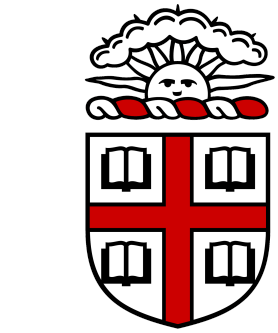

BROWN

SUMMER RESEARCH SYMPOSIUM

2023

Sayles Hall
11:00 am – 1:00 pm

Thursday, August 3
Life Sciences and Humanities

&

Friday, August 4
Physical and Social Sciences

PRESENTED BY
The College

SUMMER RESEARCH SYMPOSIUM

Sayles Hall

Main Green

Thursday, August 3

Life Sciences and Humanities Posters

11:00am – 11:05 am Welcome and Brief remarks
Associate Dean Oludurotimi Adetunji

11:05 am – 1:00 pm Research Poster Presentations

Friday, August 4

Physical and Social Sciences

11:00 am – 11:05 am Welcome and Brief remarks
Associate Dean Oludurotimi Adetunji

11:05 am – 1:00 pm Research Poster Presentations

~ A light lunch will be provided both days ~

Descriptions of each poster session include a poster number indicating the poster's placement in Sayles. To locate a poster, refer to the layout maps below.

POSTER LAYOUT

Thursday, August 3

Humanities and Life Sciences

[STAGE]

A16		B16	C16	D16	E16	F16	G16		
A15		B15	C15	D15	E15	F15	G15	H14	
A14		B14	C14	D14	E14	F14	G14	H13	
A13		B13	C13	D13	E13	F13	G13	H12	
A12		B12	C12	D12	E12	F12	G12	H11	
A11		B11	C11	D11	E11	F11	G11	H10	
A10		B10	C10	D10	E10	F10	G10	H9	
A9		B9	C9	D9	E9	F9	G9	H8	
A8		B8	C8	D8	E8	F8	G8	H7	
A7		B7	C7	D7	E7	F7	G7	H6	
A6		B6	C6	D6	E6	F6	G6	H5	
A5		B5	C5	D5	E5	F5	G5	H4	
A4		B4	C4	D4	E4	F4	G4	H3	
A3		B3	C3	D3	E3	F3	G3	H2	
A2		B2	C2	D2	E2	F2	G2	H1	
A1		B1	C1	D1	E1	F1	G1		

[ENTRANCE]

[LOBBY]

POSTER LAYOUT

Friday, August 4

Physical and Social Sciences

[STAGE]

A17	B17	C17	D17	E17	F16
A16	B16	C16	D16	E16	F15
A15	B15	C15	D15	E15	F14
A14	B14	C14	D14	E14	F13
A13	B13	C13	D13	E13	F12
A12	B12	C12	D12	E12	F11
A11	B11	C11	D11	E11	F10
A10	B10	C10	D10	E10	F9
A9	B9	C9	D9	E9	F8
A8	B8	C8	D8	E8	F7
A7	B7	C7	D7	E7	F6
A6	B6	C6	D6	E6	F5
A5	B5	C5	D5	E5	F4
A4	B4	C4	D4	E4	F3
A3	B3	C3	D3	E3	F2
A2	B2	C2	D2	E2	F1
A1	B1	C1	D1	E1	

[ENTRANCE]

[LOBBY]

SYMPOSIUM ORGANIZERS

Oludurotimi Adetunji
Associate Dean of the College for Undergraduate Research and Inclusive Science; Director, UTRA Program

Linda Sutherland, Co-Curricular Program Manager

ACKNOWLEDGEMENTS

Christina Paxson, President

Francis J. Doyle III, Provost

Rashid Zia, Dean of the College

Brown University Library

PRESERVING YOUR RESEARCH

Students who opt to upload their posters to the Brown Digital Repository can do so using the self-deposit tool, available at **https://repository.library.brown.edu/deposits/.**

The deadline for this is **Monday, August 21, 2023**

SUMMER RESEARCH SYMPOSIUM POSTERS

Thursday, August 3rd

Humanities & Life Sciences

Humanities

Hannah Stoch; Happy Jara **Poster #A1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Laura Synder, Education Department

Humanities Reimagined

The Humanities Reimagined Curriculum Project aims to produce curricula for high school humanities classrooms that adequately reflect students, their community, and the diversity of the world around them. Researchers read and analyzed A Snake Falls to Earth by Darcie Little Badger, and created accompanying assignments related to themes of climate change, technology, language revitalization, and Lipan Apache Indigenous culture. Researchers also read and analyzed Last Night at the Telegraph Club by Malinda Lo, and created accompanying assignments related to themes of intersectionality, space exploration, and self-acceptance. Researchers curated these materials into free and publicly accessible eBooks for teachers.

Kate Choi; Brynne Miller **Poster #A2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Scott Rivkees, Public Health; Daniel Weinreich, Ecology and Evolutionary Biology

American Indian and Alaska Native Influenza Vaccinations over H1N1 and COVID-19 Pandemics

The American Indian and Alaska Native (AIAN) population in the United States has disproportionately higher rates of several infectious and vaccine preventable diseases, which result in disparities in morbidity and mortality rates. The AIAN population has a greater chance of dying from pneumonia and flu than other races in the United States. Using the Kruskal-Wallis H Test, we analyze possible factors that potentially impact the AIAN influenza vaccination rates. We analyze these rates in various states across time and compare them with non-Hispanic white, non-Hispanic Black, and overall population's rates.

Ashley Zarco **Poster #A3**

Home Institution: Heritage University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Dr. Ashley Champagne, Director of the Center for Digital Scholarship, Brown University Library Cogut Institute Lecturer in Humanities; Dr.Khanh Vo, Digital Humanities Specialist Center for Digital Scholarship | Brown University Library

Humanizing the untold stories of Indigenous Enslavement: Database Cleaning and Oral Storytelling

Stolen Relations: Recovering Stories of Indigenous Enslavement in the Americas is a community-based project housed at Brown University that seeks to collaboratively build a database of enslaved and unfree indigenous people throughout time across the Americas to promote greater understanding of the historical circumstances and ongoing trauma of settler colonialism. The database examines archival documents from 1492 to 1900 and sometimes beyond about enslaved and unfree individuals across the Americas. The goal of this project is to foster a deeper understanding of the ongoing impact of colonization on Indigenous communities and promote reconciliation efforts.

Data cleaning is crucial for Stolen Relations, ensuring accuracy in analysis and archives by removing errors and inconsistencies that an earlier researcher missed and removes the incorrect location, date, name, or any sort of messy information. This helps identify patterns and correlations, allowing for a comprehensive dataset of individuals' geographic, gender, and time distribution. Proper data cleaning also helps avoid duplication and accurately represents common individuals across multiple documents, preventing misleading information in the database.

The project collaborates with thirteen regional tribes, nations, and communities to interpret archival documents and oral storytelling histories. I have been specifically focusing on data cleaning and oral storytelling regarding settler colonialism, displacement, indigenous enslavement, and ongoing survival into the present. Data cleaning is essential for humanizing records, promoting clarity, and uncovering hidden narratives. It accurately represents marginalized communities' Oral stories and experiences, enabling a human-centered understanding of indigenous enslavement's impact on individuals and communities throughout history.

Jean Wanlass **Poster #A4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: John Bodel, Classics

Digitizing Greek and Latin Inscriptions from the MFA

The Museum of Fine Arts, Boston (MFA) has an extensive collection of inscriptions from the ancient Mediterranean. The U.S. Epigraphy Project (USEP) presents digital editions of these inscribed objects according to EpiDoc guidelines for encoding in XML the texts and metadata about the objects (including dimensions, original context, date, provenance, condition, and subsequent collection history) in an extensive digital corpus of ancient Greek and Latin inscriptions held in collections in the United States. As

the MFA is a particularly early and prominent example among American collections of ‘classical’ artifacts, adding and maintaining a record of the inscriptions in its collection allows for more than just digital, public access to the information within: it creates an opportunity to consider the role which such collections have played in the ongoing negotiation of history, colonialism, and heritage occurring in American institutions.

Alexandra Floru **Poster #A5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: John Bodel, Classics

Brickstamps of Rome

My work this summer was an extension of a Spring 2023 UTRA with Professor Bodel's U.S. Epigraphy Project. The Project is a collection and display of information about inscriptions from the classical Mediterranean world. My work focuses exclusively on Latin inscriptions. In the Spring, I studied Roman epitaphs (funerary inscriptions) and learned about cultural elements such as Roman naming conventions, dating practices, and many more. This summer I worked with Roman brickstamps, which differ from epitaphs in structure and purpose, presenting unique information and challenges. This work included updating existing entries in the database and devising new classification and translation techniques.

Da-Young Kim; Ethan Register **Poster #A6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ramu Kharel, Department of Emergency Medicine

Creating Open Source Platforms and Impact Report Infographics: Insights Gained from Assisting A Rural Nepali Health Nonprofit with their Data Science Needs

A partnership between Brown University and Nyaya Health Nepal, a healthcare non-profit in rural Nepal, in Summer 2023 yielded two major work products: an open source RShiny platform/app that automates the cleaning and visualization of community health data in Nepal and an infographic summarizing the historical patient and community impact of the organization. The RShiny platform allows users to upload spreadsheets of community health data and clean it by removing empty rows or columns, removing non-alphanumeric characters, removing duplicate columns, rounding numbers up or down, or converting them into integers. This app also generates bar charts, scatter plots, and pie charts with desired variables in a straightforward fashion. The impact infographic compiles and displays the organization’s key foundational, financial, and impact information in a concise and visually-digestible format. This infographic, created in Adobe Illustrator, serves as an institutional resource/template for future reports and will be distributed to Nyaya Health Nepal’s philanthropic partners and the Nepali government. In addition to creating work products, Brown undergraduates wrangled and analyzed facility- and community-based health information to assist the organization with its annual impact reporting and analysis. Reflections on international virtual communication, non-profit infrastructure and data analysis needs, and cross-cultural collaboration led to insights about the benefits and challenges of working within the nonprofit sector, as well as suggested best practices for similar future collaborations.

Life Science

Cara Kaminski; Jessica Hooper; Max Newman; Eloise Gacetta; Ian Wright Poster #A7

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: James Simmons, Neuroscience; Andrea Simmons, CLPS

Understanding Big Brown Bats' Biosonar: Impact of Frequency Filtering on Echolocation Detection

In this experiment, we investigated the absolute detection thresholds to virtual echoes in big brown bats (Eptesicus fuscus) using a two-alternative forced choice active listening task and the Békésy tracking method. The primary focus was on assessing changes in the bats' echolocation detection when low-frequencies were removed from virtual echoes. To understand how their sonar screening operates, we used a high-pass filter to eliminate ranges of frequencies below 35 kHz and tested how this modification affected their performance as bats rely on a narrow band of frequencies to distinguish between sounds and echoes. Bats were trained to walk on a Y-Shaped platform toward a single virtual echo. The experiment involved six bats, with three experienced bats starting at 3 meters and three newly-trained bats starting at 0.5 meters. We conducted a series of trials, progressively decreasing the attenuation by 3dB until the bats began making errors. Our experiment also employed three different tests to evaluate accurate responses: (1) no filter, (2) filter set to 35 kHz (anticipated to yield errors), and (3) the same filter turned back to 25 kHz (expected to restore performance). We predict that reducing the number of frequencies in FM sweeps would lead to a disproportionate increase in errors, demonstrating the crucial role of low frequencies in bats' perception of sonar images.

Rainy Wortelboer; Christopher Liu; Samantha Chon; Alex Hernandez-Manriquez; Joseph Suh Poster #A8

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Glenn Radice, Department of Medicine, CVRC

Vinculin Y822 phosphorylation impacts mechanical equilibrium of cardiomyocytes in the neonatal and postnatal heart

In 2021, complications from cardiovascular disease accounted for one in five of all fatalities in the United States. The neonatal mammalian heart is capable of regeneration after injury, but this ability disappears seven days after birth. Understanding mechanisms that affect neonatal cardiac growth might allow us to develop novel regenerative therapies to compensate for loss of cells upon injury. Maturation of mechanotransductive cadherin junctions sequesters transcriptional co-activators at the intercalated disc causing neonatal heart cells to exit the cell cycle. Vinculin, a cytoskeletal adaptor protein, undergoes posttranslational modification in response to mechanical force. Vinculin phosphorylation at tyrosine residue 822 (pVCL-Y822) is critical for force-induced cytoskeletal remodeling and adhesion strengthening at cadherin junctions. We show that pVCL-Y822 expression correlates with remodeling of cadherin junctions in the embryonic heart, and declines in postnatal and adult hearts. CRISPR-mediated genome editing was used to mutate the tyrosine (Y) at position 822 to a non-phosphorylatable phenylalanine (F) in

the mouse Vcl gene. We characterized the novel Vcl Y822F mouse model in terms of cardiac structure and function, junction formation, and intercalated discs, highlighting the impact of vinculin phosphorylation on mechanical equilibrium of cardiomyocytes and its implications for heart disease and growth.

Nellely Lopez-Mendez; Harper Liang **Poster #A9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: David Sheinberg, Neuroscience; Ryan Miller, Neuroscience

Within-modal and Cross-modal Recognition of Shapes through Vision and Touch in Humans: Supramodel vs Associative Learning

Sight and touch are among the most fundamental modalities humans use to recognize objects and explore the world. Initially processed by distinct neural systems, how do they converge to form an abstract representation of the world, independent of sensory modality? A hypothesis relying on supramodal representations of objects does seem intuitive; when we touch objects, we can imagine what these objects look like in our mind's eye. Perhaps we can compare this image conjured by imagination to a real visual image? Indeed, fMRI studies have found overlap between visual and haptic neural pathways that hints at the possibility of a supramodal representation's existence. Portions of the human lateral occipital cortex (LOC) and anterior intraparietal sulcus (aIPS) respond to both visual and haptic cues, and might be activated when subjects use one modality to identify objects encoded with the other.
However, testing the supramodal hypothesis directly has proven to be difficult. Thus, an alternative hypothesis called "learning association" is introduced. Learning association proposes that the mental representation of an object's appearance is not automatic but is instead learned through repeated associations between different sensory experiences and their corresponding visual representations, and thus has confounding effects that might falsely imply the use of a supramodal representation of objects. Conducting experiments to differentiate between these two models has been challenging, especially in the field of haptics. To avoid the confounding problem of learning during testing, researchers need to use a large and diverse set of different shapes, but this can be technically challenging.
To address this issue, we designed an experiment that aims to compare the two concepts by introducing two variables: congruence and modality. Incongruent trials present participants with stimuli that contradict their natural associations, while congruent trials involve linking sensory experiences with specific visual representations either deliberately or intuitively. Additionally, we examined cross-modal effects by using both visual and haptic shape representations within a trial. The analysis of this data can have broader implications for our understanding of how the human brain integrates information from multiple sensory sources to create a coherent perception of the world around us.

Jack Blocker; Olivia Maule; Jacob Lerman **Poster #A10 & #A11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: David Rand, Evolutionary Ecology and Behavioral Sciences; Faye Lemieux, Evolutionary Ecology and Behavioral Sciences

A Drosophila model of personalized medicine using genetic variation in mito-nuclear interactions underlying climbing, flight and development time

Although the vast majority of DNA in eukaryotic cells is found in the nucleus, the mitochondria contains its own distinct genome. The proper expression of these distinct genomes is necessary for standard cellular metabolism. Natural genetic variation in these two genomes modulates the way they communicate, which affects mitochondrial function and energy production. Faulty 'mitonuclear' communication often results in metabolic defects, such as exercise intolerance and delayed development. Mitochondrial diseases affect 1 in every 5,000 people, and every 30 minutes a child is born who will develop mitochondrial disease by age 10. *Drosophila melanogaster* is an ideal candidate to test the supposed disruption of the communication between the nuclear and mitochondrial genomes. Through backcrosses, eight mitochondrial genomes were paired with two different nuclear genomes (DGRP375 and OreR) producing a total of 52 unique genotypes. Each mitonuclear pair was evaluated through quantitative measures of climbing speed, flight height, and development time. To analyze an environmental impact on the mitonuclear interactions, all genotypes were split onto a control diet and an experimental diet which contained rotenone, a mitochondrial inhibitor. Rotenone is particularly helpful to investigate the communication of these two systems since it targets both nuclear and mitochondrial encoded proteins in complex I within the electron transport chain. The rotenone diet may limit mitochondrial efficiency through this mechanism, however, results where rotenone-fed *Drosophila* outperform in flight, climbing, and development time alludes to the possibility of nuclear genotypes being a better predictor of performance. Between the nuclear backgrounds DGRP375 and Ore.R, the 375 nuclear background consistently outperforms. This correlates some combinations of mito-nuc encoded proteins to much higher efficacy regardless of environmental stressors. Further research into mitonuclear interaction may be critical for the development of novel medications for individuals with mitochondrial diseases.

Lizi Zhang; Lucy Anderson **Poster #A12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Justin Fallon, Neuroscience

The Impact of Increased Hippocampal Neurogenesis on Spatial and Emotional Memory in a Mouse Model

The hippocampus plays a critical role in learning, memory, and emotion. These functions are mediated by different hippocampal subregions that are connected to distinct brain regions. The dorsal hippocampus (DH) is primarily involved in spatial navigation and cognitive processes, while the ventral hippocampus (VH) is involved more in emotional and affective processing. Adult hippocampal neurogenesis (AHN), or the generation of new neurons in the hippocampus, is essential for normal hippocampus functioning. AHN is diminished in both diseases involving cognition and memory like Alzheimer's Disease (AD), as well as affective disorders like Major Depressive Disorder (MDD), suggesting its importance in the normal functioning of both the DH and the VH. Therefore, upregulating AHN could serve as a potential therapeutic for these diseases.

BMP (bone morphogenetic proteins) signaling tonically inhibits AHN, thus, interventions that reduce BMP signaling could promote AHN. In previous studies, our lab identified MuSK (muscle-specific kinase) as a BMP co-receptor that augments BMP signaling. The Ig3 domain of MuSK is required for its high-affinity binding to BMP and for optimal activity of the MuSK-BMP pathway. Our preliminary data shows that a genetically modified mouse model that constitutively lacks the MuSK-Ig3 domain exhibits increased hippocampal neurogenesis, especially in the ventral area. In order to assess the impact of inhibiting the MuSK-BMP pathway on the functioning of both the DH and the VH, we are performing two behavioral experiments our ΔIg3-MuSK mouse model, the Y-maze, which assess spatial memory localized in the DH, and contextual fear conditioning, which assesses emotional memory that involves both the DH and the

VH. Our long-term goal is to better understand the behavioral implications of MuSK-BMP pathway manipulation and shed light on its potential application for the treatment of a variety of disorders involving the hippocampus.

