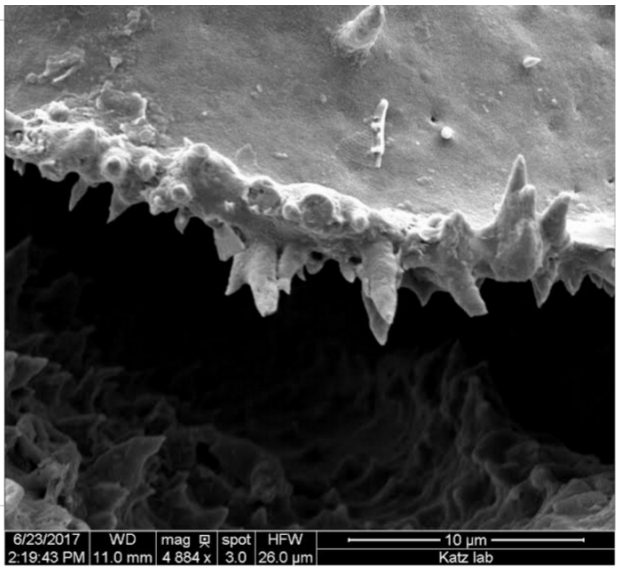
Katz lab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Katz lab

RpoS and Temperature Dependency in Biofilm Formation and Motility Assisting Genes in Uropathogenic Escherichia Coli

Salma Khan/2018

Uropathogenic (UPEC) strains of Escherichia coli are responsible for eighty percent of all urinary tract infections in women, single-handedly the most common kidney and urological disease in the world. UTIs are a major source of health care cost and morbidity within young non-pregnant women and UPEC's primary role in these infections has made it a significant topic within the medical research community.

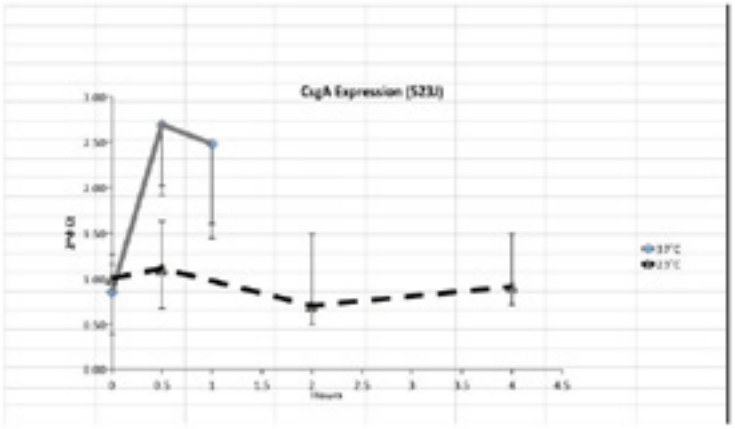
Virulence factors of UPEC allow it to successfully invade host tissues, infect their mucosal surface, and cause inflammatory responses within the host. Biofilm formation is held as one of the key pathological sources of UPEC's success as it enables the strains to endure for a lengthy period within the genitourinary tract and protect bacteria from host immune responses and antibiotics. Just as biofilm formation encourages and leads to infection through adhesion, motility driven by flagella is also a key pathogenic strategy of UPEC's success as it allows the bacterium to colonize other niches.

RpoS is a sigma stress factor protein that is responsible for the control and regulation of transcription in E. coli and is activated by different environmental conditions. Within previous studies in the CWZ lab of the nonpathogenic K-12 strain of E. coli, genes responsible for biofilm formation have been RpoS-dependent and the genetic expression of them have been influenced by temperature. In this study, use of wild type and ΔrpoS mutant strains of UPEC, grown in 23˚C and 37˚C, were completed to understand if RpoS plays a similar role in UPEC strains to sense and respond to temperature.

Through QT-PCR, the genetic expression levels of csgD, csgA, and fliC-- three genes involved in biofilm formation and motility, have been studied. The data shows that lower temperature of 23˚C in comparison to 37˚ C, increased csgA expression by an average of 2-fold in the UPEC strain regardless of presence of RpoS. For fliC, there were no differences in expression depending on temperature; expression levels of csgD also demonstrated no significant difference when temperature increased to 37˚C in the absence of RpoS. This result supports previous studies and indicates that gene expression of csgA is highest at low temperatures regardless of RpoS, which is responsible for curli formation and fibronectin binding, both critical for E. coli's capacity to produce biofilm adhesion. It is inconclusive whether or not fliC or csgD are RpoS and temperature dependent until the data is compared to the gene expression of the wild type UPEC strain, the next step of my study.

(Supported by NSF: National Science Foundation)

Advisor: Christine White-Ziegler, Biological Sciences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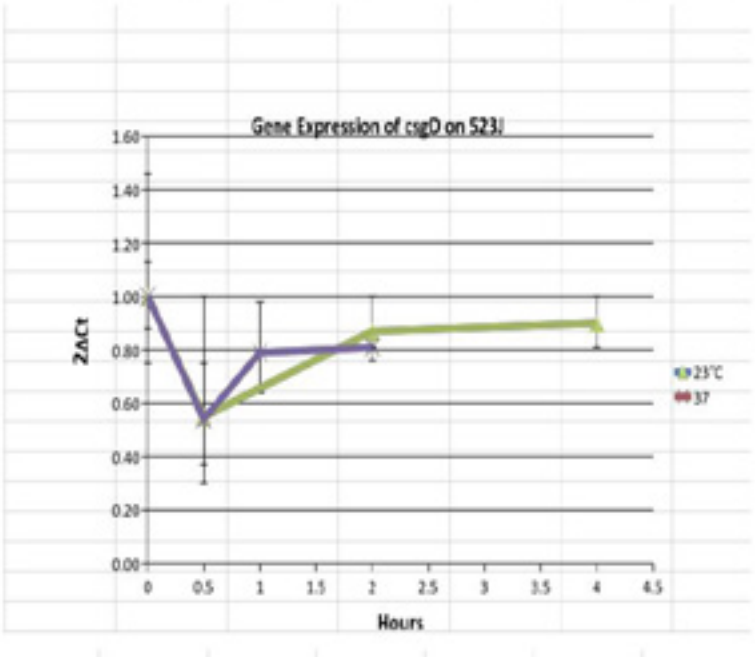
23°C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Hours
23°C
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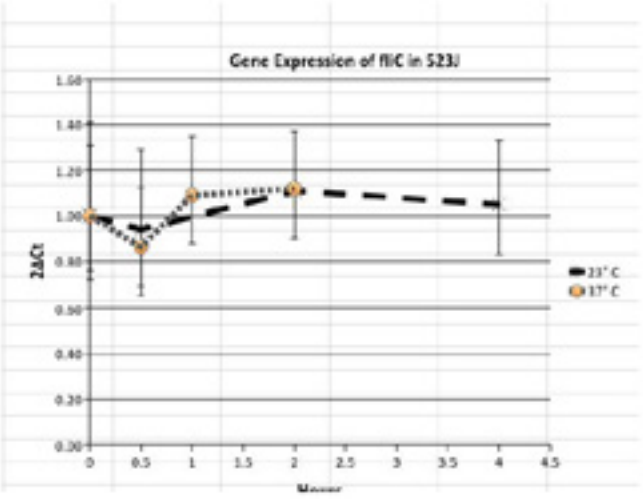

Gene Expression of flIC in 523J
2ΔCt
23° C
37° C

Just a "Wnt" of division: The role of Wnt5b in radial glial proliferation and differentiation during zebrafish spinal cord development

Julia Kim/2019, Carla Velez, Viviana Laines/2020, and Virtue Winter/2019

During embryonic development, the central nervous system is built through the precise balance of neural stem cell proliferation and differentiation. In vertebrate organisms, radial glial cells serve as the resident neural stem cell, giving rise to both neuronal and glial cell types. Secreted morphogenetic factors in the developing neural tube, like those of the wnt pathway, are known to play some of the most important regulatory roles in patterning the diversity of cell differentiation in the spinal cord. However, the complexity of morphogenetic signaling leaves much to be discovered, especially how such potent inducers of proliferation and differentiation are maintained at an appropriate balance for the careful construction of the spinal cord. Here, we are investigating the role of the non-canonical wnt5b signaling protein in radial glial development. We hypothesize that wnt5b protein functions to attenuate the canonical Wnt/β-catenin pathway, which serves to modulate radial glial proliferation. We used both genetic and pharmacological approaches to manipulate wnt5b signaling and the Wnt/β-catenin pathway. We show that loss and gain of wnt5b function results in the increase and decrease of proliferating radial glial cell numbers respectively. These data suggest that wnt5b normally functions to repress radial glial proliferation, which itself may be mediated through the attenuation of Wnt/β-catenin signaling. Ongoing experiments are designed to directly demonstrate that Wnt/β-catenin signaling has the capacity to promote either radial glial proliferation or differentiation depending on the amount of Wnt/β-catenin present, an amount that is in part kept in balance by wnt5b. Lastly, we are employing mathematical modeling of dual antagonistic Wnt secreted morphogens to ensure we are capturing the most critical parameters of Wnt-dependent radial glial development as well as to theoretically determine the most optimal amount of Wnt/β-catenin signaling needed for normal patterns of neuronal and glial differentiation in the spinal cord.

(Supported by NSF: National Science Foundation)

Advisor: Michael Baressi, Biological Sciences

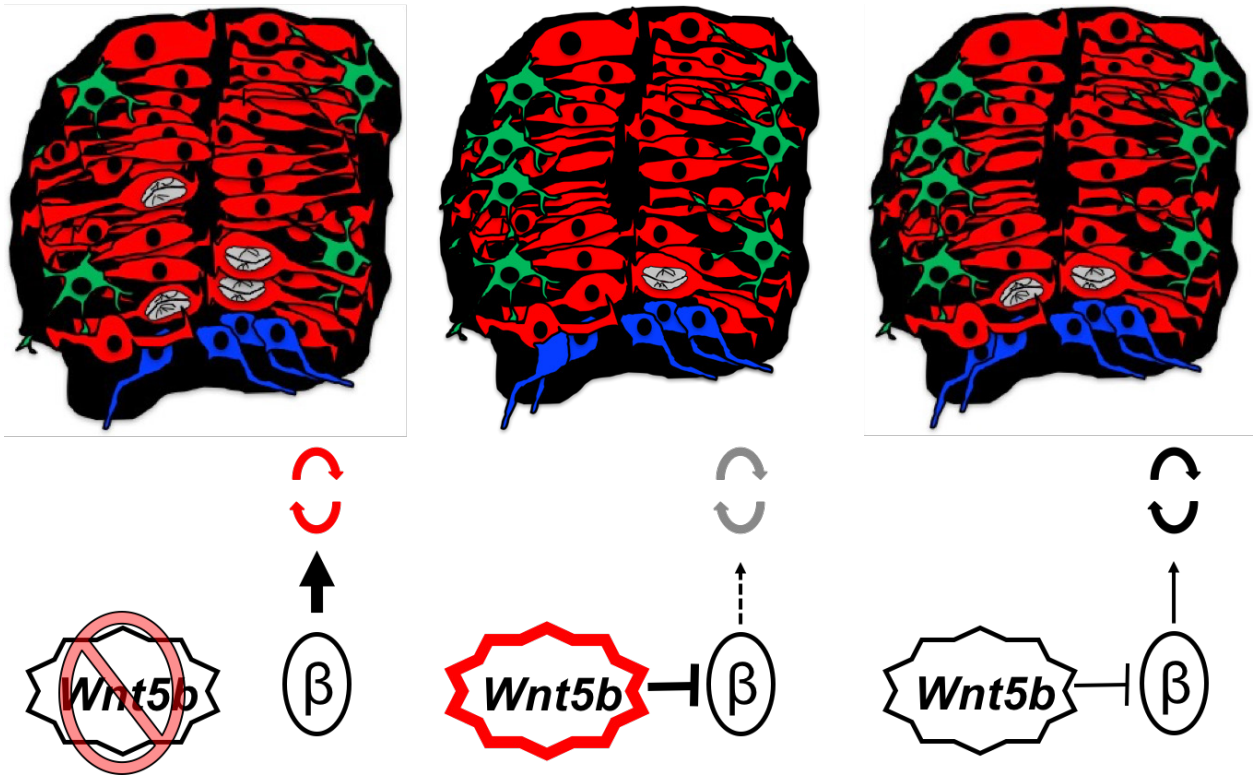


Figure 1. Hypothesized Interaction of Wnt5b and β-catenin**.** Upon loss of *wnt5b* function, the gene is not able to repress β-catenin, which goes on to promote too much proliferation of radial glia. Upon gain of *wnt5b* function, β-catenin is repressed too much and the number of divisions goes down. Taking these findings, we can conclude that *wnt5b* normally functions to repress β-catenin so that the right number of radial glial divisions take place.

Investigating the role of Slit/Robo protein signaling in the formation of the post optic commissure during zebrafish CNS development

Cassie Kemmler/2019 and Mackenzie Litz/2020

Neurodevelopment in the zebrafish is guided through a combination of axon guidance and neuronal cell movement. One key developmental point in neurodevelopment is commissure formation. This process occurs early on during neural development, and occurs when neurons send axonal projections to cross the midline of the nervous system to form structures composed of bundles of midline crossing axons, which are called commissures. The creation of the post optic commissure, the first commissure formed during development, involves the interaction of many cell types to signal these commissural axons to cross at the correct locations. Once such structure which is thought to mediate POC formation is a bridge of astroglia cells, which is thought to provide structural support and guidance for the commissural axons (Barresi et al. 2005). The development and condensation of the glial bridge and the correct crossing of the POC axons at the midline relies in part on functional expression of a family of repellant guidance proteins called Slits and their Robo receptors (Barresi et al. 2005; Rasband, Hardy, and Chien 2003). Slit and robo signaling is canonically defined as being repellant guidance signaling (Barresi et al. 2005; Brose et al. 1999; Long et al. 2004). The role of slit1a and robo4 in axon guidance however, which are expressed in the POC region, have been less well investigated. Our working hypothesis is that slit1a and robo4 have a contrasting function to the canonical repellant functions of slit and robo signals and serve as an attractant guidance cue for commissural axon midline crossing and promoting glial-axon contact.

We have also employed a new technique called parabiosis to investigate the role of slit1a as a chemoattractant guidance cue. Parabiosis, the creation of conjoined embryos, has been utilized in the zebrafish model system to study hematopoietic cell migration between conjoined embryonic bloodstreams (Demy et al. 2013). This new experimental approach allows for the in vivo analysis of cell migration following surgical blastula fusion of embryos of differing genetic backgrounds or transgenic lines. Our tg(gfap:cherry-caax) and tg(gfap:gfp-caax) transgenic embryos were successfully conjoined at the forebrain allowing for the visualization of the migration of green and red fluorescently labeled glial cells into the opposite transgenic embryonic diencephalon (Figure 1). In the future, this technique will be used to determine if the axons of one embryo are attracted to the overexpression of slit1a in its conjoined parabiotic embryo.

(Supported by NSF: National Science Foundation)

Advisor: Michael Baressi, Biological Sciences

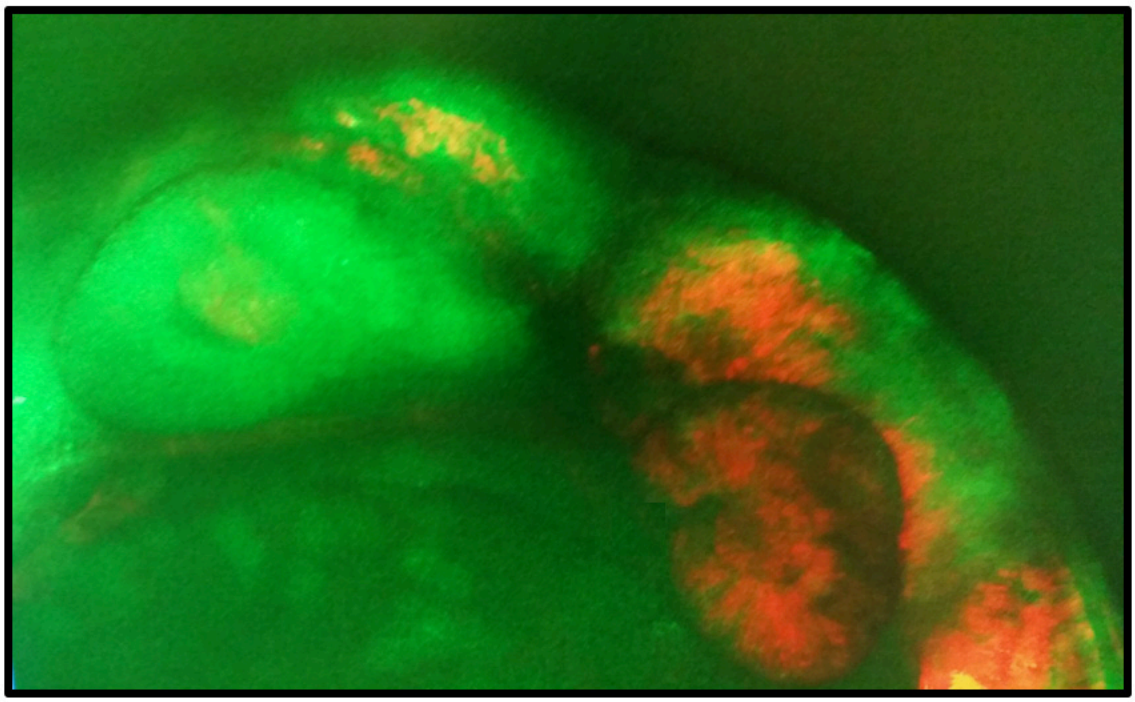


Figure 1: Conjoined tg(*afap:cherry-caax*) and tg(*afap:gfp-caax*) zebrafish forebrains showing the migration of transgenic fluorescent glial cells between the embryonic diencephalon.

Investigating the Use of Drones to Study the Grey Seal

Anastasia Konefal/2017

The Grey Seal, Halichoerus gypus, is endemic to the North Atlantic and is found throughout the year on Cape Cod. Protected population size of seals is large, averaging between six and eight meters long for adults. They reproduce late in life with a gestation period of eleven months; thus, they are very vulnerable to population crashes.

Actively monitoring these populations is one way to predict and prevent these population crashes. However, the only way to obtain weight and other morphometric data of these seals is to enter the colony and interact with the seals directly, which is invasive and creates stress for the seals. Photographs would be a time-efficient, non-invasive way to study these animals. Past work has shown that photographs taken with a handheld camera has proven ineffective, leading us to the possibility of drone photography.

The first step was to ground truth to see how a seal would look from a drone at different altitudes. While I couldn't do this on an actual seal, I used a stuffed tiger that was approximately 1 meter in length. I flew a drone overhead at an altitude of 25 meters. The tiger was then measured in Image J to use as a caliber for other images. I obtained an image taken by Beth Josephson at NOAA of a seal colony on Cape Cod also taken at 25 meters. I used the known length of 1 meter of the tiger to measure the length of the seals in the NOAA image.

Results showed that Image J was not accurate in calculating length of grey seals even with an accurate measurement of the stuffed animal. However, the average length the seals calculated in image J was 130 m for adults and 60 m for the pups, which is clearly inaccurate.

In addition to taking single aerial images of the stuffed animal, the drone also performed an orbit around the animal and took pictures throughout the orbit. These images were used to create a 3-D model of the tiger to calculate weight of the animal. Results from this test were inconclusive, as the volumes calculated were inaccurate, but time constraints prevented me from investigating these discrepancies.

This was an important first step to finding a new way to study seals and other marine mammals, even if results were inconclusive. After working with the orbit feature on the drone, I do not think that this would be a feasible way to study seals. While it is better than entering the seal colony, it is still time-consuming and requires the seal to be still in order to obtain the images which can be nearly impossible. A next possible step in this research would be to use a thermal camera to sense the heat of a seal and from that obtain weight.

(Supported by Strickler Environmental Science and Policy Student Research Fund)

Advisor: Paulette Peckol, Biological Sciences

Design and Optimization of a q-PCR Assay for the Detection of Ross River Virus

Rebecca Kuzma/2018

Ross River virus (RRV) is the most common mosquito-borne disease of humans in Australia, with approximately 5,000 infections yearly. Symptoms of RRV infection include fever, fatigue, and debilitating polyarthritis. RRV is transmitted by a broad range of mosquito vectors, with laboratory transmission confirmed in at least ten species of Aedes and Culex mosquitos. In the absence of comprehensive diagnostic facilities, RRV was believed to be maintained in zoonotic cycles of transmission involving macropod marsupials. The 1979-80 outbreak of RRV infection in the Pacific and the availability of comprehensive diagnostic facilities in Australia, provided strong evidence for cycles of human-mosquito-human transmission without a requirement for intermediate vertebrate hosts. The re-appearance of RRV transmission in Fiji and the large human population born since the 1979-80 outbreak (and so susceptible to RRV infection) highlights the need for a sensitive and specific surveillance system able to detect future outbreaks of RRV infection in this region. To this end, we have designed and optimized a quantitative polymerase chain reaction (q-PCR) assay for the detection of RRV. Preliminary data shows that this assay specifically detects RRV at high sensitivity and differentiates RRV from other alphaviruses, including the genetically similar Getah virus. These results support the use of our assay for the detection of RRV at low viral concentrations in mosquito vectors through the use of our molecular xenomonitoring platform. The next steps include testing the assay in lab-infected mosquitos and wild mosquito populations from endemic regions.

(Supported by NSF: National Science Foundation)

Advisor: Steven Williams, Biological Sciences

The Role of Wnt5b in Radial Glial Proliferation and Differentiation During Zebrafish Spinal Cord Development

Viviana Laines/2020, Julia Kim/2019, Virtue Winter/2019, and Carla Velez

Radial glial cells play an important role during neurogenesis. These cells are capable of differentiating and proliferating, producing various cells that are essential to development of the central nervous system, due to the various signals and transcriptional networks that encompass the nervous system along the anterior-posterior and dorsal-ventral axis. One of the two major gradients that guide the formation of the spinal cord is the Fgf/Wnt gradient. Wnts are a family of signaling proteins that play a role in development and cell proliferation. Wnt has two pathways: the canonical Wnt/B-catenin pathway and the non-cannonical B-catenin independent pathway.

This project investigates the role that non-canonical Wnt5b signaling protein plays in radial glial development in zebrafish. It is hypothesized that Wnt5b talks with the canonical Wnt/B-catenin pathway to negatively repress B-catenin. To test this hypothesis, a series of loss and gain of function of Wnt5b and manipulated B-catenin agonist and antagonist experiments were done. The gain of function of Wnt5b experiment consisted of collecting the embryos, heatshocking transgenic embryos at 10 hpf to try and increase the expression of Wnt5b. From there, the embryos were dechlorinated, fixed, dissected, genotyped, blocked, cryosectioned, immune, imaged, and counted. The loss of function experiment's main goal was to identify the homozygous wild types and homozygous mutant types from the PCR gel in genotyping so that the effects of loss of Wnt5b could be studied. The gain of function and loss of function experiments are nearly similar, except for heatshocking which only were done to the transgenics. The drug treatments consisted of using BIO, IWR, and DMSO to see the effect that B-catenin agonist and B-catenin antagonist would have on the embryo. The results showed that loss of Wnt5b lead to a decrease in differentiated cells and an increase in dividing cells while the gain of Wnt5b lead to an increase in differentiated cells and decrease in dividing cells. This data shows that Wnt5b regulates the division and differentiation of radial glial being that when Wnt5b was either loss or gain, it affected the number of dividing cells. Through the manipulation of B-catenin, similar results were found that related to the loss and gain of Wnt5b. In the future, more research will be done on earlier time points to get a clearer picture on embryo development. More experiments will be done to understand the relationship between wnt5b and B-catenin where both will be manipulated.

(Supported by NSF: National Science Foundation)

Advisor: Michael Baressi, Biological Sciences

The Role of Reelin Signaling in Neurogenic Development of the Spinal Cord

Wiktoria Leks/2019

Reelin is a large secreted glycoprotein, crucial for directing cell migration in the developing brain through the establishment of cortical cellular layers and synaptic activity. Reelin performs intracellular signaling with neuron and glia cells by binding to two lipoprotein receptors, either Apolipoprotein-E receptor 2 (ApoER2), or Very low density lipoprotein receptor (Vldlr), which as a result activates the intracellular adaptor Disabled 1 (Dab1) by tyrosine phosphorylation1. Activated Dab1 receives cues from the environment to regulate neurite growth cone extensions, cortical neuronal migration, cell fate specification and radial glial morphology.

The majority of research about Reelin focuses on cell migration with still images of the brain. However, little investigation has been done on the role of Reelin in conjunction with Reelin's receptors, ApoER2 and Vldlr, which may affect cell differentiation of various cell types or radial glia and neuronal proliferation in spinal cord development. The zebrafish spinal cord is a simple model to study neural development due to a limited number of neuron and glia cell type. We are currently using CRISPR/CAS9 technology to generate mutations in the genomic loci of zebrafish for Reelin, ApoER2, Vldlr and Dab1 to create a total loss of function approach. The CRISPR/CAS9 system induces double stranded breaks in an assigned location of the DNA, leading to an ideally unsuccessful repair process known as non homologous end joining. However, it takes time for CRISPR injected embryos to mature, create progenitor lines, and future generations which would then carry the homozygous recessive induced mutation.

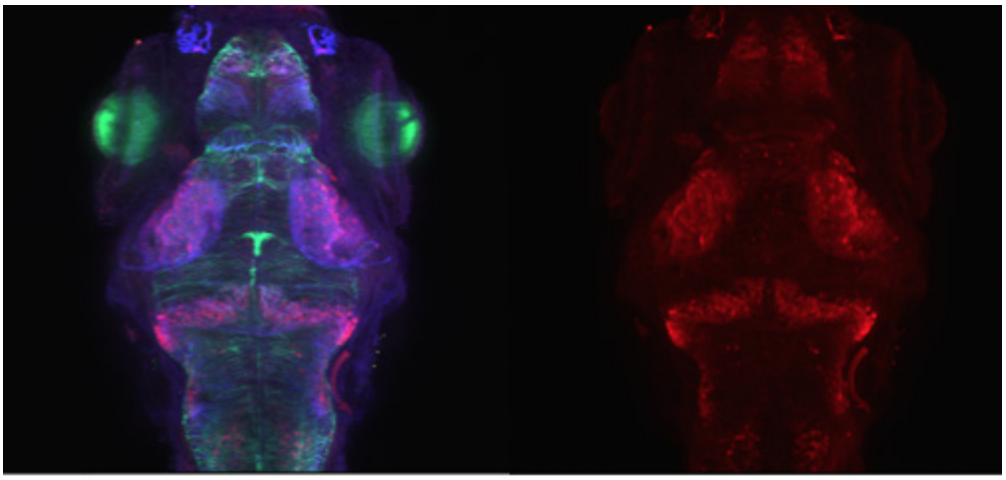
Progress was made in establishing viable CRISPR injected fish that are heterozygous for the ApoER2 gene mutation and their G2 in-crossed progeny are growing up on the zebrafish system, where a quarter of the offspring is expected to have the complete knockout mutation, which will then be further characterized via immunohistochemistry (with regards to an apoer2 and Reelin antibody), as well as in situ expression analysis. A new Reelin in situ probe was also designed to examine Reelin expression in fixed time stages of 24,48, 72hpf wild type fish. Immunohistochemistries were preformed on 24hpf 17bpd Reelin identified Mutants staining for GABAergic expression and compared against wild type data, but still need to be quantified.

Figure 1: GABAergic expression (red staining) of 24hpf 17bpd Reelin genotyped mutant. Radial glia stained in green and acetylated tubulin in blue.

1. Gabriella D'Arcangelo (2014). Reelin in the Years: Controlling Neuronal Migration and Maturation in the Mammalian Brain. Advances in Neuroscience.

(Supported by Nancy Kay Holmes Memorial Fund)

Advisor: Michael Baressi, Biological Sciences



Elucidating the Role of Slit1a in the Zebrafish Forebrain

Mackenzie Litz/2020

The nervous systems of bilaterally symmetric organisms require communication pathways between the two halves of the brain in order to function. These pathways are called commissures, which are formed by midline crossing axons which connect the two hemispheres of the brain. Commissure formation is a critical step in nervous system development, and is therefore highly conserved across organisms, and its development is highly stereotypical. Probing axon guidance in the context of commissure therefore allows for detailed and repeatable study of the molecular mechanisms of axon guidance. Proper commissure formation is achieved by the dynamic interaction of multiple signaling pathways. These pathways work together to stimulate midline crossing while also spatially restricting axon growth to ensure that midline crossing axons reach their targets on the contralateral side. One set of critical guidance cues which spatially restrict axon growth is the Slit-Robo guidance pathway, composed of Slit1a/2/3 secreted growth cues, and their Robo receptors Robo1-4. Our goal is to utilize the highly tractable zebrafish model organism to understand how the Slit-Robo guidance system mediates axon guidance. This summer I specifically focused on elucidating the role of Slit1a in POC formation and axon guidance.

One method to better understand the effect of slit1a on POC development is to eliminate the protein's function by generating mutations in the coding region of its associated gene, and observing the embryo's phenotype. A Barresi lab member, Vivian Morris, previously injected wild type embryos with CRISPR-Cas9 and guide RNA targeting the slit1a gene. The CRISPR-Cas9 system acts as a specific molecular scissor, cutting a specified region within the slit1a gene. Once cut, the cell's repair mechanisms attempt to repair the cut DNA, often leaving errors that disrupt protein function. This summer I genotyped the fish grown up from the injected wild type embryos, searching for the perfect mutation. With the help of sequencing technology and our grad student mentor Jake Schnabl, we were able to identify several slit1a mutant fish. In the following semesters we will use these mutant embryos and perform immunocytochemistry and laser confocal microscopy to analyze the effect of a loss of function of slit1a on POC development.

In combination with parabiosis experiments (please see Cassie Kemmler's abstract) and other work being done in lab, we intend to uncover the precise role of slit1a in POC axon guidance.

(Supported by NSF: National Science Foundation)

Advisor: Michael Baressi, Biological Sciences

Sourcing and Propagation Methods for Neurolaena lobata for Extraction and Analysis of Antiparasitic Compounds

Samara Loewenstein/2018

For several years, the SAW and Shea Laboratories at Smith College have been testing Neurolaena lobata for its use as a treatment for lymphatic filariasis. Drug resistance to current anti-parasitic medications is a major concern today. In laboratory trials parasites have shown vulnerability to neurolenin, a secondary metabolite that can be isolated from the leaves. There has been little research conducted on the concentration in fresh leaves and the role provenance plays in the concentration of neurolenins. The aim of this project was to obtain a reliable source of seed to propagate at Smith College as well as leaf material with its associated provenance information. This project also gave me the opportunity to work in the SAW Lab extracting parasitic DNA from human stool samples for future assays.

Provenance factors such as the micronutrients present in the soil have a profound effect on the concentration of secondary metabolites. Unfortunately provenance information was hard to come by. Seeds were obtained from two sources; one from Costa Rica and the other from Belize, as well as a leaf source from Belize. A wet paper towel germination test as well as direct propagation in a peat-based seed starter was performed. The seeds from Costa Rica had a germination rate of 0.02%. The results from the Belize seeds are not available yet. However upon microscopic examination the seeds from Costa Rica weren't viable (no embryo was present) while the seeds from Belize were fertile (endosperm present).

My conclusion is that it is not feasible to grow N. lobata at Smith College. The college does not have adequate space, staff, or systems to make this a viable endeavor. Even if the college could secure a plot of land outside there is no literature available about the survivability of the seed in cold weather. Therefore this plant has the possibility of becoming an invasive species. The most practical solutions are to secure a source of leaf through Index Seminum, enter into a relationship with a company that sells leaf material, and/or use cell cultures to manufacture the secondary metabolites present in N. lobata. I plan on continuing to monitor my plants at the Botanic Garden and to act as a liaison between the Botanic Garden and the SAW and Shea Laboratories. I have also created a dossier including sources, contacts, and notes to future researchers which will be distributed to both laboratories and the Botanic Garden.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Gaby Immerman, Biological Sciences

Costa Rican seed: no embryo present

Belize seed: endosperm present

Seasonal photosynthetic response of various deciduous species post-clearcut

Madeleine Meadows-McDonnell/2018

New England has a long history of land use change, particularly in the disturbance and recovery of forests. As agriculture moved west with settlements, New England was converted from a mostly agricultural region into a mostly forested region. These land use changes cause changes in the environment. Increased concentration of CO2 in the atmosphere has also increased global environmental change. Forests are a crucial part of the carbon cycle due to the photosynthetic, and therefore carbon storage, capacity of plants. This study delves into the effect of various environmental factors, such as water and nitrogen availability and climate, on the photosynthetic capacities of dominant plant species after a commercial clear-cut disturbance. Based on the curve analysis for each species, there were no significant differences between the two clearcut sites in Harvard Forest. Hayscented fern had a lower rate of carbon assimilation than the rest of the dominant species. All of the species had similar rates of cellular respiration. This study will be continued with assessment of how the environment factors such as water and nitrogen availability can impact the rates of photosynthesis.

(Supported by B. Elizabeth Horner Fund)

Advisor: Danielle Ignace, Biological Sciences

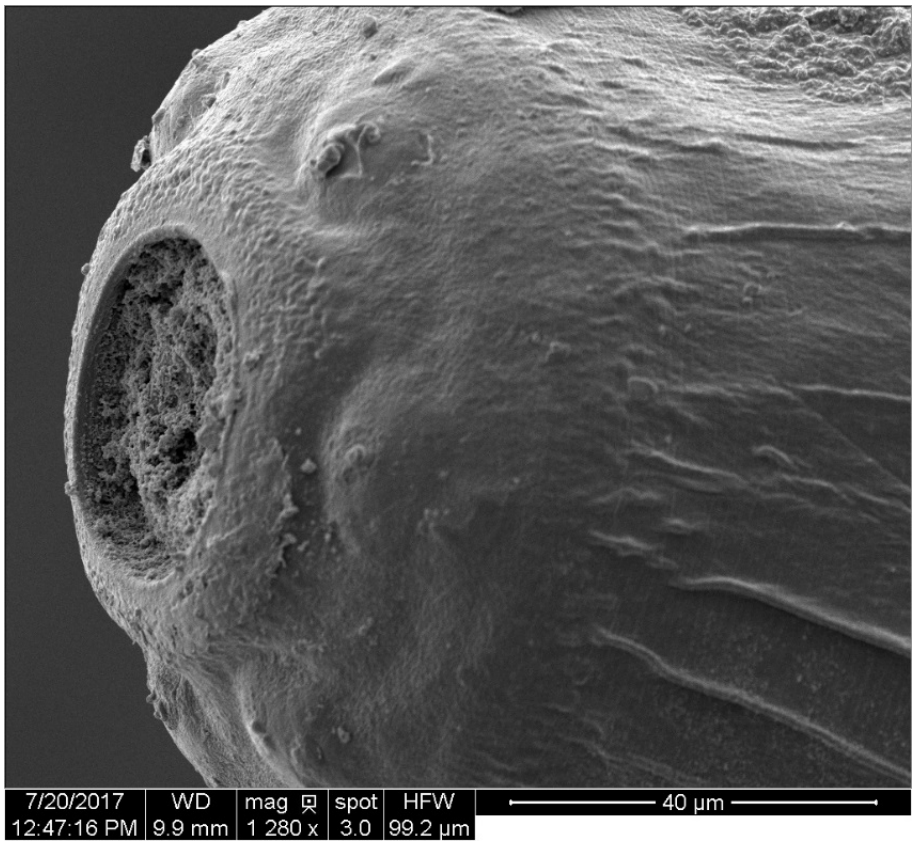
Using Microscopy Techniques to Morphologically Catalog West Coast Parasites that Infect Seals

Hafsa Mire/2019

The sea lion crisis in 2013 led to an outbreak of the lungworm Otostrongylus circumlitus resulting in the endangerment of northern elephant seals. Typically, Otostrongylus circumlitus is a parasite found in harbor seals. However, the overlapping habitats of the harbor seals and northern elephant seals introduced the latter as an intermediate host of the parasite, preying on fish infested with worm larvae capable of infecting mammals upon ingestion. Harbor seals have already developed immunity to the lungworms, but northern elephant seals were at a greater disadvantage upon infection of the previously unencountered parasites. As a result, Otostrongylus circumlitus has been blamed for wreaking havoc within the unsuspecting heart and pulmonary arteries of elephant seals, leading to problematic blood clots with the potential for sudden cardiac arrest. However, since seals often suffer from multiple parasite infections it is difficult to pinpoint exactly which species of parasite holds responsibility as the cause of death. The objective of this summer research was to investigate the various parasite samples that were collected from both harbor and elephant seals on the coast of California. Using the techniques associated with both light and electron microscopy, images of the posterior and anterior ends of each parasite sample from a single host were collected to determine if there were multiple species of parasites in one host. When genetic identification was unable to differentiate between two major species, Otostrongylus circumlitus and Anasakis pegreffii, morphological identification became a necessary tool in effectively identifying which species of parasite infected either harbor or elephant seals. The combination of both light microscopy and scanning electron microscopy images was able to shed light on prominent features, such as the presence of bursa with finger-like rays at the posterior end, and an oral capsule at anterior portion in Otostrongylus circumlitus parasites visibly distinguishable between both Otostrongylus circumlitus and Anasakis pegreffii.

(Supported by NSF: National Science Foundation)

Advisor: Steven Williams, Biological Sciences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The Role of Slit 1A In the Development of Zebrafish Forebrains

Vivian Morris/2018

During embryonic brain development, neurons extend their axons in order to make necessary connections with other neurons. To allow for communication between the left and right hemispheres of the brain, these neurons form commissures, or tight bundles of axons that cross the midline of the brain over a substrate of astroglia cells. At the midline, axons are guided in part by Slits, extracellular signaling molecules, and Roundabout receptors. Preliminary research in the Barresi lab has suggested a previously uncharacterized role for Slit1a to promote interaction between axons and astroglia cells by positively directing axon growth. This is contrary to Slit2 and Slit3, which are known to act as repellants and prevent axons from wandering into regions of the brain they are not intended occupy.

Using zebrafish as our model, one goal is to determine how the Slit1a guidance cue promotes the Post-optic commissure formation in the developing zebrafish forebrain. We will investigate this role by using zebrafish containing genetic knockdowns of Slit (1a, 2, and 3) and Roundabout (Robo1, 2, 3, and 4) to help us examine how the developing forebrain responds to global and regional loss or gain of functions of these signaling proteins and receptors. Further, we aim to determine which Robo receptor (Robo1, 2, 3, or 4) mediates the different respective Slit functions. We hypothesize that one or more of the Robo receptors mediate the positive guidance cues of Slit1a.

Research on Slit-Roundabout signaling not only expands scientific understanding of nerve pathways during embryonic development, but also has direct implications for neural regeneration. By understanding the genetic and molecular mechanisms behind these processes, we could direct important axon growth after serious injuries sustained to the nervous system.

(Supported by SURF Gifts Fund)

Advisor: Michael Baressi, Biological Sciences

Using Oxford Nanopore MINion for bacterial 16S rRNA gene diversity in soil

Yi Ning/2018

The 16S rRNA gene is used for phylogenetic studies as it is highly conserved between different species of bacteria and archaea, yet contains hypervariable regions that include species-specific sequences. The 16S rRNA gene is often used in identifying microbial diversity in soils. The 16S rRNA gene sequencing enabled researchers to shift away from cultivation-based methods and made possible to obtain information about bacteria that are unsuitable for cultivation.

Before the invention of next-generation sequencing technologies, researchers used clone-based Sanger sequencing of the 16S rRNA gene to sequence fewer than 100 16S rRNA gene sequences. Although the switch to next-generation sequencing platform has enabled researchers to identify many more gene sequences in one run, it has also restricted the screened sequence length to a maximum of around 230 bp, about the same length as a single 16S rRNA gene hypervariable (V) region. (Vasileiadis et al., 2012) This severely constrained researcher's ability to identify bacterial diversity, because taxonomy information is lost in trimmed sequences as compared to their full-length version.

New advances in single molecule sequencing technologies enable longer read with higher throughput. Specifically, the Oxford Nanopore MinION device uses nanopores to produce high-throughput sequencing read at a maximum length of 150 kb, a significant length improvement from Illumina Miseq. Therefore, near-full length 16S rRNA gene region fragments using the Oxford Nanopore MinION sequencing platform could theoretically be achieved. The present study aims to use Oxford Nanopore MINion device for massive parallel screening of bacterial 16S rRNA gene diversity in the soil environment.

Pure culture E. coli (K-12) was analyzed using the Oxford Nanopore MinION device as a proof of concept. Next, a sample of high aridity non-agricultural soil was analyzed. Since both closed and open operational taxonomic unit (OTU) picking failed, the Ribosomal Database Project classifier was used to order phylogenetical alignments of ribosomal RNA (rRNA) sequences.

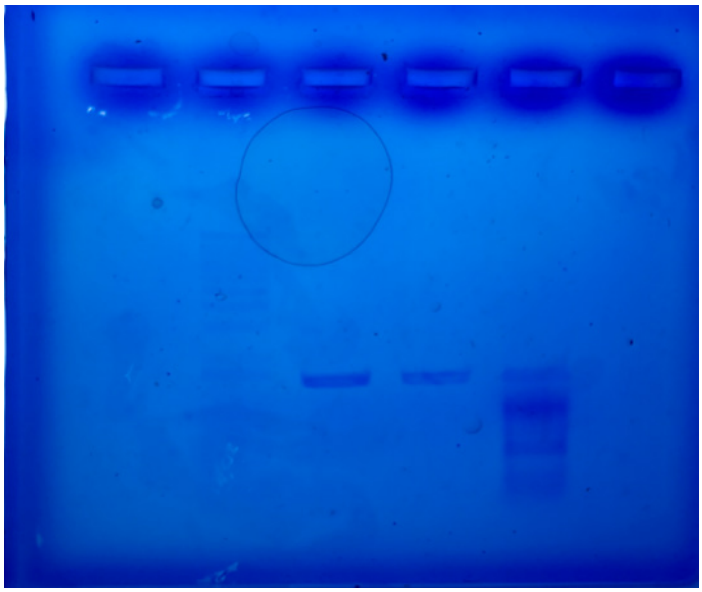
Figure 1. Visualizing PCR product of 16S amplicon. Lane 2 and 5: Molecular weight marker. Lane 3 and 4: PCR product of sample 1 and 2 respectively. The arrow points at the 1600bp marker.

Reference:

Vasileiadis, S., Puglisi, E., Arena, M., Cappa, F., Cocconcelli, P.S., and Trevisan, M. (2012). Soil Bacterial Diversity Screening Using Single 16S rRNA Gene V Regions Coupled with Multi-Million Read Generating Sequencing Technologies. PLoS ONE 7.

(Supported by Blakeslee Fund)

Advisor: Robert Dorit, Biological Sciences



The use of Transmission Electron Microscopy (TEM) to Study the Connection between Glia and Axons in the Post Optic Commissure of the Zebrafish Embryo.

Anja Nordstrom/2018

The neural patterning that occurs in early development is key to the functioning of an organism in the long run. Neurons send projections known as axons to target cells in order to form synapses. The first instance of axons crossing the midline occurs in the formation of the Postoptic Commissure (POC) and the Anterior Commissure, which form in the forebrain (Barresi, 2005). It is known that astroglia cross the midline of the forebrain before the axons cross. These glia form a bridge to support the axons crossing the midline (Barresi, 2005). Fluorescence imaging shows a large amount of axons in contact with glia, but the specific connections cannot be resolved at the light microscope level. The goal of this project was to use Transmission Electron Microscopy (TEM) to determine the types of connections between neurons and astroglia at the POC.

To this end, zebrafish embryos were fixed at 29 hpf and dehydrated, then embedded in Epon 812 resin. Thick sections (1 μm) of these resin blocks were gathered using an Ultratome V. These sections were stained using 1% toluidine blue in 1% borax and imaged using bright field microscopy to better understand the anatomy of the zebrafish brain and locate the area of interest (POC). Once the POC was located, thin sections (60-90 nm) were obtained and observed using the TEM. The POC was located based on anatomical markers determined from thick sections.

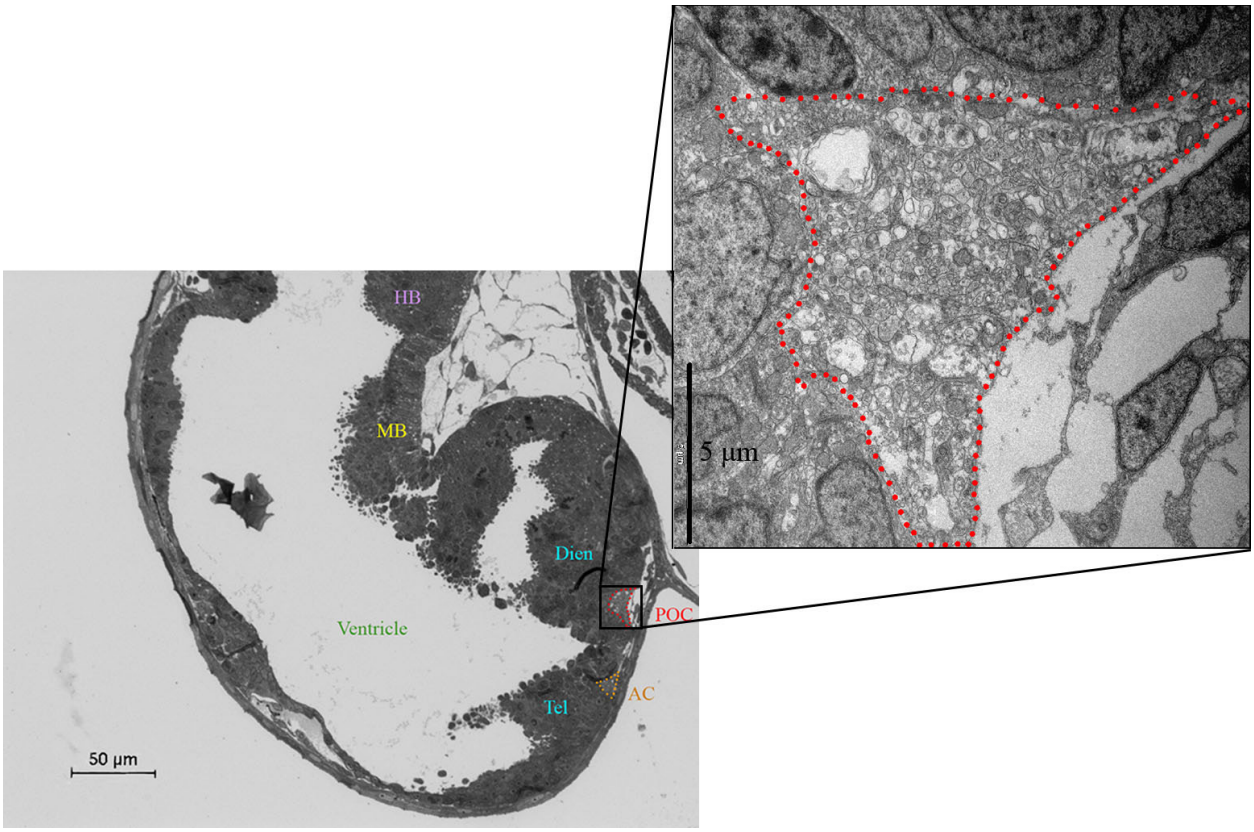
The TEM images show glia in contact with the neurons, but the exact way in which they are in contact is not entirely clear. In future research we plan to label astroglia using immunogold labeling. Once the glia can be distinguished from commissural axons the connection can be studied and documented.

Barresi MJF, Hutson LD, Chien C-B, Karlstrom RO (2005) Hedgehog regulated Slit expression determines commissure and glial cell position in the zebrafish forebrain. Development Available at: http://dev.biologists.org/content/132/16/3643 [Accessed August 2, 2017].

Figure 1. On the left, brightfield micrographs of a sagittal sections of the zebrafish brain at the midline, on the right, a Transmission Electron micrograph of the same region of the POC. The POC is outlined in red in both images. Anterior Commissure; AC, Diencephalon; Dien, Hindbrain; HB, Midbrain; MB, Postoptic Commissure; POC, Telencephalon; Tel, Ventricle.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Judith Wopereis, Biological Sciences


HB
MB
Dien
POC
Ventricle
AC
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50 µm
5 µm

Genome Architecture of Arcellinid Testate Amoebae

(Emma) Gabrielle Östlund-Sholars/2019J

Arcellinid testate amoebae are eukaryotic unicellular microorganisms that fall within the taxonomic group Amoebozoa. Their main synapomorphies are their lobopodia (lobose pseudopodia) and self-secreted organic, proteinaceous, siliceous, chitinous, calcareous, or agglutinated tests. Arcellinida are known to serve as good palaeoenvironmental bioindicators [1], and top predators in threatened wetland habitats such as bogs and fens. Their morphological variability is considered to reflect responsiveness to environmental factors such as pH, percent moisture, depth of living moss and depth to water table. Recent studies [2] suggest that the biodiversity among microorganisms has been vastly underappreciated; grouping species by phenotype alone proves insufficient in fully capturing the discordances found between phenotypes and genotypes.

Studying the genomic architecture of Arcellinid testate amoebae required a combination of microscopy and molecular tools. UV imaging using the confocal laser scanning microscope was done to gain further insight into the nucleic structure of Arcellinid taxa by fixing the cells in paraformaldehyde and staining them with 4',6-diamidino-2-phenylindole (DAPI), which binds to A-T rich regions in nuclear DNA. To resolve the genomic structure of Lesquereusia spiralis, I first performed whole genome amplifications and whole transcriptome amplifications (protein coding genes) of the cells, and then used a PCR based approach that focused on three genes (Actin, small ribosomal subunit, and cytochrome oxidase c subunit I) to analyze protein evolution. I intend on interpreting the resulting data in a molecular evolution framework this fall as I continue my research as a McKinley Honors Fellow.

