2022

Summer Research Fellowship Project Descriptions 2022

Clark Science Center's Summer Research Fellows Program

Smith College
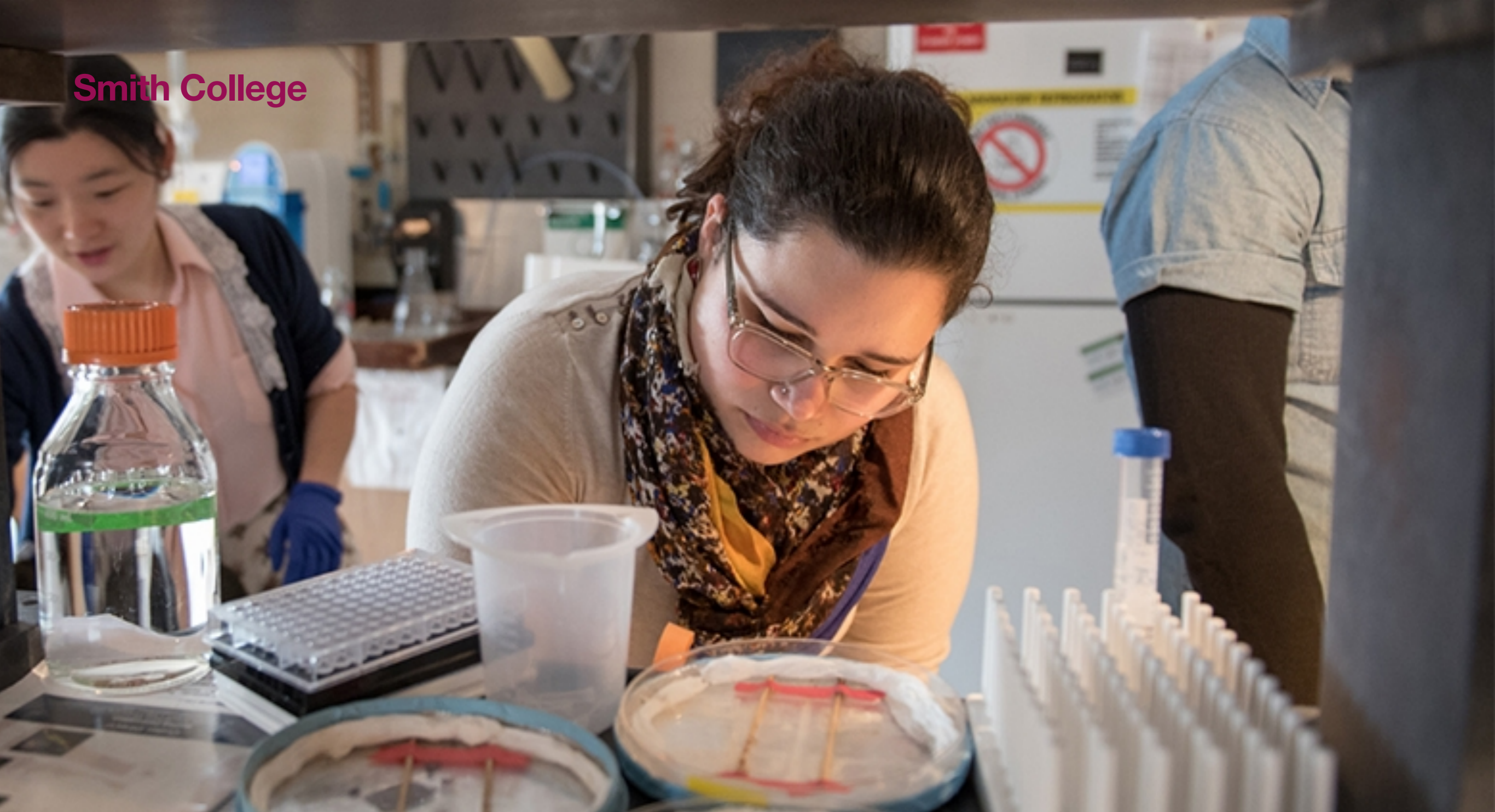
SURF

2022

2022
Abstracts

Assessing the Feasibility of Automating the Fabrication of Electrochemical

Name: Heather Schapfel
Year of Graduation: 2023
SURF Advisor(s): Mike Kinsinger, Engineering
Field of Study: Engineering
Co-Authors: Roma Taranto

Title: Assessing the Feasibility of Automating the Fabrication of Electrochemical Oxygen Sensors

Abstract:

This project focused on assessing the feasibility of automating the fabrication of electrochemical oxygen sensors used in Werfen's GEM blood gas analyzers. Werfen, a manufacturer of diagnostic instrumentation for acute-care blood analysis, was the sponsor of this project. A key element of the oxygen sensor is a membrane layer which is deposited on the sensor surface as small droplets. Currently, skilled operators manually deposit these droplets. We used a Nordson automated XYZ table equipped with a non-contact dispenser to demonstrate it is feasible to automate this process. The effects of nine different operating settings were explored to determine conditions to deposit droplets with the correct volume and shape and in the correct location. In addition, we established a protocol for creating arrays of sensors that incorporated a cleaning routine to prevent the instrument's dispensing nozzle from clogging. Over 60 completed oxygen sensors were provided to Werfen for further testing.

Investigating Climate Change and Plant Conservation in the Forests of the Eastern U.S.

Name: Daun Lee
Year of Graduation: 2024
SURF Advisor(s): Jesse Bellemare, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Investigating Climate Change and Plant Conservation in the Forests of the Eastern U.S.

Abstract:
The climate crisis poses a major threat to plant biodiversity, especially to small-ranged species that could see climate conditions change completely across their limited geographical distributions. If faced with extinction in their native ranges, some threatened plants could potentially be "assisted" by humans in migrating to cooler, northern habitats, i.e., "assisted migration". This is a fascinating, but controversial, idea among conservation biologists and ecologists. As an intermediate step and "insurance policy", botanical gardens are beginning to develop genetically-diverse conservation collections of species that could support future restoration or assisted migration efforts. To provide more empirical data on this complex issue, my SURF internship focused on researching two endemic woody plant species native to the southeastern US that might be vulnerable to climate change: Mountain Magnolia (M. fraseri) and Carolina Rhododendron (R. carolinianum). My results for M. fraseri were most significant, so I describe those here. Mountain Magnolia (Magnolia fraseri) is a tree species native to the southern Appalachian Mountains where it is found in cooler, higher elevation forests. Using tree cores collected from native populations along an elevation gradient in Virginia in October 2021, I prepared and analyzed tree core samples to age the trees and estimate their radial growth rates relative to elevation and local climate conditions. Trees sampled from cooler, higher elevation sites tended to be younger and showed significantly more radial growth per decade than those in the warmer, lower-elevation populations. This suggests that the species' preferred climatic niche is shifting to higher elevations within its native range and that lower elevation populations might already be in decline. I also explored questions around the viability of establishing an ex situ conservation collection of this rare tree species at the Smith College MacLeish Field Station. Soil characteristics, including texture and chemistry, were compared between the native population sites in VA and the proposed conservation site at the MacLeish Field Station. I found that some soil nutrients were modestly more abundant at MacLeish than at native sites in VA, and thus might support viable growth of M. fraseri. I also evaluated climate conditions in the two regions by comparing Mean Annual Temperature (MAT) and Mean Annual Precipitation (MAP) between the species' native range at higher elevations in the Southeast U.S. and counties in New England.

Cont.: Investigating Climate Change and Plant Conservation in the Forests of the Eastern U.S.

MAT and MAP were similar between the two areas, although MAT was moderately lower in New England. However, given that the field data from native populations in Virginia, including the tree cores described above, suggests that M. fraseri is already being impacted by climate warming, the moderately cooler conditions seen in the Northeast might be ideal for future growth of the species in an ex situ conservation collection at Smith College. My results indicate that Mountain Magnolia should be prioritized for conservation due to climate change and that ex situ conservation might be feasible in the Northeast U.S.

Plant Conservation Efforts in the Eastern US and Beyond

Name: Katherine Rahaim
Year of Graduation: 2023
SURF Advisor(s): Gaby Immerman, Biological Sciences/Botanic Garden; Jesse Bellemare; John Berryhill
Field of Study: Conservation Biology
Co-Authors:

Title: Plant Conservation Efforts in the Eastern US and Beyond

Abstract:
As one of the 'Plant Conservation Interns' at The Botanic Garden of Smith College for Summer 2022 working with John Berryhill and Prof. Jesse Bellemare, the primary goals of my SURF project were to support our developing collaboration with the Native Plant Trust's (NPT) regional plant conservation efforts and to contribute to ongoing research by John Berryhill in the Bellemare Lab on the Southern Appalachian endemic tree species, Magnolia fraseri.
As a key first step in the collaborative efforts with Native Plant Trust, early in the summer, I trained to become a Plant Conservation Volunteer through NPT. For this work, I worked closely with John Berryhill and other Botanic Garden staff to survey rare plants and invasive species in natural areas around western MA, and to complete an extensive field report following our searches to relocate and monitor rare plant populations. I experienced the intricacies of searching for rare plants. Sometimes these plants grow on privately owned property. We were only allowed to collect seed material if permissions were expressly granted. The collected seed will be used to establish "founder plots" of important native plant species on the Smith College campus, as outlined in the BG's Collections Management Plan. These founder plots will act as genetic repositories for plant species to grow from seed-to-plant and be used as future sources of seeds and plant material for ecological restoration projects. This approach will encourage local genetic diversity and help support the adaptive capacity of native plants, leading to increased resilience in restored native plant communities, such as after the removal of invasives. Smith College will partner with a native plant nursery and our local NPT partner, Nasami Farm, to grow these plants to their full size, then the plants will be distributed to local plant conservation groups.
For my second major project during Summer 2022 SURF, I focused on research related to M. fraseri. This distinctive tree species is endemic and native to the Southern Appalachian Mountains in states including Virginia, North Carolina, and Georgia. In support of John Berryhill's ongoing research in the Bellemare Lab with M. fraseri, we mounted and analyzed tree core samples that had been collected in October 2021. Initial tree core analysis indicated that age was poorly correlated with tree size (diameter) and that there was a significant shift in growth rates of trees in different population sites from southwestern Virginia corresponding to elevation: trees in higher elevation sites were growing much more rapidly than those at lower elevation sites.

Cont.: Plant Conservation Efforts in the Eastern US and Beyond

This pattern suggested that climate change in recent decades may already be impacting mature trees in populations at lower, warmer elevation sites. This finding parallels what John Berryhill had documented for seedlings, where seedling recruitment was seen abundantly at higher elevations but was mostly absent at lower elevation sites.

While researching literature on M. fraseri, I found little prior data on the species and noted the US Forest Service's own information seems to be outdated and not keeping pace with the changes that appear to be taking place on the ground due to climate change. John's preliminary population survey data suggest that M. fraseri, described in the past as occurring at mid- to upper elevations in the mountains, may be contracting upslope due to changing climatic factors. It appears that only higher elevation sites now support viable populations with ongoing recruitment, while the mid- to lower-elevation sites might be in decline. Based in part on these observations, John, Jesse, and I also contributed to a Conservation Gap Analysis Report for the Global Conservation Consortium for Magnolia (GCCM) to share information on M. fraseri's ecology and distribution, and to report John's findings on the species' possible range shift/contraction. Up to this point, the species had not been flagged for conservation attention.

Finally, in August, we traveled to southwestern Virginia to continue field research on in-situ species distribution and seedling recruitment, and to collect seeds from mature specimens to initiate ex situ conservation collections of this species. Most strikingly, we sampled transects from higher elevation population sites upslope into areas where adult trees do not yet occur. Our goal here was to document whether seedlings are beginning to expand their distribution upslope to adjust to climate change. However, we did not detect any seedlings at higher elevations than adult trees, suggesting that the species is not dispersing upslope at a rate that could help it offset the effects of climate change on its local distribution.

We were also very successful in collecting M. fraseri fruits and returned them to Smith College for processing. After processing the seed, we obtained over two thousand M. fraseri seeds. These will be available for future use in germination experiments, in situ recruitment trials, and for establishing conservation collections—living gene banks through the Botanic Garden of Smith College and their GCCM partners.

Blind Juror and Health Biases

Name: Andrea Rivera
Year of Graduation: 2024
SURF Advisor(s): Yael Granot, Psychology
Field of Study: Psychology
Co-Authors:

Title: Blind Juror and Health Biases

Abstract:
This summer, I worked on two projects at the intersection of psychology and law. Both projects centered on bias in justice-related contexts. For the first project, we considered biases specific to visual evidence, and how the purported shared, objective experience provided by such evidence might influence how lawyers present a case. In particular, we hypothesized that, in cases with key visual evidence, lawyers might let the evidence "speak for itself, " and expound upon it with moral and emotional language, unless they believed one of their jurors was blind. We designed vignette style survey, to be administered via Mechanical Turks, that put participants in the shoes of a lawyer and asked them to make an opening statement in defense of a potential murder victim. In the study design, one randomly assigned group of participants was told that there was a blind juror and, while a control group received no mention of a blind juror. We instructed all participants to craft a statement that presented the facts based on the evidence provided. We hypothesized that participants assigned to the control group would write statements featuring more emotion-based statements compared to those told about the blind juror. Contrarily, we hypothesized that those in the blind juror condition would be more likely to speak directly to the facts that the evidence presented. In addition to this project, I also began formulating ideas for a project exploring the intersection of weight bias, racism, and misogyny in the health field and how these biases affect overweight women of color in receiving proper access to healthcare. While this project is still being designed, the initial research allowed me to engage with existing literature and connect to important conversations around justice in healthcare.

High Precision Spectroscopy of neutral atoms

Name: Tilila Karani
Year of Graduation: 2024
SURF Advisor(s): Will Williams, Physics
Field of Study: Physics
Co-Authors: Allie Wallace, Chitose Maruko

Title: High Precision Spectroscopy of neutral atoms

Abstract:
In this SURF, we worked on a number of spectroscopic experiments. Included in the work was experimental design, building, data taking, data processing, and paper writing. Below we highlight the experiments we did this summer.
Europium spectroscopy: We performed spectroscopic measurements on three different transitions in the neutral europium atom. The experimental design for this project was already completed in the spring semester, but a data collection issue was identified and corrected at the end of the spring semester. With the data collection issue fixed, we retook all of the data for these three transitions. While doing this project, we learned about how to experimentally check for things that could skew our results, which we call systematic effects. These systematic effects include factors like pressure, laser power, and discharge voltage. After the data was collected, the data was analyzed to extract information about the europium atom. This project will result in 2 peer-reviewed publications. One of these papers is in the peer review process. The other paper will be submitted for publication soon.
Nitrogen spectroscopy: For this project, we first built an experimental setup to perform spectroscopy on neutral nitrogen atoms. The initial experimental setup did not work as well as we needed, so we redesigned and rebuilt the experimental setup twice to better improve the experiment. We searched for the spectroscopic signature of a nitrogen transition, and may have found a new, unknown nitrogen transition. We also found two more nitrogen transitions that will be explored more this fall.
Beryllium spectroscopy: The experimental setup for this project also went through multiple iterations. In the end, we finally found the spectroscopic signal. Like the nitrogen project, this project will be finished this fall.

Develop Honors Thesis and Present at APA

Name: Ruth Button
Year of Graduation: 2023
SURF Advisor(s): Nnamdi Pole, Psychology
Field of Study: Psychology
Co-Authors:

Title: Develop Honors Thesis and Present at APA

Abstract:
For the first half of the summer, we developed my research question and honors thesis proposal. This involved researching articles on sex trafficking, trauma processing, and psychological vulnerability to trauma exposure. We created a literature review and wrote a 7-page intro, methods, and hypothesis for my honors thesis. During the second half of the summer, I ran significant analysis for an existing SSW dataset in the R programming language, created and printed a poster, and then presented at the 2022 APA conference in Minneapolis MN. Significant development of abnormal psych and data analysis procedures.

A Snapshot into the Lives of Wild African Elephants: Camera Traps and Conservation

Name: Amanda Odom
Year of Graduation: 2025
SURF Advisor(s): Virginia Hayssen, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Jodie Berezin

Title: A snapshot into the Lives of wild African Elephants: Camera Traps and Conservation

Abstract:
Camera traps are widely used in conservation work because they are a less expensive and less time-consuming way to assess animal populations. In elephant research, camera traps have been used extensively to monitor both captive and wild elephants. To date, little information is available about group dynamics and patterns of African elephants living in desert and scrub-desert regions. Here, we present findings on the group dynamics of African elephants (Loxodonta africana), collected from high-resolution, camera-trap photos taken across a year at the Mushara waterhole in Etosha National Park, Namibia. Photos were captured every fifteen minutes, from 7 am – 6 pm, for a total of about 4,500 photos. We explored the average group size and number of groups for four different group types including solitary bulls, bulls, family, and mixed groups using temporal and environmental variables including (1) wet and dry season, (2) month, (3) time of the day (morning, afternoon, and evening), and (4) phase of the moon. The most common group type seen in the dry season was bulls (44% of dry season groups), while the least common was family groups (6% of dry season groups), perhaps because family groups arrive at the waterhole after dark. In the wet season, the most common group type observed was the solitary bulls (60% of wet season groups) and the least common was mixed groups (2% of wet season groups). Bull groups were larger in the dry season, with an average group size of 3.8, compared with 2.2 in the wet season. Family and mixed groups were larger in the wet season with an average group size of 14.3 and 25.7, respectively, compared with dry season averages of 9.6 and 20.2, respectively. Bull groups and solitary bulls were most often observed in the afternoon, while family and mixed groups are most often observed during the evening. These results provide insight into elephant group dynamics and patterns of scrub-desert dwelling elephants. Because in-person field work at the Mushara waterhole only occurs during June/July, camera traps allowed the monitoring of elephant group dynamics across the entire year. What was presented here is only a snapshot into the group dynamics of the elephants that visit Mushara. In the future, we will also collect and analyze several additional years of camera trap photos and collect data on social behaviors, hormonal status, movement patterns, and additional environmental variables. These data can inform management decisions for Etosha's elephants based on environmental and temporal conditions, thus allowing for more population specific management. Additionally, the data can help inform management decisions for captive elephants living in similar environmental and social contexts.

Introduction to Methods in Academic Psychology Research/Practice

Name: Hannah Desrosiers
Year of Graduation: 2024
SURF Advisor(s): Nnamdi Pole, Psychology
Field of Study: Psychology
Co-Authors:

Title: Introduction to Methods in Academic Psychology Research/Practice

Abstract:
My summer 2022 SURF experience did not pursue a single research project but rather gave me experience with the research process through the lens of several different projects. Specifically, I made important contributions to the literature review process of a study on adverse childhood experiences by organizing studies in a Zotero database. I helped another student to design an honors thesis survey instrument by taking the survey and providing critical feedback. In this way, I learned about the data collection process. I attended a three hour training on psychophysiological data reduction. I also learned to use software designed to quantify the presence of psychologically significant words in psychotherapy transcripts. I gained unusual insights into the peer review process by contributing to the examination of actual scientific papers under consideration for publication. Finally, my SURF experience included learning about teaching a doctoral level course neuroscience course. I previewed and summarized neuroscience teaching videos and also prepared and implemented Moodle quizzes. Taken together, I was able to sample a broad range of scholarly activities that have left me with unique insights into the diverse work of academic psychologists.

Loneliness in Twitch Streamers

Name: Andreea-Bianca Morecut
Year of Graduation: 2023
SURF Advisor(s): Johanna Brewer, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Loneliness in Twitch streamers

Abstract:
My research this summer explored loneliness in Twitch streamers, specifically through the way Twitch creators interact with the platform's UX/UI. I spent a good amount of time wrestling around the abstractly shaped overlap of areas of study that really makes up 'loneliness in Twitch streamers.' Out of them, Human Computer Interaction, Psychology, and Design Justice stand out the most.
As part of this process, I read 27 papers, which I found through either compilation documents, references sections of papers I'd already read, or various databases — either Smith's own, Google Scholar, the ACM Digital Library, or JSTOR. Around a third of them felt significant enough for closer study; I have gotten about halfway through this closer study, at 4 papers very closely analyzed. The papers showcased repeated topics being broached — negative impacts on mental health, addiction, parasocial relationships, the importance of knowing one's boundaries — and my question became somehow both more and less clear.
I also followed about a dozen streamers regularly (out of which I have been able to make contact with two — https://www.twitch.tv/iguesseli and https://www.twitch.tv/imiyoung — who have expressed their interest in sitting down with me to have an interview in the near future).
One of the patterns I ended up noticing was that a lot of streamers holding marginalized identities were very intentional in the communities they were building. I even 'switched sides' for a brief (somewhat terrifying) moment during which I did a test stream!
All of the above have been so that I can continue this study into the year, and so I can get a better (personal) understanding of the topic I am pursuing, academically. I plan to continue this process into the academic year; thankfully, much of my thinking around that structure has settled as well, and I have been in conversation with two prospective advisers as well.

Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Name: Lily Shannon
Year of Graduation: 2024
SURF Advisor(s): Brianna McMillan, Psychology
Field of Study: Psychology
Co-Authors: Sarah Bradford, Vivian Almaraz, Caitlin Senni

Title: Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Abstract:
Parental involvement at-home and in the community correlates with higher child academic success (Byrant et al., 2000), but what about parental involvement in their child's school? Parental depression has a negative association with the amount that a parent reads to their child (Paulson et al., 2009). So is it possible that parental involvement in school-related activities is a mediator of the relationship between parental depression and child language outcomes? The goal of our study was to explore how parental involvement mediates the relationship between parental depression and child language outcomes in 3-5 year olds enrolled in Head Start programs.

Head Start is a program designed to provide quality care and early education for children from underprivileged backgrounds, specifically low-income families. Using the Center for Epidemiologic Studies Depression Scale (CES-D) to measure parental depression, the Peabody Picture Vocabulary Test (PPVT) to measure child language, and a checklist of school-based activities to measure parental involvement from the FACES 2019 dataset from the Head Start Family and Child Experiences Survey, we set out to create a mediation model (Figure 1). First, we hypothesized that higher levels of parental depression would be associated with lower child language scores. Second, we hypothesized that higher levels of parental depression would be associated with lower parental involvement in school activities. Third, we hypothesized that the relationship between parental involvement and child language scores would be mediated by parental depression. We measured the data by using a linear regression for each relationship between the variables. Initial analyses found no significant relations between parental involvement, parental depression, and child language scores. In future analyses we will explore whether sociodemographic factors might explain our null findings.

Investigating the Motility of Cytoskeletal Motor Proteins

Name: GenevieveTorrence
Year of Graduation: 2024
SURF Advisor(s): Nathan Derr, Biological Sciences
Field of Study: Biological Sciences, Biochemistry
Co-Authors:

Title: Investigating the Motility of Cytoskeletal Motor Proteins

Abstract:
My research in the Derr lab this summer involved studying the motility of molecular motor proteins, using DNA origami scaffolding to study group motility. The motors kinesin and dynein carry cargo along cytoskeletal microtubules. Studying them as they pull a resistive load in different configurations can help us understand their binding and unbinding behaviors.

To get an idea of a baseline for Kip2 yeast kinesin movement on a microtubule, we attached a fluorophore to kinesin and observed it using the TIRF microscope. The 300 runs of kinesin I collected averaged a speed of 61.4 nanometers/second, within the expected range for Kip2.

A large part of the summer was spent preparing for experiments with multiple motor proteins on DNA chassis. Myself, my advisor and other students in the Derr lab grew and harvested yeast cells that expressed the proteins dynein and kinesin. I focused on the expression of Kip2 in yeast cells. We then purified the motor proteins and labeled them with either fluorophore and oligonucleotide tags. Simultaneously, my lab collaborators and I designed and folded DNA origami structures that would be able to attach the motor proteins at specific sites, thus creating a motor "chassis" structure with which we could study the group dynamics of motor proteins.
We used microtubule assays on the TIRF microscope to view and quantify the motor movement.

Our chassis tested the movement of motors in series and in parallel in their ability to pull rigor dynein, a mutated motor that is permanently bound to the microtubule and creates a resistive load. In our preliminary trials with this chassis series, we observed unusual runs. To treat this, we experimented with different motor dilutions and motor purifications, and eventually refolded new chassis. Possible explanations for the unusually few and long runs could have been related to improperly folded chassis, motor or dead motor concentration, or other reagents involved in the microscope slide assay.

Effects of Zooplankton Presence on Sunlight Inactivation

Name: Adeline Rickard
Year of Graduation: 2024
SURF Advisor(s): Niveen Ismail, Engineering
Field of Study: Engineering
Co-Authors: Jacqueline Wang, Hadeel Shwwa

Title: Effects of Zooplankton Presence on Sunlight Inactivation

Abstract:
Rotifers, a filter-feeding zooplankton, are able to take up microbial pollutants in aquatic systems, such as viruses. While rotifers may ingest these pollutants, it is not certain whether the rotifers inactivate them through digestion or retain them in their bodies. Retention of viruses could lead to protection from sunlight disinfection which is a critical process to inactivate viruses. The main objective of this research was to quantify the impact of rotifer presence on sunlight disinfection of viruses.

For our month-long SURF, we conducted two types of experiments on the Ford Seasons Room balcony. For each experiment we used rotifer Brachionus plicatilis as a model organism and MS2 bacteriophage as a surrogate for human pathogenic viruses. The purpose of the first rooftop experiment was to confirm that the presence of rotifers impacts the rate of sunlight disinfection of viruses. We exposed various conditions as well as corresponding controls to 12 hours of sunlight. For each condition tested, we measured MS2 concentration as a function of solar irradiance. The purpose of the second rooftop experiment was to observe whether the bodies of the rotifers may also cause a shading effect for uningested MS2. We prepared beakers with live rotifer specimens and compared the decline of MS2 concentration with beakers containing dead rotifers. Similar to the first experiment, we measured MS2 concentration as a function of solar irradiance after exposing samples to sunlight for 12 hours.

The data we obtained was consistent with our hypothesis that rotifers do indeed take up MS2, and that the concentration of viable MS2 was higher in beakers that contained rotifers. These results indicate that rotifer presence results in a reduction of sunlight inactivation of viruses and can protect MS2 from sunlight inactivation. During fall semester we will continue to obtain data from saved samples from these experiments. We will be utilizing RT-qPCR to examine the viral RNA from the MS2 in samples that we froze this summer. We will also be working on publishing our results in peer-reviewed literature.
The results of this work will help inform the management of treatment wetlands in which sunlight disinfection is a critical process for inactivation of microbial pollutants. Treatment wetlands also often contain large densities of zooplankton which may impact the overall fate of microbial pollutants.

Assessing the Processivity of Human-Yeast Chimeric Dynein

Name: Emily Swindell
Year of Graduation: 2024
SURF Advisor(s): Nathan Derr, Biological Studies
Field of Study: Biology/Biochemistry
Co-Authors:

Title: Assessing the Processivity of Human-Yeast Chimeric Dynein

Abstract:
During my time on Smith College Campus under SURF funding I began a project that will be the focus of my special studies for the next few years and will likely be my senior thesis. Over this past summer I have made a lot of headway with my project, meaning that I will be able to focus on performing experiments over the fall semester. I also developed more confidence and knowledge of standard lab procedures, and I feel much more secure in my ability to not only follow procedures, but design and develop them as well.

My project is continuing the research of a prior Derr lab student, who had created yeast-human dynein chimeras by replacing the microtubule binding domains (MTBD) of yeast dynein with that of human dynein. I am continuing to study chimeras, however I am creating the reverse chimeras: human dynein motor domains with yeast MTBD. We hypothesize that, if processivity is determined solely by the MTBD, then replacing the mammalian MTBD with the yeast MTBD should increase processivity. My project will be focused on experimenting with several constructs: wild-type mammalian dynein, chimeric mammalian dynein with the yeast MTBD, mammalian dynein with yeast MTBD and wild type dynein with a point mutation from Arg to Glu at position 3337 (an amino acid position which is theorized to play a very important role in processivity). My project is designed to assess if the MTBD is solely responsible for processivity, and to analyze if there are any other regions of mammalian dynein that affect processivity when the MTBD is manipulated.

The major portion of my work this summer involved reading, analyzing, and collecting data from academic papers to determine the ideal location to truncate human dynein for expression in yeast cells, creating an outline of what my project would entail, and learning to operate the "SeqBuilder" application from DNAStar. I used this application to design oligo primers for my planned PCRs, as well as develop a truncated human dynein sequence more suitable for expression and harvesting in yeast. During this time I continued to practice and engage in making slides for, and observing motors on, the TIRF microscope, following the Derr lab standard procedure. Additionally, as I waited for my oligo primers to arrive, I learned and updated the procedure for a "flow chamber" assay, which involved utilizing the CDF's resources to troubleshoot and improve mechanical aspects of the microscope slide stabilizer provided.

Once my oligo primers had arrived, I began performing PCRs, as well as TAE gel electrophoresis analyses to determine the success of each PCR. My project thus far has involved a lot of troubleshooting, with of course both some successes and some failures. As such, I am currently working on troubleshooting two specific PCRs and will be continuing this project into the Fall 2022 semester as my special studies project.

Delving into Microbial Eukaryotes

Name: My My Tran
Year of Graduation: 2024
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Delving into Microbial Eukaryotes

Abstract:

1. Ciliates as a Model Organism & 2. Identifying Meiosis-Specific Genes in “Asexual Lineages”,"Although the vast majority of eukaryotic life consists of microbial eukaryotes, they are heavily understudied. One such microorganism are ciliates, which fall under Alveolata in SAR (Stramenopiles, Alveolata, and Rhizaria) on the eukaryotic tree of life. Ciliates are unicellular organisms characterized by their cilia and nuclear dualism (i.e. they have both a somatic macronuclei and germline micronuclei). Although they can reproduce asexually by exchanging genetic material, they also have a unique form of sexual reproduction called conjugation, in which haploid micronuclei are exchanged (Landweber, 2013).

This summer, we aimed to characterize the nuclear architecture of the ciliate Chilodonella uncinata, by developing molecular techniques to understand stages of macronuclear development. Samples collected from Lyman pond were cultured to prepare for DAPI staining, fluorescence visualization, and whole transcriptome-amplification (WTA). DAPI is a chemical that is used to fluorescently stain the DNA in cells. In order to connect fluorescent visualization with gene expression (WTA), we experimented with using Glyoxal, a fixative that can retain genetic material in the cells. This would allow us to sequence the transcriptome of a cell after analyzing it through fluorescent microscopy. In our experiment, we varied the pH level and concentration of Glyoxal, then performed whole transcriptome amplification on cells that were fixed with glyoxal to see which had high quantification measurements.

My second project was identifying meiosis-specific genes (MSGs) in microbial eukaryotes. The life cycles of many lineages remain unobserved or heavily understudied which oftens leads to lineages being identified as asexual–unless proven otherwise. This poses the question: is sex ancestral to all eukaryotic life?–This is an open-ended question and many meiotic toolkits have been hypothesized in an effort to answer it. A meiotic toolkit combines phylogenomic approaches with bioinformatic tools to identify MSGs to detect sexual processes in microeukaryotes.

Cont.: Delving into Microbial Eukaryotes

For this project, I ran our working pipeline in the lab to identify MSGs in different eukaryotic taxa from an established list by (Mciver, 2019). A few of my contributions to this team project a Python script on subsampling protein sequences from the EGGNOG database and plotting the taxonomic distribution of sequences, and running sequences through Pre-Guidance to filter out low quality sequences to clearly represent each MSG.
Not only did SURF allow me to build on my molecular skills and complete complex protocols, but I was able to take on the initiative of starting an R learning club for other members of the lab.

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Exploring Ciliate's Microbiomes and Ciliates Underwater

Name: Jailene Gonzalez
Year of Graduation: 2024
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biological Studies
Co-Authors:

Title: Exploring Ciliate's Microbiomes and Ciliates Underwater

Abstract: Ciliates are single cell microeukaryotes belonging to the major clade, Alveolata. Ciliates are characterized by their hair-like structures called cilia and by their nuclear dualism. This feature in ciliates is fascinating because they have both a somatic macronucleus and germline micronucleus that performs different functions for the organism (Ahsan et al. 2022). For example, their somatic macronuclei helps ciliates with their metabolism, cell growth and division, while their germline micronuclei helps form the cell's new macronucleus after conjugation (Ahsan et al.2022). Thus, playing a key role in their nuclear architecture and development. Furthermore, ciliates are known for having the capacity to harbor a microbiome of symbionts, however, there have only been a couple of studies addressing who these symbionts are and what they are doing (Schrallhammer 2020). In Schrallhammer 2020, they described 7 studies that showed that these new or rediscovered endosymbionts on ciliates provides insight into the biological concept of intracellular symbionts, their host range, and how they may protect their host from ultraviolet irradiation (Beliavskaia et al. 2020; Korotaev et al. 2020; Fleming et al. 2020; Schrallhammer 2020; Sonntag et al, 2020; Spanner et al. 2020). As a result, symbionts play a key role in understanding the interactions between the organisms and their ecological and evolutionary process. Hence, I conducted a preliminary study to further investigate this topic.

This summer, I worked in collaboration with another undergraduate student in the Katz Lab to find suitable methods for this experiment. We tried out two different single cell total RNA isolation kits to extract all of the RNA of the ciliate cell we picked and all of its associated microbiome. The goal is to use molecular techniques to identify the species of ciliates and their associated endosymbionts and see what genes are being expressed by them. During this process, we managed to get a good understanding of the kits we were using and how to develop a more accessible protocol that would aid us when conducting the experiment. For instance, we collected a series of cells we knew that would generate positive results to see which RNA extraction kit was easiest to use and/or yielded better results. In conclusion, we determined that we would continue this experiment in the fall using a different kit to compare to the one we've tested thoroughly.

Additionally, I also worked on a project related to single-cell ciliate samples collected from a UConn research cruise members of the Katz Lab went on earlier this summer. Our lab had joined this research cruise in order to assess what ciliates are living deep in the ocean, at the deep chlorophyll maximum (DCM). The team had gone far offshore into the blue water to sample from many depths. At the surface, they set up sampling stations, took notes of their sampling points and data, as well as used microscopes to identify and pick ciliate species to transfer into tubes for wet work at the lab. The team collected 43 cells and I had the opportunity to kick start the processing of these cells for Whole

Cont.: Exploring Ciliate's Microbiomes and Ciliates Underwater

Transcriptome Amplification (WTA) on 12 cells. This process allowed us to amplify total RNA of the cell to learn more about their transcriptomes and gene expression.

On another note, I was able to dedicate my time during SURF to start preparing and writing up my undergraduate thesis for publication. I also had the opportunity to do more fieldwork and go sample at Madison, CT and both Lyman and Paradise Pond on Smith's campus. In addition, I started learning how to implement bioinformatic tools into my research projects and learn how to write scripts and run new software in the lab, e.g. Barrnap, HISAT2, Geneious Prime, etc. Overall, I hope to be able to continue all of these projects and make them applicable to my thesis as a graduate student at Smith.

Analysis of Silica-Undersaturated Lava from Bermuda: Insights into eruptive and post-eruptive history

Name: Anne Lepow
Year of Graduation: 2022
SURF Advisor(s): Sarah Mazza, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Analysis of Silica-Undersaturated Lava from Bermuda: Insights into eruptive and post-eruptive history

Abstract:
Bermuda is an intraplate volcano located ~1,000 km off the coast of North America. Long thought to fall under the mantle plume model for intraplate volcanism, Bermuda lacks key characteristics of hotspot volcanism (Vogt & Jung, 2007). Recent geochemical research supports a different model with a source reservoir of geologically young, recycled material in the mantle transition zone. Under this model, melting and upwelling of volatile-rich material are attributed to mantle convection (Mazza et al., 2019).
Analysis of core samples from the Bermuda Deep Drill of 1972 is ongoing. Carbonate and silicate globules—or "ocelli" as they are oft termed—permeate the core. Originally assumed to be secondary alteration products, initial analysis of the core deliberately avoided sections containing ocelli. Textural analysis performed last year revealed features inconsistent with a purely secondary origin for these features. Preliminary trace element work also supported a more complex petrogenetic history.
During SURF 2022, we performed a more thorough analysis of existing core samples with special attention paid to ocelli-rich sections. In addition to textural analysis, ocelli were also classified into different groups—carbonate- and silicate-rich—based on composition. Major and trace element data on several different ocellus types were also collected.
A comprehensive analysis of geochemical data for the ocelli, combined with whole-rock geochemical data reveals more about the role of carbonate fluids in Bermuda's petrogenesis.

Characterizing meteorin and meteorin-like expression using a Danio rerio

Name: Shariqa Sheila
Year of Graduation: 2024
SURF Advisor(s): Michael Barresi, Biological Sciences
Field of Study: Neuroscience/Biological Sciences
Co-Authors: Lilly Mearsheimer

Title: Characterizing meteorin and meteorin-like expression using a Danio rerio model

Abstract: There is evidence that suggests that meteorin (metrn) and meteorin-like (metrnl) proteins play a role in cell differentiation, development and proliferation in the central nervous system (CNS). Studying expression of metrn and metrnl genes might help us understand how different types of neural stem cells, such as radial glia, are guided to differentiate and develop in order to form the matured CNS. Radial glial cells are extremely important to the formation of the brain, and there is consensus that some brian tumors originate from these cells. The reality, however, is that not much is known about radial glial cells and even less is known about their potential regulators, metrn and metrnl. Metrn is a secreted protein that has been found to influence the formation and differentiation of radial glial cells as well as contributing to axonal growth.

In this project, we attempted to characterize the expression of metrn and metrnl by utilizing a Danio rerio model. Zebrafish (Danio rerio) is a model organism to study as it is a vertebrate which shares a high percentage of genetic similarity with humans, and as its embryos are nearly transparent, making it easier to observe. To characterize the expression of metrn and metrnl, we carried out a technique known as Hybridization Chain Reaction (HCR) which fluorescently tags mRNAs coding for metrn and metrnl. This allowed us to image patterns of metrn and metrnl expression on the laser-scanning confocal microscope. One challenge we ran into was finding the optimum microscopy settings to visualize the metrn expression so this is something we hope to refine in our work further beyond SURF.

We also attempted to characterize loss of metrn and metrnl functions by using zebrafish that were injected with CRISPR guide RNAs. The injections were intended to target different locations in the DNA promoter region upstream of the metrn gene so as to disrupt the metrn expression. The idea was that if the injections were successful, the off-springs of the injected zebrafish would be lacking the metrn gene in the targeted DNA segment. To explore this, we mated several pairs of injected fish and then genotyped their embryos. After genotyping, we carried out gel electrophoresis to screen for whether any or what percentage of embryos showed mutations (unexpected band pattern compared to wildtype zebrafish DNA). An overarching goal for this experiment was to identify founder parents: injected zebrafish whose mutation successfully occurred at germline and has the ability to produce offsprings that carry the same metrn knock-out mutation). After repeated screening of tens of pairs of zebrafish, we are hopeful to have found one promising founder pair. The off-springs of this founder pair can be further studied for the effect of loss of function in future lab projects.

Magmatism in the White Mountains, New Hampshire

Name: Julia Walker
Year of Graduation: 2022
SURF Advisor(s): Sarah Mazza, Geoscience
Field of Study: Geosciences
Co-Authors:

Title: Magmatism in the White Mountains, New Hampshire

Abstract: During SURF 2022, we continued to investigate the magmatic history of the White Mountains, NH. We focus on the relationships between mafic rocks from the Three Ponds area and multiple igneous provinces documented in the New England region, as well as the processes responsible for generating those provinces. Samples were collected during summers 2021 and 2022. Whole rock major and trace element analysis was performed using XRF and LA-ICP-MS. Mineral and textural analysis was done in hand sample and thin section. Additional mineral chemistry data was collected using SEM-EDS and XRD.

The Three Ponds area has been previously mapped as Jurassic gabbro, part of the White Mountain Magma Series. However, the geochemistry of Three Ponds gabbro sampled in summer 2021 is remarkably similar to that of the Central Atlantic Magmatic Province (CAMP) associated with Pangea break-up. Kinney et al. (2022) use zircon dates to claim the Three Ponds gabbro is instead part of the Devonian New Hampshire Plutonic Suite. Field work during summer 2022 confirmed that the Kinney et al. sample has been heavily metamorphosed and is therefore unlikely to be the same rock as the gabbro we collected and studied in 2021. However, to further complicate the story the newly collected gabbro samples are geochemically distinct from gabbro collected nearby in 2021. In 2022 we also sampled a previously undocumented diabase that is geochemically distinct from the Three Ponds gabbros and from CAMP and is instead more similar to the Coastal New England (CNE) province that predates CAMP. However, the CNE province is not known to extend into the White Mountains. We are unable to compare these samples to the Cretaceous New England Quebec (NEQ) province, which has been documented in the White Mountains, because no geochemical data has been published for mafic NEQ rocks.

The Three Ponds area is more complicated than previously believed, and many questions remain regarding the relevant dates, magmatic provinces, and geologic processes. Future work includes processing gabbros and pyroxenites from elsewhere in New Hampshire, some of which are known to be Cretaceous, in order to expand our geochemical data set.

Geospatial Analysis of Demarcation Pillars in Dhaka

Name: Rana Gahwagy
Year of Graduation: 2022
SURF Advisor(s): Efadul Hum, Environmental Science and Policy
Field of Study: Environmental Science and Ploicy
Co-Authors:

Title: Geospatial Analysis of Demarcation Pillars in Dhaka

Abstract: Urban rivers and wetlands are drawing renewed attention as cities envision pathways for climate resilience. Urban rivers and wetlands provide multiple ecosystem services from provisioning to regulating to supporting, such as water supply and filtration, flood control, and reducing heat island effect. In the case of Dhaka, Bangladesh, where rivers face pollution and encroachment, the respective planning authorities implemented a multi-year project to define the boundaries of rivers. The demarcation project, which quickly became controversial, erected concrete pillars to mark the river's edge. The summer research project analyzes the location of these demarcation pillars in relation to the historic water flow in the rivers. The pillars, costing up to 3 million dollars, are cement structures meant to mark the boundaries of multiple rivers that run over 110 km. They are used to prevent unauthorized people from taking over the river banks. However, environmentalists contend that the pillars were inaccurately placed, and claimed that 'misplaced' pillars disproportionately affected small landowners by taking away their land.

The primary goal of the research project is to understand and visualize the location of the pillars in relation to the seasonal changes in the rivers. The analysis conducted will have several complementing components. We used GPS location from a previous report to map and verify the locations of the demarcations. We found that, indeed, a lot of the pillars are in the river and will allow people to encroach farther into the river.

The other component is to measure the extent of the river and the seasonal changes. We used satellite images from the freely available Landsat database that goes back to the 1970s. This specifically sheds light on the position of the pillars and the ecological basis for the demarcation lines. ArcGIS was used for the analysis of river flow by using ISO Cluster Unsupervised Classification to map the river for about 30 years during wet and dry seasons. We noticed that the area of the river and surrounding water bodies have gone almost in half during the wet season since the start of the demarcation project, which indicates how it did not stop river encroachment.

The importance of this research project lies in its potential to generate policy implications for the environmental, socioeconomic, and governance aspects of demarcation pillars in urban rivers. Understanding the working of the river and the placement of the demarcation pillars will answer questions and contribute to resolving disputes that are of importance to urban planners, river management authorities, environmentalists, and people living on the banks of the rivers.

References:
RDRC. (2021). Report on Field Survey of the Demarcation Pillars by BIWTA on Buriganga and Turagh River. River & Delta Research Centre. https://www.rdrc.info/report-on-field-survey-of-the-demarcation-pillars-sat-by-biwta-on-buriganga-and-turagh-river/
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The effect of buffer and pH on two populations of antagonistic bacteria isolate

Name: Madeleine Soyster
Year of Graduation: 2024
SURF Advisor(s): Chris Vriezen, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: The effect of buffer and pH on two populations of antagonistic bacteria isolate samples and the development of mathematical models.

Abstract: Urban rivers and wetlands are drawing renewed attention as cities envision pathways for climate resilience. Urban rivers and wetlands provide multiple ecosystem services from provisioning to regulating to supporting, such as water supply and filtration, flood control, and reducing heat island effect. In the case of Dhaka, Bangladesh, where rivers face pollution and encroachment, the respective planning authorities implemented a multi-year project to define the boundaries of rivers. The demarcation project, which quickly became controversial, erected concrete pillars to mark the river's edge. The summer research project analyzes the location of these demarcation pillars in relation to the historic water flow in the rivers. The pillars, costing up to 3 million dollars, are cement structures meant to mark the boundaries of multiple rivers that run over 110 km. They are used to prevent unauthorized people from taking over the river banks. However, environmentalists contend that the pillars were inaccurately placed, and claimed that 'misplaced' pillars disproportionately affected small landowners by taking away their land.