Mason Romantic; Octavia Rowe **Poster #A13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mark Johnson, Cell and Molecular Biology

Analysis of Tomato HAP2 Mutants

Title: Analysis of Tomato HAP2 Mutants
Authors: Mason Romantic, Octavia Rowe, Jonathan Dow, Mark Johnson, Department of Molecular Biology, Cell biology, and Biochemistry, Brown university

With the human populations growing and climate change progressing the molecular and cellular mechanisms that create our food and fruits have become increasingly important. In plants, it is necessary for two sperm to fuse with an egg and central cell, respectively, to produce a seed, and then fruit. Sperm fussion to the egg and central cell is dependent on HAP2. This process is dependent on HAP2, a sperm-expressed transmembrane protein that drives gamete fusion in multiple species and is broadly important for fruit production in plants. However, HAP2 protein and gamete fusion has not been studied in one plant that produces our food: tomatoes. Two loss-of-function mutations were created and are maintained as both heterozygous and CRISPR-CAS9 active plants. One has early frameshift and the other an in-frame deletion of 77 N-terminal amino acids. We have used PCR to observe and sequence the genotypes of these plants and a western blot will show the size of the mutant sterile plant as well as the wild-type plant. CRISPR-CAS9 active plants are male sterile, and crosses between heterozygous mutant plants and wild-type plants both suggest that the mutant completely blocks sperm function. The seed-set data for these crosses remains the same as in wild-type though, suggesting some form of unknown fertilization recovery that may not be limited by the number of synergid cells, as is the case in Arabidopsis. We are using these tomato HAP2 mutants to explore differences between tomato and Arabidopsis fertilization and to determine the mechanisms of fertilization recovery present in tomatoes.

Nate Nigrin; Sanyu Rajakumar; Zining Chen **Poster #A14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Erica Larschan, Molecular Biology, Cell Biology, and Biochemistry

Y does your X still affect your life? Investigating the Relationship Between Dosage Compensation and Sex-based Aging

A majority of species display sex-based differences in the process of aging. In humans, these sexual dimorphisms lead to an average longer lifespan in females. Moreover, neurodegenerative diseases such as Alzheimer's and Parkinson's show varying incidence rates based on sex. Despite the apparent

relevance of these outcomes, sex-based aging is relatively understudied. Therefore, investigating the genetic basis of brain aging between the sexes could provide translational benefits in addressing longevity and neurodegenerative disease.

To interrogate this differential speed of aging, we study dosage compensation with a specific focus on the aging brain. Dosage compensation (DC) is the genetic process in which a given species equilibrates the expression of sex-linked genes. Thus the dysregulation of this pathway with age could result in sexually dimorphic traits. Indeed, previous work has shown that DC is linked to sex differences in cognitive aging and several neurological disorders. We use Drosophila melanogaster to study dosage compensation during aging as they share many fundamental biological processes and genetic pathways with humans and they are a well-established model for DC.

To study the impact of dosage compensation on sex-based aging, we use the CRY2 and GeneSwitch Gal4/UAS systems in vivo to disrupt dosage compensation molecular machinery and observe its respective effect on male and female drosophila's aging pattern and longevity. Additionally, we use in silico methods to analyze transcriptomic data from the "Aging Fly Cell Atlas", thus revealing genome-wide effects relevant to aging and dosage compensation. Together, we hope to build an understanding of the genetic basis for sex-based differences in fly aging, and how dosage compensation specifically plays a role in this broadly conserved phenomenon.

Our preliminary findings, although inconclusive, suggest a potential association between the disruption of the dosage compensation complex and the aging process of both male and female Drosophila. These preliminary observations warrant further in-depth investigations to reach a conclusive understanding of the role dosage compensation plays in the aging process of the two sexes. The ambiguous nature of our initial results underscore the complexity of the genetic mechanisms governing sex-based aging and highlight the need for additional data collection and analyses.

Elisa Dong; Ayla Taylor-Robichaud; Brown Bulloch **Poster #A15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Christian Nixon, Pathology and Laboratory Medicine

Expression and Purification of a Novel Malaria Transmission Blocking Vaccine Candidate Antigen

Malaria presents a significant global health problem, resulting in 619,000 deaths in 2021 (WHO), the majority of whom are sub-Saharan African children under the age of 5. The current vaccine against *P. falciparum*, the most prevalent and deadly species involved in malaria infection, has exhibited limited efficacy. The Nixon Lab currently aims to characterize a novel vaccine candidate of unknown function previously identified from a gametocyte-specific phage display library whose antibody levels are inversely correlated with gametocyte density levels over time. The protein shares homology with human Talin1, responsible for enabling cytoskeletal deformation via actin-integrin linking. It also contains an important cleavage site for Plasmepsin IX, an aspartic malarial protease involved in erythrocyte invasion, and is among the *P. falciparum* virulence-associated genes. Current confocal imaging has determined its position in either the rhoptries or micronemes, which are specialized secretory organelles. It is therefore hypothesized that this antigen of interest may be involved in parasite invasion or egress.

We approach the topic of protein characterization through a multi-pronged approach. Firstly, we aim to immunolocalize the protein in transgenic *P. falciparum* lines encoding the V5 epitope tag. Immunofluorescence assays (IFAs) will probe the protein expression and localization at different parasite stages with antibodies targeting the V5 tag and affinity-purified rat antibody to our protein of interest, visualized with an in-house confocal microscope. Immuno-Expansion Microscopy (Immuno-ExM) will elucidate the protein's subcellular localization and function, with NHS-Ester grayscale, lipid stains, and organelle-specific antibodies (CYTOX Deep Red for nuclei, anti-AMA1/EBA75 for micronemes, anti-RAP1 for the rhoptries). We will also prepare samples for Transmission Electron Microscopy (TEM) to gain insight on ultrastructural localization of our protein of interest throughout the plasmodium life cycle.

Secondly, we aim to express, isolate, and purify the protein for further functional tests, including cleavage experiments on the putative cleavage site by Plasmepsin IX. We will produce the His-tagged recombinant protein in an *E. coli* bacterial expression vector and a CHO cell mammalian expression vector, and purify with nickel columns, cation exchange columns, and size exclusion chromatography. Due to the high isoelectronic point and large size of the recombinant protein, continued optimization is necessary to increase protein yield. Current efforts are focused on trialing different vectors to generate sufficient protein for future structural, cleavage, and binding studies. The difficulty of heterologous protein expression in *P. falciparum* has served as a barrier to characterization of many potential therapeutic targets, underlying the need for elucidating the function of our protein of interest.

Celia Johnson; Cassandra Travis **Poster #A16**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mark Johnson, Department of Molecular Biology, Cell Biology, and Biochemistry

What Doesn't Kill You Makes You Longer: Anchored Heinz Tomato Pollen Tubes Can Grow Under Heat Stress In Vivo

Fruits are a vital component of our food supply. For flowering plants to produce fruit, sperm cells must fertilize the ovules, a process regulated by the pistil. Pollen grains containing sperm cells land on the pistil and form elongated structures called pollen tubes, which grow through the pistil. It is thought that complex interactions between the pistil and pollen tubes allow for rapid, directed growth of pollen tubes toward the ovules. Climate change has caused rising temperatures globally, exposing plants to higher-than-typical temperatures. In vitro, a significant fraction of tomato pollen tubes burst when exposed to heat stress, demonstrating the heat sensitivity of this developmental phase. We wanted to determine if the pistil has a protective effect on pollen tube development. We focused on the Heinz tomato variety, a cultivar that produces fewer fruits under heat stress compared to non-stress conditions. Using aniline blue staining, we measured pollen tube length and number of pollen grains. Under sustained heat stress in vivo, we saw no evidence of pollen tube growth, as well as fewer pollen grains compared to pistils grown at 28°C. To test whether this difference in pollen grain count was due to heat stress preventing pollen grains from anchoring on the pistil, we grew pistils at 28°C, allowing them to anchor before exposure to heat stress. We found evidence of pollen tube growth during heat stress under these conditions. However, the pollen tubes grew at a slower rate than pollen tubes grown solely at 28°C for the same duration, differing from the heat-independent rate observed in vitro. We also conducted trials in which pistils were incubated at 28°C, then exposed to heat stress, and then returned to 28°C. After being returned to non-stress temperatures, pollen tube growth rate increased from the heat stress growth rate. Overall, these experiments highlight the protective role of the pistil in supporting pollen tube growth during heat stress. While heat stress can impede pollen tube growth in vitro, the presence of the pistil appears to reduce the

negative effects by promoting slower growth under stress and facilitating recovery under normal conditions.

Mareesa Islam; Noah Medina **Poster #B1**

Home Institution: University of California, Berkeley

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Kenny Breuer, Department of Engineering

Characterizing individual bird trajectory preferences in wind tunnel flight

From the cross-continental 24 hour migratory flights of the albatross to the split second pathing decisions of a house finch dodging cars, understanding the flight paths birds choose is fundamental to the study of avian flight. However, knowledge of individual variation among birds—termed here as a bird's 'flight personality'—remains underrepresented in the scientific literature due to methodological limitations. This summer, our team hoped to shine more light on this under-studied aspect of bird behavior through how bird flight path preferences change on an individual level. Our study, carried out at the Breuer Lab, investigates individual flight paths among ten European Starlings using advanced flight tracking in the Barus and Holley wind tunnel. We hypothesize that birds demonstrate unique flight preferences that significantly vary on an individual basis. To test this hypothesis, we first measure individual flight preferences by conducting a series of solo wind tunnel flights for each bird. We utilize machine learning cameras placed throughout the wind tunnel to track the bird's position, and quantify each flight by collecting average location, standard deviation, and skewness values for the x, y and z axes separately. We then place those same birds in the tunnel with the presence of a wake-generating robotic flapper that acts as a disruptor of flow, and quantify each flight the same way. Once we have this flapper/no flapper treatment factor, we can analyze each bird’s flight path change in response to substantial flight disturbance, in doing so quantifying the significance of each individual bird’s flight “personality” on overall flight path and position. We will conduct this analysis using paired T-tests between the treatment factor and each flight variable, as well as an overall MANCOVA including covariates of sex and weight. The findings from this study will enhance our understanding of whether changes in flight paths significantly differ on a bird-by-bird level.

Victoria El-Khoury; Sara Santacruz **Poster #B2**

Home Institution: Brown University

Summer Research Program: Summer Research Assistantship in Biomedical Sciences

Faculty Mentor: Kate O'Connor-Giles, Neuroscience; Scott Gratz, Neuroscience

Functional Analysis of Candidate Synaptic Genes

The transfer of information in the brain is governed by the release and uptake of neurotransmitters at synapses. However, our understanding of how functional synapses are established and how these processes are altered in neurodevelopmental disorders is still evolving. To address these open questions and identify novel conserved regulators of synapse formation and function, we are conducting both behavior assays and genetic screening on a set of genes with spatiotemporal expression profiles similar to known synaptic genes. We used CRISPR to generate endogenously tagged and knockout alleles in Drosophila Melanogaster to assess their roles in vivo. The Drosophila larval neuromuscular junction

(NMJ) is a well-established model Glutamatergic synapse. In our screen, we quantified synapse-containing boutons to assess synaptic growth in knockout alleles. To quantify bouton number, we dissect larvae, use immunostaining to label synapses, and conduct confocal imaging and image analysis. To assess synapse function, we used larval crawling to assess locomotion, which we predict will be impaired if synapse number and function are altered. Overall, the combination of morphological and behavioral analysis has revealed multiple genes with distinct roles.

Bryce Okihiro; Yahir Oseguera **Poster #B3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mark Johnson, Molecular, Cellular Biology, and Biochemistry (MCB)

Hot Potato? More Like Hot Tomato… The Importance of High Pollen Tube Integrity for Securing Food Amidst a Warming Global Climate

One of the mechanisms critical to maintaining agricultural yields amidst rising global temperatures is proper plant sexual reproduction–a critical component of which is the successful double fertilization of an ovule with two sperm cells, which is required for fruit and seed production. Yet, for many agricultural crop varieties, this critical component becomes compromised with increases in environmental temperatures. In flowering plants such as tomato, sperm cells are delivered to ovules via an elongated structure called the pollen tube. Once a pollen grain lands on the stigma and hydrates, it germinates and elongates a pollen tube through the style to reach the ovary where the ovules are located. Previous studies have demonstrated that under heat stress, pollen tube integrity is compromised, leading to reduced fertilization success. However, thermotolerant tomato varieties have been found to better maintain pollen tube integrity under heat stress compared to thermosensitive varieties. Our project aims to identify genes found in thermotolerant tomato varieties that confer increased pollen tube integrity under heat stress conditions. We first sought to determine whether pollen tube integrity is controlled by the haploid pollen genome or the diploid genome of cells that support pollen maturation. We tested whether the pollen tube integrity of a tomato hybrid–the cross between a thermotolerant variety Tamaulipas and a thermosensitive variety Heinz–behaved similarly to either parent, which would indicate control by diploid cells; or whether pollen tube integrity was intermediate between the parents, which would indicate control by the haploid pollen genome. The results from our research show that the pollen tube integrity of thermotolerant Tamaulipas is higher than that of thermosensitive Heinz under heat stress and that the integrity of the Tamaulipas-Heinz hybrid pollen tubes is Tamaulipas-like. This suggests that the Tamaulipas genome contains at least one dominant allele that confers enhanced pollen tube integrity under heat stress. This study provides novel insight into the responses of thermotolerant-thermosensitive hybrid pollen tubes to heat stress and advances efforts toward identifying genes that confer higher pollen tube integrities in heat stress environments.

Camilla Regalia **Poster #B4**

Home Institution: Brown University

Summer Research Program: Paid [through a grant] research assistant position in the Wharton Laboratory

Faculty Mentor: Kristi Wharton, MCB & Carnegie Institute

Atf6 identified as a dominant modifier of (G4C2)30+ toxicity associated with adult-onset, motor-neuron-specific model of C9orf72-ALS in Drosophila

A (G4C2)30+ hexanucleotide repeat expansion in C9orf72 is the most common genetic cause of amyotrophic lateral sclerosis (ALS). Previous deficiency screens have identified modifiers of (G4C2)30+ toxicity on the second and third Drosophila chromosomes, but never in an adult-onset, motor-specific context.

In an unbiased screen for modifiers of C9orf72-ALS pathogenesis, we tested 371 deficiency lines on the X, second, and third chromosomes for their ability to modify a lifespan defect associated with (G4C2)49 expression in adult motor neurons. We compared the set of Dfs we identified with the Dfs found in two other screens for dominant modification of C9orf72-ALS-related neurodegeneration, which employed rough eye or wing phenotypes. While this revealed some overlap, no Df line was found in all three screens. Indeed, a number of novel genomic regions and genes extended lifespan in our model, including Atf6, a transcription factor involved in ER stress signaling. Reduction of Atf6 dosage by the loss-of-function mutant Atf6c05057 and Atf6-RNAi significantly extended lifespan. Given that knockdown of ATF6 in mice leads to decreased apoptosis, a process by which neurons could be eliminated in ALS, a lowering of Atf6 levels may act similarly in our C9-ALS model to reduce neuron death and extend lifespan. We explored whether Atf6 could ameliorate neurodegeneration associated with GMR>hTDP43M337V and GMR>hFUSR521C models of ALS, and found that Atf6-RNAi again conferred substantial rescue.

Overall, we sought to identify genetic modifiers of (G4C2)30+ toxicity in an adult-onset, motor-neuron-specific context as it may better address cellular processes leading to motor circuit dysfunction, a hallmark of ALS. Here, we show that Atf6 knockdown can alleviate neurodegeneration associated with C9-(G4C2)49, TDP43M337V, and FUSR521C, suggesting that these three genetic causes of ALS may share a common defect. Further studies are underway to pinpoint the molecular basis of Atf6-mediated suppression

Melissa Aldana **Poster #B5**

Home Institution: Brown University

Summer Research Program: NSF REU

Faculty Mentor: Erica Larschan, MCB

Targeting an Active Chromatin Domain to the Drosophila X-chromosome

In male Drosophila, the Dosage Compensation Complex (DCC) is targeted to the X-chromosome via a transcription factor-Chromatin-linked Adaptor for MSL complex (CLAMP). Targeting the DCC to the X-chromosome upregulates the active genes along the single X-chromosome in males two-fold, equalizing the X-chromosome transcriptional output with that from the two autosomes. Different regions of CLAMP were excised to dissect the regions necessary for proper DCC distribution along the X-chromosome. However, CLAMP binds to all chromosomes and therefore the key question is: How does CLAMP specifically target the DCC to all chromosomes? I performed Cleavage Under Targets and Release Using Nuclease (CUT&RUN) to better understand DCC targeting the X-chromosome in CLAMP mutants. After isolating the DNA fragments post-CUT&RUN, I prepared for Next Generation Sequencing. I obtained my sequencing data, I performed analyses to investigate DCC binding with Deeptools. Looking at the conserved motifs in this region, high promiscuity suggests other transcription factors can bind at the sites where there are not as many conserved motifs. Using ReactomePA, the pathway and gene ontology enrichment clusters in clamp mutants but not wild type are significantly associated with programmed cell death suggesting that CLAMP prevents binding to genes that induce cell death.

Amber Wang **Poster #B6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Arthur Salomon, MCB; Kenneth Callahan, MCB

Elucidating mechanistic variation in T cell activation networks from chimeric antigen receptors with varying costimulatory domains

Chimeric antigen receptors (CARs) are a novel, modular cancer immunotherapeutics with incredible promise for treating a wide variety of cancers. Currently, there are six CARs approved for use in patients with subtle structural differences that impact the longevity and intensity of the treatment.. In particular, the inclusion of intracellular signaling domains from T cell costimulatory receptors (hereafter costimulatory domains) is known to have profound consequences on the success and side effects of CAR T cell therapy. For example, using a CD28 costimulatory domain leads to hyperactive CAR T cells with robust but short lived antitumor responses, whereas a 4-1BB costimulatory domain generates CAR T cells that survive and differentiate into memory CAR T cells for prolonged antitumor effects. Although this has been observed clinically, the precise mechanisms behind these phenotypes are unclear. By understanding how CAR T cell activation varies as a function of costimulation, we will learn how to design CARs that can avoid the shortcomings of currently approved CAR T cell therapies.