The Katz Lab is currently underway with rebuilding its phylogenomic pipeline3 to resolve the eukaryotic tree of life. This summer, I familiarized myself with bioinformatics via running biopython scripts that assemble post-transcriptome high-throughput sequencing data generated in lab.Gaining further knowledge about the phylogenies of Arcellinid taxa will contribute to the appreciation of biodiversity at large and further the understanding of the causes driving morphology-lineage discordances.

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2. Lahr, D. J., Laughinghouse, H. D., Oliverio, A. M., Gao, F., & Katz, L. A. (2014). How discordant morphological and molecular evolution among microorganisms can revise our notions of biodiversity on Earth. BioEssays, 36(10), 950-959.

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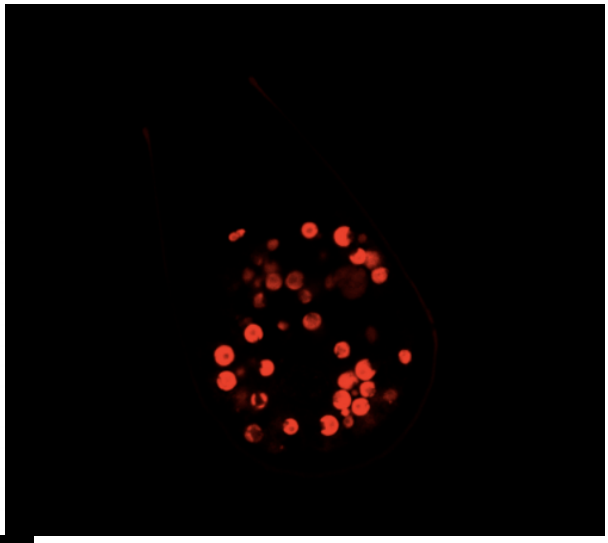
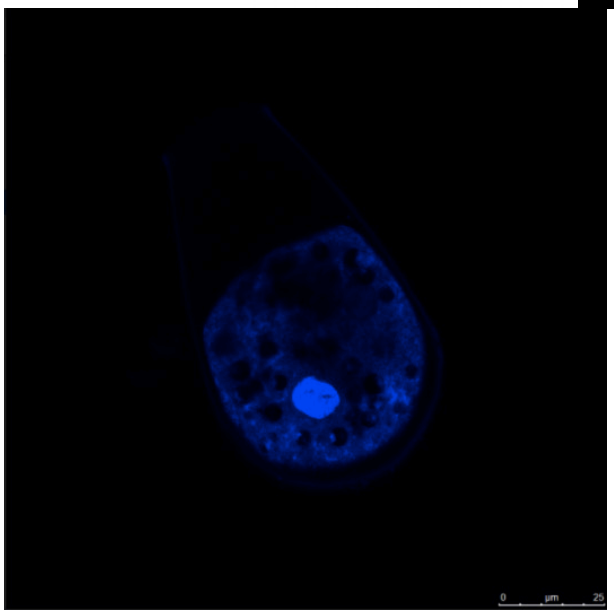
Hyalosphenia papilio captured with the Confocal Laser Scanning Microscope at different excitation wavelengths.

Left to right: UV Diode 405 nm/DAPI staining of nuclear DNA, HeNe 633 nm/Autofluorescent algae, Brightfield.

(Supported by NSF: National Science Foundation)

Advisor: Laura Katz, Biological Sciences





Atata Coral Reef Assessment: A Diversity Survey

Hayley Reifeiss/2018 and Emiline Koopman/2018J

Coral reefs are intrinsically, socially, culturally, environmentally, and economically valuable. Reefs provide shore protection, water filtration and support the pelagic food web (Moberg & Folke 1999). In addition, they are hot spots for biodiversity enhancing the diversity of the entire ocean (Plaisance et al. 2011). This makes them sources for fisheries and a desirable part of the tourist industry. However, they are highly susceptible to changing abiotic and biotic factors in the environment which leaves at risk on both the local and global scale. In order to better understand the threats that coral reefs face as well as their impacts it is essential to assess coral reef health. One indicator of reef health is coral diversity. Our study seeks to assess the diversity of the Atata reef in Tonga in order to better understand its condition and establish a diversity baseline. Small Island Developing States (SIDS), such as Tonga, are particularly vulnerable to climate change factors such as weather variability and sea level rise (Mead et al. 2015). While it is known that the Pacific Island nation of Tonga faces similar problems as the rest of the Pacific in terms of coral reef decline, few studies focus specifically on this island. Furthermore, although decline in reef cover has been highly documented worldwide (Pandolfi et al. 2003) and in the Pacific (Bruno & Selig 2007), research that focuses solely on the size of reefs does not provide a holistic picture of reef resilience and health. Therefore, obtaining baseline data showing which reef species are present and the levels of reef diversity are highly important to predicting the trajectory of reef communities.

This data was obtained using 1m2 photo quadrats on 50m transects established parallel to the shore approximately 10m from the reef edge. Twenty-five points were randomly overlaid on the photos and coded for using the program Coral Point Count. Through the examination of 194 photo quadrats a data set of 4,850 points was produced from which the percent composition of the transects was calculated. The Atata reef was found to be comprised of 2.20% Acropora cytherea, 10.40% Acropora micropthalma, 6.52% Acropora aspera, 0.77% Acropora gemmifera, 34.23% Acropora globiceps, 1.01% Astreopora gracilis, 0.74% Isopora crateriformis, 0.11% Leptoseris incrustans, 0.03% Millipora sp. and 0.34% Isopora cuneata (figure one). Furthermore it was found that 22.27% of coral were dead and another 13.63% were dead and covered in algae (figure one). Of those corals present, 12.60% showed signs of bleaching.

This relatively poor species richness coupled with an uneven abundance across species produced low diversity indices of 1.26 (Shannon Index) and 0.58 (Simpson Index). Due to this low diversity, we predict Atata Reef to be highly susceptible to future disturbances. Locally, this includes the overfishing of herbivorous fish, the use of damaging fishing practices such with trawl or gill nets, physical damage to the reef from boats, anchors, moorings, and swimmers, increased sedimentation and toxic runoff from additional development, or a loss of nearby nursery habitats such as eelgrass beds and mangroves. Globally, Atata Reef is threatened by climate related factors such as sea level rise, increased ocean warming, ocean acidification, and an increase in the frequency and intensity of storms. While localized management strategies will not be able to combat these global threats, reducing local anthropogenic stressors to the reef will allow the coral to better cope with climate related changes (Smith et al 2016).

While this study provides a baseline measurement of coral health and diversity in Atata, further research could expand on our conclusions. Experimental research on the dominant corals found in Atata Reef (Acropora globiceps and Acropora aspera) would illuminate how these specific corals respond to particular disturbances, thus providing a more accurate assessment of the future trajectory of this reef. Therefore, we hope to continue this research throughout the semester as part of an honors project building upon this baseline as well as examining newly acquired data.

Figure One: Percent composition of the sampled Atata reef, including the species present, the percent dead and the percent affected by algal growth.

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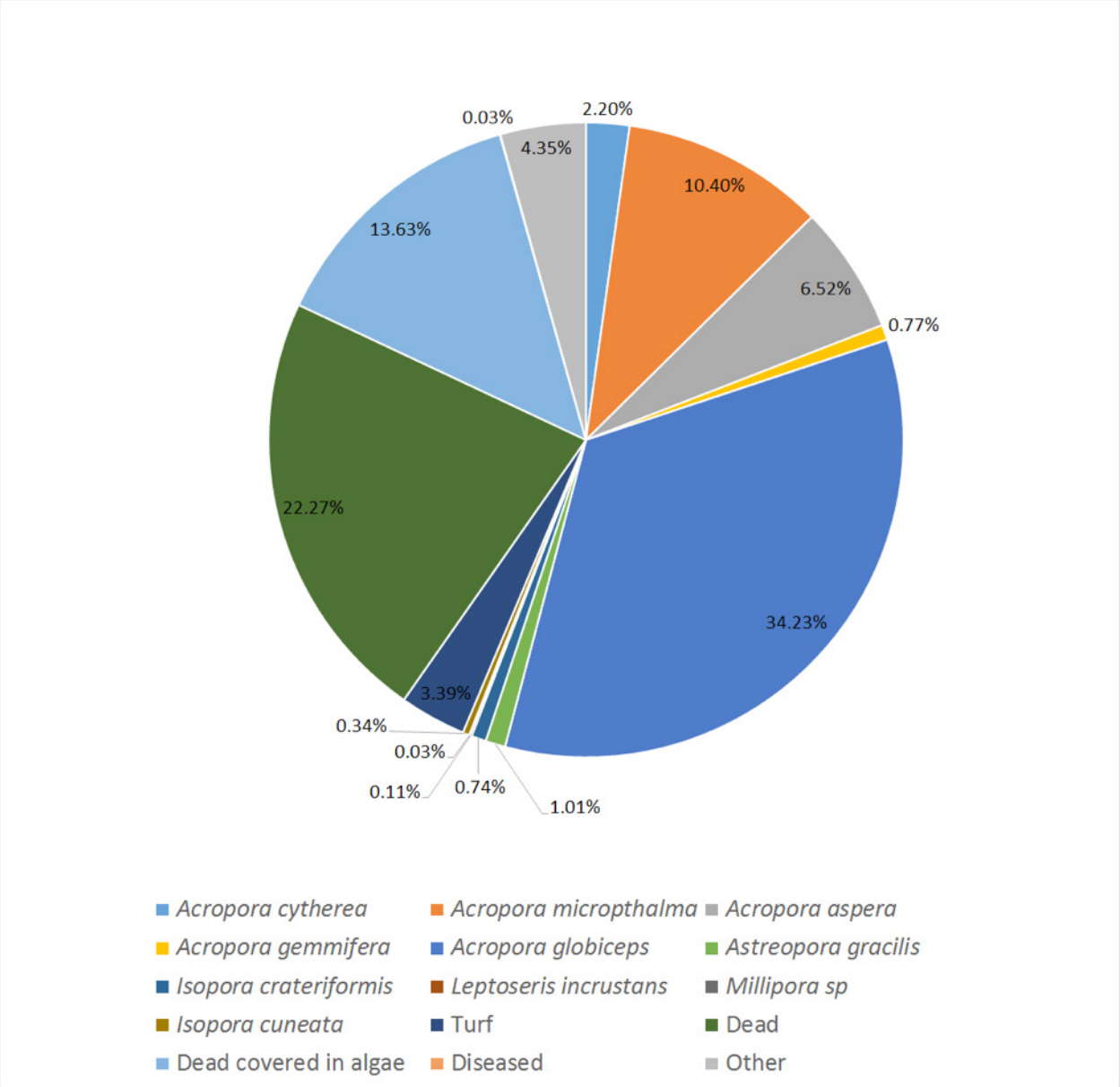
(Supported by SURF Gifts Fund)

Advisor: L.David Smith, Biological Sciences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Acropora cytherea
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Acropora gemmifera
Acropora globiceps
Astreopora gracilis
Isopora crateriformis
Leptoseris incrustans
Millipora sp
Isopora cuneata
Turf
Dead
Dead covered in algae
Diseased
Other

Is pH a cue for antibiotic production in grassland and forest soil bacteria?

Orielle Rollinson/2018

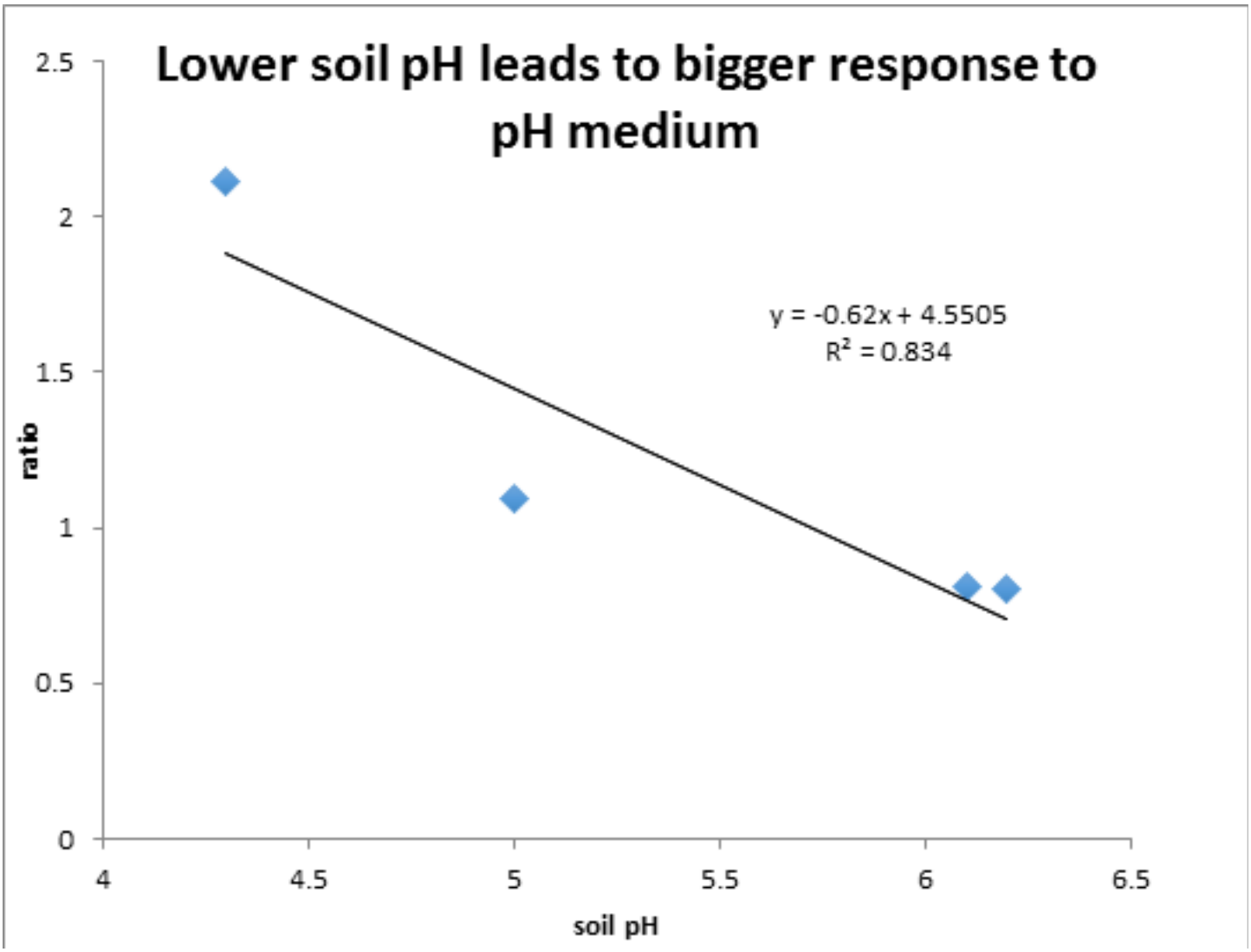
I worked with 152 isolates from soil samples collected by the Chris Vriezen lab at MaCleish Field station in Whately, MA. Prior screens have found that all 152 isolates have the ability to produce antibiotics and inhibit growth of S.epidermidis. My primary objective was to further investigate whether or not pH is a cue for antibiotic production, and if the response to pH differs between populations. Previous screens of the 152 isolates were done on 100% TSA at pH 7.3. The pH of the soil at each original sample site varies from the more acidic forest surface (4.3) and subsurface (5.0) soil to the more neutral grassland surface (6.2) and subsurface (6.1) soil. All 152 isolates were screened for inhibition of S.epidermidis at three pH levels (5.5, 7.3, 8.5).

Two distinct patterns were observed. With increasing pH of medium, the percentage of forest surface and forest subsurface isolates that inhibited growth of S.epidermidis increased. The highest percentages were found on pH 8.5. This was the most dramatic for the forest surface isolates. Where only 19% of isolates scored positive for inhibition on pH 5.5 and 26% scored positive on pH 7.3, 48% scored positive on pH 8.5. The forest subsurface isolates behaved in a similar trend, but with a much smaller difference between conditions (pH 5.5= 42%, pH 7.3= 44%, pH 8.5= 48%. The grassland surface and subsurface isolates showed a different response. The highest percentage of isolates that inhibited growth of S.epidermidis was observed for both populations on pH 7.3 (GS=64%, GSS=67%), with a decrease in positive scores on pH 5.3 (GS= 9%, GSS= 58%) and pH 8.5 (GS=51%, GSS=54%). Overall, it appears that a lower soil pH correlates with a greater response to the pH medium.

What explains the different trends observed among these four populations? Are isolates from the more acidic forest soil more sensitive to more alkaline conditions? If this is a stress response to being grown on a higher pH, why do the grassland surface and subsurface isolates not respond similarly to being grown on a higher or lower pH? Are there certain species that are responsible for these different trends? The predominant species from both the forest surface and subsurface samples is Bacillus mycoides and the predominant species from both the grassland surface and subsurface samples is Bacillus thuringiensis. Isolates identified as B. mycoides from both forest sample types followed a similar trend to their larger data set. This was the same for B. thuringiensis from the grassland samples.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Jan Vriezen, Biological Sciences



	dpH	ratio
GS	1.1	0.8
GSS	1.2	0.81
FS	3	2.11
FSS	2.3	1.09
	pH	ratio
	6.2	0.8
	6.1	0.81
	4.3	2.11
	5	1.09

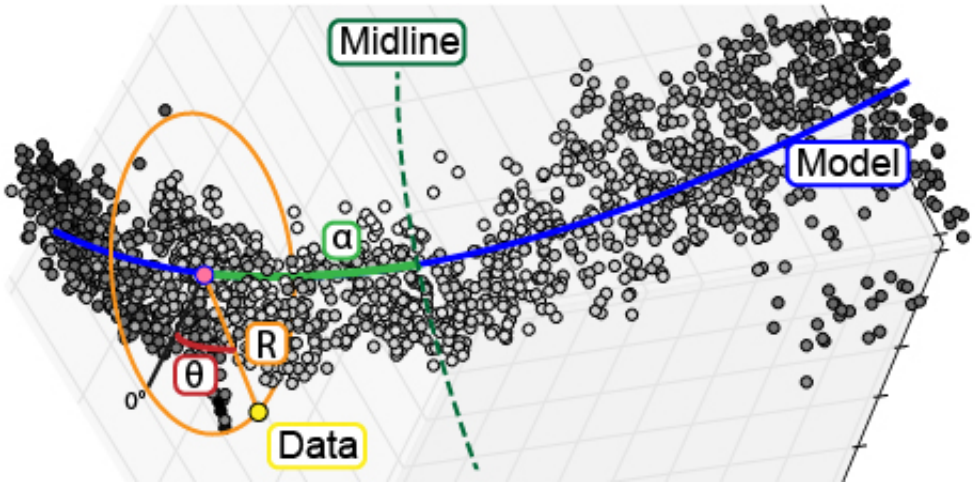
A new computational method to quantify 3D image data to detail changes in morphological structure and spatial relationships during nervous system development

Morgan Schwartz/2018

Research in developmental biology has relied on the analysis of morphological phenotypes through qualitative examination of maximum intensity projections that surrender the power of three dimensional data. Statistical methods to analyze visual data are needed, particularly to detect subtle phenotypes. In addition, these methods would best serve the community if they could leverage all the data contained within 3D datasets that are becoming common with the advent of sophisticated microscopy techniques. One barrier to achieving statistical power in image analyses has been the misalignment of spatial relationships between different images. We have created a program for biological image analysis that enables quantification and statistical analysis of 3D multichannel signals that are positioned around a well-defined structure. Our method enables description of the biological structure using a mathematical model that aligns and compares different samples while also accounting for individual variation. We demonstrated the utility of this program by quantifying the phenotypes associated with post optic commissure (POC) development following manipulation of axon guidance cues. Our method has successfully quantified a severe non-midline crossing phenotype in the you-too (Gli2-DR). We are currently building this method into a user-friendly, open source program that the community can use to similarly quantify 3D, multichannel datasets, which will provide statistical rigor and novel insight often lost in the qualitative inspection of subtle phenotypic changes. The preliminary results of this work were awarded first place undergraduate poster award at the National Society for Developmental Biology conference in July.

(Supported by 4CBC NSF)

Advisor: Michael Baressi, Biological Sciences



GABA Production by Gut Bacteria

Julia Silver/2019

Your body is colonized by an abundance of bacteria that outnumber your cells 10 to 1 and thrive on every inch of your skin. The majority of these organisms inhabit your digestive tract and communicate with your brain via afferent neurons along the vagus nerve (Galland). In recent years, science has begun to shift from viewing bacteria as carriers of death to livelihood regulators. The bacterial microbiome in the gut control our entire physiology from nutrient absorption and immune system functioning to vitamin and neurotransmitter production, as described in Figure 1. Our emotional and physical health is dominated by the state of our gut microbiome (Perlmutter).

The gut-brain connection was studied in this research to determine whether neurotransmitters, namely, GABA, are: (1) produced by the gut bacteria and (2) whether a conclusion can be drawn between the strains that produce GABA and the main bacterial strains in the infant gut. Previous studies have shown that bifidobacterium species produce GABA, since the microbiota are responsive to human hormones and neurotransmitters (Smith). However, not much research has been done on whether GABA is synthesized to the same extent in an infant's gut microbiome and whether its profusion is a result of the bacterial components found in breast milk.

Over the course of the summer, I was able to analyze the effects of adding MSG, a precursor for GABA, to MRS growth medium so as to determine which of the various strains of lactobacilius brevis in the gut could survive a GABA-rich environment like that of the colon. This was done to narrow down which strains to test for their GABA production. Then, following several experiments in total phenolic content in cranberries to hone in on assay creating skills, I was able to create a standard curve for GABA. This standard curve is crucial because it will serve as a comparison for when GABA production will be measured in the bacterial supernatants we will eventually create and study. Because the goal is to eventually determine whether GABA is produced by the infant colon, B infantis, the primary bacteria found in the infant gut, will be fed milk oligosaccharides (found in breast milk) and glucose (as a control) in future experiments to determine under what conditions GABA is synthesized in the colon, if it is at all.

Figure 1: The coordination of gut-brain axis and microbiota. The pathway by which the brain influences colonic microbiota is on the left. The method by which the microbiota influences the brain and behavior is on the right (Collins).

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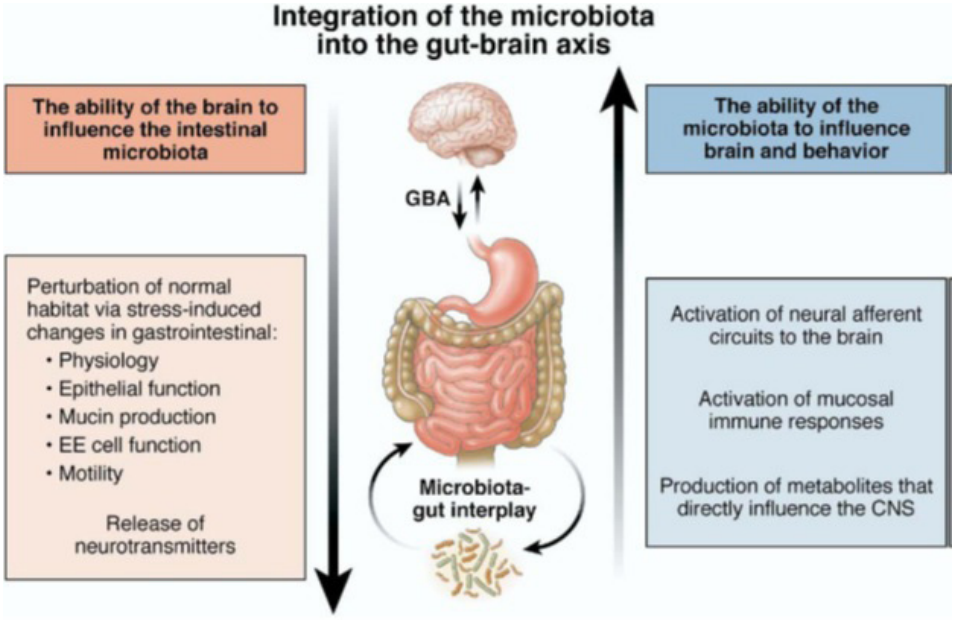
(Supported by Frances Baker Holmes Internship Fund)

Advisor: Adam Hall, Biological Sciences


Integration of the microbiota into the gut-brain axis
The ability of the brain to influence the intestinal microbiota
Perturbation of normal habitat via stress-induced changes in gastrointestinal:
• Physiology
• Epithelial function
• Mucin production
• EE cell function
• Motility
Release of neurotransmitters
GBA
Microbiota-gut interplay
The ability of the microbiota to influence brain and behavior
Activation of neural afferent circuits to the brain
Activation of mucosal immune responses
Production of metabolites that directly influence the CNS

Androgenic Modulation of Foot-Flagging Behavior in the Bornean rock frog (Staurois parvus)

Sarah Smith/2018

Many species perform elaborate physical gestures that require the adaptation of the brain, spinal cord, peripheral nerves, and muscles to precisely control movement. Yet little is known about how these systems are modified by evolution to incorporate gestural signaling into animal communication repertoires.

One possible explanation involves testosterone, which can act on androgen receptors (ARs) in the skeletal muscles and/or spinal cord to mediate the reproductive behavioral displays of many male vertebrates [1]. For instance, testosterone may stimulate male Bornean rock frogs (Staurois parvus) to wave their rear limbs to "foot flag," which deters sexual rivals [2]. I examined whether selection for the foot flag led to the evolution of androgenic sensitivity in the muscles that move the hind leg, the spinal cord neurons that control these muscles, or both, to support this new motor skill.

Adult male S. parvus frogs (n = 38) received an injection that either inhibited ARs in the skeletal muscles (Bical) or throughout the entire body (Flut). Inclusion of these two groups helped determine whether the ARs that mediate foot-flagging behavior are only in the muscles or if modulation of the spinal cord/brain by testosterone is also necessary for foot-flagging behavior. Two males receiving the same treatment were placed in a transparent mesh arena with one randomly-chosen female to stimulate foot flagging. Following a two-hour acclimation period, foot-flagging behavior was videotaped for seven hours and the number of foot flags per hour was recorded.

Preliminary results (n = 9) indicated that individuals exposed to Flut did not show a significant decrease in the number of foot flags at any hour compared to the control group ($0.16 < p < 0.77$) (Figure 1). This suggests that foot flagging is not dependent on testosterone or ARs, which contradicts previous studies [2]. However, a complete data analysis will be performed during my honors thesis. Future research will suggest whether androgenic sensitivity is associated with the emergence of gestural signals, which could provide a novel perspective on how evolution shapes the nervous system to produce adaptive motor skills.

This research was presented at the Amphibian Conservation Research Symposium and the Vienna Zoo.

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(Supported by B. Elizabeth Horner Fund)

Advisor: Lisa Mangiamele, Biological Sciences

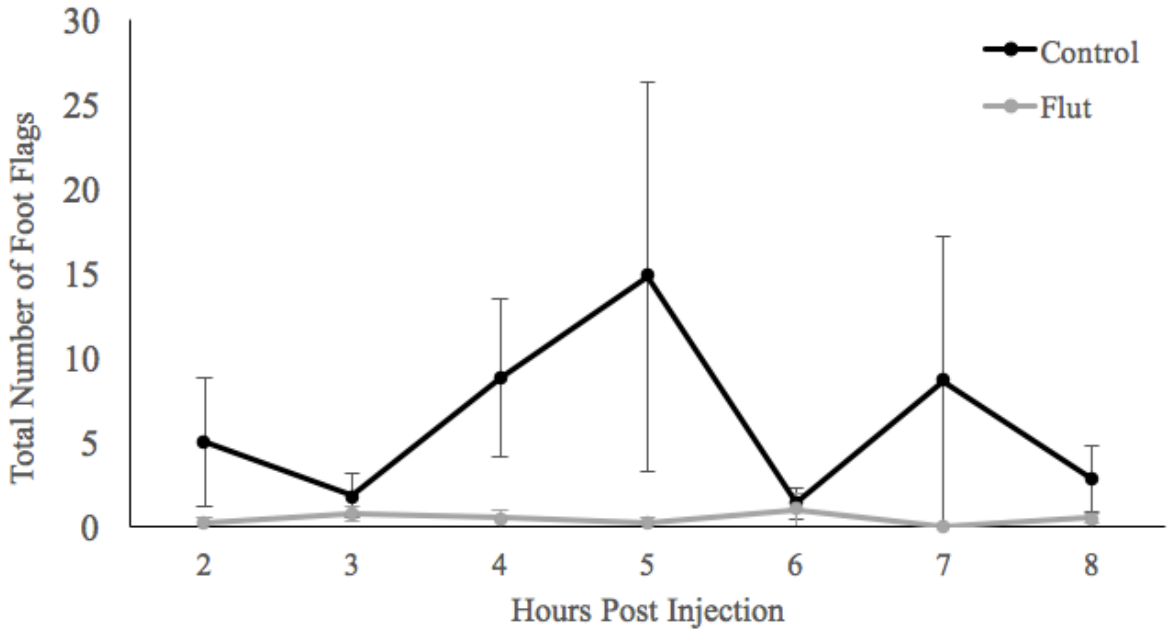

Figure 1. The total number of foot flags performed by *S. parvus* individuals exposed to the AR inhibitor Flut did not significantly differ from control individuals ($0.16 < p < 0.77$).

The Role of Reelin Signaling in Neurogenic Development of the Spinal Cord

Raegan Stokes/2019

Reelin is a large glycoprotein that is secreted in the extracellular matrix of the central nervous system. It binds to the receptors ApoER2 and Vldlr, which then activate Dab1a/b kinases and causes downstream pathways that regulate neuronal migration. The question that we study is: does the Reelin signaling pathway play a role in proper regulation of radial glia stem cells and neuroglial progenitors in the zebrafish spinal cord?

To answer this research question, we use a loss of function approach using the CRISPR/CAS9 system. The CRISPR/CAS9 system induces double stranded breaks in an assigned location of the DNA, leading to an unsuccessful repair process known as non homologous end joining. Currently we are screening through crispr injected zebrafish lines of Reelin and ApoER2 (no crispr has been created for Vldlr yet and the Dabla/b crispr needs to be reinjected). Once we identify homozygous mutants for these lines, we will complete phenotypical and morphological testing to see how a knockout of all these genes influences neuronal migration.

As shown in the figures below, immunohistochemical staining was done on Reln 17bp deletion mutants and wildtype zebrafish to stain for oligodendrocytes, GABAergic neurons and axons. This allows us to examine whether mutants exhibit defects of proliferation, differentiation and/or migration in specific types of cells within the spinal cord. No quantitative data has been collected yet.

We are in the process of creating a successful in situ hybridization at various developmental timepoints for Apoer2, Reelin, Metrn, Vldlr, and Dab1a/b which labels where each gene is expressed in the zebrafish embryo. This approach is used to determine which cell types express the Reelin pathway genes within the neural tube.

Figure 1a: (10x) Dorsal and lateral images of Reln 17bp deletion mutant at 4dpf: staining for oligodendrocyte progenitor cells (green), GABAergic neurons (red), and all axons (blue).

Figure: 1b: (20x) Dorsal images of the telencephalon, midbrain and hindbrain of Reln 17bp deletion mutant at 4dpf: staining for oligodendrocyte progenitor cells (green), GABAergic neurons (red), and all axons (blue).

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Michael Baressi, Biological Sciences

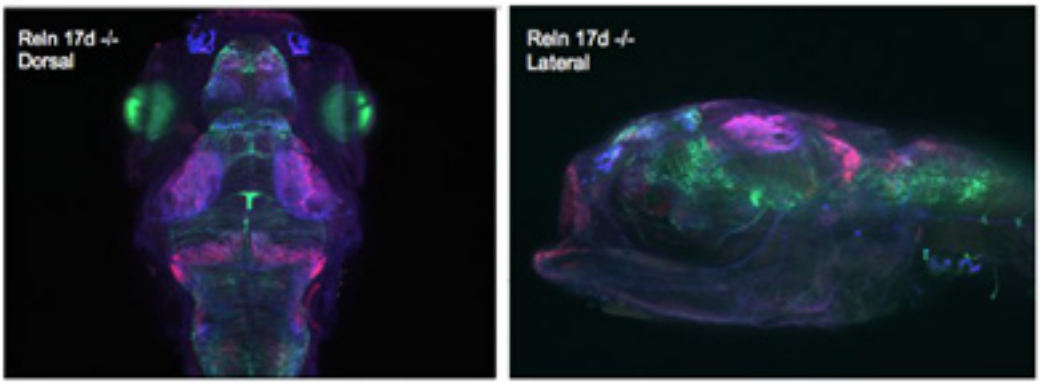

Figure 1a: (10x) Dorsal and Lateral View of Reln 17bp deletion mutant at 4dpf: staining for oligodendrocyte progenitor cells (green), GABAergic neurons (red), and all axons (blue).

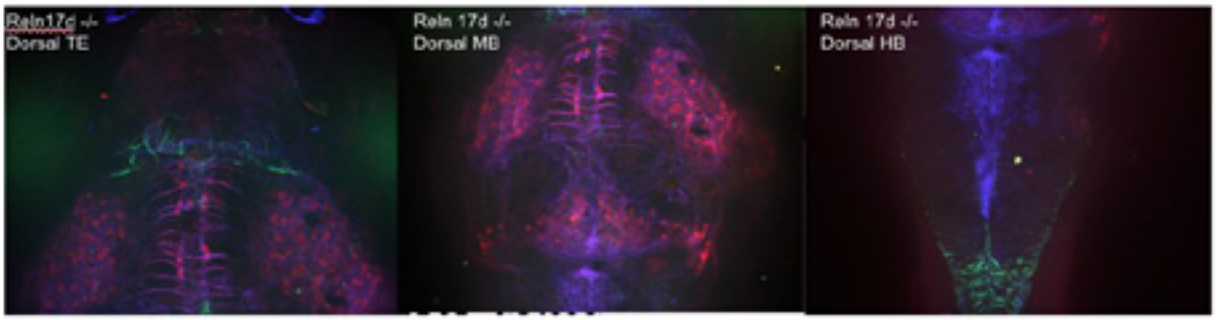

Figure: 1b: (20x) Dorsal images of the telencephalon, midbrain and hindbrain of Reln 17bp deletion mutant at 4dpf: staining for oligodendrocyte progenitor cells (green), GABAergic neurons (red), and all axons (blue).

Skeletal Muscle Protein Changes Throughout the Stages of Myogenesis

Jacqueline Urdang/2020

Myogenesis is the process of skeletal muscle development which occurs not only in embryonic tissue, but in adult tissue as well. This study analyzed protein changes, including stress proteins, throughout in vitro myogenesis. Stress proteins are upregulated when cells are exposed to stressful stimuli to help ameliorate the stress and facilitate repair. Therefore, understanding their changes in expression during development can aid in our understanding of normal myogenesis and of myogenic disorders such as the muscular dystrophies.

Murine C2C12 cells are an immortal mouse myoblast cell line (Yaffe and Saxel, 1977) derived from adult dystrophic mice thigh muscles that recapitulate in vivo myogenesis in vitro. Beginning as mononucleate myoblasts, these cells fuse forming multinucleate early myotubes that then form contracting myofibrils as late myotubes. This study postulates that this fusion event is a stressful stimulus.

The analysis was accomplished by quantitative immunoblotting using one-dimensional SDS gels of whole cell extracts at the three stages (n=5). The gels were transferred to PVDF immunoblot membranes and probed with mono-specific primary antibodies to various proteins and visualized by HRP-coupled secondary antibodies. The blots were then stripped and probed for GAPDH as a loading control.

The developed blots (Figure 1) were scanned and analyzed with ImageJ and the integrated pixel intensities analyzed statistically by JMP, which adjusted the experimental data for loading uniformity and intrablot protein standards. The means (+/- SD) were calculated and compared using the Dunnett's test ($p<0.05$) to assess statistical significance and used to calculate the fold-change in expression (Figure 2).

Three different patterns of expression changes were observed. Immunoblot data in Figure 1 show the antibody staining for each myogenic stage, as well as the GAPDH staining as loading controls. Heat shock protein 70 and creatine kinase muscle isoform (CK-M) exhibit continuous increase during myogenesis, whereas heat shock protein 60 is unchanged. Heat shock protein 25 increased between the myoblast and early myotube stages and then decreased between the early and late myotube stages. These three patterns are shown quantitatively in Figure 2 with indications for statistically significant changes from the myoblast (Day 0) stage.

The proteins that were found to increase throughout myogenesis aid in protein folding and the maintenance of energy homeostasis. These results show that fusion is a stressful event because proteins that protect against the stress, allowing the cell to avoid the apoptosis which might otherwise occur, are upregulated. This research will be continued in the fall as a STRIDE project with the hopes of explaining the patterns of expression and analyzing more proteins.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: *Stylianos Scordillis, Biochemistry*

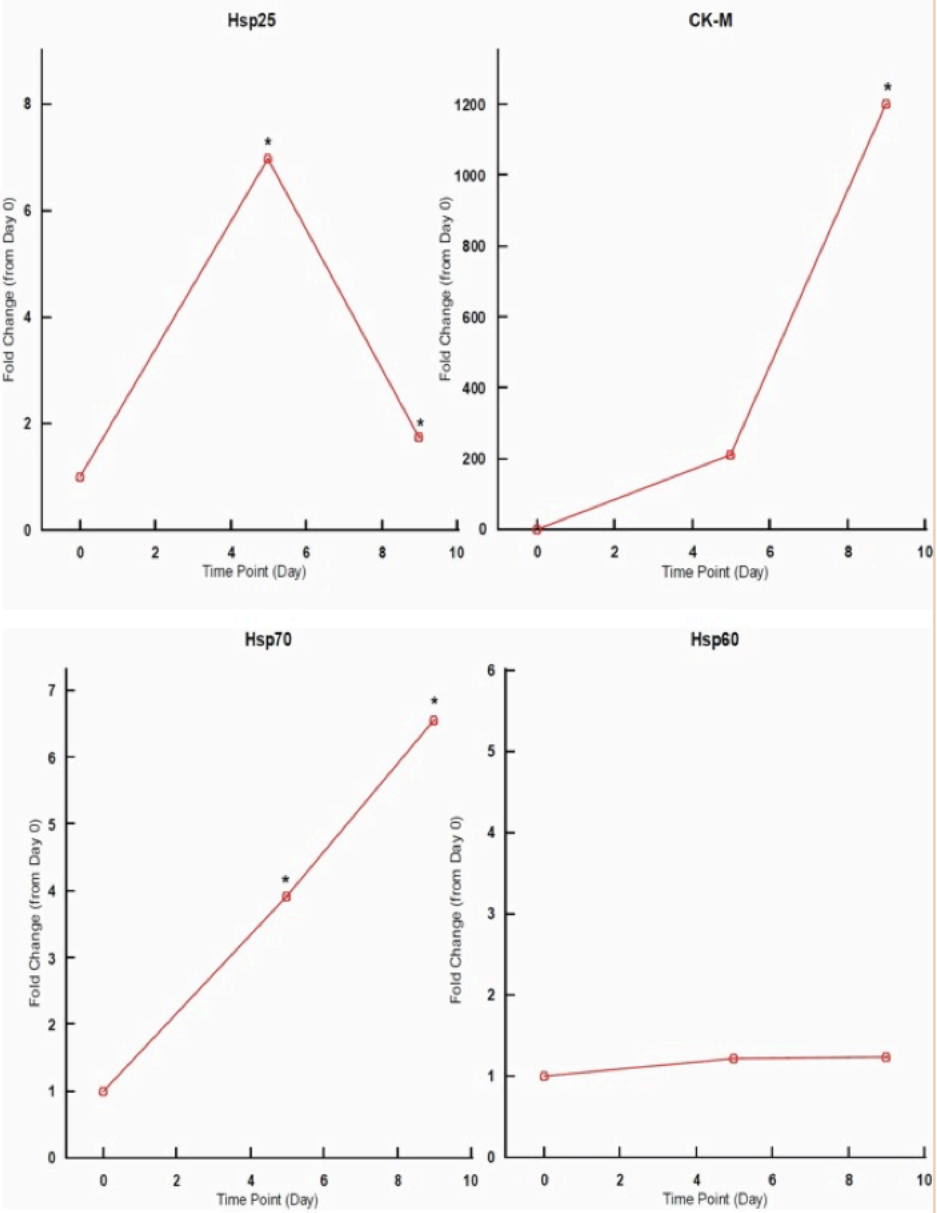

Figure 2. Graphs of the fold change in various proteins during myogenesis (myoblasts (Day 0), early myotubes (Day 5), late myotbues (Day 9)). * indicates significant difference ($p<0.05$) from Day 0.

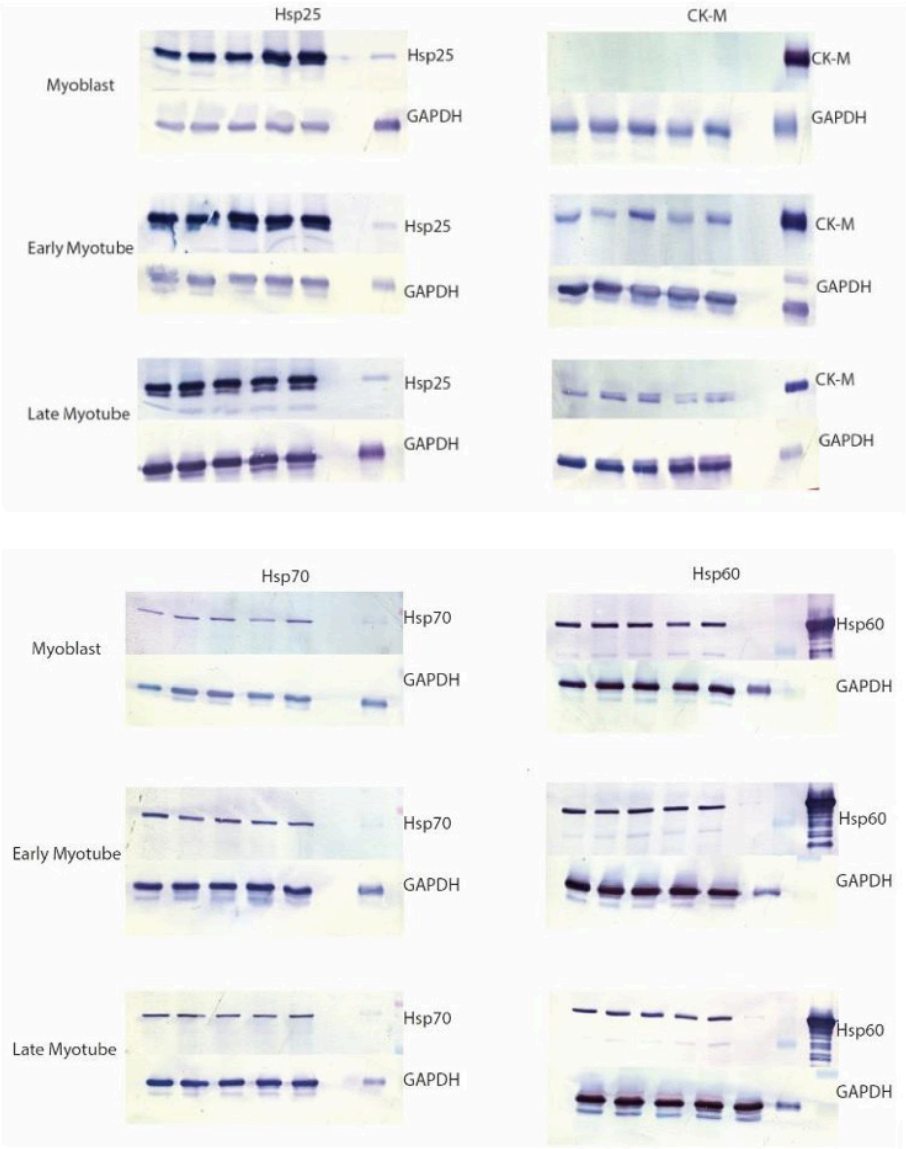

Figure 1. Immunoblots of C2C12 cells probed with various antibodies. From left to right: 20 µg of each whole cell extract (n=5), 2.7 µg mouse skeletal muscle extract, 5 µL molecular weight standard.

The analysis of genome-wide changes in gene expression in Enteropathogenic E. coli upon environmental stimulation

Nhi Van/2018

Escherichia coli are Gram negative bacteria that are commonly found in warm-blooded mammalian lower intestines. Even though most E. coli are harmless, there are some serotypes of E. coli that cause disease [1,2]. Enteropathogenic E. coli (EPEC) are a major cause of diarrhea and infant mortality in developing countries. It accounts for about 1.3 million of death annually [11]. Even though EPEC is such a notable threat, more investigation of the molecular mechanisms by which EPEC causes disease are needed to identify novel therapies to battle infection [2]. Inside the host, bacteria need to adapt to changing environments that differ in such factors as temperature, pH, osmolarity, or nutritional access. How well bacteria respond to such alteration is important in determining whether they survive or die. These environmental factors are thought to act as an on and off switches for specific genes that can enhance their fitness inside the host and prevent expression of unused genes.

Previous studies from the White-Ziegler lab demonstrated that 10% of non-pathogenic E. coli genes are controlled by temperature in comparing to bacteria grown at room temperature (23℃) and host temperature (37℃). Additionally, other studies from the lab demonstrated that virulence genes are expressed at host temperature [3]. Thus, it proved that change in temperature is an important cue that E. coli uses to determine if virulence genes should be expressed within the host. By understanding the regulatory factors, we will be able to develop direct therapeutic drugs that target these molecular on and off switches in such a way that virulence genes cannot be expressed; consequently, bacteria will not be able to invade the host and cause diseases [3].

My experimental focus is attempting to mimic the environment inside the human gastrointestinal (GI) tract by altering not just temperature, but also the pH. Beside temperature, EPEC also encounter different pH levels in this environment; saliva pH is around 7 to 7.5, the stomach region has a lower pH of 2 to 3, while the cecum, where EPEC is known to bind to colonize has a pH of 5.5. Previous studies have shown that Enterohemorrhagic E. coli (EHEC) adhesion to host's epithelial cells are enhanced by low pH [4]. Thus, we hypothesize that the combination of temperature and pH lead to the expression of a wide range of genes that enhance the fitness of EPEC inside the host.

To assess the impact of both temperature and pH on global gene expression, we conducted an RNA-seq experiment in the EPEC in which bacteria were shifted from 23℃ to pH of 3 for 2 hours, followed by a shift to pH 5.5 for an additional 2 hours at 37℃. Bacterial cells were harvested and RNA was isolated. Ribosomal RNA was depleted from the samples and library construction was completed from the mRNA for Next-generation sequencing (NGS).

Results from biostatistical analyses of the EPEC transcriptome demonstrated that many genes were regulated by pH, temperature or both. 532 genes were changed by temperature, while 376 genes were changed by pH. The effect of both temperature and pH changed the expression of 373 genes. This result indicates that temperature remain the most important cues for EPEC genes regulation. However, pH also plays a significant role in controlling the expression of many genes. Most of them are genes related to type 3 secretion system (T3SS), iron acquisition and storage, as well as transporter genes.

One focus of my project was on the impact of these environmental cues on small regulatory RNAs (sRNAs). Despite their small size, sRNAs were found to play a role in regulating virulence genes in EPEC [10]. Preliminary data showed that temperature shift alter the expression of 16 sRNAs, while the pH shift changes the expression of 9 sRNAs. Interestingly, 3 sRNAs - DsrA, GcvB, PsrO - are significantly changed in both pH and temperature shift. However, temperature and pH lead to an opposite effect. The expression of DsrA was upregulated by temperature while downregulated by pH; the expression of GcvB and PsrO was downregulated by temperature while upregulated by pH. DsrA are genes that control RpoS and H-NS, which in turn regulate the expression of proteins involve in stress response and virulence factor for pathogenic E. coli [8]. GcvB is a non-coding protein that regulate many amino acid transport and amino acid biosynthesis genes [9]. Little research has been done on PsrO. However, research showed what the expression of PsrO increases under temperature stress response [10]. Thus, our long-term target is to build a model that connect these sRNAs to the proteins that are known to be a master transcriptional regulators of temperature responses (such as Per, Ler and Grl). Future studies will be focused to either knocking out or overexpressing these sRNAs of interest to determine their impact on virulence gene expression in EPEC.

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(Supported by Blakeslee Fund)

Advisor: Christine White-Ziegler, Biological Sciences

Identification of Clock Gene Functional Conservation between Caenorhabditis elegans (C.elegans) and Brugia malayi (B. malayi)

Josselyn Vergara/2019

Endogenous circadian rhythms have been demonstrated in several model systems. Cycles in behavior, physiology, and gene expression have also been reported in microfilarial transmission where the movement between the peripheral bloodstream and surrounding tissues operates under an approximate 24-hour rhythm [1]. B. malayi is a parasitic nematode responsible for 10 % of lymphatic filariasis infections [2]. C. elegans has been selected as the nematode reference species in the elucidation of B. malayi gene function due to phylogenetic similarity and detailed annotation of C. elegans circadian functionality.

PER and PDF signaling proteins have been key in confirming if an organism possess circadian clock [3]. In C. elegans, the Per homologue Lin-42 is the major protein responsible for correct timing of ecdysis and PDF signaling has been identified to regulate the central timing machinery [4]. Operating with observed Per and PDF conservation between C. elegans and B. malayi, it can be proven that the periodic patterning of microfilarial production in B. malayi are dictated by functional homologues to Per and PDF proteins. To identify our Lin-42 homologues in B. malayi, the Lin-42 protein sequence was subjected to protein BLAST (BLASTp) against all similar protein sequence available on NCBI's genomic. BLASTp identified one significant match from B. malayi, a functionally un-annotated hypothetical protein (XP_001896444.1). In the same way, different homologues were annotated from C. elegans clock genes including the ones in Table 1.