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Alam, N., & Azaz, M. (2021). What went wrong with Dhaka rivers re-demarcation? The Business Standard. https://www.tbsnews.net/analysis/what-went-wrong-dhaka-rivers-re-demarcation-186595

Metagenomic Analysis of South African Wildlife Fauna

Name: Margaret Weber
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences; Mary Doherty
Field of Study: Genomics
Co-Authors:

Title: Metagenomic Analysis of South African Wildlife Fauna

Abstract:
An uptick in South African ecotourism has caused increased food-driven livestock demand. Regions containing imported livestock will continually expand, and spatial overlap of livestock and wildlife will, therefore, grow too. Concern over increased parasite transmission, specifically gut-borne nematodes, in nature reserves such as Tswalu is paramount (Bird, 2016). It is already understood that parasitic infection increases co-infection vulnerability, decreases fitness, alters feeding patterns, and hinders growth, among other symptoms (Milner et al., 2013). Through uncovering the gastrointestinal biodiversity of these hosts, we can better understand parasite transmission—between and among host species—thereby improving wildlife management and preservation in South Africa.

For the duration of SURF 2022, I was able to successfully sequence fifty DNA samples of previously extracted wildlife scat via Illumina Miseq Next Generation Sequencing in preparation for parasitic helminth presence and load discovery. Once the protocol was optimized through pilot studies, the 18S rRNA gene was amplified via polymerase chain reaction (PCR) for triplicates of each sample and were verified through gel electrophoresis. All 150 PCR products were pooled (triplicates of each sample), purified via left-sided bead cleanup, and amplicon sizes were verified with fragment analysis. Concentrations were then normalized to 4nM, pooled together, and quantified. The final library was then diluted to 9pM and sequenced on an Illumina Miseq sequencer. Future directions include following the Qiime II workflow for Metagenome data analysis to identify amplified filarial parasite species and the biodiversity within wildlife fauna from the Illumina Miseq run data.

Bird, C. (2016). The biodiversity of gastrointestinal nematodes in South African wildlife. Smith College.
Milner, J., Wedul, S., and Laaksonen, S. "Gastrointestinal Nematodes of Moose (Alces Alces) in Relation to Supplementary Feeding." Journal of Wildlife Diseases, vol 49 (2013): 69-79.

IDL Software Engineering Research—Improving Moderation System for Anykey GLHF Pledge

Name: Waken Ninohira
Year of Graduation: 2022
SURF Advisor(s): Johanna Brewer, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: IDL Software Engineering Research—Improving Moderation System for Anykey GLHF Pledge

Abstract: Harassment, especially of marginalized individuals, on networked gaming and social media platforms has been identified as a significant issue, yet few Human Computer Interaction practitioners have attempted to create interventions tackling toxicity online. There is, however, a growing cohort of technology design activists whose work attempts to take an intentional stance on social change. In this SURF research, I aligned myself with these efforts by continuing the development of a community-driven moderation intervention called the AnyKey GLHF pledge. Specifically, I analyzed this online system which has reached over 1.3 million users, and improved upon its existing features in order to better support the inclusive communities on Twitch, who rely on the technology.

During SURF, I implemented two major features and two minor changes. To decide on features to implement in the moderation system, I based on the input from researchers that performed moderation on Anykey's system including myself. First, we focused on how some moderator feels the need for a tool to consult with more experienced moderator about how to deal with some difficult report cases. I designed and implemented a feature that allows mods to leave comments on a specific report so that they can better communicate with other mods and get advice on how to resolve the reports.

Another major feature I worked on highlights reports about users that have been reported before. Anykey's moderation philosophy is to give a warning to users when first time getting reported as long as their act is not severely harmful, so that they can have a learning moment on how to better behave in online space. Following this policy, moderators tell them that their badge will be revoked when getting reported again. However, Anykey's existing system did not provide a way for mods to find if a reported user has been reported and warned before. With this new feature, mods can better detect more urgent reports about users continuously abusing the badge.

Other than those major features, I added pagination on the reports list view to follow the best practices. I also worked on email confirmation upon report submission which was requested by our community.

The Effect of Bedrock Lithology Weathering on Vernal Pool Water Chemistry at MacLeish Field Station

Name: Natalie Nathanson
Year of Graduation: 2023
SURF Advisor(s): Amy Rhodes, Geoscience
Field of Study: Environmental Geoscience
Co-Authors:

Title: The Effect of Bedrock Lithology Weathering on Vernal Pool Water Chemistry at MacLeish Field Station

Abstract: Vernal Pools are seasonal, shallow wetlands. They are critical ecosystems for both flora and faunal reproduction due to the seasonality of water present during the winter and spring. At Smith College, forested vernal pools are present in the MacLeish Field Station. This study examined water and soil samples to better understand the hydrology and geologic setting of the vernal pools at MacLeish. The two guiding research questions are " How does mineral weathering of the sediment and glacial till affect the water chemistry of vernal pools?" and "What is the mineralogy of the soil and how might weathering of these minerals affect the water chemistry of vernal pools?". To address these questions this summer, I collected samples of water in the vernal pools and associated streams, and I examined soil samples collected previously by students in GEO 301, Aqueous Geochemistry class, of which I was a member. I also examined the weathering results (water chemistry and mineralogy) of schist minerals from the Waits River Formation, which makes up some of the bedrock underlying the vernal pools and that can include pyrite, which produces acidity and sulfate when it weathers. The soil samples collected were weathered in bottles with rain water over a two-week period to determine its effects on the chemistry of water. Water samples were analyzed for cation, anions, trace metals, and alkalinity, and mineralogy was determined by X-ray diffraction. Overall, the alkalinity of water extracted from the soil weathering experiment shows initial pH values that ranged between 4 and 5 and a much broader range of alkalinity results (-842- 64.8 ueq/L). X-ray diffraction results revealed that quartz, muscovite, and biotite make up the composition of vernal pool soil. Further, possible clay weathered from the experiment is Illite or Kaolinite which is determined using dA° values from databases and that best match with the samples. Additionally, when using dA°values from the samples, it was determined that pyrite was not found in the more acidic vernal pools soil samples. Based on the results from this study, my future work will focus on examining additional geochemistry and mineralogy data in order to determine possible relationships between minerals present in soils based on the compositions of the bedrock and the vernal pool water chemistry.

The Identification of Insulin Receptor Expression in Skeletal Muscle Myogenesis

Name: Katelyn Diaz
Year of Graduation: 2023
SURF Advisor(s): Stylianos Scordilis, Biological Sciences
Field of Study: Biochemistry

Title: The Identification of Insulin Receptor Expression in Skeletal Muscle Myogenesis
Abstract:

Background
The insulin receptor (INSR) is involved in signaling and glucose homeostasis and is an important regulator of cell growth, metabolism, and differentiation. Glucose transporter type 4 (GLUT4) is another protein involved in glucose metabolism, acting as an insulin-regulated glucose transporter that is responsible for insulin-regulated glucose uptake into muscle and adipose cells. Insulin's main purpose is regulating the energy supply in the body, and is essential to metabolic health. The aim of this study was to determine at what stage of myogenesis insulin receptors start being expressed.

Methods
Using control cells from days zero, five, and nine, a Lowry assay was conducted to test for peptide bonds and obtain a protein concentration. Using these values, Western blots were run with samples from days zero, five, and nine on both a 10% separating gel and a 7.5% separating gel. Following completion, the blots were transferred to PVDF (polyvinylidene difluoride) membrane in preparation for the immunoblotting protocol. First, optimization blots were conducted using INSR and GLUT4 as the primary antibodies, and (goat anti-rabbit IgG horse radish peroxidase linked) (Gt x Rb IgG-HRP) as the secondary antibody. Next, using determined optimal dilutions, the experiment was performed, and the gels were analyzed to see which day of myogenesis INSR and GLUT4 appeared.

Results
The optimal antibody dilutions were determined to be 1:1500 on a 7.5% separating gel for INSR, and 1:2000 on a 10% separating gel for GLUT4. Preliminary results show that INSR and GLUT4 bands had the strongest intensity on day zero, but further research is required to confirm and quantify how insulin receptor expression changes through myogenesis.

Conclusion/Discussion
This research has further implications for studies on metabolic health. A decline in metabolic health is associated with a decline in musculoskeletal health during aging, illness, and menopause. Prior studies have shown that post-menopausal women are at an increased risk for type 2 diabetes, and as both INSR and GLUT4 increase insulin sensitivity, less GLUT4 and INSR in the system makes the body less sensitive to insulin.

Physical Activity and Hot Flash Study

Name: Sara Buszkiewicz
Year of Graduation: 2025
SURF Advisor(s): Sarah Witkowski, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies
Co-Authors:

Title: Physical Activity and Hot Flash Study

Abstract:
I worked primarily on a study examining the relationship between exercise and hot flashes in perimenopausal people aged 43-55. Cardiovascular disease (CVD) is the leading cause of death in menopausal people and CVD risk increases with the progression of menopause, unrelated to aging. Hot flashes have been associated with higher CVD risk for perimenopausal people, however the impact of physical activity on this relationship is unknown. This study included 3 participant visits to the Vascular Function Lab where various measurements were collected, including vascular tests, physical activity and hot flash monitoring, and blood. Twice a week I traveled to businesses in the area and put up flyers advertising our study to recruit participants. Before visits, I helped set up equipment, and during visits I collected data. Additionally, I learned the protocols involved in the tests conducted during visits and implemented them during participant visits.
Endothelial dysfunction is an early indicator of CVD and can be measured via brachial artery Flow Mediated Dilation (FMD). The procedure involves ultrasound imaging of the brachial artery for a total of 11 minutes. First, 2 minutes of baseline measurements are recorded, including vessel diameter and the shear rate of the blood moving through the vessel. Next, a cuff placed on the participant's lower arm inflates to 200 mmHg. After 5 minutes of inflation, the cuff releases and measurements are recorded following the response of the vessel. Ideally, the vessel will expand in response to the spike in shear rate, and quickly (30-60 seconds). FMD % is calculated by dividing the change in arterial diameter by the initial diameter and multiplying by 100. A lower FMD % could indicate endothelial dysfunction, as the endothelial cells along the vessel walls are not responding as they should to the increased shear rate. I worked on learning how to find the brachial artery using the ultrasound and running a few FMD studies for participants this summer. Additionally, after a study is finished, I used CardiovascularSuite software to make sure we had the best analysis of the study. The tracking along the vessel walls could be misplaced, or the calibration could have been incorrect, and I go back and fix it so we know we have the most accurate numbers for our study. I worked with Tint Tha Ra Wun to analyze this data and create an abstract to submit for the NEACSM conference this fall where we will present our findings.

Wenjun,Zhao,Anya,2025,"Sarah Moore, Engineering",,Engineering,,,Fn3 therapeutic effect on MSLN positive cancer cells.,"Mesothelin (MSLN) is a

Fn3 therapeutic effect on MSLN positive cancer cells

Name: Wenjun Zhao
Year of Graduation: 2025
SURF Advisor(s): Sarah Moore, Engineering
Field of Study: Engineering
Co-Authors:

Title: Fn3 therapeutic effect on MSLN positive cancer cells.

Abstract:
Mesothelin (MSLN) is a tumor-associated antigen that can be considered as a specific biomarker for targeted immunotherapy. MSLN is overexpressed on cancer cells, including ovarian, breast and pancreatic cancers, and interacts with CA125 (MUC16) for metastasis and proliferation.The Moore lab has previously engineered several variants of the fibronectin type III domain (Fn3) non-antibody protein that binds selectively to MSLN on cancer cells, and showed that the protein can induce apoptosis in MSLN positive cancer cells. This summer we aimed to measure the binding affinity and killing ability of a variant named Fn3 5.3.2 and a non-binding negative control Fn3-RDG. Mouse anti-MSLN antibody (K1) and goat anti-mouse PE conjugate (PE) were used as positive controls to show MSLN expression by flow cytometry. Binding assays were performed using two different MSLN-positive cancer cell lines, named OVCAR-3 and KB-3-1 cells. . Samples were analyzed by flow cytometry. Verification of results is ongoing.
Apoptosis is a form of programmed cell death that the engineered Fn3 proteins were previously shown to induce in cancer cell lines. We developed apoptosis experiments using the negative control protein Fn3 RDG and a positive control molecule, chemotherapeutic mitomycin C (MMC). In future work, the cytotoxic effect of 5.3.2 will be measured.

Using Single Cell Transcriptomic Data to Investigate the Evolution and Ecology of Freshwater Testate Amoeba Arcellinida

Name: Beatrice Wendling
Year of Graduation: 2025
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study:
Co-Authors:

Title: Using Single Cell Transcriptomic Data to Investigate the Evolution and Ecology of Freshwater Testate Amoeba Arcellinida

Abstract: Arcellinida are a freshwater clade of shelled, or testate, amoebae within Amoebozoa whose unique shells make them useful for many environmental and paleontological studies (Strullu-Derrien et al., 2019). Both of my SURF projects focused on the application of Arcellinida single-cell transcriptomes to learn about their evolution throughout geologic history and their modern ecological relationships.

Molecular Clock of Arcellinida Using Single Cell Transcriptomes

Arcellinida are some of the oldest extant eukaryotes found in the fossil record (Lahr, 2021), so modeling their evolution provides a greater perspective on eukaryotic evolution and diversity in Earth's history. My study aims to use Katzlab-specific molecular data in combination with current molecular clock analysis software to create a more robust representation of Arcellinida evolution. Additionally, a reevaluation of the fossil record will yield more accurate depictions of the age of groups within Arcellinida.
Over SURF, I started the first stages of this project: curating a list of fossils to be used as calibration points(Fig 1), familiarizing myself with methods for protist-specific molecular clocks, and beginning to learn the molecular clocks software.

Identifying Unknown Flagellate Symbionts and Their Relationship to Arcellinida Hosts

Some freshwater samples from Katzlab sampling locations in Acadia National Park contain Arcellinida with unknown flagellates living inside their tests (Fig 2). These flagellates are present in multiple species of Arcellinida that have varying morphologies. Videos show that the flagellates exhibit a consistent size (typically [sic]

Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Name: Vivian Almaraz
Year of Graduation: 2023
SURF Advisor(s): Brianna McMillan, Psychology
Field of Study: Psychology
Co-Authors: Caitlin Senni, Lily Shannon, Sarah Bradford

Title: Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Abstract: Parental involvement at-home and in the community correlates with higher child academic success (Byrant et al., 2000), but what about parental involvement in their child's school? Parental depression has a negative association with the amount that a parent reads to their child (Paulson et al., 2009). So is it possible that parental involvement in school-related activities is a mediator of the relationship between parental depression and child language outcomes? The goal of our study was to explore how parental involvement mediates the relationship between parental depression and child language outcomes in 3-5 year olds enrolled in Head Start programs.

Head Start is a program designed to provide quality care and early education for children from underprivileged backgrounds, specifically low-income families. Using the Center for Epidemiologic Studies Depression Scale (CES-D) to measure parental depression, the Peabody Picture Vocabulary Test (PPVT) to measure child language, and a checklist of school-based activities to measure parental involvement from the FACES 2019 dataset from the Head Start Family and Child Experiences Survey, we set out to create a mediation model (Figure 1). First, we hypothesized that higher levels of parental depression would be associated with lower child language scores. Second, we hypothesized that higher levels of parental depression would be associated with lower parental involvement in school activities. Third, we hypothesized that the relationship between parental involvement and child language scores would be mediated by parental depression. We measured the data by using a linear regression for each relationship between the variables. Initial analyses found no significant relations between parental involvement, parental depression, and child language scores. In future analyses we will explore whether sociodemographic factors might explain our null findings.

HRV Analysis Training & Statistical Reviewing

Name: Aushanae Haller
Year of Graduation: 2023
SURF Advisor(s): Nnamdi Pole, Psychology
Field of Study: Psychology
Co-Authors:

Title: HRV Analysis Training & Statistical Reviewing

Abstract: Heart Rate Variability (HRV) is a measure of stress resilience, associated with positive health and mental health outcomes. This summer I worked with Professor Nnamdi Pole in HRV Software training, to prepare for the analysis of a dataset consisting of beat-by-beat heart rate data collected on Five College students, whom participated in a three-hour intervention aimed at teaching them to manage difficult conversations about sociopolitical topics. In the training I learned how to synchronize the dataset so that each participant's data is aligned in time and how to inspect the data for errors and statistical outliers.

In addition to this primary project, I devoted part of my SURF time assisting Professor Pole with his Associate Editor work. I specifically provided statistical reviews focused on critiquing data analysis practices, data reporting, and data visualization. I wrote point by point reviews that were incorporated into Professor Pole's decision letters at the end of peer review.

The Effects of Zoom Self-View Distraction on Daily Self-Objectification and Well-Being

Name: Jessica Pardim Araujo
Year of Graduation: 2023
SURF Advisor(s): Randi Garcia, Psychology
Field of Study: Psychology
Co-Authors: Randi L. Garcia, Jessica Pardim Araujo, Pamela Kramer and Sarah Bingham

Title: The Effects of Zoom Self-View Distraction on Daily Self-Objectification and Well-Being

Abstract: Self-objectification is defined as internalizing others' views on one's body and seeing oneself as a body or an object (Fredrickson and Roberts, 1997). Recent research has found that higher self-objectification leads to spending more time looking at oneself on video calls and showing less satisfaction with their body and facial features (Pfund et al., 2020; Ratan et al., 2022). Additionally, mirror anxiety–anxiety experienced due to prolonged self-focused attention has been shown as a reason for more Zoom fatigue in women (Fauville et al., 2021). The present research examined if daily Zoom use, specifically, distraction due to seeing one's self on Zoom, increased the state of self-objectification among college-aged young women. Additionally, the study tested if self-objectification was related to daily well-being variables such as state self-esteem, mental fatigue, and cognitive functioning.
The study concluded that using the hide self-view features on zoom and being less distracted by one's own image can decrease self-objectification. In addition, self-objectification can lead to higher mental fatigue and negative feelings throughout the day.

Resilience, race, and sexual orientation as predictors of posttraumatic growth in college students during the COVID-19 pandemic

Name: Kristin Cirulli
Year of Graduation: 2023
SURF Advisor(s): Nnamdi Pole, Psychology
Field of Study: Psychology
Co-Authors:

Title: Resilience, race, and sexual orientation as predictors of posttraumatic growth in college students during the COVID-19 pandemic

Abstract: I have spent this summer exploring the psychological effects of COVID-19 on college students. I reviewed hundreds of articles about how COVID-19 interacts with race, gender, sexual orientation, social class, adverse mental health, resilience, posttraumatic growth, among many other topics. After reviewing this literature, I have chosen to further explore how psychological resilience and posttraumatic growth (PTG) are prevalent in the lives of college women with marginalized and intersecting identities during the COVID-19 pandemic. It is no secret that the pandemic has challenged society tremendously and affected the lives of everyone, however it has impacted some demographics more than others, including women and marginalized racial communities. We are also interested in how COVID-19 has affected the LGBTQ community, however this area is not yet well-researched. Though COVID-19 has had many adverse outcomes, psychological resilience can be a protective factor and PTG can be a positive outcome. PTG is a meaningful psychological change that occurs as a result of facing adversity (Tedeschi & Calhoun, 2004), while resilience is more of a trait that one might already possess which allows them to return back to normal following adversity (Herman et al., 2011). The present study aims to assess the relationship between resilience and PTG especially within marginalized racial communities. Prior research has observed increased levels of resilience in Black (Campbell-Sills et al., 2009), Asian (Raghavan et al., 2019), and Latinx participants (Morgan Consoli et al., 2015). Additional research has shown posttraumatic growth in the Asian American community amidst this pandemic (Kiang et al., 2022). Data from a COVID-19 wellness survey for Smith College students will be used to assess the relationship between resilience and PTG during COVID-19. Exploratory analysis of the dataset showed that the sample was fairly representative of race with the majority of participants being white. However, this sample is unique in that the majority of participants identify as non-heterosexual. We predict that non-white participants will have higher resilience scores and will experience more PTG as a result of the COVID-19 pandemic. We are unable to make predictions about the LGBTQ community's survey responses due to the lack of literature, but this study will serve as a means of assessing pre-COVID resilience and post-COVID growth.

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2022 Summer Research Abstract

Name: Anne-Marie Martin
Year of Graduation: 2025
SURF Advisor(s): Alexandra Strom, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: 2022 Summer Research Abstract

Abstract: For the first half of this summer, I worked on synthesizing sulfonamides by reacting an amine with tosyl chloride in a solvent solution of DCM and triethylamine or pyridine. I was able to successfully synthesize five sulfonamides and I was able to get a large percent yield in my synthesis of N-tosyl-p-toluidine, N(p-methoxybenzyl)sulfonamide, and N-benzyl-p-tolusulfonamide. I found that I was able to produce a higher percent yield when I used triethylamine as the base rather than pyridine, and there could be multiple reasons as to why that is. The sulfonamides that I produced were used by a fellow student in the lab, Christine Wu, who was working on testing the sulfonamides. She was reacting the sulfonamides I produced with different ketones to find evidence of the amination reaction. For the second half of the summer, I worked on synthesizing benzyl ketones using a two-step process where I used the benzyl Grignard reagent to produce alcohol from an aldehyde and then oxidized the alcohol using DMP. I will be continuing these experiments this academic year.

A Divide & Concur Approach to Collaborative Goal Modeling with Merge in Early-RE

Name: Kathleen Hablutzel
Year of Graduation: 2023
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: A Divide & Concur Approach to Collaborative Goal Modeling with Merge in Early-RE
Abstract: Student worked to finalize manuscript and prepare for publication at the 30th IEEE International Requirements Engineering 2022 conference of the paper ""A Divide & Concur Approach to Collaborative Goal Modeling with Merge in Early-RE"": Goal modeling enables the elicitation of stakeholders' intentionality in the earlier stages of a project. Often, approaches are limited by the effort required to create an initial goal model. In this paper, we investigate the problem of model merging for Tropos goal models. Specifically, we propose a formal approach to the problem of automatically merging the attributes of intentions and actors, once these elements have been matched. Additionally, recent approaches have investigated answering questions about future evolutions of stakeholders' projects with goal models. In this work we consider both static models, as well as those with timing information, using the principles of gullibility, contradiction, and consensus. We study our implementation and validate the merge operation on a variety of models from the literature.

Examining the influence of Sonic Hedgehog on Forebrain Development and Cranial Neural Crest Cell Migration

Name: Nalini Oliver
Year of Graduation: 2023
SURF Advisor(s): Michael Barresi, Biological Sciences
Field of Study: Developmental Biology and Neuroscience
Co-Authors: Nadia Penkoff Lidbeck

Title: Examining the influence of Sonic Hedgehog on Forebrain Development and Cranial Neural Crest Cell Migration

Abstract: Neural crest cells (NCCs) are a neural progenitor cell type that typically contribute to structures of the peripheral nervous system (PNS). After the neural tube closes, NCCs delaminate and differentiate into a variety of subtypes, including trunk, sacral, vagal, and cranial neural crest cells. While cranial neural crest cells (CNCCs) have been known to contribute to craniofacial structures, recent work within our lab has found that a small stream of CNCCs migrate anteriorly back into the forebrain by tracking this cell type with the marker Sox10. Our work within the lab this summer has sought to continue the thesis work of Nadia PenkoffLidbeck over the past year. This includes determining what may be guiding the migration of CNCCs into the forebrain and the effect this guidance cue may have on other structures within this region. One candidate that was investigated was the chemoattractant known as Sonic hedgehog (Shha). The effect of this morphogen was evaluated in two ways: through overexpression of Shha through heatshock of our Tg(hsp701:shha-EGFP) line and by repressing Smoothened, a G-protein coupled receptor that is activated when Shha is expressed, through treatment with Cyclopamine on wild type embryos. These embryos were treated at 10 hours post fertilization (hpf) (when NCCs begin to migrate out of the neural tube) and 15 hpf (during CNCC migration into the midbrain). Along with looking at changes to CNCC presence, we evaluated the effect this would have on broader forebrain development by looking at its principal structures, the anterior and post-optic commissures. This includes the glial bridge substrate that is initially formed, and the migratory axons that cross the midline to connect the two hemispheres of the forebrain. We visualized CNCCs, glial bridge formation, and commissural axons at 22 hpf and 28 hpf through immunohistochemical labeling, which were then imaged on the confocal. Moreover, we visualized the population of CNCCs that are responsive to Shha. This was achieved by performing hybridization chain reaction (HCR) to label for Sox10 as well as the receptor for Shha, patched-2 (ptch2). This was imaged on both the MuVI light sheet microscope as well as the confocal. These samples were also further processed through cryosectioning, which was also imaged on the confocal.

Characterizing meteorin and meteorin-like expression using a Danio rerio model

Name: Lillian Mearsheimer
Year of Graduation: 2025
SURF Advisor(s): Michael Barresi, Biological Sciences
Field of Study: Developmental Biology
Co-Authors: Shariqa Shaila

Title: Characterizing meteorin and meteorin-like expression using a Danio rerio model

Abstract: There is evidence that suggests that meteorin (metrn) and meteorin-like (metrnl) proteins play a role in cell differentiation, development and proliferation in the central nervous system (CNS). Studying expression of metrn and metrnl genes might help us understand how different types of neural stem cells, such as radial glia, are guided to differentiate and develop in order to form the matured CNS. Radial glial cells are extremely important to the formation of the brain, and there is consensus that some brian tumors originate from these cells. The reality, however, is that not much is known about radial glial cells and even less is known about their potential regulators, metrn and metrnl. Metrn is a secreted protein that has been found to influence the formation and differentiation of radial glial cells as well as contributing to axonal growth.

In this project, we attempted to characterize the expression of metrn and metrnl by utilizing a Danio rerio model. Zebrafish (Danio rerio) is a model organism to study as it is a vertebrate which shares a high percentage of genetic similarity with humans, and as its embryos are nearly transparent, making it easier to observe. To characterize the expression of metrn and metrnl, we carried out a technique known as Hybridization Chain Reaction (HCR) which fluorescently tags mRNAs coding for metrn and metrnl. This allowed us to image patterns of metrn and metrnl expression on the laser-scanning confocal microscope. One challenge we ran into was finding the optimum microscopy settings to visualize the metrn expression so this is something we hope to refine in our work further beyond SURF.

We also attempted to characterize loss of metrn and metrnl functions by using zebrafish that were injected with CRISPR guide RNAs. The injections were intended to target different locations in the DNA promoter region upstream of the metrn gene so as to disrupt the metrn expression. The idea was that if the injections were successful, the off-springs of the injected zebrafish would be lacking the metrn gene in the targeted DNA segment. To explore this, we mated several pairs of injected fish and then genotyped their embryos. After genotyping, we carried out gel electrophoresis to screen for whether any or what percentage of embryos showed mutations (unexpected band pattern compared to wildtype zebrafish DNA). An overarching goal for this experiment was to identify founder parents: injected zebrafish whose mutation successfully occurred at germline and has the ability to produce offsprings that carry the same metrn knock-out mutation). After repeated screening of tens of pairs of zebrafish, we are hopeful to have found one promising founder pair. The off-springs of this founder pair can be further studied for the effect of loss of function in future lab projects.

Assess Motility at 37°C & 23 °C on Various strains: K-12, UPEC in wt, and ΔrpoS Mutants

Name: Asmae Lichir
Year of Graduation: 2024
SURF Advisor(s): Christine White-Ziegler, Biological Sciences
Field of Study: Microbiology
Co-Authors:

Title: Assess Motility at 37°C & 23 °C on Various strains: K-12, UPEC in wt, and ΔrpoS Mutants

Abstract: When a microbe, such as pathogenic E. coli, infects a human host, its temperature rises to 37°C. Changes in this upshift from room temperature to human body temperatures in nonpathogenic E. coli strains demonstrate that human temperature increase motility. My project broadened this finding to investigate how temperature and the global regulator RpoS impact motility in u CFT073 strains compared to the nonpathogen. This pathogenic bacterium is the most common cause of acquired urinary tract infections. To complete my experiments, I used a motility assay that reduces the amount of agar in the medium so that bacterial swimming can be measured. On high-energy LB media, motility was found to be greater at 37°C than at 23°C for both the Uropathogen and the nonpathogen. The Uropathogenic showed lower motility in comparison to the nonpathogen at both temperatures. RpoS is known to increase motility in the nonpathogen. Our results with the ΔrpoS CFT073 strain reveal that deletion of this gene increases the microorganism's motility at 23°C without affecting its growth. The CFT073 ΔrpoS mutants are more motile than the CFT073 wild-type strain (time = 12 to 16 hours). CFT073 rpoS mutant move faster than CFT073 wild-type strains (time = 12 to 16 hours). In contrast to the MG1655 K-12 ΔrpoS mutant strain where the deletion of the rpoS gene improved cell motility without reducing cell growth. It has lower intrinsic motility than the wild-type UPEC strain (at 37 °C and 23 °C, respectively. My study is significant because evaluating the gene expression signals of these pathogens at different temperatures leads to new findings that lead to a better understanding of how pathogenic bacteria vary their motility. In addition, these findings might lead to new anti-infective chemotherapeutic medications or microbial disinfection targets.

Creating a bioinformatics pipeline to distinguish differentially expressed gene pathways in pathogenic E. coli under varying human host environmental growth conditions

Name: Melissa Bolick
Year of Graduation: 2022
SURF Advisor(s): Christine White-Ziegler, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Creating a bioinformatics pipeline to distinguish differentially expressed gene pathways in pathogenic E. coli under varying human host environmental growth conditions

Abstract: We in the White-Ziegler lab study gene expression in model disease-causing Escherichia coli strains to discover the adaptations they employ in different environments. I studied a specific enteropathogenic strain that causes diarrhea, particularly of concern for children in developing countries, E. coli 0127:H6 strain E2348/69 (EPEC). EPEC experiences changing environmental conditions as it moves through the gastrointestinal tract with virulence characteristics that differentiate it from other strains. Studying this organism is a multi-step collaborative project that began with growth experiments and the isolation of RNA (a skill I also developed during this project with a urinary pathogenic strain). These RNA samples were then sequenced via a next-generation sequencing technique, RNA-seq, producing a complete file of all RNA present in a sample called a transcriptome. My research began with these data wherein I created a bioinformatics pipeline to quality control, compare, and ultimately map these RNA data to represent the relative expression genes and therefore expressed proteins in each sample.

The transcriptomes that I studied were generated by another lab member, Nhi Van, who grew EPEC in varying pH and temperature conditions alongside a Δhfq mutant (an RNA chaperone involved in stress response). While comparing gene expression across different growth environments, it is important to account for differences that could be because of non-biological variations between experimental conditions, known as batch effects. The primary assessment of these batch effects was via Principal Component Analysis Plots before and after normalization using the limma package in R. I determined we could make comparisons changing a single variable, but not multiple. I could compare changes in pH or changes in temperature with our data, but not both together based on our experimental design. Comparing pH was of greatest interest because, over the course of the disease state, the gastrointestinal tract drops from a pH of about 7.5 in the ileum of the small intestine to around 5.5 in the caecum of the large intestine. I selected data from growth experiments that represented these different environments. Subsequently, I performed a gene set enrichment analysis of named gene outputs tagged by Rockhopper using the ClusterProfiler package in R. Key differentially expressed pathways between pH 7.5 and 5.5 emerged in the generation of metabolic and energy precursors, RNA binding, and carbohydrate derivative biosynthetic processes. These results suggest that, in the 37°C host environment, environmental pH may influence gene expression, accounting for EPEC's proliferation in the gastrointestinal tract.

Bacterial microbiome variation across body part and symbiotic state in a cnidarian model

Name: Kaylin Curtis
Year of Graduation: 2023
SURF Advisor(s): Rachel Wright, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Bacterial microbiome variation across body part and symbiotic state in a cnidarian model

Abstract: Exaiptasia diaphana is a popular model organism for exploring the symbiotic relationship observed between cnidarians and their microsymbionts. While physiological roles of algal photosymbionts (Symbiodinaceae) are well studied, the contributions of bacterial communities are less defined in this system. We investigated microbial variation between distinct parts of the body and symbiotic state across four genets held in identical environmental conditions using 16s rRNA gene amplicon sequencing. We found differentially abundant taxa between body part and symbiotic state that highlight the roles these bacteria may play in holobiont heterotrophy and nutrient cycling. Beta-diversity analysis revealed distinct communities between symbiotic states consistent with previous studies; however, we did not observe the presence of previously reported core microbiota. We also found community differences across clonal lines, despite years of identical rearing conditions. These findings suggest the Exaiptasia bacterial microbiome is greatly influenced by host genetics.","My funding was split between two sources which felt overly complicated and hard to track. Perhaps unavoidable, but being a low-income student off-campus and having the extra burden of time tracking and being taxed when my peers weren't was difficult. "
Zhixin,Liao,,2023,"Sharon Owino, Neuroscience",,Neuroscience,Yuqi Wang,https://www.jotform.com/uploads/SmithCollegeSURF/221873834409159/5384715151122605676/Z Liao_SURF2022Image.png,Characterization of Zebrafish GPR37 Paralogs in Early Development,"   G Protein-Coupled Receptor 37 (GPR37) is an orphan transmembrane receptor highly expressed in oligodendrocytes and retinal Müller glia cells (Roesch et al., 2008; Karlsson et al., 2021). Although previous studies have established a role for GPR37 in oligodendrocyte maturation and protection against demyelination (Yang et al., 2016), its expression in early development and functional role in Müller glia remain largely unknown. It is noteworthy that recent research has discovered that zebrafish Müller glia can be reprogrammed to progenitor cells upon injury, and migrate to the site of injury to regenerate damaged neurons (Powell et al., 2016). This discovery makes zebrafish an exciting new model for studying regeneration. However, little is known about GPR37 in zebrafish and its expression has not yet been characterized.

Cont. Bacterial microbiome variation across body part and symbiotic state in a cnidarian model

This project characterized the expression of GPR37 mRNA in zebrafish early embryonic development with hybridization chain reaction RNA-in situ hybridization (HCR RNA-FISH) and began expression quantification using real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR). Some preliminary results regarding the two paralogs of gpr37 in zebrafish, gpr37a and gpr37b, have been attained. Specifically, gpr37a is only detected in the periphery of the brain at 1 day post fertilization (dpf). Starting from 2 dpf, gpr37a expression diminishes in the brain and is only detected in the inner nuclear layer (INL) and ciliary marginal zone (CMZ) of the retina, colocalizing with the Müller cell marker gfap-GFP. This expression sustains through the first six days and until adulthood. Gp37b, on the other hand, has not only been found in the retina, but also in the brain in early development. It is found in the retinal ganglion cell layer (GCL) in addition to INL and CMZ, but have little coexpression with gpr37a. As for in the brain, it is ubiquitously expressed in the forebrain, midbrain, and hindbrain but downregulated starting at 4 dpf.

Since GPR37 is known to mediate glial cells' injury response (McCrary et al., 2019), and Müller glia repairs injury through dedifferentiation, future experiments may be designed to determine the role of gpr37a in retinal regeneration via morpholino knockdown. GPR37's potential role in Müller cell-mediated injury repair may provide novel insight into regenerative therapies.

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Characterization of Zebrafish GPR37 Paralogs in Early Development

Name: Yuqi Wang
Year of Graduation: 2024
SURF Advisor(s): Sharon Owino, Neuroscience
Field of Study: Neuroscience
Co-Authors: Zhixin Liao

Title: Characterization of Zebrafish GPR37 Paralogs in Early Development

Abstract: G Protein-Coupled Receptor 37 (GPR37) is an orphan transmembrane receptor highly expressed in oligodendrocytes and retinal Müller glia cells (Roesch et al., 2008; Karlsson et al., 2021). Although previous studies have established a role for GPR37 in oligodendrocyte maturation and protection against demyelination (Yang et al., 2016), its expression in early development and functional role in Müller glia remain largely unknown. It is noteworthy that recent research has discovered that zebrafish Müller glia can be reprogrammed to progenitor cells upon injury, and migrate to the site of injury to regenerate damaged neurons (Powell et al., 2016). This discovery makes zebrafish an exciting new model for studying regeneration. However, little is known about GPR37 in zebrafish and its expression has not yet been characterized.

This project characterized the expression of GPR37 mRNA in zebrafish early embryonic development with hybridization chain reaction RNA-in situ hybridization (HCR RNA-FISH) and began expression quantification using real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR). Some preliminary results regarding the two paralogs of gpr37 in zebrafish, gpr37a and gpr37b, have been attained. Specifically, gpr37a is only detected in the periphery of the brain at 1 day post fertilization (dpf). Starting from 2 dpf, gpr37a expression diminishes in the brain and is only detected in the inner nuclear layer (INL) and ciliary marginal zone (CMZ) of the retina, colocalizing with the Müller cell marker gfap-GFP. This expression sustains through the first six days and until adulthood. Gp37b, on the other hand, has not only been found in the retina, but also in the brain in early development. It is found in the retinal ganglion cell layer (GCL) in addition to INL and CMZ, but have little coexpression with gpr37a. As for in the brain, it is ubiquitously expressed in the forebrain, midbrain, and hindbrain but downregulated starting at 4 dpf.

Since GPR37 is known to mediate glial cells' injury response (McCrary et al., 2019), and Müller glia repairs injury through dedifferentiation, future experiments may be designed to determine the role of gpr37a in retinal regeneration via morpholino knockdown. GPR37's potential role in Müller cell-mediated injury repair may provide novel insight into regenerative therapies.

Horizontal Gene Transfer of Carbon Fixation Pathways in the Chloroflexi Phylum

Name: Camille Wenick
Year of Graduation: 2025
SURF Advisor(s): Luce Ward, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Horizontal Gene Transfer of Carbon Fixation Pathways in the Chloroflexi Phylum

Abstract: Although the process of carbon fixation is the foundation for all life on Earth, the evolutionary histories of different carbon-fixing metabolic pathways are poorly understood. This summer's research harnesses recent advancements in phylogenetics and comparative genomics to unravel these histories, establishing a basis for multiple future publications.

In the absence of a useful fossil record to directly observe ancient prokaryotic organisms, modern methodologies focus on genetic analysis of extant species to reconstruct their ancestors' stories, comparing closely related species against each other to construct phylogenetic models that loosely estimate when and how these species diverged. The 16S rRNA amplicon sequence data processed during SURF, obtained from a richly diverse test site in New Zealand, proved particularly promising within the Chloroflexi phylum: the phylum is known for its diverse metabolic capabilities, and various Chloroflexi are capable of surviving as anoxygenic photosynthesizers, photoheterotrophs, and/ or mixotrophs using multiple different carbon fixation pathways. One upcoming manuscript will focus on defining newly discovered Chloroflexi draft genomes, with particular focus on which species are able to use the globally dominant Calvin-Benson-Bassham cycle to fix carbon and which organisms rely on the less common 3-hydroxypropionate bi-cycle.

Additionally, increasingly efficient computational tools allow for the construction of similar phylogenetic models that target individual proteins and segments of genetic code. Juxtaposing these targeted phylogenetic trees with overall organismal trees offers clues to the diverse methods of genetic transfer available to prokaryotes: in particular, vertical inheritance from parent to child follows different patterns than horizontal gene transfer (HGT), which is lateral and can cross borders between species. Recent publications have provided substantial evidence for HGT of proteins essential to carbon fixation, including the HGT-enabled origin of oxygenic photosynthesis in Cyanobacteria (Soo et al. 2017), indicating that lateral transfer may be a driving mechanism behind bacterial metabolic evolution. Analysis of the extensive genetic information of the bacteria sampled at the New Zealand site, including the newly discovered Chloroflexi taxa, clearly displays patterns of HGT in several trees for proteins that mediate carbon fixation. This discovery adds to the emerging understanding of HGT's role in biological innovation; a second manuscript will build on the Chloroflexi taxonomy paper to explore the histories of transfer within the phylum, placing them within a larger ecological framework that interprets the prevalence of different carbon fixation pathways over time.

RNAi of Aedes polynesiensis Clock Genes

Name: Zhuoxi Ye
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: RNAi of Aedes polynesiensis Clock Genes

Abstract: The Williams lab studies neglected tropical diseases (NTDs), which cause substantial illnesses (often resulting in physical and cognitive development impairment) in developing countries in tropical regions. Prior studies have shown that mosquitoes' feeding behavior is determined and operated by circadian rhythms, a transcriptional and translational feedback loop consisting of multiple genes. We hypothesize that disrupting the circadian cycle of feeding could reduce the transmission of parasitic infectious diseases they transmit. (Takekata et al. 2021) Previous work on this project targeted three circadian rhythm genes: clk, cyc, and cry 1, using RNAi on cell lines (U4.4 and C6/36), and the combination of clk and U4.4 showed the most promising results. (Roberts et al. 2017) My main focus over the summer was to run real-time PCR samples from the Spring semester and optimize the transfection results by focusing on one clock gene with one cell line. Based on the results from the Spring, we decided that: 1. Clk and U4.4 cell line showed the most significant and consistent results probably since U4.4 is DICER competent. 2. While doing the real-time PCR, in order to establish a standard amount of starting material, the amount of RNA put into cDNA synthesis for real-time PCR should be calculated and standardized. 3. Smaller cell concentration and greater amount of dsRNA yielded better results. (Altinli et al. 2022) With all the observations and researching the literature, I decided to try another round of transfection with two new dsRNA amounts and a cell concentration of 1×10^5. The results are shown in the two images below. The results were significant, however, the number of cells transfected was low, which means that further optimization is needed with the transfection step. This fall, I am planning to continue my project with clock genes, perhaps incorporating other transfection methods to yield more dramatic changes in gene expression.

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Effects of the co-expression of GPR3,6, and 12 with Amyloid Precursor Protein

Name: Sabra Mouhi
Year of Graduation: 2023
SURF Advisor(s): Sharon Owino, Neuroscience
Field of Study: Neuroscience
Co-Authors:

Title: Effects of the co-expression of GPR3,6, and 12 with Amyloid Precursor Protein

Abstract: Alzheimer's disease (AD) is a neurodegenerative disease and the most common form of dementia. One of its defining elements is the accumulation of amyloid beta peptides in plaques, through the deleterious processing of Amyloid Precursor Protein (APP). The goal of our study was to understand the molecular elements responsible for regulating APP cleavage, such as G protein-coupled receptor (GPCR) signaling.

The honors thesis of Jessie G. Jiang from Emory university, entitled "Amyloid Precursor Protein Regulation by G Protein-Coupled Receptor 12", served as a preliminary study that shaped the design of our experiments. Jessie was able to show that GPR12 was able to induce APP dimerization, a unique effect of GPR12 that enables two APP molecules to be joined together, forming a dimer. However, we decided to assess the effect of GPR3, GPR6, and GPR12 on APP expression levels and its dimerization. We chose to work with all three receptors because they are a group of highly similar orphan receptors, that don't have a known ligand (Laun S, 2018).

We primarily used a HEK293T cell line, which we regularly transfected with the three receptor constructs (GPR3, GPR6, and GPR12) as well as an HA-tagged APP construct in variable concentrations. The transfection was done using the Fugene 6 transfection reagent. Forty-eight hours post-transfection, the lysates of the transfected cells were collected before doing a western blot, which allowed us to identify the molecular weights of the proteins present in the lysates using specific antibodies. These studies allowed us to directly analyze the effect of the co-expression of each receptor construct with APP and revealed that APP expression levels were significantly higher when co-expressed with each GPCR. Interestingly, we also observed the appearance of an additional band of APP which could correspond to a protein dimer. Further studies would be needed to confirm true dimerization since western blotting detects the denatured form of the protein.

The increase of APP levels, however, is not specific to GPCRs alone, but can also be due to cAMP activity which occurs independently from GPCR signaling. To test for this in our assay, we opted to use a forskolin treatment. Forskolin increases intracellular cAMP levels and analyzing its western blot allows us to evaluate the difference between cAMP activity alone and GPR3, 6, and 12 regulation on APP. This was further analyzed using a luciferase signaling assay.