Ju-Woo Nho **Poster #B7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jun Feng, Cardiothoracic Surgery Laboratory of Warren Alpert Medical School

The role of protein kinase Cαβ inhibition on endothelial apoptosis signaling

Simultaneously stimulating protein kinase C (PKC) and reactive oxygen species (ROS) is associated with dysfunctionality in human coronary artery endothelial cells (HCAECs) in the context of diabetes and cardioplegic-ischemia/reperfusion (C-I/R)-related injuries. Moreover, constantly activating PKCα/β, which regulate ROS, produces an unneeded amount of ROS and results in cell death and dysfunction caused by C-I/R injuries. Therefore, we will examine the role of PKCα/β inhibition on endothelial apoptosis signaling, hypothesizing that inhibiting both PKCα and PKCβ will shield endothelial cells from C-I/R induced injuries in patients with or without diabetes mellitus (DM). By culturing both non-DM and DM HCAECs, pretreating with selective PKCα/βinhibitors, simulating C-I/R injury, and measuring cellular apoptosis, the protective ability of PKCα/β inhibition can be quantified. Utilizing this translational research model holds great importance in connecting bench to bedside treatments, as it would help develop novel treatments for the coronary vasculature of diabetic and non-diabetic cardiac patients.

David Okoh **Poster #B8**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anubhav Tripathi, Biomedical Engineering

Capillary Flow Sample Preparation Device for Amphetamine Detection using LC-MS/MS

Liquid Chromatography tandem Mass Spectrometry has garnered attention in recent times due to its versatile range of applications. However, limitations still exist when it comes to effective sample preparation methods. Current methods often have limitations due to limited poor analyte recovery, especially when dealing with a complicated matrix like the human serum. Microfluidic techniques can be exploited to address this issue, and can introduce simplification of the workflow when it comes to LC0MS/MS- based translational research. The goal of this study is to design and develop a microfluidic device that utilizes the principles of capillary flow for a faster sample preparation of human serum for the detection of Amphetamine, a drug of abuse. Analyte separation and extraction will be compared on the device against current gold-standard sample preparation techniques, such as protein precipitation, and liquid-liquid extraction, that requires a large sample volume, and the drug recovery will be quantified using a QSight 220CR LC-MS/MS.

Jordan Feldman **Poster #B9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Wilson Truccolo, Neuroscience

Epileptic-seizure spreading dynamics in nonlinear brain networks under pulse perturbations

Epilepsy is one of the most common neurological disorders affecting approximately 65 million people worldwide. About 30% of the cases are diagnosed as pharmacologically resistant epilepsy. One of the main approaches for treating these cases is the use of intracranial electrical stimulation devices for seizure control. The approach is based on the fact that seizure spreading, rather than its initial localized onset, is the main event typically leading to major disruptions in sensorimotor and cognitive processing, as well as loss-of-consciousness. It thus makes sense to detect a seizure soon after its onset and deliver electrical stimulation to the seizing and related surrounding brain areas to prevent seizure spread. Currently, very simple methods to guide stimulation are used: stereotypical stimulation patterns based on a few parameters such as number and duration of pulses, and amount of current, which are trial-and-error learned and then fixed to specific values depending on patient case. There is a consensus that both better theoretical and algorithmic foundations based on dynamical systems, control theory and network science, are needed. Towards this goal, the Truccolo Lab has developed patient-specific network models (epileptor networks) to predict whether a seizure will spread and how. Given the developed foundations for predicting seizure spread, the next step is to develop better approaches for how to control it. Our ongoing work shows that linear quadratic Gaussian (LQG) regulators can successfully control seizure spread in our patient-specific epileptor network models, provided that feedback is constrained to be localized. This result was based on the full knowledge of the nonlinear network equations in order to derive a linear approximation (Jacobian matrix) and a linear Gaussian state-space model for (Kalman filter) state estimation. Over the summer, I've worked on using pulse perturbations of the network to uncover spreading dynamics and learn data-driven controls that don't rely on full network knowledge.

Kenia Sanchez **Poster #B10**

Home Institution: Farmingdale State College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Karla Kaun, Neuroscience

The effects of fluoxetine on serotonin levels within Drosophila melanogaster brains

A wide range of internal and external stresses trigger activation of highly conserved molecular signaling pathways termed the Integrated Stress Response. The fruit fly, Drosophila melanogaster, has served as a useful model for characterizing the molecular basis of stressful events. Animals activate the Integrated Stress Response pathway in response to several modes of stress, including starvation, oxygen deprivation, and heat. We do not yet understand whether male and female Drosophila differentially demonstrate behavioral or pharmacological responses to stress. Therefore, the current study aims to describe the effects of fluoxetine treatment on behavioral responses of male and female D. melanogaster exposed to chronic, unpredictable, variable stressors. The hypothesis of this experiment is that fluoxetine will increase serotonin in the brain. The flies will be treated with 10 mM of fluoxetine during 24h-72h. After this time, the fly brains will be dissected, and immunohistochemistry will be performed on their central brains using a serotonin antibody to determine how fluoxetine treatment influences serotonin levels.

Conenicus Weeden **Poster #B11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mandar Naik, Department of Molecular Biology, Cell Biology & Biochemistry

Predicting future trends in antimicrobial resistance using NMR spectroscopy

Bacteria use various mechanisms to evade the action of antibiotics leading to drug-resistant phenotypes. Over the past three decades, the widespread increase in antimicrobial resistance (AMR) continues to limit our capability to treat bacterial infections. β-lactamases are bacterial enzymes that facilitate the hydrolysis of the β-lactam ring and render the largest class of antibiotic drugs currently prescribed ineffective. Here, we will present a new methodology that uses the combined power of NMR spectroscopy and computational analysis to predict β-lactamase mutants that will show resistance to inhibition by second-generation diazabicyclooctane inhibitors. This proposal aims to identify potential resistant phenotypes by structure-directed evolution before such mutants emerge in nature, and eventually identified in clinical samples.

Pranav Gundrala **Poster #B12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Wentian Yang, Orthopedics

Role of CHSY3 in Cartilage Homeostasis and Carpometacarpal Joint Osteoarthritis

Carpometacarpal joint osteoarthritis (CMCJ OA) is a joint degenerative disease of the hand which can cause severe pain and loss of mobility that often requires surgical intervention to correct. Current understanding about the disease attributes the development of this form of OA to aging, lifestyle, and possible genetic factors which are poorly understood. In order to investigate possible genetic risk factors, a recent study by Jurynec et. al identified cohorts of CMCJ OA patients and their families in Utah to construct pedigrees and analyze whole human exomes of affected individuals. In one pedigree where

“CMCJ OA segregated as an apparent autosomal dominant trait,” the researchers identified a rare coding variant for the gene encoding CHSY3, chondroitin sulfate synthase 3, which was linked to the incidence of CMCJ OA in affected individuals of the family. The variant is a point mutation causing a substitution of glycine to arginine (G613R) in a region of the protein that participates in the production of chondroitin sulfate (CS). Proteoglycans like aggrecan rely on CS for their functions in the lubrication and tensile strength of cartilage, suggesting that an alteration in this process is a major risk factor for the development of OA. Currently, this coding variant and its role in the function of CHSY3 as well as the role of CHSY3 in CMCJ OA is not well understood. This project aims to clarify these processes by first developing novel cell lines which either lack CHSY3 or expresses CHSY3G613R variant and then studying the impacts of the mutation in-vitro. Murine chondrocytes were used as a model because of their highly conserved CHSY3 sequence at the region of the mutation. PCR primers were designed to introduce the G613R point mutation into a template plasmid vector which was amplified and further processed to introduce the CHSY3 coding variant into lentiviral vector plasmids. Currently, CRISPR-Cas9 technology is being used to develop a CHSY3 K/O cell line, with the goal of stable transfection of both mutated and wild-type CHSY3 genes using a lentivirus. Current sequence data of plasmids show successful clones expressing the point mutation, and a screening is being conducted to identify successful CRISPR K/O cell lines. Once a stable cell line has been established, in-vitro gain- and loss-of-function studies can be conducted to understand the role of CHSY3 in cell proliferation, survival, and morphology.

Adrian Lin **Poster #B13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: David Lin, Engineering

Motion Captured 3D Kinematics to Examine Upper Extremity Movement Synergies After Stroke

Introduction: Upper extremity hemiparesis is the most common cause of functional disability after stroke. Upper extremity hemiparesis consists of multiple different components—strength, dexterity, and movement synergies. Methods to quantify the different components of hemiparesis are lacking.

Objective: The aim of this project is to develop a quantitative pipeline for quantifying upper extremity movement synergies by measuring individuation of the shoulder, elbow, and wrist joint movements using 3D kinematic (motion capture) data. We specifically measure joint angles during highly instructed single joint movements.

Methods: We developed our methods in an able-bodied dataset. Data collection comprised of a series of highly instructed upper extremity movement tasks, including the individuation of wrist, elbow, and shoulder joints. Participants were also instructed to perform functional tasks, consisting of a reach out, reach up, and drinking task. To assess movement synergies, we calculated joint excursion and joint individuation indices, calculated as functions of the joint angles of instructed and non-instructed joints. Trial data were pre-processed, segmented, and analyzed using Qualisys Track Manager (QTM) and MATLAB (MathWorks, Inc).

Results: Preliminary results demonstrate the feasibility of our approach in an able-bodied dataset. Instructed joints showed significantly different joint excursion and joint individuation indices as compared to non-instructed joints.

Discussion: Our next steps are to apply this pipeline to a dataset of chronic stroke survivors with hemiparesis. Our ultimate aim is to (1) relate these movement synergy results with strength and dexterity measurements (to examine relationships between different components of hemiparesis) and (2) investigate how movement synergies map onto the neuroanatomy and neurophysiology of descending motor tracts. Such mapping will inform the development of personalized neurorehabilitation therapies for post-stroke hemiparesis.

Colin Baker **Poster #B14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ritambhara Singh, CCMB; Tuan Pham, CCMB

The new SCOOTR website helps align unpaired single-cell multi-omics datasets using co-optimal transport

New advances in single-cell multi-omics technology have allowed biologists to examine how various different factors regulate processes in concert on the cellular level. However, measuring multiple cellular features on a single cell can be quite expensive or impossible with current technology. By using optimal transport to align cells and features across disparate datasets produced by separate assays, SCOOTR, an unsupervised manifold alignment tool developed in the Singh Lab, allows biologists to align their data and examine factors not practically possible to compare on singular samples. While other tools do exist to solve this problem, SCOOTR performs just as well as or better than these state-of-the-art algorithms in addition to having fewer hyperparameters, many of which can be self-tuned. SCOOTR, unlike other alignment tools, also allows for supervision on the sample or feature alignment based on prior knowledge, which can yield more meaningful results. Here, we have now leveraged SCOOTR into a user-friendly website with easy-to-follow tutorials that give intuition on how the tool achieves its strong alignment performance. The new SCOOTR tool, as demonstrated in the website, will help improve biological analyses by allowing for more accurate downstream analyses on the same sample set.

Justin Currie **Poster #B15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Erica Larschan, Department of Molecular Biology, Cellular Biology and Biochemistry

Coordinated Regulation of Synaptic Gene Expression in D. melanogaster

Coordinated gene regulation is essential for the generation and maintenance of diverse cellular states. The expression of cell-type specific genes is primarily controlled by transcription factors (TFs) that form gene regulatory networks (GRNs) amongst themselves and with target genes. Therefore, understanding how GRNs change over developmental time is critical to understanding the determination of cell fate and formation of cellular structures. Here, we use the D. melanogaster nervous system as a model for studying coordinated gene regulation. Genes involved in synapse formation, maintenance, and function have a common temporal expression profile during embryonic development. However, the upstream TFs and GRNs responsible for the coordinated regulation of these synaptic genes are unknown. Using an atlas of scRNA-seq and scATAC-seq data from the Drosophila embryo, we have defined candidate GRNs

that modulate synaptic genes. This was accomplished using the SCENIC+ pipeline, which integrates gene expression and chromatin accessibility data for GRN prediction. Our GRNs reveal new regulators of synaptic genes as well as new interactions among TFs that have previously been implicated in nervous system development.

Miauaxochitl Haskie **Poster #B16**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Karla Kaun, Neuroscience

Drosophila as a model system to study behavior of nicotine use

Approximately 40 million Americans regularly smoke cigarettes, and nearly 2.55 million middle and high school students often use a form of tobacco product, such as e-cigarettes. Nicotine is a highly addictive stimulant primarily found in cigarettes and e-cigarettes. Its use is the leading cause of preventable disease, disability, and death, in the United States. The prevalence of smoking in adults and increased use of vaping among youth, indicates the significance of understanding how nicotine influences behavioral decisions.

Drugs of abuse including nicotine directly modify memory circuits, influencing physiological reactions and molecular mechanisms in cue-encoding neurons. Studying how nicotine can affect behavioral response in Drosophila is the first step in understanding the molecular and neural mechanisms of impaired circuits. The quick life cycle and remarkable similarities with mammals in nicotine-induced behavior make Drosophila an effective model system to study the neural and molecular mechanisms underlying nicotine use.

The aim of this study is to characterize Drosophila drug-seeking behavior in response to a nicotine-paired odor. I hypothesize that wildtype flies will exhibit increased time spent with a cue paired with nicotine vapor. These results will provide insight into potential treatment options for changes in impulsivity and depression associated with nicotine inhalation. This fundamental preliminary research could lead to a variety of future treatment options for nicotine addiction.

Blaire Williams **Poster #C1**

Home Institution: California State University, Bakersfield

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Dioscaris Garcia, Department of Orthopaedics; Christopher Born, Department of Orthopaedics

Silver Carboxylate Antibiotic-Independent Antimicrobial: Exploration of Potential Solutions for the Post-Antibiotic Era

Silver Carboxylate Antibiotic-Independent Antimicrobial: Exploration of Potential Solutions for the Post-Antibiotic Era
Williams, Blaire; Garcia, Geronimo; Rezk, Anna; Barhouse, Patrick; Marquez-Garcia, Josue; Stone,

Benjamin; Whitaker, Colin; Allu, Sai; Connolly, Liam; Garcia, Dioscaris; Born, Christopher
The Diane N. Weiss Center for Orthopaedic Trauma Research, Brown University, Providence, RI.
Since the discovery of the first naturally derived antibiotic in 1928, there has been a prompt rise in antibiotic resistance. The increased use of synthetic antibiotics, a lack of novel antibiotic development, and poor antibiotic stewardship has led to a perilous “post-antibiotic era”. Without prompt innovation, millions of deaths will likely occur from antibiotic resistant infections by 2050. A potential solution is the use of organometallics which possess antimicrobial efficacy. Our group has developed a non-antibiotic silver carboxylate compound that triggers several distinct bactericidal mechanisms. Pharmacokinetic release and loading are controlled through a ratiometric matrix of titanium dioxide and polydimethylsiloxane. To test antimicrobial efficacy, bacterial strains of Vancomycin-Resistant Enterococcus faecalis, Methicillin-sensitive Staphylococcus aureus, and Methicillin-resistant Staphylococcus aureus strains MW2 and VRS1 were utilized. Bacteria were exposed to varying concentrations of silver carboxylate for 24hrs and compared to “last resort” antibiotics and nanoparticle silver. The safety of silver carboxylate on primary human-derived cell lines involved in wound healing (osteoblasts, keratinocytes, and skeletal muscle cells) which were also exposed parallel conditions to the antimicrobial conditions was assessed via the MTT assay. In this study, we present an overview of the pharmacokinetics of release, safety on primary human-derived cell lines, antimicrobial efficacy, biofilm dysregulation, and effect of the viability of persister cells by silver carboxylate.

Tsunami Núñez-Irizarry **Poster #C2**

Home Institution: University of Puerto Rico in Aguadilla

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Jessica Plavicki, Pathology and Laboratory Medicine; Michelle Kossack, Pathology and Laboratory Medicine

Illuminating the Connection: Optogenetic Activation of Macrophage Modulates Zebrafish Heart Rate

Macrophage are best known for their essential functions in immune defense; however, more recent work has highlighted their non-canonical roles in organogenesis. Given that the etiology of most congenital conduction disorders is unknown, uncovering the factors that influence cardiac conduction system development is an important research question. Previous research using adult mice demonstrated that macrophage are electrically coupled to cardiomyocytes at the atrio-ventricular node; however, it remains unclear whether cardiac macrophage can influence the development or function of the embryonic cardiac conduction system. Work from our lab has revealed that in larval zebrafish, macrophage are present at the sinoatrial (SA) node, the electrical pacemaker responsible for initiating heart contractions. Zebrafish are a well-established model for cardiac research based on the conserved molecular signaling pathways in heart development. Zebrafish also offer specific advantages for optogenetic studies, as they are initially transparent and develop externally, allowing for the visualization of heart development and function in vivo. In this study, we investigated if optogenetic manipulation of cardiac macrophage is sufficient to modulate heart rate in developing zebrafish. We generated zebrafish with macrophage-specific expression of channelrhodopsin, a light-gated cation channel, using the Gal4/UAS system. Here, we show that optogenetic manipulation of macrophage using 405 nm light directly modulates cardiac rhythm in developing zebrafish. We are now investigating whether macrophage effects on heart function is direct or acting indirectly through stimulation of the CNS by looking at heart rate following neuronal stimulation. Our results, therefore, support the hypothesis that cardiac macrophage are functionally important in larval cardiac conduction. Further investigations into the precise mechanisms by which macrophage can

influence heart rate could have implications for therapeutic interventions targeting cardiac dysfunction.

Samir Samadov **Poster #C3**

Home Institution: Brooklyn College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Diane Lipscombe, Carney Institute

Behavioral Phenotyping of Optogenetically-Evoked Sensory Responses

The rapid development of hypersensitivity to sensory stimuli in skin is protective and is one of the most familiar examples of adaptation of the nervous system to changes in the environment. Assessing rodent behavior in response to these stimuli typically involves manual positioning of probes or von Frey filaments, which is labor-intensive. With collaboration from Carney Institute, we have created an automated system to objectively evaluate rodent responses to light-evoked stimulation of skin nerve endings using optogenetics. The system utilizes mice expressing a light-sensitive opsin, ChannelRhodopsin2, in heat nociceptors and low-threshold mechanoreceptors. These mice exhibit classic reflex paw withdrawal responses to light directed at the plantar surface of the hind paws. We also combined machine learning, and optogenetics to automatically position the light probe and capture high-resolution video of mouse behavior. The light intensity can be controlled to establish stimulus intensity-behavior relationships. We used the VGG image annotator to classify mouse behaviors, such as paw shaking, licking, guarding, resting, walking, and flinching. Our manual annotations were 94% consistent and we feed that into a machine learning platform. We compared behaviors across different mouse strains, stimulus intensities, and we assessed accuracy of the machine learning platform to classify rodent behavior. This automated platform, combined with optogenetics, allows precise modulation of nociceptive responses and deep behavioral phenotyping. It improves accuracy and enhances data acquisition during experiments. Additionally, it facilitates analysis of large datasets, enhancing data interpretation efficiency. The platform is particularly valuable for studying pain-related behaviors and potential discoveries for novel non-stimulant therapeutics.