If a rescue-of-phenotype analysis demonstrates that candidate B. malayi clock gene homologues are capable of rescuing phenotypic defects in C. elegans mutant lines, it can be concluded that the candidate B. malayi genes possess functional homology between the two species. This will prompt further research into function of these B. malayi genes to confirm if they participate in the parasite's clock gene regulatory network.

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Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Steven Williams, Biological Sciences

Table 1.- Core circadian oscillator homologues in *B. malayi* identified by BLASTp.

C. elegans clock genes	Expression pattern in *C. elegans*	*B.malayi* homolog (protein)
pdf-1/pdf-2	Expressed in interneurons, amphid neurons, motor neurons, and certain sensory neurons.	Calcitonin receptor-like protein Seb-1 (XM_001894483.1)
sur-5	Exhibits strong and constitutive expression throughout all developmental stages	Acetyl-Coenzyme A synthetase 2 (XP_001900923.1)
TAX2	Expressed in the primary thermosensory neuron	Bm3873, isoform a (CDP99526.1)
tim-1	mRNA levels reach their highest levels at the adult stage.	Timeless protein (XP_001895789.1)
aha-1	High levels during embryogenesis	Aryl hydrocarbon receptor nuclear translocator protein (XP_001901421.1)
atf-2	Levels peak between comma stage and movement in developmental stage	Hypothetical protein Bm1_19605 (XP_001895376.1)
nlp-36	Expressed in the head, tail, and the intestine	Hypothetical protein Bm1_22820 (XP_001896020.1)

Developing and Testing a PCR-based Diagnostic Test for Giardia

Sabine Vernon/2019

Diarrheal diseases are a major cause of death among children in developing countries. Giardia, a single celled parasite, likely accounts for many of these cases (CDC, 2015). Typically spread to humans through water contaminated with fecal matter, Giardia reproduces in the small intestine leading to infection and symptoms such as diarrhea and vomiting (Pulitzer et al. 2010). Currently, the common process used to detect Giardia is slow and inefficient. Over the summer, I worked on optimizing and testing sensitive PCR-based diagnostic tests to target and amplify Giardia DNA.

The PCR-based diagnostic tests were developed by the Williams lab using bioinformatics techniques to identify highly repeated sequences in the Giardia genome. Several primers and probes were then designed to target these sequences. Over the summer, I compared, optimized, and tested two assays that target and amplify distinct sequences of the Giardia genome, on Giardia samples from Bangladesh. The two assays, named CL47 and CL52, were first tested on DNA from the Giardia assemblages known to infect humans, assemblage A (strains Wb and Be), and assemblage B. Using qPCR, I tested two assays at different annealing temperatures and with different Giardia DNA concentrations to determine whether they both effectively detected Giardia across all strains and assemblages and, if so, which assay worked better. Ultimately, I determined that both assays amplified the DNA from both assemblages, and neither worked significantly better than the other.

Once it was determined both assays worked, I tested them on DNA isolated from 30 fecal samples from Bangladesh, some of which were previously determined to be Giardia positive. Both assays amplified Giardia DNA in the Giardia-positive samples and did not detect any DNA in negative samples, indicating that they did not generate false positives. In these tests with fecal DNA samples, assay CL52 proved more effective: it consistently had lower CT values, indicating it was able to amplify smaller amounts of Giardia DNA and therefore was more sensitive.

Thus, we were able to confirm that the assays do successfully detect Giardia. Work still needs to be done, however, to design highly sensitive assays that specifically target each individual Giardia strain.

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(Supported by Blakeslee Fund)

Advisor: Steven Williams, Biological Sciences

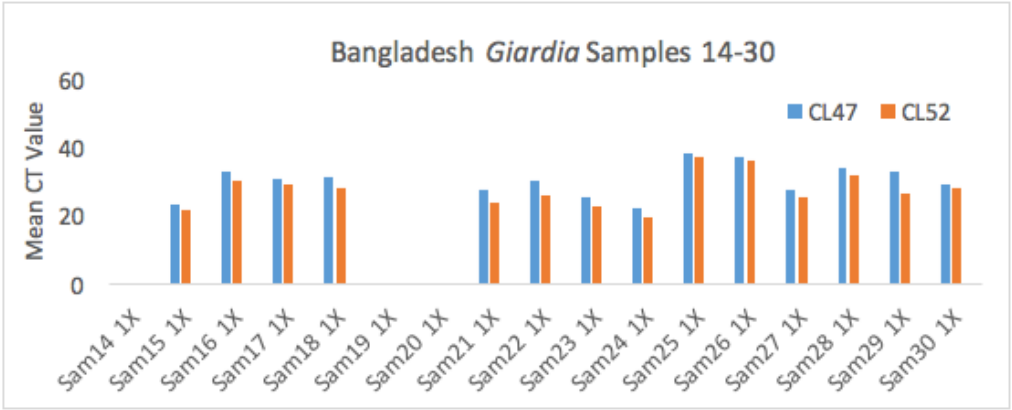


Figure 1: Successful detection of Giardia DNA by qPCR. Average CT values for *Giardia* samples 14-30, undiluted. CL52 CT values were consistently lower across all samples, a trend also seen in samples 1-13.

Neural Stem Cell Research

Virtue Winter/2019

The Barresi lab's work is focused on neural development, and the group I was a part of looked specifically at how neural stem cell development might be affected by the WNT5b gene. It is theorized that WNT5b functions as a suppressor for WNT/β-catenin non-canonical signaling, which regulates the balance of differentiation and proliferation in radial glial cells. Increased WNT5b expression should lead to decreased levels of WNT/β-catenin, causing balance to shift in favor of differentiation rather than proliferation. Conversely, decreased WNT5b expression would mean increased levels of WNT/β-catenin, leading to more proliferation than differentiation.

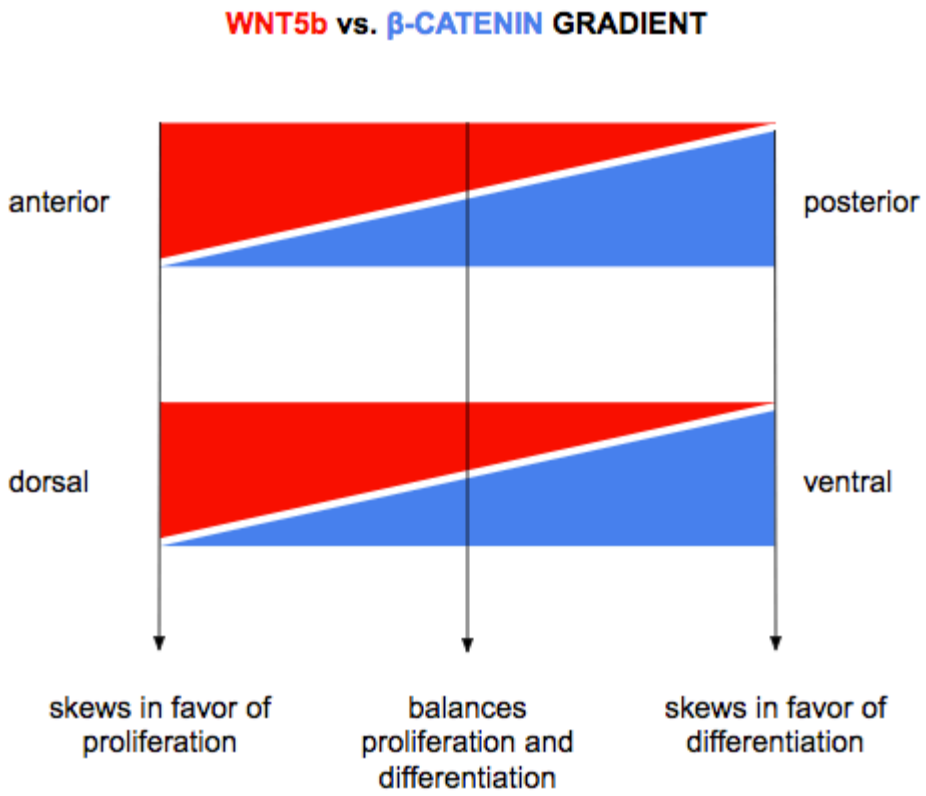
The model organism used for our experiment was the zebrafish, due to several key characteristics: they provide a clear chorion for easy viewing of embryonic development, produce large clutch sizes in short periods of time, and possess great similarity to the human nervous system. In order to create loss-of-function (LOF) and gain-of-function (GOF) models, transgenic lines and pharmaceutical drugs were used. During SURF, I worked primarily with the transgenic lines. For the LOF transgenic line, embryos were fixed with formaldehyde at specific time points in early development. The GOF embryos, a heat shock line, required the additional step of being immersed in a warm water bath for activation of heat shock proteins before being fixed. The fixed embryos were then screened for our desired genotypes: heterozygous mutant and homozygous wild type.

Next was cryosectioning and imaging. After imaging, the spinal cord was divided into three equal areas. The number of nuclei, radial glial cells, differentiated neurons, and dividing cells were then counted, recorded, and averaged for each area. These counts allowed for comparison against control levels of cell proliferation and differentiation.

The data obtained supports our original hypothesis. Furthermore, it suggests that WNT5b and β-catenin act as a morphogen gradient along the spinal cord. The WNT5b gradient goes from high to low along the anterior to posterior axis as well as the dorsal to ventral axis, with the inverse holding true for β-catenin. Moreover, the gradient itself may be time specific to early development. In future experiments, it is hoped that we can better understand how exactly WNT5b regulates β-catenin for suppression, and that a more biomathematical approach can be taken so as to better analyze and understand our results.

(Supported by NSF: National Science Foundation)

Advisor: Michael Baressi, Biological Sciences


WNT5b vs. β-CATENIN GRADIENT
anterior
posterior
dorsal
ventral
skews in favor of proliferation
balances proliferation and differentiation
skews in favor of differentiation

Roll-up Polymer Gels: A Candidate for Cell Encapsulation and Drug Delivery

Jenny Banh/2018

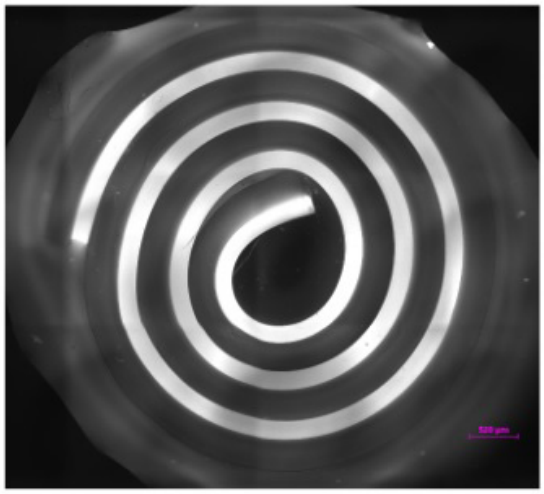
Tissue engineering is a growing scientific field in which we try to mimic the extracellular matrix (ECM) for a variety of different reasons. Reasons for this study involve creating innovative methods for developing tissues which may be used for cell culture, regenerative medicine, drug delivery as well as fabricating synthetic organs. Though there are various means of developing tissue substances which are similar to the ECM, seldom are they biologically compatible, non-immunogenic, consistent, or composed of functionalizable, synthetic and natural materials.

In Professor Maren Buck's lab, we introduce the use of polymer chemistry to produce polymer hydrogels as a potential means for regenerative medicine, drug delivery, and cell encapsulation. My project involved studying the synthesis of these polymer hydrogels and the varying characteristics of the bi-layered gels which roll into a tube. To create these bi-layered rolled gels, a polymer hydrogel composed of a higher swelling percent (eg. 25% crosslinked Jeffamine 2000) is casted upon a microscope slide, allowed to solidify at the thickness of 1 micrometer before casting another layer of a lower swelling percent (eg. 25% crosslinked Jeffamine 600) on top. Once this bilayer gel is submerged in sodium hydroxide, the two layers begin to swell at different percents with the lower swelled gel making up the inner coil of the rolled tube. Among various different tasks, one experiment was to image the cross-section of a rolled tube which had one layer fluorescently labeled with dansylcadaverine to confirm gels swelled and rolled in the manner that we hypothesized (image below).

Future plans for my research involve a continuation of studying the topic so that I may pursue it for my Master's degree. In my final year at Smith College, I will be conducting a special studies course so that I may continue to study and understand the mechanistic properties of these gels and provide definitive conclusions for how these gels behave.\

(Supported by NSF: National Science Foundation)

Advisor: Maren Buck, Chemistry



A bi-layered gel of 25% crosslinked Jeffamine-600 and 25% crosslinked Jeffamine-2000 taken by a Nikon light microscope on a 500μm scale. The bright fluorescent layer was labeled with dansylcadaverine, indicating the Jeffamine-600 layer.

Copper-Mediated O-H Methylation of Phenols with Methylboronic Acid

Mairead Bartlett/2018

The methylation of oxygen nucleophiles is not a new concept; aryl methyl ethers are very common in consumer products, including pharmaceutical compounds that treat conditions from Alzheimer's to cancer to HIV (1). However, current methodology focuses predominantly on electrophilic sources of methyl, using reagents such as diazomethane, TMS-diazomethane, methyl iodide, and dimethyl sulfate. While highly efficient, electrophiles are inherently toxic to humans, causing the death of multiple chemists since 2008 (2,3), signaling the need for an alternative, safe, regioselective methylating reagent to perform such reactions.

Our attention turned to nucleophilic sources of methyl that could be cross-coupled with oxygen to avoid the inherent toxicity of electrophiles. The Chan-Lam reaction pairs a nucleophile and boronic acid using a copper catalysts and oxidant. Although typically performed with an arylboronic acid, there is limited precedent for alkylation, including two examples of methylation (one on nitrogen nucleophiles, and one using carboxylic acids, published by the Gorin lab). After screening these sets of methylation conditions, as well as other Chan-Lam conditions, we were able to successfully methylate 4-fluorophenol. Optimization studies were performed using 19F NMR quantification.

The optimized conditions were tested on a variety of substrates to obtain isolated yields. Para-substituted electron-withdrawing groups (EWGs) underwent conversion most successfully, with isolated yields as high as 99%. We were able to successfully methylate ortho-substituted EWGs using the same conditions. When using weaker withdrawing groups or donating groups, the temperature and/or copper equivalents were increased to encourage conversion.

Further study should probe more ortho- and meta-substituted substrates, as well as electron donating groups, especially alkyl groups. Aliphatic alcohols and carboxylic acids are also an area of interest, to see if our method might be expandable to other types of alcohols, not solely phenols. I will continue this work as a thesis in September.

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(Supported by Katherine C. Hauch 1921 Fund)

Advisor: David Gorin, Chemistry

The specificity of oxidation on nanoscale silicon

Xinyuan Chen/2018, Claire Vinson/2019, and Amanda Barriscale/2018

The topography and chemical properties of a surface are known to be important in the adhesion of bacteria and the growth of biofilm on a particular surface [1,2]. To further understand the behavior of bacteria on Si(100) surfaces with varied chemistry and topography, increasing the library of available Si(100) surfaces might be helpful. Toward this end the Queeney Lab seeks to understand the site-specificity of oxidation on "rough" Si(100) surfaces with nanoscale topography. This study examined the placement of OH group in the early stages of oxidation on these surfaces.

All samples were treated by an mRCA cleaning procedure to remove impurities on the surfaces. The samples were then etched by HF to create a H-terminated Si(100) surface. After 24 hours of water etching, the surfaces are H-terminated with nanoscale topography. Samples were then oxidized for either 10 minutes or 20 minutes. The same experiment was repeated without water etching to produce flat surfaces that underwent the same oxidation process. Fourier transform infrared (FTIR) spectroscopy was used to analyzed the oxidation sites on the Si(100) surfaces. Contact angle measurements were taken to measure the wettability of the surfaces and provide possible insight into the spatial distribution of OH groups.

According to our hypothesis, oxidation would occur preferentially on the sides of the hillocks on the rough surfaces. We expect maximum site specificity at the lowest oxidation coverages, since this is a kinetic, rather than a thermodynamic, effect. The more hydrophilic our surface, the smaller the contact angle;3 nanoscale topography should cause a slight increase in contact angle relative to the flat surface.

According to Figure 1, our hypothesis was true before 50% of oxidation. However, at 50% of oxidation, flat surfaces were less hydrophilic than rough surfaces for the same oxidation extent. Moreover, according to Figure 2, in the first 10 minutes of oxidation, significant loss of the Si-H species on the tops of the hillocks (2100 cm-1 - 2150 cm-1) occurs. This might suggest that the dihydrides on the top of the hillocks will be oxidized at first. More loss of the Si-H on the sides of the hillocks occurs after 50% of oxidation. This suggested that after a certain amount of oxidation, oxidation might start to happen on the sides of the hillocks. Thus, lower oxidation extent did not result in the predicted specificity in the early oxidation. Further research would be conducted to verify our results as well as figure out the turning point when oxidation starts to happen on the sides of the hillocks on our surfaces.

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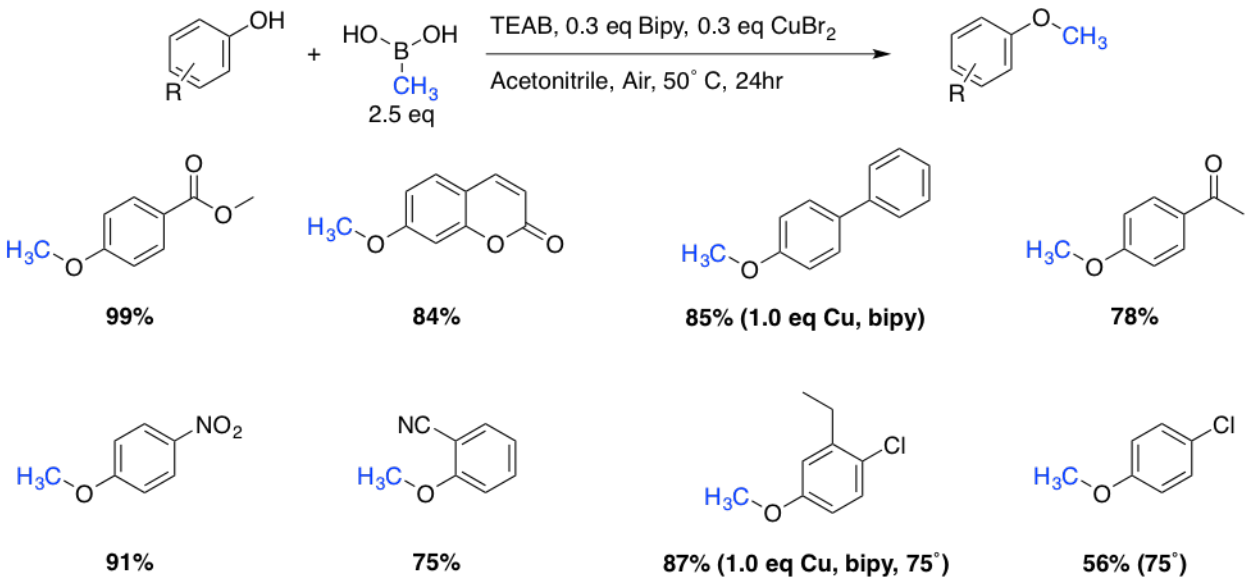
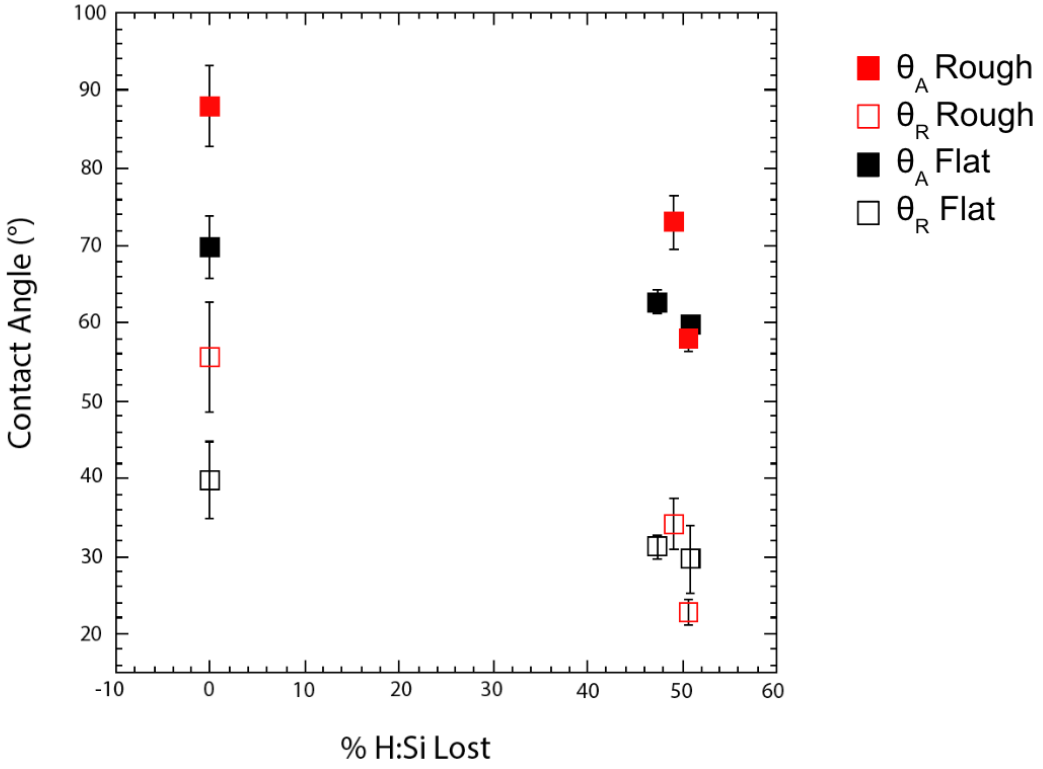
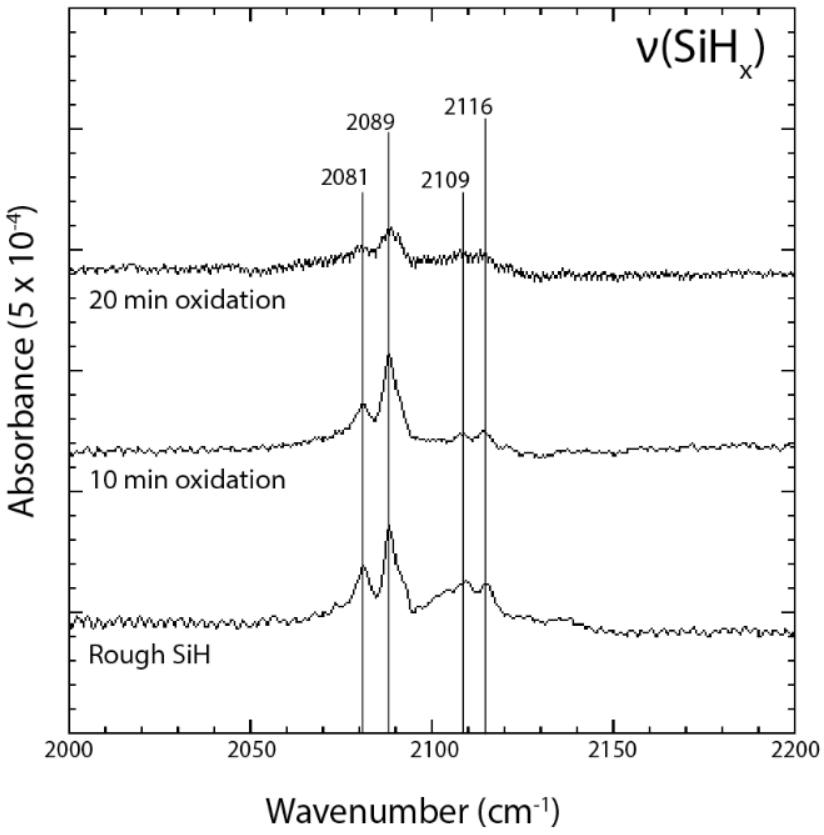
(Supported by SURF Gifts Fund)

Advisor: Kate Queeney, Chemistry

Figure 1. Substrate Scope of Chan-Lam Methylation of Oxygen Nucleophiles




Contact Angle (°)
% H:Si Lost
θA Rough
θR Rough
θA Flat
θR Flat


ν(SiHx)
2116
2089
2081
2109
20 min oxidation
10 min oxidation
Rough SiH
Absorbance (5 x 10-4)
Wavenumber (cm-1)

NMR studies on a Cisplatin-Modified DNA 12-mer

Xingyi Guan/2019

Cisplatin is known as a chemotherapy medication used to treat a variety of cancers. Its mechanism as a drug has been widely studied by scientists. Cisplatin interferes with cell replication by forming an aquo complex, cis-[PtCl(NH3)2(H2O)]+ and entering the cell by passive diffusion. It is able to form 1,2-intrastrand cross-links with purine bases, distorting the helical structure of DNA [1]. The cisplatin-modified DNA might hinder DNA repair mechanisms, and thus lead to apoptosis.

The purpose of this research is to investigate how cisplatin lesions affect DNA properties. Previous studies show that its structural distortion does not go beyond three flanking base pairs next to lesion, and therefore it may not be a significant repair marker [2]. It is now hypothesized that changes in base pair opening rate might be crucial to the damage recognition. To examine the lesion's influence on base-pair opening rates, the following DNA 12-mer sequence was used:

5'-CCTCTGGTCTCC-3'
3'-GGAGACCAGAGG-5'

A sample of the undamaged DNA was prepared by Sheng Tian, who is also currently working on preparing cisplatin-modified duplex.

To investigate how the cisplatin lesion affects base-pair stability, a temperature study was done using 1H NMR. Spectra were obtained at 5 degree steps from 278K to 323K, which is the melting temperature of this sequence. Since the imino peaks broaden and disappear as temperature rises, presumably because the hydrogen bonds break and imino protons exchange with water, the rough melting temperature of each imino peak was obtained. After the cisplatin-modified DNA is available, a comparison between the modified and unmodified strand will be made. The optimum temperature to run the base pair opening experiments and possible 2D NOESY NMR was also determined to be 296K, where imino peaks are intense and clear with least overlap.

DNA base pairs are constantly in a flux between an open and closed state, and this process is thought to play a role in the functioning of DNA. To quantify this base pair opening rate, the exchange of imino protons with the solvent (water) will be monitored through 1H NMR. To see the full picture of how the cisplatin lesion affects DNA stability and kinetics, temperature studies and base pair opening kinetics studies will also be done on the cisplatin-modified strand in future.

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(Supported by M.T. & J.P. Schiffer Endowed Fund)

Advisor: Cristina Suarez, Chemistry

The Effect of pH on Aerosol Mimicking Solutions

Emma Gubbins/2018

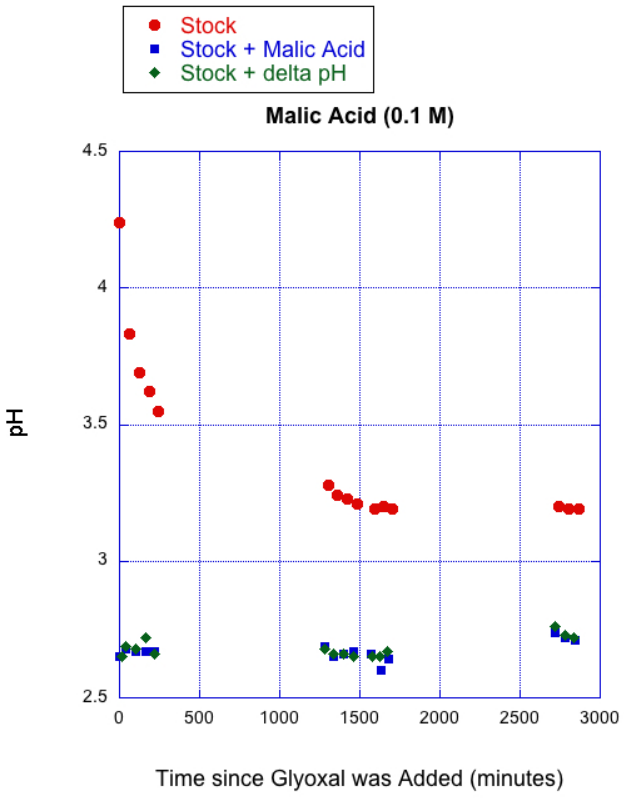
Aerosol research is important because the extent to which aerosols affect climate change is not well known, as there are large error bars associated with the cooling effects of aerosols. The study of secondary organic aerosols can help us understand more about how SOA's interact with other molecules in the atmosphere as well as their rates of formation. Aqueous aerosol mimicking solutions made with glyoxal and ammonium sulfate were used to gain a better understanding of the kinetics of SOA formation by manipulating this system with different alcohols that are present in the atmosphere at varying concentrations. The effect of different small, atmospherically prevalent acids on aerosol kinetics and the extent to which this effect is dependent on pH was also studied.

The following three solutions were tested for each acid: the stock solution (ammonium sulfate, glyoxal, and ultra pure water), the stock solution with the addition of an acid, and the stock solution with the pH adjusted to match the pH of the stock and acid solution. Malic acid, succinic acid, oxalic acid, glutaric acid, acetic acid, and adipic acid were all tested. The three solutions for each acid were run on the Thermo uv-vis for two days and the pH's of the solutions were monitored. Graphs of the pH's of these solutions versus time since the glyoxal was added show a trend where the pH of the stock solutions decreased and the pH's of the "stock + acid" and "stock + delta pH" solutions remained relatively stable.

The purpose of these tests were to determine how the pH of the solutions affected aerosol formation and kinetics and to determine if there was something else besides pH that drove the kinetics for the acid solutions. By comparing the uv-vis kinetics data of the three solutions at the same wavelength we can get a better understanding of how the pH of the solution affects the behavior of aerosol growth. The uv-vis data for the acid tests still needs to be graphed and analyzed to determine if trends for SOA formation exist. Moving forward, once the existing data is analyzed there are more acids to test and tests involving intermediates in SOA formation that can be done in order to better understand this process.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Andrew Berke, Chemistry



Using safer organocarbonates for methylation and ethoxylation

Bezawit Habtesellassie/2018

Methylation is a very important method in polymer synthesis and medicinal chemistry. However, the current methylating reagents used are toxic and deadly. Commonly used methylating reagents are diazomethane, highly toxic and an explosive gas that must be made in the lab before use and trimethylsilydiazomethane, "safer" because it is the liquid form. However, trimethylsilydiazomethane caused the death of two sciences since 2008. Gorin lab's mission is to find a better and safer reagent to do methylation. We propose Dimethyl carbonate (DMC) as a greener and safer alternative reagent for performing methylation reactions.

Previous work in the lab revealed that a methyl group can be transferred from DMC to a carboxylic acid. The optimized condition showed for each carboxylic acid nucleophile, 20 equivalents of DMC, 0.4 equivalents of cesium carbonate are required. The reaction was heated to 90oC and run over night. Mechanistic studies suggested that our reaction undergoes SN2 mechanism. However, to confidently come to this conclusion, multiple equilibrium tests had to be done to show the addition of methanol does not affect the reaction. I ran the reaction with and without methanol multiple times using Florine 19 NMR to quantify the data. Results showed that addition of methanol did not affect the reaction, which eliminated the equilibrium path way. Unlike a comparable Shei's condition that followed an equilibrium path way, our methylation reaction follows SN2 like mechanism. The successful SN2 methylation reaction inspired us to expand this method to other organ carbonates such as indoles to do ethoxylation.

Ethoxylation is a highly applicable reaction in medicinal chemistry. However, like methylation, current methods of ethoxylation use toxic reagents such as ethylene oxide, chloroethanol, and bromethanol. The Gorin lab put forth ethylene carbonate as an inexpensive, nontoxic, and "green" alternative reagent to perform ethoxylation. Previous work showed the transfer of ethyl alcohol from ethylene carbonate to indole. My goal was to optimize the reaction condition to increase the yield from 67%. Fluorine 19 NMR was used to quantify each data. I was able to replace dimethylformamide (DMF), toxic catalyst, to 1,8-Diazabicyclo[5.4.0]undec-7-ene (DBU). Experimenting with solvents, anisole gave a better yield and dissolved the reagents homogenously. To date, the optimized condition is for every indole, 25 equivalents of ethylene carbonate, 0.5 equivalent of DBU and 90oC are required for 71% yield. In the future, I will further optimize the condition by testing for strong bases such as NaH- and raising the temperature.

(Supported by NSF: National Science Foundation)

Advisor: David Gorin, Chemistry

Site-selective chemistry in complex systems

Sarah Krejci/2018

Site-selective reactions in biological systems have posed a significant challenge for scientists. While it is relatively easy to use a catalyst to target one functional group, it is more difficult to design a selective catalyst to target one instance of that functional group. DNA-small molecule catalyst conjugates, or DCats, aim to achieve site-selectivity by linking a DNA aptamer, which provides selectivity, to a small molecule catalyst, which provides reactivity. The DNA aptamer has a high binding affinity for the target molecule, and the small molecule catalyst performs the desired reaction. We hypothesize that when the DNA aptamer binds its target, the catalyst is held near the target molecule, letting it react with its target while leaving all other molecules intact. My research aims to assess and improve the function of DCats which selectively hydrolyze adenosine esters.

This summer, I synthesized a methyl umbelliferone ester using acetyl chloride, umbelliferone, and triethylamine. The methyl umbelliferone ester was used to test the selectivity of DCats which target cholic acid esters. The cholic acid DCats were tested with a cholic acid umbelliferone ester and with the methyl umbelliferone ester to see if it would react with a non-target molecule. I also synthesized DCats that target adenosine esters using imidazole as a catalyst and linkers with different lengths and attachment sites on the DNA aptamer. I assessed the function of these DCats using an adenosine umbelliferone ester. Hydrolyzing the ester releases umbelliferone, which fluoresces, so we can track reaction progress by measuring fluorescence intensity. The reaction rate is compared to imidazole controls.

The selectivity trials showed that 5 μM of cholic acid DCats hydrolyzed the cholic acid ester near the same rate as 500 μM imidazole, but did not hydrolyze the methyl umbelliferone ester. 10 μM of the adenosine DCats worked faster than equivalent concentrations of imidazole, with some DCats working as well as 100 μM imidazole.

The cholic acid DCats show almost perfect selectivity when comparing the cholic acid esters to the methyl ester, suggesting that they will be selective in a mixed system. The adenosine DCats provide an increased reaction rate in the presence of their target molecule. Further testing will reveal what qualities (such as linker length and attachment site) make the DCats most effective. This research has been presented at Celebrating Collaborations in 2016/2017 and will be continued as an honors thesis in this coming year.

(Supported by NSF: National Science Foundation)

Advisor: David Gorin, Chemistry

Base Pair Opening Kinetics of Damaged DNA Bases

Sally Kyale/2019

Damage to DNA bases is insidious as the genomic information stored within the DNA can be lost, and if the damage is left unrepaired, covalent chemical changes to the bases can lead to carcinogenesis or apoptosis. DNA bases occasionally undergo oxidation mediated by reactive oxygen species such as hydrogen peroxide, superoxide and hydroxyl radicals. Guanine bases are particularly susceptible to oxidation due to guanine's low reduction potential, which leads to a variety of oxidized guanine products. The most well studied guanine oxidation product is 7,8-dihydro-8-oxoguanine [1]. This lesion easily undergoes further oxidation to form the spirominohydratonin (Sp) lesion [2].

In an effort to understand the enzyme repair mechanism for the Sp lesion within the body, the goal of my research has been to compare and contrast the opening rates of a canonical GC base pair in an 11-mer DNA duplex with that of an 11-mer duplex containing an Sp lesion using Nuclear Magnetic Resonance Spectroscopy (NMR). The opening and closing of DNA base pairs occurs spontaneously and is important for DNA function It is proposed that the base pair opening may be important for the recognition of lesion by DNA repair enzymes. Using NMR analysis, quantitative data can be gathered detailing the opening rates in the control DNA duplex and the damaged DNA duplex containing the lesion further contributing to the discussion of how repair proteins recognition of damages Sp-DNA adduct.

In the course of my research this summer, I have succesfully been able to perform the preliminary experiments necessary for determining the rate of base pair opening. I have additionally been able to establish the ideal temperature to perform the experiments which offers maximal peak sepearation (Figure 1). I am currently working on experiments with added ammonia catalyst that will be necessary to measure the rates of base pair opening. I hope to continue with this research in the fall to arrive at conclusive base pair opening rates from which I will be able to move my research in other directions and hopefully analyze results from the Sp lesion and other DNA adducts as well.

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An Exploration of Mechanisms for the Transformation of 8-Oxoguanine to Guanidinohydantoin and Spiroiminodihydantoin by Density Functional Theory.

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(Supported by CFCD Committee on Faculty Compensation and Development)

Advisor: Elizabeth Jamieson, Chemistry and Biochemistry

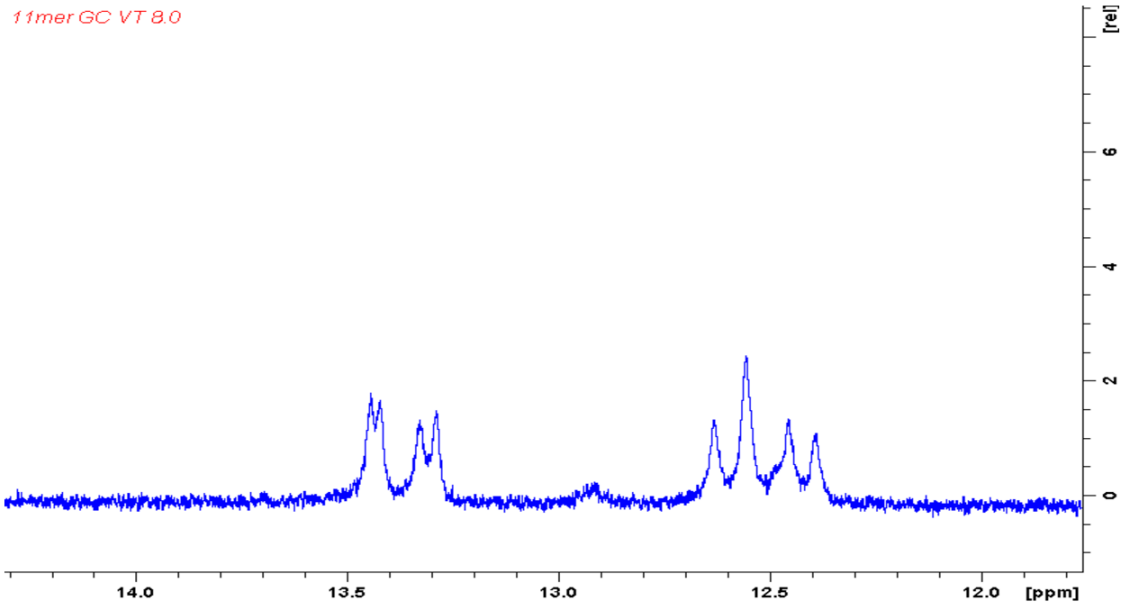


Figure 1.1D ^{1}H NMR Proton Spectrum showing Thymine and Guanine imino protons exhibiting optimal peak separation at 8 °C.

Synthesis and Isolation of Potential Cyclohexanol Anesthetics

Emma Livernois/2018

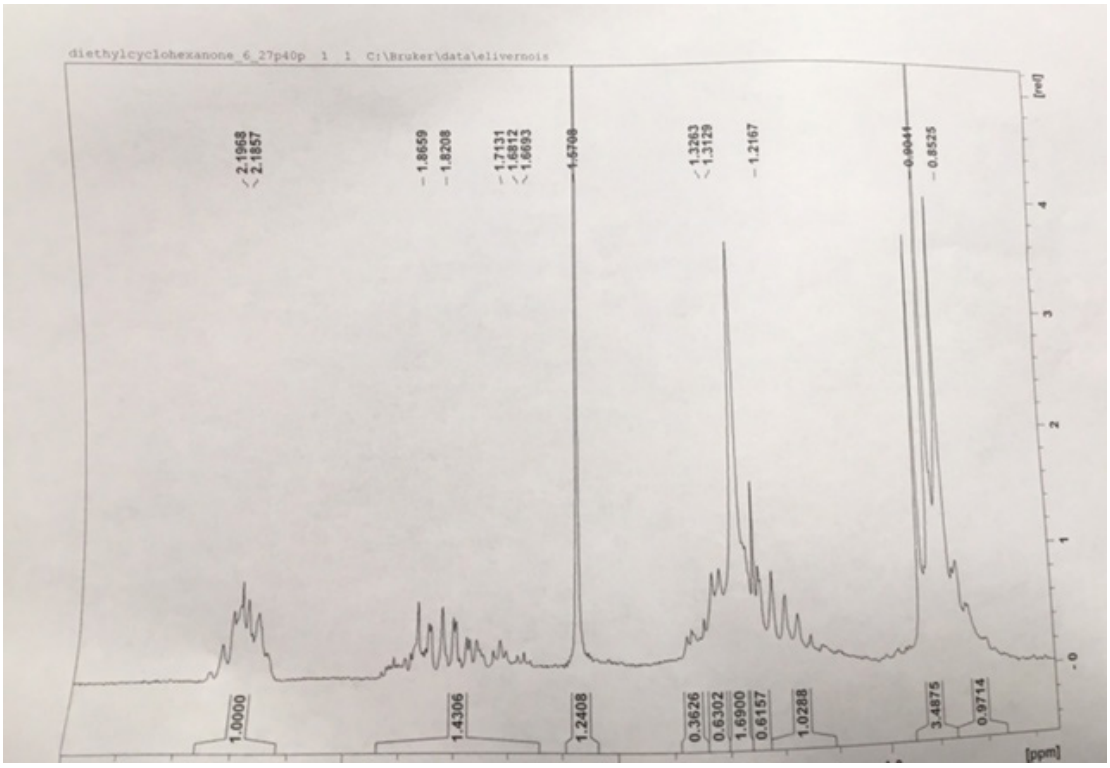
Propophol, or 2,6 Diisopropolphenol is a commonly used anesthetic; Professor Adam Hall has been doing research exploring whether geometrically similar disubstituted cyclohexanols had similar effects, potentially with fewer side effects or slightly different activity. In the Shea Lab, the focus is on isolating diastereomers of potential anesthetics for Professor Hall to use in his research.

This summer two disubstituted cyclohexanols were used in research, 2,6 Diethylcyclohexanol and 2,6 Dimethylcyclohexanol. Isolating the diastereomers of these compounds is not a straightforward task; pure mixtures cannot be separated into the diastereomers directly using common methods like column chromatography. Instead, both Diethylcyclohexanol and Dimethylcyclohexanol are oxidized into their respective ketones, Diethylcyclohexanone and Dimethylcyclohexanone. This can be accomplished through a Swern oxidation or an oxidation using Dess-Martin Periodinane. The ketone forms can be separated into a cis form where both ethyl or methyl groups are on the same side and a trans form where the ethyl or methyl groups are on opposite sides. These separated ketones can then be reduced with Lithium Aluminum Hydride. The cis ketone is reduced to a pair of alcohols which can be separated using column chromatography. The trans ketone is reduced to a pair of alcohols as well but these are inseparable. Thus it is possible to obtain trans-trans Diethylcyclohexanol, cis-cis Diethylcyclohexanol, and a mixture of trans-cis and cis-trans Diethylcyclohexanol.

These separations had been achieved previously but with low yield. The substances are quite volatile and must be purified carefully, usually via bubbling nitrogen through the sample to evaporate solvent. Over the course of the summer three samples of Diethylcyclohexanol were purified, oxidized, separated and reduced, and a sample of Dimethylcyclohexanone which had previously separated was reduced and further separated. Further work on this project will include attempts at further improving the methods to increase yield and to isolate other similar compounds which might have similar activity.

(Supported by CFCD Committee on Faculty Compensation and Development)

Advisor: Kevin Shea, Chemistry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Controlled Post-Polymerization Reaction Via Photolabile 1º Amine Protecting Group

Autumn Mineo/2019

The bulk of Dr. Maren Buck's previous research is based on various applications of azlactone-functionalized polymers with emphasis on the radically initiated polymerization of 2-vinyl-4,4-dimethylazlactone (VDMA) to synthesize poly(2-vinyl-4,4-dimethylazlactone) (PVDMA). Unique to PVDMA polymer networks, post-polymerization ring opening reactions are possible when in the presence of nucleophiles, such as primary amines, alcohols, or thiols [1].

A photo-caging strategy utilized by Christopher Bowman, in relation to a 'click' thiol Michael reaction commonly used in polymer network formation, provided inspiration for my summer research [2]. Post-polymerization crosslinking and functionalization reactions between PVDMA networks and photo-caged primary amines can be initiated by UV irradiation, via the degradation of 2-nitrobenzyl photolabile primary amine protecting groups.

To synthesize the photo-protected monoamine, 2-(2-nitrophenyl)propyloxycarbonyl hexylamine, and diamine, di 2-(2-nitrophenyl) propyloxycarbonyl hexamethylenediamine, modifications were made to the Bowman synthesis by the use of the starting material, 2,5-dioxopyrrolidin-1-yl(2-(2-nitrophenyl)propyl) carbonate, which was synthesized by methods discussed by Deforest et. al. [3]. Hydrogen nuclear magnetic resonance spectroscopy was used to demonstrate that the photo-protected monoamine and diamine were successfully synthesized with reasonable purity.

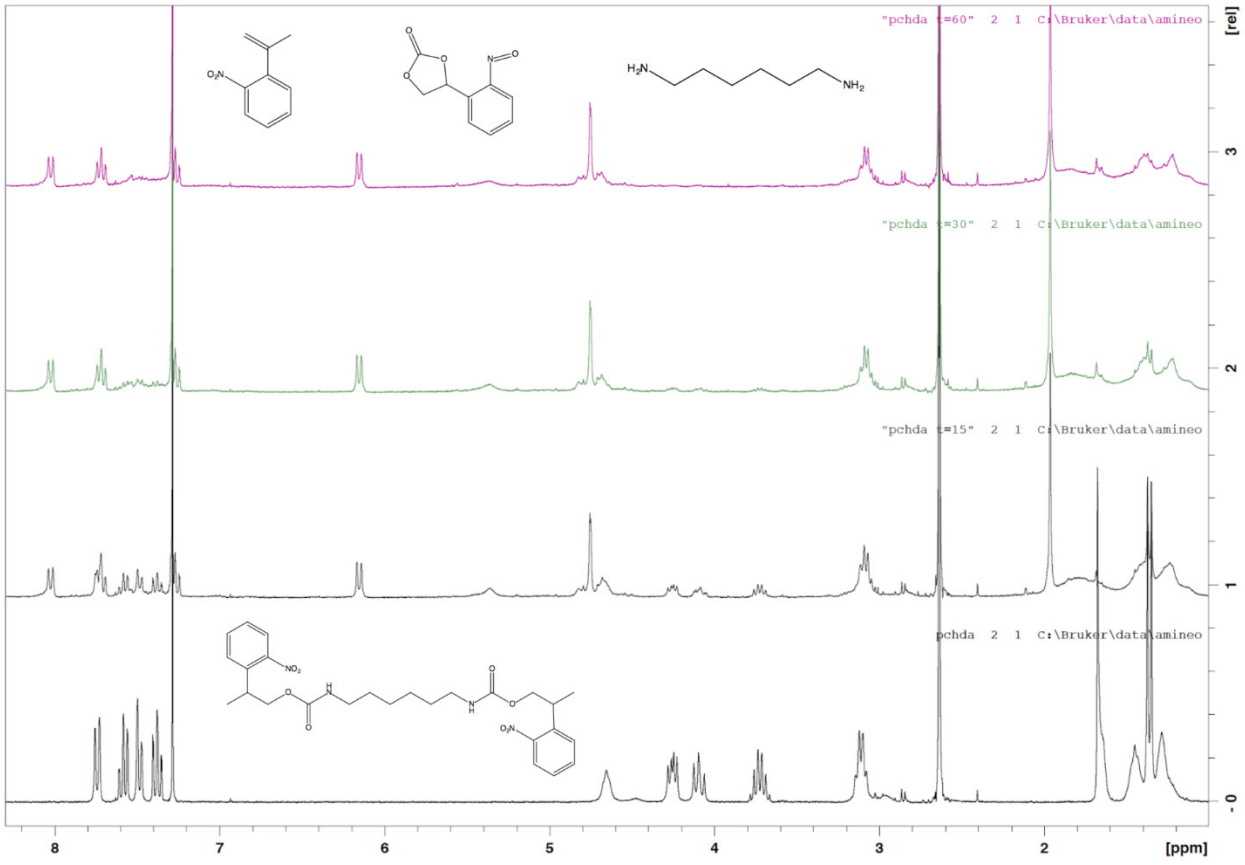
Functionalization studies of PVDMA by the photo-protected monoamine and diamine, monitored by infrared spectroscopy, yielded inconsistent data regarding the complete functionalization of available PVDMA, as the peak at 1820 cm-1, indicative of the carbonyl bond in PVDMA, did not decrease. This peak's presence could be the explained by a chemically similar carbonyl present in a byproduct of the photo-degradation: 4-(o-nitrosophenyl)-1,3-dioxolan-2-one.

Promising evidence of the complete degradation of the photo-protected diamine is seen in Fig. 1, which shows the 1H NMR spectra recorded at time 0, 15, 30, and 60 minutes under UV irradiation. The disappearance of the 4.26, 4.10, and 3.73 ppm hydrogen environments indicate that the photo-degradation had gone to completion, as these environments are not found in product molecules. Additionally, two new peaks form at 1.13 and 2.86 ppm, which are indicative of the formation of the intended diamine product. Moreover, all novel peaks have corresponding assignments in the two resulting byproducts of photo-degradation: 2-(2-nitrophenyl)-1-propene, 4-(o-nitrosophenyl)-1,3-dioxolan-2-one.