In general, over the summer we worked on optimizing various molecular techniques such as cell transfection and maxi prepping for plasmid extraction. We hope to continue with our experiments this fall and do more data analysis.

Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Name: Anna Peel
Year of Graduation: 2022
SURF Advisor(s): Benita Jackson, Psychology
Field of Study: Psychology
Co-Authors: Benita Jackson, Maya Kiernan, Leyla Akin, Uzma Malik, Lana Sabbah

Title: Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Abstract: Studies show that even brief time in settings with nature (e.g., a park) increases cognitive function, compared to similar time spent with less nature-based elements (e.g., buildings; Nisbet & Zelenski, 2011). One important predictor of cognitive function that, to our knowledge, has yet to be linked to exposure to nature is psychological flexibility. Arguably a critical key common pathway to mental and physical health (Kashdan & Rottenberg, 2010), psychological flexibility is a psychological characteristic holding promise as a potent point of intervention. For this project we sought to test for a unique association between nature exposure and psychological flexibility. Additionally, we identified potential pathways (e.g., time perspective), amplifiers (e.g., self-compassion), and dampeners (e.g., rumination) for the link between nature exposure and psychological flexibility, should they exist. We designed two sets of empirical examinations: a correlational study to test initial associations, and an experimental study, to test a replication and extension Nisbet and Zelenski's (2011) research on nature exposure and cognition, in our version, focusing on psychological flexibility as the dependent variable. Our pilot correlational study drawing from data collected on a sample of college students Fall 2021 (N = 52) showed statistically significant negative correlations between exposure to nature and present fatalist time perspective (r = -.28, p = .042), the latter of which was also inversely associated with psychological flexibility (r = -.29, p = -.044). Relevant to our increasingly online world, building on these findings we will further investigate the effects of virtual exposure to natural and built environments on psychological flexibility and potential pathways linking them in a randomized control trial. We created, edited, and piloted a range of film clips of natural and built environments on campus as an experimental manipulation that we will test among students in the 2022-2023 school year. If such a link exists, this can lay groundwork for later intervention research testing the 'minimal nature dose' - including amount of time and type (in person v. virtual) - to boost psychological flexibility.

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Analyzing and Curating Deeply sequenced Loxodes genomes

Name: Emma Schumacher
Year of Graduation: 2023
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Analyzing and Curating Deeply sequenced Loxodes genomes

Abstract: Ciliates, a clade of single celled eukaryotes with cilia, have fascinating and complex genomes, with unique features like having two distinct nuclei, variable mating types (Maurer-Alcalá, 2018), and variable codon usage (Ying, 2017). Their genomes are very different from more well studied genomes, such as those of humans and yeast cells. Studying ciliate genomes is important because it allows us to explore new angles on how genes are organized and structured. My project looked at the sequencing results of the Loxodes genome, and attempted to analyze trends found there. By understanding this architecture, we hoped to better understand how Loxodes functioned and what their evolutionary relationship was with other organisms (Ying, 2019).

The first step in this project was to prepare the raw read sequences from the Loxodes genome to be analyzed. To do this, I trimmed them to remove primer sequences and assembled them into contigs, longer contiguous sequences. Then, I needed to verify the identity of the sequences. While we intended to sequence Loxodes only, when a sample is collected there are normally other organisms, like bacteria, that get caught in the mix. To verify the identity of my sequences, I used tools like HISAT2 and Barrnap to compare my reads and contigs to a Loxodes reference genome. The sequences that did not match well to my reference genome could be excluded from my data. I also used DFAST, dotplots, phylogenetic trees, Clustal omega, and sequence alignments to check the quality of my sequences. Tools like Clustal Omega and sequence alignment let me compare the sequences to each other and a reference sequence to see how closely related they were to each other. I also used geneious to evaluate how robust my sequences were.

Cont. Analyzing and Curating Deeply sequenced Loxodes genomes

This allowed me to filter some of our sequences from the Loxodes pool when they seemed to be unrelated to our target organism. I also began investigating trends in the sequences that seemed to be Loxodes, such as the relationship between their GC content, length, and coverage. To identify contaminants in our data, I also created codon usage bias plots that showed the distribution of GC content in my whole genome data through python scripts I wrote. Loxodes have a unique footprint, since their GC3 content tends to fall between 20-60% on a codon usage bias plot. Therefore, when we had data that was widely distributed or clustered somewhere else, we could assume it was a contaminant.

The assembly process took longer than I had anticipated, so in the future I would like to focus my efforts on doing more analysis of my now assembled sequences. My work this summer focused on familiarizing myself with my data and the tools I plan to use, familiarizing myself with prior research, and curating my data by repeating my process and removing unreliable sequences.

Figure 1: Codon usage plot from a deeply sequenced Loxodes genome. The typical fingerprint of GC content of Loxodes is on the left, between ~20-40%, while a likely contaminant seems to be on the right between 60-80%

Figure 2: Phylogenetic tree showing evolutionary distance between my deeply sequenced Loxodes genomes (all labeled LKH) and some references taken from Genbank.

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Development and Optimization of Diagnostic Assay for Sensitive Detection of Asian Schistosoma Species

Name: Yuezhi Gu
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Development and Optimization of Diagnostic Assay for Sensitive Detection of Asian Schistosoma Species

Abstract: S.japonicum and S.mekongi are the two important agents causing a Neglected Tropical Disease (NTD), Schistosomiasis, in Asian countries. The Kato-Katz technique, which makes use of a small spatula and slides to examine feces and count eggs, is the conventional method for diagnosing Schistosomiasis. However, the diagnosis using Kato-Katz lacks the specificity to distinguish between the infection by the S. japonicum and S. mekongi species. During the summer, I was working on optimizing a novel real-time polymerase chain reaction (RT-PCR) assay for the diagnosis of S. japonicum and S. mekongi species. Previous SAW lab students have worked on designing RT-PCR assays for both species. Though the assay is more sensitive than the conventional method, it still lacks the specificity to distinguish between S. japponicum and S. mekongi species. Our group hypothesized that the possible contributing factor to that amplification was because of the occurrence of hybridization between the two species. We next targeted a different sequence of the tandem repeats where the most variation occurs with the hope of finding an alternative method for diagnosing Schistosoma species in a specific and cost-efficient manner. The newly developed assay was tested with purified DNA samples on the sensitivity and specificity of the assay. Then, we were able to further validate the new assay and compared the results of the new assay with other published diagnostic assays on clinical samples. With the preliminary results on the clinical samples, we are planning to further explore possible reasons behind the differences in results on the clinical samples using my new assay with different qPCR assays in the coming academic year.

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Investigating the Biogeography of Arcellinida

Name: Amelia Babb
Year of Graduation: 2025
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Investigating the Biogeography of Arcellinida

Abstract: Arcellinida is an order of testate (shell building) amoebae, which can be identified morphologically by their different test or shell shapes, and by their pseudopods that can be seen emerging from the aperture of the test. Arcellinida live in freshwater environments such as freshwater bogs, and play an important ecological role in low pH bogs and fens. Arcellinida are also important bioindicators for both present and past environments, as their tests are preserved in the fossil record, providing information on past environments (Oliverio et at., 2015).

This summer I worked on a review paper focusing on the biogeography of Arcellinida. The goal of this review paper is to synthesize research and better determine global distribution patterns of Arcellinida, as well as the environmental influences affecting these patterns. Research on Arcellinida has been conducted globally, specifically in five key regions: Northeastern US, Canada, Brazil, China, and Europe. For this paper, I worked on the section focusing on the biogeography of Arcellinida in China. I reviewed literature in order to determine both the major genuses and species groups found in various parts of China, and environmental factors that influence Arcellinida distribution and community composition.

In addition, my contributions to the Amoeba Team consisted of working with the postdoctoral researcher Taylor Sehein to learn the current FISH (fluorescence in situ hybridization) protocol. After observing low fluorescence, we adapted the protocol by comparing 1µM vs 2µM probe concentrations and washing cells at 37°C and 46°C. The different probe concentrations showed no difference in labeling, but washing the cells at a lower temperature appeared to have better results (Figure 1). We observed the most successful labeling in Hyalosphenia elegans cells. In addition, we ordered a new Arcella FISH probe, and I learned about probe design.

During my 5 Week SURF I also gained many new wet work skills, such as cell picking and being trained in WTA and PCR. Along with other members of the lab, I went sample collecting at Hawley Bog in Whately, MA, and created plates using the moss from our samples. I continued plate husbandry, made microscope observations, and learned to identify testate amoeba commonly found in our samples. I worked on building my bioinformatics skills through participating in an R learning club with other students from the Katz Lab. I was also trained in PhyloToL (Ceron-Romero et al., 2019), the phylogenomic pipeline used in the Katzlab to run phylogenetic trees. My next steps for the fall semester will be to continue work on the Arcellinida biogeography review paper, as well as to continue improving the FISH protocol.

Figure 1: Hybridized Hyalosphenia elegans cell, the blue-green color is showing successful labeling.

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Exploring Foraminifera: Miliolids, Allogromia, and other hard-shelled forams

Name: Sri Tejasvi Kumaran
Year of Graduation: 2025
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Exploring Foraminifera: Miliolids, Allogromia, and other hard-shelled forams

Abstract: Foraminifera are single-celled microbial eukaryotes that belong to Rhizaria, a group within the SAR clade (Stramenopiles, Alveloates and Rhizaria). Foraminifera are largely testate organisms that can be identified by extensive pseudopodial networks that display bidirectional streaming (Sen Gupta 1999). This summer, I worked on different projects studying various kinds of foraminifera, e.g. Miliolids, Allogromia, and other forms that were calcareous or agglutinated.

Miliolids are a group of marine benthic foraminifera that are characterized by their porcelaneous tests with tubular chambers (Figure 1) (Pawlowski et al. 2013, Gupta et al. 2002). Over the course of the summer, I took a leadership role in maintaining and expanding the miliolid culture in the Katz Lab for further study. As the species and even genus of the miliolid is unknown, I worked to obtain high quality SEM (scanning electron microscope) images and WTAs (whole transcriptome amplifications) to aid in identifying them. For this, I tested several methods of preparing cells for the SEM that would preserve the morphological features of the miliolid calcite shell. I also attempted different treatments of fixing and freezing for obtaining good WTA results. In addition, I worked on staining miliolid DNA using Hoechst. In this process, I began developing a protocol for staining tailored to the miliolids, such as comparing different permeabilization agents and changing conditions to preserve the most cells.

Additionally, I helped with the Allogromia project, studying the life cycle and nuclear dynamics of Allogromia latocollaris through confocal and light microscopy, which other members of the Foram team in the Katz Lab were working on. In order to determine their life cycle and test for synchrony in CSH populations, we tracked individual isolated cells through multiple generations, recorded changes in their developmental stages and sizes, and in parallel, stained their nuclei and imaged them.

Cont. Exploring Foraminifera: Miliolids, Allogromia, and other hard-shelled

Lastly, collaborating with Adri Grow, a graduate student in the lab, I worked to develop a method for fixing "wild" foraminifera from field samples with calcareous or agglutinated tests, using glyoxal as a fixative, to prevent degradation of RNA during the WTA process. Much of this work was troubleshooting the procedure and testing various treatments, including altering proportions of reagents, changing the temperature and incubation times during the process, checking different pHs and testing using saltwater versus freshwater. No conclusion has been drawn so far, but we now have a better understanding of the reagents and how to proceed from here to test for the most optimal conditions.

Alongside working on these projects, I also gained some fieldwork experience by going on sampling trips to Hawley Bog in Massachusetts and a salt marsh in Madison, CT. Furthermore, I improved my wet lab work skills in picking cells, conducting PCRs through PCR trainings, and doing more WTAs. In addition to that, I also began to gain more exposure to bioinformatics through learning R and PhyloToL (Ceron-Romero et al. 2019).

Figure 1. SEM image of a Miliolid test. Miliolids were cleaned with a paintbrush, treated with three washes of 70% ethanol, and then air dried over two days. The samples were mounted using an eyelash onto an SEM mount and coated before imaging.

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Investigation of the Characteristics and Timeline of Macronuclear Development in the Ciliate Chilodonella uncinata

Name: Anna-Lee Thompson
Year of Graduation: 2025
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Investigation of the Characteristics and Timeline of Macronuclear Development in the Ciliate Chilodonella uncinata
Abstract: Ciliates are single-celled microeukaryotic organisms that are characterized by their nuclear dimorphism (i.e. the presence of both germline and somatic nuclei in each cell/organism; Ahsan et al, 2022). Our model organism, Chilodonella uncinata, is a ciliate within the class Phyllopharyngea that contains a transcriptionally inactive germline micronucleus and a functional somatic macronucleus (Maurer-Alcalá, 2018). Currently, many ciliates are known to undergo DNA deletion, scrambling (in some ciliates including C. uncinata), fragmentation, telomere addition, and amplification during macronuclear development.There is also evidence suggesting that there is an initial round of amplification in the beginning stages of development and a DNA poor stage following fragmentation in C. uncinata (Rodger honors thesis, 2017). To study the process of somatic development we stained the DNA of vegetative and post-conjugated cells using DAPI. After which, I visualized the cells using a confocal microscope to further characterize the nuclear architecture of C. uncinata macronuclei at different developmental stages. Additionally, we began experimenting with rDNA and telomere fluorescent in situ hybridization (FISH) probe staining methods.
This summer, I also developed procedures to fix C. uncinata using Glyoxal, a fixative that enables transcriptome analysis after staining. Within these experiments I determined which variation of Glyoxal works best for C. uncinata. In both marine and freshwater samples, I compared the effects of varying pH and concentration on cell morphology, heterochromatin structure, and ease of cell picking afterwards. Using Glyoxal, we will be able to combine microscopy and sequence data to study the gene expression corresponding to each stage of macronuclear development.
In addition, I also began working on another project that investigates symbiosis in single-celled wild-caught ciliates. I wrote protocols for and experimented with two total RNA isolation kits. I had some success with both kits and assessed their outputs using fragment analysis. Going forward, we now have a better understanding of which kit we should proceed with, and have begun preparations for next steps. Some of these include PCR and Sanger sequencing to verify the precedence of rDNA's and eventually amplification of total RNA preps.
Aside from my projects, I continued my literature review, improved lab skills (cell picking, culturing, molecular work, etc.), gained a better understanding of bioinformatics, and began learning how to create data visualizations using R. I also went on a research cruise off the coast of Connecticut with the McManus lab at the University of Connecticut. We collected community marine samples to be analyzed through metatranscriptomics and isolated single-cells to undergo whole transcriptome amplification.

Figure 1. Image of a DAPI stained C. uncinata cell post-conjugation. The more pigmented region is the new developing macronucleus.

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Fn3 therapeutic effect on MSLN positive cancer cells

Name: Wenjun Zhao
Year of Graduation: 2025
SURF Advisor(s): Sarah Moore, Engineering
Field of Study: Biochemistry
Co-Authors:

Title: Fn3 therapeutic effect on MSLN positive cancer cells

Abstract:
Mesothelin (MSLN) is a tumor-associated antigen that can be considered as a specific biomarker for targeted immunotherapy. MSLN is overexpressed on cancer cells, including ovarian, breast and pancreatic cancers, and interacts with CA125 (MUC16) for metastasis and proliferation. However, it is less expressed in healthy cells. In addition, the higher binding affinity protein Fn3 can selectively recognize and bind MSLN on cancer cell lines as a potential therapeutic tool. Moore lab has already engineered several variants of the fibronectin type III domain (Fn3) non-antibody protein and showed the protein can induce apoptosis to MSLN positive cancer cells. This summer we aimed to test pEThk-Fn3 5.3.2 and Fn3-RDG binding affinity and killing ability and tried to understand the mechanism of causing apoptosis.

Mouse anti-MSLN antibody (K1) and goat anti-mouse PE conjugate (PE) are used as positive controls to show MSLN expression by yellow fluorescence detection (flow cytometry). Binding assays are performed by setting 5.3.2 and RDG concentrations from 0.01 nM to 200 nM, followed by treatment with OVCAR-3,and KB3-1 cell lines respectively. An anti-his antibody with green fluorescence was treated as a secondary antibody to bind the his tag on the Fn3 protein. Samples were analyzed by flow cytometry and kailegraph. The results showed a Kd value of 78 for OVCAR-5.3.2 and 7 for KB3-1-5.3.2, both with high binding affinity and the binding level is in the range of 10^2 to 10^3. Also it was concluded that the RDG protein does not bind MSLN by doing background subtraction of the anti-his antibody.

Apoptosis is named as programmed cell death. Apoptosis assays were performed using cells only and Fn3 RDG as negative controls and treated with Mitomycin C (MMC), a chemotherapeutic agent that kills cells, as a positive control. After treatment with 5.3.2 protein in OVCAR-3 and KB3-1 cell lines for 48 h, the samples were analyzed by flow cytometry. Annexin V, green fluorescence, labeled with Alexa Fluor 488 (green) was used to stain phosphatidylserine (PS) to show the percentage of early apoptosis. Propidium iodide (PI) can also be stained for DNA to show necrosis. The results showed that mitomycin C resulted in 68% necrosis and 32% early apoptosis, and 90% viable cells for negative controls. However, the desired cytotoxic effect of 5.3.2 still needs to be obtained in the future.

SOA SOLVENT STUDIES

Name: Liangnuo Zhang
Year of Graduation: 2025
SURF Advisor(s): Andrew Burke, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: SOA SOLVENT STUDIES
Abstract: In Berke lab's previous research, the reaction environment for generating secondary organic aerosols (SOA) from organic aerosols (OA) has been investigated, in particular, ammonium sulfate in a complex solvation environment that consists of glyoxal and other alcohols forming imidazole-2- carboxaldehyde (IC) and biimidazole (BI). With an aim to further investigate the liquid-liquid phase separation (LLPS) system in SOA, my research focuses on unraveling the nitrogen-containing compounds' liquid–liquid phase separation (LLPS) and kinetics of brown carbon aerosol formation in more complicated solutions over time.

To better understand how the reaction could be influenced by ammonium compounds and alcohols, in this research, we mixed three components to build the alcoholic solvent systems: organic and inorganic ammonium compounds—including ammonium acetate, ammonium bicarbonate, ammonium carbonate, ammonium formate, ammonium oxalate, and ammonium dihydrogen phosphate—with diverse alcohols(methanol, 1-propanol, 2-propanol, 3-methyl-2-butanol) and glyoxal.

Techniques, including GC/MS, Mass spetrum, UV-Vis spectroscopy, and viscosity measurements, were used to identify products (IC and BI) and kinetics of reactions between glyoxal and ammonium compounds. FTIR was applied to explore the liquid-liquid phase separation in ammonium systems by the articulated straw coring analysis method. And Raman spectroscopy is left to be carried out in the future.

Ref:
Probing Liquid–Liquid Phase Separation in Secondary Organic Aerosol Mimicking Solutions Using Articulated Straws

Impact of Zooplankton Filter Feeding on Sunlight Inactivation of Viruses

Name: Jackie Wang
Year of Graduation: 2023
SURF Advisor(s): Niveen Ismail, Engineering
Field of Study: Environmental Engineering
Co-Authors: Hadeel Shwwa, Adeline Rickard

Title: Impact of Zooplankton Filter Feeding on Sunlight Inactivation of Viruses

Abstract: Rotifers, a filter-feeding zooplankton, are able to take up microbial pollutants in aquatic systems, such as viruses. While rotifers may ingest these pollutants, it is not certain whether the rotifers inactivate them through digestion or retain them in their bodies. Retention of viruses could lead to protection from sunlight disinfection which is a critical process to inactivate viruses. The main objective of this research was to quantify the impact of rotifer presence on sunlight disinfection of viruses.

For our month-long SURF, we conducted two types of experiments on the Ford Seasons Room balcony. For each experiment we used rotifer Brachionus plicatilis as a model organism and MS2 bacteriophage as a surrogate for human pathogenic viruses. The purpose of the first rooftop experiment was to confirm that the presence of rotifers impacts the rate of sunlight disinfection of viruses. We exposed various conditions as well as corresponding controls to 12 hours of sunlight. For each condition tested, we measured MS2 concentration as a function of solar irradiance. The purpose of the second rooftop experiment was to observe whether the bodies of the rotifers may also cause a shading effect for uningested MS2. We prepared beakers with live rotifer specimens and compared the decline of MS2 concentration with beakers containing dead rotifers. Similar to the first experiment, we measured MS2 concentration as a function of solar irradiance after exposing samples to sunlight for 12 hours.

The data we obtained was consistent with our hypothesis that rotifers do indeed take up MS2, and that the concentration of viable MS2 was higher in beakers that contained rotifers. These results indicate that rotifer presence results in a reduction of sunlight inactivation of viruses and can protect MS2 from sunlight inactivation. During fall semester we will continue to obtain data from saved samples from these experiments. We will be utilizing RT-qPCR to examine the viral RNA from the MS2 in samples that we froze this summer. We will also be working on publishing our results in peer-reviewed literature.

The results of this work will help inform the management of treatment wetlands in which sunlight disinfection is a critical process for inactivation of microbial pollutants. Treatment wetlands also often contain large densities of zooplankton which may impact the overall fate of microbial pollutants.

Title

Name: Emily Hafken
Year of Graduation: 2024
SURF Advisor(s): Julianna Tymoczko, Mathematics and Statistics
Field of Study: Mathematics
Co-Authors:

Title: The Geometry and Combinatorics of Springer Fibers
Abstract: Springer fibers are a topic of mathematical research that utilize aspects of linear algebra and combinatorics. Each Springer fiber is a set of matrices where there are certain linear conditions on the columns. We can easily calculate whether a matrix, or cell, is in a certain Springer fiber, but this process grows more time consuming as the size of the matrix increases. Thus, it is an important goal to find a way to determine the pieces of a Springer fiber without calculation.

One way to do this is to use arc diagrams made from words called balanced Yamanouchi words. A balanced Yamanouchi word of b's, m's, and t's is one where there is an equal number of each letter, and, from left to right, there must always be as many b's as there are m's and t's and as many m's as there are t's. For a linked word and matrix, each letter corresponds simultaneously to a variable in the matrix and to an arc in the diagram. Our goal is to describe entries in terms of crossing and nesting of arcs. This process has been proven to work for matrices with two blocks by the work of Goldwasser, Tymoczko, and Sun, and we have focused on discovering and proving how the same process works for matrices of three blocks too. However, as matrices increase in size and number of blocks, their entries increase in complexity, with some becoming expressions depending on multiple variables.

My primary work this summer has been to figure out exactly how these expressions connect to the arc behaviors in the corresponding diagrams. To this end, I generated a lot of data by calculating Springer cells with templates that I also worked to create. One example is shown below of a finished matrix. This collection of data enabled me to find the patterns that occur both in the diagrams and the entries of cells. From this process of analysis, I developed a theory that describes all of the observed expressions in a given matrix by connecting them to specific arc behaviors in the corresponding diagram. My theory is that every entry with an expression follows the same basic structure but is complicated by four rules. Each rule describes exactly how a specific behavior is represented in the expressions. So far, my theory has worked in every example we have done but is yet to be proven. ",

Effectiveness of RNAi Knockdown of Cactus and Caspar in A. albopictus

Name: Selin Kubali
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Effectiveness of RNAi Knockdown of Cactus and Caspar in A. albopictus

Abstract: This project is a continuation of honors student Rachel Pietrow's research on immunity genes in the mosquito species Aedes polynesiensis and Aedes albopictus. These species are vectors for multiple neglected tropical diseases (NTDs) such as dengue fever and lymphatic filariasis (Benedict et al. 2017, Richard and Cao-Lormeau 2019). Editing genes responsible for mosquito immunity may prevent the spread of these diseases by increasing immune activation against the pathogens that cause the disease. Mosquitoes do not have acquired immunity, but they do possess an innate immune system made up of four pathways. Knockdown of certain genes along these pathways can upregulate mosquitoes' immunity. An experiment in Aedes aegypti – a relative of A. polynesiensis and A. albopictus – measured the ability of these mosquitoes to transmit filarial nematodes such as Brugia malayi, which causes lymphatic filariasis, after immunity gene knockdown. When genes controlling the Toll, IMD, and JAK-STAT innate immunity pathways were knocked down, the mosquitoes hosted fewer transmissible B. malayi larvae (Edgerton et al. 2020).

Our project aims to use RNA interference (RNAi) to knock down the Cactus and Caspar genes, which are respectively located in the Toll and IMD pathways. RNAi regulates gene expression by binding to mRNA transcripts of expressed genes, leading to degradation of the transcripts. Two A. albopictus cell lines were transfected by Rachel with RNA that would interfere with either Cactus or Caspar expression. (Unfortunately, there is no A. polynesiensis cell line yet.) My part in the project this summer was to determine the results of the transfections. The ultimate goal was to measure how much the Cactus and Caspar genes were expressed in transfected wells compared to controls. I converted the mRNA transcripts in each transfected well to cDNA, and measured the amount of DNA present with quantitative PCR. Along the way, I realized some of my samples were contaminated with genomic DNA produced by the cell itself, rendering some data unusable. After I realized this, I cleaned each sample of gDNA and have not found contamination subsequently. I am hoping to collect more data this year, since it is difficult to draw conclusions from the current data. The difference in gene expression between Cactus-transfected wells and controls is slight, but the Caspar transfections seem to have consistent reduced expression. After collecting the remaining data, I will investigate whether transfections using CRISPR rather than RNAi will be more effective.

Citations
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Fate of Microbial Pollutants exposed to Zooplankton

Name: Hadeel Shwwa
Year of Graduation: 2024
SURF Advisor(s): Niveen Ismail, Engineering
Field of Study: Engineering
Co-Authors: Jackie Wang, Adeline Rickard

Title: Fate of Microbial Pollutants exposed to Zooplankton

Abstract: Rotifers, a filter-feeding zooplankton, are able to take up microbial pollutants in aquatic systems, such as viruses. While rotifers may ingest these pollutants, it is not certain whether the rotifers inactivate them through digestion or retain them in their bodies. Retention of viruses could lead to protection from sunlight disinfection which is a critical process to inactivate viruses. The main objective of this research was to quantify the impact of rotifer presence on sunlight disinfection of viruses.

For our month-long SURF, we conducted two types of experiments on the Ford Seasons Room balcony. For each experiment we used rotifer Brachionus plicatilis as a model organism and MS2 bacteriophage as a surrogate for human pathogenic viruses. The purpose of the first rooftop experiment was to confirm that the presence of rotifers impacts the rate of sunlight disinfection of viruses. We exposed various conditions as well as corresponding controls to 12 hours of sunlight. For each condition tested, we measured MS2 concentration as a function of solar irradiance. The purpose of the second rooftop experiment was to observe whether the bodies of the rotifers may also cause a shading effect for uningested MS2. We prepared beakers with live rotifer specimens and compared the decline of MS2 concentration with beakers containing dead rotifers. Similar to the first experiment, we measured MS2 concentration as a function of solar irradiance after exposing samples to sunlight for 12 hours.

The data we obtained was consistent with our hypothesis that rotifers do indeed take up MS2, and that the concentration of viable MS2 was higher in beakers that contained rotifers. These results indicate that rotifer presence results in a reduction of sunlight inactivation of viruses and can protect MS2 from sunlight inactivation. During fall semester we will continue to obtain data from saved samples from these experiments. We will be utilizing RT-qPCR to examine the viral RNA from the MS2 in samples that we froze this summer. We will also be working on publishing our results in peer-reviewed literature.

The results of this work will help inform the management of treatment wetlands in which sunlight disinfection is a critical process for inactivation of microbial pollutants. Treatment wetlands also often contain large densities of zooplankton which may impact the overall fate of microbial pollutants.

Building Story Generator

Name: Jingwen Xiang
Year of Graduation: 2024
SURF Advisor(s): Jamie Macbeth, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Building Story Generator

Abstract: Within our research group, we focused on building a story generator that can produce logical and interesting content. We used GPT3 to generate stories about modern life with an interleaving process, which aims to mitigate biases in complex decision-making environments.

In addition, we combined GPT3 with TALE-SPIN which is a story generator that produces Aesop- like fables in English. A TALE-SPIN story focuses on the main character who carries out plans to resolve some problems. The output may also be viewed as the narration of problem-solving procedures. A TALE-SPIN story begins with some characters and various facts about them, such as individual personalities and their relationships. The initial state of the world is often defined by the reader. To make the plot more interesting, various obstacles are introduced and the reader is asked to make decisions during the process of story generation. We did experiments with GPT3 by trying various inputs and prompts with TALE-SPIN's outputs, and there are two main output categories— embellishing stories and interleaving stories.

Engineering Protein-Drug Conjugates

Name: Sheher-Bano Ahmed
Year of Graduation: 2024
SURF Advisor(s): Sarah Moore, Engineering
Field of Study: Biology/Engineering
Co-Authors:

Title: Engineering Protein-Drug Conjugates

Abstract: The goal of this SURF was to produce a protein-drug conjugateThe goal of this SURF project was to create a protein that selectively binds to cancer biomarker mesothelin while incorporating a non-canonical amino acid to enable specific drug conjugation. This was a short-term goal in the process of eventually creating a protein-drug conjugate capable of performing targeted drug delivery in the body. A protein-drug conjugate is a therapeutic that selectively binds to specific tissues in the body. Such therapeutics can reduce harmful side effects caused by a drug acting on healthy tissue. The protein-drug conjugate that I worked on this summer uses a protein that binds to mesothelin receptors, which are overexpressed on cancer cells. The specific protein that I worked on was an engineered fibronectin protein (Fn3), which was modified to include an additional methionine at its N-terminal. Our hope was to use methionine auxotrophs to replace the methionine with the non-canonical amino acid azidohomoalanine. I am working to add a non-canonical amino acid called azidohomoalanine to the cancer-binding protein. The amino acid takes advantage of its azide group to react with alkynes through click chemistry reactions to attach a cancer drug. To make the protein-drug conjugate, I first worked with DNA to code for the desired protein. I have designed and inserted the appropriate gene into the appropriate plasmid using restriction and ligation enzymes. The plasmid was then transformed into colonies, and those colonies allowed to propagate in order to increase plasmid count. I have also tested several versions of transformed bacteria to find some that express the correct plasmid, using DNA sequencing.

Wettability of Polymer Films

Name: Kallie Fisher
Year of Graduation: 2024
SURF Advisor(s): Kate Queeney, Chemistry
Field of Study: Chemistry
Co-Authors: Elizabeth Rehwinkel

Title: Wettability of Polymer Films

Abstract: Our research focused on the wettability of polymer films deposited on surfaces with varying underlying surface chemistry. The larger goal of this research is to create surfaces that are reproducible, have tunable wettability, and display the same surface chemistry when the topography of the underlying substrate is changed. Because wettability impacts how biological entities like bacteria and eukaryotic cells interact with surfaces, control of surface wettability is critical to our ability to probe the molecular-level interactions that govern processes like biofilm nucleation and cell proliferation. Our specific goal for the summer was to explore whether and how we can use pH-dependent wettability measurements (dynamic contact angle goniometry) to probe for the appearance of certain functional groups at the surface of a polymer film.

Our model polymer is poly(allylamine hydrochloride) (PAH), which contains amine groups that are positively charged at low pH and neutral at high pH. The optimal deposition conditions for maximum PAH adsorption were determined experimentally. We adsorbed PAH onto two surfaces: the native silica layer of silicon substrates (hydrophilic) and surfaces prepared by silanization of silica surfaces with octyldimethylchlorosilane (hydrophobic). The resulting polymer films were characterized by ellipsometry and dynamic contact angle. The contact angle was initially measured manually, but we also developed a reproducible procedure to take measurements with an image capture system, accounting for droplet size-dependent variation in contact angle.

After PAH deposition, the contact angle of the hydrophilic surfaces increased, the contact angle of the hydrophobic surfaces decreased, and the ellipsometric thickness of both surfaces increased. To investigate the quantity of exposed amine groups on the polymer coated surfaces, we measured contact angles with buffered drops of different pH values. Since amine groups are neutral and therefore less hydrophilic at pH 9, contact angles measured at this pH would increase if there is sufficient density of surface amines. Since we found no observable pH-dependence of contact angle for a single layer of PAH on hydrophilic surfaces, we conclude that the electrostatic interactions between positively charged amine groups on PAH and negatively charged silanol groups on the surface reduce the number of amine groups free to interact with the buffered drops. Preliminary results suggest that there might be a pH-dependence for PAH on hydrophobic surfaces, where the amine groups on PAH do not tether the polymer to the (electrically neutral) surface.

Research regarding a single layer of PAH on hydrophobic silicon wafers will be continued in the Fall, and will hopefully yield more precise data on the pH-dependent wettability. Additional research in the Fall will investigate the pH-dependent wettability of alternating multilayers of PAH and poly(acrylic acid) (PAA) on hydrophilic silicon wafers.

Phenotypic plasticity of Littorina obtusata when exposed to Hemigrapsus

Name: Rosalind Lao-Brooks
Year of Graduation: 2023
SURF Advisor(s): L. David Smith, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Phenotypic plasticity of Littorina obtusata when exposed to Hemigrapsus sanuineus

Abstract: My summer SURF project consisted of two projects. In the first, I assisted with Maggie Stoffer's honors thesis project, where we examined the phenotypic plasticity of the snail Littorina obtusata in the presence of the invasive crab species Hemigrapsus sanuineus. We collected snails from both Massachusetts, where H.sanguineus has been observed, and Maine, where they have not. To mimic summertime temperatures at each location, half the Massachusetts snails and half the Maine snails went into one 14°C incubator (Maine temperature), while the rest went into a 19°C incubator (Massachusetts temperature). Snails were separated into replicate jars in incubators with three snails each per jar. A randomized half of the snail jars in each incubator received water that had been in a seawater aquarium that contained H.sanguineus (crab cue), while the other half of jars received seawater that had not been exposed to H.sanguineus. Overall, the goal was to see whether the presence of H.sanguineus in the water affected L.obtusata shell growth and whether background temperature or prior exposure to the crabs were important.. The snails were measured at the beginning of the experiment (a 10 week period), the middle, and are to be measured again at the end.
My independent project focused on gravid female H.sanguineus and how much of their total mass is devoted to their eggs versus their claws.   Claws are important tools for defense, feeding, and competition for both sexes, yet female H. sanguineus have relatively smaller claws than males. I wanted to see if energetic resources devoted to growing larger claws in males were instead put toward egg production in females. For the first set of measurements, I measured carapace width, claw length, claw height, claw depth, and total weight of the live crab. I repeated weight measurements three more times, while also measuring abdomen length and width. After this first set of measurements, every time a crab expelled her eggs, I would remeasure carapace length and width as well as her total weight. By subtracting the two weights I was able to determine the total mass of just the eggs. Overall I found that the average weight of the egg mass was 8.48% of the total body weight. I also sacrificed five still-gravid crabs to count subsets of their eggs. I weighed the subsets and then counted the individual eggs within each. On average, each egg weighed 0.00004426646563 grams. By separating the claws of the sacrificed crabs, I was also able to determine that the claws made up 4.16% of the total body weight of a gravid crab. Therefore, according to the calculations I have done so far, a gravid H.sanguineus devotes about twice as much mass to its eggs compared to its claws.

The Role of Habitual Physical Activity on Flow-Mediated Dilation in Healthy Peri-Menopausal People

Name: Tint Tha Ra Wun
Year of Graduation: 2024
SURF Advisor(s): Sarah Witkowski, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies, Biological Sciences, Statistics and Data Sciences
Co-Authors:

Title: The Role of Habitual Physical Activity on Flow-Mediated Dilation in Healthy Peri-Menopausal People

Abstract: The Role of Habitual Physical Activity on Flow-Mediated Dilation in Healthy Peri-Menopausal People,"I did my SURF project in the Vascular Function Research Lab in the Exercise and Sport Studies Department. I worked on different aspects of our study on how habitual physical activity affects symptoms related to the menopause transition and influences cardiovascular disease risks.
Perimenopause is characterized by variable menstrual cycle length, symptoms (e.g., hot flashes), and increased cardiovascular disease (CVD) risk. Endothelial dysfunction is an early CVD indicator assessed via flow-mediated dilation (FMD). High habitual physical activity (PA) is associated with enhanced endothelial health in various populations. However, the role of habitual PA on endothelial function during perimenopause remains unclear.
In this project, we investigated the differences in FMD between high- and low-active healthy perimenopausal people. I performed a literature review on FMD and physical activity analysis. My lab mates and I, along with Dr. Witkowski, recruited study participants who were healthy and peri-menopausal. The peri-menopausal status of participants was determined via the STRAW+10 criteria and the habitual PA level was scored using the International Physical Activity Questionnaire. We assessed their endothelial function via the brachial artery and used the data to measure the baseline diameter, peak diameter, absolute (mm) and relative (%) FMD response, and the shear rate stimulus. CVD risk factors (e.g., age, blood pressure, body mass index, cholesterol levels, glucose level) and FMD outcome variables were compared between high- and low-active groups using Mann Whitney U test, Shapiro-Wilk normality test, and two-tailed independent t-test. All the data analysis was performed in R studio software. We found that absolute FMD response was significantly higher in the high-PA group (high=0.17±0.14mm, low=0.11±0.08mm, p=0.01). No other outcome variables were significantly different between groups. Our preliminary results suggest that in healthy, peri-menopausal people, high habitual PA is related to greater absolute FMD. In this population, high habitual PA may be an important component for delaying endothelial dysfunction.
Furthermore, to test whether habitual physical activity is a strong predictor for FMD response, I performed stepwise backward regression for all FMD variables with CVD risk factors. To expand the list of CVD risk factors, I explored subjective- and objective- hot flash data using the FlashTrax Analysis software and objective- 7-day physical activity data using ActiLife software. I also searched methods to measure four sex hormones in participants for future analyses. Subsequent research will be continued via a McKinley pre-honors fellowship in Fall 2022 and my honor thesis project in Spring and Fall 2023.

Inclusive Streamers Through the Inclusive Design Lab

Name: Meredith Diamond
Year of Graduation: 2023
SURF Advisor(s): Johanna Brewer, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Inclusive Streamers Through the Inclusive Design Lab

Abstract: witch.tv is a streaming site where users can watch live streams of content creators playing their favorite games, participating in tournaments, or even just chatting with their audience. Streaming has become increasingly more popular with more people tuning in and more people streaming their own gameplay. Twitch provides a unique environment for viewers and streamers to interact and a platform with the potential to reach thousands. Twitch's chat feature can breed a group mindset or give viewers the opportunity to speak with others who have different experiences than their own. In the Inclusive Design Lab, I studied how Twitch streamers cultivate inclusive communities on their platforms.

Twitch is designed to encourage user interaction with the streamer and with other users. Besides the main screen displaying the content creator's stream, there is an additional window displaying "chat." Any user can type in chat where everyone else, including the streamer, can see. Because of this, many viewers form relationships with each other and pursue friendships outside of Twitch. How the streamer treats their community often shapes how the viewers react and interact with each other. I looked to study streamers whose communities were supportive, inclusive, and kind.

My area of focus was female streamers who play first person shooter games. I started my research by browsing Twitch to find streamers who fit those requirements with inclusive audiences. I spent time surveying the streamer and their chat to see how they interacted.I did not participate in chat so as not to influence the streamer's view of me when interviewing them. From there, I curated a list of streamers including information about their engagement style, their chat's environment, and methods of contacting them. Once I had a definite list, I began reaching out through email and Twitter DMs to ask for an interview. I set up times for interviews and then went over a carefully curated list of questions over Zoom call with them. After the interview finished, I transcribed it and began coding through the text for recurring themes.

Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Name: Caitlin Senni
Year of Graduation: 2023
SURF Advisor(s): Brianna McMillan, Psychology
Field of Study: Psychology
Co-Authors: Sarah Bradford, Lily Shannon, Vivian Almaraz

Title: Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes
Abstract: Parental involvement at-home and in the community correlates with higher child academic success (Byrant et al., 2000), but what about parental involvement in their child's school? Parental depression has a negative association with the amount that a parent reads to their child (Paulson et al., 2009). So is it possible that parental involvement in school-related activities is a mediator of the relationship between parental depression and child language outcomes? The goal of our study was to explore how parental involvement mediates the relationship between parental depression and child language outcomes in 3-5 year olds enrolled in Head Start programs.
Head Start is a program designed to provide quality care and early education for children from underprivileged backgrounds, specifically low-income families. Using the Center for Epidemiologic Studies Depression Scale (CES-D) to measure parental depression, the Peabody Picture Vocabulary Test (PPVT) to measure child language, and a checklist of school-based activities to measure parental involvement from the FACES 2019 dataset from the Head Start Family and Child Experiences Survey, we set out to create a mediation model (Figure 1). First, we hypothesized that higher levels of parental depression would be associated with lower child language scores. Second, we hypothesized that higher levels of parental depression would be associated with lower parental involvement in school activities. Third, we hypothesized that the relationship between parental involvement and child language scores would be mediated by parental depression. We measured the data by using a linear regression for each relationship between the variables. Initial analyses found no significant relations between parental involvement, parental depression, and child language scores. In future analyses we will explore whether sociodemographic factors might explain our null findings.

References:

Bryant, D., Peisner-Feinberg, E., & Miller-Johnson, S. (2000). Head Start parents' roles in the educational lives of their children. East Lansing, MI: National Center for Research on Teacher Learning.
Paulson, J.F., Keefe, H.A. and Leiferman, J.A. (2009), Early parental depression and child language development. Journal of Child Psychology and Psychiatry, 50: 254-262. https://doi.org/10.1111/j.1469-7610.2008.01973.x

Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes

Name: Sarah Bradford
Year of Graduation: 2023
SURF Advisor(s): Brianna McMillan, Psychology
Field of Study: Psychology
Co-Authors: Vivian Almarez, Lily Shannon, Caitlin Senni

Title: Examining How Parental School-based Involvement Mediates Relations between Parental Depression and Child Language Outcomes
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Paulson, J.F., Keefe, H.A. and Leiferman, J.A. (2009), Early parental depression and child language development. Journal of Child Psychology and Psychiatry, 50: 254-262. https://doi.org/10.1111/j.1469-7610.2008.01973.x

An LLM- and Script-Based Story Generator for Product Planning

Name: Kexin Zhao
Year of Graduation: 2024
SURF Advisor(s): Jamie Macbeth, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: An LLM- and Script-Based Story Generator for Product Planning

Abstract: In the topic of Large Language Models, one high-level research question is often asked: How can AI help counteract biases in complex decision-making environments and make exploration of a decision space more comprehensive and balanced? To explore this question, this summer we (Team with Professor Jamie C. Macbeth) explored how to make a system that generates fictional storied in natural language be a part of a toolset for de-biasing decision making. This project is a continuous one from previous years, and this summer we focused on improving algorithm, examining the result, and we also submitted a short paper about the project. First, we did experiments on different parameters to solve a non-responding issue, which is basically the story generator responding an empty blank instead of a continuous sentence for the story. After that, we tuned various parameters to achieve an optimized combination of parameters for the algorithm so in a sense the story being created is more comprehensible and understandable. Then, we optimized the process of saving results from manually writing in files to automatically saving data in logs. The final step of the programming side is to combine the GPT-3 story generator with another similar algorithm called Tale-Spin and make the entire process automotive. In the end, we also submitted an ACS paper about this story generator algorithm and its use in the field.

Comparing physiological responses to hot and cold stress in a cnidarian–algal holobiont, Exaiptasia diaphana

Name: Nicole Capozzi
Year of Graduation: 2024
SURF Advisor(s): Rachel Wright, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Comparing physiological responses to hot and cold stress in a cnidarian–algal holobiont, Exaiptasia diaphana
Abstract: Coral bleaching—the breakdown of the cnidarian–algal symbiosis—is a major cause of reef decline. The sea anemone Exaiptasia diaphana, commonly known as Aiptasia, is used as a model to study cnidarian-algal symbiosis in laboratory settings. Aiptasia can live with or without symbionts, which allows scientists to study the host combined and separate from the influence of the symbionts. Scientists are able to trigger the breakdown of the symbiosis using heat or cold stress. Cold stress is more commonly used to render aposymbiotic Aiptasia because it seems to be less harmful to the host than bleaching under heat stress. Is cold really less harmful than heat stress? We compared hot and cold stress responses to different stress regiments: a gradual temperature change, a gradual temperature change followed by a sudden temperature change, and a sudden temperature change from ambient conditions. We explored multiple physiological responses of the anemones to determine their level of stress response. We measured mortality and algal density in the host, as well as carbohydrate in the host and symbiont fractions. We also measured peroxide production in algal cultures exposed to the same treatment regimes. After repeating the experiment twice, we found that anemones had different responses, which emphasizes the necessity for repeated experiments in research conducted with live subjects.