Tayler Leonard **Poster #C4**

Home Institution: North Carolina A&T State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Eric Jutkowitz, School of Public Health; Katherine Rieke, N/A

A Literature Review on The Effects of Radiation Therapy for Benign Conditions in Veterans

Over the last three decades, there has been an increase in the use of radiation therapy (RT) for the treatment of benign musculoskeletal, orthopedic, and soft tissue diseases. The Veteran Health Administration seeks to understand this evidence base to support clinical guidance. The goal of this project was to understand the prevalence of 9 benign conditions in Veterans that may benefit from RT and understand the clinical motivation to use this treatment for these diseases in Veterans.

Literature searches were conducted for the prevalence of musculoskeletal, orthopedic, and soft tissue diseases in Veterans. Data from published studies compiled by the Providence ESP for the 9 benign

diseases were graphically visualized. This information was synthesized to understand the efficacy of RT for benign conditions in the VA.

Veterans may have higher prevalence rates of each disease as a result of the trauma and injuries associated with military service. Evidence of the negative impact these diseases had on Veterans' well-being and quality of life was one motivation to use RT for these conditions. A non-invasive treatment, RT works in benign diseases to inhibit cell proliferation, suppress inflammation, and reduce pain. It can be an alternative for surgery or non-steroidal anti-inflammatory drugs (NSAIDs).

This review demonstrates potential for RT as an effective treatment of benign diseases in Veterans and provides motivation for further investigation of RT in these conditions.

Ian Joe **Poster #C5**

Home Institution: Brown University

Summer Research Program: SPRINT/LINK

Faculty Mentor: Brian Zerbe, Ophthalmology

A chart review of the results of selective laser trabeculoplasty treating open angle glaucoma in Tajikistan

RELEVANCE:
Selective laser trabeculoplasty (SLT) has been shown to be an effective treatment for open angle glaucoma since 1998. Recent studies have shown that compared to medication as initial therapy, SLT decreased visual field progression, increased the number of visits with target intraocular pressure (IOP), and decreased the need for future surgical procedures. SLT may have an even greater role in Tajikistan, given the unusually high rate of pseudoexfoliative glaucoma and studies that show that SLT may have a greater IOP lowering effect in pseudoexfoliation.
OBJECTIVE:
To investigate the effect of SLT on eyes with chronic open angle glaucoma in Tajikistan.
MATERIALS AND METHODS:
This was a retrospective chart review of 64 SLTs performed at Solim Med Clinic from 2011 to 2021. SLT was performed with Frequency-doubled, Q-switched, 532-nm wavelength Nd:YAG laser at a 400 micrometer spot size, with the trabecular meshwork treated with 100 spots over 360 degrees. IOP, measured with Goldmann applanation tonometry, was compared pre- and 4-6 weeks post laser, and yearly for as long as follow-up data was available. A student T test was used to determine statistical significance.
RESULTS AND DISCUSSION:
Average pressure was 23.6 mmHg pre-SLT, dropping to 17.4 mmHg 4-6 weeks after SLT (26% drop, $p<0.001$). At 6-12 months this was maintained with an average IOP of 18.0 mmHg (24% drop, $p=0.004$). The percentage of eyes with >20% IOP drop from baseline was 48% at 4-6 weeks, 25% at 1-2 years, 40% at 2-3 years, and 40% at over 5 years.
CONCLUSIONS:
The results of our study are consistent with findings internationally which have shown the effect of SLT to be similar to the effect of latanoprost. Based on recent larger studies, it would be good to expand SLT use as initial treatment for open angle glaucoma, and to repeat SLT more often, even when initial SLT was ineffective. One of the limitations of our study was that relatively few patients followed-up beyond 1-2 years. This highlights the challenges with compliance that makes treating glaucoma difficult, regardless of the treatment modality.

Hassan Alemara **Poster #C6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Alan Morrison, Medicine

Detection of Macrophage Rac1-NF-kB Interaction in Human Atherosclerotic Plaques

Coronary artery calcification is associated with increased cardiovascular event risk. Macrophage Rac1 and NF-kB drive the upregulation of inflammatory cytokines in plaque that promote the calcification process in experimental models; however, the interaction between Rac1 and NF-kB has not been detected in human coronary plaques. To see if this signaling association is present in human atherosclerotic plaque, we obtained human coronary artery specimens from individuals with varying degrees of coronary artery disease. The samples were paraffin-embedded and underwent histological staining for calcification using Alizarin Red staining. A proximity ligation assay (PLA) was performed to highlight areas within the tissue where Rac1 and NF-kB come within 40 nm of each other. We then imaged the coronary artery slides using an automated slide scanner followed by quantification of the relative amounts of calcification and PLA signal, using semiautomated ImageJ software analysis. Our results demonstrated that Rac1 and NF-kB are closely associated in CD115+ cells (macrophages) in areas of atherosclerotic calcification. Disrupting this Rac1-NF-kB interaction that appears important for inflammation may have therapeutic potential in preventing calcification of human atherosclerotic plaque.

Timothy Reiad **Poster #C7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brett Owens, Brown University Alpert Medical School Department of Orthopaedics

Epidemiology of 9.3 Million Shoulder Injuries Presenting to United States Emergency Departments From 2006 Through 2021

Shoulder injuries are a significant health concern, representing the third most injured joint and accounting for approximately 16% of all emergency department (ED) visits related to joint injuries. This research paper examines the epidemiology of shoulder injuries presenting to EDs in the United States using data from the Consumer Product Safety Commission's National Electronic Injury Surveillance System (NEISS) database from 2006 to 2021.

A total of 9,393,512 shoulder injuries were recorded in U.S. emergency departments during this period, resulting in an average injury rate of 1.85 shoulder injuries per 1,000 population. Males had a significantly higher injury rate compared to females (2.25 vs. 1.47; $p < 0.05$). Shoulder injury rates varied among age groups, with the highest rate observed among individuals aged 15 to 24 years and the lowest among children under 5 years. Injury rates decreased across most age ranges, except for those aged 45 to 64 and above 65, which experienced an increase during the study period. Fractures, dislocations, and lacerations were the most common diagnoses associated with shoulder injuries. Males had a higher proportion of fractures, while burns were more prevalent among females. Sports and recreation were the primary contributors to shoulder injuries, followed by home structures and furnishings.

These findings provide valuable insights into the demographics and injury patterns of shoulder injuries. Recognizing the significant sex and age group differences highlights the importance of tailored

approaches to injury prevention. Utilizing the NEISS database, this study may inform healthcare professionals and policymakers and may work to facilitate the implementation of effective measures to reduce shoulder injury rates and enhance safety at home and in the workplace. Further research is required to understand the underlying causes and risk factors associated with shoulder injuries and to assess the impact of preventive interventions.

Rosa Rijo Benitez **Poster #C8**

Home Institution: Rochester Institute of Technology

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Alger Fredericks, Division of Biology and Medicine

Using Deep RNA Sequencing As A Novel Diagnostic And Therapeutic Tool In Critical Illness

The global impact of COVID-19 has significantly affected millions of patients worldwide. While technological developments have enabled the detection of viral RNA in patients, they provide no insight into the host response during the active phase of the illness. The purpose of this study is to utilize deep-RNA sequencing as a diagnostic tool to identify gene expression and pathogen presence, ultimately enabling the prediction of mortality in COVID-19 in septic patients. In this study, our objective is to find discernible patterns in gene analysis that can significantly enhance the accuracy of patient prognosis. Additionally, we aim to identify secondary infections, which could potentially facilitate more effective pathogen-directed antibody treatments. In this study, a total of 31 COVID-19 patients admitted to the intensive care unit underwent deep-RNA sequencing of peripheral blood samples. The analysis revealed the presence of not only SARS-CoV-2 RNA but also RNA from other viruses and bacteria in all patients. Using computational biology analysis, the data was collected and examined using principal component analysis (PCA). The implementation of deep RNA sequencing offers enhanced accuracy in identifying and characterizing the multitude of genes that pose potential threats to the well-being and health of patients. Integrating this approach into hospital settings and incorporating it within a patient's care plan has the potential to improve the accuracy of prognoses, ultimately leading to more effective treatment outcomes.

Victoria Chen **Poster #C9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Erica Larschan, Molecular Biology

Transcription Factor Regulates Splicing through Protein-Nucleic Acid Interactions

Splicing and transcription are crucial biological processes involved in development, contributing to the generation of diverse transcripts and proteins. The resulting protein diversity gives rise to function- and sex-specific differences among cells, which play significant roles in disease response and pharmacological outcomes. We aim to investigate how splicing and transcription is regulated by transcription factors (TFs) and RNA-binding proteins (RBPs). We hypothesize that the phase separation property of TFs and RBPs is responsible for the coordinated regulation of splicing and transcription. Phase separation refers to the ability of proteins to form liquid droplets, known as speckles, through interactions with DNA or RNA. Splicing speckles contain essential components involved in splicing,

including spliceosomes, RNA molecules, and various proteins.

We plan to utilize the maternal transcription factor Chromatin-linked adapter for MSL proteins (CLAMP) as a model to gain insights into the role of TFs in splicing speckles. CLAMP is an ideal candidate gene due to its direct binding to RNA and DNA, linking them at sex-specifically spliced genes. Furthermore, CLAMP is known to sex-specifically interact with spliceosomal RNA and RBPs and regulate the distribution of MLE (Maleless), a spliceosome component, in males.

We aim to investigate how CLAMP's phase separation property influences its ability to co-regulate splicing and transcription. To accomplish this, we intend to create deletions in the MSL2BD, ZnF, and PRLD+6Q domains of the CLAMP gene and assess the ability of CLAMP mutants to bind to DNA and RNA and to form splicing speckles. Additionally, we will examine the importance of RNA length and sequence diversity in phase separation by utilizing a variety of RNAs with differing characteristics.

Charles Finch Stowers **Poster #C10**

Home Institution: Colorado State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Nicholas Antonson, Department of Evolution, Ecology, and Organismal Biology; Matthew Fuxjager, Department of Evolution, Ecology, and Organismal Biology

Comparison of muscle activation in woodpeckers during impact vs. non-impact head behaviors

The eponymous behavior of most species of woodpecker has many functions; depending on the behavior's speed and intensity, forcefully striking the bill against a surface can be referred to as 1) drumming, which plays a significant role in territorial defense, or 2) tapping or drilling, the methods by which woodpeckers search for and acquire food. Drilling specifically is the primary technique woodpeckers use to extract insects from the ground tissue of trees, making the behavior vital for their survival. Despite its clear importance, however, the neuromuscular mechanisms behind this behavior aren't well understood. In this experiment, we utilized electromyography (EMG) to examine the extent to which certain muscles, predicted to be used in drilling, activated as a Downy Woodpecker (Dryobates pubescens) performed behaviors involving flexion and retraction of the head and neck, with varying degrees of beak impact. We found that more intense beak behaviors, such as drilling, engaged more muscles than lower impact beak behaviors, like tapping, or non-beak behaviors, such as head turning. These findings demonstrate that impact-related head movements engage a larger suite of muscles to perform these intense behaviors. We believe this experiment can be a starting point for more specific myologic analysis of beak behavior, potentially involving an examination of when exactly each muscle fires during the performance of the behavior or a comparative study of specific muscles between several species which perform said behaviors at different lengths or intensities. These studies, in turn, may shed light on the evolutionary origin and development of specialized animal behavior as a whole.

Flavia Maria Galeazzi **Poster #C11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ahmed Abdelfattah, Neuroscience

Engineering genetically encoded voltage indicators using photoinduced electron transfer.

Brain circuits process and transmit information in the form of electrical signals. One of the most important challenges of neuroscience is to record this electrical activity. There has been considerable progress in developing genetically-encoded voltage indicators (GEVIs). These are protein-based sensors that translate the voltage response into an optical readout. However, a far-red, and fast voltage indicator for in vivo use has not yet been developed. Far-red fluorescence allows for the greatest spectral separation from tissue autofluorescence, minimizes light scattering, allows deeper tissue penetration, and facilitates the simultaneous recording of other physiological parameters using spectrally orthogonal tools. To address this gap, the Abdelfattah lab has been developing a novel platform to engineer far-red GEVIs. In our design a voltage-sensitive domain (VSD) is fused to a self-labeling HaloTag protein and an electron-rich tryptophan amino acid is introduced near the dye binding location. Depolarization-induced motions of the voltage sensor domain modulate the distance between the HaloTag-bound dye and the tryptophan leading to a change in dye brightness via Photoinduced Electron Transfer (PeT).
In this work, we explore different tryptophan positions within the protein to maximize PeT response to membrane potential changes. To determine distances to the dye binding site, we used an existing crystal structure of HaloTag (PDB ID: 6U32) and PyMOL. We measure distances between the dye center of mass and the nearby residues, identifying 17 potential locations to add a tryptophan amino acid close enough (within ~15 Angstroms) to undergo PeT with the bound HaloTag dye. In addition, we consider four different circular permutations of the HaloTag protein proximal to the dye binding site to position the dye close to the conformational movement of the VSD. To verify whether multiple tryptophans could have an additive dye quenching effect, we generated variants with two tryptophan mutations. We cloned these constructs in a mammalian expression vector using Gibson assembly, purified the plasmid using NEB Turbo E. Coli cells, and verified the sequence using Sanger Sequencing. We are now testing responses in transfected primary neuron culture to test protein localization and response amplitude to action potentials using simultaneous fluorescence imaging and field stimulation.

Mallory Tucker **Poster #C12**

Home Institution: Rice University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Sophia Piggott, EEOB; Matthew Fuxjager, EEOB

Developing a non-invasive, open source workflow for analyzing biomechanical & morphological characteristics in long bones

Having consistent, low-cost, and precise tools with which to assess characteristics of skeletal anatomy is a valuable component of the study of bone evolution and development. Particularly, other techniques for assessing bone stresses fail to adequately account for eccentricities in shape in long bones or require access to proprietary software. Here, we developed and streamlined a workflow which measures the morphological and biomechanical characteristics in long bones. Because of its bone measurement accuracy and precise assessment of bone shape, this procedure overcomes the limitations of other techniques and is suitable for hollow, small, and/or non-circular bones. By non-invasively preparing detailed images of bones using microCT and then analyzing them with open-source software (3D Slicer and ImageJ/Fiji), our workflow expands the potential for understanding bone morphology and evolution across diverse taxa and lends itself to comparative studies of bone anatomy.

Rolake Feyisetan **Poster #C13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Theresa Desrochers, Department of Neuroscience, Robert J and Nancy D. Carney Institute for Brain Science, Department of Psychiatry and Human Behavior, Brown University

Comparing resting state fronto-parietal network connectivity in OCD patients and healthy controls

Obsessive-Compulsive Disorder (OCD) is a mental health disorder characterized by recurrent, intrusive thoughts (obsessions) and repetitive behaviors (compulsions). These compulsive behaviors often follow specific patterns or rituals known as sequences, such as handwashing or counting in order to reduce anxiety. The fronto-parietal network (FPN), consisting of interconnected brain regions in the frontal and parietal lobes, plays a role in cognitive processes like attention, working memory, and decision-making. Dysfunctions within the FPN have been implicated in OCD, contributing to cognitive and behavioral abnormalities such as difficulty suppressing intrusive thoughts and regulating attention. However, there is still a knowledge gap regarding the specific alterations in functional connectivity within the FPN in individuals with OCD. For instance, performing a sequential task may alter the FPN connectivity in OCD differently than in healthy controls (HCs).

My research investigates my hypothesis that the FPN at rest is modulated by a preceding sequence task and that connectivity differs between OCD and HCs. The sequence task involves participants memorizing brief sequence categorization decisions based on shape and color (e.g., shape, color, shape, color). To see how tasks might affect the FPN, I defined a task-active region of the FPN and compared connectivity between OCD and HCs in the task active region of the FPN. Task-active areas refer to regions that show activity during the sequence task and overlap with the established region of the FPN. To study this phenomenon, the lab collected functional magnetic resonance imaging (fMRI) data from both OCD patients and healthy controls. Participants performed the sequence task followed by a resting state scan.

I then performed a group-level comparison to determine if there are significant differences in network connectivity between OCD patients and HC. By focusing on task-active regions of the FPN during a specific sequence task and investigating their connectivity at rest, my research aims to provide insights into the specific alterations in connectivity associated with OCD. I predict the results will show that people with OCD have increased network connectivity at rest in areas of the FPN that are task active during the sequence task compared to HC.

Kanny Barry **Poster #C14**

Home Institution: Brooklyn College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Gerwald Jogl, Molecular Biology, Cell Biology and Biochemistry

Expression and Inhibition of the ORF2 protein from the LINE-1 retrotransposon and implications for human health

Retrotransposons are genetic elements that can replicate and insert themselves into new locations within the genome. The life cycle of retrotransposons begins with transcription of the DNA into RNA by the host cell's RNA polymerase enzyme. The RNA transcript is then reverse transcribed by the retrotransposon

encoded reverse transcriptase (RT) enzyme which synthesizes a DNA copy of the RNA transcript, which then is inserted randomly into the human genome. This causes genomic instability with negative implications possibly on human health. LINE-1 is a retrotransposon that makes up a significant portion of the human genome. ORF2 protein is one of the two main proteins encoded by LINE-1. It is essential for retrotransposition of L1 elements and an important target protein for understanding the molecular mechanisms. However, ORF2 expression and purification is very difficult. This protein is not very stable and is not folding correctly. We wanted to test how tuning the level of protein expression or by expressing in the presence of chaperones improves protein folding and ORF2 purification. Our results will hypothesize and enable further research to fully understand the role of ORF2 in human health and disease and to help develop effective therapies to target this protein.