In order to further study the intended ring opening reaction between PVDMA and UV liberated photo-protected primary amines, methods of cleaning the photo-degradation byproducts from the polymer networks will be explored, as a means of proving its occurrence by IR spectroscopy.

(Supported by CFCD Committee on Faculty Compensation and Development)

Advisor: Maren Buck, Chemistry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Diagnosing Parkinson's Disease Using Salivary Dopamine Levels

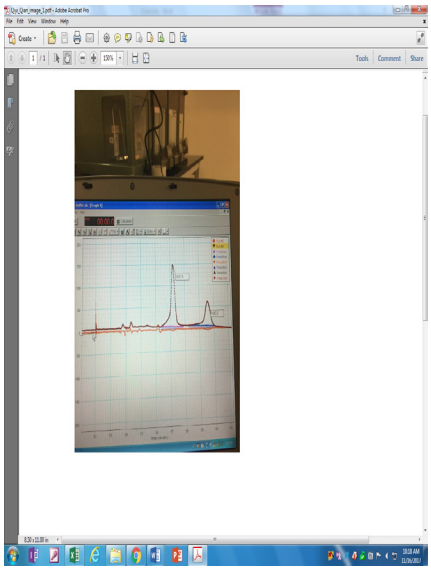
Qiyi Qian/2020

Diagnosing Parkinson's disease early and accurately is essential for effective medical intervention. The pathological symptoms of Parkinson's disease are caused by the loss of dopaminergic neurons in the substantia nigra. We believe that before the loss of these neurons occurs, dopaminergic neurons in the "enteric nervous system" (neurons associated with the digestive tract) are destroyed. If so, changes in the dopamine levels in enteric fluids, such as saliva, could provide an early biomarker for the diagnosis of Parkinson's disease.

To determine the dopamine levels in saliva samples, we first collected saliva using an oral swab placed under the tongue for two minutes. This method allowed us to collect saliva that was almost exclusively from the submandibular gland. The dopamine was then removed from the saliva chromatographically and quantified using high performance liquid chromatography with electrochemical detection (HPLC-ECD). We found that dopamine is unstable in saliva, and its concentration decreases over time. To identify where dopamine was being lost, we examined our dopamine purification procedures and carefully adjusted each step to improve the dopamine yield and the reliability of the assay. After many adjustments, our assay protocol was significantly improved. A critical improvement was the addition of "protectants," compounds that stabilize dopamine, to the saliva immediately after its collection. This decreased the rate of dopamine loss during its purification and elution. We are currently testing different methods for adding the protectants to saliva that will preserve as much dopamine as possible.

(Supported by CFCD Committee on Faculty Compensation and Development)

Advisor: David Bickar, Chemistry



Synthesis and Thermodynamic Analysis of a Cisplatin-Modified DNA 12-MER

Sheng Tian/2018

Cisplatin is a member of the platinum-containing anti-cancer drugs including carboplatin and oxaliplatin. It is widely used in the treatment of testicular cancer. Cisplatin binds to DNA, forming adducts that alter the helical structure of DNA, causing inhibition of DNA synthesis and leading to apoptosis. Cisplatin selectively binds to the N-7 atom of purine bases and forms 1,2-intrastrand cross-links as the major adducts (1).

In order to study the effect of a 1,2-intrastrand GG cisplatin adduct on a DNA duplex, I reacted the top strand of the 12-mer duplex below with a cisplatin solution that had been activated by silver nitrate to remove the chlorine ligands:

5'-CCT CTG GTC TCC-3' top strand

3'-GGA GAC CAG AGG-5' bottom strandThe resulting cisplatin-modified DNA top strand was separated and purified from the unmodified DNA top strand by using HPLC (Agilent 1200 Instrument). The cisplatin-modified top strand produced a peak with a high intensity that eluted at around 20 minutes that we collected, desalted, and concentrated. The purified cisplatin-modified 12-mer top strand was tested by ESI mass spectrometry to see if the right product was made. 12-mer DNA duplexes were made by annealing either the unmodified top strand or the cisplatin-modified top strand to the bottom strand. UV melting curves were obtained for the unmodified 12-mer control duplex at several different concentrations using a Hewlett Packard diode array spectrophotometer.

Thermodynamic data was obtained for the unmodified 12-mer duplex by performing a van't Hoff analysis of the melting curve data (Figure 1). The thermodynamic data for the unmodified DNA 12-mer duplex was compared to the data for a 9-mer DNA duplex that I obtained last summer (Table 1):

Table 1. Thermodynamic Data for 9-mer and 12-mer DNA Duplexes

Duplex	ΔH°	ΔS°	ΔG° at 298K
Unmodified Control 9-mer	-166 kJ mol-1	-404 J K-1	-45.9 kJ mol-1
Cisplatin-Modified 9-mer	-184 kJ mol-1	-478 J K-1	-41.4 kJ mol-1
Unmodified Control 12-mer	-305 kJ mol-1	-828 J K-1	-58.4 kJ mol-1

The thermodynamic data for the DNA 12-mer showed that it was enthalpically (ΔH°) more stable than the DNA 9-mer, presumably because more hydrogen bonds were made during duplex formation. The 12-mer showed a larger entropic (ΔS°) destabilization, consistent with the "enthalpy-entropy compensation" that is often observed in melting temperature studies of DNA duplexes (2). The Gibbs free energy values (ΔG°) showed that the DNA 12-mer overall was more thermodynamically stable than the 9-mer, again presumably because it has three additional base pairs. Thermodynamic studies with the cisplatin-modified 12-mer duplex will be carried out in the fall as part of my senior honors thesis project.

(Supported by Katherine C. Hauch 1921 Fund)

Advisor: Elizabeth Jamieson, Chemistry and Biochemistry

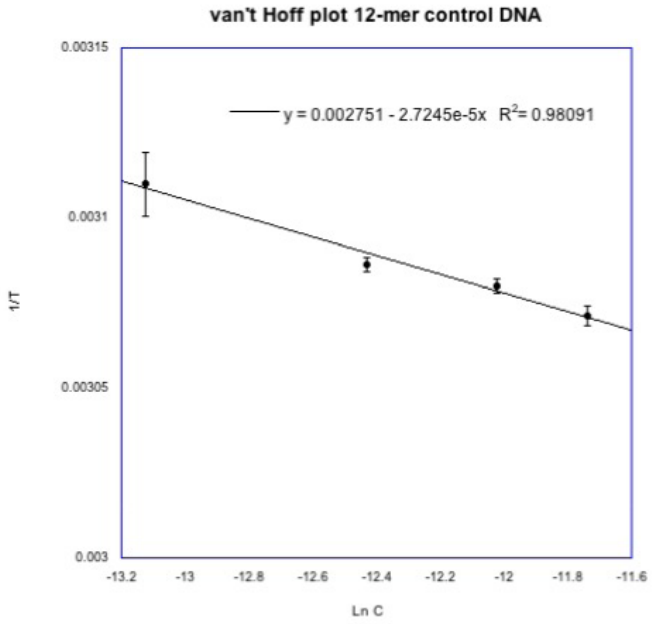


Figure 1. van't Hoff plot for DNA 12-mer. The melting temperatures, T_m, were measured at $\lambda = 260$ nm.

Hydrosilylation of oxidized Si(100) surfaces

Claire Vinson/2019, Amanda Barriscale/2018, and Xinyuan Chen/2018

The chemical and topographical functionalization of silicon surfaces is biologically significant: exploring the multifunctionalization of these surfaces could provide insights into biofilm growth [1,2]. In past work, the Queeney Lab has striven to increase the library of Si(100) surfaces through multifunctionalization [3,4]. Previous results have suggested that hydrosilylation is not site specific and occurs on both hydrogen-terminated and oxidized Si(100) surfaces [3]. However, a paper published by the Bent group suggests that hydrosilylation only occurs on hydrogen-terminated surfaces [5]. Research conducted this summer attempted to explain the discrepancies between the Bent group and the Queeney Lab and to enhance understanding of the hydrosilylation of oxidized Si(100) surfaces.

Sample surfaces initially underwent either an mRCA or Piranha cleaning procedure. Treatment with HF etchant yielded hydrogen-terminated Si(100) surfaces. Surfaces underwent two-hour hydrosilylation and standard post-hydrosilylation cleaning procedures [3]. Surface infrared spectroscopy (FTIR) was used to analyze the CHx region while ellipsometry was used to determine the thickness of the alkyl layer formed after hydrosilylation.

Our initial hypothesis surrounding hydrosilylation of oxidized surfaces relied on the presence of SiH bonds as defects in the wet chemical oxide layer [6]. Under this assumption, hydrosilylation would occur to a lesser extent on samples with a wet chemical oxide layer than those that were hydrogen-terminated and would not occur at all on samples retaining a thermal oxide layer. However, hydrosilylation took place in equal amounts on thermal oxide (74%) and wet chemical oxide (73%) samples, as shown in Figure 1. It is important to note that the quality of the alkyl layers on the H-terminated and oxidized samples differs: because the asymmetric CH2 stretch is red-shifted for the H-terminated surface when compared to the two oxidized surfaces, the alkyl layer on the H-terminated surface is more crystalline [7].

In an attempt to match procedures used by the Bent group, hydrosilylated samples were cleaned through Piranha treatment.5 Hydrosilylation occurred, but to a lesser extent (41%) than on samples that had undergone mRCA cleaning. Changes in post-hydrosilylation cleaning procedures, such as sonicating for longer amounts of time or in less polar solvents (hexanes, petroleum ether), were proposed to investigate whether physisorbed or polymerized alkyl chains were providing misleading evidence for hydrosilylation. However, the thickness of the alkyl layer remained relatively consistent (~ 20 □) despite changes in cleaning procedures.

Since specific procedures used by the Bent group are referenced in an as-of-yet unpublished paper, we have been unable to replicate their cleaning and hydrosilylation procedures. Gaining access to these details would allow us to better understand differences between the Bent group's practices and our own. We also aim to investigate whether there is precedent for radical reactions, like hydrosilylation, to occur with an alkene and a silanol. Further research will be conducted via a special studies course in the upcoming fall semester.

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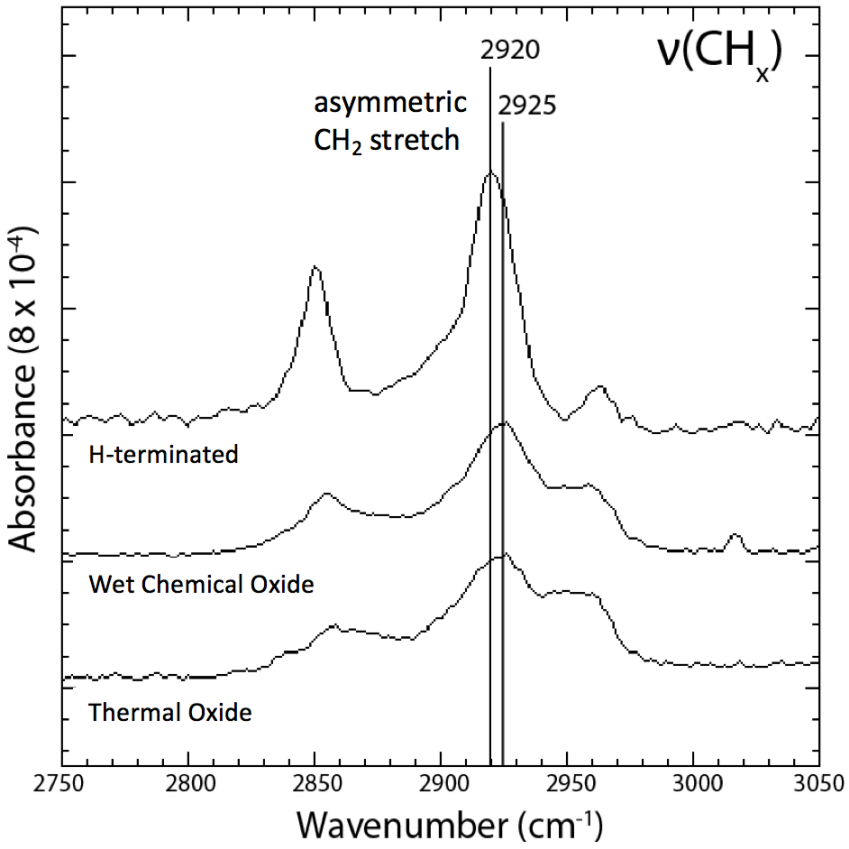
Figure 1. FTIR spectra of hydrogen-terminated, wet chemical oxide, and thermal oxide Si(100) surfaces after hydrosilylation.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Kate Queeney, Chemistry



Development of a Tandem Diels-Alder/Pauson-Khand Strategy for the Synthesis of Tetracycles

Eve Xu/2020 and Sarah Lee/2019

The Diels-Alder reaction dominates the developments in steroid synthesis (1). To further study the role of Diels-Alder reaction in steroid synthesis, we hope to develop a one-pot, tandem Diels-Alder/Pauson-Khand reaction strategy to convert acyclic molecules to cyclic compounds in one step. Specifically, we hope to transform an acyclic tetraenyne into a tetracyclic molecule that resembles steroid molecules by using a cobalt-complexed alkyne to promote the Diels-Alder reaction followed by a Pauson-Khand reaction. It is believed that the cobalt-complexed alkyne can be used as an electron-donating group to activate the diene in a Diels-Alder reaction, in which the diene and a dienophile react to form a six-membered ring. The overarching goal is to determine whether the cobalt-complexed alkyne plays a role in increasing the rate of the Diels-Alder reaction, which will provide a new, faster synthesis of the carbon backbone of steroids.

Research this summer focused on the modification of Wittig and Grignard reactions, the last two steps of tetraenyne synthesis proposed by Katie Blackford '17. The two-step yield Katie got from aldehyde 8 to molecule 9 was only 8%. Due to this low yield at the last two steps of the synthesis, we devised two methods to optimize the Wittig and Grignard reactions: 1) To synthesize Wittig reagent 13, eliminating one step in the transformation from compound 8 to compound 9. 2) To alter Katie's reaction sequence, moving low yielding Wittig and Grignard reactions toward the beginning of the synthesis. For the first method, we could not form the new Wittig reaction since the Grignard reaction that yields Wittig reagent 13 failed to work for all of our attempts. The second method was more promising with the new Grignard reaction going to completion within an hour. Future work on this project includes the accumulation of molecule 9 with our new synthesis scheme to successfully run the tandem Diels-Alder/Pauson-Khand reaction. Both of us will continue the work on this investigation as our special studies project in the upcoming school year.

Reference

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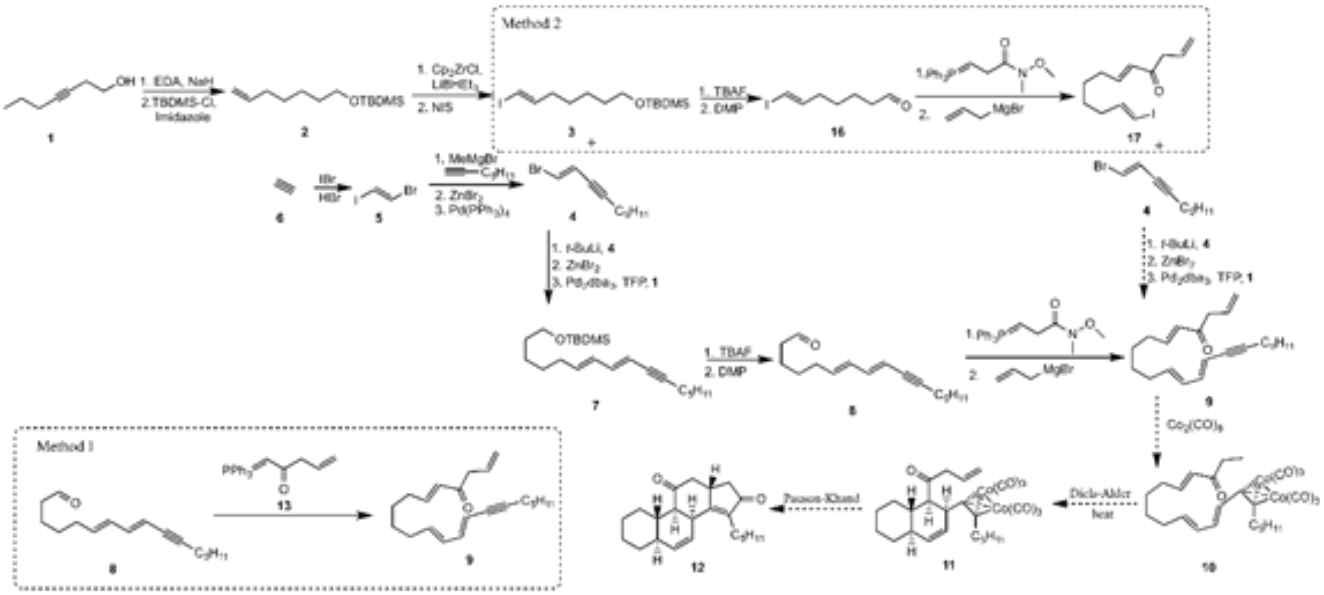
(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Kevin Shea, Chemistry



Scheme 1. Reaction scheme with the new synthesis methods boxed.

Photoinitiated RAFT Polymerization of VDMA and Characterization of Photodegradable PVDMA Hydrogels

Shuran Yang/2019

Because the reactivity of azlactone enables hydrogels to attain more tailored properties, poly(2-vinyl-4,4'-dimethylazlactone), or PVDMA is selected as the main polymer to make gels in the Buck lab [1]. As we aim to investigate the influence of molecular weight on gel properties and to make block copolymers, the prerequisite is to produce well-defined PVDMA via controlled polymerizations, such as reversible addition−fragmentation chain transfer (RAFT) polymerization [2]. Previous work in the lab has proved that well-defined PVDMA can be made by thermal-initiated RAFT in the presence of AIBN as the thermal initiator and S-1-dodecyl-S'-(α,α'-dimethyl-α"-acetic acid) trithiocarbonate (DDMAT) as the chain transfer agent (CTA). In order to make more well-defined PVDMA under mild conditions and with easier operation, we attempted to polymerize VDMA through photo-initiated RAFT (Figure 1) [3]. Based on literature, polymerization of VDMA was conducted under long-wave UV irradiation with a high concentration of DDMAT, but there was no sign of polymer shown in the GPC data. In future studies, different monomers will be tested for photo-initiated RAFT using DDMAT as the CTA. We will also work with other CTAs to make photo-RAFT PVDMA.

With their physical and chemical properties tunable temporally and spatially with light, photodegradable hydrogels are valuable biomaterials for regulating cellular microenvironments and have found numerous applications in tissue scaffolding and drug delivery [4]. The Buck lab continues to synthesize and study photodegradable hydrogels in the hopes that they will aid in the topographical and chemical patterning of PVDMA hydrogels and controlled photorelease of potential drugs [5]. Following the work of Isabella McNamara ('16), I repeated the assembly of the photo-cleavable PVDMA hydrogel (Figure 2) using 2-nitro-1,3-benzene dimethanol as the crosslinker and further characterized gel degradation under UV irradiation by NMR and ATR-IR spectroscopy. It was proposed that after the crosslinker reacted with PVDMA polymeric chains, an ortho-nitrobenzyl (o-NB) ester functionality formed at the crosslinking joint, and by UV irradiation it can photoisomerize into a corresponding ortho-nitrosobenzaldehyde, releasing a free carboxylic acid [5]. However, the spectral data collected were not convincing enough to prove the proposed degradation. We will continue to improve the way of characterizing the degradation and will work with different o-NB-based photolabile crosslinkers.

Figure 1. Proposed photoinitiated RAFT polymerization of VDMA with DDMAT as the CTA.

Figure 2. Assembly of photodegradable PVDMA hydrogel using 2-nitro-1,3-benzene dimethanol as the crosslinker and proposed degradation of the gel based on the light degradable property of the o-NB ester.

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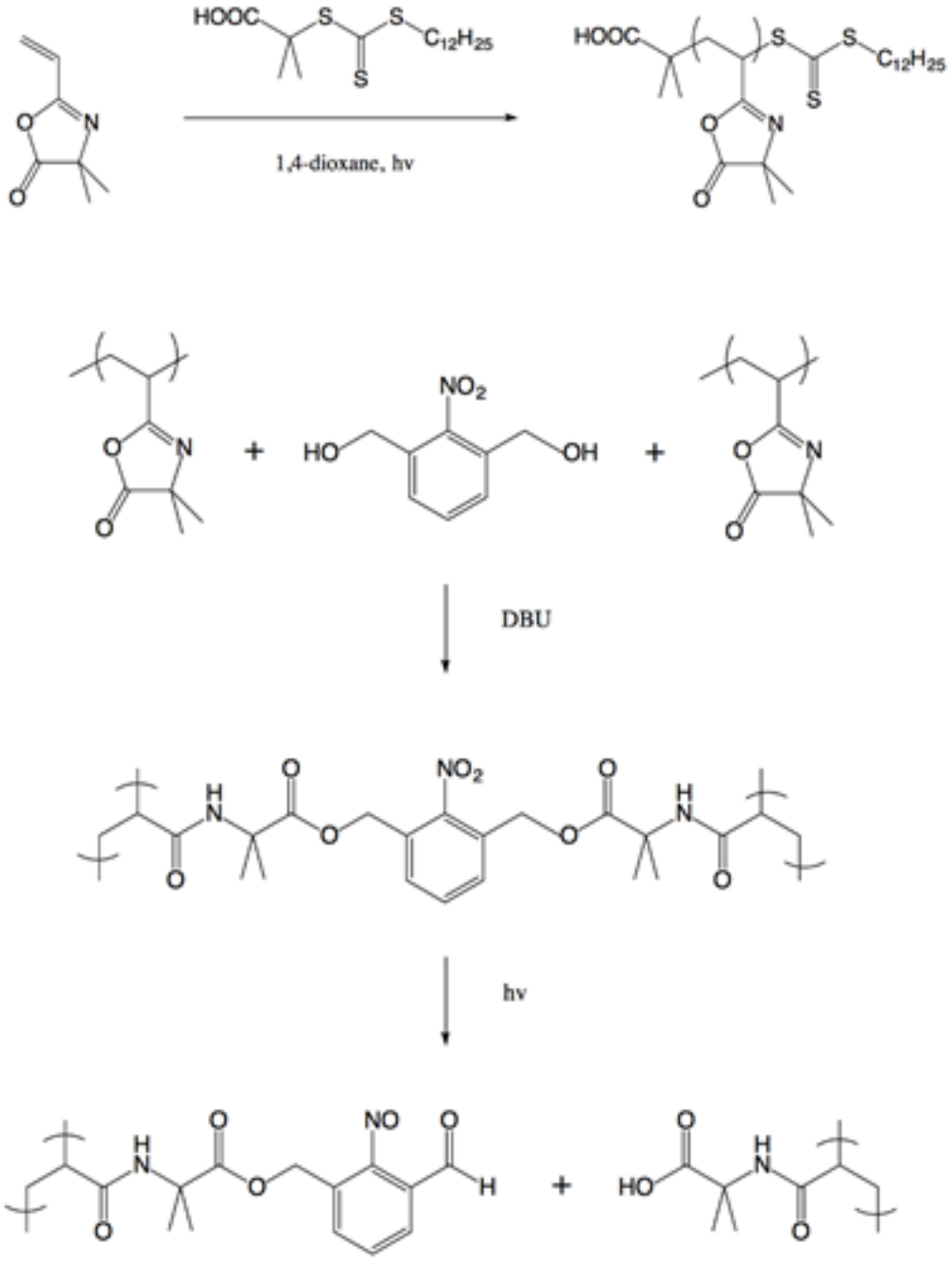
(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Maren Buck, Chemistry


HOOC
S
S
$C_{12}H_{25}$
S
1,4-dioxane, hv
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H

A DNA-Catalyst Enzyme Mimic for Site-Selective Transformations in Biological Systems

Yueyu Yao/2018

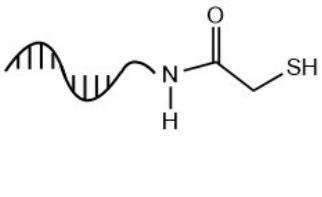
When more than one instance of a functional group is present in a mixture, strategies to selectively modify the target molecule and leave other substances undisturbed are needed to pursue synthesis of desired product or labeling of a specific target. For instance, introducing a non-selective catalyst into a biological system enhances the rates of desired and undesirable reactions comparable, and it may destroy the system. In the past, many approaches have been developed to deal with the problem, but we keep thinking if there is a method that can be generalized to have a potentially unlimited scope of applications.

To address the problem, we propose to use conjugates of DNA aptamers and small molecule to perform site-selective reactions. Inspired by that most enzymes possess selectivity due to their nature of having a binding domain and a catalytic domain, we designed DNA-catalyst (DCat) enzyme mimics, in which the DNA aptamer functions as the binding domain for substrates and the small molecule catalyzes the intended reaction. The DNA aptamers are short artificial DNA strand, developed to have high affinity for desired substrates through specific three-dimensional interaction. Nucleophilic catalysts are covalently linked to the DNA aptamers, and they attack the substrate once it binds. By physically holding the target substrate and catalyst close to each other, DCat is theorized to increase the effective concentration of substrate, thus enhancing the reaction rate selectively.

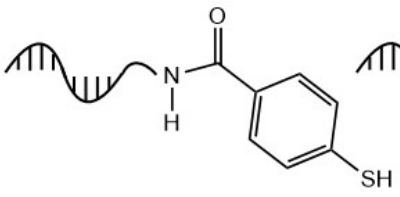
Previous research in our lab has demonstrated that DCat 1 is capable of increasing the reaction rate of umbelliferone-cholic acid ester hydrolysis as efficiently as small molecule catalyst on its own with 100 fold concentration. To prove the enhancement of reaction rate is selective, we tested DCat 1 against esters that it does not has an affinity for. During the summer, I worked on the synthesis of esters that can be used in control experiments and collaborated with others in lab to synthesize umbelliferone methyl ester. The next step is to vary the small molecule catalysts installed onto DCat, to prove the potential of generalizing this concept. Started with imidazole, we are now looking forward to 4-Dimethylaminopyridine (DMAP), thiols, and thiophenols. As the steps for proof-of-concept process built up gradually, DCat is a promising tool for doing site-selective chemistry in future.

(Supported by NSF: National Science Foundation)

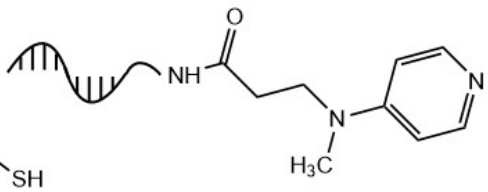
Advisor: David Gorin, Chemistry



Thiol-DCat



Thiophenol-DCat



DMAP-DCat

Machine Learning Experiments on Isolated Character Samples from Syriac Manuscripts

Minyue Dai/2020

A large data set of securely dated Syriac letters is available for future research, and several experiments based on convolutional neural networks(CNN), such as character classification, character denoising, and style detection for characters are tested on this data set. These applications will be set up as a baseline for possible future work, and all of them are built on similar network structure.

The basic architecture of these models (Fig. 1) relies on combination of convolutional layers and fully connected layers. This model consists of 3 convolutional layers with 2x2 pooling layers, and each uses 5x5 kernels with a stride of 2. Then the output is unfolded and fed into 2 fully connected layers. The generator in style detection mirrors this architecture and instead uses 3 deconvolutional layers with unpooling layers. In practice, the input and output will be modified based on different applications.

For the letter classification, the model tests on two different data sets: cleaned and raw data. The size of Syriac letter can vary dramatically for different types of letters, and the extra noises in raw data will add on difficulty. The classification accuracy on test set is 93.2% on raw data and 99.2% on cleaned data.

The goal of the Denoise experiment is removing extra noises on raw data. There are two modes: Denoise and conditional Denoise (CDDenoise), and the later one takes both images and images' labels as input. The denoising results are shown in the picture (Fig. 2), and F-measure evaluated in test set are 79% and 82% for each, proving that conditional structure adds little improvement on this task.

The most complicated application is the style detection for characters. A conditional generative adversarial network (GAN) plays an adversarial game: generator, which takes a randomly generated z vector (length 100 in this experiment) as input, wants to produce fake image that are as realistic as possible to fool discriminator; discriminator aims to distinguish fake inputs from real ones. Then this model will be transferred to be an autoencoder, which encoder(discriminator) can generate z vector from real images. This z vector encodes writing style information for future experiments, such as dating.

Figure 1: Architecture Details of Models (Discrminator in GAN)

Figure 2: Examples of Denoise Result. The top to bottom rows are: original input, target cleaned images, row output from the model, binary output with threshold of 0.5.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Nicholas Howe, Computer Science

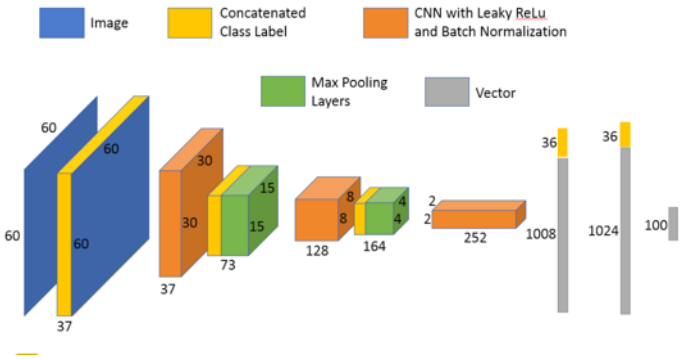


Image
Concatenated Class Label
CNN with Leaky ReLu and Batch Normalization
Max Pooling Layers
Vector
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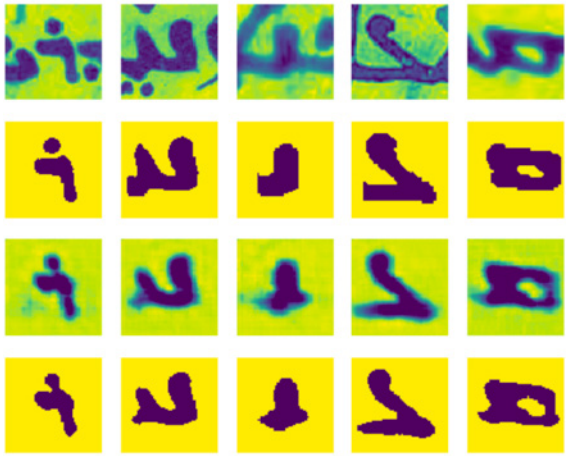


Collaborative:RUI: Mathematical foundations of reconfiguration algorithms for geometrically constraint structures

Xuanqi Lyu/2020

During the summer, I worked on small projects that extracts data from protein and molecules downloaded form RCSB. The data I extract is mainly the atoms labels, their element symbols, and their x, y, and z coordinates in three dimensions. However, some proteins might appear with different models which are the same proteins, but in different unit position when viewed. To extract the models, I had to keep track of the fact that despite of the fact that the atoms have different positions, they are still the same atoms. Other than models, proteins also contains irregular atoms and residues, like solvents and ligands. Solvents are atoms or small molecules like water molecules floating around the protein, and ligands are non-standard residues, other than the 20 regular residues, which are connected to the regular molecules and proteins. I got to write programs extracting just the ligand, and read lines in original protein files to get the pairs of atoms that are connected by all the bonds. Other than that, I have adapted the way of invoking programs and other apps on my laptop from the command line, and to invoke programs and apps from other programs. There are also macromolecules of proteins. There exist in RCSB proteins and viruses with more than 100,000 atoms. The number of atoms in these files is over the capacity of pdb file and cif files. Therefore, they invent another file type called pdbx, which split a macromolecule into several 100,000 atoms, and put each section into its own pdb file. I have also written programs to extract different residues and certain clips of a protein, that can either take just the residue names, or a list of residues. The program would open and write to a file that contains only the atoms that belong to that residue or a certain chip of the protein chain. I have also written a program that can be used to test the files other people write on a large dataset. It basically runs the program over and over again on the data file in a folder. That worked very well during the whole SURF process when I was debugging the code.

(Supported by SURF Gifts Fund)

Advisor: Ileana Streinu, Computer Science

Uptake of E. coli and MS2 by B. calyciflorus and Daphnia Magna in Natural Systems

Brittney Blokker/2017 and Rowan Turner/2018

Ecosystems are more resilient when water is pollutant-free, since clean water is a necessity to maintaining life. Filter feeding organisms have the potential to remove water contaminants therefore increasing the quality of water sources they are present in. Our project aims to develop an understanding of uptake rates of the bacteria E. coli K12 the the MS2 bacteriophage by Brachionus calyciflorus, a species of Rotifer, and Daphnia Magna. This information can be used in the future to develop a model to predict performance of filter feeding organisms in natural systems.

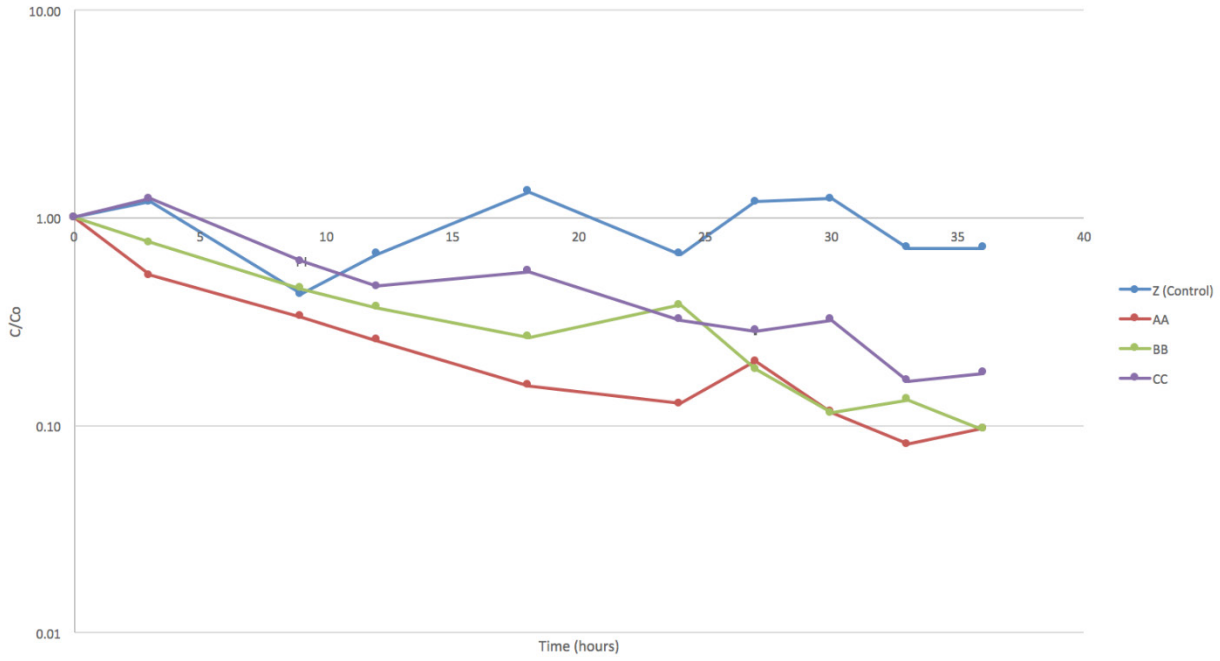
Feeding experiments with daphnia and rotifers were carried out with varying experimental parameters, including temperature, initial contaminant concentration, and zooplankton concentration, in order to gain a holistic understanding of their feeding habits on E. coli K12. Zooplankton were divided into beakers - the rotifers were concentrated at this time - and starved for 24 hours before being spiked with the contaminant. Water samples were taken at set intervals for up to 48 hours. These water samples underwent membrane filtration, then the filters were placed on selective mTEC agar plates before being incubated and analyzed. By analyzing the plates, it was possible to determine the exact concentration of E. coli in the water at the time of the sample.

Additionally, MS2 was propagated and enumerated using a double-layer plaque assay method. Preliminary feeding experiments with daphnia, in which water spiked with MS2 was sampled at set intervals over a span of 24 hours, were carried out using similar experimental conditions to those of the E. coli and daphnia experiments. To determine if MS2 retains its infectivity under the typical conditions of rotifer and daphnia feeding experiments, along with daphnia's ability to tolerate specific changes in water quality parameters, tests were conducted to understand the resilience of MS2 and daphnia following various treatments. This included resuspending MS2 pellets after centrifugation and altering the conductivity of daphnia-containing water, among other treatments. This preliminary data will allow us to proceed with feeding experiments and gather data relating to MS2 uptake rates by daphnia and rotifers.

Moving forward, we will continue feeding experiments on MS2 with varying experimental parameters just as we did with with the E. coli K12 experiments. We eventually plan to conduct feeding experiments with these contaminants and algae, the natural food source for these organisms. This will allow us to gain a greater understanding of the preferential feeding habits of these zooplankton species and how the sorption of E. coli and MS2 to larger algal particles impacts the rate of uptake.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Niveen Ismail, Engineering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Origami and Kirigami for Auxetic Materials

Elizabeth Boahen/2020

Paper engineering is a tool that can solve problems in a multitude of fields by folding and cutting paper can inexpensively display traits or mimic fabric that is rare or expensive. This allows engineers and material scientists to observe the behaviors of auxetic materials. Auxetic materials are mediums where when pulled in one direction, the volume of the medium increases in all directions. This is similar to a Hoberman sphere—where a rubber band would become longer and thinner when stretched, a Hoberman sphere becomes a larger sphere. A paper model of auxetic material would allow researchers to understand and physically interact with aspects of auxetics that occur on a microscopic level and the models can apply these patterns to materials.

This can be achieved through tessellations. Multiple tessellations and folds expressing auxetic qualities were created and observed (Fig 1).

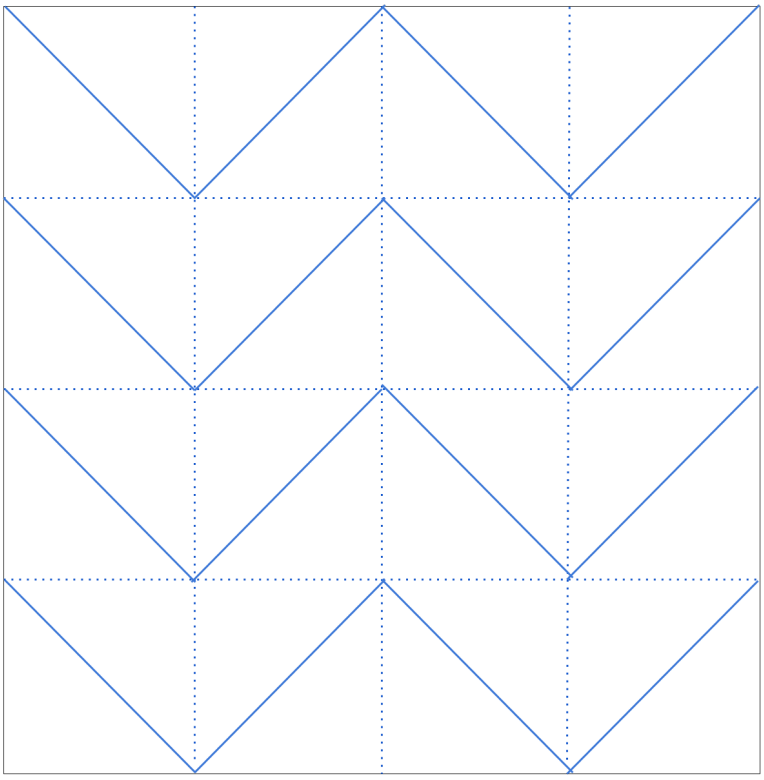
The Twisted Squares were simple and accurate paper models of the functions of an auxetic material but were difficult to translate into a material. However, the tessellations could be called auxetic materials all on their own. Though each model was created from single sheets of paper, the tessellations responded to force as auxetic material should and had a pattern to them which made the tessellations more like a fabric than paper. The Water Bomb naturally curves thus—if applied on a larger scale—the pattern could be a used in material aimed to respond to respond bending curves such as knees. The Herringbone became the focus of this research due to its simple and resilient nature. When flattened, the tessellation is a grid—16 by 16 on the tessellation second from the right and 32 by 32 on the other (Fig 1)—with alternating diagonals in each row (Fig 2). The tessellation twisted, turned, stretched, expanded, and stiffened in response to force making it adaptable to curves, corners, and hyperbolic paraboloid. Thus, the Herringbone would be a versatile pattern to use in a polymer.

After the Herringbone tessellation was chosen, the rest of this project revolved around Eco-flex. Eco-flex is a biodegradable polymer. Researchers can make elastic molds with capacitance using Eco-flex and the Herringbone tessellation can make that mold responsive to arms and wrists. This is a fascinating collaboration between engineering an art but one that needs further research due to the infinite possibilities of the Herringbone. The diagonals created in the grid for the Herringbone can be any value that is greater than 0° and less than 90° and the angles created when folded still need to be measured. Further research is needed to develop the equation that would show the relationship between these dimensions for the Herringbone to be used as a mold.

Fig 1: The Twisted Square on the left and left of center, the Water Bomb to the right of center, and two Herringbone tessellations to the right.

(Supported by SURF Gifts Fund)

Advisor: Kristen Dorsey, Engineering



The Fabrication of Soft Sensors that Detect the Rotation of Human Forearm

Meng Cao/2019

Soft sensors are often made to attach to skin to detect motion. The movement of limbs and joints will cause deformation of the sensor and therefore results in changes in its electrical properties like capacitance, resistance, and inductance. This paper will focus on how the capacitance of the soft sensor reacts to torsion, such as in the rotation of human forearm, which ranges approximately 180° from supination to pronation.

The goal of this project is to design a capacitive torsion sensor spanning the length of the forearm. Capacitors with twisted tubes and capacitors with parallel tubes are fabricated and compared to find out which one is able to give a one-to-one relationship between the rotation angle and the capacitance. With the relationship, the sensor can reflect the rotation of forearm from the change in its capacitance. This will allow scientists to better understand how the forearm rotates to complete daily tasks and to design robotic prostheses or exosuits to help people who have problem with forearm rotation.

To ensure the stretchiness of the sensor, Ecoflex, a type of silicone rubber, is used as the substrate and two parallel pieces of silicone tubing are used as the channels in which liquid metal (galinstan) is injected to form the electrodes. The capacitive sensor is 20 cm long and a 3D printer is used to fabricate the mold for the sensor. Three device types are fabricated and differ by the number of times the electrode tubes are twisted around each other: none, twice, or three times. Each device is tested on a torsion tester and a human forearm to study the relationship between the capacitance and the rotation angle.

Data shows that capacitors with tubes twisted three times act the best as torsion sensors on forearm. The maximum capacitance shift measured is 0.1 pF from 0° to 180°. However, the capacitors have a detection limit of 30°.

For future work, capacitors with more twists could be fabricated and studied to understand the phenomenon and therefore reduce the limit. In addition, a testbed will be built in order to better simulate the movement of a forearm.

My lab partner Becky Shen and I submitted a full paper to the 2017 IEEE MIT Undergraduate Research Technology Conference. If selected, we will present our work in the conference.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Kristen Dorsey, Engineering

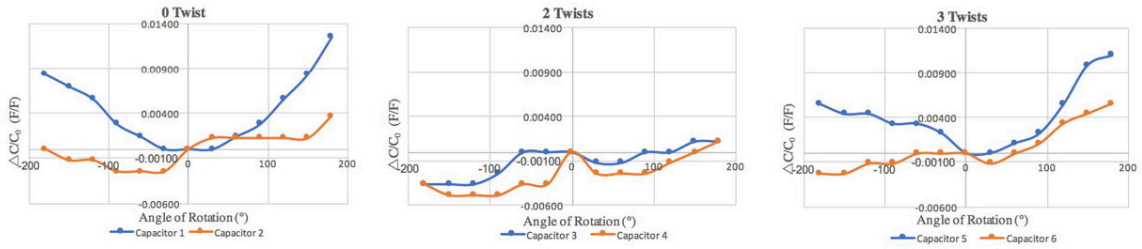


Fig. 2. Normalized capacitance for three types of capacitors on torsion tester

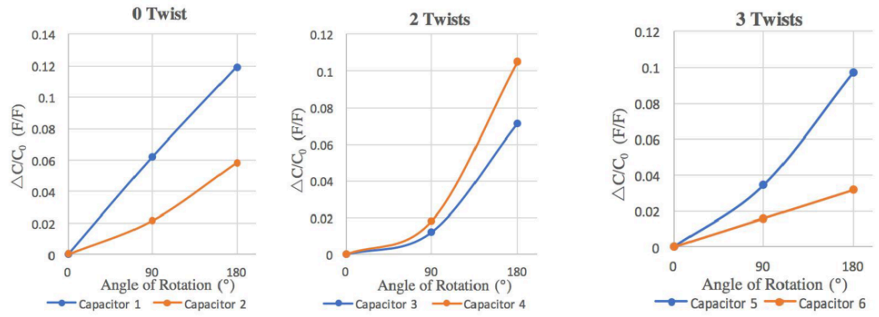


Fig. 3. Normalized capacitance for three types of capacitors on a human forearm at supination (0°), neutral position (90°) and pronation (180°).

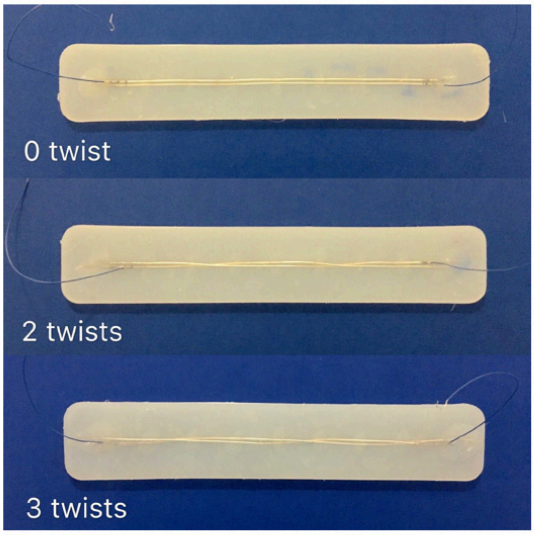


Fig. 1. Three types of completed capacitors with wires inserted

Estimating Thermal Dynamics in a Continuous Feed Biomass Torrefier

Isabella Casini/2017

This research used experimental data from continuous feed torrefaction of woody biomass to create a simple thermal model of that system. Biomass torrefaction is a heat treatment process that chemically converts woody biomass to more physically and energetically favorable gas and solid products. A computationally simple model produces faster responses, which is attractive when using the model for real time control with embedded controllers, potential future work. The research considered woody biomass species from the Northwest of the United States including redwood, tanoak, hardwood slash, Douglas fir, and Douglas fir tops. This biomass is currently being slashed and burned; however, torrefaction provides a way to access this wasted energy. This study, joint with the Schatz Energy Research Center (under the U.S. DOE "Waste to Wisdom" project), used a pilot-scale continuous feed electrically heated screw conveyance torrefier. Proximate analysis data was first analyzed finding that as degree of torrefaction increases (mass yield decreases), the volatile matter mass fraction decreases, the fixed carbon mass fraction increases, and the ash mass fraction stays roughly constant.

During experimentation, there was evidence of combustion, which given the operating temperatures would have been possible only if air had entered the system (possibly through the inlet and outlet airlocks). To confirm this suspicion, elemental composition through an elemental balance was used to attempt and estimate the quantity and composition of the products leaving in gaseous phase, of which there is little experimental data. Reducing the need for expensive specialized instrumentation, the proximate analysis data with two different models was used to predict elemental composition for the raw and torrefied biomass. To complete an elemental balance, while assuming that the gaseous phase product is primarily composed of carbon monoxide, carbon dioxide, and water vapor, it is confirmed that air must have entered the reactor. Under these assumptions, an experimentally motivated range of the quantity of air entering the torrefier was calculated and used to better model the thermal dynamics of the torrefier, the next part of this research.

The thermal model was designed depicting the thermal dynamics occurring to constituents in the torrefier during torrefaction. The thermal data gathered from thermocouples placed along the length of the torrefier are used as reference for the model. During experimentation, air (at top of the torrefier) and product or biomass (at bottom of the torrefier) temperatures were measured. The current model was optimized by reducing the sum of the squared residuals between the experimental data and the modeled values. This optimization was completed using an unconstrained cost function in MATLAB to tune parameters.

An error analysis was conducted on previously calculated higher heating values. A sensitivity analysis showed that temperature was the most influential parameter when determining higher heating values. Variation (standard deviation) for the higher heating values was found using first order error propagation and showed that feedstock was not a statistically significant parameter.

(Supported by SURF Gifts Fund)

Advisor: Denise McKahn, Engineering

Evaluating the Global Water and Sanitation crisis: A Case Study on Bangladesh

Tasbiha Chowdhury/2019

1 in 10 people lack access to clean water. In 2015, it is estimated that 663 million people worldwide still use unimproved drinking water sources, including unprotected wells, springs, and surface water. The majority of them now live in two developing regions; nearly half of all people using unimproved drinking water sources live in sub-Saharan Africa, while one fifth live in Southern Asia. The aim of my research project was to identify the factors that influence water and energy shortages in developing countries. I conducted a case study on a South Asian country, Bangladesh.

Primarily through literature review, I built a thorough understanding of how water and energy resources are distributed in Bangladesh. I examined existing international developmental efforts and connected with organizations as well as interviewed relevant people to collect data. I identified two possible pathways that can help mitigate Bangladesh's water and sanitation crisis; One of which is to persuade large institutions such as universities and hospitals to harvest rainwater at least for non-potable use. Another way is to educate and train the poverty-driven slum population about building appropriate cost-effective latrines for their communities which can recover waste that can be converted into nutrients as well as energy.