Invasive Crab Predator and Native Snail Prey Interactions in the Rocky Intertidal

Name: Sophie Schneider
Year of Graduation: 2023
SURF Advisor(s): L. David Smith, Biological Sciences
Field of Study: Marine Ecology
Co-Authors:

Title: Invasive Crab Predator and Native Snail Prey Interactions in the Rocky Intertidal

Abstract: The oceans are changing in ways humans have caused but cannot control. Climate change has already begun to change temperatures and seasonality in the world's seas at the same time that ever-increasing human trade and travel has facilitated the movement and invasion of organisms to novel habitats. The Gulf of Maine is a perfect location for studying and analyzing these changes as they happen. This body of water, spanning from Cape Cod in Massachusetts to the Southern tip of Nova Scotia, is warming at a rate faster than 90% of the world's oceans. Additionally, the intertidal zone of this region has been subject to invasive crab predators with the European green crab (Carcinus maenas) from the times of European colonization to the ongoing invasion of the Asian shore crab (Hemigrapsus sanguineus). It is essential to understand the compounding effects of warming waters and invasive species on this region.To that end, my research this summer involved the support of Maggie Stoffer ('23 J) with their thesis exploring the developmental effects of Asian shore crabs on a native snail species (Littorina obtusata) as well as my own project collecting and analyzing census data on these organisms in the field to compare with historical data. Stoffer's project explores phenotypic plasticity, the ability for organisms to adapt their bodies to better suit their environment within their lifetime (as opposed to passing down favorable genes). This phenomenon has been observed on this same snail species in reaction to cues from European green crabs so this project aims to understand if there are similar effects from Asian shore crabs. Unlike with the green crabs, these snails do not share an evolutionary history with Asian shore crabs so it is hypothesized that they may not respond similarly (via thickening their shell) to this novel predator.

To further understand this relationship, I surveyed crab and snail populations at a northern site, Carrying Place Cove in Lubec, ME, and a southern site, Back Beach in Rockport, MA in the Gulf of Maine. At each site, snails and crabs were collected and brought back to the lab to be measured. For snails shell color was noted and shell length, height and lip thickness were measured. For crabs, sex was noted, claw length, height and depth were measured as well as carapace width. I then analyzed these data in R Studio to generate graphs and summary statistics to compare with historical data collected in (give years) by former students in the Smith lab. The data show that Asian shore crabs have come to entirely outnumber European green crabs at the southern site. The northern site still has an absence of Asian shore crabs, perhaps due to cold temperature restriction, and the green crab population has stayed relatively stable in the past 13 years. This relationship between native prey and invasive predator has implications for the health and balance of this ecosystem and several others facing similar threats around the world.

Identifying lineage-specific genes in testate lobose Amoebae (Arcellinida)

Name: Angela Jiang
Year of Graduation: 2023
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Identifying lineage-specific genes in testate lobose Amoebae (Arcellinida)

Abstract: The order Arcellinida consists of single-celled protists that fall under the major taxonomic group Amoebozoa. Despite their ubiquity and usefulness as bioindicators, they are understudied and much remains to be learned with respect to their gene family evolution. Lineage-specific genes, genes found in one taxonomic group but not others, offer insight into evolutionary events such as gene duplication and de novo events. My project aims to elucidate Arcellinida evolution by identifying lineage-specific gene families through bioinformatic methods. Another goal of the project is to identify lineage-specific genes of two ubiquitous Arcellinida species of the genus Hyalosphenia: H. papilio and H. elegans. The first step in my pipeline was to cluster sequences using the tools Barrnap and CD-Hit, and then identifying Orthologs (OGs) using the bioinformatics tool OrthoFinder. I then wrote an R script to find genes only present in Arcellinida (lineage-specific) and not other groups from the output gene count table. This summer, my aim was to curate lineage-specific genes identified through curating short sequences and identifying contaminants. To identify contaminants, I created codon usage bias plots of the GC content in OGs through writing python scripts. Since Arcellinida have a unique footprint of GC content on a codon usage bias plot, we are able to verify whether each OG is an Arcellinida gene or a contaminant. In addition, I experimented with different minimum sequence lengths set in OrthoFinder, and found that setting a minimum length of 100 amino acids was sufficient to eliminate very short sequence fragments. I then used a python script to curate very short and very long sequences in each OG to remove fragments. Future work involves assessing confidence in OG sequence alignments through the use of the algorithm Guidance and conducting phylogenetic analyses on these lineage-specific gene families.

Starting Ketone Variation in Nucleophilic Cross-Coupling α-Amination

Name: Nicole Arends
Year of Graduation: 2024
SURF Advisor(s): Alexandra Strom, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Starting Ketone Variation in Nucleophilic Cross-Coupling α-Amination

Abstract: This research project used the typical α-amination nucleophilic cross-coupling reaction in the Strom Lab, using $FeBr_3$ as the metallic catalyst. We looked into the effects that variations of the starting ketone had on the ratios between α-amination, α-halogenation, and the remaining starting materials.

Initial research focused on the isovalerophenone α-amination reaction with no additions in efforts to determine if amination occurred and if so, to find a replicable ratio of starting material to aminated product. No amination was observed, but this research stage also served to standardize the reaction setup.

For the next research stage, ligands of various types (acac, catechols) were added to the reaction to observe their effects on three different starting ketones. For the standard ketone (4-chloro) we looked for a change in the ratio of α-amination to starting ketone, and for isovalerophenone and acetophenone ketones we looked for a change in the ratio of α-halogenation to starting ketone along with signs of any amination. The silver salt $AgBF_4$ was also attempted, and 1H NMR spectra indicated possible synthesis of the desired product (Fig 1, upper) in isovalerophenone. Future research will focus on different equivalencies of $AgBF_4$ and other silver salts, to determine which materials promote amination. This may also aid in mechanistic studies.

The Electricity of the Embryo: Visualizing bioelectric patterns during early embryonic development in Danio rerio

Name: Ruiyi Song
Year of Graduation: 2025
SURF Advisor(s): Michael Barresi, Biological Sciences; Narendra Pathak, Neuroscience
Field of Study:
Co-Authors:

Title: The Electricity of the Embryo: Visualizing bioelectric patterns during early embryonic development in Danio rerio

Abstract: Bioelectric signals, also known as changes in the membrane potentials of non-excitable cells, have been shown to influence stem cell differentiation, regeneration, left right symmetry, and organogenesis in diverse organisms. We focus on the role that bioelectric signaling plays during early axis development using zebrafish (Danio rerio) as a vertebrate model organism, we have developed a stable transgenic line of zebrafish that ubiquitously expresses the genetically encoded voltage indicator (GEVI) Marina whose relative fluorescence is expected to increase in response to membrane depolarization. Using fluorescent light sheet microscopy, we present our initial characterization of Marina expression during the blastula and gastrula stages of Zebrafish development and establish that membrane potential is not uniform across the embryo. Consistent with our earlier findings using two Fluorescent Voltage Reporter (FVR) dyes DiBAC and Rhodamine 6G, we found that Marina fluorescence is maximum toward the dorsal aspect of a shield stage embryo and gradually reduces toward the anterior / ventral regions of the embryo. We describe the utility of this transgenic tool in visualizing how manipulation of bioelectric could impact germ lawyer morphogenesis, cell behavior, and cell fate specification during the early embryonic development of vertebrates.

Research this summer has focused on completion of the transgenic GEVI Marina line, which will open up future experiments. My effort was mainly identifying founder from un-id G0 fish. 14 founders were identified. F1 were obtained to maximize stable fluorescent expression. Using fluorescent light sheet microscopy, the founder embryos showed membrane labeling at lower level, which will be improved with f1 transgenic fish. Characterization of individual founder was done. Smaller experiments with dyes, drugs and HCR were performed to better understand the bioelectric patterns. Hyperpolarizing drug made with Ivermectin and NMDG chloride and depolarizing drug with 4 Amino pyridine were used with. HCR were done with wt embryos and depolarized embryos to examine difference. One challenge was the high death rate of embryos with hyperpolarizing drug, which will be further examined.

The plan for the fall is focused on the quantitative analyses for the bioelectric pattern in the transgenic line. Experiments with HCR and drugs need to be repeated. Further study will have more possibilities with this stable transgenic line.

Development of a Diagnostic Multiplex qPCR Assay for Schistosoma mansoni and S. haematobium

Name: Siobhan Dietz
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Molecular Biology
Co-Authors:

Title: Development of a Diagnostic Multiplex qPCR Assay for Schistosoma mansoni and S. haematobium

Abstract: Schistosomiasis is a debilitating neglected tropical disease caused by many species of the parasitic flatworm Schistosoma. The two species of interest for my summer research were S. mansoni (SM) and S. haematobium (SH), which are co-endemic in much of sub-Saharan Africa. Current treatment is prophylactic administration of the anti-parasitic drug praziquantel, which is distributed en masse. The typical diagnostic protocol is the Kato-Katz method, which requires a skilled microscopist to look at urine and/or stool and to characterize and count any parasitic eggs found in the sample. This misses low-parasite burden infections and can easily lead to diagnosis of the wrong species, so the need for sensitive and specific molecular assays is crucial. A multiplex assay where one sample could be tested for both species would be beneficial because it would cut the amount of tests needed for diagnosis of these species in half.

The Williams Lab has previously developed two diagnostic qPCR assays for both species, and the data on their sensitivity and specificity were evaluated to decide which assays to include in the multiplex. The first SM assay, SmR1, and the second SH assay, ShR2, were determined to be the best candidates to multiplex. More tests for specificity were conducted, using SM DNA in ShR2 or vice versa, because there was previous concern for cross-amplification of the other species' genome. It was eventually decided that minimal aerosol contamination was most likely responsible for those data. Limit of detection tests were performed on each assay and they were both found to be sensitive and specific down to 2fg of DNA, giving enough confidence to move on to multiplexing. It was clear from the validation testing of each assay that ShR2 was less sensitive, as it consistently took more cycles to be detected by qPCR. When multiplexing the two assays, the same results for the sporadic cross-amplification as well as the delayed detection of SH DNA in ShR2 were seen - despite adjusting the concentration of ShR2 and SmR1 primers in the master mix.

The final two weeks were spent attending the New England BioLabs Summer Molecular Biology Workshop, run by Prof. Steven A. Williams. The course aimed to cover a vast array of topics in molecular biology, and I gained skills and knowledge in many areas of the field I've never gotten to learn - it was invaluable to my development as a scientist.

Analysis of Bermudan Garnet

Name: A. Elvidge
Year of Graduation: 2023
SURF Advisor(s): Sarah Mazza, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Analysis of Bermudan Garnet

Abstract: We collaborated with a geologist from Bermuda who collected sedimentary rock samples which he thought contained volcanic glass. This "discovery" was unexpected as no volcanic rocks are preserved on the surface of the island; while Bermuda was formed due to volcanism, the surface is completely covered by sedimentary rocks. The rock samples were sent to Smith College for identification. Using XRD analysis, it was determined that the rock contained garnet and perovskite, not glass. Garnet was also an unexpected find within the sample because the metamorphic process needed to form the mineral is not known to have occurred in Bermuda.

My SURF project involved analyzing the mineral composition of the rock samples, with a particular focus on the garnet. Images were made of thin sections of each sample in plane and cross polarized light. The bulk mineral composition of the samples was determined using XRD, the rocks were predominantly composed of calcite, perovskite, garnet, and clinopyroxene. Further analysis on the chemical composition of the minerals was done using SEM-EDS. This revealed that there were three types of garnet present in the sample- andradite, grossular, and almandine. Other minerals such as titanite, apatite, magnesiochromite, iron oxide, and zircon were also identified using SEM-EDS. Further study will be done to determine if the iron oxide is maghemite, magnesite, or hematite.

This project fits into the larger goal of determining why garnets were found in the Bermudan rock samples. The most likely explanation is that the garnets were formed outside of Bermuda then transported to the island and lithified along with other sediment to form the sample rock. However, the source of the garnet, along with the transportation method to Bermuda is yet to be determined. The data collected about the chemical composition of the garnets will be used to match the garnets to potential sources.

High Precision Spectroscopy of Neutral Atoms

Name: Alicia Wallace
Year of Graduation: 2025
SURF Advisor(s): Will Williams, Physics
Field of Study: Physics
Co-Authors: Tilila Karani, Chitose Maruko

Title: High Precision Spectroscopy of Neutral Atoms

Abstract: In this SURF, we worked on a number of spectroscopic experiments. Included in the work was experimental design, building, data taking, data processing, and paper writing. Below we highlight the experiments we did this summer.

Europium spectroscopy: We performed spectroscopic measurements on three different transitions in the neutral europium atom. The experimental design for this project was already completed in the spring semester, but a data collection issue was identified and corrected at the end of the spring semester. With the data collection issue fixed, we retook all of the data for these three transitions. While doing this project, we learned about how to experimentally check for things that could skew our results, which we call systematic effects. These systematic effects include factors like pressure, laser power, and discharge voltage. After the data was collected, the data was analyzed to extract information about the europium atom. This project will result in 2 peer-reviewed publications. One of these papers is in the peer review process. The other paper will be submitted for publication soon.

Nitrogen spectroscopy: For this project, we first built an experimental setup to perform spectroscopy on neutral nitrogen atoms. The initial experimental setup did not work as well as we needed, so we redesigned and rebuilt the experimental setup twice to better improve the experiment. We searched for the spectroscopic signature of a nitrogen transition, and may have found a new, unknown nitrogen transition. We also found two more nitrogen transitions that will be explored more this fall.

Beryllium spectroscopy: The experimental setup for this project also went through multiple iterations. In the end, we finally found the spectroscopic signal. Like the nitrogen project, this project will be finished this fall.

Wettability of Polymer Films

Name: Elizabeth Rehwinkel
Year of Graduation: 2025
SURF Advisor(s): Kate Queeney, Chemistry
Field of Study: Chemistry
Co-Authors: Kallie Fisher

Title: Wettability of Polymer Films

Abstract: Our research focused on the wettability of polymer films deposited on surfaces with varying underlying surface chemistry. The larger goal of this research is to create surfaces that are reproducible, have tunable wettability, and display the same surface chemistry when the topography of the underlying substrate is changed. Because wettability impacts how biological entities like bacteria and eukaryotic cells interact with surfaces, control of surface wettability is critical to our ability to probe the molecular-level interactions that govern processes like biofilm nucleation and cell proliferation. Our specific goal for the summer was to explore whether and how we can use pH-dependent wettability measurements (dynamic contact angle goniometry) to probe for the appearance of certain functional groups at the surface of a polymer film.

Our model polymer is poly(allylamine hydrochloride) (PAH), which contains amine groups that are positively charged at low pH and neutral at high pH. The optimal deposition conditions for maximum PAH adsorption were determined experimentally. We adsorbed PAH onto two surfaces: the native silica layer of silicon substrates (hydrophilic) and surfaces prepared by silanization of silica surfaces with octyldimethylchlorosilane (hydrophobic). The resulting polymer films were characterized by ellipsometry and dynamic contact angle. The contact angle was initially measured manually, but we also developed a reproducible procedure to take measurements with an image capture system, accounting for droplet size-dependent variation in contact angle.

After PAH deposition, the contact angle of the hydrophilic surfaces increased, the contact angle of the hydrophobic surfaces decreased, and the ellipsometric thickness of both surfaces increased. To investigate the quantity of exposed amine groups on the polymer coated surfaces, we measured contact angles with buffered drops of different pH values. Since amine groups are neutral and therefore less hydrophilic at pH 9, contact angles measured at this pH would increase if there is sufficient density of surface amines. Since we found no observable pH-dependence of contact angle for a single layer of PAH on hydrophilic surfaces, we conclude that the electrostatic interactions between positively charged amine groups on PAH and negatively charged silanol groups on the surface reduce the number of amine groups free to interact with the buffered drops. Preliminary results suggest that there might be a pH-dependence for PAH on hydrophobic surfaces, where the amine groups on PAH do not tether the polymer to the (electrically neutral) surface.

Research regarding a single layer of PAH on hydrophobic silicon wafers will be continued in the Fall, and will hopefully yield more precise data on the pH-dependent wettability. Additional research in the Fall will investigate the pH-dependent wettability of alternating multilayers of PAH and poly(acrylic acid) (PAA) on hydrophilic silicon wafers.

Bridging the Gap: Developing Self-Rolling Azlactone Hydrogels for Nerve Injury Applications

Name: Annabelle Hendrickson
Year of Graduation: 202
SURF Advisor(s): Maren Buck, Chemistry; Alexis Ziemba
Field of Study: Neuroscience and Chemistry
Co-Authors: Arshiyan Alam Laaj

Title: Bridging the Gap: Developing Self-Rolling Azlactone Hydrogels for Nerve Injury Applications
Abstract: The NeuroHydrogel project in the Buck lab aims to model a nerve guidance conduit (NGC), which is a structure that aids nerve regeneration, for nerve injury applications (1). The NGC is created using hydrogel bilayers synthesized with the reactive polymer poly(2-vinyl-4,4'-dimethyl azlactone) (PVDMA) and crosslinker Jeffamine-600. Varying the crosslinking density (CL%) of the bilayers, thus changing the swelling capacity of each layer, allows the hydrogel bilayer to roll into a tube once placed in water. During the first half of SURF, the goal was to optimize the methods used to cast the hydrogel bilayers to create tubes with smaller diameters.
Hydrogel tubes with optimized diameters ensure stronger guidance cues for neurite outgrowth (2). Previously, the thickness of each layer was that of a single microscope coverslip (~150 um), resulting in a tube with an unsupportive diameter (Figure 1). To further reduce the thickness of each layer, which would, in turn, allow for more tightly rolled tubes, aluminum foil (~48 um) was used as spacers. The new material brought with it new challenges. For example, the gels would not solidify, resulting in dissociating and fragile bilayers. This led us to experiment with various casting methods, which we will continue to explore further throughout the coming semesters.
The second half of SURF was spent in collaboration with the Peyton Lab at the University of Massachusetts - Amherst. Here, we gained key chemical engineering and cell culture skills that are transferable to our own project in the Buck Lab. Sonu Kizhakkepura, a postdoctoral fellow at the Peyton Lab, had synthesized a novel polymer that would be used to mimic force-responsive breast tissue. Our goal with this project was to fabricate hydrogels that would model Dr. Kizhakkepura's original hydrogel and carry out the following tests. We used sulfobetaine methacrylate - poly(ethylene glycol) (SBMA-PEG) hydrogels at various CL% and measured their elastic modulus using rheology. Once the CL% corresponding with the elastic modulus comparable to the original novel hydrogel was determined, gels were cast on treated coverslips and subsequently conjugated with collagen. Then, MDA-MB231 breast cancer cells were seeded on the conjugated hydrogels and their morphology and viability were monitored using brightfield microscopy. Unfortunately, near the end of SURF, we were unable to observe cell viability on our conjugated model hydrogels.

Citations: (1) Vijayavenkataraman, S., et al (2020) Acta Biomater 106, 54–69. (2) Wang, HB., et al. (2010) Acta Biomaterialia 6, 2970-2978.

Bridging the Gap: Developing Self-Rolling Azlactone Hydrogels for Nerve Injury Applications

Name: Arshiyan Alam Laaj
Year of Graduation: 2023
SURF Advisor(s): Maren Buck, Chemistry; Alexis Ziemba
Field of Study: Neuroscience and Chemistry
Co-Authors: Annabelle Hendrickson

Title: Bridging the Gap: Developing Self-Rolling Azlactone Hydrogels for Nerve Injury Applications

Abstract The NeuroHydrogel project in the Buck lab aims to model a nerve guidance conduit (NGC), which is a structure that aids nerve regeneration, for nerve injury applications (1). The NGC is created using hydrogel bilayers synthesized with the reactive polymer poly(2-vinyl-4,4'-dimethyl azlactone) (PVDMA) and crosslinker Jeffamine-600. Varying the crosslinking density (CL%) of the bilayers, thus changing the swelling capacity of each layer, allows the hydrogel bilayer to roll into a tube once placed in water. During the first half of SURF, the goal was to optimize the methods used to cast the hydrogel bilayers to create tubes with smaller diameters.

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Phyllotaxis Project

Name: Shaotong Cao
Year of Graduation: 2024
SURF Advisor(s): Christophe Gole, Mathematics and Statistics
Field of Study: Bio-Math
Co-Authors: Elaine Demetrion, Xinyun Guo, Xiaoman Xu

Title: Phyllotaxis Project
Abstract: Phyllotaxis is the arrangement of plant organs on a stem. Frequently, these organs are arranged into spirals; the numbers of spirals in each direction are often two consecutive Fibonacci numbers. However, some plants display similar numbers of spirals in each direction. Stephane Douady coined the term "quasi-symmetric" to describe this. The goal of our research is to statistically distinguish quasi-symmetric from Fibonacci phyllotaxis, and determine which conditions prompt the formation of each. Throughout, we use the geometric tool of primordia fronts, which gives a local count of spirals.
During the first half of SURF, Elaine and Xinyun worked on a MATLAB application for generating fronts, converting code written by a previous student into an app with an improved user interface. Lisa and Xiaoman explored FIJI and Mathematica to improve the quality of photos of unrolled plants, wrote a FIJI use instruction, and used the MATLAB app developed by the team to process photos.
During the second part of SURF, Xinyun worked on another front app for circular samples with Xiaoman. The app is formed with some converted code either in MATLAB code or in separate functions adapted and modified with new abilities and others are newly written code and functions by Xinyun. This app adds a possible top view procedure for analyzing fronts.
Xiaoman worked on a new Phyllotaxis website using WordPress. This is an interactive site for the mathematical study of plant pattern formation, aiming to show what phyllotaxis is and provide opportunities for them to play with plant models. Some interactive apps developed by the surf team are available for access on the website.
Lisa wrote R code to analyze if the geographical location affects the phyllotaxis, which will also serve as a template for future comparison between samples. As a person who experienced each step of the analysis in this phyllotaxis project, Lisa wrote an overall protocol which included all the detailed instructions of how to use a specific app by different members in the team.
Elaine built a simulation of primordia growth using the cone model developed by Mitchell and Atela. This models a plant stem as a cone, and primordia as disks. The user can modify the cone angle and the first disk's placement. While adding disks, a chart of spiral counts is generated. This app helps determine the phyllotaxis type certain parameters produce, and is a resource for our website.

Combinatory Approaches for the Synthesis of High-Affinity Protein-Polymer Conjugates (PPC) for Drug Delivery

Name: Ama Boamah
Year of Graduation: 2023
SURF Advisor(s): Maren Buck, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Combinatory Approaches for the Synthesis of High-Affinity Protein-Polymer Conjugates (PPC) for Drug Delivery

Abstract: Cancer is responsible for 9.6 million global deaths as of 2018. The traditional cancer therapies are surgery, chemotherapy, and radiation therapy, and the most recent one is antibody-drug conjugates. However, the side effects of these treatments can be harmful to patient health1 because of the struggles in making conjugates required to transport drugs and the therapeutical toxicity they have, although the targeting is beneficial.2 Therefore, current research aims to develop next-generation therapy with low off-target toxicity and high efficiency.1 Next-generation targeted therapy aims to deliver drugs that block the spread of cancer by interfering with genes or proteins that promote cancer growth, progression, and metastasis.3

Targeted therapies recognize and attack molecules that are selectively important for cancer cell biology but less crucial for normal tissues, resulting in low off-target cytotoxicity and fewer side effects, unlike chemotherapy, which targets fast-growing cells. The conjugation of proteins to polymers will seek to harness exquisite and precise functions in medicine, engineering, (bio)chemistry, biotechnology, and enzymatic catalysis.2 PPCs are better for conjugating drugs because they are customizable and easy to synthesize.

I focused on synthesizing, polymerizing, functionalizing, and running dynamic light scattering (DLS) on polymers during SURF. This process involved troubleshooting and optimizing different conditions from varying amounts of azobisisobutyronitrile and tetrahydrofuran for polymerization and trying other time points and different heat levels for functionalization. I optimized conditions that yielded

Fate and Impacts of Silver Nanoparticles and Microplastics on Daphnia magna in Natural Systems

Name: Hannah Hutton
Year of Graduation: 2024
SURF Advisor(s): Niveen Ismail, Engineering
Field of Study: Engineering
Co-Authors:

Title: Fate and Impacts of Silver Nanoparticles and Microplastics on Daphnia magna in Natural Systems
Abstract: The production of both engineered nanoparticles (NPs) and microplastics (MPs) are greatly increasing. NPs are used in fields such as biomaterials, polymers, ceramics, agriculture, and energy while MPs are manufactured in personal care products, textiles, and in the majority of plastic items. A type of NP, silver nanoparticles (AgNPs), play a key role in innovative applications in both the commercial and technological industry. Therefore, much larger quantities of AgNPs and MPs are released into the environment, and majority of the time end up in wastewater treatment plants (WWTPs). Daphnia magna are filter feeders often found in WWTPs and are known to be negatively affected by AgNPs. However little is known about how MPs interact with the AgNPs.
Our overarching research objective is to characterize aqueous uptake of isotopically labeled $^{109}AgNP$ (20 nm, citrate-coated) and polystyrene microplastics (PSMP) (monodisperse, 0.5 µm) in D. magna at environmentally relevant concentrations (i.e. 0.02 - 2.5 µg L-1 AgNP; 100 µg L-1 PSMP). We readily develop effective methods for digesting and running samples with PSMP, daphnids, and $^{109}AgNP$ on an inductively coupled plasma mass spectrometer (ICP-MS). During SURF I worked collaboratively with a postdoctoral research fellow to perform all experiments, run equipment and complete data analysis. In addition I collaborated with another SURF student, Piper MacDonald, who ran the samples on the transmission electron microscope (TEM) in order to determine the location of the digested $^{109}AgNP$ within the daphnia. Data generated to date show increased waterborne uptake when the daphnia were exposed to MPs. The presence of MPs also significantly affects long-term elimination of AgNPs.

Evidence for primary carbonate in Bermuda Si-undersaturated magmas

Name: Caroline Ruppert
Year of Graduation: 2024
SURF Advisor(s): Sarah Mazza, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Evidence for primary carbonate in Bermuda Si-undersaturated magmas

Abstract: The Bermuda Rise, located east of the North American continent, contains ~30 Myr old silica-undersaturated lavas. They have some of the most radiogenic $206Pb/204Pb$ ratios found in ocean island basalts (Mazza et al., 2019), equalling that of HIMU end-members. Bermuda is unique among HIMU localities for having low $207Pb/204Pb$ ratios. The difference in $207Pb/204Pb$ ratios between Bermuda and HIMU 'sensu-stricto' shows the mantle reservoirs have different ages, with Bermuda tapping into a young (~650 Ma) mantle reservoir (Mazza et al., 2019) that may be unusually volatile-rich.

Carbonate veins, assumed to be secondary, are common throughout samples from the Bermuda Deep Drill of 1972. Additionally, other carbonate textures are present in some core sections, including occasional carbonate-silicate ocelli and what appears to be primary groundmass carbonate. We conducted leaching studies and Pb isotopic analysis to see to what extent the carbonate is a primary carbonate related to the mantle source or a secondary carbonate.

Two leaching methods were used to remove carbonates from the samples. The first was a "countertop" leaching method where the coarsely crushed sample was left in 10% HCl for 10 minutes before being rinsed, dried, and powdered. The second was a more intense method where powdered samples were left in 6 M HCl for two hours in a 100℃ oven before the leachate was removed and the sample was digested. The leachate from the second method was then saved for analysis. The Pb isotopic composition of the leached and unleached samples are not very different and plot on the extant $206Pb/204Pb$ vs. $207Pb/204Pb$ trend, which rules out the possibility of substantial seawater Pb in the carbonate that was removed by leaching. When combined with petrographic and textural analysis, the negligible difference in ratios between leaching techniques and leached and unleached samples have the potential to determine if the carbonate is magmatic in origin and a petrogenic feature of the Bermuda silica-undersaturated lavas.

Reference

Mazza S.E., Gazel E., Bizimis M. et al. 2019, Sampling the volatile-rich transition zone beneath Bermuda. Nature. 569, 398–403.

Induced defensive responses in a native snail species, Littorina obtusata, under differing temperatures and exposure to an invasive crab, Hemigrapsus sanguineus

Name: Maggie Stoffer
Year of Graduation: 2023
SURF Advisor(s): L. David Smith, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Induced defensive responses in a native snail species, Littorina obtusata, under differing temperatures and exposure to an invasive crab, Hemigrapsus sanguineus

Abstract: This summer I completed the experimental portion of my honors thesis with assistance from 3 other students. My project, titled "Induced defensive responses in a native snail species, Littorina obtusata, under differing temperatures and exposure to an invasive crab, Hemigrapsus sanguineus" aims to understand how the arrival of a novel crab invader may impact native snail populations in the Gulf of Maine. The Gulf of Maine has historically been subject to several biological invasions, including from another crab, Carcinus maenas, the European Green Crab. This system is also particularly vulnerable to climate change, as it is warming faster than over 90% of the world's oceans. The climatic vulnerability of this system paired with the unknown ecological impacts H. sanguineus may have on native communities make this system particularly important to study, especially as the water temperatures continue to rise and this novel invader continues to successfully expand its range northward. Snails are known to respond to predators by altering their shell morphology, specifically by thickening their shells in order to hinder the predatory ability of crabs to crush their shells. In order to display this induced response, snails must be able to recognize crabs as being a threat by sensing the presence of water-borne predatory cues. L. obtusata has been known to display this form of induced defensive response in the presence of C. maenas, but because H. sanguineus is such a recent invader and lacks an evolutionary history with L. obtusata, it is unknown how the snails will respond. To test induced defensive responses by Littorina obtusata populations to Hemigrapsus sanguineus at different temperatures, we collected snails by hand in two locations within the Gulf of Maine: a southern site in Rockport Massachusetts, and a northern site in Lubec, Maine. We collected all crabs from Rockport. Snails in Massachusetts have been exposed to cues from H. sanguineus for 20-30 years. Snails in northern Maine have yet to be exposed to cues from this crab. Upon return to the lab, we processed the snails by sorting individuals into 3 rough size classes based on shell length and marked snails within each size class with a distinct color. Each experimental jar contained one snail of each size class from either the northern or southern site and was assigned to one of 8 treatment combinations differentiated by the source population (snails collected from north or south), the rearing location (warm or cool incubator), and whether the snails were reared in seawater containing crab cue or not. At 4 separate times during the summer we took several morphological measurements on each snail (shell length, shell height, lip thickness) and utilized a nondestructive technique to determine tissue and shell weights. Currently, I am working on finishing the experiment and will analyze the data using analysis of covariance models..

The required forced to unfold a single

Name: Charisa Quinonez
Year of Graduation: 2023
SURF Advisor(s): Nathan Derr, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: The required forced to unfold a single

Abstract: The required forced to unfold a single
drinks so studies I have been researching a lot of what is needed in order to unfold a single strand protein. We've discussed in our studies the simplicity of a double strand and the difference between denaturing and unfolding of a protein. I have been studying and understanding the bio physical force of pico Newton that is required to unfold a single protein using dyneins.
The question becomes how many dinings would've been required to connect both ends of a single strand protein without breaking it. This is only the beginning in understanding how much force is required in doing so to understand the Connecticor and the microtubules that are connected inside the cell work together to unfold and re-fold during myosis and mitosis. The spindle assembly checkpoint has also been a part of my studies to understand each single protein that is listed inside the cell and how it is broken down and understanding each of the proteins function and structure, so far I have been figuring out the difference between human proteins that's versus the fruit fly drosophila. so far we have reviewed that not many studies have shown the amount of forest that it required to unfold a protein that is 500bp most of the research has shown that it's been proteins longer than 1000 BP and the study has become a little difficult to map down based on the length and the force in the heart the calculations are quite different from what the lab is trying to figure out. currently we have tested one KNL1 on one side only to a DNA origami platform. Used to test KNL1 binding to DNA origami and Bub3 binding to KNL1. Does not include motors or MTs. and has proven successful on the second test where we need to figure out KNL1 linked between 2 DNA origami 12HBs. Used for putting tension on the KNL1 protein. Requires motors and MTs.
is the most challenging part because we still need to figure out the amount of force required to unfold and not denture a single strand knl1. More study needs to be conducted.

DNA Coupled Small Molecule Catalysts

Name: Jingyi Sze
Year of Graduation: 2025
SURF Advisor(s): David Groin, Chemistry
Field of Study: Biochemistry
Co-Authors:

Title: DNA Coupled Small Molecule Catalysts

Abstract: Complex chemical reactions that take place in biological systems often lack site selectivity, which is the ability to distinguish between different functional groups and react with only one of them. This difficulty of site selectivity motivates the Gorin lab to synthesize DNA Coupled Small Molecule Catalysts (DCats) that allow for site selectivity. One application of DCats includes targeted drug delivery, so it is important that site selectivity is achieved. DCats are comprised of a DNA aptamer that is covalently linked to a small molecule catalyst. Currently, the lab is working on the second generation of DCats in which we use a Palladium catalyst. In order to covalently link the DNA aptamer to the Palladium catalyst, a ligand must be synthesized.

My work this summer has focused on synthesizing the ligand that attaches Palladium to the DNA aptamer. Previous members of the lab had been working on this multistep synthesis, but were stopped short due to the pandemic. As a result, I spent a significant amount of time performing NMR and GCSM analysis to determine if the starting material that was left over from previous experiments were the starting material needed to continue with the synthesis. Once I determined that the materials we had were in fact not the compounds we needed, I began the multistep synthesis from the beginning. In the total eight step synthesis, I was able to perform the first two steps, which included an enolate alkylation to attach the alkyl group and a carbonyl reduction to reduce the esters into alcohols. Restarting this synthesis allowed me to learn important organic chemistry skills such as product purification via column chromatography, NMR analysis to determine if I formed the correct product, and conduct literature reviews.

Comparative porosity analysis of carbonate coral reef deposits with thick microbial encrusters: New insights from X-ray Computed Tomography (CT) imaging of core segments from Pleistocene (Eemian, MIS 5e) Cockburn Town Member, Grotto Beach Formation on San Salvador Island, Bahamas

Name: Rory Haff
Year of Graduation: 202
SURF Advisor(s): Bosiljka Glumac, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Comparative porosity analysis of carbonate coral reef deposits with thick microbial encrusters: New insights from X-ray Computed Tomography (CT) imaging of core segments from Pleistocene (Eemian, MIS 5e) Cockburn Town Member, Grotto Beach Formation on San Salvador Island, Bahamas

Abstract: Two segments of a 54 mm-diameter, 34 m-deep core drilled into the Grotto Beach Formation at The Gulf site on the south coast of San Salvador Island were scanned at the High-Resolution X-ray CT Facility, University of Texas, Austin and analyzed using Dragonfly software. Comparison between Acropora cervicornis coral encrusted with 10 cm-thick laminated microbialite from -9.3 m and the same type of coral surrounded by skeletal-peloidal-ooid sand from -13 m provides insights into the role of encrusters in reducing porosity of coral-bearing subtidal carbonate deposits.

This study complements previous analyses that aimed at evaluating reservoir properties of cored subtidal deposits, overlain by 7+ m of eolian and beach grainstones, and capped by a Holocene-Pleistocene boundary terra rossa paleosol. Core-plug samples were analyzed for porosity, permeability and grain density, and made into petrographic thin sections. Fiji/ImageJ software was used to analyze porosity in high-resolution scans of thin sections with blue epoxy, and selected slides were point-counted for porosity determination. Radiographs of selected core segments were recorded on an ITRAX core scanner, and gamma-density data were collected on a GeoTek core logger to document relative variations in bulk density.

CT-scan analysis of the core segment with thick microbialite revealed porosity of 3.8% as compared with 14.5% for the segment with non-encrusted coral in sand. Since porosity of A. cervicornis was similar between these two samples (10.7% and 11.8%, respectively), the difference in overall core segment porosity stems from contrasting properties of the surrounding deposits: well-lithified micritic microbialites vs friable carbonate grainstone. These results support and expand the range of standard core-plug measurements, which indicated that the heterogeneous subtidal deposits have variable and generally lower porosity and permeability (15.5-48.5% and ~2-1600 mD, respectively) in comparison with overlying beach and eolian grainstones (40-50% and ~4500-19000 mD). CT scans also augment petrographic observations of the distribution of various pore types, ranging from small intergranular voids in sandy deposits and primary porosity within coral skeletons to larger, cm-scale secondary porosity created by bioerosion.

Jetlag and internal desynchrony

Name: Zhen Nie
Year of Graduation: 2023
SURF Advisor(s): Mary Harrington, Psychology
Field of Study: Neuroscience, Chronobiology
Co-Authors:

Title: Jetlag ad internal desynchrony

Abstract: Jetlag is a common circadian disruption to internal synchronicity between the central clock, the suprachiasmatic nucleus, and peripheral organs, like the liver. Escobar et al. found that chocolate, as palatable food, can accelerate rat's locomotor activity re-entrainment to a 6-hour advancement. Based on this study, we became interested in knowing if chocolate can also accelerate the liver's re-entrainment.

Starting in spring 2020, we conducted two behavioral experiments to 1) replicate Escobar's study on mice, and 2) investigate if locomotor activity and liver shifts at the same rate. Using Lumicycle Invivo, we were able to simultaneously record mice locomotor activity and liver bioluminescence, as indications of central and peripheral clock rhythm, respectively.

The statistical analysis results demonstrate that the liver re-entrains much slower than locomotor activity, and chocolate does accelerate both locomotor activity and liver re-entrainment. The future goal of this project is to identify if chocolate is shifting the clock through the metabolic or reward pathways and if chocolate is changing mice eating behaviors. We also found some sex differences in terms of female and male mice's rate of re-entrainment.

Meanwhile, we are also looking at if skin cells can generate their own peripheral rhythm when the central clock is broken. We performed SCN lesion surgeries on transgenic skin reporter mice. Following 12 days of constant darkness in Lumicycle Invivo, we record mice locomotor activity and skin bioluminescence rhythm. The experiment is currently ongoing and will be replicated in Fall 2022.

The optimization of iron-catalyzed α-amination on ketone derivatives

Name: Christine Wu
Year of Graduation: 2024
SURF Advisor(s): Alexandra Strom, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: The optimization of iron-catalyzed α-amination on ketone derivatives

Abstract: Catalytic reactions typically involve other transition metal catalysts such as copper, a more environmentally expensive metal, in cataylic reactions. Iron, however, is the most naturally abundant metal on earth leading it to be cheaper in production. The Strom Lab focuses on the usage of iron-catalytic reactions for α-animated carbonyls which are essential structures in drugs such as Argatroban. Argatroban is a drug used to reduce blood clots occuring in veins or arteries. The usage of iron catalytic reactions are less explored in coupling sulfonamides and nitrogen sources. The lab aims to develop an oxidative α-amination method that utilizes iron with a low environmental cost to couple these sulfonamides with carbonyl derivatives. During SURF, I aimed to test different carbonyl derivatives with p-toluene sulfonamide and analyze for evidence of amination and calculate percent yield. My focus was to study iron (III) in catalytic reactions for the formation of the C–N bond between ketones and a variety of sulfonamides under optimal oxidative conditions. Under the optimal conditions developed, the lab's approach used different derivatives of ketones and p-toluene sulfonamide as the nitrogen source. (Scheme 2). Additionally, I tested different sulfonamides with benzyl-4-chlorophenyl ketone. (Scheme 1). The hope is that these conditions result in α-animated carbonyls with high yields and results demonstrated that under these conditions our expected product was formed with high yields ranging from 50-70%. Future projects will focus on testing more ketones with p-toluene sulfonamides and amines. We will continue to optimize the experimental conditions to try to increase the yield.

The Knock Out of the Nix Gene with CRISPR/Cas9 in C6/36 Cells

Name: Elena Reshetnikoff
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: The Knock Out of the Nix Gene with CRISPR/Cas9 in C6/36 Cells

Abstract: The mosquito Aedes albopictus is one of the most dangerous invasive species and is a major vector of arboviruses, growing public health concerns globally (Vega-Rúa et al. 2020). The ability to understand sex determination and identify sex determination genes in Aedes mosquitos is a fundamental step for potential future projects involving transgenic mosquitoes (de Araújo et al. 2018). Knocking out important genes for sex determination using molecular tools, we may be able to prevent a population of mosquitoes from reproducing and spreading disease (de Araújo et al, 2018). The Nix gene acts as a "dominant master switch" for male sex determination and has great potential for developing mosquito control strategies to reduce vector populations of Aedes mosquitos through female-to-male sex conversion (Aryan et al, 2019).

This summer, as a starting point, I used a paper by Liu et al. 2020 which investigated if the Nix gene is a male-determining factor in the Aedes albopictus mosquito. My focus was transfection of C6/36 cells with CRISPR/Cas9 and puromycin expression cassettes. C6/36 is a cell line established in 1967 from Aedes albopictus larvae. These cells are commercially available and widely used to study virus-mosquito interactions. (Miller et al. 2018).

The goal of my project was to transfect the cells with a CRISPR/Cas9 vector that contained sgRNA designed during the previous semester and a linear donor sequence of the: puromycin gene which would add an additional level of cell selection. Cells were plated in 24 wells at 2 x 10^5 cells per ml concentration. Transfection was done in triplicate: the DNA amount was kept constant and the lipofectamine reagent was increased 1µl, 3µl, 5µl. After 72h the reduced serum medium (Opti-MEM) was replaced with a minimum essential medium containing penicillin, streptomycin and puromycin (5 µg/ml). After 5 days cells from 1µl and 3µl were transferred to T25 flasks for an easier selection. The cells plated with 5µl lipofectamine died in the first 3 days, suggesting that this concentration of the reagent is harmful for the cells. Post transfection cells plated with puromycin in the T25 died after 5 days. This implies that the transfection did not work properly or was not stable enough. I will continue working on the optimization of the transfection, sequencing of the extracted DNA and qPCR to confirm that Nix gene removal leads to Dsx and Fru being split into female forms with alternative splicing according to Liu et al., 2019.

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The Effects of Protamine on E.coli

Name: Elle Jamieson
Year of Graduation: 2024
SURF Advisor(s): Christine White-Ziegler, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Christine White-Ziegler

Title: The Effects of Protamine on E.coli

Abstract: Professor White-Ziegler's lab aims to explore how temperature dictates gene expression in bacteria. This work is particularly relevant when developing drugs to treat infectious diseases. Previously, published papers by the White-Ziegler lab, such as "A Shift to Human Body Temperature (37°C) Rapidly Reprograms Multiple Adaptive Responses in Escherichia coli That Would Facilitate Niche Survival and Colonization", begins to explore the importance of ompT, a thermoregulated gene in Escherichia coli. When E. coli enters a host, it experiences a temperature change from 23°C to 37°C. OmpT is responsible for cleaving antimicrobial peptides, including protamine, which are part of the host's immune and defense system. Dr. White-Ziegler has found that ompT is more highly expressed at 37°C, making it a promising target for antibacterial treatments. As concerns grow over antibiotic resistance in E. coli, new anti-infective are being tested. A paper "Potential Application of Protamine for Antimicrobial Biomaterials in Bone Tissue Engineering" by Honda et al. suggests the use of protamine, an antimicrobial peptide, in fighting bacterial infections. These researchers found that certain levels of protamine both inhibited bacterial growth and induced cell toxicity. To further investigate protamine's effectiveness at controlling infections from E. coli, growth curve and microtiter plate experiments were developed in the White-Ziegler lab to address if protamine inhibited growth and/or killed cells and whether cells grown at 37°C showed a higher resistance to protamine, presumably through higher OmpT expression 23°C versus 37°C. Through extensive testing, it was found that protamine did not seem to have a significant effect on bacterial growth, nor did it induce cell death at 23°C or 37°C. Growth curves of cells inoculated with protamine versus without protamine were virtually identical. This could be due to protamine's interference with spectroscopy technology, leading to inaccurate results, or more simply, protamine is not effective at controlling bacterial infections at a concentration of 6400 ug/mL and less. To further explore the role of antimicrobial peptides as bacteria fighting agents, it is hoped to run similar experiments with the antimicrobial peptide LL-37, which shows promising antibacterial qualities. Additionally, running the same experiments with ompT mutants, could shed light on the importance of OmpT in cleaving antimicrobial peptides as a defense against the host immune system.