Hoon Hee Ryan Rhew **Poster #C15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Carolina Haass-Koffler, Center for Alcohol and Addiction Studies, School of Public Health; Nazzareno Cannella, School of Pharmacy, Center for Neuroscience, Pharmacology Unit, University of Camerino, Italy

Inverse-translational pharmacological approach to validate the heterogeneous NIH-HS rat line as preclinical model of AUD

BACKGROUND: Alcohol use disorder (AUD) is a leading cause of death in the US, with significant variability in vulnerability among individuals. Currently, only three drugs are approved by the FDA for the treatment of AUD, while many preclinically promising drugs have failed at the clinical stage. The present research aims to validate the use of the outbred NIH-heterogeneous stock (HS) rat line as a model of individual variability in response to pharmacological treatment within the human population, as an alternative to the inbred (homogeneous) rat lines typically used in preclinical studies. We applied an inverse-translational pharmacological approach, testing a drug that has been approved for AUD therapy (Naltrexone) and a drug that failed in clinical trials (Memantine) on alcohol self-administration (ASA).
METHODS: HS rats (N=40, 50% female) were trained to self-administer 10% alcohol, in 30-minute daily sessions under a fixed-ratio 1 reinforcement schedule. We tested the effect of Naltrexone (0.0, 0.3, 1.0 mg/kg) and Memantine (0.0, 6.0, 12.5, 25.0 mg/kg) on ASA using a within-subject design. The effective doses were also tested on saccharin self-administration (SSA) as a natural reward control. We hypothesized that memantine but not naltrexone would selectively reduce alcohol seeking.
RESULTS: At the population level, both doses of naltrexone and the highest dose of memantine significantly reduced ASA. 25 mg/kg of memantine also reduced SSA, while only the highest dose of naltrexone (1.0 mg/kg) did so. As only naltrexone demonstrated alcohol-selective effects, the degree of change in ASA induced by each naltrexone dose was used in a k-mean analysis (k=2) to allocate rats into “high-responder” (HR; N=10) and “low-responder” (LR, N=25) clusters; five rats were excluded from this analysis because of negligible ASA baseline. In LR, only the highest dose of naltrexone reduced ASA, but this dose also reduced SSA. In HR, both doses of naltrexone reduced ASA, while neither affected SSA.
CONCLUSION: Consistent with our hypothesis, Memantine failed to selectively reduce alcohol seeking in the genetically heterogeneous HS rat population while Naltrexone succeeded in selectively reducing ASA in a subset of rats. The findings emphasize the importance of considering individual variability in developing personalized pharmacological interventions for AUD, enabling the identification of responder subpopulations and tailoring clinical AUD treatment at the personal level.

Rachel Kaniuk **Poster #C16**

Home Institution: Rutgers University - New Brunswick

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Luke Rosedahl, CLPS

Humans and neural networks are impacted by different difficulty factors in category learning tasks

Category learning is essential to our everyday lives. Whether deciding if a pear looks ripe, or if a passing vehicle is an ice cream truck or just a white van, people constantly categorize objects and events in their environment, often without conscious awareness. Categories can be more or less difficult to learn depending on 'difficulty factors', such as how much variability there is within and between categories. Artificial Neural Networks (ANNs) are composed of interconnected nodes (or neurons) in a layered structure that resembles the human brain. The strength of the connection between these nodes is updated over the course of training to allow the network to learn which visual features correspond to specific categories. However, it is unknown whether they are impacted by the same difficulty factors as humans, providing a potential challenge when using such models to explore human learning. Additionally, finding ways in which ANNs learn differently from humans can help clarify potential mechanisms that could be added to networks to improve their performance. This motivates the goal of this study: to compare how ANNs and humans are impacted by difficulty factors during category learning. To do this, we trained fifteen commonly used pre-trained neural networks on eight different category structures from the human category learning literature. By analyzing performance across these structures, we determined that humans and ANNs are impacted by different difficulty factors. Our work could lead to improvements in ANN performance for many visually demanding tasks.

Samara Cummings **Poster #D1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Nicolas Fawzi, The Department of Molecular Biology, Cell Biology & Biochemistry

Structural study of Fused in Sarcoma aggregation caused by ALS mutations

Fused in Sarcoma (FUS) is an RNA-binding protein with several intrinsically disordered domains that are essential for FUS's role in facilitating transcription and splicing events throughout the RNA life cycle. FUS accomplishes some of these functions within liquid-like, protein-rich condensates formed through a biological phenomenon known as liquid-liquid phase separation (LLPS). Upon mutation, FUS can undergo aggregation and cytoplasmic mislocalization in motor neurons, both of which are observed in patients with some of the most aggressive forms of amyotrophic lateral sclerosis (ALS). Although several point mutations in FUS have been linked to ALS pathogenesis through clinical studies, the molecular details underpinning how different FUS mutations cause the disease remain poorly understood. Here, we investigate five ALS-associated mutations (S96Δ, G156E, G174-175Δ, G191S, and R234C) in the intrinsically disordered N-terminus of FUS, the region of the protein that is critical for LLPS. Through time-dependent aggregation assays, we show that several mutations accelerate FUS aggregation in vitro, while minimally impacting its phase separation propensity. Moreover, we identify distinct aggregate structures formed by disease mutants using NMR-based hydrogen/deuterium exchange (HDX) experiments, allowing us to probe core and surface regions of FUS aggregates with residue-by-residue

specificity. Overall, this project details the structural impacts of FUS disease mutations that lead to aggregation and provides valuable molecular insights that can inform novel ALS therapies.

Nicole Melendez **Poster #D2**

Home Institution: University of Puerto Rico, Mayaguez Campus

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Nicole Moody, Department of Ecology, Evolution, and Organismal Biology; Matthew Fuxjager, Department of Ecology, Evolution, and Organismal Biology

Exploring Motoneuron Structure and Specialization for Woodpecker Drumming

Neuromuscular coordination is critical in avian communication behaviors used in territorial defense, social displays, and mating. Woodpecker drumming is prime example of one such territorial signal. The rapid hammering of the beak on a hard substrate requires precise and skilled contractions of the bird's neck muscles. Given the level of precision involved in this display, the motoneurons which control the muscles' contraction must fire within controlled rates of rhythm, speed, and duration. However, the neuronal basis of this behavior is not well-understood. Our investigation delves into the structure of motoneurons responsible for woodpecker drumming which are innervating two primary neck muscles (longus colli ventralis and longus colli dorsalis). In contrast, we're using the scapulohumeralis flight muscle (SH), as our control group to provide a comparative basis against the non-drumming movements. Cell size can serve as an essential indicator of cellular specialization, with variations in dimensions often reflecting specific functional roles and adaptive strategies used in this sound production. Accurate cell measurements are crucial to elucidating this biological dynamic, as they provide insight into intricacies of the cellular structure. Here we show that using a 0.30% to 0.50% contrast enhancement in the motoneuron measurements from Image J will result with a high accuracy and precision essential for future analysis in the motoneuron structural differences. Moreover, by performing a rigorous analysis in morphometry characterization it will provide a rapid and accurate measurement of neuron morphologies and better understanding of the cell detection and shape expected in the neck muscles' motoneurons.

Aleah Davidsen **Poster #D3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kristi Wharton, MCB

Investigating sex-specific defects in SOD1 models of ALS

Amyotrophic lateral sclerosis (ALS) is a lethal neurodegenerative disease characterized by progressive loss of upper and lower motor neurons leading to motor defects and paralysis. Mutations in the antioxidant enzyme superoxide dismutase one (SOD1) have been implicated in familial cases of ALS. In humans, it has been observed that ALS is more prevalent and has an earlier onset in males than females, but the basis of this skewed sex difference is not understood. We utilize CRISPR-derived G85R and A4V SOD1 mutants in Drosophila melanogaster to investigate sex-specific differences in the onset and presentation of ALS-related symptoms. Our investigations demonstrate that male A4V mutants exhibit higher severity and earlier onset of neuromuscular defects than A4V females. We characterize these defects through analysis of lifespan, axonal projections in the femur of the third leg, and climbing ability

throughout disease progression. Interestingly, analysis of sex ratios of G85R mutants at various developmental stages suggests that homozygous G85R mutant females exhibit higher levels of lethality than males early in development. This finding suggests a reversal in the sex most severely affected. This could reflect a difference in the mutation or in the developmental stage examined. We intend to distinguish between these possibilities in future work. An understanding of the sex-specificity of defects associated with SOD1 mutations can increase our understanding of ALS disease pathology.

Joanne Lee **Poster #D4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kate O'Connor-Giles, neuroscience

Structural and functional analysis of TRAPP complexes in the Drosophila larval central nervous system and neuromuscular junction

Communication in the nervous system regulates behaviors like movement and cognitive functions such as learning and memory. Synapses, the sites of this communication, are composed of signal-sending (presynaptic) and signal-receiving (postsynaptic) cells. At specialized presynaptic regions called active zones, synaptic vesicles (SVs) are coupled to calcium channels to achieve a high-probability Ca2+-dependent fusion and neurotransmitter release. However, the molecular mechanisms underlying how synaptic vesicles are recruited to active zones is not well understood. Ultrastructural analysis of synapses across species reveals protein tethers linking synaptic vesicles one another and to active zone membranes, but the composition of these tethers remains unknown.The Transport Protein Particle (TRAPP) complex is a complex of tethering proteins that mediate ER-Golgi vesicle trafficking in non-neuronal contexts. Disruptive variants in TRAPP subunits have been implicated in motor dysfunction, intellectual disability, and developmental delay. However, it remains unknown why these changes would predominantly affect the nervous system given the universal role of the complex. We hypothesize that the TRAPP may play a role in tethering synaptic vesicles at synapses, and that TRAPP variants disrupt this process leading to diminished synaptic communication throughout the nervous system.
My results have demonstrated TRAPP is expressed in the nervous system and strongly co-localizes with synaptic vesicles. I found that downregulation of TRAPP leads to reduced levels of synaptic vesicle proteins. Interestingly, I did not observe any changes in the levels of synaptic vesicle proteins in the brain, which suggests that the lack of TRAPP may be causing a transport deficit, leading to cargo accumulation. These data support the model that TRAPP complexes play an important role in synaptic vesicle recruitment and, thus, neurotransmission, and that studying their function will provide new insights into disease mechanisms while answering long-standing questions about synaptic vesicle trafficking.

Brandon Ulin **Poster #D5**

Home Institution: Brown University

Summer Research Program: NSF REU

Faculty Mentor: Rebecca Kartzinel, Department of Ecology, Evolutionary, and Organismal Biology

Leaflet Diversity Amongst American Hog-Peanut Lineages

The American hog-peanut (Amphicarpea bracteata) is an amphicarpic annual legume found throughout

the mid-west and eastern United States. Although, there is currently only one recognized hog-peanut species in the United States, recent work has called such taxonomic assessment into question based on ecological, genetic, and morphological data, suggesting that there are at least three cryptic-lineages. One phenotype used to identify these proposed cryptic-lineages is the length-to-width ratio among leaflets. Here, we re-asses previous claims about proposed cryptic lineages by utilizing the largest geographic sampling of American hog-peanuts to date and performing morphometric analyses on leaflet length-to-width ratios. Our findings not only contribute to a better understanding of the natural history among Amphicarpea species, but also provide more insights into the diversification process among amphicarphic plants.

Dan Bernstein **Poster #D6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mamiko Yajima, Molecular Biology, Cell Biology and Biochemistry

Identifying the mRNA Targets and Targeting Mechanism of Vasa, an RNA-Helicase in Sea Urchin Embryos

The sea urchin embryo undergoes both symmetric and asymmetric cell divisions early after fertilization, which results in specialized and unspecialized blastomeres. Vasa, an RNA-Helicase, forms granules and localizes on the spindle during these divisions and appears to play critical roles in them by regulating mRNA translation on the spindle. However, little is known about what RNAs Vasa targets or how it regulates their translation on the spindle.

To address these questions, we here take two approaches. First, to understand what mRNAs and proteins Vasa interacts with on the spindle, we aim to identify the components of Vasa granules using APEX-seq. APEX-seq is a sequencing procedure that uses an APEX2 peroxidase protein to catalyze the biotinylation of all macromolecules within 20nm. We fused an APEX2 peroxidase protein to Vasa to biotinylate all macromolecules within 20nm of Vasa proteins. Biotin-labeled macromolecules were then visualized by immunofluorescence using streptavidin-tagged Alexa fluorophore to validate the experimental procedure. Using the same method, in the future, we plan to pull down biotinylated proteins and mRNAs to identify the specific components of Vasa granules through RNA sequencing and Mass Spectrometry.

Second, to understand how Vasa selects its mRNA targets, we investigate G-quadruplex (G4) secondary structure as a possible targeting mechanism. G4s are stable square structures common in DNA and RNA and have been shown to be involved in translation regulation. Among previously predicted mRNA targets of Vasa, we focused on RNABind mRNA and analyzed how Vasa recruits its mRNA and/or protein through its G4 motif using live imaging. We observed the recruitment of wild-type RNABind mRNA to ectopically expressed Vasa, which decreased when using a mutant RNABind transcript without a G4 motif. These results suggest that Vasa may recruit mRNAs through the G4 motif, which we plan to further validate in other target mRNAs of Vasa in the future. Overall, these experiments will provide insight into Vasa's functional mechanism in localized translation, which is critical for efficient embryogenesis in the sea urchin.

Mary Avella **Poster #D7**

Home Institution: Hunter College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Matt Nassar, Neuroscience

How Does Attention to Detail Update Our Way of Learning in the Face of Change?

Autism Spectrum Disorder is a neurological disorder that affects how a person communicates and interacts with others. One way people on the spectrum are different from neurotypical people is by paying close attention to detail instead of looking at “the bigger picture”. One way these contrasts manifest is through learning, where attention to detail might reflect focusing attention on the most recent information, rather than integrating over longer time periods. Because neurodiversity is a wide spectrum, it is hard to measure the difference between every autistic and normal learning style. Previous work from the Nassar lab has identified relationships between "attention to detail, " as measured by the autism spectrum questionnaire, and specific learning strategies that are overly focused on specific data points. This work was conducted as part of a small in-person study, and we hope to conduct a larger, online study to validate and extend the results. To do so, we used an online video game experiment to analyze how people learned based on the movements and changes on the screen. The video game measured how participants moved a bucket to catch money dropped by an invisible helicopter. The participant had to infer where the helicopter was, so they could catch the money to earn points. The movements of the helicopter once each new trial started varied between similar patterns and spontaneous movements, so we could measure how people would decide on where to move the bucket. We have a working, online version of the task and plan to collect behavioral data and measures of attention to detail using an Autism Spectrum Questionnaire. The data that we collect will allow us to examine the similarities and differences in learning styles of autistic people to better understand the complexity of ASD.

Ava Nemerovski **Poster #D8**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ahmed Abdelfattah, Neuroscience

Engineering Far-Red Chemigenetic PET-Based Neuromodulator Biosensors

Uncovering the dynamics of neuromodulators, such as dopamine, is crucial to determining their function within the nervous system. Fluorescent biosensors allow for the non-invasive visualization of neuromodulators with high spatial and temporal resolution. However, most existing neuromodulator biosensors absorb and emit short-wavelength light. This is disadvantageous for imaging in tissue because of increased scattering and autofluorescence. While other sensors achieve red spectral shifts by utilizing red fluorescent proteins (RFP), these proteins lack the brightness and photostability required for long-term, in vivo imaging.

We produced a brighter sensor by a chemigenetic approach, which combines the advantages of genetically-encodable proteins with bright and photostable synthetic dyes. We fused a circularly-permuted self-labeling HaloTag protein between a dopamine G-protein-coupled-receptor and the corresponding miniG protein. The binding of dopamine causes a conformational change that modulates the fluorescence

intensity of a Halo-Tag-bound, far-red dye.

In order to translate a conformational change into a change in brightness, we utilized photoinduced electron transfer (PET) as a quenching mechanism. This distance-dependent electron transfer prevents the fluorescence-emitting relaxation of electrons to the ground state, allowing fluorophore brightness to vary depending on how close the fluorophore is to its oxidation-reduction partner. Tryptophan has the redox potential to be able to undergo PET with rhodamine dyes. Because of this, we utilized molecular cloning techniques to mutate various residues within cpHaloTag into Trp.

In order to improve the response, stability, and dye-binding kinetics of our biosensor, we tested three different circular permutations of HaloTag. For each of these circular permutations, we tested multiple Trp mutation sites. These constructs were transfected into HEK cells, visualized under a microscope, and assessed for expression and trafficking to the cell membrane. Dopamine was then added to test for response. Several of these constructs localized well and responded to dopamine. To improve membrane trafficking, we added an ER-export sequence. Additionally, we tested varying linker lengths between protein sections. Decreasing these linker lengths from three amino acids lead to an increase in response with no loss in stability or trafficking.

Chloe Kim **Poster #D9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Nicole James, Obstetrics and Gynecology; Kathryn Grive, Obstetrics and Gynecology

Elucidating the Role of Amphiregulin in the Ovarian Tumor Immune Microenvironment

High grade serous ovarian cancer (HGSOC) is a deadly gynecologic malignancy, with many patients experiencing chemoresistant recurrence after platinum-based therapy. Immunotherapies have shown limited success, making it crucial to understand chemotherapy's impact on the ovarian tumor immune microenvironment (TIME). Previous data identified amphiregulin (AREG) as significantly induced in HGSOC tumors after chemotherapy, prompting a study on the role of increased AREG in the ovarian TIME post-chemotherapy.

The study used OVCAR8WT cells stimulated with recombinant AREG (rAREG) for genomic analysis. Over 770 genes related to tumor immunology were assessed using NanoString nCounter® PanCancer IO360 analysis. rAREG led to significant increases in tumor-intrinsic immune factors, including DUSP5, DUSP1, IL6, CXCL8, CXCL2, and CXCL1 genes. Phospho-kinase proteome profiling revealed increased STAT3 expression after rAREG exposure in OVCAR8WT and PEA1 cells, confirmed by Western blot. Phospho-AKT, phospho-ERK, and programmed death ligand 1 (PD-L1) were also increased following rAREG treatment in HGSOC cells. Co-culturing OVCAR8WT and PEA1 cells with peripheral blood mononuclear cells (PBMCs) stimulated with rAREG resulted in higher cell viability than PBMCs alone. Combining carboplatin with an AREG neutralizing antibody (AREG nab) synergistically decreased cell viability in chemoresistant PEA2 cells.

In an in vivo study using an immunocompetent HGSOC mouse model (ID8p53-/- C57/BL6), daily rAREG treatment led to significantly lower levels of IL-2, IL-5, and IL-11 in ascites and higher serum IL-20 levels. Intratumoral levels of PD-L1 were upregulated in rAREG-treated mouse tumors, while CD8+ T cell levels were significantly lower.

These findings indicate that increased AREG activates key immune pathways and associated genes, promoting tumor immune evasion in HGSOC. Future studies will explore the effects of targeting AREG alone and in combination with chemotherapy in vivo. Understanding the role of AREG in the ovarian TIME may offer new insights into combating chemoresistance and improving patient outcomes in HGSOC.