This research experience was valuable for me as it provided me with a direction that I can now take to work towards implementing a human-centered design project that will deal with the water, energy and sanitation crisis in Bangladesh.

Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Denise McKahn, Engineering

Environmental Effects on Water Quality and E. coli Concentrations in an Ephemeral Stream at MacLeish Field Station

Ruby Kohn/2019 and Tyler Feeney/2019

At the Ada and Archibald MacLeish Field Station, an ephemeral stream currently runs through a forested area before flowing into a cattle pasture where water quality has been impaired by fecal inputs from grazing cattle. According to the United States Environmental Protection Agency (USEPA), fecal indicator bacteria (FIB) are the leading cause of impaired water bodies. Not all FIB are pathogenic but they are good indicators of fecal contamination that has the potential for human infectious diseases (1). Escherichia coli (E. coli) is a useful and well-studied FIB found in freshwater because it is a common gut bacteria in mammals and birds. The Smith College Center for the Environment, Ecological Design, and Sustainability (CEEDS) is currently planning a restoration project for the stream that will include rechanneling and limiting access by cattle. This summer, we collected additional baseline data regarding water quality before restoration to augment initial data collected in summer of 2016.

To measure the effect of the cows' fecal input on water quality, we sampled 15 locations in both the upstream forested region and the downstream cattle pasture on 5 separate occasions. At each sample point the turbidity, pH, conductivity, temperature, and dissolved oxygen were measured with probes. E. coli was enumerated by dilution, membrane filtration, and plating on a selective media. We found that the upstream E.coli concentrations were on the same order of magnitude of the EPA standards for recreational water of 126 colony forming units/100 mL (1), while the downstream concentrations tended to be 10 to 100 times higher. To compare E. coli concentrations and water conditions to location in the stream, a full statistical analysis will be completed.

Zooplankton abundance can be used as another measure of water quality because select species of zooplankton uptake microbial pollutants through filter feeding. These species feed on microbial pollutants like E. coli by pushing the surrounding water over permeable tissue to absorb food. We have previously quantified the uptake rates of E. coli by specific species of zooplankton through batch experiments in laboratory conditions. To gain a broader understanding of the ephemeral stream's water quality and the function of zooplankton in natural systems, we collected and preserved concentrated samples from both up and downstream of the cow pasture. To further understand the role of zooplankton in the system we will enumerate them in these samples and compare the data to the E. coli levels and water conditions to determine if there is a correlation.

Studies have shown that solar radiation can inactivate E. coli in water (2). To explore the role of sunlight inactivation on E. coli levels of the ephemeral stream, we completed a diurnal study where we sampled one point upstream and one point downstream every hour for 36 hours. The forested upstream region has more tree coverage than downstream, so there was variation in sunlight. We collected data using the same water quality parameters and enumerated E. coli using the same methods. We compared our data to solar irradiance collected continuously by the weather station at MacLeish. While a full statistical analysis needs to be completed, our preliminary findings show that there was no significant sunlight inactivation in the stream.

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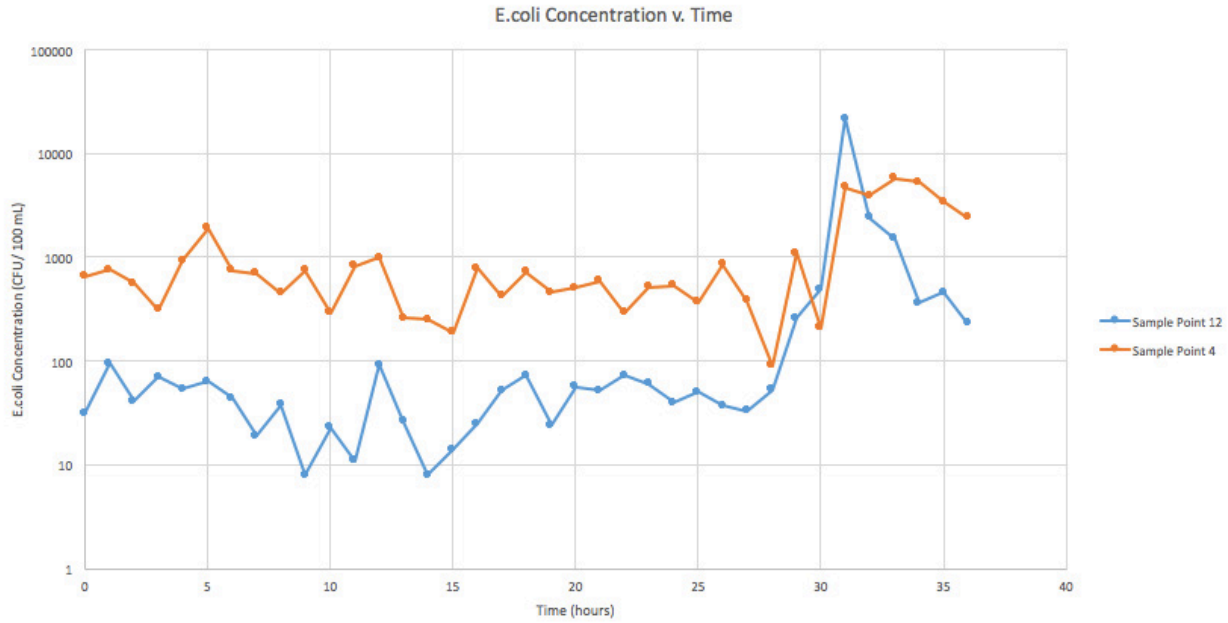
2. Whitman, R. L., M. B. Nevers, G. C. Korinek, and M. N. Byappanahalli. "Solar and Temporal Effects on Escherichia Coli Concentration at a Lake Michigan Swimming Beach."Applied and Environmental Microbiology 70.7 (2004): 4276-285. Web.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Niveen Ismail, Engineering


E.coli Concentration v. Time
E.coli Concentration (CFU/ 100 mL)
100000
10000
1000
100
10
1
0
5
10
15
20
25
30
35
40
Time (hours)
Sample Point 12
Sample Point 4

Engineering Proteins for Health Application

Naomi Murata/2019 and Analia Vazquez Cegla/2018

Our project focuses on engineering proteins that would transport therapeutic drugs into the brain to treat diseases such as Alzheimer's. The goal is to create a protein that gets transported into the brain using naturally occurring transport processes. We would then attach a specific drug to this protein to be delivered into the brain. We know that native transferrin protein passes into the brain through receptor mediated transcytosis. Previous members of the lab have engineered proteins that binds to transferrin receptors, using a fibronectin protein scaffold, in hopes that our protein-drug conjugates will also be internalized into the cell and transported into the brain. As the cells in the blood brain barrier contain a high concentration of transferrin receptors, this ensures a targeted delivery of drugs to the brain.

This summer, we focused on producing and purifying engineered proteins. We transformed BL21(DE3) bacteria with plasmids that contain the DNA sequences of our desired proteins. We then grew a large scale culture and induce it to produce the proteins. The cells were lysed to release proteins into the supernatant, and the resulting mixture was purified through His-purification as our proteins were made with a hexahistidine tag. To further purify the proteins, we conducted size exclusion chromatography and checked samples using western blots to see which protein peak corresponded to our engineered protein. We are currently working on optimizing the cell lysing procedure.

This summer, we also worked on a collaboration project with the Buck Lab which consists of conjugating our engineered proteins to polymers. The idea behind this is that although our proteins are target specific, they lack the ability to carry a therapeutic drug to their target. This issue could be addressed by conjugating our proteins to polymeric micelles, which do have the potential of encapsulating therapeutic drugs. Previous work showed conjugation of model proteins, lysozyme and BSA, to linear polymeric structures. We decided to test the same principle using transferrin, a natural occurring protein that transports iron. Through titration binding assays, we obtained triplicate data of the binding affinity of transferrin to its receptor on MCF-7 cells. Through internalization experiments, we saw encouraging data that suggests that transferrin could be internalized by cells even when conjugated to polymer. We are currently planning more experiments to determine the binding affinity of transferrin conjugated to polymer and to get more conclusive data about its internalization.

(*Supported by NIH: National Institute of Health)*

Advisor: Sarah Moore, Engineering

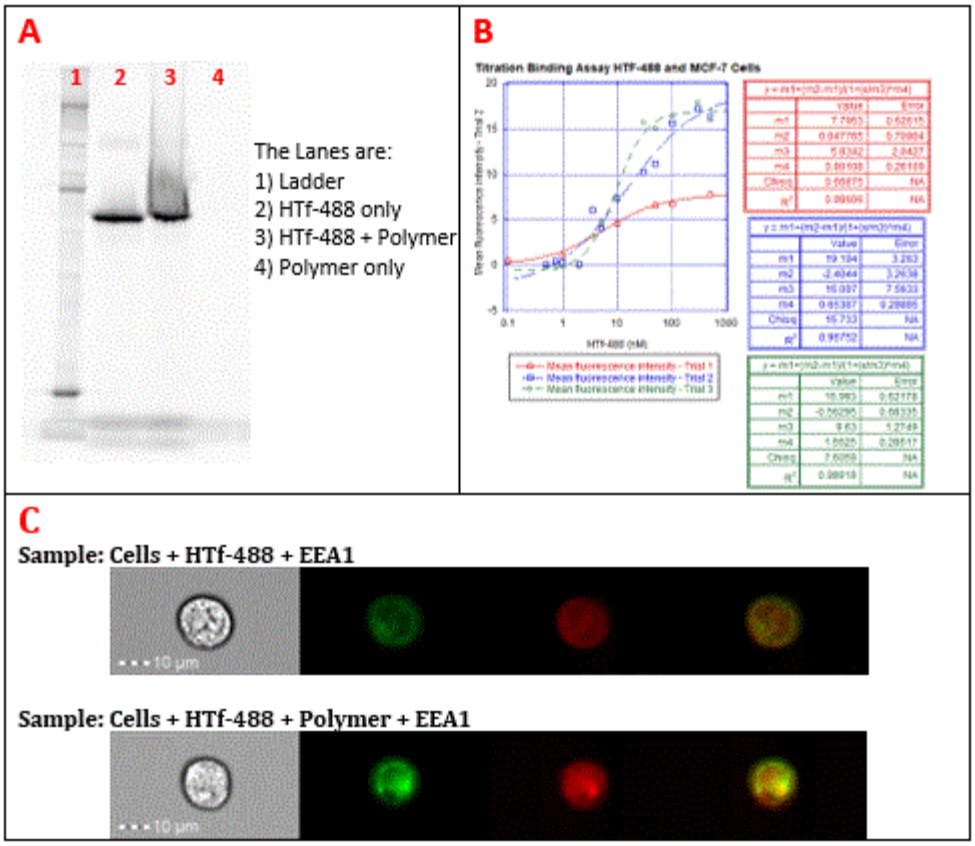


Figure 1. **A)** Results of the protein to polymer conjugation experiment. Lane 3 shows that the protein stretched at high molecular weights, which indicates conjugation of protein to polymer. **B)** Triplicate data of the binding affinity of Holo-transferrin to the transferrin receptor on MCF-7 cells. The binding affinity was found to be K_D = 10 +/- 4 nM. **C)** Results of the internalization experiment of HTf-488 and MCF-7 cells, using an endosomal marker labeled with Alexa 647 (EEA1). Results show that protein got internalized by cells.

Investigating Alternative Geothermal Energy Sources for Smith College

Gwenyth Naness/2019

Smith College has set a goal to achieve carbon neutrality by 2030. They hired an external energy consultant group which develop a multistep plan, involving the installation of a geothermal heat pump at Smith. Geothermal heat pumps draw energy from the Earth for heating and cooling for buildings. A set of pipes is installed in underground with a conducting fluid circulating through them. Throughout the year, at a certain depth, the ground remains a moderately constant temperature, therefore with a geothermal heat pump, heat from the ground is transferred through the pipes to heat the buildings in the winter and heat is dumped into the ground from the buildings in the summer.

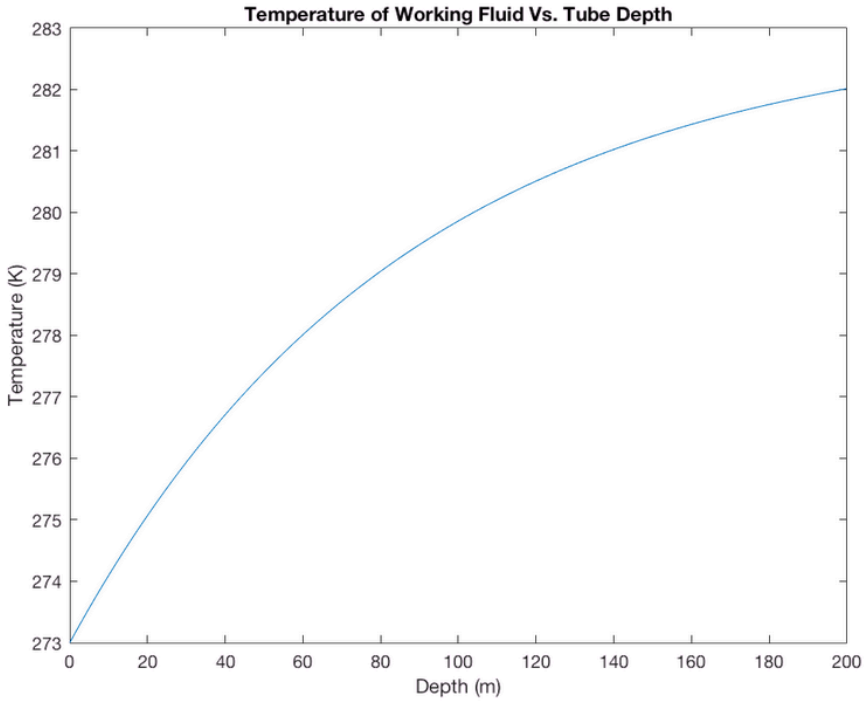
For my SURF project, I looked into the feasibility of installing the geothermal heat pump at Smith by researching multiple methods and configurations used by large institutions. A spreadsheet was created to collect data from known facilities with a heat exchange system, focusing on universities including Skidmore College, Ball State University, and Stockton University. A survey was sent to these facilities to gain more insight on their process and learn which ones could be most helpful to Smith. The survey gathered data points such as their prior heating and cooling systems and the amount of heating and cooling that the exchange system supplies for their current needs.

Parameters for the geothermal heat exchange system were collected from these universities and a model of how heat is transferred to the pipes was developed using those parameters. Figure 1 is a simple 1-D model showing the heat transfer. As the parameters are shifted in the model, the shape of the curve shifts. With this set of parameters, the curve begins to level off at around 200 m which shows what an approximate depth for the pipes could be. The model proved useful in determining which factors were significant and which had little impact on the heat transfer.

During the 2017 Fall Semester, I will continue working on this project to determine the feasibility of installing a geothermal heat pump at Smith College.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Denise McKahn, Engineering


Temperature of Working Fluid Vs. Tube Depth
Temperature (K)
283
282
281
280
279
278
277
276
275
274
273
0
20
40
60
80
100
120
140
160
180
200
Depth (m)

Materials and Animal Mimicry - Teaching Mechanical and Bioengineering through Adventures

Ha Le Phuong/2019

The study of materials fathoms almost all branches of engineering. An early understanding of basic concepts of materials' properties can advance children to a deeper understanding and quicker interpretation of the behaviors of numerous objects in real life: why can a rubber band be stretched, why it is easier to break a glass mug rather than a plastic mug? However, in order to deliver related mechanics concepts such as stress, strain, ductility, brittleness, and fatigue, to children of 10-13 years old, it requires more than simple verbal definitions.

Understanding this challenge, the "Through My Window" project led by Professors Glenn Ellis and Alan Rudnitsky is using Kieran Egan's "an imaginative approach to teaching" to design online learning adventures associated with Sonia Ellis's second book "The TimeTilter," which focuses on mechanical engineers and bioengineers.

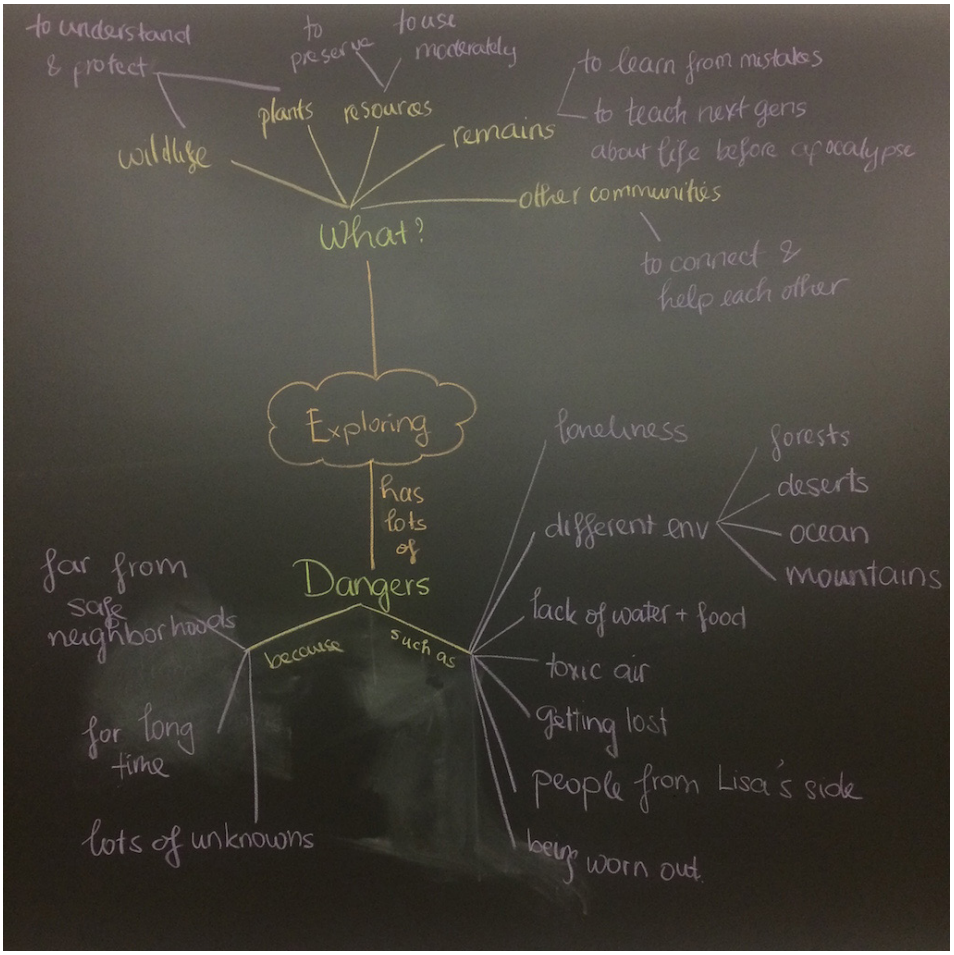
This summer, I played a crucial part in the project's substantial progress by using my knowledge in engineering and other sciences to create a captivating follow-up story that can engage students in learning about properties of materials and useful mechanisms in nature (biomimicry) in order to unfold the mystery of the book. With the help of the professors and other team members, I managed to incorporate a wide range of knowledge such as types of heat transfer, strength of materials, and camouflage strategies to build up some designing failures, which not only framed the requirements for the final designing task, but also acquainted students with the idea of learning from mistakes. Moreover, with a view to guiding students' thinking during need-finding, we created many scenarios analyzed by engineer characters in the story to model real-life discussions among engineers. We also referred to experiments done by scientists and famous engineering accidents such as Tacoma Narrow Bridge Collapse to enrich students understanding of an engineer's duties, ethics, and qualities.

In addition, I was able to create a set of resources that can assist students during their learning adventure. This includes a materials toolbox written in suitable language to children that comprises materials of extreme abilities, such as low density, high strength, high thermal protection, and good camouflage. Besides this toolbox, there are also a wide variety of external links to biomimicry ideas that can be of use along the way.

When the website is launched and becomes a part of the curriculum, the effect of this imaginative approach will be assessed and the adventures will be improved as needed.

(Supported by SURF Gifts Fund)

Advisor: Glenn Ellis, Engineering


to understand & protect
to preserve
to use moderately
wildlife
plants
resources
remains
to learn from mistakes
to teach next gens about life before apocalypse
other communities
to connect & help each other
What?
Exploring
has lots of
Dangers
because
such as
far from safe neighborhoods
for long time
lots of unknowns
loneliness
different env
forests
deserts
ocean
mountains
lack of water + food
toxic air
getting lost
people from Lisa's side
being worn out

Technical Education Satellite

Sarah Chu/2019

The development of CubeSats provide a cost-effective platform for scientific investigation and the testing of new technologies. The purpose of the Technical Education Satellite (TechEdSat) project is to demonstrate the efficiency and effectiveness of two different technologies. The first being a communication and tracking system using the Iridium constellation. Currently, the team is using the Iridium modem to uplink and downlink packets between the satellite and the ground. Eventually, a swarm tactic would be utilized to communicate between a series of CubeSats. There would be an uplink to the closest satellite which would then send the signal through the swarm until the command reaches the correct satellite to execute. The second being the development of an Exo-Brake. The Exo-Brake is a high-density parachute-like drag device with the ability to rapidly de-orbit the payload. This device uses two hard struts and two soft struts connected to the payload. This allows us to send a signal to the system that will turn on the winches to modify the ballistic coefficient of the Exo-Brake and guide the spacecraft to a desired location in the atmosphere. The final goal for the Exo-Brake is to direct a controlled payload and land back on the ground. TechEdSat will be a great step towards retrieving samples from space, and a profound opportunity for interplanetary nano-satellites to be utilized on small missions to the surface of Mars.

(Supported by SURF Gifts Fund)

Advisor: Andrew Guswa, Engineering


sarah_chu_1.pdf - Adobe Acrobat Pro
File Edit View Window Help
Create
Tools
Comment
Share
National Aeronautics and Space Administration
Technical Education Satellite
Sarah Chu [1], Hailey Johnson[2], Marcus Murbach [3], Ali Guarneros Luna [3]
[1] Smith College, [2] University of Idaho, [3] NASA Ames Research Center
ABSTRACT
The purpose of the Technical Education Satellite (TechEdSat) project is to demonstrate the efficiency and effectiveness of two different technologies. The first being a communication and tracking system using the Iridium constellation. Currently, the team is using the Iridium modem to uplink and downlink packets between the satellite and the ground. There would be an uplink to the closest satellite which would then send the signal through the swarm until the command reaches the correct satellite to execute. The second being the development of an Exo-Brake. The Exo-Brake is a high-density parachute-like drag device with the ability to rapidly de-orbit the payload. This device uses two hard struts and two soft struts connected to the payload. This allows us to send a signal to the system that will turn on the winches to modify the ballistic coefficient of the Exo-Brake and guide the spacecraft to a desired location in the atmosphere.
Small Payload Quick Return
ATROMOS
Image result for galaxy background
EXO-BRAKE
The exploded diagram to the right shows the modulated tension drag device that guides spacecraft to a desired location.
The graph on the right shows that a lower ballistic coefficient allows for a faster deorbit. The target ballistic coefficient is 1 kg/m² and the drag coefficient is 2.2 kg/m².
COMMUNICATION & TRACKING
Cricket Wireless Sensor Module
Sends packets to satellite
Wi-fi capabilities
Data & video downlink
Iridium
Uplink & downlink
Control & Data
GPS
ACKNOWLEDGEMENTS
A special thank you to Marcus Murbach, Ali Guarneros Luna and the TechEdSat team for their support and guidance.
www.nasa.gov
SMITH COLLEGE
10:09 AM
11/16/2017

Automation of Strain Tester and Reaction of Capacitance of Soft Sensors According to Rotation of Human Forearm

Qinghan Shen/2019

The recent development of flexible sensors leads to the potential for new applications, such as biomedical monitoring, robotics and wearable communications. The research on how the characteristics of sensors react to deformation caused by strain or torsion is of great significance. This project focuses on two parts: the automation of the strain tester and the reaction of the capacitance of the soft sensor according to torsion, such as in the rotation of human forearm.

Methods

A. Automation of Strain Tester

The first part of the project is divided into two main steps: designing the structure of the tester and programming the motor. A Sherline 6559 Single-Axis slide and a Sherline 67130 Stepper Motor are used. A pair of film grippers is designed with Solidworks and then printed on a 3D printer. The two grippers are used to fix the soft sensors. They are installed on the slide and one of them can be moved by the motor. Therefore, the operator is able to stretch the samples automatically by sending commands to the motor.

In order to program the motor, I used a motor shield (Synthetos gShield V5) installed onto an Arduino Uno board. The gShield is powered by a voltage supply of 24V and the Arduino board is plugged into the wall. Processing is used to communicate with the gShield through the USB port. The Processing program asks the user for how far the motor should move in total and how far it should move between each capacitance measurement. The motor will then be moved to a certain distance accordingly.

B. Reaction of Capacitance of Soft Sensors According to Rotation of Human Forearm.

Capacitors with tubes twisted twice and three times and those with parallel tubes are fabricated. The capacitors were tested firstly on a torsion tester and then on a human forearm. A torsion tester (Instron 55MT Micro Torsion Testing System) are used to simulation forearm rotation. The dimensions of the socket drives of the torsion tester are taken. A pair of clamps that can fit onto the socket drives are designed with Solidworks and then printed with a 3D printer. The two clamps were installed onto the torsion tester. The capacitor was clamped by two opposite edges and suspended horizontally. Then the left edge was rotated from -180° to 180° to twist the capacitor. The rotation was stopped every 30° and the corresponding capacitance was measured with a capacitance-to-digital converter (Analog Devices EVAL-7746) when the capacitor was at rest. After the test on a torsion tester, the capacitor is attached to a human forearm with Elmer's glue to test the efficiency of simulating forearm motion with a torsion tester. The forearm was rotated to three positions— supination (0°), neutral position (90°), and pronation (180°) and the capacitances at these positions were measured.

Results

A. Automation of Strain Tester

The Processing program takes two variables in mm— the total distance moved and the distance moved per interval. The program can then calculate how many times the motor should move. If the total distance cannot be divided exactly by the interval distance, the motor will move further than the total distance to keep each interval distance constant. The motor stops for 3 seconds between each movement to allow the capacitance of the sensor to be read. The coordinates of the motor and the total distance moved are printed out after each movement.

B. Reaction of Capacitance of Soft Sensors According to Rotation of Human Forearm.

The direction of twist of the two tubes in the capacitors is defined as the positive direction. A successful sensor for measuring this rotation should monotonically increase or decrease its capacitance from 0° to180° and have sufficient sensitivity to distinguish 0°, 90°, and 180°. Both the capacitors with no twist and the capacitors with tubes twisted twice fail to achieve this goal. However, for the capacitors with three twists, the capacitance increases monotonically after 30° in the positive direction: the relationship between the angle of rotation and the normalized capacitance can be described by a one to one function. Therefore, the capacitors with three twists perform the best as a torsion sensor, but have a detection limit of 30°.

The test on human forearm shows that a torsion tester cannot fully simulate the motion of human forearm, but it can serve as an initial measurement to compare the sensitivity of each kind of capacitors.

Discussion

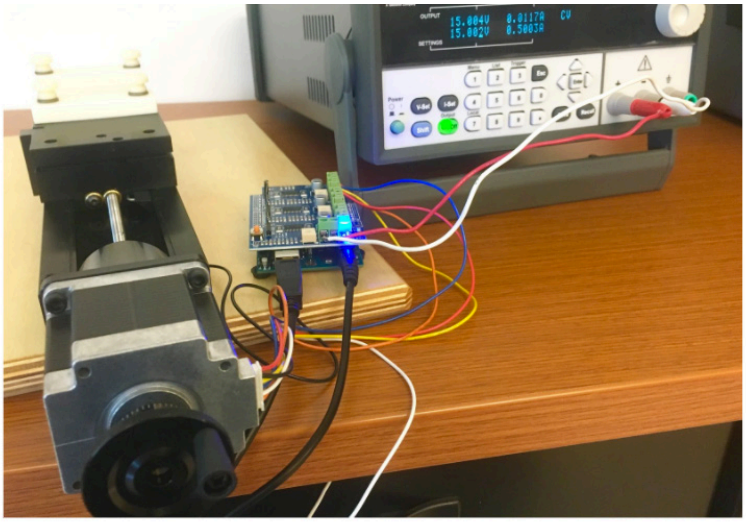
The new strain tester will significantly save the cost of research on flexible sensors, since human testers will not be required to move the grippers and the result will be free from human error. In the future, the program will be improved to control the capacitance-to-digital converter to read the capacitance automatically when the motor stops and to save both the coordinates and the capacitances to a certain text file.

For the study on the reaction of the soft sensors capacitances according to human forearm rotation, capacitors with more twists will be fabricated and studied to understand the relationship better and to minimalize the detection limit. A testbed that can better simulate forearm rotation will be built as well. Since the sensors are soft, stretchable and non-toxic, they have wide application in areas, such as artificial muscles, soft robotics and wearable devices.

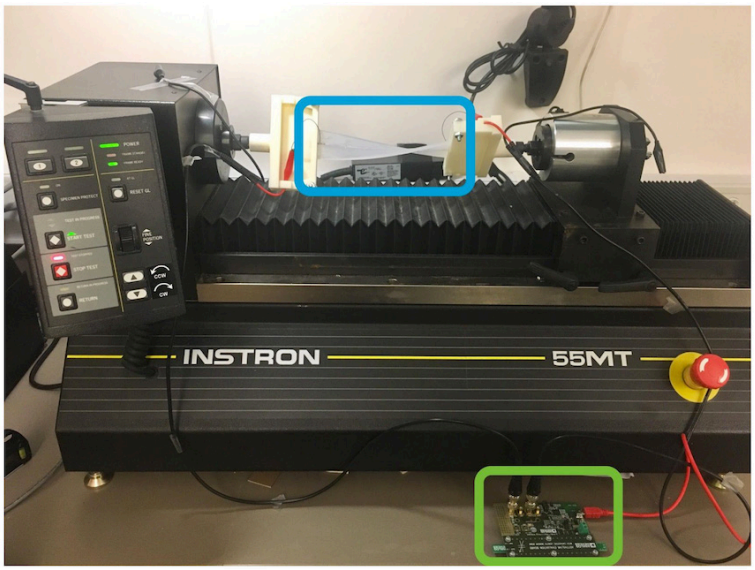
*My partner, Meng Cao and I submitted a paper about the reaction of soft sensors capacitances according to human forearm rotation to IEEE MIT Undergraduate Research Technology Conference.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

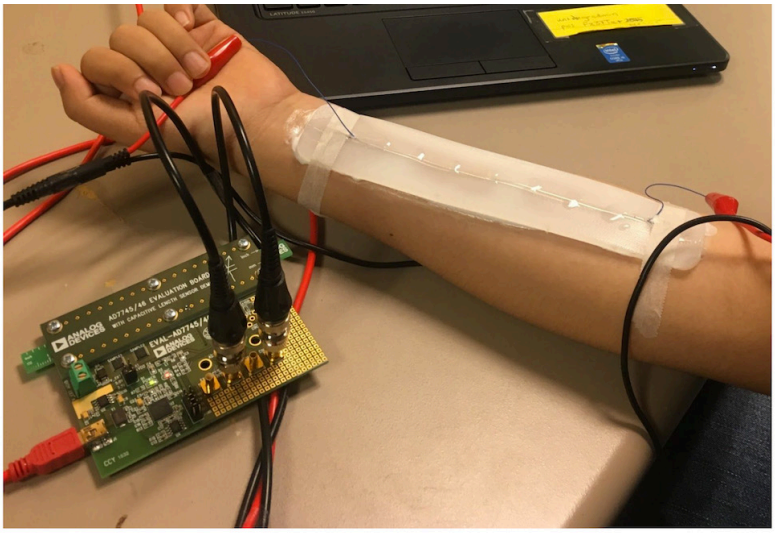
Advisor: Kristen Dorsey, Engineering



Strain tester setup



Test setup on torsion tester. The capacitor is in the blue box and the Analog Devices EVAL-7746 is in the green box.



Test setup on a human forearm

Utilizing the High Affinity of Proteins Targeting Mesothelin to Develop Cancer Therapeutics

Emely Tejada Jaquez/2020 and Leanna Troncoso/2020

Each and every day new cancer cases are discovered; according to the American Cancer Society there will be an estimated 1,688,780 new cancer cases discovered in 2017. As a result, our lab's major goal is to successfully engineer effective and targeted treatment methods for patients suffering from ovarian, triple negative breast, lung, and pancreatic cancer. These cancer types lack FDA-approved targeted therapeutic methods and are instead treated with aggressive therapies that have many toxic side effects. Chemotherapy, for example, targets all healthy dividing cells such as stomach lining and hair follicle cells and causes negative effects like hair loss, nausea and fatigue. In order to develop new targeted therapies, our lab specifically has focused on developing therapies that recognize mesothelin (MSLN), a cell surface protein that is overexpressed by many cancer cells and less prominent in healthy human tissues. Previous members of the lab have utilized a fibronectin protein scaffold to engineer a protein, named anti-MSLN 1.4.1, that has a high affinity for MSLN. This engineered protein's characteristics can be used to develop a targeted therapeutic method that could also allow physicians to non-invasively diagnose tumors and monitor the cancer's molecular level response to treatment.

This summer, our project specifically focused on improving both the therapeutic and diagnostic potential of 1.4.1 by direct drug conjugation to the small, fluorescent, and cytotoxic drug, Doxorubicin (DOX). Previously collected lab data shows that cancer cells internalize protein 1.4.1 and preliminary data shows that 1.4.1 may kills tumor cells. By attaching this anticancer drug to 1.4.1, we can develop a drug-protein conjugate that may have enhanced therapeutic effects. The conjugation reaction was completed by rotating a mixture containing 1.4.1 and crosslinker, disuccinimidyl glutarate (DSG), at room temperature. Next, the reaction was completed by adding DOX to the mixture and rotating at room temperature. Then purification occurred in various steps: Amicon spin filtration with a molecular weight exclusion membrane, microscale desalting, and high pressure liquid chromatography. Lastly, our sample was analyzed using protein gels (SDS-PAGE), western blot, nanodrop UV-Vis, and MALDI-TOF mass spectrometry.

However, difficulty arose when we could not locate our protein on the MALDI-TOF spectra, this was due to the aggregation of DOX which resulted in the Amicon filter membrane adsorbing our protein during the purification process. We responded by changing the protein to linker to drug ratio from 1:4:2 to a 1:1:1. However, when analyzing the MALDI-TOF spectra of the new sample, we noticed a variety of unaccounted for peaks. This leads us to believe that our protein control sample had multiple smaller proteins in it and that our sample was not as pure as we initially thought.

Our future directions include relying on more specific chemistry for our conjugation reaction due to the difficulty in limiting side reactions with amine chemistry. Previous members engineered a cysteine tagged anti-MSLN 1.4.1 which could do specific and favorable thiol-amine chemistry. To conjugate doxorubicin to this version of our protein we will use a PEGylated SMCC cross linker instead of DSG. Using this cross linker will not only limit side products but will increase the circulation time of our conjugate in the body. Furthermore, DOX is most effective in its unhydrolyzed form, and by using this linker, the linker can be cleaved to release doxorubicin by a pH shift. Instead of using the Amicon filter, which adsorbs our protein, we will utilize gel filtration chromatography beads to purify our final product. Once we have confirmed the creation and stability of our conjugate we will be able to perform competition and cytotoxicity binding assays using cell lines that overexpress MSLN.

Overall, our goal is to create a protein drug conjugate that will be used as both a diagnostic and therapeutic method for patients who suffer from ovarian, triple negative breast, lung, and pancreatic cancer.

(Supported by NIH: National Institute of Health)

Advisor: Sarah Moore, Engineering

Evaluation of energy harvesting technologies on passenger vehicles based on Parametric Model of Vehicle Energy Consumption

Yuhan Wen/2020

The automobile industry of fossil vehicles has been lagged by limited improvements in engine efficiency, of which the common value is 25%, while the limitation is estimated 50% [1]. Traditional methods of enhancement to break this bottleneck are no longer efficacious. Therefore, energy harvesting technology on passenger vehicles is an active area of research in improving driving mileage per cycle and are compatible to the original vehicle without major changes of the engine or the frame. The research project was focused on regenerative suspension system, braking system, raindrop energy harvester, self-sustainable sensors, and solar car roof.

First, I reviewed literature and collected data on emerging energy harvesting technologies. Then, I applied them on passenger vehicles, using a quarter car model. After that, I used Parametric Model of Vehicle Energy Consumption [2] to calculate the theoretical value of minimal energy consumption of the engine and the aiding subsystems, where the air conditioning (A/C) system is a major factor. Since data were given as ranges, I chose the Tesla model and analyzed the relationship between energy consumption of the A/C system and outside temperature. Then, I designed an energy storage system, where the supercapacitor is an aiding source, coupled with the main battery. All calculations, evaluations, and graphs were done using Python and matplotlib. Finally, I analyzed the results and assessed the feasibility of the application of the model. Light-weight material, carbon fiber reinforced plastics (CFRP), was considered but was not the focus of the research.

Results show that theoretically, up to 94% of the energy consumption can be recovered, meaning the driving range can be improved by 94%. Since the raindrop harvester and solar cells are way less efficient in the real-world setting, the actual recovery may be less. Figure 1 is an example of the performance of individual harvesters and their combinations. Not only the vehicle becomes more energy-efficient, but also is the major concern of electric vehicles that battery size limits the driving range, is mitigated.

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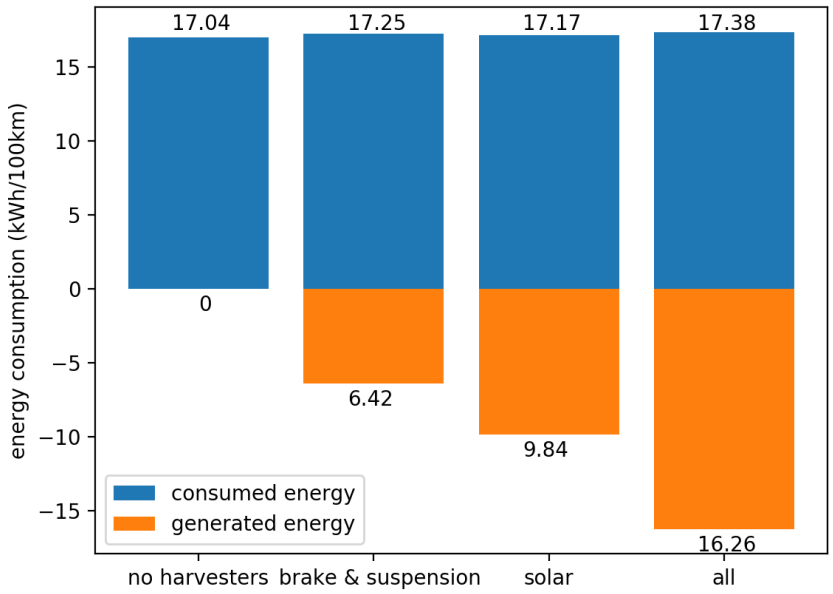
(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Paramjeet Pati, Engineering

Figure 1. Energy consumption and recovery conditions when the AC system is off



Microgrids and Machine Learning

Jessica Wert/2018

During SURF this summer, I spent some time learning about both microgrids and genetic algorithms. Microgrids employ distributed generation and energy storage to provide power to loads on a more local level. Microgrids can function in conjunction with the larger power grid and also when islanded. When islanded, certain loads may need to be prioritized. In transitioning in and out of the islanded configuration, it is important that this can be done smoothly. In entering the islanded configuration, energy storage needs to be relied upon and as such should be readily available for immediate integration. In reconnecting to the macrogrid, synchronization methods must be carefully employed to prevent issues in the power grid. Benefits of adopting microgrids lay in energy security, increased implementation of renewable energy, localized control, improved stability (voltage regulation), and fewer outages.

Genetic algorithms are a machine learning technique that is modeled after natural selection. A random initial population is generated, evaluated for fitness, the fittest are selected and the least fit are eliminated, the selected individuals are then crossed over at a random point in the string, then an element of random mutation is added and this repeats until the "fittest" individual solution is found. Genetic algorithms are applied to solve optimization problems with particular constraints. I thought that it would be a good fit as it is effective as a generalized tool (unlike artificial neural networks), and works to optimize under constraints. In the power grid, there are many physical constraints (line limits, voltage limits) to ensure proper functioning of equipment in addition to economic and environmental constraints (cost and emissions of any configuration).

My time in lab was spent conducting literature reviews to learn both about microgrids and genetic algorithms in preparation for my honors senior thesis. Through completing the SURF program, I feel that I have a much better understanding of these topics than I did before and am looking forward to applying this knowledge through the actual implementation of GAs on power systems in my thesis.

(Supported by NSF: National Science Foundation)

Advisor: Judith Cardell, Engineering

Management of Risk and Uncertainty through Optimized Co-operation of Transmission Systems and Microgrids with Responsive Loads

Yuqing Zhu/2019

Power networks are complex that in power units are scheduled to meet demands at different nodes of very large networks under constraints imposed by generators, transmission lines, and the need to balance load and demand for electricity in real-time. Responsive demand has the benefit of being well-distributed and rapidly deployable, as well as requiring little additional infrastructure. The existing projects on implementation of responsive demand share the commonality of implementing responsive demand and renewables into the high-voltage transmission system.

This project works on the development of a comprehensive optimization framework that incorporates the generation and transmission system, with micro grids that include responsive loads and distributed generation. The objective of this work includes investigating demand response, DR, strategies to mitigate the impacts of renewables intermittency on operation costs through micro grid modeling that integrates the energy management of the micro grid with the DR strategies. Viable strategies and models will be identified and developed for integrating demand response in the low voltage grid, and evaluating the potential application to mitigating risk and uncertainty in the grid. Micro grid-based DR strategies will be investigated to mitigate the impacts of the intermittency of renewables on the transmission system.

The project addresses risk and uncertainty of the future power system by participating in the solicited research areas of wholesale market operations through the integration a responsive demand in the unit commitment and economic dispatch process of the wholesale market. The project will benefit manifesting in the development of a framework and associated computational methods that will enhance the integration of renewables, storage, and responsive demand within the transmission and distributions systems.

I have read through articles to get to know this comparatively new field, demand response. I learned about smart grid, distributed energy resources, the economics of electricity supply and power plants from IEEE Power & Energy magazine. PowerWorld and HOMER are two softwares used for modeling and data analysis. I also read through tutorials to learn to use both softwares. Then I focused on collecting and organizing data and descriptions of the demand response programs offered by Independent System Operators, ISO. More specifically, I worked to organize information about whether the programs are economic based or reliability based, offered years, number of participants and kinds of these programs.

(Supported by NSF: National Science Foundation)

Advisor: Judith Cardell, Engineering

Sustainable Labs

Kelilah Abner/2019

Sustainable Labs examines and targets how to make laboratory spaces more energy efficient and sustainable. Two of the projects this summer focused on freezers and fume heads. The fume head campaign continued efforts from last summer to close sashes when not in use.

The Smith College Science Center can improve energy efficiency and reduce electricity usage by targeting the 18 Ultra Low Temperature Freezers in Ford Hall and Sabin-Reed. Ultra Low Temperature freezers are set as low as -80 Celsius. These freezers use up to 30 kwh of electricity a day, equivalent to the average New England home.

Methods surveyed for efficiency improvements includes proper maintenance, regular defrosting, raising the temperature, and placement. A well maintained and defrosted freezer can increase efficiency up to 20%. Raising the temperature of an ULT freezer from-80 Celsius to -70 Celsius increases efficiency from 15 - 25%. Some samples stored in the ULT freezers can be preserved at -70 Celsius and perform identical to samples stored at -80. Some samples stored in the Smith College ULT freezers include these. Other methods for improving efficiency includes improving sample storage and increasing communication.

Placement of ULT freezers affects the efficiency and performance of freezers. Ford 131 is an equipment room containing 6 ULT Freezers and other pieces of the equipment. The freezers in 131 are currently not placed correctly and the room is unable to handle the additional heating and cooling loads. Future recommendations should examine the placement of freezers. Smith College can both conserve energy and resources and costs with proper freezer management.

(Supported by Science Center Undergraduate)

Advisor: Margaret Rakas, Clark Science Center, Environmental Science and Policy

Atata Coral Reef Assessment: A Diversity Survey

Emiline Koopman/2018 and Hayley Reifeiss/2018

Coral reefs are intrinsically, socially, culturally, environmentally and economically valuable. Reefs provide shore protection, water filtration, and support the pelagic food web (Moberg & Folke 1999). In addition, they are hot spots for biodiversity enhancing the diversity of the entire ocean (Plaisance et al. 2011). This makes them sources for fisheries and a desirable part of the tourist industry. However, they are highly susceptible to changing abiotic and biotic factors in the environment which leaves at risk on both the local and global scale. In order to better understand the threats that coral reefs face as well as their impacts, it is essential to assess coral reef health. One indicator of reef health is coral diversity. Our study seeks to assess the diversity of the Atata reef in Tonga in order to better understand its condition and establish a diversity baseline. Small Island Developing States (SIDS), such as Tonga, are particularly vulnerable to climate change factors such as weather variability and sea level rise (Mead et al. 2015). While it is known that the Pacific Island nation of Tonga faces similar problems as the rest of the Pacific in terms of coral reef decline, few studies focus specifically on this island. Furthermore, although decline in reef cover has been highly documented worldwide (Pandolfi et al. 2003) and in the Pacific (Bruno & Selig 2007), research that focuses solely on the size of reefs does not provide a holistic picture of reef resilience and health. Therefore, obtaining baseline data showing which reef species are present and the levels of reef diversity are highly important to predicting the trajectory of reef communities.

This data was obtained using 1m2 photo quadrats on 50m transects established parallel to the shore approximately 10m from the reef edge. Twenty-five points were randomly overlaid on the photos and coded for using the program Coral Point Count. Through the examination of 194 photo quadrats a data set of 4,850 points was produced from which the percent composition of the transects was calculated. The Atata reef was found to be comprised of 2.20% Acropora cytherea, 10.40% Acropora micropthalma, 6.52% Acropora aspera, 0.77% Acropora gemmifera, 34.23% Acropora globiceps, 1.01% Astreopora gracilis, 0.74% Isopora crateriformis, 0.11% Leptoseris incrustans, 0.03% Millipora sp. and 0.34% Isopora cuneata (figure one). Furthermore it was found that 22.27% of coral were dead and another 13.63% were dead and covered in algae (figure one). Of those corals present, 12.60% showed signs of bleaching.

This relatively poor species richness coupled with an uneven abundance across species produced low diversity indices of 1.26 (Shannon Index) and 0.58 (Simpson Index). Due to this low diversity, we predict Atata Reef to be highly susceptible to future disturbances. Locally, this includes the overfishing of herbivorous fish, the use of damaging fishing practices such with trawl or gill nets, physical damage to the reef from boats, anchors, moorings, and swimmers, increased sedimentation and toxic runoff from additional development, or a loss of nearby nursery habitats such as eelgrass beds and mangroves. Globally, Atata Reef is threatened by climate related factors such as sea level rise, increased ocean warming, ocean acidification, and an increase in the frequency and intensity of storms. While localized management strategies will not be able to combat these global threats, reducing local anthropogenic stressors to the reef will allow the coral to better cope with climate related changes (Smith et al 2016).

While this study provides a baseline measurement of coral health and diversity in Atata, further research could expand on our conclusions. Experimental research on the dominant corals found in Atata Reef (Acropora globiceps and Acropora aspera) would illuminate how these specific corals respond to particular disturbances, thus providing a more accurate assessment of the future trajectory of this reef. Therefore, we hope to continue this research throughout the semester as part of an honors project building upon this baseline as well as examining newly acquired data.

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(Supported by Science Center Undergraduate Research Fellowships)

Advisor: L.David Smith, Biological Sciences, Environmental Science and Policy

Where does atmospheric mercury come from? Tracking mercury fate and transport

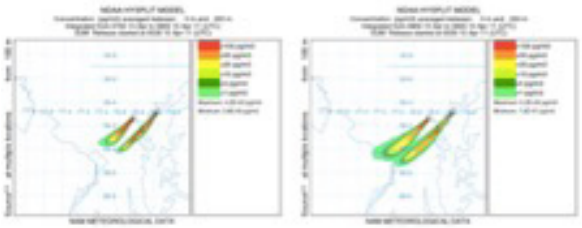
Zhuoran Li/2019

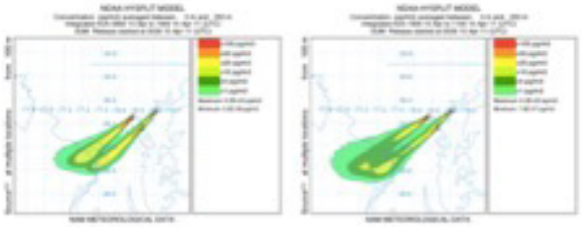
Mercury is a persistent global pollutant that imposes negative effects on both the ecosystem and human health, damaging nervous systems of humans and other animal species. The majority of mercury released into the environment is emitted into the atmosphere and then deposits on the ground some distance from the polluting source. Hence, it is crucial to identify the sources of atmospheric mercury and understand its atmospheric transport, transformation, and deposition. The purpose of my internship was to trace the potential sources of gaseous elemental mercury peaks and create a 3-dimentional visualization of the pollution plume coming from the sources.