Phyllotaxis Project

Name: Xinyun Guo
Year of Graduation: 2025
SURF Advisor(s): Christophe Gole, Mathematics and Statistics
Field of Study: Mathematics
Co-Authors: Lisa Cao, Elaine Demetrion, Xiaoman Xu

Title: Phyllotaxis Project
Abstract: Phyllotaxis is the arrangement of plant organs on a stem. Frequently, these organs are arranged into spirals; the numbers of spirals in each direction are often two consecutive Fibonacci numbers. However, some plants display similar numbers of spirals in each direction. Stephane Douady coined the term "quasi-symmetric" to describe this. The goal of our research is to statistically distinguish quasi-symmetric from Fibonacci phyllotaxis, and determine which conditions prompt the formation of each. Throughout, we use the geometric tool of primordia fronts, which gives a local count of spirals.
During the first half of SURF, Elaine and Xinyun worked on a MATLAB application for generating fronts, converting code written by a previous student into an app with an improved user interface. Lisa and Xiaoman explored FIJI and Mathematica to improve the quality of photos of unrolled plants, wrote a FIJI use instruction, and used the MATLAB app developed by the team to process photos.
During the second part of SURF, Xinyun worked on another front app for circular samples with Xiaoman. The app is formed with some converted code either in MATLAB code or in separate functions adapted and modified with new abilities and others are newly written code and functions by Xinyun. This app adds a possible top view procedure for analyzing fronts.
Xiaoman worked on a new Phyllotaxis website using WordPress. This is an interactive site for the mathematical study of plant pattern formation, aiming to show what phyllotaxis is and provide opportunities for them to play with plant models. Some interactive apps developed by the surf team are available for access on the website.
Lisa wrote R code to analyze if the geographical location affects the phyllotaxis, which will also serve as a template for future comparison between samples. As a person who experienced each step of the analysis in this phyllotaxis project, Lisa wrote an overall protocol which included all the detailed instructions of how to use a specific app by different members in the team.
Elaine built a simulation of primordia growth using the cone model developed by Mitchell and Atela. This models a plant stem as a cone, and primordia as disks. The user can modify the cone angle and the first disk's placement. While adding disks, a chart of spiral counts is generated. This app helps determine the phyllotaxis type certain parameters produce, and is a resource for our website.

Illuminating the life cycle and nuclear dynamics of Allogromia laticollaris, a single-chambered foraminiferan, through light and confocal microscopy

Name: Kristine Le
Year of Graduation: 2025
SURF Advisor(s): Laura Katz, Biological Sciences
Field of Study: Microbiology
Co-Authors:

Title: Illuminating the life cycle and nuclear dynamics of Allogromia laticollaris, a single-chambered foraminiferan, through light and confocal microscopy

Abstract: Allogromia laticollaris are single-celled micro-eukaryotes characterized by their organic tests and granular reticulo-pseudopodia. Despite their ecological ubiquity, allogromiids are poorly understood due to a lack of research in combination with their non-canonical, facultative life cycles. Understanding allogromiids and learning from their varied approaches to life can expand how we understand eukaryotic life as they redefine what eukaryotic life can be. My team's research this summer focused on studying Allogromia laticollaris CSH (Cold Spring Harbor strain) through light and confocal microscopy in order to understand their life cycles.

To study the life cycle of these organisms using light microscopy, I isolated individual cells in 24-well plates and observed and photo-documented them consistently over the summer months. Through this experiment I successfully gathered data to (1) propose a life cycle based on distinct morphological stages (2) estimate the duration of each life cycle stage of Allogromia latocollaris CSH (3) estimate growth rates and (4) explore synchrony among cells.

This summer we also combined our life cycle tracking work with confocal microscopy. We stained the DNA of cells using Hoechst and visualized the nuclear architecture of Allogromia laticollaris cells as they moved through their life cycle. We also experimented with Click-iT technology staining (RNA) and FISH probes (rDNA and rRNA). With the images and z-stacks collected we were able to better understand the changes in nuclear architecture as cells move through their life cycle, visualize rare nuclear stages, and estimate genome content to gain insight on ploidy. All together, the data collected this summer has enabled my team and I to begin writing a manuscript reporting what we have discovered.

In addition to this project, I was able to experience field work in Sapelo, Georgia, on a research cruise through the University of Connecticut, and in Madison, Connecticut. Field work primarily consisted of sampling forams from various environments, processing the samples, and preparing the forams for further molecular work. I was also able to strengthen my wet-lab skills overall by gaining experience in whole transcriptome amplification and whole genome amplification.

Fibonacci vs Quasi Symmetric Phyllotaxis

Name: Elaine Demetrion
Year of Graduation: 2025
SURF Advisor(s): Christophe Gole, Mathematics and Statistics
Field of Study: Biomathematics
Co-Authors: Lisa Cao, Elaine Demetrion, Xinyun Guo, Xiaoman Xu

Title: Fibonacci vs Quasi Symmetric Phyllotaxis

Abstract: Phyllotaxis is the arrangement of plant organs on a stem. Frequently, these organs are arranged into spirals; the numbers of spirals in each direction are often two consecutive Fibonacci numbers. However, some plants display similar numbers of spirals in each direction. Stephane Douady coined the term "quasi-symmetric" to describe this. The goal of our research is to statistically distinguish quasi-symmetric from Fibonacci phyllotaxis, and determine which conditions prompt the formation of each. Throughout, we use the geometric tool of primordia fronts, which gives a local count of spirals.

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Chan-Evans-Lam Oxidative Oxygen Cyclopropylation

Name: Abigail Perce
Year of Graduation: 2024
SURF Advisor(s): David Gorin, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Chan-Evans-Lam Oxidative Oxygen Cyclopropylation

Abstract: While cyclopropylation of aliphatic alcohols to synthesize cyclopropyl ethers is essential in medicinal and natural products chemistry, few conditions have been established for industrial and laboratory synthesis. Cyclopropanes have high metabolic stability due to their high C-H bond dissociation energy. Traditional methods for alkylation utilize electrophilic agents, many of which are toxic and unstable. Chan-Evans-Lam oxidative cross coupling makes use of nucleophilic coupling to avoid electrophiles. While there is precedence- established by the Molander group at UPenn- in aliphatic alcohol arylation, aliphatic alcohol alkylation via Chan-Evans-lam mechanisms was unknown until the Gorin lab started this work. In the exploration of various reaction conditions, a 1H NMR quantification methodology was developed to quantify reaction yield efficiently. It was determined via this quantification system that the addition of a strong base was vital in the reaction progression. Additional screens were carried out to test the importance of the copper source, ligand, reaction run time, equivalence of additives, and oxidant. It was found that the addition of NaH (1.0 eqv) to the standard reaction conditions yielded 23% product formation, while the addition of other additives did little to yield product. Further work aims to determine the true role of the base in the reaction mechanism, expand to additional substrates, and develop conditions for alternative alkylations.

Using the FTIRS Method to Estimate Biogenic Silica and Total Organic Carbon from Lake Lacawac

Name: Molly Fischer
Year of Graduation: 2024
SURF Advisor(s): Gregory de Wet, Geosciences
Field of Study: EnvironmentalSciences, Geosciences
Co-Authors:

Title: Using the FTIRS Method to Estimate Biogenic Silica and Total Organic Carbon from Lake Lacawac
Abstract: Broadly, this research project aims to study past climate in northeastern Pennsylvania. In collaboration with Dr. Matt Finkenbinder from Wilkes University, we analyzed 68 sediment samples from Lacawac Lake for biogenic silica (BSi) and total organic carbon (TOC).
In previous studies, BSi and TOC have been used as proxies for past temperatures, with relatively higher amounts of BSi and TOC per sample representing warmer conditions.
BSi and TOC were measured using Fourier Transform Infrared Spectroscopy (FTIRS) in the FTIRS lab at UMass Amherst. All samples were dried at 60°C for at least 72 hours before analysis. 0.5 milligrams of potassium bromide (KBr) powder were mixed with 0.1 milligrams of sediment. The prepared samples were run through the FTIR spectrometer, and data points on BSi and TOC were generated as wavelength versus relative absorbance line graphs. To interpret the results, we graphed relative absorbance versus the rough composite core depth for each sample. Based on these graphs, we can say the following about climate in the Lake Lacawac region — however, it is worth noting that we do not have data on the age of the samples. Generally, we can say that newer sediment is located at the top of the core (0cm) and older sediment is located toward the bottom (500cm). The relative absorbance of BSi and TOC change in a similar way throughout the core. Additionally, there is relatively more BSi and TOC toward the top of the core, and less towards the bottom.
Another goal of this project was to create a standard set of instructions for preparing and running each sample, which provided an opportunity to think deeply and critically about the science. One experiment we set up explores the results when the ratio of lake sediment to KBr powder is changed. The control is the mass of the KBr powder, 0.5 grams. We chose five sediment masses to test (in milligrams): 9.0, 9.5, 10.0, 10.5, and 11. When working with lake sediments, preserving sediment is a significant concern. We hope to glean from this experiment that less sediment can be used to generate BSi and TOC data while maintaining high-quality results. Furthermore, creating a standard set of instructions decreases the chance of errors or mistakes while generating data. Ultimately, the experiment and the instructions will help to generate the highest-quality data possible.

A Script-Based Story Generator for Electric Vehicle Planning

Name: Megan McKenzie
Year of Graduation: 2023
SURF Advisor(s): Jamie Macbeth, Computer Science
Field of Study: Computer Science, Cognitive AI
Co-Authors:

Title: A Script-Based Story Generator for Electric Vehicle Planning
Abstract: The main goal of our SURF project was to develop a story generator that creates stories about electric vehicles in hopes to aid and inspire vehicle design. This is done in collaboration with and sponsored by the Toyota Research Institute (TRI).

This summer I contributed to two papers that will be published this September. My work included conducting literature reviews, providing information on the tools we utilized for this project, meeting with an English professor at Smith to discuss quality of generated stories, creating citations, making edits, and reflecting on drawbacks of large language models (LLMs).

Additionally, I attended a TRI conference and hackathon for the work we have been doing in the Macbeth Lab. I helped create a poster and present our research to the TRI community.

A significant part of this work are scripts and script-based representations. Per our paper, 'a script is a form of knowledge that defines the stereotypical sequence of events in a common situation, allowing people to know what behavior is appropriate in that situation. Scripts were traditionally used in story understanding systems to simulate the ways in which people can reference a script to recover unstated details in understanding a story'. We use this script-based approach to develop the stories about electric vehicles.

Another area of language modeling we explore is OpenAI's GPT-3. GPT-3 is a third generation deep learning neural network model made by OpenAI trained on internet data. The training data are masses of text from information available on the internet. GPT-3 takes in a small amount of user input text and generates large amounts of relevant, proper text that closely mimics human-generated texts.

To finish, the papers will be submitted to this year's upcoming Advances in Cognitive Systems Conference!

Monitoring Macroinvertebrates in the Mill River

Name: Runpeng Hu
Year of Graduation: 2023
SURF Advisor(s): Marney Pratt, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Brianna Bell, Rae Ettenger, Rachel Slater

Title: Monitoring Macroinvertebrates in the Mill River

Abstract: Paradise Pond is a well-known landmark in the Smith College community, where it serves both recreational and educational needs of the students and the public of the Northampton area and beyond. However, the sediment redistribution (formerly dredging) required to maintain the pond has the potential to disrupt the Mill River ecosystem, including the macroinvertebrates that reside in it. Macroinvertebrates are important bioindicators of the health of an aquatic ecosystem. In addition to abiotic measurements of water quality, such as levels of dissolved oxygen, pH, and nitrogen/phosphate levels, macroinvertebrate sampling offers an especially dynamic method of testing for water systems of interest. We used freshwater benthic macroinvertebrates to gain insight into the health of the Mill River as affected by recent (2016 and 2018) sediment redistribution events.

To minimize the ecological effects of sedimentation, Smith is required by the government to monitor the impacts of the pond, therefore providing us with the opportunity to monitor the health of the river by collecting and identifying samples of macroinvertebrates from two macrohabitats (upstream and downstream of the pond) and five microhabitats within them.

In order to measure impacts of sediment redistribution on macroinvertebrate populations, Dr. Pratt uses a BACI (Before-After-Control-Impact) design. A BACI design has at least one sample before and after an impact (sediment redistribution) and has a sample that is likely to be affected by the impact as well as for a sample that should not be affected by the impact (Control sample). The impact site for this Mill River study is the rocky riffle habitat downstream of Paradise Pond, while the control site is a rocky riffle habitat upstream of the pond.

Through this project, our group became familiar with fieldwork sampling techniques and gained macroinvertebrate identification skills as well as knowledge of the general ecological research process. Sampling for macroinvertebrates in the Mill River consists of multiple important factors, namely large rocks and riffle area, which is the preferred habitat of macroinvertebrates. We then place a quadrat over the rocks and a D-net just downstream of the quadrat. Rocks are lifted into a bucket and gently rubbed off. After the rocks are gently rubbed off we use our feet to shuffle sand for 20-30 seconds. Macroinvertebrates are then transferred to the lab for preservation in a 70% ethanol solution.

Through data analysis in R, we found an increase in abundance of scrapers and collector filterers downstream compared to the previous two years (Figure 1). We also found an increased abundance of collector gatherers upstream in comparison to downstream this year. In addition, scrapers are more prevalent in the downstream region.

Determining the Mutagenicity of Sesquiterpene Lactone Compounds Derived from Neurolena lobota and the Effect of These Compounds on Brugia pahangi

Name: Chloe Leach
Year of Graduation: 2023
SURF Advisor(s): Steven Williams, Biological Sciences
Field of Study: Biochemistry
Co-Authors:

Title: Determining the Mutagenicity of Sesquiterpene Lactone Compounds Derived from Neurolena lobota and the Effect of These Compounds on Brugia pahangi

Abstract: Lymphatic filariasis is one of many neglected tropical diseases that affect millions of people. An aspect of this issue is the inaccessibility to effective drugs that can treat the parasites that cause this disease. The Williams lab has tested different derivatives of the Neurolenin D drug synthesized in the Shea lab, which is naturally occuring in Neurolena lobota, on the filarial nematode Brugia pahangi. B. pahangi is a parasitic nematode that is biologically similar to Brugia malayi, a nematode that causes lymphatic filariasis in humans via mosquito bite. The main difference between the two is that B. pahangi doesn't infect humans. From the work we've done this semester, it appears that one of the derivatives in particular is the most promising candidate for treating lymphatic filariasis. The toxicity and mutagenicity of this compound must be tested to show the safety of it as a potential drug candidate in order for pharmaceutical companies to show interest in it.

This summer, I tested Neurolenin D derivatives against B. pahangi in cultures of 30 adult male and 30 adult female worms. The nematodes were washed with an antimicrobial solution and were plated in a culture medium (10% FBS and antimicrobial solutions in Minimum Essential Medium Alpha). After 48 hours, the worms were treated with 70% ethanol as a negative control, Neurolenin B as a positive control, and a Neurolenin D derivative as the experimental condition. The mortality and motility of B. pahangi were observed every six hours over a 120 hour period. It was found that the Neurolenin D derivative resulted in a slower mortality rate than the Neurolenin B, but this may be beneficial as a rapid accumulation of dead filarial worms may trigger an allergic reaction in an infected organism.

The mutagenicity of the Neurolenin D derivative was assessed with the Ames assay; a reverse mutation assay that detects mutations of histidine-synthesizing genes in Salmonella typhimurium DNA. S. typhimurium cannot produce histidine on its own, and is plated in a medium containing a small amount of histidine with either a negative or positive control (70% ethanol or a known mutagen, respectively), or a drug candidate. Each condition was tested in the presence and absence of hepatic dehydrogenases, a system that replicates how the liver breaks down toxins. The amount of existing colonies after a 48 hour incubation period is directly proportional to the mutagenicity of the test material.

Four strains of the bacterium were tested, two of which had genes mutated with a base pair substitution and two of which had genes mutated with a frameshift mutation. The results showed that for strains TA98, TA1537 (frameshift), and TA1535 (base-pair substitution), the number of revertant colonies that appeared when in the presence of the Neurolenin D derivative weren't large enough to be considered mutagenic. For the test material doses in the absence of hepatic enzymes that were plated with TA100, an alarming amount of colonies formed in a decreasing fashion as the concentration of the doses increased. This is abnormal behavior for a mutagen, so these plates will have to be retested in the future. One final strain, TA102, which is genetically encoded for a transversion mutation, will be tested in the future as well.

IEEE Visual Analytics Science and Technology (VAST) Challenge 2022

Name: Yutong Zhang
Year of Graduation: 2023
SURF Advisor(s): Jordan Crouser, Computer Science
Field of Study: Computer Science (Human Computation Visualization)
Co-Authors:

Title: IEEE Visual Analytics Science and Technology (VAST) Challenge 2022

Abstract: Background:
The IEEE Visual Analytics Science and Technology (VAST) Challenge is an annual event designed to advance the field of visual analytics through competition. The challenge is designed to give researchers, commercial toolbuilders, and other contributors opportunities to test how their software might be used in a variety of realistic analytic tasks. Prof. Crouser is one of the co-chairs of this event, and the HCV Lab plays a key role in data and storyline generation.

The impact of the challenge stretches beyond each individual year's competition. From the Challenge website: "Researchers and software providers often use VAST Challenge data sets as benchmarks to demonstrate and test the capabilities of their systems. The ground truth embedded in the data sets helps researchers evaluate and strengthen the utility of their visual analytic techniques." In this way, the Smith team's preparatory efforts help to shape future advances in visual analytics and related fields.

The 2022 Challenge asks participants to analyze data, conduct urban planning, and make decisions on the allocation of a city renewal grant. The data for this challenge simulates 1000 city-dweller representatives, who checked in at each place they visited, recording variables of UserId, CheckinTime, VenueId, VenueType, the X-, Y- coordinates, and commute time. This simulated behavior is generated via a Location-Based Social Network (LBSN) model, which was developed by Kim et al. (2020) and then deployed to a local machine housed in the HCV Lab.

My work involved setting up and connecting to the database on scidb.smith.edu and doing preliminary analysis in RStudio. I conducted data analysis and superimposed a scatter plot of the check-in venues, colored by venue types, onto a map of the city to characterize the demographics of the place, find patterns in the social networks in the town, describe the daily routines of individuals, and build rationales for its residents. I investigated the count of check-in times by venue type for the most active and inactive users. In an attempt to visualize or trace the track of movements of individual users, I extracted the year, month, day, hour, and minute data from the raw CheckinTime variable and grouped by different combinations of UserId and other time variables to calculate how long each person has spent at each venue and their total number of check-ins. The next step is to make sense of overlaps in the movements of individuals to construct social rationales.
Reference:
Joon-Seok Kim, Hyunjee Jin, Hamdi Kavak, Ovi Chris Rouly, Andrew Crooks, Dieter Pfoser, Carola Wenk and Andreas Züfle, Location-Based Social Network Data Generation Based on Patterns of Life, IEEE International Conference on Mobile Data Management (MDM 2020)

Fate and Impacts of Silver Nanoparticles and Microplastics on Daphnia magna in Natural Systems

Name: Piper MacDonald
Year of Graduation: 2023
SURF Advisor(s): Niveen Ismail, Engineering
Field of Study: Environmental Engineering
Co-Authors:

Title: Fate and Impacts of Silver Nanoparticles and Microplastics on Daphnia magna in Natural Systems
Abstract: Grazing by filter-feeding zooplankton, like Daphnia magna, is a biological process that can remove pollutants from treatment wetlands. Silver nanoparticles (AgNP) are used in many household products due to their antibacterial properties, and frequently end up in freshwater systems. Plastics are also widely present in the environment and are broken down over time into microplastics (MP) and nanoplastics. Both these contaminants are considered ubiquitous in the environment and have been identified in many different types of aquatic systems, yet little is known about the interaction between these contaminants. The objective of this project is to research interactions between microplastics, AgNP, and filter-feeding zooplankton.
Considering AgNP can have negative health effects on aquatic organisms, and are known to adsorb to plastics in a lab setting, understanding the impacts of AgNP in conjunction with microplastics on zooplankton is critical to natural system function. During the summer, members of the Ismail lab conducted uptake experiments revealing that the daphnids uptake rate of ^{109}AgNP was significantly higher in the presence of PSMP. My focus this summer was to develop methods to view ^{109}AgNP within daphnid tissue on a transmission electron microscope (TEM) and determine qualitatively the difference in fate of ^{109}AgNP based on presence and absences of PSMP. In my individual exploration this summer, I discovered that when high concentrations of AgNP and PSMP (i.e. 500 µg L-1 AgNP; 50 mg L-1 PSMP) were employed, there were noticeable dark clumps of matter visible in the gut lumen in addition to AgNP-sized black specks, whereas daphnids exposed to 500 µg L-1 AgNP alone had only the specks. I will continue this research during the 2022-2023 academic year to further understand the significance of these qualitative findings, and study the components and structure of the 'dark clumps'. It is my intention to visualize how these same materials behave together in and outside of daphnid tissue.
While this project work is currently focused on laboratory experiments, the application of this work can extend to aquatic systems that are impacted by stormwater runoff and wastewater effluent. Future work is planned to consider the interaction of plastics and nanoparticles in environmentally relevant complex water matrices such as stream water from MacLeish field station as well as wastewater from Northampton wastewater treatment facility. In addition we plan to consider other zooplankton species that have been isolated from water from MacLeish and the Northampton wastewater treatment facility to further increase the environmental relevance of this work.

Effects of Campus Deicing Agents and Stormwater Design on Water Chemistry of Lyman and Paradise Ponds at Smith College, Northampton, MA

Name: Wenxi Li
Year of Graduation: 2023
SURF Advisor(s): Amy Rhodes, Geosciences
Field of Study: Environmental Science& Policy (water pollution)
Co-Authors:

Title: Effects of Campus Deicing Agents and Stormwater Design on Water Chemistry of Lyman and Paradise Ponds at Smith College, Northampton, MA

Abstract: In the wintertime, the ice formed by snow on the road can cause a lot of harmful, even lethal accidents. In the 20th century, people discovered that salt could effectively prevent roads from icing over during snowstorms by lowering the freezing point of water. Because road salt is cheap and abundant, and it is also ""nontoxic"" compared to other chemicals, road salt is heavily used in the winter. However, road salt is becoming one of the major contaminants to the freshwater ecosystem and threatening not only the freshwater ecosystem but also humans themselves.

The major ingredient of salt is sodium and chloride. When these two elements are dissolved in the water,¬ they are steadily accumulating in the freshwater system and becoming a permanent contaminant. When the salt level increases in the freshwater body, it will affect the population of organisms and even change the structure of the local ecosystem. A lot of worldwide news has reported the increasing salt level in the water causes a bad crop and hurts the local economic system. A study shows that the accumulation of salts in the freshwater system has significant effects over a longer period and affects a range of ecological processes. Collins found that road salt influenced ecological community structure by excluding salt intolerant species. Research also indicates that modern stormwater management is creating contaminated plumes of groundwater that deliver Cl– and Na+ to streams throughout the year and influence the whole groundwater system. A review found that the negative effects of road salt are not limited to freshwater ecosystems but have an indirect influence on a broader scale and even might increase the release of greenhouse gases in wetlands and exacerbate climate change.

Paradise Pond and Lyman Pond are two water bodies of Smith Campus. Paradise Pond is the major landscape feature of Smith College, and it is also a part of the Mill River. There are some frogs and other small organisms that live in the ponds. Also, some wild geese come to visit Paradise Pond each winter. A lot of farms nearby live on the water from the Mill River. Therefore, the study of the pond is important to both the Smith Campus and the local ecosystem. Lyman Pond next to the Botanic Garden is covered by green algae all summer. It is an impressive water symbol of Smith College, and it is also a very interesting water sample to study. During the wintertime, Smith College uses road salt to reduce forming of ice. The local salt practices not only have an influence on the surrounding ecosystem but also potentially could have a large effect on watershed chemistry.

This study seeks to answer the question: How does Smith College's winter salting practice, in addition to the way that Lyman Pond functions, affect Paradise Pond's water chemistry?

Cont: Effects of Campus Deicing Agents and Stormwater Design on Water Chemistry of Lyman and Paradise Ponds at Smith College, Northampton, MA

This study provides an opportunity to evaluate the potential impact of campus road salt practices and potentially identify opportunities to make a change. From our current study, at least six drainage pipes are connecting the college campus and Paradise Pond. Through our project, we will have a better understanding of the campus stormwater drainage system that would potentially deliver road runoff to this pond. And we are going to see if the water from Lyman Pond is draining directly to the Paradise Pond and might consider it as a unique point source of water pollution to the Mill River. We will find where the pipes are discharging the stormwater and Lyman Pond Water to the Paradise Pond and measure each of their influence on water quality.

The chemistry of water also can be changed by a lot of factors such as temperature, precipitation, stormwater input, etc. Through our year-long study, we will develop a picture of seasonal changes in water chemistry. We will measure the current chemical situation of the Paradise Pond and Lyman Pond and track their changing pattern during this snowstorm period and the last 20 years. From some current data from both my environmental chemistry course and Professor Rhodes, we know there is a lot of chloride and nitrogen in the Lyman Pond. We are also going to study the water source of the Lyman Pond and try to figure out the reason for that phenomenon. We assume that Lyman Pond is a point source to Paradise Pond. If we are correct, we will determine if it has a strong impact on the Mill River water chemistry. Or maybe Lyman Pond is a feature that helps to mitigate non-point source pollution to the Mill River.

Smith College uses de-icing agents on its roads and walkways. We are going to study the strategy of using de-icing agents on campus and describe the situation around college problems with road salt. As we know, currently, Smith College uses different de-icing agents, and the de-icing strategy was changed during the last decades. This project will examine the chemical composition of every kind of de-icing agent that Smith College used and how these de-icing agents may affect the water quality of Lyman Pond, Paradise Pond, within the larger Mill River wetland by testing the sodium and chloride levels. Since salt usage in the past has a steadily effect on current water chemistry, we will also try to find detailed records of the amount of de-icing agent used by Smith as far back as possible, especially for the '80s and '90s before the ""green movement."" Also, Lyman Pond appears to be a place where stormwater is discharged from the upper campus. If true, this project will evaluate the effectiveness of having a retention pond on water quality.

Sport for Social Change Lab-Qualitative Research on Trauma Informed Sport Coaching

Name: Sierra Steinwert
Year of Graduation: 2023
SURF Advisor(s): Erica Tibbets, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies
Co-Authors:

Title: Sport for Social Change Lab-Qualitative Research on Trauma Informed Sport Coaching
Abstract: Trauma Informed Sport Coaching at the Collegiate Level: A Qualitative Analysis,"Trouble managing behavior, emotional regulation, lack of motivation, inattention, lack of self-awareness, a lack of sense of identity, elevated threat alertness, and difficulty in peer interactions are all associated with the experience of significant trauma (Cloitre et al., 2009; Bergholz et al., 2016). As a result of trauma symptoms, athletic activities, particularly team sports where navigating physical, interpersonal, emotional, and intellectual challenges simultaneously become incredibly difficult for those who have experienced trauma and can even retraumatize the athlete. Carello and Butler (2015) found that 66-94% of college students had experienced one or more traumatic events. While statistics vary, there is a general consensus among scholars that US undergraduate students experience high rates of trauma. Due to the pervasiveness of trauma across many populations, trauma informed practices are being implemented in a variety of settings in order to limit the risk of retraumatization and adequately support trauma affected individuals. Trauma informed youth sport confers a range of benefits to trauma impacted youth in residential treatment and community outreach contexts (Bergholz et al., 2016; D'Andrea et al., 2014; Henley, 2005; Spinazzola et al., 2011; Weiss et al., 2016; Whitley et al., 2018). However, there is a lack of research done with college students, college athletes, and individuals between the ages of 18 and 22. These populations could benefit greatly from implementing trauma-informed sport coaching practices, particularly because trauma is so prevalent in these groups (Mountjoy et al., 2016; Carello & Butler, 2015).
Each individual experiences situations and emotions differently which calls for the use of qualitative research methods in order to fully understand the athlete experience and craft guidelines for trauma-informed coaching practices (Schools et al., 2020). In order to look at the impact of trauma-informed coaching across various demographics and get an idea of trends within collegiate coaching at all levels, we chose to use semi structured interviews and snowball sampling as our base format. This allowed us to work one-on-one with participants in order to build trust and tailor each interview to each individual in order to ensure the comfort and safety of participants. Over the course of the 2022 summer, 5 participants were interviewed from a variety of backgrounds and colleges across the country. This data was then analyzed and will continue to be analyzed throughout the fall using a blended approach to qualitative research in order to extract themes regarding the impact of coaching styles on athlete experiences.

The microtubule cytoskeleton during C2C12 myogenesis

Name: Ziyue Yang
Year of Graduation: 2023
SURF Advisor(s): Stylianos Scordilis, Biological Sciences
Field of Study: Myogenesis, Cell cytoskeleton
Co-Authors:

Title: The microtubule cytoskeleton during C2C12 myogenesis

Abstract: The development of a multinucleated myotube from a single myoblast is a complex morphological process that requires significant cytoskeletal reorganizations. This multistep process includes myoblast differentiation, cell cycle withdrawal, and myoblast fusion (Moran et al., 2002). Microtubules are one of the cell cytoskeleton components and are essential to normal muscle ontogeny. This was characterized by studies in which myotube formation was made aberrant by either disrupting microtubules in vivo or in vitro in non-mammalian organisms (Warren, 1968; Saitoh et al., 1988).
The goal of this project is to investigate the overall microtubule cytoskeleton during C2C12 myogenesis. This summer, I studied both the abundance and localization of the tubulin proteins and a few microtubule-associated proteins (MAPs).
To investigate the change in abundance of tubulins and MAPs, C2C12 cells were grown and extracted at three stages – myoblast (Day 0), early myotube (Day 5), and late myotube (Day 9). C2C12 cells were grown (n = 5) in 10% Fetal Bovine Serum/Dulbecco's modified Eagle's medium (DMEM). Once they reached 80% confluency, I extracted the Day 0 cells and performed a step-down procedure on the Day 5 and Day 9 cells by changing the media to 5% horse serum/DMEM to facilitate differentiation and fusion of the myoblasts to myotubes. The cells were fed every 48 hours and were extracted on Day 5 or Day 9 after step-down. Lowry Assay, SDS-PAGE, and western blots were performed on the cell extracts to determine some protein changes that occurred during myogenesis. The results showed that no statistically significant change occurred in either alpha- or beta-tubulins. Given the importance of tubulins as housekeeping proteins, it is understandable that a relatively large amount of alpha- and beta-tubulin is present at all stages. Conventional kinesin, a motor protein that moves cargoes along microtubules, increased on Day 5, which is the stage with the most drastic morphological change. An increase in MAPT, predominately found in the brain cells, showed up on day 9. However, the function of MAPT in skeletal muscle is not yet understood.
To investigate the localization of tubulins and MAPs, C2C12 cells were grown on No. 1 glass coverslips and were fixed and permeabilized by 5% paraformaldehyde/PBS and 0.3% Triton X-100 at all three timepoints. Cells were then stained with antibodies against tubulins and MAPs conjugated with fluorescent labels. Phalloidin stained actin filaments and DAPI stained nuclei. The multistained cells were imaged with laser scanning confocal microscopy.

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Warren R (1968), The effect of colchicine on myogenesis in vivo in Rana pipiens and Rhodnius prolixus. J Cell Biol 39: 544–555.

Phyllotaxis Project

Name: Xiaoman Xu
Year of Graduation: 2025
SURF Advisor(s): Christophe Gole, Mathematics and Statistics
Field of Study: Biomath
Co-Authors: Xinyun Guo, Elaine Demetrion, Lisa Cao

Title: Phyllotaxis Project

Abstract: Phyllotaxis is the arrangement of plant organs on a stem. Frequently, these organs are arranged into spirals; the numbers of spirals in each direction are often two consecutive Fibonacci numbers. However, some plants display similar numbers of spirals in each direction. Stephane Douady coined the term "quasi-symmetric" to describe this. The goal of our research is to statistically distinguish quasi-symmetric from Fibonacci phyllotaxis, and determine which conditions prompt the formation of each. Throughout, we use the geometric tool of primordia fronts, which gives a local count of spirals.

During the first half of SURF, Elaine and Xinyun worked on a MATLAB application for generating fronts, converting code written by a previous student into an app with an improved user interface. Lisa and Xiaoman explored FIJI and Mathematica to improve the quality of photos of unrolled plants, wrote a FIJI use instruction, and used the MATLAB app developed by the team to process photos.

During the second part of SURF, Xinyun worked on another front app for circular samples with Xiaoman. The app is formed with some converted code either in MATLAB code or in separate functions adapted and modified with new abilities and others are newly written code and functions by Xinyun. This app adds a possible top view procedure for analyzing fronts.

Xiaoman worked on a new Phyllotaxis website using WordPress. This is an interactive site for the mathematical study of plant pattern formation, aiming to show what phyllotaxis is and provide opportunities for them to play with plant models. Some interactive apps developed by the surf team are available for access on the website.

Lisa wrote R code to analyze if the geographical location affects the phyllotaxis, which will also serve as a template for future comparison between samples. As a person who experienced each step of the analysis in this phyllotaxis project, Lisa wrote an overall protocol which included all the detailed instructions of how to use a specific app by different members in the team.

Elaine built a simulation of primordia growth using the cone model developed by Mitchell and Atela. This models a plant stem as a cone, and primordia as disks. The user can modify the cone angle and the first disk's placement. While adding disks, a chart of spiral counts is generated. This app helps determine the phyllotaxis type certain parameters produce, and is a resource for our website.

Measurements of ear canal geometry

Name: Karen Bekhazi
Year of Graduation: 2025
SURF Advisor(s): Susan Voss, Engineering
Field of Study: Engineering
Co-Authors: Rebecca Farrar

Title: Measurements of ear canal geometry

Abstract: This summer we continued to refine and support the method established by prior students to measure ear canal geometry, using the software OsiriX to view CT scans in Multi-Planar Reconstruction, or across three planes (transverse, coronal, and sagittal). Measurements were taken along a central spline that we created through the ear canal, dallfirst every 2 millimeters and then every millimeter, starting at a certain location, to determine the curvature and length of the ear canal. We started recording our measurements at regular intervals of one millimeter at location 16 for pediatric subjects (ages ranging between 0 and 17 years old) and at location 24 for adult subjects (18 to 99 years old). Additionally, cross sectional areas of the ear canal were taken at every location. The most obvious location along the canal is called the first bend, which is defined as "the location of the most lateral sharp change in curvature of the canal central axis."

This method of measuring the canal is the primary way to determine more specific information about the canal's dimensions and geometry, and indicates the variability in geometry across different subjects. We use these measurements to analyze trends including total length of the ear canal vs distance of the first bend, as well as considering the subjects age vs canal length. Measurements will be used to highlight the correlation between ear canal geometry and peripheral sound flow. This understanding of the ear canal geometry can help to influence the development of future audiology technology.

Graphs of some of our measured ears are shown below. 40 unique subjects are shown below, graphing the length of the ear canal vs the cross sectional area. The first bend is denoted along the line with a more prominent point. Blue lines represent the left ear, while red represents the right ear; plots with multiple lines indicate repeated measurements from different investigators

Reflectance of 3D printed healthy ear canals

Name: Maya Gilliom
Year of Graduation: 2025
SURF Advisor(s): Susan Voss, Engineering
Field of Study: Engineering
Co-Authors: Jessica Feng

Title: Reflectance of 3D printed healthy ear canals

Abstract: Auditory diagnostic tests assume ear canals are cylindrical with a diameter of 7.5 mm and that all reflectance occurs at the tympanic membrane and more medial locations. They use this assumption to designate a fixed healthy range of reflectance values for human ears. From previous studies, however, we learned that there is more variability in reflectance than these tests acknowledge in healthy ears. Our goal was to show whether or not the shapes of ear canals contribute to reflectance.

We used CT scans, OsiriX MD (a radiology software), and 3D modeling softwares to create 3D prints of 10 different human ear canals. We also made an artificial ear based on a design by Kren Monrad Norgaard that has the same reflectance as the industry-standard Larson-Davis artificial ear. We attached each canal to the artificial ear we made, and by doing this, we controlled tympanic membrane reflectance so that all the differences in reflectance were caused by differences in canal geometry and not the terminating ear.

To ensure our results were accurate, we developed a method to ensure that the connection between the artificial ear and the printed ear canal was acoustically sealed. We also designed experiments to show that the properties of our printed material did not affect reflectance. We did this by printing several control cylinders of different lengths and resolution and comparing them to smooth copper tubes of corresponding lengths.

The next step will be to calculate the individual reflectance of each printed human ear canal using each ear canal's actual cross sectional area at the location of the measurement probe, which other members of our lab measured. This will help us to define the range for reflectance for normal hearing ears, therefore validating that variability of reflectance values from diagnostic acoustic tests rely on individual ear canal geometry.

Automated Moth Monitoring System-"Mothitor"

Name: Ruize Qin
Year of Graduation: 2025
SURF Advisor(s): Mariana Abarca, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Kate Nash

Title: Automated Moth Monitoring System-"Mothitor"

Abstract: In the age of climate change, data on insect, and more specifically moth, populations is vital to understanding how these climatic changes affect these species. This data must be collected as regularly as possible in order to create a long-term data set that can observe trends in moth populations. Manual mothing, as it is commonly performed, with a person identifying or photographing moths on a large sheet through the night, is labor intensive, especially to achieve a long-term data set. In addition, the human skill needed to identify large quantities of moths is considerable.

Over this summer, we designed, tested, and fabricated the "Mothitor", an automated moth monitoring device. We first researched existing mothing methods and automation techniques. After that, we performed lab and field tests to determine the best materials, dimensions, and light schedule.

Materials and dimensions- We tested large canvases, smaller cotton and nylon sheets, and different distances from the camera. We concluded that treated nylon fabric would be the most attractive to moths and the most durable for seasons in the field. In addition, we discovered that the size of the device could be reduced in order to take higher quality photos of the moths. The landing area of our first prototype was supported by a wooden frame, but as we keep decreasing the area and finally to 18*13.5 inches, we decided to use a nylon sheet covered plywood board to make it durable, compact, and simple to fabricate. The fabric must not be too tight on the frame of the device, or they cannot land on the fabric as easily. The back of the device is painted green, both to deter moths from landing on that side and to blend in with the surrounding environment. We utilized a waterproof camera (RICOH WG-6) 15.5 inches away from the center of the landing surface. This distance allows the entire landing surface to be photographed, and the resulting photos are detailed enough for counting purposes. This camera will be maintained by cleaning off the lens area, replacing the battery and SD card on a regular interval. The camera will be used with its flash in order to achieve better views in the dark.

Light schedule- We analyzed an accumulation curve of moths on the landing surface in order to optimize the time the mercury vapor blacklight is on to both reduce light pollution and attract the highest amount of moths. From our test, we concluded that one hour of blacklight is the ideal length of time before a photo is taken, and two hours with the blacklight off will allow the moths to disperse so that the Mothitor can attract new moths in the next cycle.

Future work- We will collaborate with computer scientists to automate moth counting and identification using machine learning programs. Additionally, we are communicating with the Massachusetts conservation service to develop a customized Mothitor to track endangered moths in local conservation areas.

TEM Study of Thin Film Cermets and Fabrication of low temperature cermet thermometers

Name: Aayushma Uprety
Year of Graduation: 2025
SURF Advisor(s): Joyce Palmer-Fortune, Physics
Field of Study: Physics
Co-Authors:

Title: TEM Study of Thin Film Cermets and Fabrication of low temperature cermet thermometers

Abstract: Cermet films are ceramic metal composite films that are promising as temperature sensitive resistors for measuring low temperatures (less than 0.1K). Transmission Electron Microscope is the tool used to study the microstructure of the films. The image from TEM will help determine the conduction mechanism within the film. This in turn will determine the sensitivity of film's resistance with temperature. This layer is incorporated into a calorimeter and hence this study would help to determine the accuracy of calorimeters.

For the first part, I prepared TEM specimens from the samples that were grown last year. For plan view specimens, we first cut the sample into a 3mm circular shape using an ultrasonic cutter. We used a hand polishing tool and a grit paper to thin the samples down to 70-100um followed by a dimple grinder which will eventually thin the center of the sample to around 5um. We then used an ion mill to make the center thin enough to pass electron beams through it. The specimens were then viewed under TEM and diffraction image Cross section specimens are also produced in the similar except for some additional processes which includes stacking the sample, cutting off the cylindrical core, securing in a copper ring and slicing them prior to the polishing.

I also got an opportunity to get involved with fabrication of calorimeters this summer. I learnt the process like photolithography, mask aligning and thin film processing using sputtering PVD and e beam system. We had two different types of wafers(substrates), one which was silicon coated with silicon dioxide and the other was sapphire. There were several devices in a single wafer. Some of the wafers we worked with had electrodes, thermometers and heaters while some had a thermalization layer instead of heater. Insulators were deposited between each of these layers for protection. We deposited chrome gold or chrome silver for electrodes, TiCr and SiO2 for the thermometer layer, titanium for the heater and titanium with gold for the thermalization layer. Before depositing each layer performed photolithography and formed desired patterns using the mask aligner. After depositing each layer we measured the resistance and thickness to check if the devices were being formed as expected.

I learnt better sample handling techniques and the fabrication process. I came to know that sensors and chips are also fabricated in a similar way. Now, the patterns that I can see in chips makes more sense.

Investigating Methods of Data Acquisition to find the Specific Heat Value of Samarium Hexaboride (SmB6) with the Aim of Precise Classification

Name: Lillian Phillips
Year of Graduation: 2025
SURF Advisor(s): Nat Fortune, Physics
Field of Study: Physics
Co-Authors: Grant Roll

Title: Investigating Methods of Data Acquisition to find the Specific Heat Value of Samarium Hexaboride (SmB6) with the Aim of Precise Classification
Abstract: A topological insulator is a material that maintains two seemingly-contradicting properties: one side behaves as an insulator, while the other is able to conduct electricity. The compound samarium hexaboride (SmB6) is considered a topological insulator–however, while its magnetoresistance supports this definition, its magnetic torque suggests it is actually a metal. In hopes of unraveling this mystery, Professor Fortune led our experimental efforts concerning the material's ability to absorb and dissipate thermal energy–its specific heat–and how these definitive observations might offer better insight into its precise classification.
We began our research by familiarizing ourselves with python to explore various methods of data acquisition and analysis. Our primary task was to develop a practical approach for a specific heat measurement. To simulate this crucial step, we built an RC circuit by adding a resistance and a capacitor in series. We then employed a LabJack T7, a multifunction DAQ device designed to receive, interpret, and send voltages between the computer and the lab equipment. We programmed the LabJack to output a steady voltage punctuated by brief rests, thereby allowing us to view how the material might heat and cool in controlled conditions.
Further, we utilized a fit program written by our professor to expand upon a range of previously-collected data, and developed the code such that the information produced could be communicated (via python) across a diverse range of lab equipment. We concurrently readied several heaters, thermometers, and devices for use at the National High Magnetic Field Laboratory (NHMFL) in Tallahassee, Florida, where we would continue our work under a generous NSF grant. There we implemented our methods of calibration, manufactured small-scale equipment, and began some preliminary data collection that will propel our research on campus.
While our investigation is far from complete, we begin the school year with a strong foundation in methods of data acquisition, analysis, and experimentation, and we look forward to exploring the question of samarium hexaboride's nebulous classification further.