Lily Zhou **Poster #D10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Gideon Koren, Department of Molecular Biology, Cell Biology, and Biochemistry

Targeting Senescent Cells with Fisetin: A Novel Therapy for Preventing Atrial Fibrillation

Atrial fibrillation (AF), one of the most common arrhythmias in the aging population, is expected to affect more than 5.6 million Americans in the year 2050. The prognosis of AF has been associated with an increase in inflammatory biomarkers, suggesting that inflammation plays a major role in the pathogenesis and prognosis of AF. An age-related disease, AF is also associated with an accumulation of senescent cells in the atria. Senescence-associated secretory phenotype (SASP) is an important physiological manifestation of senescence involving increased expression and secretion of cytokines, chemokines, growth factors, and tissue-remodeling metalloproteinases and is therefore often a pro-inflammatory and pro-fibrotic process. We hypothesize that the accumulation of senescent atrial myocytes and myofibroblasts in the left and right atria with age predisposes the heart to AF through a SASP-mediated inflammatory response. We therefore investigated Fisetin, a senolytic drug, hypothesizing that the treatment with Fisetin could decrease the susceptibility of the aged heart to developing spontaneous and inducible AF by decreasing the number of senescent cells in the left and right atria.

The data of our pilot study of 22 aged rabbits treated with either Fisetin or vehicle control show that treatment with Fisetin eliminated nearly all senescence-associated beta-galactosidase (SA-β-Gal) positive (senescent) cells from the atria, with a significant decrease as compared to the control group. An ECG monitoring (11 rabbits in each group) and optical mapping study of Fisetin-treated rabbits (5 animals in each group) showed a trend toward reduction in spontaneous AF incidence and inducible reentrant arrhythmias without causing any detrimental effect on atrial function. As a result, targeting senescent cells with Fisetin may represent a novel strategy for modulating inflammation and fibrosis. This presents a possible novel therapy for preventing AF and decreasing its incidence in the future.

Mya Collins **Poster #D11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Daniel Rubin, Neurologist at MGH and Leigh Hochberg, Prof. of Engineering and Brain Science

Speech Neuroprosthesis: Decoding Cortical Activity Patterns for Organic Communication in Individuals with Severe Paralysis

Many individuals with severe paralysis face immense challenges in expressing their thoughts and

emotions due to the inability to control their vocal tract. This research strives to create a speech neuroprosthesis system that empowers individuals with severe paralysis to express themselves through sentences. By directly translating signals from their brain to the vocal tract, the system displays words as text on a screen, ultimately enabling the spoken expression of these words

For individuals who retain some movement ability, we investigate mapping the cortical activity patterns associated with vocal tract movements for each consonant and vowel. By decoding these patterns, we aim to achieve speech recognition of full words, facilitating more rapid and natural communication. For individuals who have limited or no movement, we explore the detection of speech attempts through more subtle patterns in brain activity. By identifying the specific words participants intend to say, even without actual vocalization, we aim to enable meaningful communication.

This study utilizes an intracortical brain-computer interface, machine learning techniques, and language models to decode neurosignals of intended muscle control into a mode of communication that is both efficient and organic. In-home sessions are conducted with the assistance of a CRNA to record cortical activity using a high-density multielectrode array implanted in the sensorimotor cortex. In these experimental sessions, we investigate the path the brain follows during speech execution. By presenting a variety of phrases, individual words, and stories, we also aim to discern whether the motor cortex encodes individual mouth movements (phoneme encoding) or recognizes well-practiced phrases and movement patterns associated with them.

This research has profound implications for the mental health and quality of life of individuals with severe paralysis by providing them with a less frustrating and laborious means to communicate their ideas and feelings. Moreover, the findings may inform the development of advanced speech synthesis technologies, paving the way for improved neuroprosthetic interventions in the future.

Jonathan Li **Poster #D12**
Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Gerwald Jogl, Brown Dept. of MCB

NanoLuc Luciferase as a potential reporter in assessing ribosome function in E. coli, Thermus thermophilus, and Rhodothermus marinus wild-type and mutant variants

In order to investigate the antibiotic resistance of mutant ribosomes, a reporter gene is necessary to reliability compare mutant and wild-type variants. Analyzing these effects in Thermus thermophilus and Rhodothermus marinus ribosomes present specific challenges due to the thermophilicity of these organisms as well as the potential temperature sensitivities of certain mutations. We have shown the potential for NanoLuc Luciferase, a luminescent reporter enzyme, to be a viable reporter due to its high sensitivity for signal detection at low concentrations, reliability in in vitro transcription/translation systems, expressivity in various ribosomes, increased temperature stability, and function in cell-extract based in vitro translations. Nanoluciferase is shown to operate with high linearity spanning a dynamic 10¬4-fold low concentration range. This allows small protein production levels to be analyzed across a large detection range through a luminescence assay. The enzyme has also been reliably produced in established in vitro transcription/translation systems with the ribosomes of interest. Protein synthesis in these systems has been achieved from both plasmid DNA and mRNA through successful transcription in preparation for use in cell-based extracts. The temperature stability of the enzyme to continue luminescent production has been shown to produce detectable, but reduced signals through 60°C. The final component to establish a reliable reporter method is to develop an in vitro translation system in bacterial extracts to allow for organism specificity in analyzing temperature sensitivity of various

mutations. So far, Nanoluciferase has been established to be a reliable reporter gene through a luminescence assay and shows promise in being an effective comparator of mutant and wild-type ribosome function in select ribosomes.

Elena Pearson **Poster #D13**

Home Institution: New Mexico State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Jun Feng, Cardiovascular; Hang Xing, Cardiovascular

Effects of PKCαβ and mROS Inhibition on Streptozotocin-Induced Alzheimer's Disease in Mice

Alzheimer's disease (AD) is a common form of brain disease leading to loss of cognitive functions with symptoms including loss of memory, behavior changes, and confusion. Previous studies have suggested a link towards metabolic alterations and mitochondrial dysfunction and Alzheimer's (AD). Therefore, we hypothesize that stabilizing these signaling pathways can give us insight into possible treatment for Alzheimer's Disease. The parameters for this evaluation included a single dose of the Streptozotocin (STZ) (3mg/kg) intracerebral ventricular injection within mice for induction of AD. For the treatment groups, STZ-AD mice were also treated with vehicles or PKC inhibitor LY333531 (orally, 1 mg/kg/day) or mitochondria ROS (mROS) inhibitor Mito-Tempo (IP injection, 1 mg/kg/day). In the last 5 days of the 28 day period, the induced STZ-AD and treatment groups were all given the Morris water maze test followed by brain harvest for protein analysis. Within STZ-AD mice, they exhibited higher escape latency and lower path efficiency than the control mice, allowing us to recognize damaged cognitive function. Interestingly, within both treatments of the PKC and mROS inhibitors, the escape latency was partially restored, suggesting an improvement in cognitive function. For protein analysis, we expect to see a decrease in Tau proteins within the treated groups, as well as a decrease within apoptosis signaling. Our work has demonstrated that with the use of PKCαβ or mROS inhibitors, STZ- induced AD mice had the escape latency partially restored. Further analysis within these treatment groups can provide substantial information on possible treatment for Alzheimer's disease.

Nicole Dennis Talley **Poster #D14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anne Hart, Neuroscience

Assessing Alternative Glutamatergic and Cholinergic Degeneration in Amyotrophic Lateral Sclerosis

Amyotrophic Lateral Sclerosis (ALS) is a devastating disease that results in the progressive degeneration of motor neurons, and disease onset typically occurs in older adults. Mutations to superoxide dismutase type 1 (SOD1) specifically affect spinal cholinergic and cortical layer 5 glutamatergic neurons via unknown mechanisms. This neurodegenerative specificity is also seen in the model nematode C. elegans, where expression of the patient allele sod-1 G85R leads to degeneration in a subset of cholinergic and glutamatergic neurons (Baskoylou et al, 2018). However, only this subgroup of glutamatergic and cholinergic neurons have been thoroughly investigated for degeneration phenotypes,

and these current models are unable to visualize axonal degeneration. We hypothesize that alternative glutamatergic and cholinergic neurons also degenerate in the presence of the sod-1 G85R mutation. By determining how alternative neurons react in sod-1 G85R expression, we can understand the cellular mechanisms underlying neurodegeneration. We further predict that neurons with long processes could be more sensitive to oxidative stress because of their need for extra support and maintenance, and thus we focused on assessing glutamatergic and cholinergic neurons with long axons. Two types of glutamatergic neurons were studied: ALM, a sensory neuron with a long dendrite that runs along the anterior side of C. elegans, and PVQ, an interneuron whose axon spans the entire length of the body. We defined degeneration as the shortening of the axon or the complete death of the cell. The PVQ neuron did not demonstrate any stress-induced defects or degeneration with sod-1 G85Rs knock-in model, but the ALM neuron showed stress-induced defects through a blebbing phenotype, which could indicate an unhealthy neuron. Future experiments for this project include determining if blebbing or degeneration has a higher prevalence in aged C. elegans, and testing the cholinergic motor neuron DA9 for neurodegeneration or stress-induced defects.

Avi Lukacher **Poster #D15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Walter Atwood, MCB

The Microvascular Endothelium of the Blood-Brain Barrier Restricts JC Polyomavirus Entry to the Brain under Native Conditions

JC Polyomavirus (JCPyV) is the causative agent of progressive multifocal leukoencephalopathy (PML), an often-fatal demyelinating disease. Approximately 60% of the United States population is seropositive for JCPyV, which typically establishes a persistent, asymptomatic infection in the kidneys. However, in a subset of immunosuppressed individuals, JCPyV can mutate to a pathogenic strain that lytically infects glial cells, including astrocytes and oligodendrocytes, to cause PML. Although cases of PML have been officially documented since the 1950s, the route of viral invasion to the brain has not yet been established. Here, we investigate the microvascular endothelium of the blood-brain barrier (BBB) as a potential gatekeeper for JCPyV neuroinvasion. First, we show that the hTERT/SV40-transformed brain microvascular endothelial cell line hCMEC/D3 expresses the LSTc viral attachment receptor. Expression of LSTc is significantly less than that of SVGAs, an immortalized glial cell line that is well-established to be permissive to JCPyV infection. Consistent with these results, we show that hCMEC/D3 cells bind significantly less JCPyV than SVGAs. However, both cell lines internalize similar amounts of virus. These results support the idea that the BBB endothelium binds and internalizes JCPyV viral particles in circulation. To investigate JCPyV passage from peripheral circulation to the brain, we modeled the BBB endothelium using a monolayer of hCMEC/D3 cells in the Transwell barrier system. Under native conditions, we found that the endothelial monolayer restricts passage of purified, extracellular vesicle-associated, and JCPyV viral lysate over 72 hours, and barrier integrity is unaffected by viral exposure. In humans, JCPyV may require an inflammatory environment to achieve neuroinvasion across the BBB. To investigate this relationship, we plan to treat the endothelial monolayer with the proinflammatory cytokine tumor necrosis-α (TNFα) before introducing virus. We expect to find that TNFα exposure increases JCPyV passage across the monolayer, which would indicate that the microvascular endothelium of the BBB mediates JCPyV entry to the brain under proinflammatory conditions.

CJ Abeshaus **Poster #D16**

Home Institution: Scripps College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Darcy Diesburg, Neuroscience; Stephanie Jones, Neuroscience

Modeling the biophysical dynamics of frontocentral ERP given transient beta events during the stop-signal task

The act of stopping an action, such as preventing oneself from running into a wall, is essential to human movement. Previous studies have used the stop-signal task (SST) to show that beta events, activity patterns in the brain, predict motor inhibition (Soh et al., 2021, Wessel et al., 2015, Wessel, 2020). Often, this relationship is studied through non-invasive techniques, such as electroencephalography (EEG) and magnetoencephalography (MEG), which record macroscopic scalp signals during behavioral tasks. However, the underlying cellular processes that compose these signals and their relationship to motor inhibition in the SST are unknown. To address this gap, we use Human Neocortical Neurosolver (HNN; Neymotion et al., 2020), a biophysical neocortical column under thalamocortical drive, to predict the neural mechanisms that compose such EEG/MEG signals. We examine how beta events affect an updated calcium model (Law et al., 2021) in successful and failed SST trials, in order to analyze their potential function in motor inhibition. For successful and failed trials, the model predicted that beta events affect the voltage of the event related potential (ERP) from 15 to 400 ms before the first proximal drive by inhibiting L2 pyramidal cells. However, empirical frontocentral-ERPs from the SST did not show similar differences for trials with beta events in this period. This suggests that beta events in the frontal cortex may not have a similar effect on evoked responses as in the somatosensory cortex. Further work will elucidate how beta events in the frontal cortex impact movement suppression.

Jaden Zhang **Poster #E1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mamiko Yajima, MCB

The Role of Sox Transcription factors in sea urchin embryogenesis

A cell's fate is the primary factor that determines its essential characteristics like its morphology, proliferation, and function inside tissues. Despite its importance, the mechanisms of cell fate determination during embryonic development are not yet fully understood. Wnt/β-catenin signaling is one pathway that has been shown to regulate cell and tissue organization in various organisms. Previous studies have shown that canonical Wnt signaling prevents the degradation of β-catenin, allowing it to associate with T-cell factor/Lymphoid enhancer factor (TCF/LEF) transcription factors, which bind to Wnt enhancers and promote specific gene expressions in the nucleus. However, a recent study in human pluripotent stem cells suggests that β-catenin may also bind other transcription factors such as Sox2 and Sox17 in the nucleus to promote other gene expressions independently of TCF/LEF transcription factors, which contributes to different germ layer formation. To test this finding in the context of embryogenesis, we here use sea urchins, Strongylocentrotus purpuratus, as a model organism to identify the possible function of Sox proteins in the Wnt/β-catenin pathway. Immunofluorescence results of Sox2 and Sox17 suggest that Sox2 localizes to the nucleus in embryos from the 16-cell to Day 2 stages, while Sox17 remains in the cytoplasm throughout early development. This suggests that Sox2 may drive transcription

to facilitate different germ layer formation during embryogenesis, which will be further tested in the future in conjunction with its possible interaction with β-catenin using knockdown and immunoprecipitation approaches.

Byron Butaney **Poster #E2**

Home Institution: Brown University

Summer Research Program: Research Assistant of Ritambhara Singh, CCMB

Faculty Mentor: Ritambhara Singh, Computer Science

scGrapHiC: A Graph Generative Scheme for Single Cell Hi-C Data Augmentation

The emerging field of single-cell genomic analysis has allowed researchers to gain unique insights into intra-population genetic variation and rare disease treatment. In particular, single-cell Hi-C (scHi-C) analysis has allowed researchers to understand cell-specific chromatin architectural rearrangements and their role in disease development. However, given the technical constraints of the single-cell protocol, it is challenging to get coverage across 5%-10% of the linear genome; this limitation is further exacerbated in scHi-C, which is represented as a 2D contact map. Researchers have developed various algorithms to combat this issue, ranging from hyper-graph neural networks to relying on random graph walks to impute missing scHi-C reads to generate dense scHi-C contact maps. These existing methods are constrained in their application because they rely on sparse scHi-C contact maps that are typically unavailable, given the technical challenges associated with conducting scHi-C experiments. A recently developed method, GrapHiC, employs a graph generative scheme with structural prior and cell-specific signals through bulk ChIP-seq experiments to impute bulk Hi-C contact maps. We propose a similar approach called scGrapHiC that relies on single-cell specific signals that we can acquire through commonly conducted experiments such as scATAC-seq and scRNA-seq in conjunction with a structural prior to imputing a scHi-C contact map without requiring a sparse scHi-C contact map. Our method would allow us to impute scHi-C experiments for samples with no scHi-C experiments.

Nishitha Chaayanath **Poster #E3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Dr. Alison DeLong, Molecular Biology, Cell Biology & Biochemistry Department

Tying Up Loose N's: The N-terminal Story in The B72 Canon

Although protein kinases regulate key cellular events, protein phosphatases exercise an equally important role in the control of subcellular functions potentially resulting in phenotypic changes within model organisms. In particular Protein Phosphatase 2A (PP2A) plays an important role in processes such as mitotic entry as well as MAPK and TOR signaling to name a few. The PP2A holoenzyme is composed of three parts: subunit C (catalytic), subunit A (a structural) and finally subunit B (regulatory unit) all of which are encoded by at least one gene family. Plants express B subunits belonging to three different families, B55, B56 and B72, with the B72 family having been investigated by the DeLong lab. Previous experimentation in the Arabidopsis thaliana system has shown that b72 loss of function mutants exhibit a larger leaf phenotype, indicating that PP2A complexes containing B72 regulatory subunits contribute to the regulation of leaf area/morphology. While single, double and triple mutants for the B subunit and their resulting leaf phenotype have been studied, the function of N-terminal extension for the B subunit has been largely untouched. B72 subunits have a conserved "B72 domain" plus an amino terminal extension

of variable length and unknown function. Crispr mediated mutagenesis yielded an in-frame deletion which yielded a deletion of 100 amino acids from the 115 in the N-terminal extension.This allele provides an opportunity to determine whether the amino terminus contributes to regulation to leaf size/morphology.

Maliha Tasnim **Poster #E4**

Home Institution: Macaulay Honors at CUNY Hunter College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Mark Daley, Biomedical Engineering; Kareen Coulombe, Biomedical Engineering

Determining the role of AMPK activation in increasing the risk of atrial fibrillation for Wolff-Parkinson-White Syndrome patients using engineered human cardiac microtissues

Wolff-Parkinson-White Syndrome (WPW), a type of abnormal heart rhythm, affects 1 to 3 in 1,000 people worldwide. Patients with WPW often possess an extra electrical pathway in the heart, leading to rapid heartbeats and palpitations. They also possess an increased risk of atrial fibrillation, increasing lifetime risk of heart attack and stroke, but the origin of the trigger that causes atrial fibrillation in WPW patients is still unknown. In recent years, however, inherited forms of WPW have been linked to mutations of the PRKAG2 gene that cause over-activation of 5' adenosine monophosphate-activated protein kinase (AMPK), a critical metabolic regulator. The main goal of this project was to determine if AMPK activation contributes to the onset of atrial fibrillation in WPW patients by studying human atrial electrophysiology in vitro. Self-assembled micro-tissues were generated by combining human induced pluripotent stem cell-derived atrial cardiomyocytes and primary human cardiac fibroblasts in a 95:5 ratio in agarose round-bottom micro-wells. After one week in culture, the micro-tissues were treated with a vehicle control (DMSO) or an AMPK activator (compound 991) at a low (1μM) and high concentration (10μM) for an additional week. By monitoring changes in cellular glycogen levels and AMPK phosphorylation, we were able to validate AMPK activation. Changes in electrophysiology were evaluated by recording micro-tissue beat rate and recording action potentials using high-speed optical mapping with a voltage-sensitive dye. Combined, these data can be used to elucidate the role of AMPK activation in triggering atrial fibrillation. Future work will use cardiomyocytes derived from WPW patients to evaluate the expression of different ion channels and their contribution to altered atrial electrophysiology and the role of AMPK. With this work we aim to create the foundation for pinpointing therapeutic targets for new therapies and, in turn, enhance the quality of life for WPW patients.