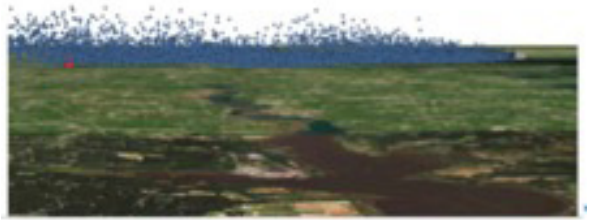
The first task at my internship at the Air Resources Laboratory (Oceanic and Atmospheric laboratory, NOAA) was learning how to use the HYSPLIT model, which was developed by NOAA, and used to make forward and backward pollutant trajectories and concentration of the pollutant. After learning about the model from the Graphic User Interface (GUI), I learned and practiced running the model from the command line using Kornshell files on Mac and Dos Batch files on Windows machines. Following the learning period, I ran case studies on peaks of gaseous elemental mercury at a data-collecting site in Beltsville, MD working with data from the past 10 years. In order to trace back to the sources that potentially caused the peak, I used the HYSPLIT model to make a backward trajectory of 72 hours, and then made a forward concentration prediction of the mercury plume. Once I had used the HYSPLIT model to generate the data for each released pollutant particles (modeled in the run), I took the 3D Visualization course on the ESRI website to learn how to use this GIS tool. I needed to convert the data from HYSPLIT into a format that could be read by ArcGIS, and then brought the file into ArcGIS Pro to create the 3-dimentional visualization of the pollutant plume. These 3D visualizations show how pollutants are emitted and disperse in the atmosphere, and when combined with local map containing emission information, help identify the sources and areas of deposition of atmosphere mercury pollution.

(Supported by Agnes Shedd Andreae '32 Research Fund)

Advisor: Non-Smith Advisor, Environmental Science and Policy







The Idaho Project

Ellie Mason/2018

My internship focused on the Idaho Project, a long-term study of salmon spawning streams that feed into the Salmon River in Idaho, where Pacific sockeye and chinook salmon return each summer. The Salmon River lies in the headwaters of the Columbia River watershed and is considered one of the last truly "wild" salmon habitats as it has not been historically dammed. Ending at its confluence with the Snake River (a tributary of the Columbia River) 640 miles from the mouth of the Columbia at the Pacific coast, the Salmon River extends another 260 miles into Idaho reaching elevations of near 5,000 feet, making this one of the longest and most energy intensive salmon migrations in the world.

This project aims to understand how marine-derived nutrients, particularly nitrogen, bound in the body tissue of the returning salmon impact the freshwater ecosystem of the Salmon River tributaries. Marine-derived nutrients enter the freshwater ecosystems from the decaying carcasses of the returning adult salmon, which die in the freshwater tributaries after spawning. Organisms that feed on the carcasses take up these nutrients and make the nutrients available in the freshwater ecosystem. Through an analysis of stable isotopes in the invertebrates, particularly nitrogen-15, a stable isotope of marine origin, a better understanding of how much the salmon enrich the ecosystem can be assessed.

We collected field data in an intensive week, while camping in the Frank Church River of No Return Wilderness in Idaho. We sampled from five sites at each of the seven streams that had been historically sampled. At three of the five sites, hess and drift net samples of invertebrates were taken to understand relative species diversity and abundance in the stream. At all sites, water quality samples, rock samples, periphyton and invertebrate samples were taken. Back at the lab I helped process these samples. Organic matter measurements of productivity per rock unit of each stream were analyzed through chlorophyll analysis and ash free dry weight measurements. Invertebrates were also identified and readied for isotope analysis using the mass spectrometer. These data contribute to a larger data set which aims to better understand freshwater stream ecology, especially the impact of wild salmon on riparian ecosystems. In light of proposed salmon farming, destruction of important coastal salmon habitat, and climate change, this study provides important insight as to how regulatory measures should be crafted to help conserve the salmon populations.

(Supported by Agnes Shedd Andreae '32 Research Fund)

Advisor: Non-Smith Advisor, Environmental Science and Policy

Hawaii Coastal Resilience: wetland restoration in the He‘eia National Estuarine Research Reserve

Rachel Moskowitz/2018

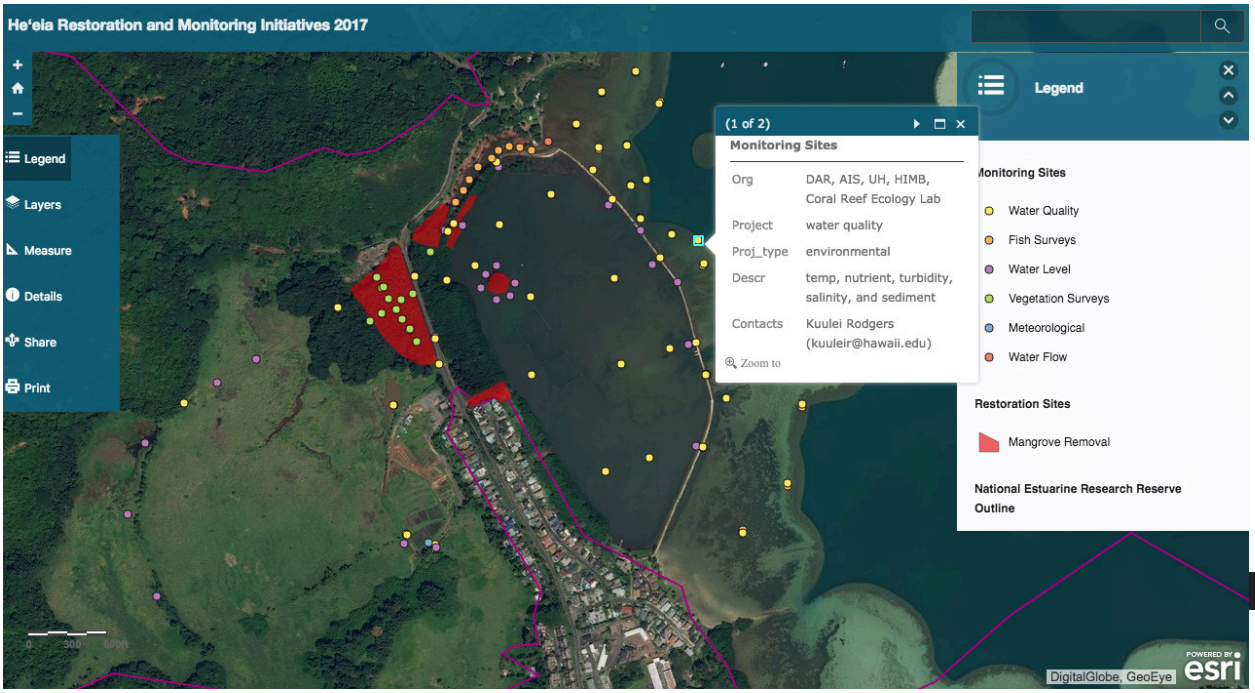
This summer I interned at NOAA’s Office for Coastal Management in the Pacific Islands Regional Office. My internship focused on aiding coastal resilience efforts on the island of Oahu through community and resource management. Earlier this year, the He‘eia ahupua‘a (the traditional Hawaiian term for subdivision of land) was designated as the 29th National Estuarine Research Reserve (NERR). I began my internship by establishing guidelines and frameworks for the He‘eia NERR, through updating old management plans, grant documents, and creating talking points regarding the site. NOAA contributes to the He‘eia NERR by providing funding, guidance, and technical assistance to community partners who manage the site on the ground. I met with researchers and resource managers at the NERR site to identify needs and opportunities for technical assistance. We identified a large need for assistance and coordination of wetland restoration projects at the He‘eia NERR site, which became the focus of my internship.

The wetland restoration project I focused on was preparing for the removal of Red mangrove (Rhizophora mangle), which was brought to Hawai‘i in 1902 to stabilize soil, but has since spread, causing detrimental impacts to coastal wetland ecosystems. Resource managers in the NERR site have decided to engage in large-scale mangrove removal projects to restore the He‘eia wetland to its native ecosystem. I used geospatial technology to coordinate removal projects, created a series of community outreach materials, and assisted with mangrove-related research at the reserve. Through creating a comprehensive map of mangrove removal and associated monitoring sites, I was able to foster communication between researchers and resource managers. I developed community outreach materials regarding coastal resilience, including a series of StoryMaps detailing different projects underway at the He‘eia NERR site. Lastly, I assisted researchers based at The Nature Conservancy and UH-Manoa with an ecosystem service analysis paper of the He‘eia watershed.

This internship allowed me to gain insight on the process of resource management, improve my understanding of geospatial technology, and contribute to wetland restoration projects and research first-hand. I not only had the opportunity to work at NOAA, but was able to work with community organizations, state partners, and academics to contribute to coastal resiliency in the state. Through these experiences, I learned how environmental restoration projects function across a wide range of institutions and increased my understanding of how communities address coastal resiliency.

(Supported by Agnes Shedd Andreae ‘32 Research Fund)

Advisor: Non-Smith Advisor, Environmental Science and Policy



Integrating Natural Capital Principles into the Ocean Economy

Breanna Parker/2018

This summer I was an intern in the Office of the Chief Economist at the NOAA headquarters, in Silver Spring, MD, where I worked on the Natural Capital Project. There are two major veins of this project: one is to integrate natural capital principles into American businesses and the other is to assist in the development of the Oceans Supplement to the Natural Capital Protocol (NCP). Essentially, natural capital is any stock of natural resource, or ecosystem service that provides a benefit to people. Some of the apparent benefits from natural capital include food, water, and the raw materials we use to create products, as well as less obvious ones like flood defense, pollination, and recreation.

Often natural capital, especially the less obvious, is not included in business decisions and cost assessments, contributing to the depletion of natural resources essential for society and the economy (1). In response, the Natural Capital Coalition (NCC) was formed as a global, multi-stakeholder collaboration to create the NCP aiming to help businesses identify, measure, and value their direct and indirect impacts and dependencies on natural capital and to generate credible and actionable information for business decisions. NOAA, through the US Department of Commerce, has the goal to integrate natural capital planning into American businesses and is a key member of the NCC. This summer, I attended meetings with NOAA and the International Trade Administration (ITA) to discuss strategies to accomplish this goal. We realized the Protocol is very useful for large corporations, but needs to be simplified for small and medium sized enterprises.

While the NCP provides a general framework for businesses, there is a need for an Oceans Supplement to guide businesses engaged in the ocean economy, because of the unique impacts and dependencies they have on the ocean. The NCC, in collaboration with NOAA and Conservation International is writing the supplement. The primary part of my internship was to develop the foundation for the Oceans Supplement. One of my contributions was to identify the key sectors of the ocean economy and organize them by their impacts and dependencies on the ocean. The sectors are marine engineering, transportation, cultural services, natural resources, and energy extraction. Additionally, I coauthored an engagement document to make the businesses case for natural capital and to engage businesses in the development of the Oceans Supplement. This internship was an excellent opportunity for me to learn about developing global environmental economic protocols.

1. World Wildlife Fund (WWF). 2016. "Living Planet Report 2016." World Wildlife Fund.

(Supported by Agnes Shedd Andreae '32 Research Fund)

Advisor: Non-Smith Advisor, Environmental Science and Policy


STOCKS
Natural capital
Biodiversity
FLOWS
Ecosystem and
abiotic services
VALUE
Benefits to business
and to society

Investigating acid mine drainage controls on the geochemistry of Davis Mine Brook, MA

Casey Armanetti/2018

This study explores how acidification from acid mine drainage (AMD) affects geochemistry in the Davis Mine Brook watershed in Rowe, Massachusetts (Fig. 1). Davis Mine is an abandoned century-old pyrite mine where tailing piles of waste rock containing pyrite (FeS_2) are within the runoff zone of the brook, causing them to oxidize, acidifying the water and lowering its pH. This project focuses on how dissolved CO_2 in the water (pCO_2), which is dependent on pH, is affected by the increased acidity from AMD. It is hypothesized that AMD will result in the release of CO_2 gas from the water into the atmosphere, and acidic waters will have higher pCO_2 than non-acidic waters. This will be tested by comparing conditions in Davis Mine Book watershed with neighboring watersheds in similar geologic settings but not receiving AMD.

Preliminary data collection included 22 sample sites within Davis Mine Brook and its neighboring watersheds (Fig. 1). At each site, water samples were collected with field measurements of pH, specific conductance, water temperature, and dissolved oxygen. Each sample was analyzed directly for inorganic carbon (IC), total carbon (TC), and total organic carbon (TOC), and then filtered for dissolved organic carbon (DOC), using the Lotix carbon analyzer. Filtered and acidified samples were tested for dissolved silica and concentrations of cations and trace metals (Ca, Mg, Na, K; total Fe, Pb, Cr, Al) on the ICP-OES. Filtered samples were tested for anions (SO_4, NO_3, PO_4, and Cl) using ion chromatography. Acid neutralizing capacity and acidity is calculated by the gran function method (Drever, 1988), using both an autotitrator and hand titration techniques.

This summer's work culminated in a theoretical proof for calculating pCO_2 using measurements collected in the field and lab. This study will continue in 2017/2018 as an honors thesis project including repeated water sampling and deeper investigation of the bedrock mineralogy. This will provide further insight into the pyrite weathering process and its impacts on water chemistry and mineral composition of the tailings at different depths of submergence. The ultimate question of how carbon sequestration patterns are affected within the Davis Mine Brook watershed will especially require interpretation of inorganic carbon and alkalinity data using equations to calculate pCO_2 from measured values of samples.

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(Supported by SURF Gifts Fund)

Advisor: Amy Rhodes, Geosciences

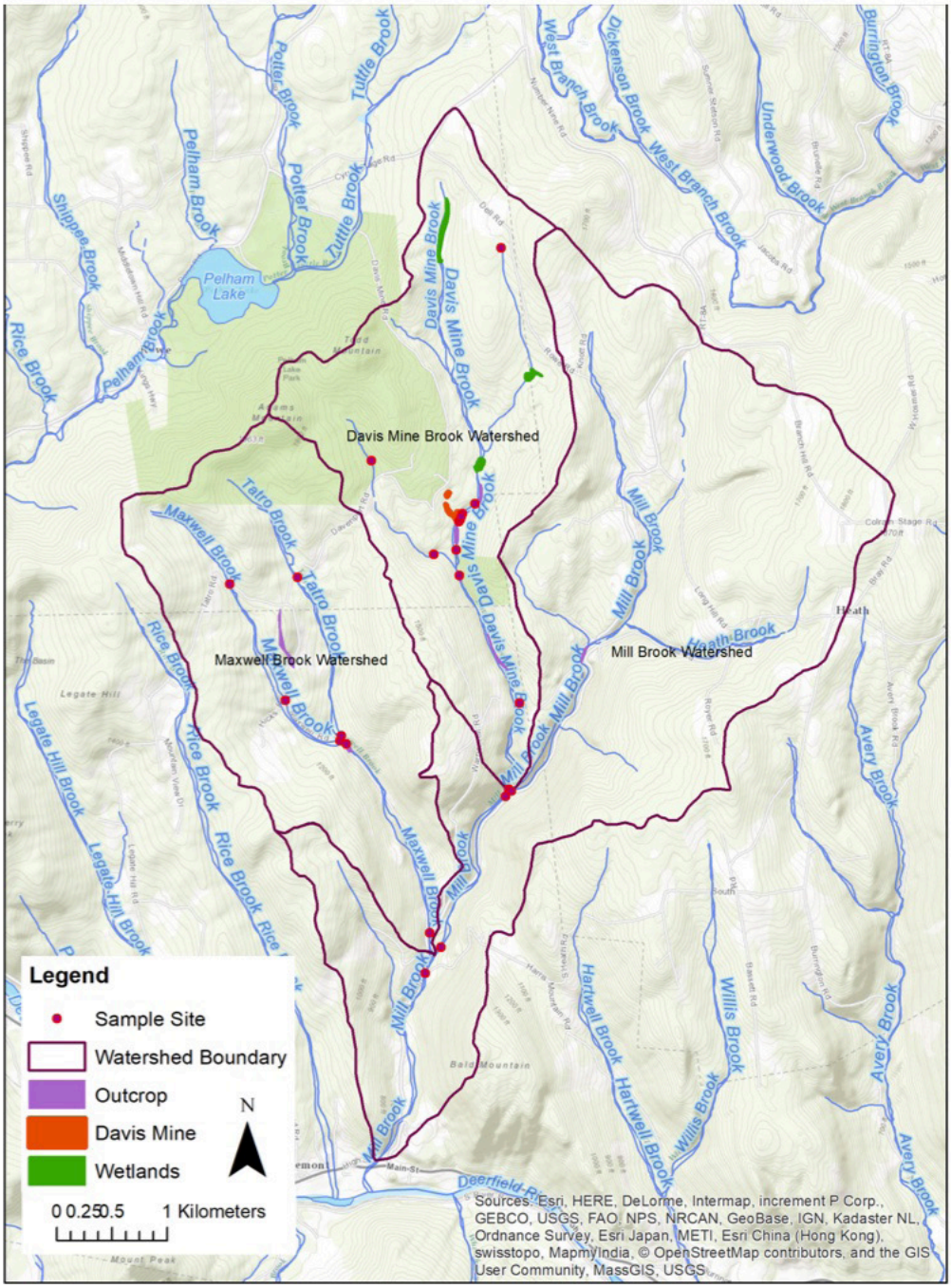


Figure 1: Map of Davis Mine Brook, Maxwell Brook, and Mill Brook watersheds.

Impact of Bioturbation on Pleistocene Carbonate Subtidal Sediments, Harry Cay Site, Little Exuma, Bahamas: Insights from Petrographic Analysis

Abigail Beckham/2019

Different kinds of stone used in the last Maya capital city of Mayapán c. 1100 to 1450 AD were examined to develop a practical classification for communicating information about stone artifacts and architecture at this site (Figure 1). The Yucatán peninsula is a relatively flat, low-elevation terrain made of Cenozoic carbonates deposited on a broad, gently sloping ramp. Mayapán is in NW Yucatán, just inside the ring of cenotes (sinkholes) marking the rim of the end-Cretaceous Chicxulub impact crater.

Our work identified the following stone types, origins, and uses: 1) porous coquina limestone from shallow subtidal, low energy, relatively open settings; this most common rock type was used extensively for building blocks, lime production, grinding tools, and disk-shaped beehive covers; 2) medium- to coarse-grained calcarenite, a subtidal peloidal-skeletal (echinoids, mollusks, algae, ostracods) packstone-grainstone used for tools and sculptures; 3) well indurated (piedra dura), fine-grained, muddy, bioturbated, lagoonal peloidal-skeletal wackestone-packstone; commonly found as rounded pseudoclasts in extensively weathered limestone (sascab); used for grinding (grains, plaster, pigment), pounding (bark for paper), and smoothing (paper, plaster) tools; 4) friable sascab quarried in shallow pits (sascaberas) for fill; 5) terra rossa paleosol, including breccia, used as building blocks; 6) up to 5-6 cm thick, indurated calcrete or caliche crust, formed during subaerial exposure of limestone, used as building blocks with naturally flat surfaces; 7) sucrosic dolostone, interpreted as mixed zone dolomitization, used for grinding and abrading tools; 8) coarse crystalline fracture fill and speleothem limestone found rarely as tools; 9) chert nodules used to make cutting and scraping tools; other chert and obsidian tools are from the Sierra Madre Mountains of Mexico and Guatemala; and 10) Fe-oxide impregnated skeletal (foraminifera, algae, mollusks) packstone-grainstone formed by pedogenisis of marine limestone; ornamentally carved and reused building blocks, and small traded dishes made of Uxmal or Ticul stone from the Sierra de Ticul or Puuc Ridge. This extensive list reflects the resourceful and diverse use of locally available stone, with some examples of reuse and trade of externally sourced material.

With co-authors Sydney Reyes Beattie '19, Marilyn Masson (The University at Albany, SUNY), Carlos Peraza Lope (Centro INAH - Yucatán, Mexico) and Bradley Russell (College of St. Rose) this work will be presented at the Geological Society of America Annual Meeting in Seattle in October 2017.

Figure 1: This large boulder, moved during construction of the marina at the Harry Cay site on Little Exuma Island in the Bahamas, was in the focus of this study. The boulder reveals a succession of three different limestone rock types or units with various biogenic and physical sedimentary structures.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Bosiljka Glumac, Geosciences


Unit 3
Unit 2
Unit 1

Contribution of Suspended Sediment to Total Sediment Accumulation in Paradise Pond

Emily DeWitt/2019

Damming the Mill River to create Paradise Pond has lead to a persistent sedimentation problem as the decrease in stream velocity leads to deposition. Periodic dredging is required to maintain an appropriate pond depth. Both suspended and bedload sediment is deposited in the pond. This study evaluates the contribution of suspended sediment to the amount of total sediment accumulating in the pond. An estimate of suspended sediment accumulation during the period from November 2016 to May 2017 was determined through analysis of turbidity measurements at both the inlet and outlet of the pond. This volume will help determine the amount of sediment that will have to be removed by sediment sluicing.

A turbidity sensor (Campbell Scientific OBS501) and pressure transducer (Campbell Scientific CS451) are located just upstream of the pond, while a second set is located downstream of the pond at the Lamont Bridge. A Campbell Scientific CR1000 datalogger was used to record the data every 15 minutes for turbidity and 10 minutes for stage. Periodic discharge measurements at the gage station were taken using a SonTek FlowTracker Acoustic Doppler Velocity meter (low flow conditions) or a Teledyne RD RiverRay Acoustic Doppler Current Profiler (high flow conditions). From this data, a stage discharge relationship was determined. This relationship was used to estimate discharge from all stage measurements. A discharge value was calculated for each of these 10 minute stages. These were selectively averaged to create a series of 15 minute discharge data, which would match the turbidity data.

Turbidity measurements are recorded in Nephelometric Turbidity Units (NTUs). An auto-sampler deployed during storm events collected samples that were analyzed for total suspended load in mg/L. These results were compared to simultaneous turbidity measurements and a suspended sediment-turbidity relationship was determined (Fig. 1). This relationship was then used to convert all of the turbidity measurements from NTUs to mg/L.

The total mass of suspended sediment, in kilograms, was calculated for each 15 minute interval by multiplying the suspended sediment concentration by the volume of flow within that 15 minute period.

Storm events increase discharge and turbidity to levels where suspended sediment are of size and concentration to have an appreciable impact on net accumulation or release in the pond. Baseflow conditions are only able to transport small, silt-sized particles, while storm conditions can transport sand sized and larger. To determine how much sediment is accumulating in the pond, several high discharge events were analyzed. A hydrograph covering November 2016 to May 2017 was generated. The events containing the top three highest flows were selected. The highest occurred during a May 2017 event at 1167 cfs, followed by a February 2017 event at 984 cfs, and an April 2017 event at 915 cfs.

Each event was isolated on the day versus tonne/day plot. The area beneath the upstream curve and the Lamont Bridge curve were separately integrated to give the total mass entering and exiting the pond for that particular event. Subtracting these values from each other indicated whether the event had a net positive or negative accumulation of sediment. All three events produced net accumulation of sediment in the pond.

The total mass of sediment accumulating in the pond over the time period of the three events (February-May 2017), was 190 tonnes. This value is the combined net masses from each of the storm events.

This mass can be converted into a volume to compare with the sediment redistribution results. This requires a series of estimations. The sediment most trapped by the pond is a sand composed of feldspar grains. Porosity of these grains was estimated at 30% and grain density estimated at 2.6 g/cm3. From these values, bulk density was calculated to be 1.82 g/cm3 (1). The estimated mass of sediment was then converted to grams. Using bulk density the volume was calculated in cubic centimeters and as to be more applicable, converted to cubic yards (2).

(1-0.3)*2.6 =1.82 g cm^-3 (1).

((187.84 tonnes*1e6 grams)/1.82 g cm^-3)*1.30795e-6 yd^3 = 134.99 yd^3 (2).

Knowing that ~135 yd3 of sediment entered the pond over this four month period provides a better understanding of how much sediment should be removed at the next sluicing event.

(Supported by Pond Project)

Advisor: Robert Newton, Geosciences

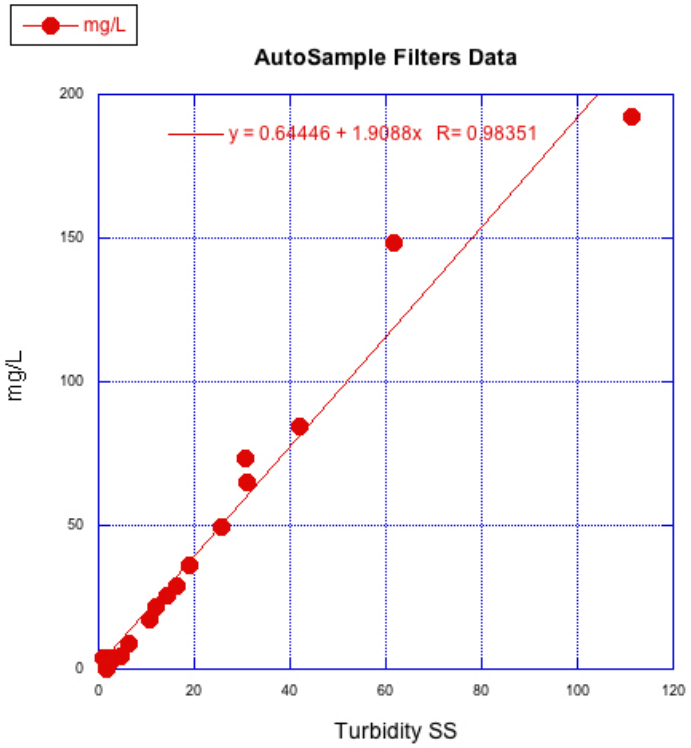


Figure 1. Turbidity measurements plotted against corresponding auto-sampler readings produce a suspended sediment-turbidity relationship

Practical Classification of Stone Used by Pre-Columbian Maya People in and around the City of Mayapán, Yucatán Peninsula, Mexico

Susannah Howard/2019

Different kinds of stone used in the last Maya capital city of Mayapán c. 1100 to 1450 AD were examined to develop a practical classification for communicating information about stone artifacts and architecture at this site (Figure 1). The Yucatán peninsula is a relatively flat, low-elevation terrain made of Cenozoic carbonates deposited on a broad, gently sloping ramp. Mayapán is in NW Yucatán, just inside the ring of cenotes (sinkholes) marking the rim of the end-Cretaceous Chicxulub impact crater.

Our work identified the following stone types, origins, and uses: 1) porous coquina limestone from shallow subtidal, low energy, relatively open settings; this most common rock type was used extensively for building blocks, lime production, grinding tools, and disk-shaped beehive covers; 2) medium- to coarse-grained calcarenite, a subtidal peloidal-skeletal (echinoids, mollusks, algae, ostracods) packstone-grainstone used for tools and sculptures; 3) well indurated (piedra dura), fine-grained, muddy, bioturbated, lagoonal peloidal-skeletal wackestone-packstone; commonly found as rounded pseudoclasts in extensively weathered limestone (sascab); used for grinding (grains, plaster, pigment), pounding (bark for paper), and smoothing (paper, plaster) tools; 4) friable sascab quarried in shallow pits (sascaberas) for fill; 5) terra rossa paleosol, including breccia, used as building blocks; 6) up to 5-6 cm thick, indurated calcrete or caliche crust, formed during subaerial exposure of limestone, used as building blocks with naturally flat surfaces; 7) sucrosic dolostone, interpreted as mixed zone dolomitization, used for grinding and abrading tools; 8) coarse crystalline fracture fill and speleothem limestone found rarely as tools; 9) chert nodules used to make cutting and scraping tools; other chert and obsidian tools are from the Sierra Madre Mountains of Mexico and Guatemala; and 10) Fe-oxide impregnated skeletal (foraminifera, algae, mollusks) packstone-grainstone formed by pedogenisis of marine limestone; ornamentally carved and reused building blocks, and small traded dishes made of Uxmal or Ticul stone from the Sierra de Ticul or Puuc Ridge. This extensive list reflects the resourceful and diverse use of locally available stone, with some examples of reuse and trade of externally sourced material.

With co-authors Sydney Reyes Beattie '19, Marilyn Masson (The University at Albany, SUNY), Carlos Peraza Lope (Centro INAH - Yucatán, Mexico) and Bradley Russell (College of St. Rose) this work will be presented at the Geological Society of America Annual Meeting in Seattle in October 2017.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Bosiljka Glumac, Geosciences

Figure 1: City of Mayapán, Yucatán Peninsula, Mexico. Geological fieldwork was conducted in and around the city to identify different stones types (mainly limestone) used

Understanding and analyzing the coupling patterns of Cascadia Subduction Zone

Sofia Johnson/2019

The Cascadia Subduction Zone is a tectonic plate boundary located along the west coast of North America from Central California to British Columbia, Canada. A subduction zone is where one tectonic plate subducts under another plate. Using the movement of the ground recorded by GPS receivers, we can study how the plates are stuck together, which leads to the accumulation of stress that will eventually be released in an earthquake.

I have applied two methods, both of which use data from GPS stations, to estimate patterns of coupling, which is the degree to which the two tectonic plates are stuck together. The difference between the two methods is that one smoothes the coupling values (Fig. 1, left) and is thus called the Smoothing method, while the other method makes the coupling more patchy (Fig. 1, right); this is called the Total Variation Regularization (TVR) method. The TVR method has never been used before in the context of understanding coupling patterns in a subduction zone, while the Smoothing method has. The methods predict movements of the GPS stations, and these are then compared to the actual observed results to analyze the goodness-of-fit of the model results. I ran two types of tests to assess the accuracy of the two methods. The first test calculates the percentage of the subduction zone that is "too coupled" and the other test run is calculating the mean residual GPS velocity.

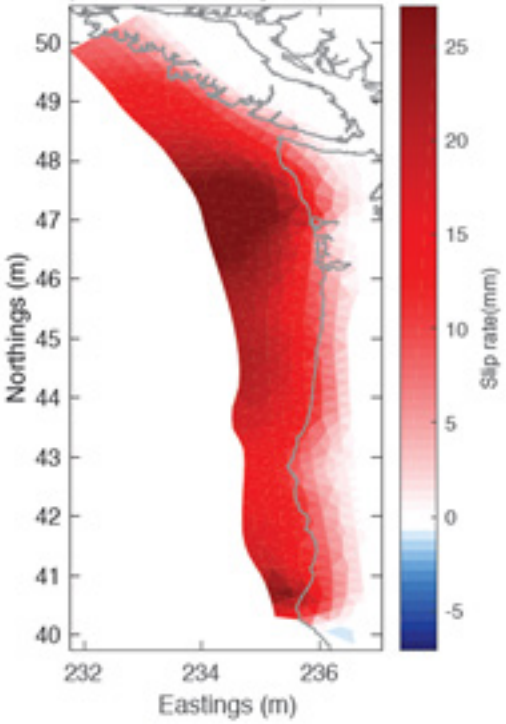
The most exciting part of this project has been looking at the model results using total variation regularization (TVR). Both the Smoothing and TVR methods can fit the observed GPS station movements with mean residual magnitudes of 0.92 mm/yr and 1.05 mm/yr, respectively. The overall patterns in coupling from the Smoothing and TVR models are broadly similar but, as expected, the TVR distribution varies more abruptly in space than the Smoothing model. This work validates TVR as an alternative method for analyzing subduction zone coupling and will enable comparison between the coupling and other processes, including slip during major earthquakes.\

Figure 1: Patterns of subduction zone coupling using the Smoothing method (left) and total variation regularization method (right).

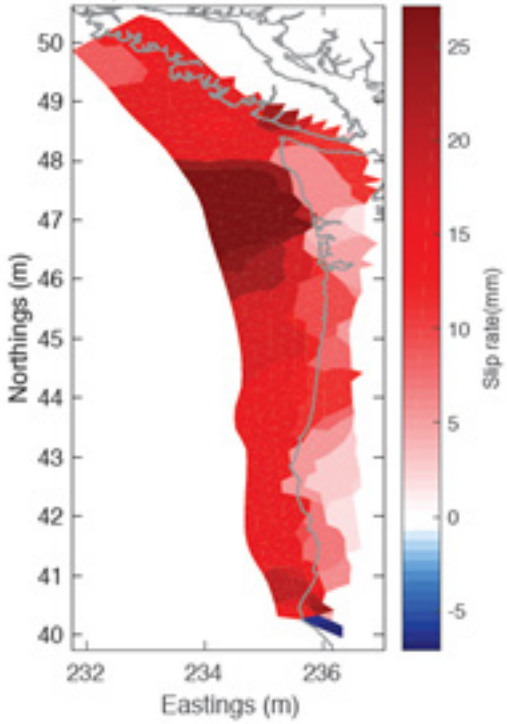
(Supported by USGS: United States Geological Survey-Loveless "Cascadia")

Advisor: John Loveless, Geosciences

Example of Smoothing method results



Example of TVR method results



Exploring the Possibilities of "Big Data" as a Tool for Education in Igneous and Metamorphic Petrology

Olivia Leadbetter/2019

Igneous and Metamorphic petrology databases were studied to assess ways in which their big data libraries can be used to aid students and researchers studying the field.

Databases studied include information regarding regional petrology and tectonic setting. This information can be used to show the correlation between the two, demonstrating the tectonic implications of igneous rock classifications. Interactive mapping could further place this information into a geographic context. Because navigating each database can require significant time/trouble shooting, there is a question of whether it is more beneficial to have students navigate the databases themselves, or simply provide selected datasets on the petrology text website to use for specific assignments. It may be useful to provide precompiled datasets for specific assignments, but additionally include instructions for navigating the databases if students and researchers want to do so independently.

In addition to researching databases, other projects were carried out that will contribute to the Igneous and Metamorphic petrology text that Professor John Brady is currently working on.

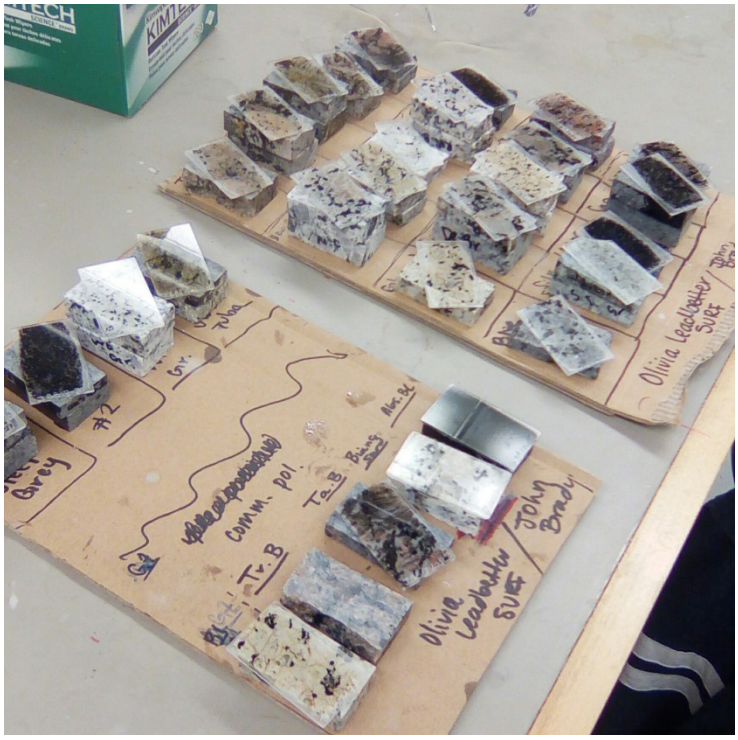
Thin sections were made and rock chemistry was carried out using common commercial granite types that one might find at any commercial granite supplier across the US. This was done to aid the Granite Rock Library section of the text. The goal is to show how one might determine the QAPF classification of a plutonic rock using modal analysis and rock chemistry. The use of common commercial granite types makes this project one that can be repeated in a classroom anywhere. This project will continue in the fall, when plane polarized and crossed polarized photomicrographs of the thin sections will be taken and added to the rock library.

Hand sample, outcrop, and thin section images were also collected for the library from other databases and web resources. QAPF classifications that are missing data will be completed using our own rock samples and field photos.

Various phase diagrams were constructed for the text, using Adobe Illustrator to create a uniform format for pre-existing temperature and composition data determined experimentally. Phase/element maps imaged from a SEM, as well as their spectra, were also edited/formatted for the text. An inverted microscope was used to take photomicrographs of the thin section areas displayed in the phase/element maps, and adobe photoshop was used to align the images. This way, someone using the text can easily move between map and thin section images of the same frame.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: John Brady, Geosciences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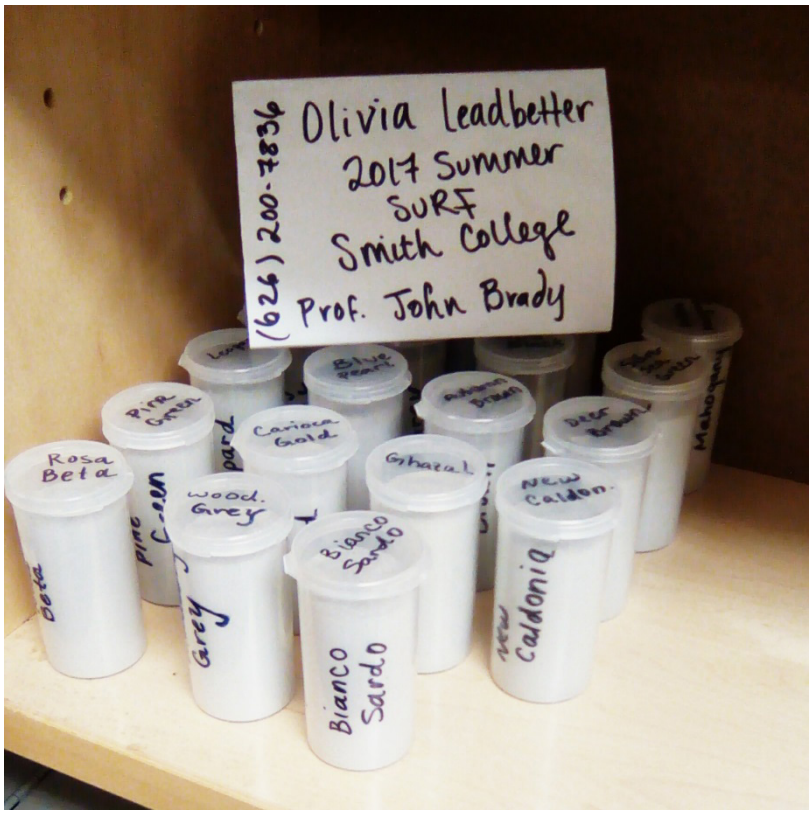
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New Caldonia

Carbonates of the Cheshire Formation, Zimbabwe

Chiza Mwinde/2018

The Cheshire Formation, part of the Belingwe Greenstone Belt (Zimbabwe), hosts exceptionally well-preserved Archean carbonates. Geochronological data suggest deposition at ~2650 Ma (1). Despite their long history, the Cheshire Formation carbonates have excellent textural preservation (2) which implies that they did not undergo massive metamorphism or chemical exchange. Therefore, these carbonates are some of the best records to give us insight into Archean carbonate depositional processes. Cheshire Formation lithofacies include shale, grainstone, microbial laminite, nodular-domal stromatolitic limestone, and microbial limestone.

The goal of this study was to provide a detailed mineralogical description of the carbonates and the aragonite pseudomorphs of the Cheshire Formation. The original mineralogy of the carbonates and knowledge of associated trace elements would provide insight into processes affecting carbonate precipitation, and better our understanding of carbonate deposition in the Archean.

Over the summer, I examined a series of Cheshire Formation carbonate samples that were collected during a field excursion to Zimbabwe in 2016 and shared with me by Professor Noah Planavsky at Yale University. My research was conducted through the preparation of polished slabs which were used to examine the macroscopic texture of the samples. Thin sections were also prepared for use in determining the mineralogy of the samples and examining the microscopic textures. Some promising samples were dissolved in dilute hydrochloric acid to analyze any siliciclastic residues that remained. The samples were also drilled by microfacies for further XRD analysis.

The petrographic analyses show dominant laminated microbial textures in the carbonates, with occasional influxes of fine grained siliciclastic sediments. Most laminations also hosted abundant pyrite grains and rusty grains interpreted as possible remnants of sulfide minerals. Some of the grains showed fanning morphologies but were not apparent enough to qualify as aragonite pseudomorphs. XRD data will help determine the exact mineralogy of the samples and help us make informed conclusions on the depositional conditions and processes for the Cheshire Formation.

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(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: Sara Pruss, Geosciences


Aby
River

What Was the Ecological Impact of the Demise of the First Animal Reefs?

Rhiannon Nolan/2019

In the lower Cambrian Period, the "Cambrian Explosion" of animal diversity was beginning, and animals began to produce reefs for the first time (e.g., Rowland and Shapiro, 2002). Reefs have been shown to be a major driver of evolutionary diversity and abundance during the Cambrian Explosion (Rowland and Shapiro, 2002), but these archaeocyath sponge reefs were a short-lived experiment, becoming extinct by the close of the early Cambrian (Zhuravlev and Wood, 1996). Although this extinction is well documented, the underlying cause(s) of the event remains unknown (Knoll and Fischer, 2011). In the western United States White-Inyo Mountains and surrounding regions, rocks that both host archaeocyaths as well as their extinction are well exposed. For example, the Poleta Formation, as well as the Harkless Formation which sits above it, preserve abundant archaeocyath reefs (Rowland et al., 2008). However, archaeocyaths do not appear in the Mule Spring Formation, which sits directly above the Harkless. Therefore, the archaeocyaths went extinct either within the upper Harkless Formation or the basal Mule Spring Formation, and my work has focused both on constraining the interval of extinction as well as examining the impact of extinction on other skeletal organisms during this time.

In May 2017, samples were collected from the Harkless Formation at Palmetto Mountain and near Gold Point, Nevada; from the Mule Spring Formation at Palmetto Mountain and Jackson Mountain, Nevada; and from the Poleta Formation near Mount Dunfee, Nevada. Each sample was cut and drilled to be run for carbon isotope data in future analyses, which may help to constrain the ages of the formations within the early Cambrian. After drilling, a subset of samples at roughly equal stratigraphic intervals were thin sectioned to be point counted and analyzed for diversity and abundance of organisms across each formation.

Preliminary analysis of thin sections from the Harkless Formation section show abundances of archaeocyaths, trilobites, echinoderms and other unidentified small shelly fossils. More detailed counting of archaeocyath abundances might reveal the relative time frame of the extinction and the environmental factors that may have contributed to it. The successive Mule Spring Formation thin sections contain mainly ooids and oncoids, which are very well-preserved Palmetto Mountain locality. This shift from more skeletal material to non-skeletal grains may be a reflection of extinction. The same formation at the Jackson Mountain locality has suffered extensive recrystallization within the oncoids, so fabrics are less well preserved. Even so, our initial analysis suggests that a major shift in carbonate deposition occurs from the Harkless to the Mule Spring formations: Harkless carbonates are dominated by diverse and abundant skeletal organisms, including archaeocyaths, whereas Mule Spring carbonates are dominated by microbial and other non-skeletal grains. We suggest that the extinction of archaeocyaths had more wide-ranging impacts than just the extinction of reefs.

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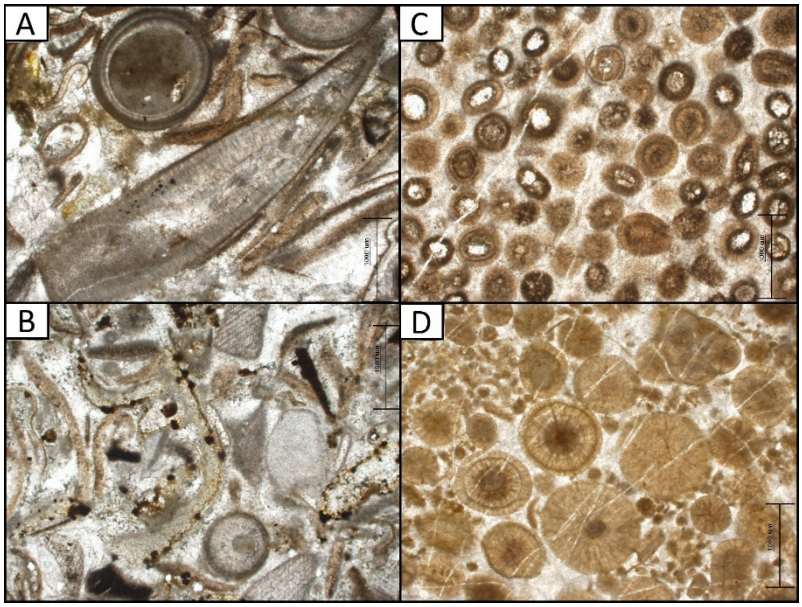
Figure 1: Thin section photomicrographs of Harkless and Mule Spring Formations. A: Sample P1-4; B: Sample P1-5.5; both showing small shelly fossils present in the Harkless at Palmetto Mt. C: Sample P2-13; D: Sample P2-23, both showing ooids found in the Mule Spring at Palmetto mountain.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: Sara Pruss, Geosciences



Bathymetric Mapping for the Management of Sediment Accumulated in Paradise Pond, Northampton, MA

Lizzie Sturtevant/2018

Every 8-10 years, accumulated sediment needs to be removed from Paradise Pond to preserve the look and recreational functionality of this central campus landmark. Sediment accumulation occurs in the pond in response to decreased water velocity due to the presence of the dam that disrupts the natural downstream transport of sediment by the Mill River.

In previous years, costly dredging operations required the excavation and transport of the sediment to a nearby landfill. An alternative method of sediment removal has been proposed that minimizes both cost and environmental impact using the natural flow of the river to flush sediment downstream during high flow events. This is a two-step process where sediment is first moved from the upstream portion of the pond down to the area just above the dam by a combination of mechanical excavation and stream transport during a partial pond drawdown. The accumulated sediment is then released at a later time when the sluice gate at the base of the dam is opened during a high flow event.

In July of 2016, an experiment was conducted to test the feasibility of the first step of this process. The pond was drawn down and sediment was moved with a bulldozer into the newly formed channel to be transported down in front of the sluice gate.

In June of 2017, in order to continue monitoring the distribution of sediment along the pond bottom, a digital elevation model (DEM) was produced for bathymetric data collected using a depth sounder. Depth data in feet from the depth sounder was subtracted from the elevation of the pond level at the time of data collection and then converted to meters to produce the elevation above sea level of each data point. Raster interpolation was performed separately on the June and October elevation points using universal kriging in ArcGIS with a 1m x 1m grid. The results show that the channel leading to the sluice gate at the base of the dam remains and that there is a mound of sediment just before the gate, ready to be released at the next large storm event.

(Supported by Pond Project)

Advisor: Robert Newton, Geosciences

Splines on Graphs with Two Distinct Degree-2 Polynomial Edge Labels

Portia Anderson/2017

Given a graph with fixed edge labels, a spline is a set of vertex labels such that the labels of any two adjacent vertices are congruent modulo the edge label between them. The focus of this project is studying splines on planar graphs whose edges are labeled with exactly two distinct degree-2 homogeneous polynomials. For an arbitrary graph of this type, we are interested in finding the minimal generating set, that is, a minimal set of splines that, via linear combination, can generate any arbitrary spline on a given graph.

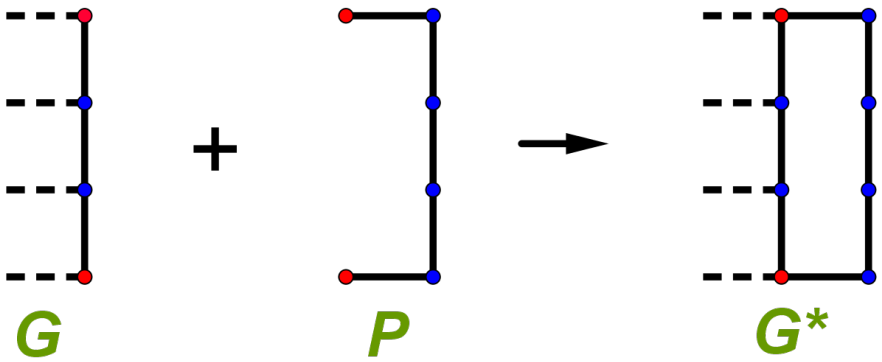
We devised two different strategies for achieving this goal. The first strategy involves finding the minimal generating set of an arbitrary graph by relating it to simpler graphs with known minimal generating sets. Specifically, we want to be able to construct an arbitrary graph (along with its minimal generating set) by inductively gluing together these simpler graphs while keeping track of the minimal generating set as we go. Thus, we are interested in finding rules to describe how the minimal generating set of a graph changes when we glue a particular type of graph onto it. In fact, the crucial research question is the following: If we glue the endpoints of a path P onto a graph G to get G* (see figure for example), how is the minimal generating set of G* related to those of P and G? This question naturally splits into two types of cases; we proved a rule for the first type and are working on a rule for the other.

The second strategy is an algorithm for direct flow-up construction of a minimal generating set for an arbitrary graph. Our idea involves assigning the vertices of the graph an ordering by which we inductively label them with zero. Each time we add a new zero, we label the remaining vertices, following specific rules that yield a spline of smallest possible degree for inclusion in the minimal generating set. A proof of the validity of this method is in progress.

I presented the work done on this project at two conferences during the summer: the Summer Combo in Vermont and the 5th Northeast Mathematics Undergraduate Research Mini-Symposium. Going forward, we aim to completely develop the two strategies described and prove that they do indeed generate minimal generating sets for arbitrary graphs.

(Supported by NSF: National Science Foundation)

Advisor: Julianna Tymoczko, Mathematics and Statistics



Generalizations of Lie(k)

Sarah Brauner/2017

We study the representations of the Symmetric group on a generalization of multi-linear component of the free Lie algebra. This generalization, called a Lie Algebra of the n^{th} Kind (LAnKe), is a space equipped with an n-linear, antisymmetric commutator and a generalized Jacobi Identity.