Hemigrapsus sanguineus: Cardiac Stomach Dissection and Prey Identification // Littorina obtusata and Hemigrapsus sanguineus: Predator-prey interactions

Name: Leah Corckran
Year of Graduation: 2025
SURF Advisor(s): L. David Smith, Biological Sciences
Field of Study: Marine Ecology
Co-Authors:

Title: Hemigrapsus sanguineus: Cardiac Stomach Dissection and Prey Identification // Littorina obtusata and Hemigrapsus sanguineus: Predator-prey interactions

Abstract: Hemigrapsus sanguineus: Cardiac Stomach Dissection and Prey Identification

The Asian Shore Crab Hemigrapsus sanguineus is an invasive crab species that have been introduced to the Gulf of Maine. They are competing with the native crab species as well as the established invasive crab Carcinus maenas. H. sanguineus is an omnivore. The species is currently expanding its invasive range north in the Gulf of Maine. By analyzing the gut contents of H. sanguineus, their impact on native prey species can be evaluated. Crabs were collected from Plum Cove, Massachusetts, and transported in a state of cold torpor before being frozen for dissection. Dissection and analysis of the cardiac stomach of 33 crabs showed various food items, including algae, small arthropods, and mussels. The dissections were completed following a dissection guide for the striped shore crab, Pachygrapsus crassipes. The stomachs, once isolated, were flushed with sea water and photographed under a dissection microscope. I found no conclusive evidence of shell fragments, which suggests that H. saguineus may not prey heavily on Littorina obtusata, the native periwinkle snail. Preliminary conclusions suggest a greater consumption of plant matter by crabs with smaller carapace widths and claws. Seven crabs were found to have fragments of the bodies of small arthropods and copepods. Future experiments could consider the tides during which the crabs were collected versus the tides in which they feed. Future research could also attempt to identify stomach contents through DNA isolation and identification and observe Littorina obtusata stomach contents following predation in controlled lab feedings.

Littorina obtusata and Hemigrapsus sanguineus: Predator-prey interactions

The invasive crab species Hemigrapsus sanguineus is present in the southern Gulf of Maine, the native habitat of L. obtusata. The purpose of this study is to determine the effect of predation cues from H. sanguineus on shell thickness and size of L. obtusata. L. obtusata respond to chemical cues from the invasive European Green Crab, Carcinus maenas, but the interaction between L. obtusata and H. sanguineus is unknown as it spreads into the northern territory of the snail. L. obtusata were collected from Back Beach, MA, and Carrying Place Cove, ME. The snails were then separated into four treatment groups: Northern (cold) temperature with crab cue, Northern temperature without crab cue, Southern (warm) temperature with crab cue, and Southern temperature without crab cue. Half the snails from each source region were reared at the temperature of the opposite region. The purpose of these four groups is to determine if the temperature or crab cue affects the shell thickness and size of the snail.

Preliminary study of Baltimore Checkerspot

Name: Laura Dreher
Year of Graduation: 2024
SURF Advisor(s): Mariana Abarca, Biological Sciences
Field of Study: Insect ecology
Co-Authors: Valeria Bastardo Brito

Title: Preliminary study of Baltimore Checkerspot

Abstract: This summer we worked with Dr. Mariana Abarca on her research study that aims to assess the role of maternal environment on offspring performance and resilience to environmental stress of the imperiled Baltimore Checkerspot and to. We planned to do this by exposing mothers and their offspring to environmental treatments, which are either cold snap, heat wave, or control conditions. By comparing survival and development time among groups, we would assess the role of maternal environment on offspring performance and quantify variation in stress tolerance among genetic families. This work is important to understand the impact that global climate change will have on populations of Baltimore Checkerspots. However, our colony of Checkerspots became parasitized by a wasp that we believe to be Cotesia euphydryadis. Only one checkerspot reached adulthood, making our planned experiment impossible to complete.

Although we didn't accomplish the goal we set out to, the research we did this summer was useful to look into different aspects of checkerspot development, and make a solid foundation for the future of working with both lab-raised and wild checkerspots. Checkerspot eggs were collected from the wild and raised in the lab, producing around 1500 pre-diapause caterpillars with which to start a future lab colony. We wrote up a detailed account of how we took care of the checkerspots to provide a foundation for future students and researchers raising checkerspots in the lab, as well as created an outline for a conservation plan to maintain checkerspot habitat at MacLeish field station and create habitat on the Smith College campus.

We weren't able to get any statistically viable data out of this summer's research, but we did notice some trends that encourage future research with the checkerspots. The caterpillars were split into two feeding groups, one group feeding on newly acquired exotic host plantain (Plantago lanceolata) and the other on their native host turtlehead (Chelone glabra). Measurements of the amount of food eaten, caterpillar mass, pupal mass, and final life stage provided insight that aligned with previous knowledge of the checkerspot, that the exotic plantain is a lower quality host than native turtlehead. We also found that the caterpillars' diet had an effect on the parasitoids as well, where only 1 of 7 successfully parasitized caterpillars had been feeding on plantain. This trend invites many questions about how the two hosts can impact the success of this parasitoid. We will continue to explore these questions with the lab colony that we reared this summer.

Fig 1. This figure shows the final life stage (Cat: caterpillar, Pup: pupa, Fe: adult with malformations, But: butterfly, Wasp: parasitoid wasp) of every caterpillar in our initial colony, depending on which host they were feeding on. Larvae were collected in Franklin county, from the roadside between Nasami nursery and Mass Wildlife great swamp management area

Justified MCQ Design and Trial

Name: Hanna Lee
Year of Graduation: 2024
SURF Advisor(s): Pablo Bolton, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Justified MCQ Design and Trial

Abstract: Exams are essential for evaluating students' understanding of various concepts; however, there is a tradeoff between tests that allow quick grading and those that have more informative answers, and that allow better feedback.Therefore, a middle ground could be found where insights into the student's reasoning can be found and where relatively quick grading is possible. I collaborated on developing a hybrid exam protocol, called the Justified Multiple-Choice Question Exam (JMCQ), that addresses several shortcomings of traditional MCQ and Free-form answer exams. A JMCQ is a multiple-choice question in which a student must justify why each discarded answer is wrong, therefore offering an insight into their reasoning that can be used to craft feedback, refine grading, or even detect/deter cheating. The goal of this SURF project was to finalize the exam protocol, question items, to refine the experimental design, and to help prepare a trial run of the protocol during the summer, and the first full run during the Fall. I started by performing a literature review on the evaluation of short answer, multiple choice, and hybrid exam formats which, in collaboration with the JMCQ protocol team, allowed me to develop the exam format. In addition, I helped produce sample justifications for each question to help as a reference when grading. By the end of the SURF period, I was able to complete the question templates for the exams that would be implemented in the summer trial and the fall semester. In addition, I helped design the pre/post feedback surveys needed to evaluate the effectiveness of the tests.
The second part of my project was to design an automatic system that could analyze justification similarities in order to provide a likelihood that they reflect the reference justifications. These would allow the grader to get a sense of which justification is most likely correct. A literature review on Automatic Short-Answer Grading helped determine the best approach to use for Justification checking, which will be implemented once Fall data is obtained.
The literature review process developed my synthesis and analysis skills; my work on the protocol design and materials allowed me to use and refine skills related to broad experimental design, data analysis through statistics, and organizing a research project involving human subjects. Future work will focus on the automatic system for justification grading; this is to be completed after the Fall semester during a Special Studies Course.

Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Name: Lana Sabbah
Year of Graduation: 202
SURF Advisor(s): Benita Jackson, Psychology
Field of Study: Psychology
Co-Authors: Benita Jackson, Maya Kiernan, Leyla Akin, Uzma Malik, Lana Sabbah, & Anna Peel

Title: Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Abstract: Studies show that even brief time in settings with nature (e.g., a park) increases cognitive function, compared to similar time spent with less nature-based elements (e.g., buildings; Nisbet & Zelenski, 2011). One important predictor of cognitive function that, to our knowledge, has yet to be linked to exposure to nature is psychological flexibility. Arguably a critical key common pathway to mental and physical health (Kashdan & Rottenberg, 2010), psychological flexibility is a psychological characteristic holding promise as a potent point of intervention. For this project we sought to test for a unique association between nature exposure and psychological flexibility. Additionally, we identified potential pathways (e.g., time perspective), amplifiers (e.g., self-compassion), and dampeners (e.g., rumination) for the link between nature exposure and psychological flexibility, should they exist. We designed two sets of empirical examinations: a correlational study to test initial associations, and an experimental study, to test a replication and extension Nisbet and Zelenski's (2011) research on nature exposure and cognition, in our version, focusing on psychological flexibility as the dependent variable. Our pilot correlational study drawing from data collected on a sample of college students Fall 2021 (N = 52) showed statistically significant negative correlations between exposure to nature and present fatalist time perspective (r = -.28, p = .042), the latter of which was also inversely associated with psychological flexibility (r = -.29, p = -.044). Relevant to our increasingly online world, building on these findings we will further investigate the effects of virtual exposure to natural and built environments on psychological flexibility and potential pathways linking them in a randomized control trial. We created, edited, and piloted a range of film clips of natural and built environments on campus as an experimental manipulation that we will test among students in the 2022-2023 school year. If such a link exists, this can lay groundwork for later intervention research testing the 'minimal nature dose' - including amount of time and type (in person v. virtual) - to boost psychological flexibility.

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Developing Inclusive Health Education Curricula for Smith College Performing Arts Programs & Organizations

Name: Ava Silverman
Year of Graduation: 2024
SURF Advisor(s): Erica Tibbets, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies
Co-Authors: Ava Silverman, Erica Tibbetts

Title: Developing Inclusive Health Education Curricula for Smith College Performing Arts Programs & Organizations

Abstract: Background: Inspired by previous work on a literature review investigating eating disorder risk factors for trans and gender-nonconforming (TGNC) commercial dancers, this project attempts to identify and address issues impacting student-performers at Smith College at the community and organizational level, while simultaneously supporting individuals at the intrapersonal level.

Methods: A survey identifying needs of Smith College students participating in curricular or co-curricular performing arts programs and organizations was conducted. The goal of this survey was to identify the needs of a wide range of student-performers at Smith College in order to (1) devise a series of evidence-based curricula designed for the purpose of student-performer health education and (2) formulate an informational guide for instructors on creating healthy performing arts spaces for performers of all identities. Participants were asked about what performing arts activities they participate in, what they believe the most pertinent issues impacting student-performers are, what they wish their instructors and organization leaders knew about supporting performer wellness, and the types of activities they enjoy in an educational setting. We encouraged participants to consider not only a holistic conception of wellness which includes physical, mental, emotional, social, spiritual, financial, occupational, and environmental contributions, but also one that is aware and affirming of all areas of identity, placing emphasis on identities which have been marginalized in the performing arts and the world.

Current Work: Based on priorities identified through the survey, we are currently developing a series of evidence-based health education curricula, accompanied by guides for instructors and leadership. By using these strategies in tandem, we seek to address the issues at an organizational level, as well as empower individuals to advocate for themselves in environments that are not attuned to their needs. This summer, we focused on creating content on vocal health and self-advocacy, with future plans to cover topics such as injury prevention & recovery, collaborative leadership, body image & eating disorders, general mental health & emotional well-being, and supportive community-building. The curricula will be released periodically as they are completed and reviewed by both the Sport for Social Change Lab, the Schacht Center for Health & Wellness, and Smith College Community Health Organizers (CHOs). Once released, academic departments and student organizations will be able to request workshops with CHOs, who will take on the outreach and implementation arm of the project.

A Dormancy Mystery: Pedicularis canadensis

Name: Virginia,Griswold
Year of Graduation: 2023
SURF Advisor(s): Tim Johnson, Biological Sciences/Botanic Garden
Field of Study: Biological Sciences
Co-Authors:

Title: A Dormancy Mystery: Pedicularis canadensis

Abstract: With climate change threatening plant diversity, conservation efforts such as seed banks and living collections at botanic gardens will become increasingly important. Consequently, studying how seeds break their dormancy and germinate will be vital to preserving native species that cannot be stored in seed banks for long periods. Pedicularis canadensis, a perennial forb and hemiparasite native to North America, is neither a rare species nor threatened but its seeds are difficult to germinate, and there is a lack of research on P. canadensis's dormancy type. Studying dormancy of P. canadensis serves to expand gaps in the literature on this species and build the Smith College Botanic Garden's protocols for studying seed dormancy and conservation.

During the 2021-2022 academic year, Larz von Huene '22, work-study intern with Director Tim Johnson, did gibberellic acid (GA; plant hormone) trials on P. canadensis and found that GA was a condition that would germinate the seeds despite trying cold stratification in darkness. Larz's results suggested that the seeds showed signs of physiological dormancy, but there appeared to be an unknown morphological component involved (Baskin and Baskin, 2014). Expanding on Larz's work, my initial review of their results suggested the dormancy type could be intermediate simple morphophysiological dormancy, meaning that the seeds would need warm temperatures in the summer to break physiological dormancy and autumn temperatures to break morphological dormancy and promote embryo elongation, then germinate in the spring (Baskin and Baskin, 2014).

Finding that warm temperatures (15-25°C) grow other Pedicularis species' (Li et al., 2007) and grow embryos of species with intermediate simple morphophysiological dormancy (Cho et al., 2020; Galíndez et al., 2018), I hypothesized that warm temperatures (20-30°C) promote embryo growth in P. canadensis. The experiment consisted of three incubation temperatures to test embryo growth: 30/20°C, 18°C, and 15/5°C. Over 10 weeks, embryo length, seed length, embryo width, and seed width were measured every two weeks for each temperature. Prior to conducting the experiment, seed collection and harvesting, tetrazolium (seed viability) testing, and protocol review took longer than anticipated, so the experiment is still underway and will conclude in September 2022. So far, a key finding is that embryos are growing inside the seed prior to germination, which supports the presence of a morphological dormancy component.

Preliminary study of the Baltimore Checkerspot

Name: Valeria Bastardo Brito
Year of Graduation: 2025
SURF Advisor(s): Mariana Abarca, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Laura Dreher

Title: Preliminary study of the Baltimore Checkerspot

Abstract: This summer we worked with Dr. Mariana Abarca on her research study that aims to assess the role of maternal environment on offspring performance and resilience to environmental stress of the imperiled Baltimore Checkerspot. We planned to do this by exposing mothers and their offspring to environmental treatments, which are either cold snap, heat wave, or control conditions. By comparing survival and development time among groups, we would assess the role of maternal environment on offspring performance and quantify variation in stress tolerance among genetic families. This work is important to understand the impact that global climate change will have on populations of Baltimore Checkerspots. However, our colony of Checkerspots became parasitized by a wasp that we believe to be Cotesia euphydryadis. Only one Checkerspot reached adulthood, making our planned experiment impossible to complete.

Although we didn't accomplish the goal we set out to, the research we did this summer was useful to look into different aspects of Checkerspot development, and make a solid foundation for the future of working with both lab-raised and wild Checkerspots. Checkerspot eggs were collected from the wild and raised in the lab, producing over 1000 pre-diapause caterpillars with which to start a future lab colony. We wrote up a detailed account of how we took care of the Checkerspots to provide a foundation for future students and researchers raising Checkerspots in the lab, as well as created an outline for a conservation plan to maintain Checkerspot habitat at MacLeish field station and create habitat on the Smith College campus.

We weren't able to get any statistically viable data out of this summer's research, but we did notice some trends that encourage future research with the Checkerspots. The caterpillars were split into two feeding groups, one group feeding on newly acquired exotic host plantain (Plantago lanceolata) and the other on their native host turtlehead (Chelone glabra). Measurements of the amount of food eaten, caterpillar mass, pupal mass, and final life stage provided insight that aligned with previous knowledge of the Checkerspot, that the exotic plantain is a lower quality host than native turtlehead. We also found that the caterpillars' diet had an effect on the parasitoids as well, where only 1 of 7 successfully parasitized caterpillars had been feeding on plantain. This trend invites many questions about how the two hosts can impact the success of this parasitoid. We will continue to explore these questions with the lab colony that we reared this summer. Fig 1. Shows the final life stage (Cat: caterpillar, Pup: pupa, Fe: adult with malformations, But: butterfly, Wasp: parasitoid wasp) of every caterpillar in our initial colony, based on which host they were feeding on. Larvae were collected at a roadside between Nasami nursery and Mass Wildlife great swamp management area.

Bridging Conservation Efforts Between the Smith College Botanic Garden and Beyond

Name: Krystal Bagnaschi
Year of Graduation: 2022
SURF Advisor(s): Jesse Bellemare, Biological Sciences; John Berryhill
Field of Study: Biology, Conservation Ecology
Co-Authors:

Title: Bridging Conservation Efforts Between the Smith College Botanic Garden and Beyond

Abstract: The focus of this SURF project was the investigation and implementation of Priority 1 in the Smith College Botanic Garden Collections Management Plan, which is "Putting Collections to Work For Regional Plant Conservation." My work this summer was split into two distinct projects, one focused on regional plant conservation efforts in southern New England and one focused on larger-scale conservation of a threatened tree species from the southeastern U.S. For the first project, I assisted Landscape Curator John Berryhill with work pertaining to the Smith College Botanic Garden's work in rare plant monitoring and establishing conservation collections of local native plants for horticultural use and ecological restoration. In this work, I was responsible for conducting data and seed collection through conservation partnerships between the Botanic Garden and the Native Plant Trust. I focused on rare plant monitoring and identifying collection sites for target species for conservation collections. In order to conduct rare plant surveys, I was responsible for compiling resources for the identification of assigned species as well as generating reports for Native Plant Trust that will serve to guide future conservation action.

For the second project, I traveled to southwestern Virginia in August and contributed to field surveys that supported the ongoing graduate research of John Berryhill in the Bellemare Lab to evaluate in situ population dynamics of mountain magnolia (Magnolia fraseri), a tree species native to the southern Appalachians in the southeastern U.S. This species is limited to higher elevation forests in the region and is of conservation concern because it might be susceptible to the "escalator effect" with climate change, as its distributions retreat to higher and higher elevations. This work was built off of previous research done by Jesse Bellemare and John Berryhill, and last summer's SURF student McKenzie Swart. My participation in this week-long field expedition was possible thanks to supplemental research support funds from the E.B. Horner Fund. We surveyed populations of Magnolia fraseri in its native forest habitat, deployed environmental sensors, and collected seed. Most strikingly, our upslope surveys at and above the upper elevation limit of adult trees found little evidence of upslope migration by seedlings or saplings even though lower elevation populations are in decline. This suggests an alarming contraction of the species' distribution in the mountains might be underway due to climate change. This research will contribute to future conservation efforts for Magnolia fraseri and the seeds we collected will help establish a long-term ex situ conservation collection at the Smith College Botanic Garden.

This experience contributed greatly to my understanding of conservation efforts and the research needed to guide them. I was able to expand my knowledge and tools as an early conservationist and recent graduate of Smith College, and this will be an invaluable experience going forward.

The effect of ear canal shape on Reflectance measurements

Name: Jingxin Feng
Year of Graduation: 2024
SURF Advisor(s): Susan Voss, Engineering
Field of Study: auditory testing
Co-Authors: Maya Gilliom

Title: The effect of ear canal shape on Reflectance measurements

Abstract: Auditory diagnostic tests assume ear canals are cylindrical with a diameter of 7.5mm. They use this assumption to designate a fixed healthy range of reflectance values for human ears, and that all reflectance occurs at the tympanic membrane and more medial locations. From previous studies, however, we learned that there is more variability in reflectance than these tests acknowledge in healthy ears. Our goal was to show whether or not the shapes of ear canals contribute to reflectance.

We used CT scans, OsiriX MD (a radiology software), and 3D modeling softwares to create 3D prints of 10 different human ear canals. We also made an artificial ear based on a design by Kren Monrad Norgaard that has the same reflectance as the industry-standard Larson-Davis artificial ear. We attached each canal to the artificial ear we made, and by doing this, we controlled tympanic membrane reflectance so that all the differences in reflectance were caused by differences in canal geometry and not the terminating ear.

To ensure our results were accurate, we developed a method to ensure that the connection between the artificial ear and the printed ear canal was acoustically sealed. We also designed experiments to show that the properties of our printed material did not affect reflectance. We did this by printing several control cylinders of different lengths and resolution and comparing them to smooth copper tubes of corresponding lengths.

The next step will be to calculate the individual reflectance of each printed human ear canal using each ear canal's actual cross sectional area at the location of the measurement probe, which other members of our lab measured. This will help us to define the range for reflectance for normal hearing ears, therefore validating that variability of reflectance values from diagnostic acoustic tests rely on individual ear canal geometry.

Investigating Methods of Data Acquisition to find the Specific Heat Value of Samarium Hexaboride (SmB6) with the Aim of Precise Classification

Name: Katherine Roll
Year of Graduation: 2025
SURF Advisor(s): Nat Fortune, Physics
Field of Study: Physics
Co-Authors: Lily Phillips

Title: Investigating Methods of Data Acquisition to find the Specific Heat Value of Samarium Hexaboride (SmB6) with the Aim of Precise Classification

Abstract: A topological insulator is a material that maintains two seemingly-contradicting properties: one side behaves as an insulator, while the other is able to conduct electricity. The compound samarium hexaboride (SmB6) is considered a topological insulator–however, while its magnetoresistance supports this definition, its magnetic torque suggests it is actually a metal. In hopes of unraveling this mystery, Professor Fortune led our experimental efforts concerning the material's ability to absorb and dissipate thermal energy–its specific heat–and how these definitive observations might offer better insight into its precise classification.
We began our research by familiarizing ourselves with python to explore various methods of data acquisition and analysis. Our primary task was to develop a practical approach for a specific heat measurement. To simulate this crucial step, we built an RC circuit by adding a resistance and a capacitor in series. We then employed a LabJack T7, a multifunction DAQ device designed to receive, interpret, and send voltages between the computer and the lab equipment. We programmed the LabJack to output a steady voltage punctuated by brief rests, thereby allowing us to view how the material might heat and cool in controlled conditions.
Further, we utilized a fit program written by our professor to expand upon a range of previously-collected data, and developed the code such that the information produced could be communicated (via python) across a diverse range of lab equipment. We concurrently readied several heaters, thermometers, and devices for use at the National High Magnetic Field Laboratory (NHMFL) in Tallahassee, Florida, where we would continue our work under a generous NSF grant. There we implemented our methods of calibration, manufactured small-scale equipment, and began some preliminary data collection that will propel our research on campus.
While our investigation is far from complete, we begin the school year with a strong foundation in methods of data acquisition, analysis, and experimentation, and we look forward to exploring the question of samarium hexaboride's nebulous classification further.

Comparative Genomics of Diverse Ammonia Oxidizing Archaea from Waikite Valley, New Zealand

Name: Tillie Slosser
Year of Graduation: 2025
SURF Advisor(s): Luce Ward, Geosciences
Field of Study: Geobiology
Co-Authors: Luce Ward

Title: Comparative Genomics of Diverse Ammonia Oxidizing Archaea from Waikite Valley, New Zealand
Abstract: The oxidation of ammonia first to nitrite, then nitrate, is thought to be a key part of the Earth's essential biogeochemical nitrogen cycle. Ammonia-oxidizing archaea (AoA) are incredibly diverse, and outnumber their bacterial counterparts in many studied environments, but are relatively understudied (e.g. Hatzenpichler 2012).
Here, we describe a set of new ammonia oxidizing archaea from hot springs in the Taupo Volcanic Zone (TVZ) of New Zealand, specifically Waikite Valley. These genomes add to our understanding of the diversity of AoA. These new genomes, of family Nitrososphaeraceae, were isolated from hot springs in the Taupo Volcanic Zone (TVZ) of New Zealand. The geochemistry of the area, such as its large temperature gradients, near-marine pH, and moderate sulfide/sulfate concentrations, make it an ideal environment to investigate Proterozoic-analog microbial mat communities. These genomes were sequenced as part of a larger effort to characterize the metabolic potential and activity of Proterozoic-analog microbial mats.
The added diversity of these genomes improves the AoA evolutionary tree, most importantly by adding new information about early-diverging groups. These early divergences are key to our understanding of ammonia-oxidizing archaea's origin and early evolution. Ultimately, improved sampling of basal genomes–including that performed here–will help us get closer to understanding the origin of nitrification.

Expanded Diversity of Chloroflexales Revealed by Genome-Resolved Metagenomic Sequencing of Novel Environments

Name: Elm Markert
Year of Graduation: 2025
SURF Advisor(s): Luce Ward, Geosciences
Field of Study: Geobiology
Co-Authors: Luce Ward

Title: Expanded Diversity of Chloroflexales Revealed by Genome-Resolved Metagenomic Sequencing of Novel Environments

Abstract: The majority of life is microbial, and has been throughout Earth history. As such, understanding the evolution and biochemistry of microorganisms can grant us a greater understanding of environments through time. Studying the evolution of modern microorganisms is particularly important because there is little fossil record to give us an understanding of historical microorganisms. Hot springs, environments that are hospitable to communities of bacteria and archaea while generally being inhospitable to eukaryotic algae and animals, are useful natural laboratories to study unfamiliar metabolic processes that have historically been unable to be studied in culture. This is especially true because these environments often resemble conditions which may have been more common at earlier points in Earth history.

From hot springs and other environments, metagenome-assembled genomes (MAGs) provide an opportunity to sample the diversity of microbes extant today without being limited by bottlenecks of isolating and culturing individual strains. MAGs can be gathered and analyzed to gain new insights into the distribution and evolutionary history of various metabolisms in microorganisms. Chloroflexi, an incredibly diverse group of bacteria which includes anoxygenic phototrophs that may have played important roles in the evolution of photosynthesis, are a particularly promising target for MAG-based analyses to gain better insight into their metabolic diversity and history.

Utilizing a large genome set composed of MAGs as well as reference genomes, we determined the presence/absence and evolutionary relationships of a range of metabolic proteins across a uniquely diverse set of Chloroflexi genomes. VWhere previous culture work only allowed for this kind of characterization of a few genera, comparative genomics and phylogenetics with MAGs has revealed far greater diversity, specifically within the Chloroflexi. This new knowledge leads us closer to understanding how carbon fixation pathways, phototrophy, and other metabolisms evolved over hundreds of millions of years.

Characterization of Fn3-PVDMA Conjugates Synthesized via Primary Amine-Azlactone Chemistry

Name: Yeji Lee
Year of Graduation: 2022
SURF Advisor(s): Maren Buck, Chemistry; Sarah Moore, Engineering
Field of Study: Chemistry, Biology, Bioengineering
Co-Authors:

Title: Characterization of Fn3-PVDMA Conjugates Synthesized via Primary Amine-Azlactone Chemistry

Abstract: One major challenge of chemotherapy is that it lacks localization or site specificity. This results in indiscriminate apoptosis of malignant and benign cells in cancer patients, leading to demoralizing side effects. Targeted drug delivery promotes drug interactions with diseased cells to prevent uptake of toxic therapeutics by healthy cells. Protein-Polymer Conjugates (PPCs) is an attractive targeted drug delivery method for treating diseases including but not limited to cancers. In short, a protein that targets diseased sites is linked to a polymer which carries a set of the same or multiple therapeutic drugs. In my study, I use poly(2-vinyl-4,4-dimethyl-azlactone), or PVDMA, a reactive polymer with diverse chemical functionality, and fibronectin type III (Fn3) proteins which can recognize and selectively bind with high affinity to $\alpha v \beta 3$ integrin receptors overexpressed in neovasculatures at cancer site(s). To conjugate the two materials, the hydrophobic polymer is partially functionalized with a water-soluble chemical group. The Fn3 proteins are synthesized and purified to react with the functionalized polymer via primary amine chemistry. The conjugates are then characterized and analyzed mainly on SDS-PAGE and Size Exclusion Chromatography (SEC). One obstacle of PPC synthesis is the susceptibility of PVDMA to hydrolysis. Hydrolysis of the polymer generally lowers conjugation efficiency, and therefore, this summer, I aimed to better understand the rate of polymer hydrolysis using IR. Another focus was to obtain a reliable polymer control SEC data for the characterization and purification of the conjugates. However, both the conjugates and the polymer control eluted at 21 min and 24 min at 220 nm. The difference in the absorbance intensities at each elution time between the two samples suggested that the peaks represented different structures, given that the amount of samples loaded was the same. Another method, which does not (only) separate particles by their hydrodynamic radii, is required to purify the conjugates in the future.

Triangular patterns in springer fiber flags

Name: Yunxi Yan
Year of Graduation: 2025
SURF Advisor(s): Julianna Tymoczko, Mathematics and Statistics
Field of Study: Mathematics and Statistics
Co-Authors:

Title: Triangular patterns in springer fiber flags
Abstract: During the summer of 2022, I joined Professor Julianna Tymoczko's research group to study the pattern of entries in flags of Springer Fibers. We explored ways to find entries in flags using linear algebra. However, as the matrix grows, the computation behind the matrix becomes increasingly tedious. Therefore, we tried to identify potential patterns in all matrices and simplify the computation as much as possible. After collecting data based on calculations of 9*9 Springer flags, I found triangular patterns in the entries and proved some of the reasons why and when these triangular patterns show up.

Development of "Direct-Ink Painting" Functional Patterning of Azlactone Hydrogels for Actuation

Name: Anna Lynch
Year of Graduation: 2023
SURF Advisor(s): Maren Buck, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Development of "Direct-Ink Painting" Functional Patterning of Azlactone Hydrogels for Actuation

Abstract: Stimuli-responsive hydrogels are swollen polymer networks that exhibit shape-altering characteristics when introduced to a change pH, temperature, or other external stimuli. (1) The reversibility of this property is especially advantageous in the biomedical field, where these flexible materials can be used in tissue engineering and drug delivery systems as actuators. (2) Previous projects in the Buck lab have used photofunctionalization to selectively pattern poly(2-vinyl-4,4'-dimethyl azlactone) (PVDMA) hydrogels with primary amines for the development of pH-responsive actuators. Upon light irradiation, the amine is released from a protecting group and initiates ring-opening reactions with the polymer's azlactones. (2) While this has proven successful, this method is synthetically demanding and limits functionality of the network to one functional group at a time. For these reasons, new functionalization methods must be explored.

During SURF, alternative patterning techniques were investigated with the goal of improving actuation speed and repeatability while reducing material consumption. Inspiration was first taken from Sui et. al's "direct-ink writing" method by manually drawing patterns onto the surface of the hydrogel using a capillary tube as a pen and a solution of dimethyl sulfoxide and dimethylethylenediamine (DMEDA), a primary amine, as ink. (3) Although "direct-ink writing" suggested rapid actuation upon functionalization for one hour, the capillary action between the tube and the surface of the hydrogel was too weak to draw thin, precise patterns. This was improved upon by plasticizing the hydrogel with dimethyl sulfoxide and by painting on the gel using a paint brush rather than a capillary tube. Confirmed with fluorescence microscopy, functionalization through "direct-ink painting" effectively patterned the hydrogels with lines of various thicknesses. Pilot studies of actuation demonstrated rolling and unrolling upon immersion into hydrochloric acid and sodium hydroxide, respectively. Unexpectedly, this actuation was not repeatable after five cycles, as the hydrogels began to fracture. While this is still under investigation, it was hypothesized that this functionalization method prevented DMEDA from diffusing through the depth of the hydrogel. This would dramatically reduce the number of azlactones functionalized and make the network more susceptible to hydrolytic degradation. Overall, this project made significant progress towards developing "direct-ink painting" as a novel, robust functionalization method for azlactone hydrogels. This work remains in progress as it will be continued as an Honors Thesis during the Fall 2022 semester.

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Altered movement coordination may predispose to low back pain among female collegiate rowers

Name: Giovanna Rocchio
Year of Graduation: 2023
SURF Advisor(s): Stephanie Jones, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies
Co-Authors: Katelyn Pickunka

Title: Altered movement coordination may predispose to low back pain among female collegiate rowers

Abstract: Rowing is an asymmetric sport that consists of repetitive sweeping movement patterns to one side of the body. With decreased diversity of movements reinforced by significant training time and load, there may be a reduced ability of trunk musculature to protect the spine and effectively prevent lower back injury. Although there is a high incidence of low back pain in rowers, the specific mechanism of injury has not been conclusively determined.

In the Jones lab, we are researching muscle activation and movement patterns among Smith College's collegiate female rowers to understand how altered patterns may relate to back pain. For data collection, subjects had wireless EMG sensors placed on 15 muscles of the trunk, bilaterally and lower leg, unilaterally. Reflective markers were placed on the body segments to analyze segmental movements and joint angles (Figure 1). This summer, work focused on analyzing two types of data. EMG data were analyzed (Gio, Katelyn) using custom software developed in MATLAB to examine the muscle activation onsets and magnitudes to identify relative timing of muscle bursts and whether asymmetric patterns were present. EMG analysis was conducted across several conditions: fixed rowing vs. free rowing, which enabled translation of the rowing ergometer thus increasing the degrees of freedom of the motion; and low vs. high stroke rate, which increased the force and velocity requirements of the movement; in both cases enabling us to perturb and probe motor coordination. Analysis required inspecting the EMG traces to ensure data were of sufficient quality, verifying the onsets/offsets selected by the program algorithm with the ability to override and manually select. These data were also used to determine which muscles were utilized at higher levels and might therefore be susceptible to fatigue during training. In addition, marker data were tracked (Gio) for each participant using Qualisys Track Manager software. Subject-specific 3-dimensional models were created (Katelyn) using Visual 3D software in preparation for analysis of segment and joint angles (Figure 2). Finally, we contacted past participants (Gio) to complete 1-year post-study interviews to track any injuries that may have occurred since their visit to the lab. A literature review was also completed to help with future projects relating to lower back pain in rowers.

The EMG data analyzed this summer were presented in poster format at the International Society of Posture and Gait Research World Congress in Montreal at the beginning of July. SURF students were instrumental in editing and creating figures for the poster.

Images:
Figure 1. Schematic of a rower at the catch (left), midpoint (middle) and finish (right) of the drive phase of the rowing stroke acquired using motion capture.
Figure 2. 3D skeletons of participants acquired using Visual 3D professional software.
Figure 3.

Graphs and Their Motions: Developing Web-Based Graph Viewers and Interactive Motion Graph Applications

Name: Emma Civello
Year of Graduation: 2024
SURF Advisor(s): Illeana Streinu, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Graphs and Their Motions: Developing Web-Based Graph Viewers and Interactive Motion Graph Applications
Abstract: During summer 2022, I worked on two graph-related projects in Professor Streinu's Linkage Lab.
The first project was a graph-viewer program which uses HTML, CSS, Javascript, and PHP. The program reads files produced by Alexandra Camero (University of Massachusetts doctoral student) that contain information about a graph's nodes, edges, orbits, shifts, and unit cell. The program displays the information visually, through circles, lines, and adjustable labels and coloring. Because this program uses web-friendly languages, Professor Streinu can use it for academic conferences that require easily-accessible demonstrations. However, these languages have few built-in functions related to graphs, and so an important part of the project was creating such functions (for example, ones that scale coordinates to the screen and display multi-edges and loops). Collaboration was another important part of the project: Julia Ting (Smith College student) developed drawing functions, hoverable tooltip labels, and file-reading functions, and Professor Streinu guided each of us in writing modular code that would be compatible with what the other created. Next steps in this project include organizing the code and testing more graph files to confirm the program's accuracy.
In the second project, I made a series of Mathematica programs that show graphs in motion. The user can manipulate a quadrilateral, Henneberg I graphs, and more-general graphs by choosing a rigid component to pin and a node to use as a driver (the pebble game confirms that the choices are compatible). Then, the user can rotate the driver and see the resulting positions of the other nodes. The ultimate goal of this project is to develop such programs in web-friendly languages; we use the Mathematica programs to identify challenges that the final ones must overcome. For example, unexpected behavior can occur when the program calculates the new positions of nodes. The solution is chosen based on a positive or negative discriminant, and when discriminants are too close to 0 (a "singularity point"), the computer's representation of them becomes imprecise – sometimes showing negative or positive when the true value is the opposite. Thus, the incorrect positions may be chosen. A temporary solution is to limit the driver's rotation before the singularity point becomes an issue. Further steps in the project involve addressing the singularity issue more directly and expanding the web-friendly version (as before, creating Mathematica-esque features that Javascript's built-in libraries lack).

DNA-Conjugated Small Molecule Catalysts for Site-Selective Transformations

Name: Laura Bickart
Year of Graduation: 2023
SURF Advisor(s): David Gorin, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: DNA-Conjugated Small Molecule Catalysts for Site-Selective Transformations

Abstract: Carrying out complex chemical reactions in a biological system presents a number of difficulties, one of which being site selectivity, which is the ability to react with one functional group when there are multiple of that same group present. There are many applications where site selectivity would be beneficial. For example designing a catalyst to react selectively with the chemical that certain bacteria use to communicate, thus rendering the bacteria unable to replicate, and thus fighting off bacterial infection. It is for reasons such as this that the Gorin lab has been working on synthesizing DNA Coupled Small Molecule Catalysts (DCats). A DCat is composed of a DNA aptamer covalently linked to a small molecule catalyst; together they react with a specific substrate to catalyze a reaction. Previous work on this project has shown that a DNA tethered catalyst can increase the rate of ester hydrolysis by approximately 100- fold compared to its untethered counterpart. This method has also been shown to be effective on a number of different esters containing substrates.

My work this summer has focused on synthesizing a trifunctional substrate for a DCat to act upon. I am working on completing the eight step total synthesis of a novel molecule containing a cholate binding site for DNA, an allyl carbamate for a palladium catalyst to react with, and a fluorogenic leaving group to track the success of the palladium reaction. The synthesis starts with a carboxylic acid reduction, followed by a mesylation to prepare the molecule for the SN2 reaction that adds the fluorogenic umbelliferone group. The nitro group is converted to an amine in step four. A reaction is done to add protecting groups to the three alcohols in cholic acid, and then in step five of the synthesis it is bound to the amine formed in the previous step. Next is an ester hydrolysis to form a carboxylic acid. This is the group that is needed to perform the curtius rearrangement in the next step. This is a very interesting reaction that has only been done once in this lab (by me last summer), which results in the allyl carbamate group that palladium will react with. The last step will be to remove the protecting groups from the cholic acid group. I have successfully completed five of the eight steps, and have promising results for the sixth step. I will be presenting my research at a national ACS conference at the end of August, and I will continue this work throughout the fall semester as I complete my thesis.

Altered movement coordination may predispose to low back pain among female collegiate rowers

Name: Katelyn Pickunka
Year of Graduation: 2022
SURF Advisor(s): Stephanie Jones, Exercise and Sports Studies
Field of Study: Exercise and Sports Studies
Co-Authors: Gio Rocchio

Title: Altered movement coordination may predispose to low back pain among female collegiate rowers

Abstract: Rowing is an asymmetric sport that consists of repetitive sweeping movement patterns to one side of the body. With decreased diversity of movements reinforced by significant training time and load, there may be a reduced ability of trunk musculature to protect the spine and effectively prevent lower back injury. Although there is a high incidence of low back pain in rowers, the specific mechanism of injury has not been conclusively determined.

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The EMG data analyzed this summer were presented in poster format at the International Society of Posture and Gait Research World Congress in Montreal at the beginning of July. SURF students were instrumental in editing and creating figures for the poster.

Ecosystem service valuation of urban rivers in Global South cities

Name: Eugenia Rogers
Year of Graduation: 2025
SURF Advisor(s): Efadul Huq, Environmental Science and Policy
Field of Study: Environmental Science and Policy
Co-Authors:

Title: Ecosystem service valuation of urban rivers in Global South cities
Abstract: Urbanization is a major contributing factor to the degradation of river ecosystems worldwide. While being heavily dependent on ecosystem services, urbanization has rarely ever engaged in a symbiotic arrangement with river and wetland ecosystems. In formerly colonized countries, ecosystem services have been taken for granted and overly extracted without much thought to river ecologies. In contemporary global south cities, therefore, restoration is a central concern in urban environmental governance. In global south cities, the complexity of river and wetlands restoration is further complicated by widespread informality and institutional ambiguities. This research project seeks to develop a literature review on approaches to ecosystem services valuation for urban rivers and wetlands in global south cities. The review will compile the current understanding of the interaction between urban settlements and aquatic systems, summarize existing approaches to valuations, and identify their implications for valuing ecosystem services of rivers and wetlands by exploring the specific case of Dhaka, Bangladesh. The output will be a prototype conceptual valuation model based on the literature review study that may inform planning for complex social-ecological sustainability issues around rivers and wetlands in global south cities.

Title

Name: Shalom Mhanda
Year of Graduation: 2025
SURF Advisor(s): Glenn Ellis, Engineering
Field of Study: Engineering
Co-Authors:

Title: Transforming Engineering Education

Abstract: In my project, I designed a lesson activity and teachers' guide for middle schools that uses storytelling and transmedia to promote deep learning in engineering concepts. The lesson unit was about waves. The activity included a case study or scenario of Seattle and an upcoming tsunami predicted. The students were given information about ways to prevent and protect a place from a tsunami and the task was to use these devices and the information to protect this endangered space from a tsunami using the engineering design process. This activity gave the students information about actual devices used by engineers in predicting and preventing tsunamis and maps of places in Seattle to do the activity with. I also created a teachers' guide to help teachers facilitate the activity in the classrooms by providing them with information on materials required and how to navigate the online lesson resources. The second project I worked on was investigating ways to bring imaginative education in undergraduate engineering courses at Smith College to encourage engagement in classes. I looked at the EGR 270: Engineering Mechanics class and brainstormed how to bring imaginative education elements into it with the team. The first step was looking at the syllabus and redesigning it in a way that makes it accessible and allows students to engage with it. I left in the brainstorming stage of the project as I was doing another summer program.

Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Name: Maya Kiernan
Year of Graduation: 2022
SURF Advisor(s): Benita Jackson, Psychology
Field of Study: Psychology
Co-Authors: Leyla Akin, Uzma Malik, Lana Sabbah, & Anna Peel

Title: Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Abstract: Studies show that even brief time in settings with nature (e.g., a park) increases cognitive function, compared to similar time spent with less nature-based elements (e.g., buildings; Nisbet & Zelenski, 2011). One important predictor of cognitive function that, to our knowledge, has yet to be linked to exposure to nature is psychological flexibility. Arguably a critical key common pathway to mental and physical health (Kashdan & Rottenberg, 2010), psychological flexibility is a psychological characteristic holding promise as a potent point of intervention. For this project we sought to test for a unique association between nature exposure and psychological flexibility. Additionally, we identified potential pathways (e.g., time perspective), amplifiers (e.g., self-compassion), and dampeners (e.g., rumination) for the link between nature exposure and psychological flexibility, should they exist. We designed two sets of empirical examinations: a correlational study to test initial associations, and an experimental study, to test a replication and extension Nisbet and Zelenski's (2011) research on nature exposure and cognition, in our version, focusing on psychological flexibility as the dependent variable. Our pilot correlational study drawing from data collected on a sample of college students Fall 2021 (N = 52) showed statistically significant negative correlations between exposure to nature and present fatalist time perspective (r = -.28, p = .042), the latter of which was also inversely associated with psychological flexibility (r = -.29, p = -.044). Relevant to our increasingly online world, building on these findings we will further investigate the effects of virtual exposure to natural and built environments on psychological flexibility and potential pathways linking them in a randomized control trial. We created, edited, and piloted a range of film clips of natural and built environments on campus as an experimental manipulation that we will test among students in the 2022-2023 school year. If such a link exists, this can lay groundwork for later intervention research testing the 'minimal nature dose' - including amount of time and type (in person v. virtual) - to boost psychological flexibility.

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Utilization of Fusion 360 Application Programming Interface(API) on generating 3D molecule and crystal models

Name: Wantong Wu
Year of Graduation: 2025
SURF Advisor(s): Illeana Streinu, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Utilization of Fusion 360 Application Programming Interface(API) on generating 3D molecule and crystal models

Abstract: Fusion 360 is a 3D modeling, computer-aided design(CAD), manufacturing(CAM), and engineering(CAE) software platform. Our research aimed at transforming realistic molecule data into 3D molecule models through running the python scripts in Fusion 360 API. The 3D models help researchers understand molecular geometry and dynamics by visualizing the spatial arrangement of atoms and bonds. During the research, we used crystal examples especially, as crystals are often arranged in a highly ordered microscopic structure.

The scripts are object-oriented based on the Fusion 360 API environment. I used atom, atoms, bond, and bonds as objects to assign properties and create models. Different properties are related to different contexts. Atoms can be created using either realistic data (exactly as imported) or ideal data that is generated from the theoretical deduction. Different types of bonds can be created based on the need. An embedding type of bond represents a revolute joint between atom and bond, which supports a z-axis direction rotation. A magnetic type of bond represents a ball joint, which supports multi-direction rotation. The two types of bonds simulate the stable or unstable relationship between different atoms and satisfy the possible need to change the angles between bonds.

The input file includes the information to build a molecule. Information like the position and symbol of atoms and the atoms linked by the bonds is parsed and stored in instances. They are processed with Fusion 360 inner features to create models. The product is shown in the Fusion 360 user interface. An STL file (used for 3D printing) can be created in the same file location as the scripts if needed.