Jared Chung **Poster #E5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Gilad Barnea, neuroscience

Development and Validation of a Novel Assay for in vivo Neuropeptide Receptor Activation in Drosophila melanogaster

Fruit flies utilize chemical signaling to communicate information between their nervous system and the rest of their body. In addition to the well-studied neurotransmitters (glutamate, GABA, acetylcholine, etc.), various peptides have also been shown to be secreted within the nervous system in response to external

stimuli and physiological changes. One such example is Diuretic hormone 44 (DH44), an ortholog of the mammalian corticotropin-release hormone (CRH). DH44 has been shown to modulate fly behavior during periods of high physiological stress, such as starvation, or during energetically-expensive processes, such as reproduction. Although the role of the neuropeptide itself has been studied, the physiology and function of its two known receptors, (DH44-R1 and DH44-R2), are almost entirely uncharacterized. To uncover the roles of the different receptors, we employed the CRISPR/Cas9 system to develop a genetically-encoded tool, TangoMAP MKII. This novel tool is designed to allow the study of in vivo receptor activation in various physiological states. This tool is a modification of the Tango assay for G-Protein Coupled Receptor activation, where the activation of one receptor triggers a signaling cascade to promote the transcription of a chosen reporter gene. For this development, we used scarless gene editing to modify the endogenous loci of the two DH44 receptors in an isoform-specific manner. Using DNA sequencing and immunohistochemistry, we are validating this new assay and plan to employ it to further characterize DH44 receptor activation in Drosophila. The design of this scarless approach allows for other neuropeptide receptor loci to be modified with ease, leading to the generation of a library of novel TangoMAP MKII tools open to the research community at large.

Nova Dea **Poster #E6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Michelle Dawson, Molecular Biology, Cellular Biology and Biochemistry

Senescent Fibroblast Matrix Remodeling Promotes Fibrotic Lung Architecture

Chronic respiratory diseases are the third leading cause of death for those above the age of 65, making it an age-related disease. With an aging domestic population where 1 in 4 Americans will be over 65 years of age by 2050, the prevalence of age-related disease is expected to increase. Cellular senescence is a natural response to DNA damage, which prevents malignant transformation by permanently arresting the cell cycle. However, senescent cells accumulate in the tissue with age, and this accumulation has been shown to mediate pulmonary fibrosis and the subsequent decline in organ function. This study investigates fibroblast senescence-associated extracellular matrix (SA-ECM) remodeling and its ability to promote a pathological senescent matrix architecture.

Post-gamma irradiation, a senescence phenotype was established through beta-galactoside staining, fluorescent microscopy, and cell phenotype characterization. Fibroblast-derived matrices (FDM) were grown using pre-senescent and senescent pulmonary fibroblasts over 21 days. Second-harmonic generation (SHG) microscopy was used to characterize organizational changes in the collagen fibers. We observed that pre-senescent FDMs uniformly deposited aligned collagen fibers. In contrast, senescent FDMs initially decreased in density before an exponential increase to levels equal to pre-senescent FDMs. Collagen fibers in the senescent FDMs were also left much more disorganized compared to pre-senescent FDMs. Through inhibition of the TGF-□ pathway, we found that we were able to decrease local senescent fiber disorganization back to pre-senescent levels. Our findings suggest senescent FDMs undergo a temporally heterogeneous biphasic remodeling process that results in a pro-fibrotic ECM architecture, and that this disorganized architecture may be targeted therapeutically to resolve pathological senescent matrix alterations.

Will Malloy **Poster #E7**

Home Institution: Brown University

Summer Research Program: IBES Summer Internship Program

Faculty Mentor: Dawn King, Institute at Brown for Environment and Society

Sex ratios of blue crabs (Callinectes sapidus) in the Providence River Estuary

Though the Narragansett Bay and Providence River Estuary (PRE) are well established as being within the range of Callinectes sapidus, research on this economically and ecologically significant species has historically focused on locations further south in its range. As such, the population structure of C. sapidus in the Narragansett Bay and PRE is comparatively poorly understood. During ongoing juvenile and adult fish survey and monitoring projects, The Nature Conservancy has collected data on the abundance of C. sapidus at twenty-four sites in the upper Narragansett Bay and the Providence and Seekonk Rivers. Individuals were collected over a three year period during the months of May through October by hauling seines and deploying unbaited fish traps left for an approximately 96 hour soak. Both survey methods were repeated once per month per site during the period studied. Animals captured by these methods were then identified to genus or species, measured, enumerated, and released. Initial analysis of the C. sapidus observed in these surveys demonstrates an uneven distribution of sexes among the observed individuals, with a bias towards males. Ongoing research is investigating possible relationships between sex ratio and water quality factors such as salinity and dissolved oxygen. However, further research is needed to determine whether the distribution of sexes in the dataset reflects an unequal sex ratio in the population of C. sapidus in the PRE or whether this bias is a result of behavioral or other differences between sexes that result in nonrepresentative sampling. Regardless, the biased sex ratios observed in this data set warrant further investigation into sex ratio trends among C. sapidus in the Providence River Estuary.

Andres Filizzola **Poster #E8**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Chemistry

Strategies for Inducing Engineered Bacteria Designed to Bioaccumulate Arsenic from Drinking Water

Arsenic contamination in drinking water even at low levels poses a significant cancer risk for people. Both the World Health Organization (WHO) and the US Environmental Protection Agency (EPA) have set limits for arsenic in drinking water with current standards recommending no more than 10 ppb. Unfortunately, millions of people worldwide are exposed to arsenic in their drinking water. These populations may derive drinking water from groundwater wells that can contain high concentrations of arsenic released from natural geographic formation. Many of these individuals do not use arsenic testing or the specialized filters needed for arsenic removal below the recommended ppb levels. The challenges associated with existing technologies are two-fold: first, they require substantial energy and material resources which contributes to their cost, and second, their effectiveness can be variable based on local water conditions. Innovative approaches for removing trace levels of arsenic from drinking water could offer the renewability, affordability, and reliability needed for widespread adoption.
Many organisms have evolved biological mechanisms to protect against arsenic toxicity, and in this project we exploit these tools in engineered bacteria designed to bioaccumulate arsenic. We engineered E.coli to selectively adsorb arsenic by expressing a novel chimeric protein that has strong and specific

arsenic interactions; this allows our living filters to predictably remove arsenic no matter the specific composition of the input water. Our filter material can be freeze-dried into a powder and reconstituted in minimal media thereby offering a renewable sorbent for selective arsenic removal. Expression of ArsR-Loop is induced in these microorganisms using a common synthetic biology and non-natural sugar, IPTG (isopropyl-beta-D-1-thiogalactopyranoside). This substance is similar enough to lactose that it can trigger transcription of the lac operon and induce protein expressions that are under control of this operon. promoter system. While commonly used in small-scale fermentation systems for engineered bacteria, large-scale use especially for this application would ideally rely on a non-chemical agent for induction of arsenic bioaccumulation. This work describes methods to evaluate alternative induction systems based on optogenetic control and red light illumination. Effective induction can be measured by changes to microbial growth and protein expression.

Justin Moustouka **Poster #E9**

Home Institution: Brown University

Summer Research Program: Undergraduate Research Assistant in Desai Lab

Faculty Mentor: Tejal Desai, Biomedical Engineering

Optimization of synthetic paradigm for biocompatible DNA scaffold nanoparticles

Polymer-based biomaterials are extensively being used as drug delivery vehicles for cancer and autoimmune disease treatments owing to their biocompatibility, tunable surface functionality, and high drug loading capacity. However, traditional fabrication of these particles lacks the ability to control surface functionalization density. Recently, our lab investigated the use of short sequence DNA scaffolds, based on polymeric particles, for immunomodulation in vivo. The DNA scaffold nanoparticles consist of FDA-approved biocompatible polymers like poly(lactic-co-glycolic acid) (PLGA) and polyethylene glycol (PEG) along with short sequence DNA on the surface. Using the complementary DNA strand conjugated to the target ligand or therapeutic moieties, we were able to prepare bioactive materials through DNA hybridization. In this work, we are optimizing the fabrication of such DNA scaffolded nanoparticles to be used for targeted cancer therapy. The two-step fabrication process includes DNA-polymer conjugation and subsequent DNA scaffold synthesis. Previously reported DNA-polymer conjugation step followed thiol-maleimide chemistry, which includes a disulfide bond breakage step with a possibility of significant material loss. Our current approach of click chemistry between an activated alkyne and an azide provides a clean DNA-polymer conjugation. For biomaterial fabrication, previous work yielded a size range of 0.2-5 μm through the emulsion method. Nanoprecipitation has been chosen as an alternative method to produce particles sized less than 200 nm, which is more optimal for accumulation in the tumor microenvironment through enhanced permeability and retention (EPR) effect. This methodology shift from emulsion to nanoprecipitation method also allows us to bypass the use of expensive instrumentation like probe sonicator and vacuum centrifuge for the synthesis of nanoscale DNA scaffolds. As-fabricated DNA scaffold nanoparticles are characterized by TEM, SEM, and DLS, along with the surface DNA density determination through fluorescence. In vitro cellular studies on tumor cell lines are performed to test the biocompatibility and cellular uptake of DNA scaffold nanoparticles using cell viability assay and flow cytometry, respectively. Promising results from this work could provide us an insight on how the tunable surface functionality of such nanoparticles can correlate to the mechanistic understanding of biomaterial-cell interfaces.

Anna Shlimak **Poster #E10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kristi Wharton, MCB

A Tissue-Specific Approach to Assessing the Impact of Imaginal Disc Growth Factor 6 (idgf6) on Amelioration of ALS Motor Deficits

While ALS is called a “motor neuron disease,” it is truly a motor circuit disease, as it results in a loss of locomotion. Motor neurons are not the only components needed for movement; sensory neurons, non-neuronal cells like glia, and supporting adipose-like tissues in Drosophila are also critical. Thus, it becomes important to assess the systemic effects associated with ALS beyond neurons alone, focusing particularly on cells that support motor function.

One gene of interest in the study of ALS is idgf6, which encodes the secreted imaginal disc growth factor 6. Preliminary data within the Wharton lab using Drosophila melanogaster as a model system has demonstrated that modifying the expression patterns of idgf6 can suppress the neurodegenerative phenotypes associated with ALS. My work assesses the effects of manipulating idgf6 expression within the context of these supporting tissues, focusing specifically on glial cells, liver and adipose-like tissue (known as the fat body), and sensory neurons.

To better understand the correlation between different types of ALS, my research has made use of disease models of ALS including TDP43 [M337V] and dSOD1 [G85R] and [A4V] mutants. My preliminary work in these models has revealed that idgf6 acts in a dosage-sensitive manner to partially restore the motor deficits associated with ALS. In supporting cells like the fat body and glia, both the knockdown and overexpression of idgf6 led to a suppression of the diseased phenotype. This brings into question the downstream effects of idgf6, especially those pertaining to metabolic pathways sensitive to gene dosage. Through our work with idgf6, my team has revealed that secreted idgf6 protein serves as a transcriptional activator of the prominent metabolic enzyme, pyruvate carboxylase. Due to its role in regulating the flux between glycolysis and gluconeogenesis, we have begun to explore the downstream effects of idgf6 on these pathways on both a transcriptional level using qPCR and on an organismal level using lifespan, eclosion, and immunohistochemistry quantification assays.

Bryanna Vilnaigre **Poster #E11**

Home Institution: New York University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Hwamee Oh, Department of Psychiatry and Human Behavior

Differential effects of beta-amyloid and diagnostic status in hippocampal subfield volume changes across the Alzheimer's disease continuum

Background: Alzheimer’s disease (AD) is a neurodegenerative disorder characterized by cognitive impairments co-factored with beta-amyloid (Aβ) plaques, neurofibrillary tangles, and hippocampal atrophy. Past research has implicated hippocampal atrophy as a marker for AD, but we aim to elucidate whether hippocampal subfield atrophy is AD specific. This work investigates volumetric changes in hippocampal subfields in relation to Aβ positivity status across the AD continuum.

Methods: We evaluated 281 participants (ages 57-94 years) from the Alzheimer's Disease Neuroimaging Initiative (ADNI2) dataset. ADNI2 is a longitudinal study developed to analyze the effects of cognitively normal (CN) aging, early and late mild cognitive impairment (EMCI, LMCI), and AD pathologies. High resolution images of the hippocampus were obtained using structural magnetic resonance imaging (MRI), and Aβ presence was detected using positron emission tomography (PET) scans.

Results: Statistical analysis of data revealed hippocampal subfield atrophy across a range of diagnostic groups. When comparing AD to CN diagnoses, there was a significant decrease in the volume of several hippocampal subfields, including CA1 and entorhinal cortex (ps<0.001). LMCI was associated with significantly decreased CA1, CA2, and entorhinal cortex volumes (ps<0.001). There were significant interactions between amyloid positivity and EMCI diagnoses for decreases in right entorhinal cortex and dentate gyrus volumes (ps<0.05).

Conclusion: These results show specific relationships between hippocampal subfields and diagnostic status as a function of the presence of beta-amyloid plaques. Assessing volumetric differences in specific hippocampal subfields across the AD continuum could help identify individuals at the early stage of AD pathology and further our understanding of the neurobiology of AD.

Barron Clancy **Poster #E12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kristi Wharton, MCB

Analysis of genetic modifiers of TDP-43 and TBPH ALS models in Drosophila melanogaster

Approximately 1 in 400 people develop amyotrophic lateral sclerosis (ALS) in their lifetime. However, there is no current cure and limited treatment options. ALS is a neurodegenerative disease generalized as a motor neuron disease, but has widespread effects on the nervous system. It is associated with over twenty genetic mutations, but over 80% cases have unknown causes. To identify potential genetic modifiers of ALS, the Wharton Lab developed a Drosophila model for ALS based on the human C9orf72 (G4C2)49 expansion in motor neurons. Using this model, the lab conducted a genetic screen of 371 chromosomal deficiencies to identify genes modifying the phenotype associated with the G4C2 expansion. Multiple deficiencies were found to suppress the lifespan deficits associated with the (G4C2)49 model.

To further investigate the potential genes whose reduction in dosage led to suppression, I investigated the potential of knocking down three candidate Drosophila genes found in the overlap of strongly-suppressing deficiencies—CG8870, Nipped-A, and raptor—using RNA interference to lower expression levels in another ALS model, TDP-43, and the Drosophila ortholog model, TBPH. I investigated well-characterized phenotypes of the model, including eye degeneration and lifespan. Preliminary results indicate that knockdown of Nipped-A and raptor suppress the lifespan phenotype. Based on these findings, I intend to analyze neuromuscular junction bouton number in larvae using immunohistochemistry and investigate changes in the expression of genes known to act downstream of these suppressor genes. With these assays, we will better understand the behavior and potential of the genes of interest to advance our understanding of ALS.

Kareena Sandhu **Poster #E13**

Home Institution: Brown University

Summer Research Program: Stanford University School of Medicine Summer Research Internship Program

Faculty Mentor: Kattria van der Ploeg, Medicine/Infectious Diseases; Pras Jagannathan, Medicine/Infectious Diseases

The in vitro effect of flu vaccine stimulation on malaria-specific IgM antibody production in tonsil organoid systems

Malaria remains a significant global health burden, and is co-endemic with other pathogens, including influenza. Furthermore, prior exposure to malaria may influence responses to vaccination, although the mechanisms of such interactions remain unclear. I investigated the impact of in vitro malaria parasite exposure on the immune response to live attenuated influenza vaccine (LAIV) in a tonsil organoid model. I also evaluated primary immune responses to malaria in this model. Previously unexposed tonsil organoid cells were stimulated with malaria iRBCs to simulate malaria exposure. Immunoglobulin M (IgM) antibody responses to schizont lysate parasite antigens were measured using enzyme-linked immunosorbent assays (ELISA) with the supernatants of both uRBC- and iRBC-exposed tonsil organoids with and without LAIV stimulation.

My findings demonstrate that prior malaria exposure influences tonsil IgM antibody responses to schizont lysate antigens in vitro. In iRBC-exposed tonsil organoid samples, I detected a tonsil IgM response 14 days after co-culture. These findings suggest the development of a malaria-specific adaptive immune response to persistent exposure. However, intriguingly, my results also reveal a complex interaction between flu vaccine and the antibody response to schizont lysate antigens. In iRBC-exposed tonsil organoid samples that received LAIV on day 0 and day 1, I observed an attenuated IgM antibody response to the malaria antigens at day 14 compared to iRBC-exposed samples that did not receive LAIV. This suggests a potential interference in the immune system's ability to mount an effective immune response against malaria-specific antigens in the presence of influenza antigens.

This study sheds light on the complex relationship between recurrent malaria exposure and the immune system, highlighting the potential implications for vaccine efficacy and immune responses in malaria and influenza co-endemic regions. Understanding the factors that modulate immune responses to malaria antigens, such as previous malaria exposure and other vaccination, is crucial for the design and implementation of effective vaccination strategies. Lastly, using tonsil organoid systems is a potentially useful mechanism to study human immune responses in vitro.

Annika Coleman **Poster #E14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Barry Lester, Department of Psychiatry and Human Behavior; Department of Pediatrics; Marie Camerota, Department of Psychiatry and Human Behavior

The Impact of Early Adversity on Hair Cortisol in Very Preterm Infants

Children exposed to early adversity, defined as the socioeconomic, psychosocial, and medical factors that influence long term health, are at increased risk of negative cognitive and behavioral outcomes. It is hypothesized that one mechanism by which social adversity “gets under the skin” is via the excessive or

prolonged exposure to physiological stress. Chronic stress can result in hyperactivation and long term 'wear and tear' on the body's primary stress response system, the hypothalamic-pituitary-adrenal (HPA) axis, a phenomenon known as "allostatic load." HPA dysregulation can subsequently disrupt the release of cortisol, a crucial glucocorticoid hormone that allows for physiological adaptation to environmental challenges. While salivary and serum cortisol have been used extensively to measure short-term stress responses, hair cortisol, as well as the inert form cortisone, have emerged as promising biomarkers of long-term stress accumulation.

Relations between early-life stress and long term health are of particular relevance for very preterm infants. Due to their heightened medical problems and exposure to the stressful neonatal intensive care unit (NICU) environment, preterm infants are at increased risk of HPA dysregulation. Nonetheless, there exists significant heterogeneity in health outcomes within this population. This study investigates the cumulative effects of pre-, peri- and postnatal adversity on hair cortisol cumulation in a cohort of 400 infants born <30 weeks gestational age from the multi-site Neonatal Neurobehavior and Outcomes in Very Preterm Infants (NOVI) study.