Specifically, we study the representations of the Symmetric group on the LAnKe polynomials. We define $\rho_{n,k}$ to be the representation of $S_{kn-k-n+2}$ on a LAnKe polynomial with an n-linear commutator applied $k-1$ times. Our results this summer can be broken up into the following categories.

\begin{enumerate}

\item \emph{A new partial proof for $k=3$.}

Hanlon, Friedmann, Stanley and Wachs recently found a proof that the representation of $\rho_{n,3}$ is the irreducible representation of shape $2^{n-1},1$. This summer, we partially proved an alternate proof for this result by defining an explicit map $\Psi: \rho_{n,3} \to S^{2^{n-1}1}$, where $S^{2^{n-1}1}$ is the Specht module corresponding to the partition $2^{n-1}1$. This method allows us to define a natural basis for the space $\rho_{n,3}$. We were able to show that Ψ is linear by proving that the image of the Jacobi Identity under Ψ holds in the representation $S^{2^{n-1}1}$. It follows easily that Ψ is surjective, and remains to be proved that Ψ is injective. We hope to publish these results once we complete them. Moreover, we hope that this technique can be extended to higher k.

\item \emph{A Recursion for $k \leq 4$}

When we began this research at the beginning of the summer, one open problem was finding a way to link $\rho_{n,k}$ to $\rho_{n-1,k}$ or $\rho_{n,k-1}$. In the case where $k \leq 4$, using our conjectured and proven results for the representation of $\rho_{n,k}$, we were able to prove a recursive formula linking $\rho_{n,k}$ to both $\rho_{n-1,k}$ and $\rho_{n,k-1}$. Our recursion for $k \leq 4$ is given by

\[\rho_{n,k} = (\sgn_{n-1} \times \rho_{n,k-1}) \cap (\triv_{k-1} \times \rho_{n-1,k}). \]

The proof of this result relies heavily on the Littlewood-Richardson rules. Thus far, the theorem also relies on the fact that the irreducible representations that make up $\rho_{n,k}, \rho_{n-1,k}$ and $\rho_{n,k-1}$ are known. However, if we were able to find a basis for $\rho_{n,k}$, we might be able to use the recursion to give an independent proof of $\rho_{n,k}$. In the case where $k>4$, the problem becomes more complex, and we found that the recursion no longer held. In future work, we hope to find a recursion which works for any k.

(Supported by Ellen Borie Fund)

Advisor: Tamar Friedmann, Mathematics and Statistics

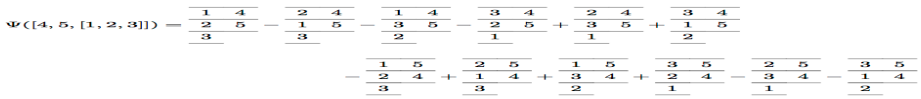


Figure 1. An example of the map Ψ in the case where $k = 3$.

1

Analyzing Predator-Prey Interaction Models

Samantha Comeau/2018

In nature, many prey species aggregate in large flocks or herds. There are several reasons prey might aggregate, including safety from predation [1]. When there are more prey, there are more eyes to watch out for predators. Thus an individual can spend more time foraging [2]. Additionally, predators can become confused in the presence of too many prey and the risk of capture for any individual subsequently decreases. Understanding how prey and predators interact with each other is essential to understanding any ecosystem.

In order to replicate prey aggregation, we make assumptions about the forces that the prey feel at any given time. It has been shown that if the prey are subjected to a long-range attraction force and a short-range repulsion force, they will exhibit aggregation [3]. Biologically, this implies that the prey have a desire to be together, but still want to retain a small amount of distance. This is most likely because other prey become competition for food or alternative resources.

More interesting formations and behaviors occur with the addition of predators. Now we must consider interactions between prey, interactions between prey and predators, and interactions between predators. The interactions between predators are the most interesting and the least explored of all the interactions. In order to determine what the interaction forces look like, we needed to decide how the predators hunt. They could be solitary hunters, they could be completely in competition with each other, or they could work cooperatively as a group.

In this project we explored existing models describing predator-prey interactions with varying numbers of prey and predators. We then broke down the different interaction forces and observed how they affected the overall behavior of the system, noting any patterns that emerged. Finally, we combined aspects of the existing models in order to create our own model that replicated actual behaviors of a pack of African wild dogs.

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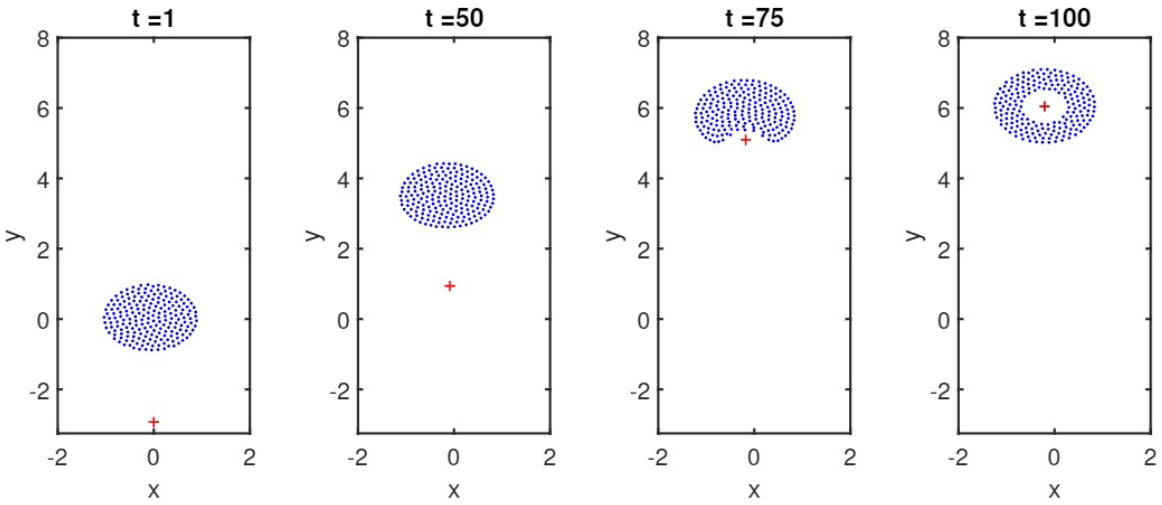
(Supported by NSF: National Science Foundation)

Advisor: Nessy Tania, Mathematics and Statistics



Optimizing a comb and a cube

Yijia Cui/2019 and Chujun He/2020

This summer we worked on optimizing a transportation network. Given a set of supply nodes, a set of demand nodes, and a set of transit nodes, we tried to find the best way to connect the nodes so that every demand could be satisfied and the total cost - our "objective function" - could be minimized. To be specific, our objective function was the sum of the fixed cost of each edge and the flow cost of every unit of flow. We mainly studied two models — the comb and the cube.

For each system, if a minimum spanning tree(MST) contains the cheapest path between every pair of supply and demand nodes, we define it as an efficient MST. We proved that if we can have an efficient MST in the graph, and the optimal graph is connected, then this MST is the optimal solution.

To set up a system on an nxm grid, the costs are assigned as follow: (1) For vertical edges between nodes (i,j) and (k,j), the fixed cost of the edge will be 1 if $|i-k| = 1$ and 60 otherwise. (2) For horizontal edges between nodes (i,j) and (i,k), the fixed cost of the edge will be 1 if $|j-k| = 1$ and i=1, and otherwise, the fixed cost will be b where b is a parameter. (3) For diagonal edges between (i,j) and (k,w), we let the fixed cost of the edge be $pa(|i-k|+|j-w|)$ where p and a are parameters. And the flow cost per unit is equal to the fixed cost of the edge.

The comb is one typical example of an efficient MST for a subset of the parameters. We found that the optimal solution will change depending on the values of the parameters. For some conditions, we located the flip point of parameters when the optimal solution is changed and we still need to keep working on other more complicated conditions.

Another example is the cube. Our professor thought of a structure that is made up of a series of connected identical cubes. Since all cubes in the big connected structure are congruent, we can also conclude that if the cube has an efficient MST, then the efficient MST for the whole structure is the optimal solution.

(Supported by Ellen Borie Fund)

Advisor: Tamar Friedmann, Mathematics and Statistics

Modeling Effects of Wnt5B on Radial Glia Proliferation and Differentiation

Selina Husain/2019

The Wnt Signaling Pathway is responsible for cell maintenance and determines developmental processes in the embryonic state. The purpose of this project was to investigate the proliferation and differentiation of a particular type of neural stem cell called radial glia. The Wnt pathway plays an important role in tumorigenesis and embryogenesis and has genes and proteins that act through different signaling pathways. Deregulation of this pathway can lead to developmental and genetic diseases such as cancer which is why examining this gene is important. We focused specifically on the Wnt5B gene which was previously identified to significantly impact neural tube development, but its exact effects on radial glia cell-cycle and differentiation are not fully known. We analyzed and further quantified data collected from Professor Michael Barresi's lab. Using mathematical modeling, we tested whether Wnt5B stimulates/represses proliferation of radial glia, changes the duration of the cell cycle, and alters differentiation into neuronal cells. We found that a mutation in Wnt5B can increase cell cycle entry and cell division but reduce cell differentiation. Our preliminary study however cannot distinguish how these processes are changing over time. In the future, we plan to incorporate other cell count data that were obtained to refine the model and test the possibility that the neuroepithelial population is impacted by the Wnt5B mutation.

Acknowledgement: Special thanks to Prof Barresi, Carla Velez, the Baressi's lab and the Four College Biomath Consortium.

(Supported by NSF: National Science Foundation)

Advisor: Nessy Tania, Mathematics and Statistics

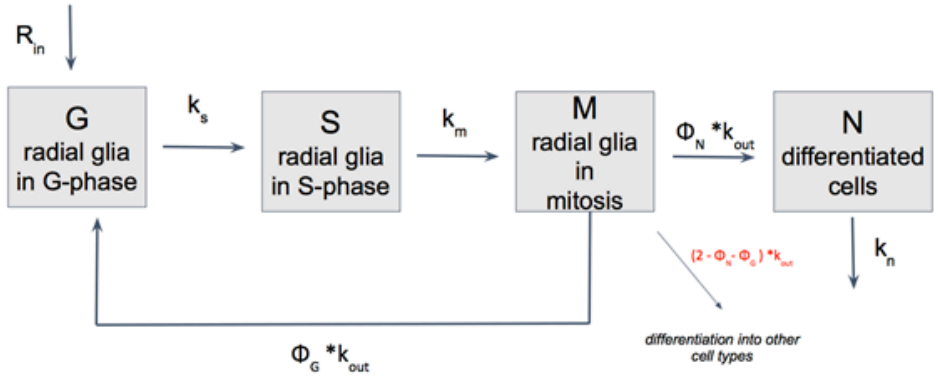


Fig 1. Proposed model schematics of the process radial glial cells undergoes. R_{in} (maximum number of radial glial cells generated by the neuroepithelial), k_s (rate of entry into S-phase), k_m (rate of entry into M-phase), ΦN (average number of daughter cells that can become differentiated cells), ΦG (average number of daughter cells can remain radial glial cells and go back to G-phase), k_{out} (exit rate from mitosis), and k_n (migration, death, or further differentiation).

Using Graph Theoretical modeling techniques in the study of neural connectivity

T

Tingshan Liu/2019

This project is a continuation of the special study I conducted during the spring semester of 2017 with Professor Gwen Spencer on the topic of identifying popular graph theory models for neural connectivity simulation.

One of the most intriguing questions in neuroscience is how the architecture of biological neural network facilitates information processing. Cortical thickness correlation has been used to investigate the anatomical connectivity patterns in the human brain [1,2]. Most of the prior studies compiled the false-discovery-rate-corrected Pearson correlation coefficients for each pair of regions of interest to generate a binary and undirected graph by applying a threshold. However, due to the lack of exploration of reproducibility in most studies and the absence of a systemic review considering the impact of sample size particularly for this method, the interpretations of the findings are likely subject to inquiry. Our project focused on examining the relationship between reproducibility of popular centrality measures and sample size and refining current edge-weighting schemes for network construction. We showed that the common cortical thickness correlation networks are not stable under re-sampling, and the graphical metrics are highly correlated with sample size. Alternative approaches were proposed and demonstrated the ability to boost reproducibility considerably.

After showing that our biased-edge-weighting scheme is practical for retaining more information in the network, we applied it to clinical data of Alzheimer Disease's patients. Apart from the network creation method identified earlier, randomized local improvement algorithm was used to maximize the difference between Spearman's footrule distances computed for healthy subjects and those for patients in pre-clinical stage of Alzheimer Disease. We were able to spot abnormal changes in the brain before symptoms can be detected by traditional neuropsychological assessment of dementia with a sensitivity of 80%.

References:

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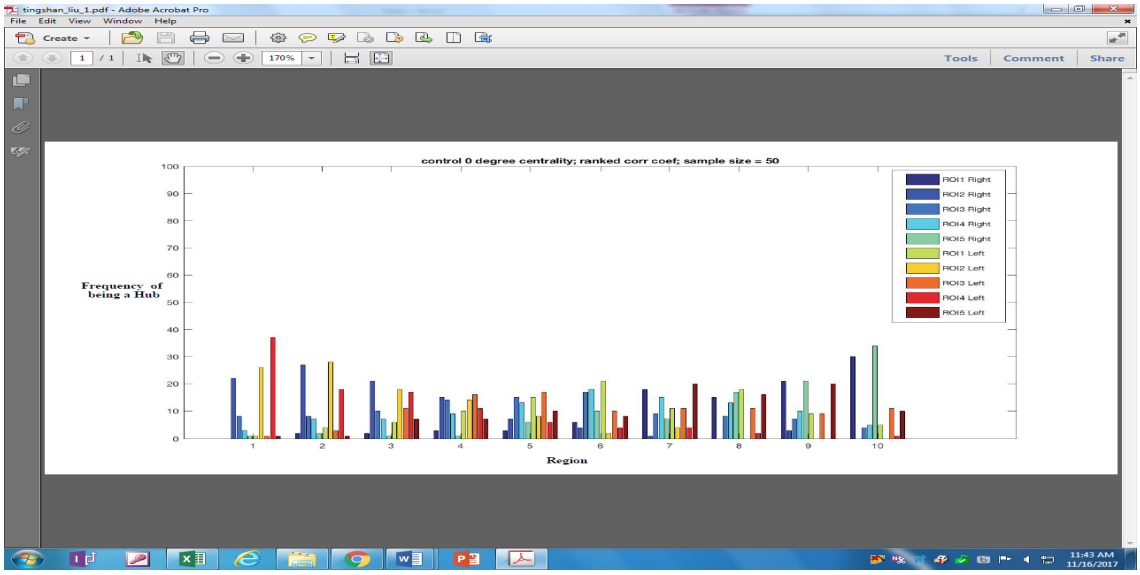
(Supported by Ellen Borie Fund)

Advisor: Gwen Spencer, Mathematics and Statistics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11/16/2017

Degree-2 Polynomial Splines on Cycles

Cleo Roberts/2017

Splines occur in several fields of applied and theoretical mathematics. It is common for researchers to try to identify bases for the set of splines on a given graph. This project focuses on characterizing the minimal generating set of splines on a given graph. It relies on and continues the research conducted by a group of students under the supervision of Prof. Julianna Tymoczko during the 2016-2017 school year.

Consider a graph G with fixed edge labels. A spline on G is a set of vertex labels in which the difference between any pair of adjacent vertices is a multiple of the edge label between them. We study splines on graphs whose edge labels are degree-2 polynomials of the form (x+ky)^2, where k is some real number. In particular, we describe the minimal generating set of splines for single and connected cycle graphs. A minimal generating set on graph G is the smallest and lowest-degree set of splines that one can combine through addition, subtraction, and multiplication to obtain all of the possible splines on G.

The splines in a minimal generating set can be expressed as a set of vectors, which can be arranged into the columns of a square matrix. This allows us to take the determinant of the minimal generating set and generalize equations for it. Gjoni (2015) has established an equation for the determinant of a minimal generating set of splines on an integer-labeled cycle graph. We show that this equation holds for polynomial splines on cycles. Mahdavi (2016) has developed an equation for the determinant of the minimal generating set of integer splines on two 3-cycles that share one edge. We simplify this equation and show that it holds for any two cycles joined by any number of edges. This result is valid for both integer splines and polynomial splines.

I presented these results at the Summer Combo Combinatorics conference at St. Michael's College in Vermont and at the 5th Northeast Mathematics Undergraduate Research Mini-Symposium at the University of Connecticut.

(Supported by NSF: National Science Foundation)

Advisor: Julianna Tymoczko, Mathematics and Statistics

Cycle MGS Determinant Theorem

Theorem (Gjoni, 2015)

Given an integer-labeled n-cycle graph, C_n, let e_i denote the label on the ith edge, where $1 \leq i \leq n$.

$$det(MGS(C_n)) = c \cdot \frac{e_1 e_2 \dots e_n}{gcd(e_1, e_2, \dots, e_n)}, \text{ where } c \in \mathbb{N}.$$

Theorem (Gjoni, 2015), adapted

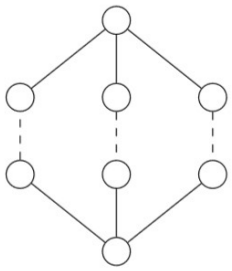
Given an n-cycle graph, C_n, whose edges are labeled by degree-2 polynomials of the form $K = (x + ky)^2$, let e_i denote the label on the ith edge, where $1 \leq i \leq n$.

$$det(MGS(C_n)) = r \cdot \frac{e_1 e_2 \dots e_n}{gcd(e_1, e_2, \dots, e_n)}, \text{ for nonzero } r \in \mathbb{R}.$$

Theorem (Mahdavi, 2016), adapted

Suppose that G is a graph composed of two connected cycles, whose edges are labeled by degree-2 polynomials of the form $K = (x + ky)^2$. Let $P_1 = \text{gcd(outer cycle edges)}$, $P_2 = \text{gcd(left inner cycle edges)}$, and $P_3 = \text{gcd(right inner cycle edges)}$.

$$det(MGS(G)) = r \cdot \frac{\text{product of all edge labels}}{lcm(P_1, P_2 P_3)}, \text{ for nonzero } r \in \mathbb{R}.$$



Modeling the Spread of Invasive Species

Emmely Rogers/2019 and Qiaomei Li/2018

Invasive species can be harmful to the environment. Our goal was to mathematically predict the spread of invasive species. Predicting the spread will aid in making adjustments to help prevent further spread. In cases of waterborne species, human behavior causes transmission of invasive species across a discrete set of locations that can be modeled as a graph.

To generate the most accurate "real life" spread process possible for a general graph, we created a simulation based on an experiment in the paper, Highly Variable Spread Rates in Replicated Biological Invasions: Fundamental Limits to Predictability. We have 7 inputs - adjacency matrix, initial node population, generations, carrying capacity, reproductive rate, death rate, and allee effect number. For each generation, the individual moves to a neighboring node or stays at the current node, and it may reproduce. If the individual moves to a neighbor that has been removed, then it dies. The reproduction rate for each individual is determined by a local reproduction rate, the individual's fitness, and allee effect.

Our simulation produced high-variability results similar to the animal experiments described in the paper (left figure). The random simulation was run 30 times (30 subgraphs). In each random simulation, an initial invasion at patch 1 spreads to the right over 13 generations.

Node removal strategy is a way to interrupt the spread of invasive species. A set of lakes can be discretized and modeled as nodes. The lakes' accessibility levels can be modeled as edges. We are looking for smart ways to choose node removals, so we implemented two objectives, minimize number of invaded nodes (IP4) and maximize time until widespread invasion (IP7), for 3 kinds of landscapes - lattice, random and gravity score (bottom figure). The spread process used in the IP's are only estimates because the spread process was designed to invade neighboring nodes in the next generation. But, the simulated spread process is the closest to "real life". We compared IP4 removals, IP7 removals, random removals, and neighbor removals under the random simulation for 30 instances (right figure).

Given a small number of invasion sites and small budget, IP7 removal has the best average performance under lattice landscape. Neighbor removal has the best average performance under random landscape. IP4 removal has the best average performance under gravity score landscape. In the future, another objective that can be implemented is minimize total cost of defending a specified percentage of nodes.

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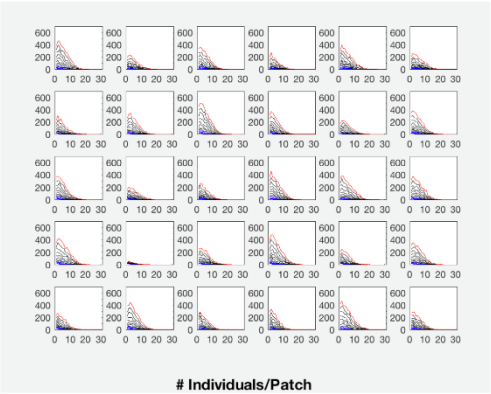
Supported by NSF: National Science Foundation)

Advisor: Gwen Spencer, Mathematics and Statistics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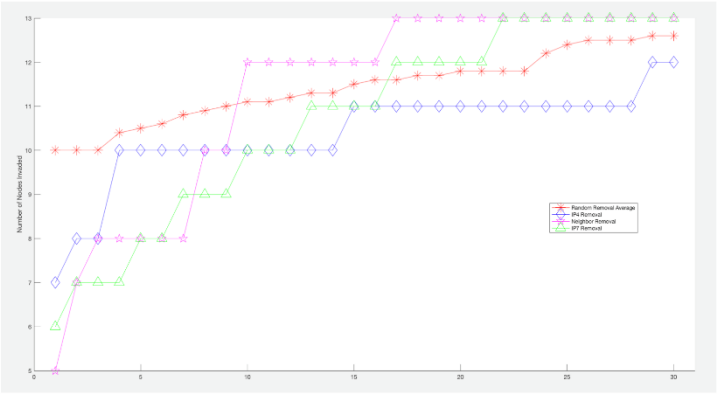
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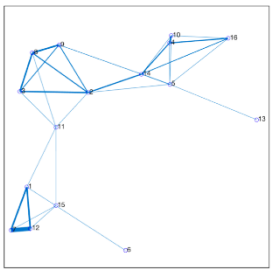
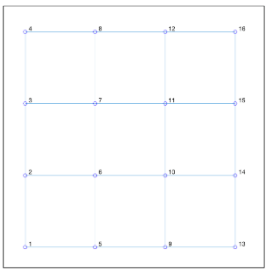
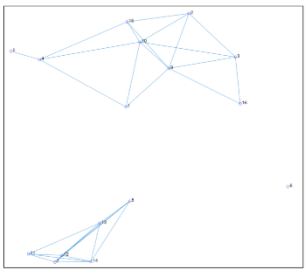






Identify the effects of Wnt5B on Stem Cell Divisions and Differentiations

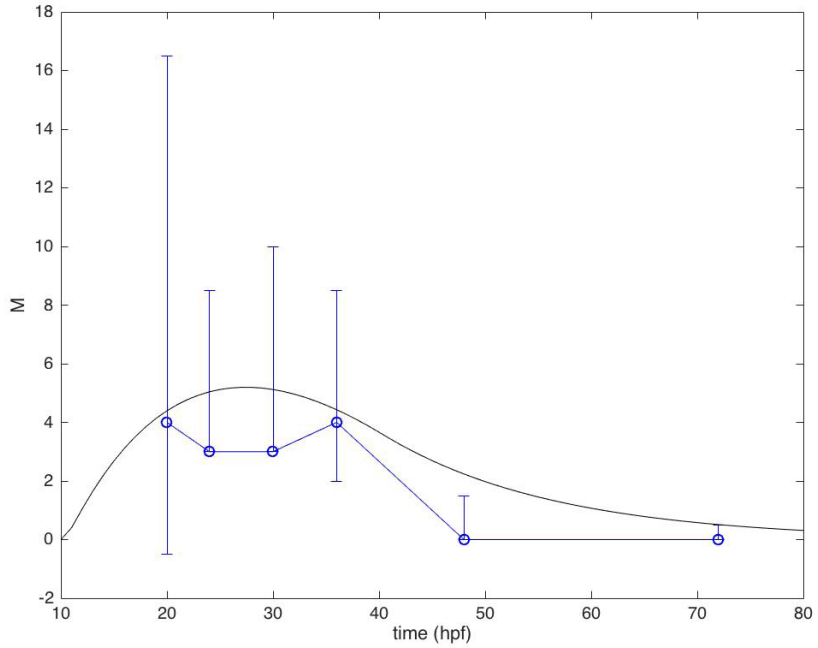
Jing Xia/2018

Regulations of stem cell division and differentiation are essential for proper embryonic development. During neurogenesis, the improper division of radial glia (neural stem cells) may lead to congenital brain disorders. During the summer, I worked with another student, Selina Husain, to build mathematical models and analyze data collected in Prof. Michael Barresi's lab. Our specific focus is to identify the effects of a particular mutation, Wnt5B, on radial glia proliferation and differentiation. We considered different mathematical models, consisting of systems of differential equations, and ranked them according to goodness-of-fit and the number of free parameters. Specifically, I implemented the Akaike Information Criterion (AIC) which considers the tradeoff between the two effects: while the model should closely fit the data, extra parameters can lead to over-fitting. Our AIC analysis suggest that a model where Wnt5B mutation leads to more frequent proliferation but lower differentiation rate in radial glia populations, is most consistent with the experimental data. We have also considered other effects such as delay in mitotic exit and changes in neuroepithelia (earlier stem cell class) proliferation/differentiation, but these models resulted in a higher AIC score (less consistent with observed data).

Through this summer research, I was not only able to gain a better understanding on the stem cell division and differentiation, but practiced the model building and research conducting skills as well. As a student who is pursuing both applied math and statistics tracks, one day in the future, I will be constructing my own models, either in graduate school or in other related fields. This experience broadened my horizon in the statistical modeling and enhanced my skills in data analyzing and manipulating. Future research for this project would include new modeling strategies and a detailed sensitivity analysis.

(Supported by CFCD Committee on Faculty Compensation and Development)

Advisor: Nessy Tania, Mathematics and Statistics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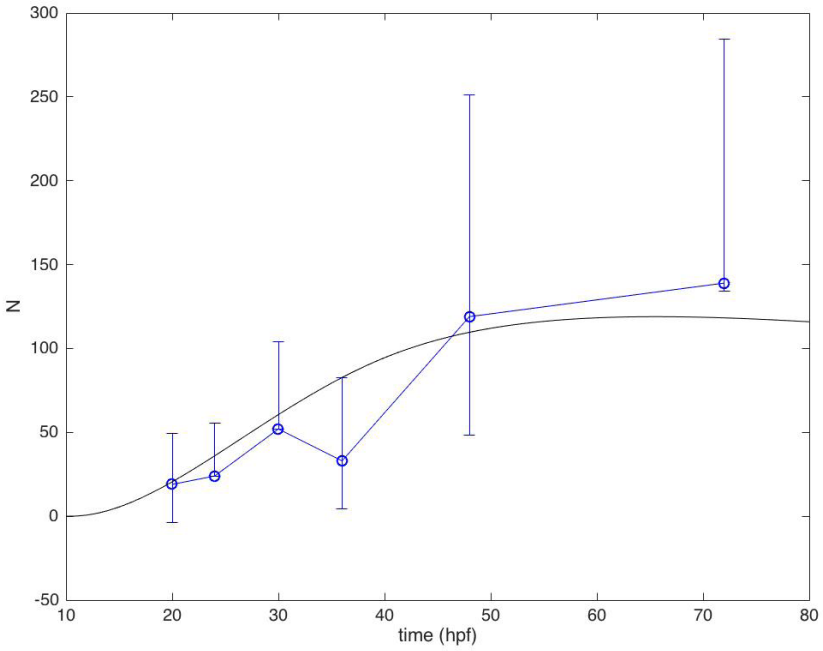
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ETL Package - Manipulate Medium-sized Data in R

Wencong (Priscilla) Li/ 2018

This research is a continuation of work that began in spring 2016 with Professor Benjamin Baumer. The objective is to learn more about 'etl' package to allow R users to work with medium data that are big and changing through time.

RStudio is a free and open source integrated development environment (IDE) for R, a programming language for statistical computing and graphics, and CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R.

R packages provide users with software that extends the core functionality of R, as well as data that illustrates the use of that functionality. However, by design the type of data that can be contained in an R package on CRAN is limited. First, packages are designed to be small, so that the amount of data stored in a package is supposed to be less than 5 megabytes. Furthermore, these data are static, in that CRAN allows only monthly releases. Alternative package repositories -- such as GitHub -- are also limited in their ability to store and deliver data that could be changing in real-time to R users.

The 'etl' package provides a CRAN-friendly framework that allows R users to work with medium data in a responsible and responsive manner. It leverages the `dplyr` package to facilitate Extract-Load-Transfer (ETL) operations that bring real-time data into local or remote databases controllable by R users. The suite of `etl`-dependent packages brings the world of medium data -- too big to store in memory, but not so big that it won't fit on a hard drive -- to a much wider audience.

SQL is a programming language that is designed for managing data held in a relational database management system. The 'etl' package helps people with no SQL experience to do data analyzation with medium data.

(Supported by the Susan M. Rambo 1905 Fund in Mathematics & Statistics))

Advisor: Benjamin Baumer, Mathematics & Statistics

Lever Pressing as a Model of Motivation for Peer Social Behavior

Natalie Bourdon/2019

The social behavior of prairie voles (Microtus ochrogaster) is unique in that they are socially monogamous, and will form same sex peer bonds in addition to mate bonds (Anacker and Beery 2013). An ongoing study in the Beery lab hopes to discover whether these peer bonds are motivated and rewarded, or simply occur out of convenience and proximity, by using a lever pressing model of operant conditioning.

Female prairie voles are trained with shaping to lever press for a food reward on a fixed ratio schedule, followed by a food reward on a progressive ratio schedule. Voles that successfully progress through this training continue to social testing, and voles that do not learn to lever press independently are discontinued from testing. Successful voles are assigned to same sex pairs or opposite sex pairs. Females assigned to opposite sex pairs are paired with a male who has been castrated and given a testosterone capsule implant. The social testing occurs in a two-chambered apparatus (Image 1). The focal vole is placed in the left chamber which contains a lever and a door that, when raised, allows access through a small tube into the right social chamber where a stimulus vole is tethered. After a sufficient number of lever presses the door opens for 60 seconds, allowing the focal vole to cross into the second chamber and interact with the tethered vole if desired. After 60 seconds the vole is returned to the left lever pressing chamber. Focal voles are given two sessions of habituation with the door taped up to allow free access between both chambers. The animals are then given two days of fixed ratio social testing. Finally, focal voles complete 8 days of progressive ratio testing with their partner or mate tethered, and 8 days of progressive ratio with rotating stranger voles tethered in the social chamber.

The number of lever presses, door openings, and time spent huddling with the tethered vole are quantifiable measures of motivation to access either a same sex peer, a mate, or a stranger vole. This research is a continuation of research completed by Sarah Lopez and Katrina Blandino, and is still in the data collection phase of the project. We hope that this data will help us understand the underlying cause of same sex peer bonds, and the difference between peer bonds and mate bonds in prairie voles.

Image 1. The social conditioning chamber. The focal vole (left) pushes a lever in order to raise a door and gain access to a stimulus vole (right) which is tethered in the social chamber.

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(Supported by Frances Baker Holmes Internship Fund)

Advisor: Annaliese Beery, Psychology, Neuroscience

The Methods of Inducing and Measuring Consequences of Jet Lag

Reja Javed/2018

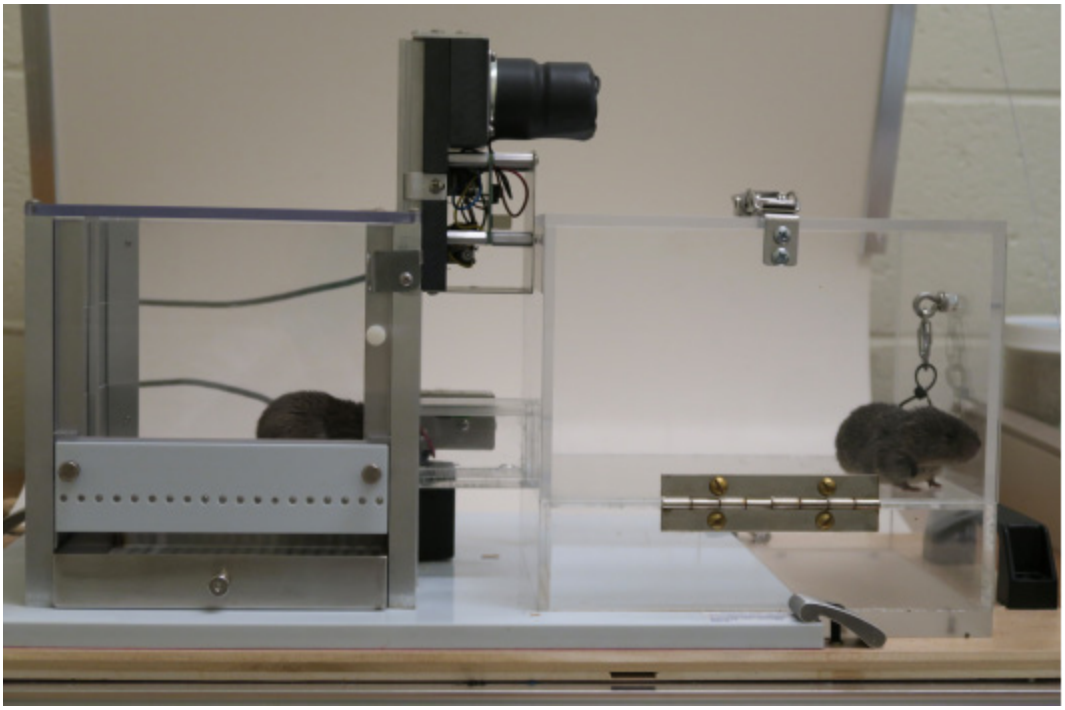
Jet lag, also known as circadian desynchrony, is when the body's internal period does not match the external environment. However it can also be when the the Suprachiasmatic Nucleus (SCN), which is the body's master pacemaker, and the peripheral tissues are misaligned in their daily rhythms.

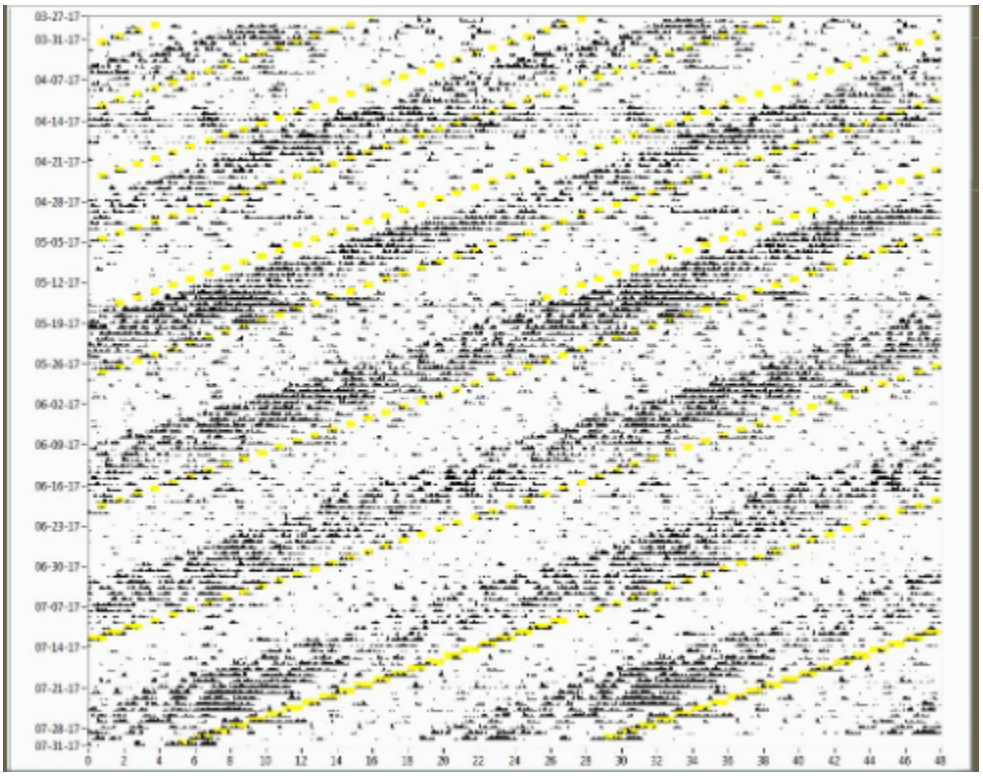
Studies have shown that jet lag caused by phase advances are much more difficult on the body than phase delays, but we are not entirely sure in what way the consequences differ. The new In Vivo bioluminescence technique allows us to look at the consequences that jet lag presents on the body while the mouse is still alive and moving. The need to kill or anesthetize the mice is no longer necessary since that often resets the rhythms of many peripheral tissues like the liver. Mice are genetically engineered to have a luciferase gene downstream of their Per2 gene that is specific to an organ and are then put into a dark chamber that has photomultiplier tubes that can read off bioluminescence. However since mice are not intrinsically bioluminescent, compounds such as D-luciferin and CycLuc1 were delivered to them via drinking water or osmotic mini-pumps. We found that drinking water was not a good option for delivery of D-luciferin or CycLuc1 because it gave us the drinking rhythm of the mouse rather than the real circadian rhythm. We also found that D-luciferin was not a good option for the osmotic mini-pumps due to insolubility, so CycLuc1 via osmotic mini- pumps was the best option in order to measure the expression of Per2 and how it changed under conditions of jet lag.

Since the In Vivo chamber needs to read the bioluminescence in the dark, we needed to come up with a way to stimulate a phase advance in the mice using as little light as possible. Studies with the phase response curve (PRC) of mice have shown that light in the late subjective night causes phase advances This was accomplished by using a skeleton photoperiod. The mice were given two half-hour light pulses separated by 12 hours administered on a 23 hour period rather than the typical 24 hour period and then switched to having only one light pulse that fell in their late activity period in order to advance the mice. The In Vivo bioluminescence technique and the skeleton photoperiod allows us to induce and measure the consequences of phase advance jet lag.

(Supported by Frances Baker Holmes Internship Fund)

Advisor: Mary Harrington, Neuroscience

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The Role of Sex and Ovarian Cycles in Rodent Behavioral and Physiological Variability

Kathleen Moshofsky/2017

Exclusive use of male test subjects is common practice in animal research, based in part on a long-held assumption that females are more variable than males because of the estrus cycle. Recent studies examining a variety of traits in rodents found no evidence of different variability between the sexes for most outcomes; for traits in which one sex was more variable, males were more variable slightly more often than females (Prendergast et al. 2014, Becker et al. 2016). These studies leave unresolved whether the sources of variability in males and females are similar. For instance, similar overall variability could arise from high variability across days in females and high variability between male individuals. Alternatively, males and females may have similar variability across days, even for traits that vary across the estrous cycle.

In the present study, we compared variability of male and female Syrian hamsters (Mesocricetus auratus) across multiple tests. Female Syrian hamsters spontaneously ovulate on a 4-day cycle, allowing exact identification of cycle phase. Ovariectomized female hamsters were compared to intact (or sham operated) females and males. Subjects were habituated to tasks and tested over two estrous cycles (or the equivalent duration) for behavior in open field, novel object recognition, and sucrose preference tests. When investigating estrous cycling, ovariectomized females and males were arbitrarily assigned an estrous cycle, with "faux estrous phases" assigned for each day. The distribution of faux estrous phases was assigned to match the distribution of estrous phase days for true cycling intact females.

Groups tracked across days of testing overlapped in mean response in most testing measures, with the exclusion of body temperature, in which males had significantly lower temperature than females. Variability differed between tests, with no one group consistently more variable than other groups across measures. When mapping testing days over estrus phases, variation between groups was mostly similar across groups. In cases when variability fluctuated, it often fluctuated most on day 3 of estrus in intact females, when the coefficient of variation tended to decrease or increase compared to variation on other days. However, significant fluctuations occurred across faux estrous cycle days in some male and ovariectomized female tests, suggesting that a larger sample size is needed to definitively claim whether the estrous cycle was controlling variability on this day, and not random variation.

(Supported by SURF Gifts Fund)

Advisor: Annaliese Beery, Psychology, Neuroscience

The behavior of ARC microglia under circadian disruption and a high-fat diet

Donna Mosley/2018

Obesity is a worldwide health issue and is implicated as a risk factor for more serious pathologies such as heart disease, diabetes, neurodegeneration, and cancer. However, the mechanisms underlying obesity are not yet well understood. It has been shown that shift workers are at an increased risk of suffering from these pathologies. Several factors have been attributed to this increased risk. Two of these are circadian disruption (CD) -- disruption to endogenous bodily rhythms because of excessive exposure to light at night -- as well as irregular and poor eating habits, namely a high-fat diet (HFD) [1]. Circadian disruption has specifically been implicated in leptin insensitivity. Since leptin is a key hormone in energy regulation, being insensitive to its effects can lead to obesity [2].

Leptin is interpreted in the brain in an area known as the arcurate nucleus (ARC) [3]. This nucleus is comprised of a network of neurons, namely POMC and AgRP neurons. This network regulates the amount of food we intake and the amount of energy we expend by interpreting leptin signals and releasing hormones that control metabolic processes. However, when the mechanisms for interpreting the leptin signals are disrupted, downstream hormones are not released and so the body does not receive the signal to decrease energy intake. In addition, if the POMC/AgRP network is interrupted at the junction of these two neurons, this can also result in the cessation of hormone release and an increased risk of obesity [4].

Microglial cells have been shown to regulate the junctions of neural networks like the one found in the ARC. However, if microglia are over-activated – possibly due to leptin insensitivity of ARC neurons -- they can degrade the network and thus the body's capacity to regulate energy intake [6].

Therefore, this study aims to assess if microglial over-activation plays a role in obesity. To that end, I raised mice in a double experimental condition of CD (to simulate shift work) and a HFD. The brains of these mice were then sliced and stained with fluorescent labels specific to proteins found in microglia. The Iba1 stain is specific to a protein found in the microglial cytoskeleton, while the CD68 stain is specific to a protein in microglial lysosomes [7]. These lysosomes are an indication of microglial phagocytosis, which is the process whereby microglia engulf and degrade material like neural terminals (e.g. the synaptic terminals within the ARC network).

This is an ongoing experiment that is part of my thesis project, and I am currently in the process of analyzing the images. Once they have been analyzed, I will use the statistical data to assess if there are more phagocytic microglia in the experimental condition than in the controls.

Figure 1. ARC microglial cells double labeled with a red immunofluorescent label specific to Iba1 (whole cells) and a green immunofluorescent label specific to lysosomal CD68 (small circular areas).

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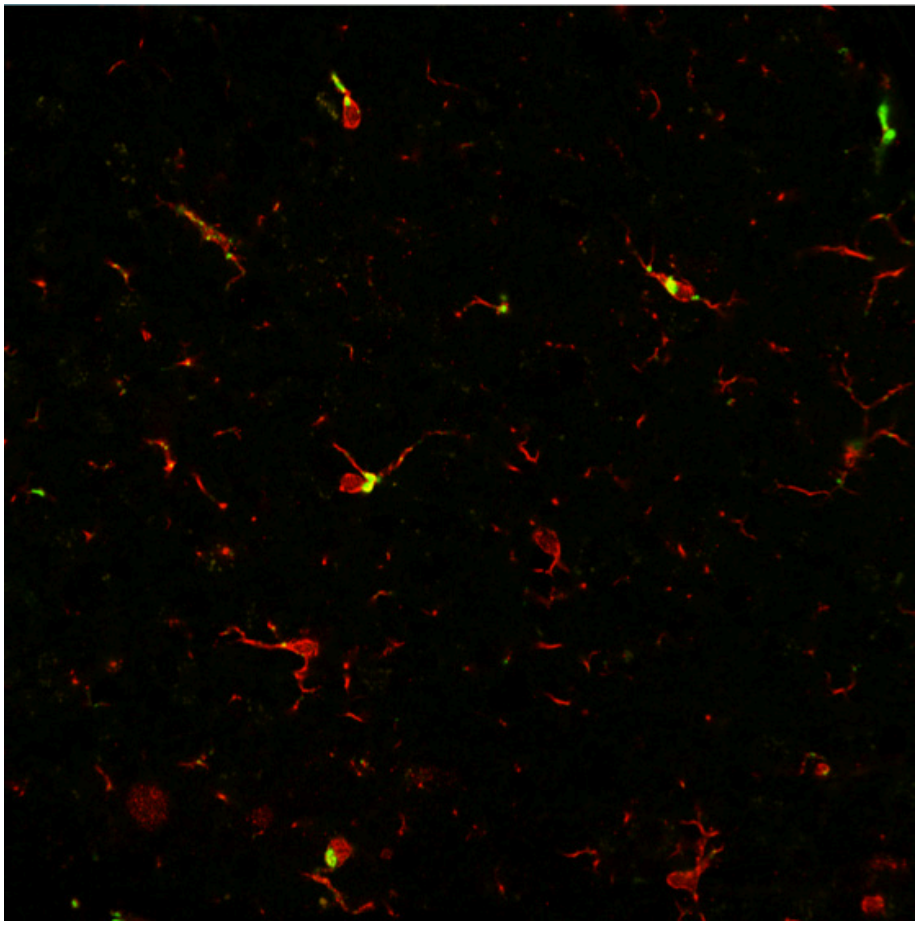
(Supported by Frances Baker Holmes Internship Fund)

Advisor: Mary Harrington, Neuroscience



Quantum Chaos and Transportation Problems

Phuong Chau/2020

Chaos is the production of complex behavior from simple rules. The chaos theory involves systems that have very similar initial conditions and diverge exponentially as they evolve. Therefore, one small change in the initial conditions can have great effect at a later time.

In order to apply this theory to a quantum mechanical system, it is required to have a quantitative measure of the difference between two points in phase space (the difference between two wave functions).

The state of a particle or system is characterized by a point in phase space. The distance between the points in phase space corresponds to these states. Therefore, we use the Wigner function, which is a real-valued function and a probability distribution in phase space to represent the quantal states. The Wigner function contains exactly same information as the wave function. The Wigner function is derived for a Gaussian wavepacket (normal distribution). The two Wigner functions are normalized so that the integration of the function over the entire space is 1.

In order to define the distance between two normalized real-valued functions, we are using such a measure that involves minimal transport of one functional shape to another. We will be working to computationally optimize the calculation of this transport function under several necessary conditions. The cheapest cost of "sand moving" is the distance between two Wigner functions.

We assume that the cost of moving one unit of sand from one box to the other box is the Pythagorean distance from the center of one box to the other box (the values will depend on the scale of the box that we are using).

Version 1: The rectangular grid box for each function

We create grid boxes that can cover all the "configurations of the sands" (the shape of the Wigner function).

n is an input that indicates the amount of small boxes that we want to divide the whole sandbox into. For example:

n=2 → we divide the whole grid box into 4 smaller boxes.

n=4 → we divide the whole grid box into 16 smaller boxes.

We predicted that as we divide the whole function into more boxes, the more accurate the result will be.

Since the contours of the Wigner functions are mostly in the ellipse shape, we create a large rectangle box that can cover most of the configuration of the sand. The grid box goes out to 2 times the width of the Gaussian in each direction. Then we divide the whole grid into many smaller boxes (n2 boxes, n4variables) so that each box will cover a portion of sand that needs to be moved. The two grid boxes of two functions have the same amount of smaller boxes. We have i,j,k,l are integers that indicate the position of the small box inside each grid while x,y (real numbers) which are the coordinate system that we use to integrate the whole function.

We assume that the amount of sands that are available to be moved out of box ij is equal to init[i][j]. Similarly, the amount of sands that are moved into box kl is equal to final[k][l].

The box can be rotated responding to the shape of the function by using the equation of rotation:

x'= xcos - ysin

y'= xsin+ycos

With x', y' are the new coordinate after rotating counterclockwise of angle around the origin.

We have tested with different n from 1 to 17. As n goes beyond 8, it took much longer to calculate the optimal value. We found that around n=12 to 14, the result will have around 1 to 5 percentage of error comparing to the analytical result that we calculated. As n >13, the optimal distance starts to decrease, and the percentage of error starts to increase. Therefore, with version 1 method, n=13 will give us the most accurate result.

Version 2: The adaptive grid box for each function

In order to make a reasonable estimation that can enclose all the relevant sand, the general grid box size depends on the function's shape (the function is not necessarily a Gaussian function)

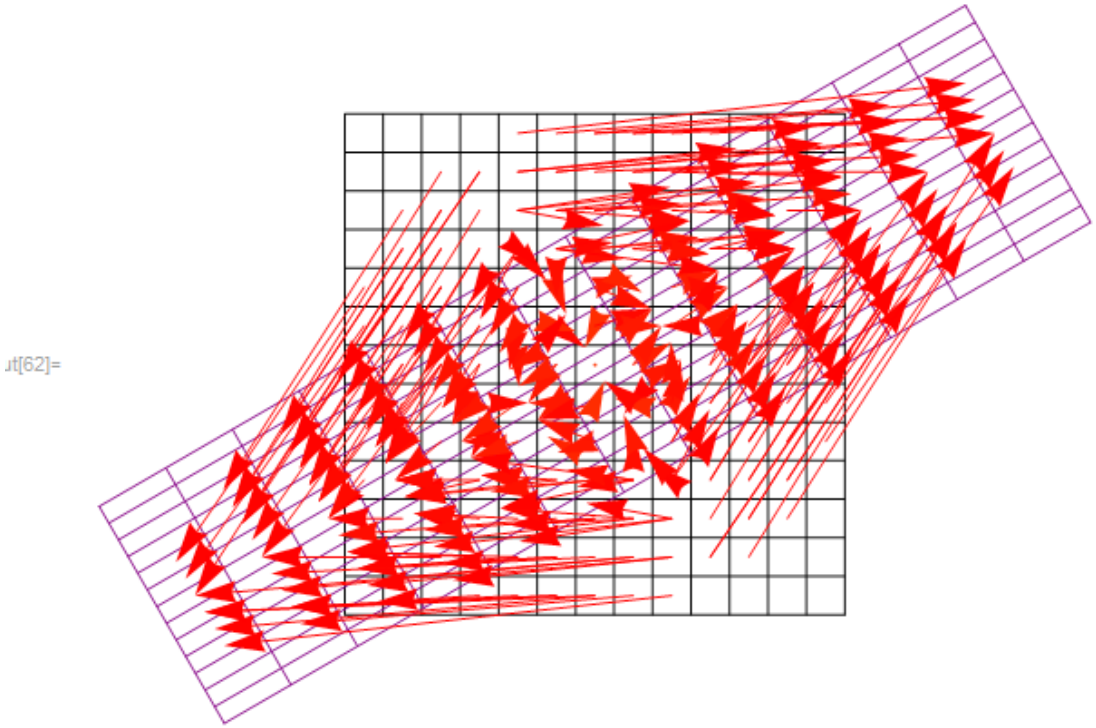
We use only the boxes that have the significant amount of sands depending on the cutoffs that we choose. Therefore, the amount of boxes that cover initial function and final function can be different.