Fusion 360 provides very strong features for creating and designing. Its API allows the possibility of computing very complex molecular structures without adding the atoms one by one. This is particularly prominent when computing crystal structures because of their repetitiveness in structure. However, the API does have an upper limit of computing, which we are still testing. Other future obstacles include the limitation of 3D printing technology. We want to 3D print the molecule while preserving its performance in the user interface. Will 3D printing allow us to print the whole molecule while keeping each part separate is still a question to find out.

Pathways to Postfeminist Sexual Agency and Sexual Efficacy: Relationships between Social Dominance Orientation, Heteronormative Sexual Beliefs, Sexual Entitlement, and Sexual Agency

Name: Ruiyi Zhang
Year of Graduation: 2023
SURF Advisor(s): Randi Garcia, Psychology
Field of Study: Psychology
Co-Authors:

Title: Pathways to Postfeminist Sexual Agency and Sexual Efficacy: Relationships between Social Dominance Orientation, Heteronormative Sexual Beliefs, Sexual Entitlement, and Sexual Agency

Abstract: Recent research on sexual agency has argued that the construct assumes a single manifestation of agency and overestimates the ability of individuals' willpower to counteract sexual vulnerability shaped by social injustices. This study is the first to create and validate a measure of postfeminist sexual agency–attitudes that regard individuals as free agents who should be completely in control of their sexual lives. It also examined how the construct is distinct from sexual efficacy, as it is commonly measured. Using Multi-Group Path Analysis, Social Dominance Orientation (SDO), heteronormative beliefs, individuals' entitlement to sex and pleasure, and beliefs about partners' entitlement were tested as predictors of postfeminist sexual agency and sexual efficacy. We found that SDO and heteronormative beliefs were associated with greater entitlement, which was associated with greater postfeminist sexual agency and weaker sexual efficacy. Findings provide insight into how different types of sexual agency are enacted among heterosexuals and suggest the postfeminist discourse that imposes constraints on individuals' sexual decision-making should be taken into account in future studies.

Meal Planning

Name: Abigail Paharsingh
Year of Graduation: 2024
SURF Advisor(s): Katie Kinnaird, Statistical and Data Sciences
Field of Study: Statistical and Data Sciences
Co-Authors: Aleksandra Kogalovski

Title: Meal Planning

Abstract: Meal planning can help households reduce food waste, save money by preventing unnecessary purchases, save time spent grocery shopping and in the kitchen, and maintain a balanced diet. What is more, effective meal planning could have positive impacts on climate change, gender equity, financial planning and health. Through our work this summer, we investigated existing meal planning solutions, such as meal kit delivery services. We noted that many of these come with hefty price tags and are not affordable for lower-income households. Subscription-based meal planning apps and websites are not built with low-income demographics in mind, and budget-friendly recipes with accessible ingredients can be challenging to find. Most meal planning apps that can support a decent variety of recipes require the planning to be done manually by the user, which can take a significant amount of time.

This project aims to use machine learning to create a meal plan recommendation system that considers each user's budget, dietary needs and preferences, and cooking skill level and uses that information to generate unique meal plans. Our goal is that this app will center on the experiences of those who are food insecure, seeking to maximize diversity of recipes while minimizing costs and food waste. To achieve these goals, we plan on using an algorithm called GraphSAGE. Once the algorithm is trained on 10,000-15,000 meal plans consisting of at least 100,000 recipes, we can predict what kinds of recipes users will be interested in cooking. GraphSAGE was previously successfully used for playlist recommendations on music streaming platforms. We plan on following a similar process, with songs being recipes, playlists being meal plans, and genres being cuisines.

Over the course of the summer, we worked together on collecting information about similar projects happening in this space to determine the viability and necessity of our project. We assessed the commercial meal planning app space as well as the academic machine learning space to ascertain what our project could do differently. We also investigated the impact of meal planning on climate change, gender equity, financial planning and health.

A Review of Trust in Relationships: Implications for Coparenting Interventions

Name: Tianmei Zhu
Year of Graduation: 2023
SURF Advisor(s): Marsha Pruett, Psychology
Field of Study: Psychology
Co-Authors: Professor Michael Saini, Dr. Kline Pruett, Jessica Pardim, Tianmei Zhu, Jonathan Alschech

Title: A Review of Trust in Relationships: Implications for Coparenting Interventions

Abstract: Trust in relationships is an understudied area in psychological research, especially in terms of its implications for coparenting relationships. The importance of trust in relationships has been accepted as an obvious part of positive, healthy, and well-functioning relationships. As a result, the concept of trust has not fully been explored in depth in psychology of close relationships, including in the creation and maintenance of positive coparenting relationships. This review highlights the importance of trust as a multi-factor, multi-determinant and complex concept that requires a comprehensive assessment of the history, dimensions, etiology, consequences and impact of trust within a family systems approach to help understand and intervene in coparenting relationship.

Experimenting with Intramoleclar Cyclization using Apha-arylation Conditions

Name: Wanbin Chen
Year of Graduation: 2024
SURF Advisor(s): Alexandra Strom, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Experimenting with Intramoleclar Cyclization using Apha-arylation Conditions

Abstract: Multi-ringed compounds are abundant in pharmaceutical compounds and natural products. Over the course of this 10-week SURF period, we experimented whether intramolecular cyclization was possible by modifying conditions used originally for alpha-arylation of deoxybenzoin with arenes. These experimental conditions, which use DDQ, $FeBr_3$, and DCE, are attractive because they are relatively safer to use and are less environmentally harmful than other potential reagents.

The intramolecular cyclization reaction was first preceded by three reactions: an acid chloride formation, a Friedel-Crafts acylation, and a Suzuki coupling. First, the acid chloride formation and a Friedel-Crafts acylation was done to make the organobromine used in the following Suzuki-Miyaura coupling.

A variety of potassium alkyl trifluoroborate salts and boronic acids were used in the Suzuki couplings. We found that in the initial conditions, where $PdCl_2(PPh_3)_2$ was the catalyst and Cs_2CO_3 was used as the weak base, the organobromine was not being completely consumed, making product isolation exceptionally difficult. We tried different eluent systems for the column chromatography such as toluene in hexane with ethyl acetate and MTBE in hexane, but none were successful in separating reagent from product. As a result, the reaction conditions were changed. $Pd(dppf)Cl_2$ was used as the new catalyst, K_3PO_4 as the new base, and 1,4 dioxane in water as the new solvent system (West, et al., 2019). In these new conditions, all of the organobromine was consumed, and a much higher yield was obtained as a result.

Finally, although we were able to run a number of cyclization reactions, we were unable to totally confirm the formation of an intramolecular cyclized product. There were also a range of side products made that were unidentifiable. Thus, for the future, we may continue to work on identifying exactly what products were made and perhaps work on tweaking current reaction conditions.

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Graph viewer and motion graph web application

Name: Julia Ting
Year of Graduation: 2024
SURF Advisor(s): Illeana Streinu, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: Graph viewer and motion graph web application

Abstract: This summer, I worked on a web application graph viewer in Javascript, PHP, and HTML. I learned to use PHP to read the contents of different types of files which represented different graph types. The app allows the user to view many graphs that are in a folder on a server. The viewer allows the user to change the labels and colors of the vertices and edges according to the information associated with the file type that the user chooses to view.
I also worked on creating another web application which would display a graph and allow the user to choose a vertex to rotate, called the driver, and an edge of the graph that would remain fixed, called the pinned edge such that the edge lengths of the graph remain the same as the driver rotates. The program worked with only Henneberg I graphs, which are graphs that start as 2 or 3 vertices connected by a single edge or 2 edges, respectively. New vertices can be added only by connecting them with 2 new edges to 2 old vertices. I worked on this app in Javascript, PHP, HTML and Python based off of a Mathematica app created by Emma Civello as Mathematica requires a subscription and is not as accessible as a web application. JavaScript was unable to easily symbolically solve the equations needed to find the coordinates of the vertices, so Python's SymPy library was used to compute the trajectory of the vertices for each angle between the driver and pinned edge as the driver rotates.

Synthesis of α-Functionalized Analogs via Iron-Catalyzed α-Functionalization of Carbonyl Derivatives with Various Coupling Partners

Name: Gloria Parrales
Year of Graduation: 202
SURF Advisor(s): Alexandra Strom, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Synthesis of α-Functionalized Analogs via Iron-Catalyzed α-Functionalization of Carbonyl Derivatives with Various Coupling Partners

Abstract: Iron-catalyzed oxidative α-functionalization of carbonyl derivatives attracts particular interest as a novel synthetic strategy for the preparation of a diverse array of compounds of varying functionality, which are valued as useful building blocks in further syntheses of pharmaceuticals and biologically active molecules (1,2). While preliminary methods have exercised a Pd or Cu-catalyzed approach, the use of iron offers a more efficient route for the preparation of α-functionalized compounds due to its greater accessibility and high reactivity (2). Our previous work has demonstrated that this strategy promotes α-amination of 4-chlorodeoxybenzoin by coupling p-toluenesulfonamide to the alpha position, producing a functionalized C-N bond instead of the intended C-C bond. Because the versatility of iron as a catalyst is dependent on the ability to produce α-functionalized analogs with a variety of functional groups, our work this summer has aimed to discover new coupling partners to diversify the substrate scope of this method for the production of α-C-C, C-N, and C-O bonds. Using DDQ and FeBr3, the compatibility of 4-chlorodeoxybenzoin in DCE with various nucleophiles of diverse functionality, including 2,4,6-trimethylphenol, succinamide, benzhydroxamic acid, and allyltrimethylsilane, was investigated. Results demonstrated that multiple of the tested nucleophiles did not couple to 4-chlorodeoxybenzoin in the described experimental conditions, which often underwent α-chlorination or α-bromination at the alpha position instead. However, reaction of 4-chlorodeoxybenzoin with allyltrimethylsilane resulted in successful α-C-C bond formation. The desired α-allylation product was isolated and characterized, but overall product yield was poor and 4-chlorodeoxybenzoin remained in large excess despite allowing the reaction to stir overnight. Subsequently, our work diverged into making alterations to the original experimental conditions to encourage product formation and increase reaction yield. Results suggested that reducing the equivalents of DDQ to 1.00 and increasing the equivalents of FeBr3 to 0.40 encouraged more of the ketone starting material to react. We thus hypothesize that DDQ may provoke degradation of the iron catalyst, hindering the success of the reaction. However, lack of product formation when DDQ is replaced with 1,4-benzoquinone justified the necessity of DDQ as the oxidant. Future experimentation intends to continue efforts to optimize reaction conditions to achieve greater product yield and elucidate the roles of DDQ and its interaction with FeBr3. Additionally, we aim to continue our work in reacting 4-chlorodeoxybenzoin with various nucleophiles to discover new coupling partners.

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Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Name: Leyla Akin
Year of Graduation: 2023
SURF Advisor(s): Benita Jackson, Psychology
Field of Study: Psychology
Co-Authors: Maya Kiernan, Uzma Malik, Lana Sabbah, and Anna Peel

Title: Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Abstract: Studies show that even brief time in settings with nature (e.g., a park) increases cognitive function, compared to similar time spent with less nature-based elements (e.g., buildings; Nisbet & Zelenski, 2011). One important predictor of cognitive function that, to our knowledge, has yet to be linked to exposure to nature is psychological flexibility. Arguably a critical key common pathway to mental and physical health (Kashdan & Rottenberg, 2010), psychological flexibility is a psychological characteristic holding promise as a potent point of intervention. For this project we sought to test for a unique association between nature exposure and psychological flexibility. Additionally, we identified potential pathways (e.g., time perspective), amplifiers (e.g., self-compassion), and dampeners (e.g., rumination) for the link between nature exposure and psychological flexibility, should they exist. We designed two sets of empirical examinations: a correlational study to test initial associations, and an experimental study, to test a replication and extension Nisbet and Zelenski's (2011) research on nature exposure and cognition, in our version, focusing on psychological flexibility as the dependent variable. Our pilot correlational study drawing from data collected on a sample of college students Fall 2021 (N = 52) showed statistically significant negative correlations between exposure to nature and present fatalist time perspective (r = -.28, p = .042), the latter of which was also inversely associated with psychological flexibility (r = -.29, p = -.044). Relevant to our increasingly online world, building on these findings we will further investigate the effects of virtual exposure to natural and built environments on psychological flexibility and potential pathways linking them in a randomized control trial. We created, edited, and piloted a range of film clips of natural and built environments on campus as an experimental manipulation that we will test among students in the 2022-2023 school year. If such a link exists, this can lay groundwork for later intervention research testing the 'minimal nature dose' - including amount of time and type (in person v. virtual) - to boost psychological flexibility.

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ASes in Tor Networks

Name: Katherine Sophie Crane
Year of Graduation: 2022
SURF Advisor(s): Shinyoung Cho, Computer Science
Field of Study: Computer Science
Co-Authors:

Title: ASes in Tor Networks

Abstract: The Tor network is designed to keep its users anonymous on the Internet. This requires using three designated Tor relays, each of which only knows where they received the packet from and where to send it to, but not where the packet originated or its ultimate destination. In theory, this should keep users anonymous, but a problem arises when both the traffic that's entering and the traffic that's exiting the Tor network happen to pass the same AS. In those cases, the anonymity of communication is put at risk due to the potential of traffic correlation attacks since the owner of that AS can try to map incoming and outgoing traffic and identify who is accessing what.

The first part of this SURF project was dedicated to writing code that could investigate if the number of Tor relays and their ASes have changed over time. I wrote codes in Bash and Python that were able to download data from the CAIDA database and the Tor Project. Using the data from the Tor Project, the codes find a list of all Tor IP addresses in a day, then remove any redundancies.

Next, the codes download information from the CAIDA database to get the IP prefixes for the ASes. Because this data gives a large list of AS numbers and their controlled IPv4 prefixes, it needs a way to quickly connect an AS number to an IP address. I addressed this need by first creating a binary tree (out of the ASes that used the binary form of an address) with one leaf being 0 and one leaf being 1. The codes convert the unique list of Tor IP addresses into binary, search for their corresponding AS in the tree, and record all ASes that contain a Tor relay.

During the final part of this SURF project, I added the option to record the bandwidth as well. In this case, doing so saves the bandwidth of each Tor relay from the Tor Project along with the list of corresponding IP addresses. Then it sums up all bandwidths of Tor relays inside a certain AS. This function was added so that I could apply AS hegemony for Tor networks using bandwidth as a weight. (A higher bandwidth means that the AS is more likely to be used—essentially that traffic is more likely to go through this node based on how the Tor protocol chooses relays.)

Knot Branched Covers in S4

Name: Annika Gonzalez-Zugasti
Year of Graduation: 2023
SURF Advisor(s): Patricia Cahn, Mathematics and Statistics
Field of Study: Mathematics (Topology, Knot theory)
Co-Authors: Georgia Gans Heng, Sylvia Song

Title: Knot Branched Covers in S4

Abstract: A mathematical knot is a positioning of a circle in space. Two knots are the same if it is possible to gradually deform one into the position of the other. Topologists want to find tools to tell knots apart. We studied one such tool, called branched covers of knots, in order to facilitate the process of telling knots apart.

The branched cover of a knot is a new three dimensional space that you can build from a labeled knot. The knot corresponds to a collection of knots in the branched cover which we call branch curves. The linking number of two knots measures how many times one knot wraps around another. A powerful knot invariant is the linking number of two branch curves in the branched cover of the original knot. This number being an invariant means that it is a valuable tool in helping us distinguish one knot from another.

We created a program which computes this invariant of a knot whose arc labelings are transpositions in S4, the symmetric group on 4 letters. This program automates the lengthy process of finding the number by hand. To calculate the number, the program requires four inputs for each crossing of the knot: the number of the crossing (which we will refer to as i), the transposition label assigned to the ith arc, the numbers of the arcs that cross over the crossing, and the sign of the ith crossing. In addition, the total number of crossings is needed for the program to run.

This program represents an algorithm which could previously only be done by hand. An automated algorithm of this sort has only existed for knots that are three-colorable or, in other terms, have arcs labeled with transpositions in S3. Thus, our work takes the next step toward automating this process for knots with any permutation labeling. The automation of this calculation allows topologists the ability to quickly and reliably tell knots apart.

Chan-Evans-Lam Oxidative O-Alkylation

Name: Angela Chavez
Year of Graduation: 2023
SURF Advisor(s): David Gorin, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Chan-Evans-Lam Oxidative O-Alkylation

Abstract: Oxygen alkylation within complicated molecules is needed for medicinal chemistry and natural product synthesis due to the highly selective nature of the human body. These ethers provide the required functional group for drug delivery and general stabilization of the molecule. Specifically for alcohol methylation, the typical methyl courses used to synthesize methyl ethers are toxic and extremely electrophilic. In 2008 a young scientist died from acute exposure to TMSD, which is a common electrophile for these reactions. The Gorin lab is developing methods to perform this reaction without these dangerous electrophiles, and therefore is working on making these important reactions safer.

In order to avoid toxic reagents, we will need to avoid the electrophiles. The typical organic chemistry reaction used involves an electron rich molecule, a nucleophile, and an electron poor molecule, an electrophile. By getting rid of these molecules, we are stepping away from the typical structure of organic synthesis; we are using two nucleophiles. This is made possible because we are using a transition metal to catalyze this reaction and using an oxidative coupling pathway. The Chan-Evans-Lam oxidative cross coupling reagents mechanism allows for alkylation reactions. Most of the previous Chan-Lam conditions use arylboronic acid, but the Gorin lab has published two papers using methylboronic acid. In the most recent publication, ethers were formed by methylating a variety of phenols using a copper catalyst, methylboronic acid, an amine ligand, and oxygen.

We have continued previous work on phenol methylation, by exploring different boron reagents for methylboronic acid. These different boron reagents have given us the opportunity to expand into different types of alkylations where the boron reagent is not in a boronic acid structure. We have started to work on alcohol benzylation using a benzyl boronic pinacol ester, using the knowledge we have gained from trying those new reagents. While Chan-Evans-Lam is a well established reaction, there is no literature about using this mechanism for cyclopropylation of aliphatic alcohols. Cyclopropyl ethers within complicated molecules provide unique properties that are beneficial for drug development and stabilization. We have been able to establish new conditions for oxidative cross coupling by using a copper catalyst and cyclopropylboronic acid.

Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Name: Uzma Malik
Year of Graduation: 2023
SURF Advisor(s): Benita Jackson, Psychology
Field of Study: Psychology
Co-Authors: Benita Jackson, Maya Kiernan, Leyla Akin, Uzma Malik, Lana Sabbah, & Anna Peel

Title: Built and Natural Environments Effects on Psychological Flexibility: Correlational Findings and Experimental Study Designs

Abstract: Studies show that even brief time in settings with nature (e.g., a park) increases cognitive function, compared to similar time spent with less nature-based elements (e.g., buildings; Nisbet & Zelenski, 2011). One important predictor of cognitive function that, to our knowledge, has yet to be linked to exposure to nature is psychological flexibility. Arguably a critical key common pathway to mental and physical health (Kashdan & Rottenberg, 2010), psychological flexibility is a psychological characteristic holding promise as a potent point of intervention. For this project we sought to test for a unique association between nature exposure and psychological flexibility. Additionally, we identified potential pathways (e.g., time perspective), amplifiers (e.g., self-compassion), and dampeners (e.g., rumination) for the link between nature exposure and psychological flexibility, should they exist. We designed two sets of empirical examinations: a correlational study to test initial associations, and an experimental study, to test a replication and extension Nisbet and Zelenski's (2011) research on nature exposure and cognition, in our version, focusing on psychological flexibility as the dependent variable. Our pilot correlational study drawing from data collected on a sample of college students Fall 2021 (N = 52) showed statistically significant negative correlations between exposure to nature and present fatalist time perspective (r = -.28, p = .042), the latter of which was also inversely associated with psychological flexibility (r = -.29, p = -.044). Relevant to our increasingly online world, building on these findings we will further investigate the effects of virtual exposure to natural and built environments on psychological flexibility and potential pathways linking them in a randomized control trial. We created, edited, and piloted a range of film clips of natural and built environments on campus as an experimental manipulation that we will test among students in the 2022-2023 school year. If such a link exists, this can lay groundwork for later intervention research testing the 'minimal nature dose' - including amount of time and type (in person v. virtual) - to boost psychological flexibility.

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Psychology of Justice

Name: Diya Seth
Year of Graduation: 2024
SURF Advisor(s): Yael Granot, Psychology
Field of Study: Psychology
Co-Authors:

Title: Psychology of Justice
Abstract: My SURF work explored the psychology of justice and legal decision-making, through three primary projects..

First, I explored whether raise-the-age (RTA) policies –intended to protect minors, often those under the age of 18, from prosecution in adult court – have unintended backlash effects, inflating the perceived culpability of 18 year olds, who are just outside the policy's purview. Preliminary analyses were run on Illinois Prison data, which showed that implementation of RTA laws did coincide with disparately greater sentencing for 18-year olds, relative to older peers, only after the passing of RTA. I searched for other states' data, including analyzing data from Utah to search for similar effects. I also designed a follow-up vignette study, to experimentally test whether learning about RTA laws, age of the defendant (18 vs. 22), and prior criminal history interacted to predict the sentence length that mock-jurors assigned to defendants.

Second, I reviewed the research literature, at the intersection of psychology and law, on the process of sentencing mitigation. I sought to understand why people are more or less willing to reduce punitive sentences, and whether systematic biases affect these judgments. This review will make up the introduction of an empirical study of public perceptions of mitigation - by learning more about public perceptions of legal responsibility we can understand jurors' mindsets and make the judicial system fairer.

Finally, I also worked with a team exploring issues of justice in schools. Specifically we worked to understand high school students' experience of discipline and school based policing. I contributed to reviewing existing manuscripts and adding to a literature review on how race, bias victimization, critical consciousness, identity development and more may interact with school disciplinary practices to affect students' experiences of safety and fairness.

repytah: An open-source Python package that builds aligned hierarchies for sequential data streams

Name: Chenhui Jia
Year of Graduation: 2022
SURF Advisor(s): Katie Kinnaird, Statistical and Data Sciences
Field of Study: Statistical and Data Sciences
Co-Authors: Amanda Liu

Title: repytah: An open-source Python package that builds aligned hierarchies for sequential data streams
Abstract: Sequential data streams often have repeated elements that build on each other, creating inherent hierarchies. The goal of extracting these repetitions and their relationships to each other to build aligned hierarchies was introduced in Katherine M. Kinnaird's thesis "Aligned Hierarchies for Sequential Data". The Python package repytah, a translation of Kinnaird's original MATLAB code, aims to fulfill this task with more accessibility. This summer, we focused on debugging and improving the existing work from the past three years and aimed toward deploying the work as a finalized Python package. First, we did line-by-line debugging to find the places that caused deviations in the output from the original MATLAB code and our Python code. Then, we optimized our Python code in both speed and memory. One big change we made is to replace the convolution method with correlation using a function from a new library that is optimized for this type of matrix calculations. Running that on Chopin's Mazurka Op.6 No.1 example, our code can be 28 times faster. We also did code unification for our four modules and the example file to make sure the code has a unified style. With the modules being revised, we also revised the corresponding vignettes, test files, and website pages to make sure all the modules work as intended. In this final stage of the project, we worked on package production so that our code is installable via standard tools such as pip and conda. Future steps for this project include further developing the package to interactive play the results of the aligned hierarchies back in a midi file or visualize the repeats, and integrate previous work with start (normalized) length diagrams into our package to compare songs.",
Joyce,Huang,Juniper,2025,"Lindsay Poirer, Statistical and Data Sciences",,,Data Ethnography and Activism,,,Federal Disclosure Datasets and Public Comment Analysis,"Disclosure datasets refer to government datasets collected by the same groups the data is meant to hold accountable. In the research project, I collaborated on this summer, we examined five federal datasets including Campaign Finance, Federal Use of Force, Home Mortgages, Toxic Release Index, and Open Payments. For changes to be made to the laws that control these datasets, agencies must propose their rules and give time for public discourse. Our work this summer examined how public comments on policies that affect disclosure datasets reveal certain perceptions, biases, and the furthering of one's agenda. On a larger scale, this will be used to understand better how public interests affect these disclosure datasets. Regulations.gov and the Federal Election Commission's website were used as archives for proposed rules and their accompanying public comments. Once we downloaded all public comments on each docket from their respective sites, they were uploaded into Dedoose to allow for coding. These codes were used to qualitatively examine trends and patterns in the discourse.
This work introduces new methods and conceptual mindsets to study social attitudes pertaining to datasets. Additionally, this will further academic knowledge of the societal context these datasets exist within and the motives for data bias. Our research will impact how data quality issues are viewed and what solutions we use to mitigate them. Data accountability and transparency will be better understood and improved by our work.

Genome Exploring and Investigation of CVAP#634 Swarming Phenotype

Name: Xin Xiong
Year of Graduation: 2024
SURF Advisor(s): Chris Vriezen, Biological Sciences
Field of Study: Microbiology
Co-Authors:

Title: Genome Exploring and Investigation of CVAP#634 Swarming Phenotype

Abstract: In the Vriezen lab, we have 152 soil isolates producing toxins against Staphylococcus sp. CWZ226, and E. coli MC4100. We are exploring these isolates for unique phenotypes. My goal this summer is two-fold. (I) Continue exploring genomic sequences of select isolates, work I initiated in the Spring 2022 semester, and (II) explore the possibility that several bacterial isolates affect a swarming phenotype in isolate CVAP#634..

Part I: In a previous manuscript (Ogawa et al. 2022), we showed that interference competition, antagonism, aggressiveness and the ability to produce exDNases are interrelated in bacterial isolates derived from a soil of low C/N and high bacterial load. In an attempt to better understand molecular mechanisms underlying these phenomena, we identified several isolates of interest from the MacLeish Fieldstation (Zukswert et al. 2014) based on similarity to published 16S sequences in NCBI databases using BLAST (Altshultz et al. 1996). We have isolated DNA from these isolates and performed Illumina sequencing on this DNA. When exploring the data, I determined a procedure about how to maximize the quality of the assembly. The next step is to find the 16S and DNase-associated genes after annotation in Patric. In addition, the assembled genome will be used to identify loci potentially involved in toxin production.

Part II: I identified one isolate, CVAP#634, which shows swarming on regular media as well as on specialized "swarming agar". Pilot experiments indicate that this behavior is affected by the presence of other isolates (CWZ226, CVAP#516, #611 and/or #614) which may inhibit swarming. 16S sequencing revealed that CVAP#634 is a Pseudomonas, while CVAP#516 and CVAP#614 are Bacillus. In the future we will further explore the environmental conditions affecting swarming and the effect of Bacillus on swarming. Furthermore, we will sequence the genomes of the isolates which will aid in the further understanding of the interaction between these isolates.

Monitoring Macroinvertebrates in the Mill River

Name: Rachel Slater
Year of Graduation: 2024
SURF Advisor(s): Marney Pratt, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Runpeng Hu, Rae Ettenger, Brianna Bell

Title: Monitoring Macroinvertebrates in the Mill River

Abstract: Paradise Pond is a well-known landmark in the Smith College community, where it serves both recreational and educational needs of the students and the public of the Northampton area and beyond. However, the sediment redistribution (formerly dredging) required to maintain the pond has the potential to disrupt the Mill River ecosystem, including the macroinvertebrates that reside in it. Macroinvertebrates are important bioindicators of the health of an aquatic ecosystem. In addition to abiotic measurements of water quality, such as levels of dissolved oxygen, pH, and nitrogen/phosphate levels, macroinvertebrate sampling offers an especially dynamic method of testing for water systems of interest. We used freshwater benthic macroinvertebrates to gain insight into the health of the Mill River as affected by recent (2016 and 2018) sediment redistribution events.

To minimize the ecological effects of sedimentation, Smith is required by the government to monitor the impacts of the pond, therefore providing us with the opportunity to monitor the health of the river by collecting and identifying samples of macroinvertebrates from two macrohabitats (upstream and downstream of the pond) and five microhabitats within them.

In order to measure impacts of sediment redistribution on macroinvertebrate populations, Dr. Pratt uses a BACI (Before-After-Control-Impact) design. A BACI design has at least one sample before and after an impact (sediment redistribution) and has a sample that is likely to be affected by the impact as well as for a sample that should not be affected by the impact (Control sample). The impact site for this Mill River study is the rocky riffle habitat downstream of Paradise Pond, while the control site is a rocky riffle habitat upstream of the pond.

Through this project, our group became familiar with fieldwork sampling techniques and gained macroinvertebrate identification skills as well as knowledge of the general ecological research process. Sampling for macroinvertebrates in the Mill River consists of multiple important factors, namely large rocks and riffle area, which is the preferred habitat of macroinvertebrates. We then place a quadrat over the rocks and a D-net just downstream of the quadrat. Rocks are lifted into a bucket and gently rubbed off. After the rocks are gently rubbed off we use our feet to shuffle sand for 20-30 seconds. Macroinvertebrates are then transferred to the lab for preservation in a 70% ethanol solution.

Through data analysis in R, we found an increase in abundance of scrapers and collector filterers downstream compared to the previous two years (Figure 1). We also found an increased abundance of collector gatherers upstream in comparison to downstream this year. In addition, scrapers are more prevalent in the downstream region.

Figure 1. Relative abundance of functional feeding groups over time in the summers of 2018-2022 in the upstream and downstream riffles of Paradise Pond in the Mill River of Northampton, MA. Relative abundance was calculated by the number of organisms of a functional feeding group divided by the total number of organisms in a sample. For each location, 15 samples were collected on three different days every year.

Lesson Scaffolding For EGR 270

Name: Sabrina Hatch
Year of Graduation: 2025
SURF Advisor(s): Glenn Ellis, Engineering
Field of Study: Engineering/Education
Co-Authors:

Title: Lesson Scaffolding For EGR 270

Abstract: This summer, I worked directly with Professor Ellis on creating a multimedia lesson plan that would incorporate the first homework and syllabus for his course being taught in the fall of 2022 (EGR 270, Engineering Mechanics I). Throughout the duration of the summer, I spent my time doing readings on deep learning, imaginative education, general concepts covered in the course, as well as scaffolding for the course itself.

Much of the time spent on the project, though, was specifically focused on the lesson planning and scaffolding of the course. And as such, we have prepared the lesson plan to be used in the beginning of the academic year which we can then set up a survey to collect data and analyze at the completion of the course.

In summation, I spent this summer learning about deep learning and producing mixed media resources as well as specific questions and homework assignments to be used by students in EGR 270 such that further data collection can be carried out through the academic year.

Synthesis and HPLC Purification of Spiroiminodihydantoin DNA Lesions

Name: Yuge Chai
Year of Graduation: 2025
SURF Advisor(s): Elizabeth Jamieson, Chemistry; Cristina Suarez
Field of Study: Chemistry
Co-Authors:

Title: Synthesis and HPLC Purification of Spiroiminodihydantoin DNA Lesions

Abstract: 8-oxo-7, 8-dihydroguanosine (8-oxoG) is a product of guanine oxidation, which can be further oxidized by cation radicals to produce the spiroiminodihydantoin (Sp) lesion (Khutsishvili et al., 2013). The Sp lesion is mutagenic and, unless it is repaired by the base excision repair system, may cause cancers associated with inflammation. (Khutsishvili et al., 2013). Previous studies have shown that 8-oxoG has similar thermodynamic values and chemical structure with its undamaged parent DNA, which prevents the base excision repair enzymes from detecting the lesions (Crenshaw, 2011). The Jamieson-Suarez Lab aims to compare the Sp lesion's base pair opening rate with that of the 11-mer oligonucleotide parent DNA by observing signals in the imino region by NMR, in order to determine if the chemical difference between Sp lesions and an undamaged DNA can make the base excision repair enzymes detect and repair the lesions.
This SURF project focused on the production of oligonucleotide samples containing Sp lesions for NMR studies. The Sp lesion was made by reacting an 8-oxoG 11-mer oligonucleotide with sodium persulfate radicals in a carbonate buffer at a temperature of 60°C. The reaction was desalted using Poly-Pak cartridges. High-performance liquid chromatography (HPLC) was used to purify the Sp-R and Sp-S diastereomers produced in the reaction using a gradient of a high salt (90% 1.5M ammonium acetate + 10% acetonitrile) and low salt (90% water + 10% acetonitrile) buffers. The purified products were collected and dialyzed to remove excess salt from the HPLC buffer. The products were lyophilized, and the final yield was calculated by using the Nanodrop spectrometer. The process was repeated to accumulate sufficient Sp lesions containing oligonucleotides to be observed by NMR. To prepare for the NMR studies, we performed water suppression and temperature calibration experiments and recorded data for a control 11-mer oligonucleotide in order to compare with Sp lesions. Future studies will be focused on analyzing the Sp lesion's base pair opening kinetics by one-dimensional (1D) NMR using the Sp lesion products collected this summer. By examining how the signals of the imino region of Sp lesions vary from its undamaged parent strands, we hope to understand how the base pair opening difference might be detected by base excision repair enzymes to repair the lesions.

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Data Ethnography and Advocacy Lab

Name: Naomi Liftman
Year of Graduation: 2024
SURF Advisor(s): Lindsay Poirer, Statistical and Data Sciences
Field of Study: Statistical and Data Sciences
Co-Authors:

Title: Data Ethnography and Advocacy Lab

Abstract: Over the past summer, I worked in the Data Ethnography and Advocacy Lab (DEAL). Currently, the lab is focused on examining five federal disclosure datasets to understand how social advocacy affects the creation, maintenance, and continuation of them. These datasets are the Toxic Release Inventory, the Campaign Finance dataset, the Home Mortgage Disclosure Act dataset, the Federal Use of Force dataset, and the Open Payments dataset. However, I worked most closely with the Campaign Finance (CF), managed by the Federal Elections Committee (FEC) and the Toxic Release Inventory (TRI), managed by the Environmental Protection Agency (EPA).

Every time a federal agency wants to make changes to a federally mandated data collection program, they must first put the proposal to the public, which in turn allows public comments to be made in favor or against the new rule. My main goals have been to aggregate submitted comments from regulations.gov and the FEC's website; analyze the public comments through a modified version of grounded theory, and deepen understanding of how people mobilize around and advocate for these datasets. I used a web scraper, for regulations.gov, along with brute manual labor to collect all the comments made on every proposed change for the TRI and CF. Once these comments were collected and imported into our qualitative data analysis software Dedoose I moved to read each and every comment. While reading there were two tasks: one was to assign descriptors to each comment; the descriptors included general ideas about the comment, such as the comment's stance, who sent the comment, how the comment was sent, etc. The second task was to look for and code themes and keywords in the comments. In total, I read through over 700 comments and marked over 2000 themes and keywords.

This approach to studying social advocacy around datasets is a fresh one in the field of critical data studies. While I read many articles surrounding critiques of the federal public comment process, as well as discussions of data accountability and audit culture, few times did the papers outline methodological approaches to studying datasets as cultural artifacts. A clear area that is lacking in this field is the methods by which to study how social advocacy shapes the values reported in datasets. To remedy this I worked towards the creation of a methods paper that outlines an approach to studying the cultural histories of datasets through qualitatively analyzing comments submitted through regulations.gov.

The overarching goal of DEAL has been to deepen our understanding of the data we use to hold institutions accountable. Moving forward our lab hopes to look at analyzing the comments and their themes, but this summer was spent laying the groundwork so that this research ahead would be possible.

Not Mussels Marinara: Effects of a Warming Ocean on Mussel Survival, Growth, and Attachment Strength

Name: Jenna Stanley
Year of Graduation: 2023
SURF Advisor(s): Paulette Peckol, Biological Sciences
Field of Study: Marine Ecology
Co-Authors: Abbey O'Meara

Title: Not Mussels Marinara: Effects of a Warming Ocean on Mussel Survival, Growth, and Attachment Strength

Abstract: The southern New England (NE) rocky intertidal zone supports the ecologically and economically important native Mytilus edulis. This mollusc species is habitat and food for other intertidal species, and provides an important ecosystem service of filtering plankton and pollutants from the water. Economically, M. edulis aquaculture is a multi-million dollar industry. Climate change and warming waters threaten survival and success of M. edulis, making it crucial to understand consequences of these changes. We investigated effects of rising water temperatures on byssal thread attachment strength, growth rates, and survivorship under ambient and elevated seawater temperatures in three size classes of M. edulis. We also collected temperature data from 5 locations spanning the CT and RI coasts. These data showed temperature differences between rock surfaces, within mussel beds, and above mussel beds. Following acclimation (10 day period) to experimental temperatures (14°C and 21.5°C), M. edulis were divided into three size categories (small: 12.21-25.68 mm; medium: 20.31-37.73 mm; and large 25.97-52.31 mm). Containers (n = 5, each size and temperature treatment) were filled with 400 mL of artificial seawater (changed every other day); a stone and polypropylene line were added as substrate. We added small (10), medium (10) or large (5) mussels to each container. Containers were aerated in darkness and fed RotiRich (commercial aquaculture formula). We took initial and final fresh weight and length of each M. edulis, and then allowed them to attach to substrates and each other during the experimental period. M. edulis showed high survival at both temperatures and we documented only a few deaths over nearly a month. At 14 and 27 days, we determined the strength of attachment (force to remove) of solitary and aggregate M. edulis, and showed our results for medium sized M. edulis (Fig. 1). Byssal thread attachment was weaker for both small and medium M. edulis (solitary and aggregates) at the higher temperature (21.5°C). Aggregates had a larger range of detachment values depending of the size of the aggregate as well as location (edge or within the aggregate).

Cont. Not Mussels Marinara: Effects of a Warming Ocean on Mussel Survival, Growth, and Attachment Strength

Mean strength of attachment varied greatly between the two temperatures, 0.235 N at 14°C and 0.057 N at 21.5°C, for solitary mussels.
We documented differences in growth among small, medium and large M. edulis at the two experimental temperatures (Fig. 2). Growth rates at 21.5°C were lower than at 14°C for all sizes. Taken together our laboratory experiments indicate that at warmer temperatures, M. edulis has a weaker attachment strength and lower growth rates; in the field, temperatures are lower within the mussel aggregates only when mussels achieve a larger size. Thus, warming ocean temperatures will affect health, attachment and growth of M. edulis, clearly resulting in negative impacts on mariculture.
(Supported by the Env. Science & Policy Program, CFCD, & Choate (Biological Sciences)
(Paulette Peckol, Faculty advisor Biological Sciences)",

Automated Mothing as a Method for Long-Term Insect Surveying

Name: Kate Nash
Year of Graduation: 2023
SURF Advisor(s): Mariana Abarca, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Automated Mothing as a Method for Long-Term Insect Surveying

Abstract: In the age of climate change, data on insect, and more specifically, moth populations are vital to understanding how these climatic changes affect these groups. These data must be collected as regularly as possible in order to create a long-term data set that observes moth population trends. Manual mothing, with a person identifying or photographing moths on a large sheet through the night, is labor intensive, especially at the scale needed to achieve a long-term data set. In addition, the human skill needed to identify large quantities of moths is considerable. Our goal was to create an automated system that will take photos of a blacklit small fabric-covered landing surface. This device eliminates the need for nightly mothing and allows for computer programs to do the work of counting and identifying the moths. Over this summer, we designed, tested, and fabricated an automated moth monitoring device (the Mothitor). We began by researching methods of mothing and automation techniques already employed. After this, we tested different designs in the lab and in the field. We tested large canvases, smaller cotton and nylon sheets, different distances from the camera, and intervals of photos and light. We concluded that a small landing surface of treated nylon fabric lit with a blacklight on for one hour with a RICOH WG-6 camera attached is the most attractive to moths, the most durable for seasons in the field, and produces the highest quality photos. This device has been installed at MacLeish Field Station and will continue to photograph the moths of Western Massachusetts until the end of the 2022 moth season and be put out again before the start of the growing season next year.

In addition, from our mothing excursions, we collected over one hundred photos which we used to contribute to citizen science efforts on the Butterflies and Moths of North America website. This required moths to be identified and cataloged. We submitted 65 sightings of individual moths to the dataset on this website.

The Mothitor is part of a global push for more automated and long-timescale-focused ecology research. In the coming year, the computer learning programs to analyze the data provided by the Mothitor will be created. Over time, this device itself will be refined to be deployed across the region for academic, conservational, and citizen science research purposes.

Post-Extinction Archaeocyath Reefs of the Early Cambrian Mule Springs Formation, Nevada

Name: Grace Karbowski
Year of Graduation: 2023
SURF Advisor(s): Sara Pruss, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Post-Extinction Archaeocyath Reefs of the Early Cambrian Mule Springs Formation, Nevada
Abstract: Archaeocyath reefs were prominent in the shallow marine environment on the western margin of Laurentia that is now the southwestern United States. The Harkless Formation—underlying the Mule Springs Formation in Esmeralda County, Nevada—contained reefs that were ecologically important to many reef-dwelling organisms including trilobites, echinoderms, mollusks, and other sponges (Pruss et al., 2019). While archaeocyaths were prominent in the Harkless Formation, it appeared that they regionally went extinct before the Mule Spring Formation. Although Cordie et al. (2019) examined the Mule Spring Formation and were successful in describing its stratigraphy, they were not able to find evidence of reefs. However, during field work in the summer of 2021, small reefs with archaeocyaths were discovered in the middle of the Mule Springs Formation. These reefs were sampled during the summer of 2021 and 2022.
My SURF research this summer was to continue research with the Mule Springs 2021 samples that were previously turned into thin sections, which were then described and analyzed for the presence of reef builders and reef-dwelling organisms. We found that there was a small presence of irregular archaeocyaths in our samples, possibly of the genera Archaeocyathus, meaning these sponges better survived the onset of the archaeocyath extinction than many of the sponges present in the Harkless Formation. Throughout the spring and summer, we have been working to characterize the different reef mounds as well as describe the morphology and ecology of archaeocyaths and the reef-dwelling organisms, such as microbes, trilobites, and echinoderms. Additionally, this summer we were able to collect supplemental data from the field in Nevada. Samples from Mule Springs 2022 were prepared for analysis, which will be continued in the fall as an Honors Project. Field work, analysis of samples, preparation of figures, and additional literary research also prepared me for further research as well as a poster presentation at the Geological Society of America conference this fall.

VPN's servers location verification

Name: Siyu Dai
Year of Graduation: 2025
SURF Advisor(s): Shinyoung Cho, Computer Science
Field of Study: Computer Science
Co-Authors: Weihe Zheng

Title: VPN's servers location verification

Abstract: A Virtual Private Network (VPN) is used to provide a secure and private connection for users and to mask their true IP addresses. Since commercial VPNs' advertised server locations cannot be relied on, a geolocation checker is required to validate server locations using round-trip time measurements from RIPE anchors operated by RIPE NCC (Réseaux IP Européens Network Coordination Centre). The existing geo-checker works by sending the network packets to RIPE anchors all over the world and measuring the roundtrip time to check whether VPN servers are in the claimed place. With the existing checker, however, we can easily exhaust unnecessary resources (i.e., all ~800 RIPE anchors) while checking for the location; thus, we worked on understanding the challenges and proposing a more accurate and faster advanced geo-checker.

In order to make the checker faster (by reducing redundant experiments), we have focused on implementing RIPE anchor selections. Before applying any anchor selection algorithms, however, we first filtered out anchors that have low or no connections. The attached CDF graph shows the connectivity of all anchors. Though we used 92 percentage connectivity as our threshold to filter out anchors with low connections, we gave a generous threshold for anchors located in Africa, since, unlike in Europe, where one city has multiple anchors, in many cases, Africa has only one anchor for each city, and those anchors may have low connectivity.

Once we filtered out the anchors with low connectivity, we applied our two proposed RIPE anchor selection algorithms. The first algorithm randomly selects an anchor for each city to reduce redundant experiments at a city level. With this algorithm, we achieved an around 44 percent reduction. The second algorithm selects one anchor for each continent. We calculate the distance from each anchor to the center of each continent by utilizing the center coordinates of the continents. By doing so, we find an anchor for each continent that represents the whole area and achieve a 99.2 percent reduction. We attached figures to show the number or location of our selected anchors.

As a next step, we will implement a third algorithm by dividing the world map into eleven regions (according to the topology of the network deployment) and selecting an anchor for each region to represent the area. After doing so, we will evaluate which algorithm is managing to give the same result as the existing geo-checker, but while using more limited resources.