The naming for each box is similar to version 1.

We assume that the amount of sands being moved out of box ij is equal to init[i][j] - final[i][j] or 0 if the difference is negative since the sands being moved out from one box only if the initial amount of sand in that box is greater than the final amount of sand in that same box. Similarly, we assume that the amount of sands moved into box ij is equal to final[i][j]- init[i][j] or 0 if the difference is negative since the sands being received by one box only if the final amount of sand in that box is great than the initial amount of sand in that same box.

(Supported by NSF: National Science Foundation)

Advisor: Gary Felder, Physics



Madden Julian Oscillation and Diurnal Amplitude Weather Oscillations in the Tropical Pacific

Sophie Shapiro/2018

The tropical Pacific is home to many important weather oscillations that affect the day-to-day weather around the globe. The most familiar of these oscillations is the daily diurnal cycle of warm temperatures in the day and cooler temperatures at night. A more esoteric oscillation is known to climate scientists as the MJO, or the Madden Julian Oscillation. This is a longer-scale oscillation of increased and decreased rainfall that appears only in the tropics. When we map the MJO, we see that it occurs in discrete events of anomalous rainfall that move eastward across the Pacific in a 30-60 day cycle.

In order to characterize the behavior of the MJO, it is important to understand how it interacts with other weather phenomenon. Just looking at each event in isolation will leave us in the dark when we try to apply our understanding to real-world scenarios such as weather prediction. This summer, I worked in the National Oceanic and Atmospheric Administration's (NOAA) Pacific Marine Environmental Laboratory to investigate what effects a passing MJO event has on the diurnal oscillation.

To do so, I used data gathered by the Tropical Atmosphere Ocean/Triangle Trans Ocean buoy Network (TAO/TRITON) array, a network of around 70 moored buoys in the Pacific that record air temperature, sea surface temperature, windspeed, and humidity, among other things. After familiarizing myself with the average diurnal cycle, I cross referenced the collected data with the dates of an MJO event, and measured how the variables differed during those days

I found that as an MJO passed by, there is a statistically significant decrease in the amplitude of the diurnal cycle. I also found that the amount of decrease is proportional to the strength of the MJO. I was more likely to observe a decrease, and that decrease tended to be larger, during a strong MJO.

This research gives us more information about the behavior of MJOs and the behavior of the diurnal cycle, and helps us to explain some of the observed variations in the diurnal cycle. It also gives us new information about how phenomena that happen on different scales and across the air-sea boundary still influence each other. This allows us to learn about the interconnectedness of climate and weather systems, helping us to understand and predict weather events and patterns.

(Supported by Agnes Shedd Andreae '32 Research Fund)

Advisor: Non-Smith Advisor, Physics

Assessing the comprehension of language in 2- year- olds using touch-screen technology

Sara Beltran/2019

Language is an integral part of our human existence. Starting in the womb (Hoff, 2013), it forms the building blocks for positive language, social, and cognitive outcomes within the first year of life (Kuhl et al., 2005). Therefore, early identification of language delay in children is essential because it helps form skills needed for school readiness such as understanding peers, following narratives, and learning math. Assessments for detecting language delay exist for ages 3-5, but we are piloting an assessment for age 2 because catching language delay at age 3 might be too late. Intervention before age 2 is not only less costly, but more effective as well (Bakermans-Kranenburg, Van IJzendoorn, & Juffer, 2008).

We are assessing the comprehension and language of 2 year olds using touch-screen technology. Referred to as "Baby Quils," our iPad test acts as a game for children with animations and entertaining sound effects. Our goal is to provide early identification risk for language delay by assessing the child's understanding of both products of children's language learning as well as the process of how they learn that language.

Baby Quils is separated into 12 different subtests. The first category of subtests is product- vocabulary: nouns, verbs, adjectives, and prepositions. The second category of subtests is product- grammar: reversible transitive sentences, WH-subject and object questions, negation, and reversible prepositions. The third category of subtests is process-vocab-grammar: fast mapping nouns, fast mapping adjectives, argument structure, and transfer of new verb to new agent + new object.

The prepositions and transitives subtests are drag while the rest are touch. Our observations show that dragging items are challenging for younger children and children without iPad experience, so we have included practice items as well. Once the children finish the game, they are rewarded with stickers as encouragement to participate again. With the help of University of Delaware and Temple University, we are piloting Baby Quils throughout many daycares in order to gain a diverse set of participants.

Our piloting will continue into the upcoming year and once we have gathered enough data, we plan to reduce the number of items per subtest and evaluate existing items that are not working. For instance, the items for negation seem to be difficult so we will adjust accordingly. After we finish narrowing the test items, we will direct our focus to test-retest reliability and write ups, leading to the dissemination of Baby Quils.

Citations:

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(Supported by Mary Sweig Wilson Undergraduate Research Fellows

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Advisor: Jill de Villiers, Psychology

Subtest	N
Nouns	123
Negation	99
Fast Mapping Nouns	71
WH Questions	106
Prepositions	80
Reversible Transitives	84
Reversible Prepositions	82
Known Verbs	80
Adjectives	104
Novel Verbs (Temple)	21
Novel Verbs (Smith)	43
Fast Mapping Adjectives	62

Table 1. Number of participants that completed each subtest

The effectiveness of the Buried in Treasures workshop in a naturalistic setting

Julianna Calabrese/2018

Now a distinct disorder in the DSM-5, there is currently a need for treatment for hoarding disorder. The Buried In Treasures (BIT) workshop is a highly structured and biblio-based facilitated support group for individuals who identify as having problems with excessive hoarding, saving, and acquiring (Tolin et al., 2014). Previous research has found that the BIT workshop significantly reduced hoarding behavior when compared to a waitlisted sample (Frost et al., 2011; Frost et al., 2012). The aim of the current study was to investigate the effectiveness of the Buried in Treasures workshop in a naturalistic setting. This study differs from previous studies as it utilizes the second edition of the accompanying book, Buried in Treasures: Help for Compulsive Acquiring, Saving, and Hoarding (Tolin et al., 2014). The workshop took place at a nonprofit organization in Santa Monica, California. The sample (N=12) consisted of 4 men and 8 women with an average age of 68. Sixteen sessions were conducted once a week over four months. Measures included Activities of Daily Living-Hoarding (ADL-H), the Adult State Hope Scale (ASHS), the Frost Multidimensional Perfectionism Scale (FMPS-II), the Saving Cognitions Inventory (SCI), and the Saving Inventory Scale-Revised (SI-R), which were administered before and after the workshop. A general linear model was used to compare pretest and posttest scores. While no participants dropped out, one participant did not complete their posttest measures and was not included in the final analysis.

Most measures significantly improved after treatment, excluding the FMPS-II. Hoarding symptoms declined, with decreases ranging from 44% to 51%, as well as hoarding beliefs, with decreases ranging from 12% to 39%. ASHS increased by 25%, indicating that participants gained hope concerning their clutter. Ten out of eleven participants successfully demonstrated response, defined as a SI-R change of 10 or more points. Remission is defined as a SI-R change of 14 or more points as well as having a posttest score of less than 42 points. All eleven participants fulfilled the first criteria while nine fulfilled the second. Our findings are consistent with previous research. This is the first study that incorporated ASHS into a BIT study. Limitations include failure to use a control group and a small sample size. Future studies should include a waitlisted control and increase their sample size by conducting multiple BIT groups.

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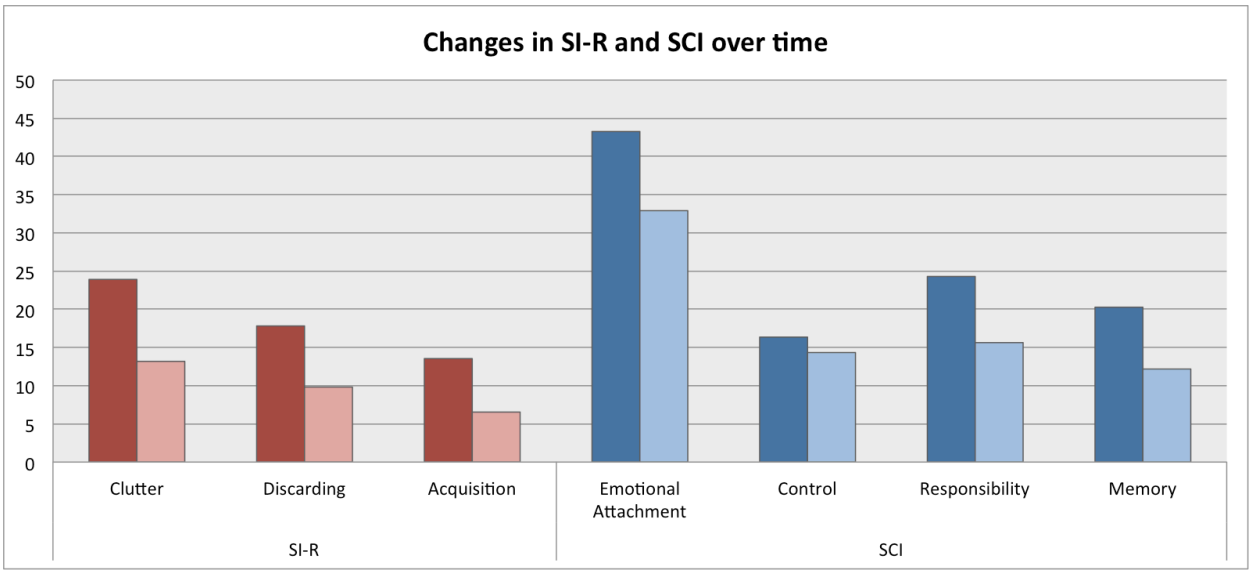
(Supported by Frances Baker Holmes Internship Fund)

Advisor: Randy Frost, Psychology


Changes in SI-R and SCI over time
50
45
40
35
30
25
20
15
10
5
0
Clutter
Discarding
Acquisition
Emotional Attachment
Control
Responsibility
Memory
SI-R
SCI

Syntax and Dialect: Effects of African American Mothers' Language to their Preschool Children on Later Reading Outcomes

Lissandra Camacho/2019

Previously, a research study by Betty Hart and Todd Risely (2003) showed that higher-income preschoolers hear 30 million more words during their childhood than low-income preschoolers, suggesting the quantity of mothers' language predicts childrens' language and literacy outcomes. However, recent studies show that it is the quality of language input, not the sheer amount of input that matters for reading development. The main purpose of this study is to see what are the effects of low socioeconomic African American mothers' language on the literacy development of their preschool children. The African American mother-child pairs were part of a longitudinal project studying the impact of curricular interventions on school readiness. 10-minute play sessions between mothers and their children were transcribed. The children were of ages 3;10 to 5;0 (mean=4;6) at the beginning of the study. The transcriptions were coded for the amount of utterances produced in the 10-minute play period, grammatical variation using the IPSyn Score (Scarborough, 1990), and the depth of AAVE dialect. The language and literacy measures analyzed for the children were the EOWPVT-R which measures vocabulary production, the TOPEL test which measures phonological awareness, and The Woodcock-Johnson III Passage Comprehension subtest which measures reading comprehension.

On a sample of 60 mothers, linear hierarchical regression analysis demonstrated that it is the grammatical richness of the parental input that independently predicts the children's first grade reading outcomes when other factors are controlled (Table 1). Other research shows that the diversity of the vocabulary used, the grammatical variety and complexity, and the quality of joint communication between the mother and child are strong predictors of children's reading outcomes. This summer the subject sample for the study has been extended to about 80 mothers and it has been found that the correlations have gotten stronger.

This study has also been extended to a sample of Hispanic mothers. The purpose of the study is to see if Hispanic mothers' data would look similar to the African American mothers' data. Some Hispanic mothers speak only English to their children, meanwhile others may speak only Spanish or a mixture of both languages. Approximately 20 Hispanic mother-child pair play sessions have been transcribed, and we are beginning coding for the mothers' language in both English and Spanish for vocabulary and syntactic "richness." This work will continue during the fall semester of 2017.

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Scarborough, H., van Kleeck, A., Gillam, R. B., Hamilton, L., & McGrath, C. (1997). Index of productive Syntax. Journal of Speech, Language, and Hearing Research, 40, 1261-1271.

Table 1. Hierarchical linear regression predicting children's 1st grade reading comprehension

(Supported by Mary Sweig Wilson Undergraduate Research Fellows)

Advisor: Peter de Villiers, Psychology

Intersectional Invisibleness: The Perception of African American Women

Jada Flint/2018

Intersectionality is the multitude of different forms of discrimination and oppression, such as racism, sexism, classism, etc., overlapping upon an individual. An example is the various levels of discrimination that occurs to African American women. African American women have been oppressed due to the color of their skin and their sex. In the 1960s, the Women's Right Movement placed African American women as the middleman because neither black men nor white women wanted to acknowledge them. African American women significantly contribute to fighting for women and black rights; however, they were not acknowledged for their contribution. Therefore, it leads to the idea of intersectional invisibleness. This hypothesis consists of the experience of social invisibility, specifically by individuals who belong to multiple subordinate social groups. Studies have shown that African American are overlooked and not efficiently heard by others. For instance, Ghavami and Peplua (2012) found that stereotypes about black people similarly correlate more with stereotypes of black men, and stereotypes about women lean more towards the stereotypes of white women. Therefore, it suggests that African American women are neither prototypical of women nor of Blacks. In addition, Sesko and Biernat (2009)'s study found that most white, female subjects had a difficult time recognizing "old" images of African American women face, which led to them assuming that the images were mostly new.

Many studies have provided evidence that African American women are "invisible" to others. However, all of the studies provided a perception of African American women through the eyes of white participants, which can lead to questioning if invisible only occurs when European Americans are the perceivers. Would invisibility still be in the picture if African Americans were the perceivers? During SURF, I was able to research and gain understanding about studies on the perception of African American women, specifically through intersectionality and invisibility. Additionally, I expanded my knowledge on studies involving the eye-tracker to learn how to incorporate it into a potential study. The knowledge gained from SURF contributed to the construction of a potential honors thesis study that examines where African American subjects' visual attention is placed when looking at images of black and white female and male faces to determine if one recognizes the faces or not. The main goal is to investigate if African Americans contribute to the association of invisibility towards African American women by not seeing them as a result of not recognizing them.

(Supported by Science Center Undergraduate Research Fellowships)

Advisor: *Fletcher Blanchard, Psychology*

Predictor	Beta	t	p
Age	-.14	-1.06	ns
CHILD Vocabulary	.17	1.10	ns
Phonological Awareness	.29	2.00	.05*
MOTHER # Utterances	-.12	-0.91	ns
AAVE dialect	-.11	-0.92	ns
Grammatical IPSyn Score	.49	3.68	.001***

Inconsistent Subject Exclusion Criteria in Studies of Police Shooter Bias

Eliza Going/2018

This is an analysis of three studies completed on the topic of police shooter bias, referring to police officers shooting unarmed black men at disturbingly high rates. The results found in the studies done by Copeland-Brock (2014), Gruescz (2017), and Shern (2016) were compared to previous research that had excluded subjects' responses using arbitrary guidelines.

To investigate the psychology behind this phenomenon, studies have utilised a video game simulation of images Black and White targets coupled with a shooting task to shoot targets holding a gun and not shoot targets holding a benign object such as a wallet or cellphone. Most have used the same or similar guidelines established by Correll, Park, Judd, & Wittenbrink (2002) in which participants are asked to shoot or not shoot by pressing specific keys on a keyboard. The response window is generally either 630 milliseconds or 850 milliseconds, depending on the focus of the particular study. Studies focusing on error rates use 630-ms response windows, while studies examining response latency scores use 850-ms response windows. Faster response times biased toward black targets indicated unfavorable racial shooter bias. Subject exclusion criteria has been brought into question, largely due to inconsistent or potentially unfair guidelines.

The pool of studies seems to follow different rules for deciding when a subject is not responding authentically; responding too fast, responding too slowly, and making too many errors have all been rules by which subjects' responses have not been counted in the final statistical analyses. Correll (2007) and Correll (2011) excluded participants who had "more than four timeouts for every error." Ma and Correll (2011) also omitted participants' data when the ratio of incorrect to correct responses was 4:1. Other studies have followed similar guidelines to the first two experiments in Correll (2002), excluding trials with incorrect responses or timeouts, typically resulting in erasure of 0-10% of all trials.

Response times of less than 300 ms have been omitted from analysis in Copeland-Brock (2014), but all subjects' responses were included in this study. No subjects were excluded from analysis in Gruesz (2017) or Shern (2016). The results have not shown statistically significant differences in response rates compared to response rates from previous research. Changing subject exclusion guidelines has not been shown to significantly change overall shooting patterns with respect to race of target.

(Supported by Frances Baker Holmes Internship Fund)

Advisor: Fletcher Blanchard, Psychology

2017 SURF De Villiers research abstract- Elizabeth Lamar

Elizabeth Lamar/2019

This summer, I worked on two main projects and one side project in Jill and Peter de Villiers' labs. I worked on Jill's Baby Quils project, Peter's parent and child language project, and translated a language assessment as a side project. The Baby Quils project is a large tri-state collaboration between Jill, Kathy Hirsh Pasek at Temple University in Philadelphia and Roberta Golinkoff and Aquiles Iglesias at the University of Delaware. The Baby Quils is a language assessment for young children between ages 2-5 whose questions focus on vocabulary, comprehension, and language learning tactics. This summer, we were in the second phase of reliability testing. In Peter's lab, we were working on another large project, that studies the effect parents' and teachers' language can have on their children's language comprehension and acquisition. The side project was translating a French Theory-of-mind animated assessment, named the DIRE (Differencier, Idee/Realite, Exercices) into English.

For Jill's lab, we had to test the reliability of the Baby Quils. We already had preschools available, with permission and viable children to test. Every weekday morning, Jill's research assistant and I traveled to different preschools (either Fort Hill, Nonotuck or the preschool summer program at First Church-Christ Scientist) and tested between 1-5 children, all aged 2. The test is an animated ipad game, made up of ten subtests, either focusing on vocabulary (like the noun subtest), comprehension (like the negation subtest) or learning tactics (like the novel verb subtest). Two interns would test together, so one intern could give the test, while the other marked the child's answer. Before every test, there are three example questions given to quickly adjust children to using the ipad. When the child selects an answer, a positive animated sound rings, whether or not the child's answer is correct. After every testing session, the child is given their choice of a sticker. For Peter's lab, my job was to transcribe vhs audio tapes of African-American parents speaking to their children, usually in African-American English (AAE) into written files. After the files were complete and compiled into an accessible excel sheet, I then had to score out of 30 how many times a particular sentence, described on the scoring sheet, was uttered. The side project was simple; I had to translate a French assessment, which focused on teaching young autistic children Theory-of-mind comprehension.

Because no research project is finished at the moment, there are no results at this time. We are still testing the reliability of the Baby Quils to decipher which questions are throw-away and which are keepers. The coding of the transcriptions has not finished either, but so far, we have seen a positive effect of the diverse syntax of AAE on children's language development. As the projects progress, we hope to gather more data that will help us strengthen our Baby Quils subtests, and we hope to gather data that will prove various positive effects of the grammar of AAE on children's language development

(Supported by Mary Sweig Wilson Undergraduate Research Fellows)

Advisor: Jill de Villiers, Psychology

How Instagram effects Body Image Satisfaction

Sophia Liu/2018

Focusing on college-aged students, this research will examine how Instagram and Instagram usage effects self-perception of body image. The goal of the study is to understand the psychological and physical effects image social media can have on the mind, focusing on female college students. We will examine this potential connection through connecting various existing psychological theories like objectification theory and attributional theory. By using the daily diary method of collecting real-time data, we hope to show that increased Instagram use will increase body image distortion.

(Supported by Frances Baker Holmes Internship Fund)

Advisor: Randi Garcia, Psychology

Exploring household task equality: An interaction of social psychological constructs with interpersonal factors

Yujia Ning/2019

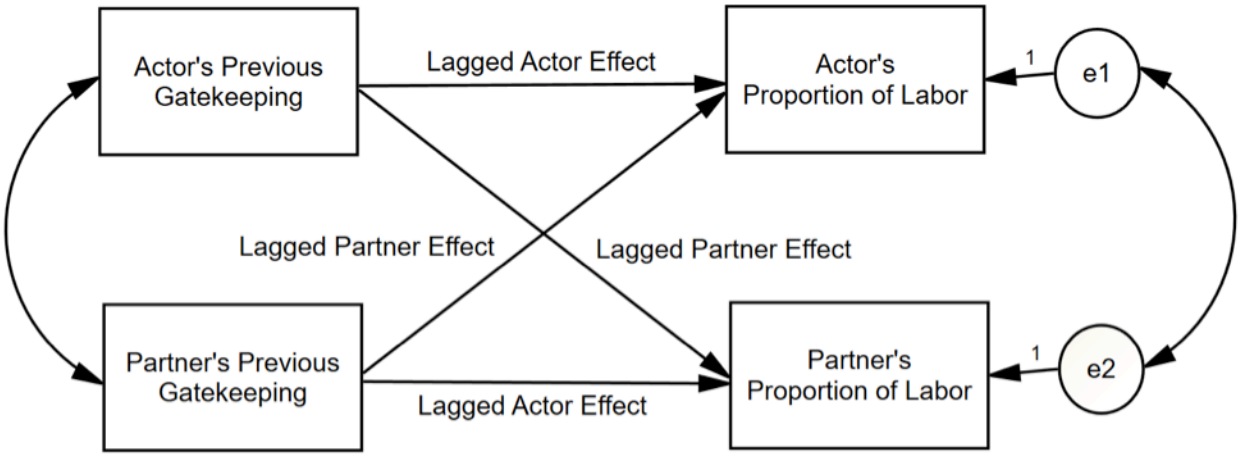
This research looks at gender equality from another perspective: while workplace gender equality is emphasized and carried out, different genders might not have the same treatment in the domestic sphere. I looked at how cohabit couples (regardless of marital status) assign household tasks between each other.

Considering that both physical and psychological reasons can influence household labor distribution, the measures include gender role adherence, sexist ideologies, masculine gender role stress, social stress dominance orientation, perfectionism, gatekeeping, etc. The study consists of 2 phases. In phase 1, couples complete a battery of questionnaires as a pre-measure (couples will be invited into the lab if they live close by). They are to engage in a videotaped interaction task (couples who cannot make it to the lab will be recorded via online video call applications). In phase 2, couples will be asked to complete a nightly questionnaire for 3 weeks (21 days) and the questionnaires will be emailed to them daily. Couples will be able to make further communications and look at their relationship more closely, and we will gain further understanding of the gender dynamics in our society.

Since this past summer was still the beginning phase of our entire study design, I spent a lot of time going through existing literature and finding possible measures that can eliminate confounds and unveil sexism that exist in people's everyday life. However measures only gave me a brief outline of what I was looking for—the next step was to find specific questions that can operationalize the wanted measures. There were many different combinations of questions for every measure, so I had to go through all the literature to make sure we would be using the most updated and most cited sources. Every measure and every design need to be supported. This process was especially hard because a lot of authors simply quoted some past research without including a specific battery of questions that he/she took the excerpt from. My professor and I also spent a lot of time designing our nightly measures: how many days should the nightly measures cover; how long of a list do we want to give volunteers everyday; what kind of pattern was to be expected; in what season and how many months should phase 2 be carried out after phase 1, etc. We will continue designing and carrying out the actual data collection in the coming semester.

(Supported by Frances Baker Holmes Internship Fund)

Advisor: Randi Garcia, Psychology



The Effect of Teacher Input on Early Reading Achievement in Low-Income Children

Hannah Searles/2018

The input a child receives affects their language and reading development. Quantity of input is significant, but studies have also shown that quality is just as important, if not more so (1, 2). While the role of mothers and primary caregivers has been studied, less attention has been paid to the role of teachers. There are also fewer studies focusing on low-income children, yet socioeconomic status can affect language development (3).

Data was used from a longitudinal curriculum intervention study spanning from the final year of preschool through first grade in multiple schools serving low-income populations in Texas and Florida. Taped interactions between teachers and children were coded for syntax and mental state references. Syntax was coded using the IPSyn, drawing from a 10-minute sample (4). The number of mental state references in a 30-minute sample were counted and labeled as desire, cognition, or emotion. Correlations, partial correlations controlling for background variables, and linear regressions were all performed.

Echoing previous studies' findings, child's own vocabulary and phonological awareness positively correlated to measures of their later reading achievement. A linear regression shows that both background measures (age, wordspan, nonverbal IQ) and language measures (narrative creation, vocabulary, phonological awareness) account for similar and significant amounts of variance in later reading achievement ($\Delta R2=.148^{**}$ for background measures; $\Delta R2=.150^{*}$ for language). However, when teacher IPSyn scores were introduced into the regression as an independent variable, it did not add significant variance. There were strong relationships between language measures and theory of mind, particularly with vocabulary and complement clause comprehension. In a linear regression, amount of cognitive references had a small but significant effect on theory of mind development ($\Delta R2=.015$, $p=.036$). However, while cognitive references were related to development, it was not greater than the child's own factors, such as vocabulary and complement clause comprehension.

One possible explanation for no syntax effect is that there appears to be less of a range of input in teacher IPSyn than there was in the mother sample from this study, which had previously found that higher IPSyn scores were correlated to better reading outcomes. Further research should investigate if this difference is significant or not. It is possible that the teachers have more standardized input and that this could act as a protective factor for low-income children. More research should continue to be done to focus on the possible positive or protective effects that teachers might have on children, particularly those who are more vulnerable.

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(Supported by Mary Sweig Wilson Undergraduate Research Fellows)

Advisor: Peter de Villiers, Psychology

American identification across racial/ethnic groups under different political contexts

Yiyin Zhang/2019

This project aims to investigate how American people of different racial/ethnic groups conceive of their own American identity and racial/ethnic identity, as well as that of people from racial/ethnic groups different from their own. We also want to see how this changes under different political context.

Our goal is to construct a questionnaire which includes both explicit and implicit measures of people's attitudes of national identification and recruit a diverse body of participants consisting of people from different racial/ethnic groups to complete the questionnaire. We will then conduct a data analysis and have a comparison of data from 2008 and our new data collected in 2017, to see how national identification across racial/ethnic groups changes under Obama years and Trump years.

Throughout the summer, we gathered relevant academic articles from 2008 to the latest and started to review the literature, create annotated bibliography, and refine our experimental design.

This project is currently on-going and we plan to continue with it through the semester.

(Supported by SURF Gifts Fund)

Advisor: Randi Garcia, Psychology

2017 Summer Data Science Research (Mental Health/Northampton Survival Center)

Yue Kuang/2019

This past summer spent in Professor Crouser's lab has been spectacular. I had the opportunity to try out data visualization tools and also accomplished what I couldn't imagine before I stepped into the lab.

Just like everyone in the lab, I was on multiple projects. I participated in designing interface to help mental health clinicians to acquire more accurate diagnosis based on the massive data set extracted from DSM (Diagnostic and Statistical Manual of Mental Disorders). During the process, I learned how to process of data wrangling, how to connect database with the front-end, how to cooperate efficiently with different people, and most importantly, how to tackle unexpected challenges. Since DSM is a text-based manual, we made the most recent progress (thanks to my co-workers Lucy, Kelly, and Maggie) by being able to re-categorize diagnosis in the book by using text-mining technics rather than relying on the original chapter division. Yet we realized the bias in the book and believed that there is still plenty of space for improvement, both regarding our interface and DSM.

We (Jiyoung, Lucy, and I) also provided data consulting to our community this summer. The Northampton Survival Center came with data of their clients and hoped that we could notice useful and distinguishable patterns from it. By using R and Tableau, we obtained information hidden in the data and discovered interesting features from it. For instance, some clients tended to come to wait much more earlier before the center even opened. According to our analysis, there was indeed an advantage of early arrival, so they didn't need to wait in long line to get food when they got into the center. However, the price of gaining less ten minutes wait in line is obviously not worthy, because they would need to wait for more than two hours outside of the center. In our visualization, we present the total waiting time in a day by aligning time to get food and time waiting outside of the center in a tornado graph. One can easily tell when will be the most efficient time to come to the center.

Besides the two projects mentioned above, I also explored the nature of streaming data. Different from traditional aggregate and stationary data, visualization of continuous and ever-changing streaming data has always been a challenge for data scientists.

All in all, working with such intelligent professor and other students this summer has been a wonderful experience, and I look forward to continuing participating in Professor Crouser's lab in the following semester

(Supported by DoD/LAS: Department of Defense/Lab for Analytical Sciences)

Advisor: R. Jordan Crouser, Statistical and Data Sciences

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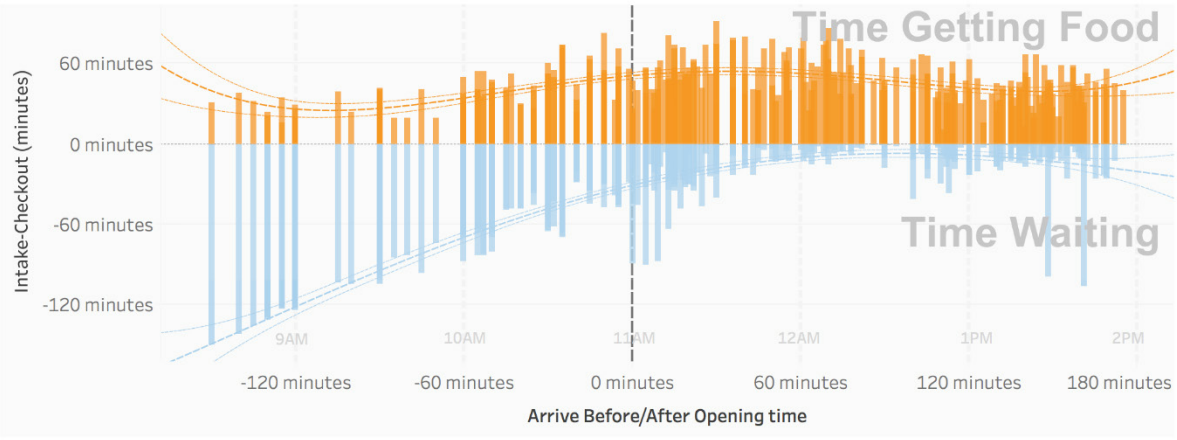
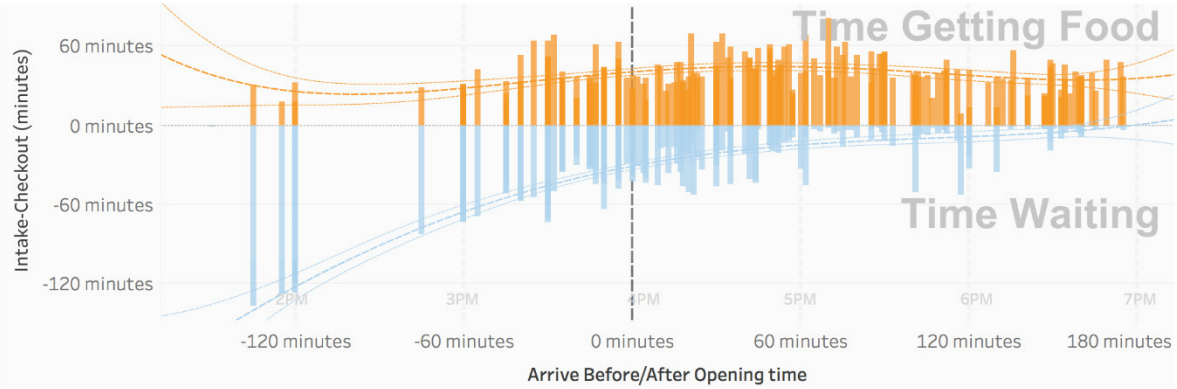


Tue/Thu



User Interface for Studying Syriac Manuscripts

Yuszu Lin/2019

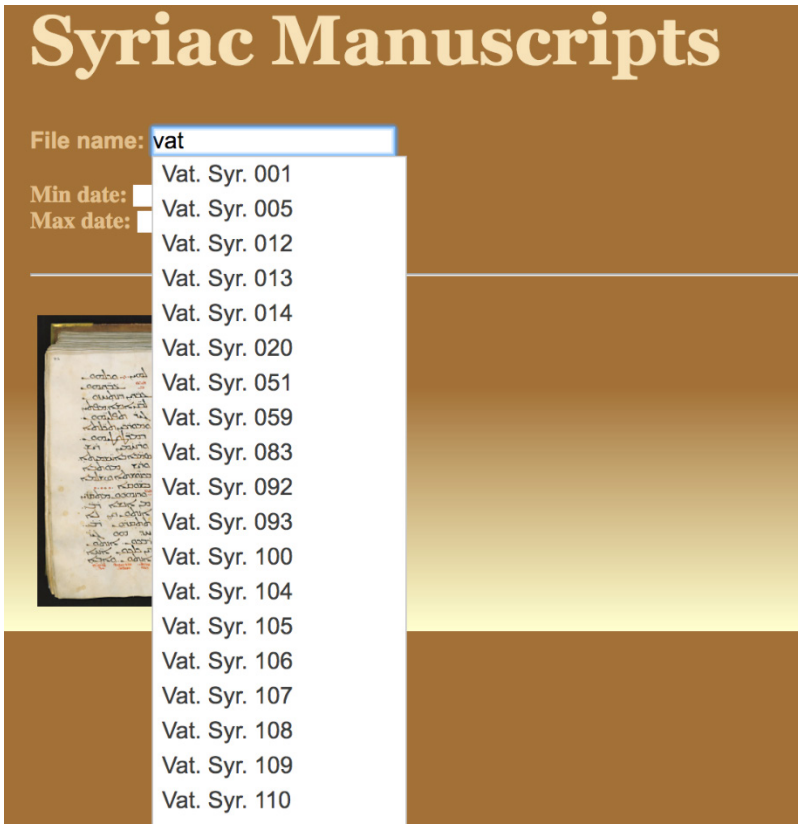
Even though few people speak it today, Syriac language used to be a major language throughout the Middle East. A few hundred manuscripts survive today and many of them remain undated. As part of my research project, I created a webpage that would allow for researchers to access a database of Syriac manuscripts, with a search engine and multiple features including selecting multiple manuscripts, filtering by dates, and simply going through all of the manuscripts in the database. The database consists of all the information on each manuscript and all the images of each page of the manuscripts. For the webpage, each manuscript is presented by only the thumbnail of the first page, and the user could then click into the manuscript that they wanted to see the full size of. By clicking into the first page thumbnail, a swipebox feature would appear and users could then swipe around through the pages of the manuscripts in full size.

The first step of the project was to use HTML to format the page, which included where the heading would be and where the content would be. After the basic structure of the page was finished, I used JavaScript to sort the data I collected from the database and grouped manuscript pages together by manuscript name, and finally displayed everything on my webpage. To get access to the database, I used PHP to send SQL queries, which retrieves the data that I need from the database to my webpage. Throughout the 10 weeks, I met several times with a professor from Stanford University who was studying these manuscripts and discussed various features that would be helpful for those who wanted to study Syriac manuscripts.

In doing this project, I went from not knowing how to write a webpage to being able to use various different programming languages to achieve what I wanted on my webpage. In the future, I hope I can continue on with building my webpage and integrating it with other people's contributions to making Syriac manuscripts easier to identify and study.

(Supported by SURF Gifts Fund)

Advisor: R. Jordan Crouser, Statistical and Data Sciences


Syriac Manuscripts
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Max date:
Vat. Syr. 001
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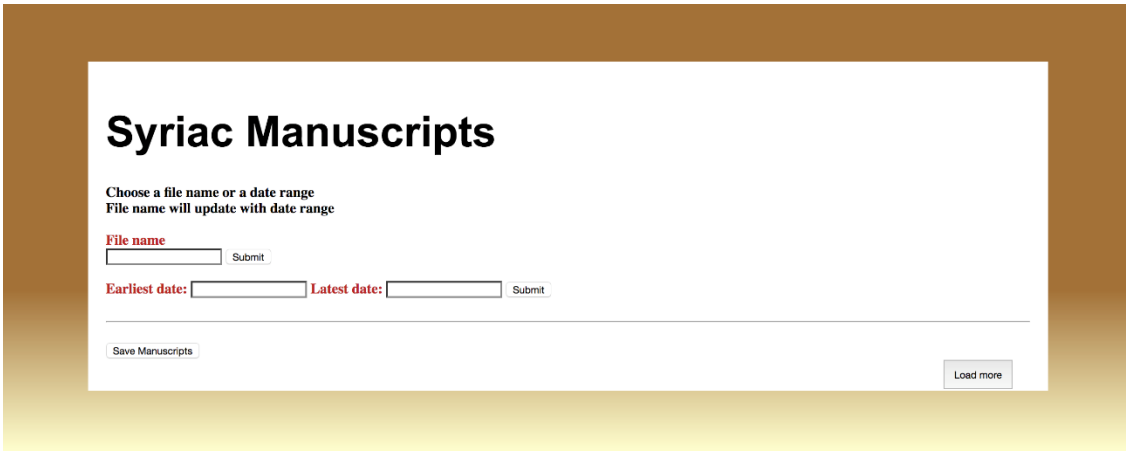

Syriac Manuscripts
Choose a file name or a date range
File name will update with date range
File name
Submit
Earliest date:
Latest date:
Submit
Save Manuscripts
Load more

Visualization of Streaming Data and Website Design of Historical Handwritten Syriac Manuscripts

Junzhou Liu/2017

It has been a challenge to visualize streaming data which usually comes in a huge amount at a high speed. To figure out how to improve existing visualization models, we used data from 2017 Visual Analytics Science and Technology (VAST) Challenge. Given the data in spreadsheet format, we tried with different tools, such as D3.js. and R, to represent them in scalable vector graphics (SVG). To our surprise, no single tool alone could generate our ideal type of data visualization, the kind requires little or minimal effort to interpret and understand. Knowing the flaws of existing data visualization tools, we tried to design and write new visual models on RAW Graphs, an open source data visualization platform. Started with a line chart model, we will enrich the RAW Graphs inventory with many more kinds of SVGs in the future.

Besides presenting data on certain graphics, we also tried to present data on web interfaces using image data of Syriac manuscripts. Most of the extant handwritten Syriac manuscripts are preserved in the British Museum and have been easily accessible to UK-based researchers solely. However, scholars interested in Syriac Paleography conduct studies in many other parts of the world as well. They are in urgent need of a solution for worldwide sharing of the manuscripts. We therefore managed to build an online interface for image data of Syriac manuscripts to resolve this issue. This user interface would be able to facilitate better collaborations and communications among Syriac Paleography scholars throughout the world, and hopefully, even lead to the achievements of significant progresses in the field of Syriac Paleography.

Given the scanned image of each manuscript page from former researchers working on this project, we extracted all these image data form their storage place, a SQL database. We then employed JavaScript to display these image data on an interface we created using PHP. We set up two filters, manuscript title and data of written, and designed drop-down lists under each filter for users to view different groups of image data. We also tried to create a separate block on the interface for users to save their selected data, and add/remove any images from their saved data sets. More user-friendly layout and functionalities will be developed and added to on this intuitive user interface that require minimal training and experience to use.

(Supported by SURF Gifts Fund)

Advisor: R. Jordan Crouser, Statistical and Data Sciences

Mining the Diagnostic and Statistical Manual of Mental Disorders

Zhu Shen/2019, Kelly Pien/2020, and Maggie Carttar/2020

The fifth edition of the Diagnostic and Statistical Manual of Mental Disorders (DSM-5) offers healthcare providers and insurance companies a common language and standard criteria for the classification of mental disorders. These disorders are currently grouped into 20 chapters by common symptoms [1]. However, 13 separate groups of experts developed different parts of the book, resulting in little cross-group collaboration or standardization between chapters [2]. We examine this inherent organizational bias and attempt to remedy it by creating new groups through k-means clustering.

We used the Natural Language Toolkit (NLTK), a Python package, to compare similarities between DSM-5 diagnoses through term frequency-inverse document frequency (tf-idf) weights, which show the normalized frequency each significant word or phrase appears in diagnoses.

Using R, we conducted principal components analysis on the tf-idf weights to reduce the number of dimensions in the data. We then k-means clustered the diagnoses into 12 (the optimal number balancing the needs to explain variance and avoid excessive similar clusters) and 20 (the number of DSM chapters) groups.

Clustered bubble charts made with D3.js enabled us to visualize the versions.

Both versions' clusters are mostly intuitive, separating developmental, elimination, neurocognitive, sexual, substance, and unknown and other specified disorders. Interestingly, four bipolar disorders and two depressive disorders were always grouped together, dovetailing with research that bipolar and depressive disorders are frequently misdiagnosed for each other[3]. In the 12 cluster version, several psychotic disorders were also grouped there.

A few clusters are unintuitive. For example, both versions contain a large and amorphous group with seemingly disparate diagnoses, like hoarding disorder, dissociative identity disorder, and gender dysphoria.

Even using 20 clusters, only nine purely contain diagnoses from one DSM chapter. This suggests that the DSM's current organization may not be optimal if truly grouped by similar symptoms.

This fall, we will find the minimum number of clusters needed for total purity and more closely analyze the clusters. The clusters will be integrated into a website to help clinicians diagnose clients while reducing bias. The same process could be applied to medical diagnoses in the International Statistical Classification of Diseases and Related Health Problems.

[1] American Psychiatric Association. (2013). Diagnostic and statistical manual of mental disorders (5th ed.)

[2] American Psychiatric Association. (2013). Diagnostic and statistical manual of mental disorders (5th ed.)

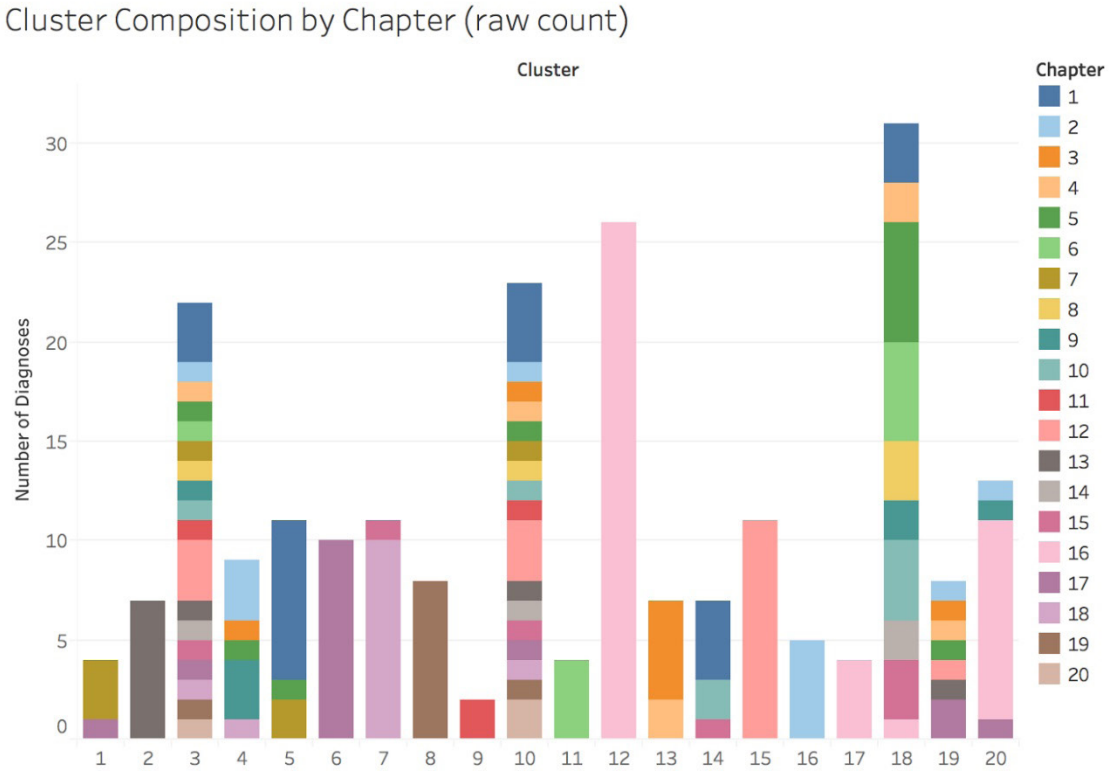
[3] Ghaemi SN, Sachs GS, Chiou AM, et al. Is bipolar disorder still underdiagnosed? Are antidepressants overutilized? J Affect Disord. 1999;52:135–44.

Figure 1: DSM diagnoses split into 20 clusters. Color indicates the diagnoses' DSM-5 chapter.

Figure 2: Stacked bar chart displaying the chapters of the conditions in each cluster.

(Supported by Schultz Foundation Undergraduate Research Fellowships)

Advisor: R.Jordan Crouser, Statistical and Data Sciences


Cluster Composition by Chapter (raw count)
Cluster
Chapter
Number of Diagnoses
0
5
10
15
20
25
30
1
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5
6
7
8
9
10
11
12
13
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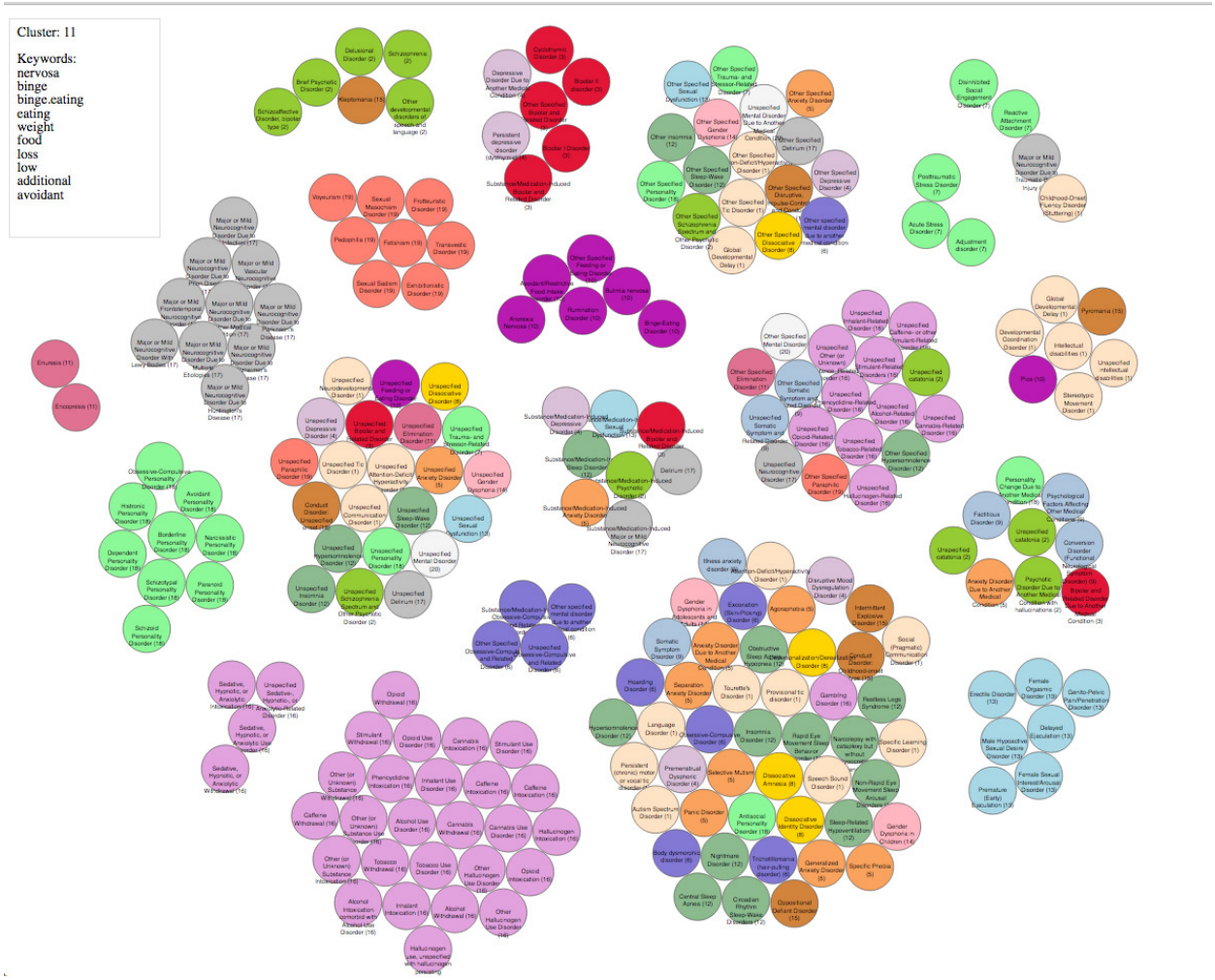
Cluster: 11
Keywords:
nervosa
binge
binge.eating
eating
weight
food
loss
low
additional
avoidant

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