VPN's servers location verification

Name: Weihe Zheng
Year of Graduation: 2024
SURF Advisor(s): Shinyoung Cho, Computer Science
Field of Study: Computer Science
Co-Authors: Sophia Dai

Title: VPN's servers location verification

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Not Mussels Marinara: Effects of a Warming Ocean on Mussel Survival, Growth, and Attachment Strength

Name: Abigail O'Meara
Year of Graduation: 2024
SURF Advisor(s): Paulette Peckol, Biological Sciences
Field of Study: Marine Ecology
Co-Authors: Jenna Stanley

Title: Not Mussels Marinara: Effects of a Warming Ocean on Mussel Survival, Growth, and Attachment Strength

Abstract: The southern New England (NE) rocky intertidal zone supports the ecologically and economically important native Mytilus edulis. This mollusc species is habitat and food for other intertidal species, and provides an important ecosystem service of filtering plankton and pollutants from the water. Economically, M. edulis aquaculture is a multi-million dollar industry. Climate change and warming waters threaten survival and success of M. edulis, making it crucial to understand consequences of these changes. We investigated effects of rising water temperatures on byssal thread attachment strength, growth rates, and survivorship under ambient and elevated seawater temperatures in three size classes of M. edulis. We also collected temperature data from 5 locations spanning the CT and RI coasts. These data showed temperature differences between rock surfaces, within mussel beds, and above mussel beds.

Following acclimation (10 day period) to experimental temperatures (14°C and 21.5°C), M. edulis were divided into three size categories (small: 12.21-25.68 mm; medium: 20.31-37.73 mm; and large 25.97-52.31 mm). Containers (n = 5, each size and temperature treatment) were filled with 400 mL of artificial seawater (changed every other day); a stone and polypropylene line were added as substrate. We added small (10), medium (10) or large (5) mussels to each container. Containers were aerated in darkness and fed RotiRich (commercial aquaculture formula). We took initial and final fresh weight and length of each M. edulis, and then allowed them to attach to substrates and each other during the experimental period. M. edulis showed high survival at both temperatures and we documented only a few deaths over nearly a month.

At 14 and 27 days, we determined the strength of attachment (force to remove) of solitary and aggregate M. edulis, and showed our results for medium sized M. edulis (Fig. 1). Byssal thread attachment was weaker for both small and medium M. edulis (solitary and aggregates) at the higher temperature (21.5°C). Aggregates had a larger range of detachment values depending of the size of the aggregate as well as location (edge or within the aggregate). Mean strength of attachment varied greatly between the two temperatures, 0.235 N at 14°C and 0.057 N at 21.5°C, for solitary mussels.

We documented differences in growth among small, medium and large M. edulis at the two experimental temperatures (Fig. 2). Growth rates at 21.5°C were lower than at 14°C for all sizes. Taken together our laboratory experiments indicate that at warmer temperatures, M. edulis has a weaker attachment strength and lower growth rates; in the field, temperatures are lower within the mussel aggregates only when mussels achieve a larger size. Thus, warming ocean temperatures will affect health, attachment and growth of M. edulis, clearly resulting in negative impacts on mariculture.

Climate Change Effects on Intertidal Gastropod Species, Littorina littorea and L. obtusata

Name: Svetlana Roth
Year of Graduation: 2023
SURF Advisor(s): Paulette Peckol, Biological Sciences
Field of Study: Marine Ecology
Co-Authors: Perryne Vega

Title: Climate Change Effects on Intertidal Gastropod Species, Littorina littorea and L. obtusata

Abstract: As Earth continues to be faced with anthropogenic stressors, the rocky intertidal zone off the New England (NE) coast is dynamically changing due to increased temperatures, rising sea level, and ocean acidification. The introduced herbivorous gastropod, Littorina littorea, and indigenous L. obtusata are abundant intertidal species that have overlapping distributions and different tolerances to widely ranging environmental conditions (Putnam and Peckol 2018). Given projections for warming seawater temperatures, particularly in the NE area, it is vital to understand consequent trophic level effects. We studied the impacts of elevated temperatures on grazing rates and attachment strengths of L. littorea and L. obtusata.

After collection, the snail species were acclimated over a 1-2 week period (maximum 1oC change per day) to ambient (14°C) and elevated (20.5°C) temperature conditions. The warm temperature treatment was chosen to simulate projected increases estimated from climate change. Glass lidded containers were filled with 300 mL of seawater, and ~1.5g FW of Fucus vesiculosus and 4 healthy snails (either L. obtusata or L. littorea) were added. Water was changed daily, and containers were held under low irradiance levels (~100-150 μmol photons/m2/sec). Grazing rates of L. littorea were significantly (t = 4.38, p < 0.001) higher at the elevated temperature, while L. obtusata showed the opposite pattern (t = 3.19, p = 0.01) (Fig. 1). Further, herbivory of L. obtusata was significantly lower when held in the presence of L. littorea under both experimental temperatures, suggesting that asymmetric interference competition (Putnam and Peckol 2018) will continue as a future threat to L. obtusata populations.

We also documented the strength of attachment of the snails' foot to their natural substrata when acclimated to the two experimental temperatures. Stainless steel coils were glued on the exterior of the species' shells. To simulate natural attachment sites in the lab, L. littorea were placed in a 38 cm x 15 cm x 5 cm plastic container filled with a dense layer of small rocks and adequate water to submerge the rocks. For L. obtusata, the container included a covering of F. vesiculosus. We measured force to remove when we were certain that the snails were well attached. There was no difference in attachment strength of L. littorea held under the two temperature conditions. In the field, the attachment strength of large (18.6 - 21.8 mm) L. littorea was 2X greater than that of small (12.5 - 16.6 mm) snails. L. obtusata acclimated to 20.5°C required greater force (t = 2.26, p = 0.03) to remove than those held under ambient conditions (Fig. 2); however, nearly half of the snails from the 20.5oC treatment refused to attach. Thus, in the field, warming temperatures may make it difficult for L. obtusata to attach in its intertidal habitat. Taken together, grazing rates and attachment strength measurements suggest that L. littorea may be more resilient than L. obtusata to warming seawater temperatures caused by global climate change.

Knot Branched Covers in S4

Name: Heng Song
Year of Graduation: 2024
SURF Advisor(s): Patricia Cahn, Mathematics and Statistics
Field of Study: Mathematics and Statisitcs
Co-Authors: Georgia Gans, Annika Gonzalez-Zugasti

Title: Knot Branched Covers in S4

Abstract: A mathematical knot is a positioning of a circle in space. Two knots are the same if it is possible to gradually deform one into the position of the other. Topologists want to find tools to tell knots apart. We studied one such tool, called branched covers of knots, in order to facilitate the process of telling knots apart.

The branched cover of a knot is a new three dimensional space that you can build from a labeled knot. The knot corresponds to a collection of knots in the branched cover which we call branch curves. The linking number of two knots measures how many times one knot wraps around another. A powerful knot invariant is the linking number of two branch curves in the branched cover of the original knot. This number being an invariant means that it is a valuable tool in helping us distinguish one knot from another.

We created a program which computes this invariant of a knot whose arc labelings are transpositions in S4, the symmetric group on 4 letters. This program automates the lengthy process of finding the number by hand. To calculate the number, the program requires four inputs for each crossing of the knot: the number of the crossing (which we will refer to as i), the transposition label assigned to the ith arc, the numbers of the arcs that cross over the crossing, and the sign of the ith crossing. In addition, the total number of crossings is needed for the program to run.

This program represents an algorithm which could previously only be done by hand. An automated algorithm of this sort has only existed for knots that are three-colorable or, in other terms, have arcs labeled with transpositions in S3. Thus, our work takes the next step toward automating this process for knots with any permutation labeling. The automation of this calculation allows topologists the ability to quickly and reliably tell knots apart.

Climate Change Effects on Intertidal Gastropod Species Littorina littorea and L. obtusata

Name: Perryne Vega
Year of Graduation: 202
SURF Advisor(s): Paulette Peckol, Biological Sciences
Field of Study: Marine Biology
Co-Authors: Svetlana Roth

Title: Climate Change Effects on Intertidal Gastropod Species Littorina littorea and L. obtusata

Abstract: As Earth continues to be faced with anthropogenic stressors, the rocky intertidal zone off the New England (NE) coast is dynamically changing due to increased temperatures, rising sea level, and ocean acidification. The introduced herbivorous gastropod, Littorina littorea, and indigenous L. obtusata are abundant intertidal species that have overlapping distributions and different tolerances to widely ranging environmental conditions (Putnam and Peckol 2018). Given projections for warming seawater temperatures, particularly in the NE area, it is vital to understand consequent trophic level effects. We studied the impacts of elevated temperatures on grazing rates and attachment strengths of L. littorea and L. obtusata.
After collection, the snail species were acclimated over a 1-2 week period (maximum 1oC change per day) to ambient (14°C) and elevated (20.5°C) temperature conditions. The warm temperature treatment was chosen to simulate projected increases estimated from climate change. Glass lidded containers were filled with 300 mL of seawater, and ~1.5g FW of Fucus vesiculosus and 4 healthy snails (either L. obtusata or L. littorea) were added. Water was changed daily, and containers were held under low irradiance levels (~100-150 µmol photons/m2/sec). Grazing rates of L. littorea were significantly (t = 4.38, p < 0.001) higher at the elevated temperature, while L. obtusata showed the opposite pattern (t = 3.19, p = 0.01) (Fig. 1). Further, herbivory of L. obtusata was significantly lower when held in the presence of L. littorea under both experimental temperatures, suggesting that asymmetric interference competition (Putnam and Peckol 2018) will continue as a future threat to L. obtusata populations.
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Monitoring Macroinvertebrates in the Mill River

Name: Brianna Bell
Year of Graduation: 2024
SURF Advisor(s): Marney Pratt, Biological Sciences
Field of Study: Biological Sciences
Co-Authors: Rae Ettenger, Rachel Slater, Runpeng Hu

Title: Monitoring Macroinvertebrates in the Mill River

Abstract: Paradise Pond is a well-known landmark in the Smith College community, where it serves both recreational and educational needs of the students and the public of the Northampton area and beyond. However, the sediment redistribution (formerly dredging) required to maintain the pond has the potential to disrupt the Mill River ecosystem, including the macroinvertebrates that reside in it. Macroinvertebrates are important bioindicators of the health of an aquatic ecosystem. In addition to abiotic measurements of water quality, such as levels of dissolved oxygen, pH, and nitrogen/phosphate levels, macroinvertebrate sampling offers an especially dynamic method of testing for water systems of interest. We used freshwater benthic macroinvertebrates to gain insight into the health of the Mill River as affected by recent (2016 and 2018) sediment redistribution events.

To minimize the ecological effects of sedimentation, Smith is required by the government to monitor the impacts of the pond, therefore providing us with the opportunity to monitor the health of the river by collecting and identifying samples of macroinvertebrates from two macrohabitats (upstream and downstream of the pond) and five microhabitats within them.

In order to measure impacts of sediment redistribution on macroinvertebrate populations, Dr. Pratt uses a BACI (Before-After-Control-Impact) design. A BACI design has at least one sample before and after an impact (sediment redistribution) and has a sample that is likely to be affected by the impact as well as for a sample that should not be affected by the impact (Control sample). The impact site for this Mill River study is the rocky riffle habitat downstream of Paradise Pond, while the control site is a rocky riffle habitat upstream of the pond.

Through this project, our group became familiar with fieldwork sampling techniques and gained macroinvertebrate identification skills as well as knowledge of the general ecological research process. Sampling for macroinvertebrates in the Mill River consists of multiple important factors, namely large rocks and riffle area, which is the preferred habitat of macroinvertebrates. We then place a quadrat over the rocks and a D-net just downstream of the quadrat. Rocks are lifted into a bucket and gently rubbed off. After the rocks are gently rubbed off we use our feet to shuffle sand for 20-30 seconds. Macroinvertebrates are then transferred to the lab for preservation in a 70% ethanol solution.

Through data analysis in R, we found an increase in abundance of scrapers and collector filterers downstream compared to the previous two years (Figure 1). We also found an increased abundance of collector gatherers upstream in comparison to downstream this year. In addition, scrapers are more prevalent in the downstream region.

Quantum Chaos

Name: Jillian Lehosky
Year of Graduation: 2024
SURF Advisor(s): Gary Felder, Physics
Field of Study: Physics
Co-Authors:

Title: Quantum Chaos

Abstract: Chaos describes a physical system so unpredictable that the outcome seems random, largely due to sensitive dependence on initial conditions. We can determine chaos by comparing the phase space representations of an initial system and the same system with a small change in its initial conditions. Most commonly, quantum mechanical wave functions are represented as complex probability distributions found using the Schrödinger equation and thus comparing the "difference" between the two is nearly impossible. We use Wigner functions to display the same information as a distribution in phase space.

We can analytically solve for the difference between two Gaussian distributions but not all Wigner functions will result in a Gaussian distribution. Thus, we need to find a way to discretize and numerically solve for the difference between any two wave functions. This becomes a type of linear programming problem known as a transportation problem. More specifically, we are attempting to solve the "Earth Movers' Distance Problem" which imagines each function as a pile of sand that must be moved from an initial shape to a final shape, with each movement having an associated cost. Our goal is to find a numerical method that will produce a total cost with 1% of the analytical cost.

Previous work on the project used a Mathematica notebook and the built-in "FindMinimumCostFlow'' function. However, we wanted to see if there were other methods that are faster and more accurate when compared to the analytical solution. I combined code from an online source and methods from a previous mathematica notebook to create a Jupyter notebook capable of solving EMD problems using the Modified Distribution (MODI) method. This notebook performed similarly with the mathematica notebook when comparing the numerical solutions each produced to the analytical solution. There were a few cases where the Jupyter notebook performed better than the mathematica notebook, however the opposite was true in other cases. Overall, the Python code was generally a bit more accurate, but took longer to execute. I noticed that having very precise bounds for integration and reducing the amount of empty sand boxes was one of the best ways to optimize the accuracy.

Moving forward, I plan to find a way to automate the process of finding these bounds, rather than looking at a plot and assigning the bounds manually. As the project progresses we will start looking at real systems which have two degrees of freedom and thus exist in a 4 dimensional phase space.This may require implementing faster algorithms to compute EMD such as EMD-L1 or using a neural network based algorithm.

Meal Planning

Name: Aleksandra Kogalovski
Year of Graduation: 2025
SURF Advisor(s): Katie Kinnaird, Statistical and Data Sciences
Field of Study: Statistical and Data Sciences
Co-Authors: Abby Paharsingh

Title: Meal Planning

Abstract: Meal planning can help households reduce food waste, maintain a balanced diet, save money by preventing unnecessary purchases, and decrease time spent grocery shopping and in the kitchen. Existing meal planning solutions, such as meal kit delivery services, come with hefty price tags and are not affordable for lower-income households. Subscription-based meal planning apps and websites are not built with low-income demographics in mind, and budget-friendly recipes with accessible ingredients can be challenging to find. Most meal planning apps that can support a decent variety of recipes require the planning to be done manually by the user, which can take a significant amount of time.

This project aims to use machine learning to create a meal plan recommendation system that considers each user's budget, dietary needs and preferences, and cooking skill level and uses that information to generate unique meal plans. Our goal is that this app will center on the experiences of those who are food insecure, seeking to maximize diversity of recipes while minimizing costs and food waste. To achieve these goals, we plan on using an algorithm called GraphSAGE. Once the algorithm is trained on 10,000-15,000 meal plans consisting of at least 100,000 recipes, we can predict what kinds of recipes users will be interested in cooking. GraphSAGE was previously successfully used for playlist recommendations on music streaming platforms. We plan on following a similar process, with songs being recipes, playlists being meal plans, and genres being cuisines.","It would be nice to have more events organized for the SURF students on campus. It was hard to meet people that I didn't already know from the academic year or wasn't directly working with, so it would have been a great opportunity to learn more about what different labs at Smith were researching and to meet new people.

Cultivating Climate Literacy through Indigenous Studies: An example from the "Climate in Arts and History" educational resource

Name: Ollie Donald
Year of Graduation: 2022
SURF Advisor(s): Bosiljka Glumac, Geosciences
Field of Study: Geosciences, Education, Indigenous Studies
Co-Authors: Bosiljka Glumac and Christen Mucher

Title: Cultivating Climate Literacy through Indigenous Studies: An example from the "Climate in Arts and History" educational resource

Abstract: Climate in Arts and History" is a web-based educational resource that strives to promote climate literacy in disciplines beyond the natural and environmental sciences. This resource highlights the impact of climate on society and culture through topical entries on the themes of history, art, literature, languages, and music. The website is intended for use by K-12 students and teachers, as well as general audiences from across the world, with the goal of helping people understand how climate intersects with every facet of human life. In consultation with experts, Smith College undergraduate students from across disciplines have been working to develop website entries, drawing from recent publications, performances, and other works.

The current stage of the project focuses on integrating Indigenous perspectives across all aspects of the website. Indigenous perspectives are essential to cultivating climate literacy; climate history and the looming climate crisis cannot be separated from the ongoing truth of settler colonialism. The new "Indigenous Studies" webpage (https://www.science.smith.edu/climatelit/indigenous-studies/) is a growing compilation of resources that connect Indigenous history and knowledge of climate with the goal of resisting the dominance of Western thought and reimagining our collective understanding of place, land, and climate. This webpage provides an introduction to the field of Indigenous studies, including the concept of land acknowledgments, settler colonialism, and the importance of decolonization, which serve as an essential framework for further exploration of Indigenous knowledges on the topic of climate. The page also lists links to the "Climate in Arts and History" website entries that center on Indigenous peoples. An example includes "The Great Dying" entry from the "History/ Social Studies" theme, which connects the widespread destruction Europeans inflicted on Indigenous peoples across the Americas at the onset of the colonial era to anthropogenically-caused changes in climate.

At this stage of project development we seek to share the in-progress work to solicit feedback from the community. View the entire Climate Literacy Resource at http://www.science.smith.edu/climatelit/ and contact us at climate@smith.edu.

Knot Branched Covers in S4

Name: Georgia Gans
Year of Graduation: 2023
SURF Advisor(s): Patricia Cahn, Mathematics and Statistics
Field of Study: Mathematics (specifically, knot theory)
Co-Authors: Annika Gonzalez-Zugasti, Heng (Silvia) Song

Title: Knot Branched Covers in S4
Abstract: A mathematical knot is a positioning of a circle in space. Two knots are the same if it is possible to gradually deform one into the position of the other. Topologists want to find tools to tell knots apart. We studied one such tool, called branched covers of knots, in order to facilitate the process of telling knots apart.

The branched cover of a knot is a new three dimensional space that you can build from a labeled knot. The knot corresponds to a collection of knots in the branched cover which we call branch curves. The linking number of two knots measures how many times one knot wraps around another. A powerful knot invariant is the linking number of two branch curves in the branched cover of the original knot. This number being an invariant means that it is a valuable tool in helping us distinguish one knot from another.

We created a program which computes this invariant of a knot whose arc labelings are transpositions in S4, the symmetric group on 4 letters. This program automates the lengthy process of finding the number by hand. To calculate the number, the program requires four inputs for each crossing of the knot: the number of the crossing (which we will refer to as i), the transposition label assigned to the ith arc, the numbers of the arcs that cross over the crossing, and the sign of the ith crossing. In addition, the total number of crossings is needed for the program to run.

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Presence Conditions Within BloomingLeaf Tool

Name: Venus Nguyen
Year of Graduation: 2025
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Xinran Bi

Title: Presence Conditions Within BloomingLeaf Tool

Abstract: We introduced presence conditions in BloomingLeaf to visualize changes within the goal model's evolution. BloomingLeaf is an analysis and modeling tool that allows users to model goals that evolve over time. These models consist of intentions, actors, and links. By evaluating the changes in intentions over time, users are better able to understand future project evolutions and make decisions from them. A presence condition states whether a model element (i.e., intention or actor) exists at a particular time point in the project's evolution.
We first determined how to make an intention invisible. The "element ID" in each intention allowed us to change the visibility of each intention, so we successfully made intentions disappear in the CSS code. We then identified intentions with their IDs and have them stored automatically from the given goal models.
Next, we started looking through the front-end code and testing out possibilities of getting intentions within our model to disappear on a time-based condition. Once a user simulates a goal model within the analysis window, BloomingLeaf creates a path of timepoints that shows the progress of a goal model through a set span of time. At each timepoint the Satisfaction value of each intention changes. Users are able to step through each time point and examine the current state of the model with the use of a slider. We tested the disappearance of intentions based on satisfaction values to allow the visibility of elements more reliant on the prebuilt attributes. Satisfaction values are values assigned to intentions indicating whether the intentions are satisfied or denied within the evolutions of the model. Ultimately, we validated we could make intentions appear or disappear with the given satisfaction values.
We then grouped actors and all the intentions within it to change the visibility of elements on the actor-level instead of a single intention. We found a list of actors containing their embedded elements (intentions and links) to make a specific actor disappear with all its embedded elements. In future work, we hope to implement presence conditions with Actors.

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Year of Graduation: 2025
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Next, we started looking through the front-end code and testing out possibilities of getting intentions within our model to disappear on a time-based condition. Once a user simulates a goal model within the analysis window, BloomingLeaf creates a path of timepoints that shows the progress of a goal model through a set span of time. At each time point the Satisfaction value of each intention changes. Users are able to step through each time point and examine the current state of the model with the use of a slider. We tested the disappearance of intentions based on satisfaction values to allow the visibility of elements more reliant on the prebuilt attributes. Satisfaction values are values assigned to intentions indicating whether the intentions are satisfied or denied within the evolutions of the model. Ultimately, we validated we could make intentions appear or disappear with the given satisfaction values.

We then grouped actors and all the intentions within it to change the visibility of elements on the actor-level instead of a single intention. We found a list of actors containing their embedded elements (intentions and links) to make a specific actor disappear with all its embedded elements. In future work, we hope to implement presence conditions with Actors.

Monitoring Macroinvertebrates in the Mill River

Name: Rachel Ettenger
Year of Graduation: 2023
SURF Advisor(s): Marney Pratt, Biological Sciences
Field of Study: Ecology and biology
Co-Authors: Runpeng Hu, Brianna Bell, Rachel Slater

Title: Monitoring Macroinvertebrates in the Mill River

Abstract: Paradise Pond is a well-known landmark in the Smith College community, where it serves both recreational and educational needs of the students and the public of the Northampton area and beyond. However, the sediment redistribution (formerly dredging) required to maintain the pond has the potential to disrupt the Mill River ecosystem, including the macroinvertebrates that reside in it. Macroinvertebrates are important bioindicators of the health of an aquatic ecosystem. In addition to abiotic measurements of water quality, such as levels of dissolved oxygen, pH, and nitrogen/phosphate levels, macroinvertebrate sampling offers an especially dynamic method of testing for water systems of interest. We used freshwater benthic macroinvertebrates to gain insight into the health of the Mill River as affected by recent (2016 and 2018) sediment redistribution events.

To minimize the ecological effects of sedimentation, Smith is required by the government to monitor the impacts of the pond, therefore providing us with the opportunity to monitor the health of the river by collecting and identifying samples of macroinvertebrates from two macrohabitats (upstream and downstream of the pond) and five microhabitats within them.

In order to measure impacts of sediment redistribution on macroinvertebrate populations, Dr. Pratt uses a BACI (Before-After-Control-Impact) design. A BACI design has at least one sample before and after an impact (sediment redistribution) and has a sample that is likely to be affected by the impact as well as for a sample that should not be affected by the impact (Control sample). The impact site for this Mill River study is the rocky riffle habitat downstream of Paradise Pond, while the control site is a rocky riffle habitat upstream of the pond.

Through this project, our group became familiar with fieldwork sampling techniques and gained macroinvertebrate identification skills as well as knowledge of the general ecological research process. Sampling for macroinvertebrates in the Mill River consists of multiple important factors, namely large rocks and riffle area, which is the preferred habitat of macroinvertebrates. We then place a quadrat over the rocks and a D-net just downstream of the quadrat. Rocks are lifted into a bucket and gently rubbed off. After the rocks are gently rubbed off we use our feet to shuffle sand for 20-30 seconds. Macroinvertebrates are then transferred to the lab for preservation in a 70% ethanol solution.

Through data analysis in R, we found an increase in abundance of scrapers and collector filterers downstream compared to the previous two years (Figure 1). We also found an increased abundance of collector gatherers upstream in comparison to downstream this year. In addition, scrapers are more prevalent in the downstream region.

Figure 1 Caption. Relative abundance of functional feeding groups over time in the summers of 2018-2022 in the upstream and downstream riffles of Paradise Pond in the Mill River of Northampton, MA. Relative abundance was calculated by the number of organisms of a functional feeding group divided by the total number of organisms in a sample. For each location, 15 samples were collected on three different days every year.

Matching Requirements with Git Artifacts

Name: Sonora Halili
Year of Graduation: 2025
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Anisha Jain

Title: Matching Requirements with Git Artifacts

Abstract: Imagine leaving a dinner party hungry. Although your friend took note of each guest's dietary needs, they failed to account for each of them while grocery shopping, unintentionally leaving you with no options. Now imagine a tool that could remind your friend after each purchase that you can't have gluten, and that your other friend can't have dairy, or that your other friend is vegetarian. This would narrow down the recipe options for the host. They'd need to decide whether it's worth cooking three separate meals or one complex dish instead. Eventually, the decision would have to please everyone.

Software development is our favorite dinner party. There may be many cooks and many recipes, but it is of utmost importance that everyone gets to eat. The dietary specifications of software development are requirements—clear-cut expectations for the final product. Requirements Management (RM) refines the coding workflow, yielding quality bespoke software. RM techniques include creating traceability links between requirements and development artifacts (i.e., issues and pull requests), an often costly task that developers are reluctant to invest in. Completing this process manually is tedious and time-consuming, given that even small and medium-scale projects come with hundreds of requirements. In this project, we investigated the feasibility of creating a lightweight, open-source, Git-based tool that can complete the mapping process semi-automatically, reducing both the time and monetary cost of fully integrating RM.

Our proposed tool will take in requirements in natural language (plain text), map them to existing Git artifacts (issues and pull requests) through Natural Language Processing (NLP), and prompt the user to select among the suggested traceability links. It will function iteratively, allowing the user to update and add links at all stages of the development process. The Git development environment is ubiquitous for small and medium sized companies, so hosting our solution through existing Git infrastructure will make RM more accessible in the software development community.

We explored cloud-based Git repository websites (GitHub, BitBucket, GitLab) and chose to extend the GitLab interface, given that it is open-source and comes with a barebones requirements feature. Additionally, Smith College Computing and Technical Services (CATS) runs a local version of GitLab and agreed to host our improvements. In future works, we will continue to research NLP techniques and Deep Learning techniques for connecting requirements with Git artifacts.

Evaluation Visualization Overlay (EVO): A User Validation Study

Name: Joey Elsbernd
Year of Graduation: 2025
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Irene Foster, Yesugen Baatartogtokh

Title: Evaluation Visualization Overlay (EVO): A User Validation Study

Abstract: BloomingLeaf is a web-based tool that allows users to model and analyze goals that evolve over time. These models consist of actors, links, and intentions that have function types and satisfaction values, which are also known as evidence pairs. By evaluating the changes in intentions over time through path analysis, users are better able to understand future project evolutions. However, running a path analysis means that each intention in the model contains evaluation information for each time point of the path. This information is difficult for the user to remember, which makes decision-making complicated.

Previous work in BloomingLeaf implemented Evaluation Visualization Overlay (EVO) as a feature that assigns each evidence pair a color. In BloomingLeaf's Modeling mode EVO colors the intentions that have evidence pairs according to the color key. In Analysis view has three mode options: Percent, Time, and State. State mode allows the user to step through each time point in the path with the intentions colored according to their satisfaction value. In Time mode, the intentions are striped chronologically with each color representing a different time point, allowing the user to see the evolution of the model over time at a glance. Percent mode colors the intentions with the percentage of time it has a specific satisfaction value, showing the values according to proportion.

To validate that adding EVO assists users in their model understanding and allows for better and faster decision making, we developed a between-subjects user study that will be taken online. Our research questions are:

RQ0: Do modelers perform similarly on understanding tests, given a consistent training protocol
RQ1: How does EVO affect modeler's understanding and comprehension of goal models
RQ2: How does EVO affect the speed at which a modeler understands a goal model

RQ1 has understanding and comprehension being broken down into the ability to interpret, exemplify, classify, summarize, infer, and compare. RQ2 looks at the time it took subjects with and without EVO to answer our questions.

This summer, we explored empirical methods of evaluation and created our study design. Additionally, we prepared study materials (including videos) and tested these materials with others in the lab.

We intend to run our study this fall, which will allow us to validate the usefulness of EVO for users.

Evaluation Visualization Overlay (EVO): A User Validation Study

Name: Irene Foster
Year of Graduation: 2023
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Yesugen Baatartogtokh , Joey Elsbernd

Title: Evaluation Visualization Overlay (EVO): A User Validation Study

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Year of Graduation: 2023
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Irene Foster, Joey Elsbernd

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Matching Requirements with Git Artifacts

Name: Anisha Jain
Year of Graduation: 2025
SURF Advisor(s): Alicia Grubb, Computer Science
Field of Study: Computer Science
Co-Authors: Sonora Halili, Joey Elsbernd

Title: Matching Requirements with Git Artifacts

Abstract: Imagine leaving a dinner party hungry. Although your friend took note of each guest's dietary needs, they failed to account for each of them while grocery shopping, unintentionally leaving you with no options. Now imagine a tool that could remind your friend after each purchase that you can't have gluten, and that your other friend can't have dairy, or that your other friend is vegetarian. This would narrow down the recipe options for the host. They'd need to decide whether it's worth cooking three separate meals or one complex dish instead. Eventually, the decision would have to please everyone.

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Identification and Genome Studies of O. ulmi inhibitors

Name: Jennifer Wise
Year of Graduation: 2023
SURF Advisor(s): Chris Vriezen, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

Title: Identification and Genome Studies of O. ulmi inhibitors

Abstract: The focus of this summer's research was to identify soil-borne bacteria inhibiting Ophiostoma ulmi, a causative agent of Dutch elm disease, and Chaetomium globosum. Using techniques and protocols developed during SURF last year, 152 soil isolates were tested for inhibition of the two fungi. We identified 11 isolates with strong or moderate inhibition of one or both of the fungi. The figure shows inhibition of O. ulmi by CVAP#434. Of those, we chose the six strains inhibiting O. ulmi which is of greater interest due to the great harm it causes. The DNA of CVAP#433, 452, and 514 were isolated. The DNA of isolates CVAP#434, 438, and 690 had been isolated and sequenced previously. Pilot studies using Comprehensive Genome Analysis in Patric showed us that CVAP#690 is most closely related to Paenibacillus, CVAP#438 is related to Collimonas, and CVAP#434 is related to Burkholderia.

AntiSMASH was used to search for gene signatures for the potential production of secondary metabolites. This search indicated the production of fusaricidin B and polymyxin in strain CVAP#690 with gene clusters of 100% similarity. Both of these substances have been shown to have strong antifungal activity. Rhizomide A/B/C (100% similarity) was found in strain CVAP#438 and has been poorly studied. However, at least one study has shown its antifungal activity. Strain CVAP#434 did not show a high similarity signature for the production of antifungals and even the low similarity metabolites have not been shown to have antifungal activity. This is incongruent with our observation that this strain inhibits O. ulmi.

The next goal is to develop protocols for the identification of (i) (novel)-genes involved in the production of antifungals and (ii) the potential antifungals produced. Our preference is for an isolate whose genome does not contain previously known antifungal secondary metabolites. To do this, transposon mutagenesis will be done on one of the isolates. We are currently in the process of identifying the isolate of interest allowing the initiation of this line of research. Considering the data obtained, CVAP#434 is our best candidate to date.

Identification and Genome Studies of O. ulmi inhibitors

Name: Jennifer Wise
Year of Graduation: 202
SURF Advisor(s): Chris Vriezen, Biological Sciences
Field of Study: Biological Sciences
Co-Authors:

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Understanding the role of reelin signaling in neurogenesis utilizing a Danio rerio model system

Name: Zoe Gardner
Year of Graduation: 2022
SURF Advisor(s): Michael Barresi, Biological Sciences
Field of Study: Biology
Co-Authors:

Title: Understanding the role of reelin signaling in neurogenesis utilizing a Danio rerio model system

Abstract: Reelin is a large glycoprotein known to be secreted by specific types of neurons. It is implicated in regulating neurogenic and synaptogenic processes during vertebrate brain development. Defects in reelin signaling have been linked to numerous human disorders including, Autism Spectrum, Schizophrenia, Bipolar, and Alzheimer's. Reelin interacts with two membrane-bound receptors Apoer2 and Vldlr. Intracellularly the signal is relayed via the cytoplasmic protein Disabled1. Reelin influences the migration and positioning of neural progenitors. Not much is known about mechanisms that regulate the expression of diverse components of the reelin signaling pathway. It is unknown whether its two membrane-bound receptors mediate specific actions in distinct types of neurons or whether they operate interchangeably. We have carefully examined expression patterns of Reelin pathway genes during early development of the nervous system in wildtype zebrafish and in mutants deficient in reelin, and apoer2 genes. We characterize these mutants by utilizing both quantitative and qualitative methods, Hybridization Chain Reaction (HCR), and quantitative Reverse Transcriptase PCR(qRT PCR). We found that in reelin mutants reelin is downregulated consistently, with apoer2 and vldlr being upregulated at 2dpf and then relatively stable at 3dpf. In apoer2 mutants, apoer2 was downregulated and reelin was upregulated consistently. Vldlr on the other hand underwent fluctuations, being upregulated at 2dpf and then downregulated at 3dpf. Our studies of the Reelin signaling pathway in zebrafish mutants of its distinct components have the potential to yield insights into the transcriptional mechanisms that regulate reelin pathway expression and how these mechanisms and the pathway more generally may be affecting early vertebrate brain development.
This summer I did further HCR analysis of wt specimens. Using confocal imaging I was able to get a better understanding of where and when reelin pathway members are being expressed in the brain. I created a poster detailing the work I have accomplished over the past 2 years which I then presented at the biannual Pan American Society for Developmental Biology meeting in Vancouver British Columbia. This poster earned me an honorable mention for best undergraduate student poster.   In addition to the more glamorous work, I also spent a lot of time breeding and caring for our zebrafish specimens in order to prepare for my departure from the lab at the end of the summer.

Generalization of Springer Fibers: Hessenberg Varieties

Name: Joy Mahoney
Year of Graduation: 2024
SURF Advisor(s): Julianna Tymoczko, Mathematics and Statistics
Field of Study: Abstract Mathematics
Co-Authors:

Title:Generalization of Springer Fibers: Hessenberg Varieties
Abstract:
Background:
A flag is defined as a matrix that satisfies the following conditions:
   1. There is one pivot in each row and column
   2. Entries below the pivot are zero
   3. Entries to the right of the pivot are zero
A Springer fiber is the subset of flags where the following condition is satisfied for each k = 1, ..., n:

$$X\vec{b_k}=\{\vec{b_1},\vec{b_2},\vec{b_3},\cdots,\vec{b_k}\}$$

The definition of a flag partitions the collection of flags of matrices of size n into $n!$ subsets according to where the pivots are. Using these definitions, we can determine which flags are included in the Springer fiber for each specific matrix X. The Springer fibers that we focus on are related to arc diagrams, an important concept in knot theory. Knot theorists study how the arcs fit together to form different kinds of loops.
Methods:
This summer, I looked at a generalization of Springer fibers often called Hessenberg varieties for which the Springer fiber condition is relaxed. We relax the condition by defining a non-decreasing function h that returns exclusively integers as an indexing function. This changes which flags are included in the Hessenberg variety of the matrix $X = \left(\begin{array}{cccc}
0 & 0 & 1 & 0 \\
0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{array} \right)$.

Cont. Generalization of Springer Fibers: Hessenberg Varieties

To collect extensive data on which sets of pivots were in each of these Hessenberg varieties and the dimension of the other entries in each part of the partition, I created a spreadsheet workbook to observe patterns in these Hessenberg varieties with different indexing functions. I then performed analysis and formed hypotheses and conjectures.

Results:
After analyzing the gathered data, I observed the following for each indexing function h:

   1. Suppose the pivot in the first row is included in the span of columns with pivots in row $n-1$ and the pivot in the second row is included in the span of columns with pivots in row n, according to the indexing function h. Then flags with this pivot are included in the Hessenberg variety of X.

   2. Conditions on the non-pivot, non-zero entries of flags disappear when the column of the flag with a pivot in the first row is in the span of the columns with pivots in row n, as defined by the indexing function h.

   3. When the condition on non-pivot, non-zero entries of the flag is present, it follows that the value of the non-zero entry above the lowest pivot is equal to the value of the free variable above the pivot in the second row of the flag.

   4. Suppose h is a function of the form $h(i)=i+c$ for some fixed c. The size of the Hessenberg variety of X, H, is given by the following formula:
$$H = H_{c-1} + 2(5-c), \text{and } H_0 = 6$$

In addition to the conjectures made above, we have drafts of proofs for Claims 2 and 3.

Oxygen-Cyclopropylations via Chan-Evans-Lam Reaction

Name: Danielle Joubran
Year of Graduation: 2024
SURF Advisor(s): David Gorin, Chemistry
Field of Study: Chemistry
Co-Authors:

Title: Oxygen-Cyclopropylations via Chan-Evans-Lam Reaction
Abstract: Cyclopropyl groups are found in many natural products and drugs, exhibiting unique chemical properties due to their strained shape and unusual bond angles. Thus, developing methods for their installation could have significant applications in pharmaceuticals and medicine. This study aimed to develop a method for oxygen cyclopropylations. The Chan-Evans-Lam reaction, which couples nucleophiles via a copper catalyst, has primarily been used to install aryl groups. Basing our method on the Chan-Evans-Lam, cyclopropyl (rather than aryl) boronic acid was reacted with an aliphatic alcohol substrate. The conditions for this O-cyclopropylation were optimized and, during SURF, methods for efficient quantification were explored. To obtain a standard curve, precedented methods for O-cyclopropylations were tested and altered in an attempt to form excess product. However, since these reactions were unsuccessful, initial spectra were taken to develop a method for 1H NMR quantification. Future work will involve testing the reaction with different aliphatic substrates and quantifying the results via NMR.

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Stable Isotope Study of Encrusters on Corals from the Cockburn Town Member (Grotto Beach Formation; Eemian, MIS 5e) from San Salvador and Great Inagua

Name: Asha Lang
Year of Graduation: 2023
SURF Advisor(s): Bosiljka Glumac, Geosciences
Field of Study: Sedimentary geology
Co-Authors:

Title: Stable Isotope Study of Encrusters on Corals from the Cockburn Town Member (Grotto Beach Formation; Eemian, MIS 5e) from San Salvador and Great Inagua Islands, Bahamas

Abstract: A 34 m-deep, 54 mm-diameter core through the Cockburn Town Member of the Grotto Beach Formation from The Gulf (TG) site on the south coast of San Salvador Island, Bahamas, contains coral reef deposits from the last Pleistocene interglacial highstand (Eemian, MIS 5e). Results of petrographic, stable isotope and XRD analyses of these deposits are compared with outcrops of this interval from the Cockburn Town Fossil Reef on the west coast of San Salvador and Matthew Town Marina and Devil's Point sites on Great Inagua Island to better understand the conditions that resulted in heavy encrustation of corals, especially Acropora cervicornis, with microbialites.

Stable isotope analyses ($\delta13C$ and $\delta18O$ in ‰ VPDB) included various carbonate components throughout the entire TG core and focused on intervals with encrusters up to 14 cm thick at -9.2 to -9.7, -23.8 and -31.1 m. There is positive covariation ($R2 = 0.7$) between data for coral (lower values; $\delta13C$ = -1.8 to 1.9‰; $\delta18O$ = -3.6 to -1.1‰) and laminated microbialites (higher values; $\delta13C$ = 1.2 to 4.4‰; $\delta18O$ = -3.1 to -0.2‰). Outcrop data have similar trends, with a sharp increase in $\delta13C$ and $\delta18O$ values at the transition between corals and microbial encrusters. These differences can in part be attributed to isotopic fractionation between aragonitic corals and mixed aragonitic and calcitic microbialites, and to vital effect and greater degree of meteoric diagenetic modification of corals.

Microbialites incorporate fine carbonate sand and mud, and their composition overlaps with skeletal-peloidal-ooid sand and micritic sediment from TG core ($\delta13C$ = -1.9 to 3.3‰; $\delta18O$ = -2.6 to 0‰). Rhizoliths from -19.4 to -24.4 m in TG core have $\delta13C$ values as low as -5.4‰, and outcrop caliche has the most negative $\delta13C$ value of -8.2‰, representing formation from meteoric water. Conversely, the most positive $\delta13C$ values of microbialites may indicate elevated organic productivity due to enhanced nutrient input to shallow marine settings, possibly during post-storm run-off. The transitions from corals to thick encrusters may also reflect changes in water depth, with elevated $\delta13C$ and $\delta18O$ values of microbialites indicating shallower and more restricted conditions. These results complement other sedimentological and paleontological studies to provide insights into reef microbialite formation. This work will be presented at the Geological Society of America Annual Meeting in Denver in October 2022.

Methods of Measurement for Ear Canal Geometry

Name: Rebecca Farrar
Year of Graduation: 2025
SURF Advisor(s): Susan Voss, Engineering
Field of Study: Engineering
Co-Authors: Karen Bekhazi

Title: Methods of Measurement for Ear Canal Geometry

Abstract: This summer we continued to refine and support the method established by prior students to measure ear canal geometry, using the software OsiriX to view CT scans in Multi-Planar Reconstruction, or across three planes (transverse, coronal, and sagittal). Measurements were taken along a central spline that we created through the ear canal, dallfirst every 2 millimeters and then every millimeter, starting at a certain location, to determine the curvature and length of the ear canal. We started recording our measurements at regular intervals of one millimeter at location 16 for pediatric subjects (ages ranging between 0 and 17 years old) and at location 24 for adult subjects (18 to 99 years old). Additionally, cross sectional areas of the ear canal were taken at every location. The most obvious location along the canal is called the first bend, which is defined as "the location of the most lateral sharp change in curvature of the canal central axis

This method of measuring the canal is the primary way to determine more specific information about the canal's dimensions and geometry, and indicates the variability in geometry across different subjects. We use these measurements to analyze trends including total length of the ear canal vs distance of the first bend, as well as considering the subjects age vs canal length. Measurements will be used to highlight the correlation between ear canal geometry and peripheral sound flow. This understanding of the ear canal geometry can help to influence the development of future audiology technology.

Graphs of some of our measured ears are shown below. 40 unique subjects are shown below, graphing the length of the ear canal vs the cross sectional area. The first bend is denoted along the line with a more prominent point. Blue lines represent the left ear, while red represents the right ear; plots with multiple lines indicate repeated measurements from different investigators.

Skeletal Abundance During the Cambrian SPICE Event, western Utah

Name: Amelia Olsen
Year of Graduation: 2022
SURF Advisor(s): Sara Pruss, Geosciences
Field of Study: Geosciences
Co-Authors:

Title: Skeletal Abundance During the Cambrian SPICE Event, western Utah

Abstract: The Steptoean Positive Isotopic Carbon Excursion (SPICE) is a globally recorded positive shift (+4-5‰) in δ13C during the Furongian Epoch of the Cambrian. The SPICE event is recorded within thick, fossiliferous sections of the Orr Formation exposed at the Lawson Cove and House Range localities in western Utah. High resolution sampling through the SPICE event provided an opportunity to observe shifts in skeletal abundance and diversity through the excursion while tracking Hg abundances, total organic carbon, and organic carbon isotope ratios. In both sections, pre-SPICE intervals are characterized by low abundance of skeletal material, followed by a brief absence at the onset of the SPICE event. The rising limb of the SPICE has the greatest abundance of skeletal material observed in thin section with as much as 49% of skeletal material per slide in both sections. In the Lawson Cove section, the most positive δ13C values are aligned with a brief absence of skeletal material, while in the House Range, an extended absence of skeletal material overlaps with peak δ13C values. This prolonged depauperate stretch in the House Range is correlated with a marine regression recorded in the facies change from the Candland Shale Member into the Johns Wash Limestone Member of the Orr Formation. The geochemical and fossil differences between these two localities illustrate the impacts of local processes on the preservation of the SPICE event itself as well as its biological consequences.