We constructed a cumulative adversity index spanning 46 pre-, peri-, and postnatal risk factors (e.g., demographic, medical, psychological, and social risk variables) collected from birth to age 4 years. Hair cortisol and cortisone were assayed from hair samples collected at age 4. We evaluated the relationship between cumulative adversity and log-transformed cortisol and cortisone using censored regression models. After adjusting for covariates, cumulative early adversity was positively correlated with both hair cortisol ($b = .55$, $p = .04$) and cortisone ($b = .25$, $p = .04$) concentrations. These results support the hypothesis that early adversity is correlated with long-term stress accumulation and suggest the need to further disentangle the timing and type of adversity factors that most significantly contribute to the observed HPA dysregulation.

Yihuan Dong **Poster #E15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Amitai Shenhav, Cognitive, Linguistic & Psychological Sciences, Carney Institute for Brain Sciences; Ivan Grahek, Cognitive, Linguistic & Psychological Sciences, Carney Institute for Brain Sciences

Leveraging Continuous Psychophysics to Investigate Cognitive Control Allocation in Dynamic Environments

Cognitive control plays a crucial role in determining how we allocate our cognitive resources. For example, we will increase how much control we allocate (e.g., top-down attention) when studying for a course that we find to be valuable (e.g., provides us with valuable skills in job interviews), but we will invest less effort into courses that are not relevant to us. Cognitive control research has demonstrated that people increase control allocation when they expect higher rewards. However, while studying is a continuous process, most cognitive control research is done using trial-based paradigms in which participants commit discrete responses to discrete stimuli. Recent work in psychophysics has focused on the use of continuous paradigms which allow measurement of continuous behavior. In such paradigms, participants continuously monitor (e.g., mouse tracking) stimuli which are changing over time (e.g., moving targets). Such paradigms are more naturalistic and very data-efficient (collecting data with high time resolution). However, it remains unclear whether performance in such paradigms depends on cognitive control. The goal of this summer research project is twofold: first, we aimed at replicating the

previous work in the domain of continuous psychophysics. Second, we investigated whether performance in continuous paradigms is sensitive to reward, which would indicate that it can be modulated by cognitive control. We developed a task in which participants used the cursor to track randomly moving targets (Gaussian blobs) of varying difficulty (spatial uncertainty). On each trial, participants tracked one target for 20s, and they could earn either high ($3) or low ($1) rewards based on their performance in each block of trials. We successfully replicated previous work, showing that tracking errors increase with stimulus difficulty. Further, we show that reward expectations impact tracking behavior, but that there are large individual differences in this effect. Having established this, we will proceed with fitting dynamic internal models to this data in order to further investigate whether difficulty and reward expectations influence attentional or motor processes. This will allow us to investigate whether continuous tracking paradigms can be used to study the dynamics of cognitive control in more naturalistic settings.

Meher Sandhu **Poster #E16**

Home Institution: Brown University

Summer Research Program: Rhode Island Hospital Research Internship Program at the Mind and Heart Lab

Faculty Mentor: Elena Salmoirago-Blotcher, Medicine, Psychiatry and Human Behavior at the Brown Alpert School of Medicine

Challenges in Recruitment of Older Patient Populations with Chronic Illness for Clinical Studies: Gaps and Strategies

Investigators at The Miriam and Rhode Island Hospitals are recruiting patients with heart failure to participate in a research study called the Mind Your Heart Study-II. Congestive heart failure is an illness most commonly found in older patients. The clinical study has experienced challenges in recruiting older patient populations with chronic illnesses. The complexities associated with recruiting older individuals for clinical trials include comorbidities, physical limitations, time commitment, transportation issues, and distrust of research institutions. Previous studies have reported challenges related to participant recruitment and retention within this specific population. Formalized approaches would effectively engage participants and address their concerns, ultimately leading to increased participation rates and representative study populations. Despite the existence of some recruitment strategies, gaps persist in developing the optimal approach for recruiting older individuals. The literature lacks a comprehensive understanding of reasons for participant attrition and low retention rates within this older population, necessitating further investigation. Drawing upon my experience with the Mind Your Heart Study-II, I have explored recruitment strategies aimed at overcoming some of the challenges faced by older populations. Despite successful screening of participants, retention remains problematic within the clinical study. Understanding the reasons behind participant withdrawal is essential to improve retention rates. Utilizing data from the Access Operational Report, I have devised innovative recruitment approaches specifically tailored for this study. Identifying the factors that contribute to withdrawals will facilitate the development of tailored interventions and foster participant engagement. Considering that these populations often include minorities, it is crucial to design strategies that are inclusive and culturally sensitive. The utilization of social media platforms and exploration of alternative recruitment methods are potential avenues to improve engagement in the future. Emphasizing the relevance of these findings in the context of the Mind Your Heart Study-II will facilitate the development of targeted strategies and enhance recruitment and retention of older individuals with chronic illnesses.

Kristine Yang **Poster #F1**

Home Institution: Brown University

Summer Research Program: MCB Summer Undergraduate Research Assistant

Faculty Mentor: Nicola Neretti, Molecular Biology, Cell Biology, and Biochemistry

Deep Learning Identification of Cellular Senescence Using Nuclear Morphology

A driver of aging and age-related diseases, cellular senescence is a state of permanent cell cycle arrest that can be induced by various factors such as DNA damage, oxidative stress, or replicative exhaustion. Senescence alters the biology of a cell in almost every aspect, increasing secretion levels of pro-inflammatory molecules to epigenetic changes of chromatin, resulting in modifications to the proteome and transcriptome. A major challenge in understanding senescence is the lack of a specific and universal marker to identify senescent cells. A multi-marker approach involving the detection of cell cycle kinase inhibitors p16 and p21 as well as senescence-associated β-galactosidase (SA-β-Gal) is commonly used to identify senescence in vivo. However, because these markers are not specific to senescence, they can be expressed irrespectively of senescence. Furthermore, with estimates below 5%, senescent cells occur in low abundance in aged tissues which makes detecting senescence in tissue more challenging. As microscopy has shown that senescent cells often have enlarged and irregularly shaped nuclei compared to those of proliferating cells, our project combines imaging methods with deep learning and computer vision capabilities to predict cellular senescence. Human fibroblasts from the Lung Fibroblast 1 (LF1) cell line were used and split into two groups, senescent and proliferating. The first group of cells were cultured and fed proper growth factors to maintain proliferation, while senescence was induced via DNA damage in the second group of cells using etoposide. All samples were stained with a fluorescent marker of DNA and DAPI, and images were captured on a fluorescent microscope. As images contained tens to thousands of cells, a cell segmentation algorithm was utilized to isolate individual nuclei, and the nuclei were extracted and saved as individual grayscale images. Feature reduction methods such as background masking, size normalization, and internal masking were applied to the nuclei images to make our classifier more robust to variations. We trained our convolutional neural network on these nuclei images and achieved high accuracy in predicting between senescent and proliferating cells. We aim to

Evan MacLure **Poster #F2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Walter Atwood, Department of Molecular Biology, Cell Biology, and Biochemistry

Screening Plant Flavonoids as a Potential Therapeutic in Significantly Reducing JC Polyomavirus Infection by Antagonizing Inflammation and Survival Pathways.

JC Polyomavirus (JCPyV) is a virus present in roughly 60% of the human population and is the cause of progressive multifocal leukoencephalopathy (PML) in immunocompromised patients, a demyelinating brain disease with a high morbidity and mortality rate. The virus passes into the brain through an unknown mechanism which establishes a lytic infection in astrocytes and glial cells. No FDA-approved antivirals are currently available for the treatment of PML. In this report, we show that plant flavonoids significantly inhibit JCPyV viral infection by blocking key inflammatory and survival signaling pathways important for viral replication. First, we found that the flavonol Quercetin and the flavone Apigenin, potent inhibitors of the NF-kB and PI3K signaling pathways, significantly inhibited JCPyV infection in SV40-transformed glial cells (SVGAs) and normal human astrocytes (NHAs). To identify this reduction,

standard infections using SVGA cells, and NHAs were examined through a 72-hour treatment with either Quercetin or Apigenin following a two-hour treatment with virus. There were significant reductions in VP1 of over 50% observed with IC50 values ranging between 10 - 20 uM in SVGA cells while being as low as 5 uM in NHA. Fisetin and Myricetin, two analog flavonols similar in structure and function to Quercetin, also comparably inhibited JCPyV infection in SVGA cells. Our lab previously identified the oxindole GW-5074 as a potent inhibitor of JCPyV infection by inhibiting the MAPK/ERK pathways. Co-treatment of Quercetin and GW-5074 synergistically inhibited JCPyV infection, suggesting alternate pathways involved in viral replication and varying functions between the two drugs. We are currently investigating the phosphorylation of specific components of the NF-kB pathway, including IKBα, p-65 subunit, and AKT without and in the presence of flavonoids added at various time points. The abundant class of plant flavonoids requires further investigation of its anti-inflammatory properties and its function as a potential therapeutic for PML.

Jasmine Xi **Poster #F3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anne Hart, Neuroscience

Exploring the effects of development on neurodegeneration using a sod-1 ALS model

Amyotrophic Lateral Sclerosis (ALS) is a fatal and incurable neurodegenerative disease affecting motor neurons. The mechanisms and cellular pathways that lead to ALS are still not fully understood, making it an important topic to study. Previous research has shown that stress during adolescent development causes changes in neuron morphology and outgrowth dynamics. Thus, the purpose of this experiment was to see if developmental changes from adolescence to adulthood would affect neurodegeneration in our ALS model. To carry out this experiment, we used a single copy ALS expression model of sod-1 G85R in Caenorhabditis elegans. A key period of development in the C. elegans lifespan occurs between the L4 and young adult stages. Accordingly, we tested our question by comparing the neurodegeneration of L4 animals versus young adult animals. Our results indicate that there is no significant difference between the neurodegeneration levels of animals in the L4 and young adult stages. This implies that in our model, developmental changes do not protect or enhance the neurodegeneration in ALS.

Tarrin Dewberry **Poster #F4**

Home Institution: Brown University

Summer Research Program: Presidential Scholar

Faculty Mentor: Gary Wessel, Cell and Molecular Biology; hg Nathalie, Cell and molecular Biology

WNTering the Pathway of Gene Expression

Sea urchins and sea stars are famous for their ability to make large numbers of sperm and eggs throughout their lifetime. They do not exhibit any reproductive senescence as seen in humans and other mammals, many vertebrates, and even many invertebrates. As such, their gonads may serve as important models for prolonged ovarian function and stem cell immortality.
I am focusing on testing the role of the wnt signaling pathway in ovarian function.
The Wnt pathway allows cells to communicate through cell surface receptors to change the transcriptional profile of a cell and its development. The Wnt pathway is known to be a critical part of embryonic

development and even homeostasis of the self-renewal adult tissues. Although it is known that the Wnt pathway has an important role in embryonic development, there's a lack of understanding of its role in the function of ovary development (and ovary regeneration). The sea urchin, Lytechinus variegatus, will be our model system in this project due to its regenerative capabilities in the production of oocytes. Here, sea urchin ovaries were treated with lithium chloride (an activator of the Wnt pathway) to identify by qPCR the genes that are affected by the Wnt pathway. In preliminary experiments, a qPCR experiment was conducted on stage IV ovary (after spawning) and the results showed that genes such as Wif (Wnt inhibitor factors) are highly upregulated in the ovary when the Wnt pathway is stimulated. I will now test other genes recently identified to respond to the Wnt pathway, and in different stages of ovaries to determine how broad this response may be. I will then determine which cells are responsive to wnt by use of in situ hybridization and single cell RNA-seq analysis. These results should be helpful to understand the prolonged, highly fecund gonad and how it may inform us in the biology of reproductive senescence in general.

Giordana Serretta Fiorentino **Poster #F5**

Home Institution: Brown University

Summer Research Program: An Integrative Treatment for Body-Focused Repetitive Behaviors: Connecting Neuroscience and Contemplative Techniques

Faculty Mentor: Larson DiFiori, Contemplative Studies

An Integrative Treatment for Body-Focused Repetitive Behaviors: Integrating Neuroscience and Contemplative Healing Techniques

My research project focuses on proposing an integrative treatment for body-focused repetitive behaviors (such as nail-biting and skin-picking), a highly common and yet understudied disorder affecting many college students. Mirroring the interdisciplinary aspect of my concentration, Contemplative Studies, my research incorporates both a neural and contemplative understanding of body-focused repetitive behaviors. As part of my research process that began this past Spring semester in my independent project with Professor Di Fiori, I first researched the different neural substrates of body-focused repetitive behaviors, as well as existing treatments and their relative effectiveness. To deepen my understanding of these relevant neural networks, I have also joined the Tiny Blue Dots research group this Summer at the Brown Mindfulness Center, in which we are leading an MRI study on brain regions affected by meditation among participants with anxiety and experienced meditators. I then explored a variety of meditation techniques and contemplative practices targeting the specific neural mechanisms underlying the disorder. Under the guidance of Professor Di Fiori, I drew from contemplative techniques founded on diverse spiritual practices, including Daoism, Tibetan Buddhism, and Sicilian shamanism. As someone who has struggled with chronic nail-biting my entire life, I tested out these different meditation techniques on myself to personally understand how they could be combined to result in a detailed and effective treatment. I plan to further this research with a pilot study this coming Fall, and I hope that my findings can have a beneficial impact on students struggling with this disorder, proposing a cost-effective, safe, and accessible treatment targeting each nuanced aspect of body-focused repetitive behaviors.

Sai Chamarthi **Poster #F6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Wael Asaad, Department of Neurosurgery

Adaptation to Distractors is Different for High and Low-Level Features in Rapid Serial Visual Presentation

Previous research has demonstrated that distractor suppression boosts task performance in goal-oriented paradigms. Specific attributes of these distractor stimuli may govern the relative degrees of inhibition and thus, the corresponding adaptation patterns. To investigate this relation, we employed a 10-image rapid serial visual presentation (RSVP) task in which subjects encoded and identified a target image ("T2") that immediately followed a pre-specified cue image ("T1"), with a defined proportion of trials further presenting a distractor ("filler") between the two images. Specifically, through 1) varying the high- and low-level filler features and 2) the proportion of filler trials, we aimed to characterize the distractor properties that promote effective filler suppression and accurate target selection. Understanding variances in performance may elucidate how distractors influence temporal attention processing of task-relevant stimuli.

Markelle Worrell **Poster #F7**

Home Institution: Georgia State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Jonathan Kurtis, Department of Pathology and Laboratory Medicine

Determining if PfGARP is Secreted from Plasmodium falciparum Infected Red Bloods Cells

As one of the leading causes of pediatric death in children under five, malaria remains a problem in sub-tropical developing countries such as Nigeria and Kenya. Malaria is a parasitic disease transmitted through the bite of an infected Anopheles mosquito. The disease is caused by the genus Plasmodium. The most fatal species in humans is caused by Plasmodium falciparum. There is still ongoing development on a highly effective vaccine against malaria. In the lab, a parasite antigen known as PfGARP was used, a parasite antigen of 80 kDa that is recognized by antibodies in the plasma of children relatively resistant to malaria. PfGARP function will not be effective in secretion on the surface of infected erythrocytes as a quorum sensor. PfGARP was secreted into a culture media from P. falciparum-infected red blood cells for the experiment. Western blots were used with 4-15% SDS protein gels, phosphate-buffered saline (PBS), and high parasitemia of 9% malaria trophozoites. In the experiment, there was no binding to the parasites with PfGARP. From the results, it is expected that PfGARP does not secrete into a culture of red blood cells infected with P. falciparum. For the future of malaria, PfGARP's inability to secrete concludes that PfGARP is unlikely to function as a soluble ligand in quorum sensing. Therefore, the results demonstrate that further study can be made regarding PfGARP and its effectiveness for malaria.

Halle Nwanne **Poster #F8**

Home Institution: Georgia State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Peter Belenky, Molecular Microbiology and Immunology

"Skin Microbial Battle: Staphylococcus epidermidis Fermentation of Glycerol Antagonizes S. aureus and Cutibacterium acnes"

Acne vulgaris is a common inflammatory skin disease of sebaceous skin pores caused by a disrupted skin microbiome and effects millions of Americans annually. Cutibacterium acnes is strongly implied as an etiological agent of acne vulgaris when it over-populates on the skin. Conventional acne treatments often try to manage acne symptoms or remove target microbes altogether from the skin during serious infections. These treatments are often transient and fail to address the underlying dysbiosis of the skin microbiome. As such, alternative approaches to managing acne vulgaris are required. One approach is to leverage other commensal skin community members to regulate the growth of C. acnes and re-establish skin microbiome homeostasis. Staphylococcus epidermidis is a ubiquitous skin commensal known to antagonize C. acnes growth through short-chain fatty acids (SCFAs) produced from glycerol fermentation. Thus, the purpose of this study was to determine if there exists a S. epidermidis body site isolation influence on fermentative antagonism. In this study, we assessed media acidification, growth kinetic inhibitions and plate-based antagonism assays to query potential body site isolation effects. The results indicate that body isolation site does not influence the acidification of media in the presence of glycerol. Likewise, we observed that the growth of C. acnes was severely inhibited in the presence of glycerol-containing media that was fermented by S. epidermidis. We also assessed this fermented media against another common skin pathogen, S. aureus, and observed a strong growth-inhibition effect. Lastly, our plate-based antagonism assay suggests that even at a concentration of C. acnes which mimics over-population during acne vulgaris, S. epidermidis was still able to inhibit the growth of C. acnes. This work suggests that the fermentative antagonistic effect of S. epidermidis is general and not body site specific. Consequently, this work supports the use of a microbiome-centric approach where native skin commensals on a person suffering from acne vulgaris may be used to effectively manage the disease.

Lella Wirth **Poster #F9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Petra Klinge, Warren Alpert Medical School Department of Neurosurgery; Christine Trask, Warren Alpert Medical School Department of Psychiatry and Human Behavior

Chiari and Cognition: Measuring Post-Surgical Change in Neurocognitive Symptoms in Adults and Children with Chiari Malformation Type I (CM1)

Chiari malformation type I (CM1) is a neurosurgical disorder in which one or both of the cerebellar tonsils are displaced below the foramen magnum, causing pressure changes on neural structures including the cerebellum. The cerebellum is known to have a role in motor learning, balance, and coordination, with emerging studies suggesting cerebellar control over cognitive and emotional processing. Cognitive dysfunction in CM1 is well-documented, but assessments have often relied on extensive neuropsychological tests which take hours to administer. In 2016, a concise way to quantify cognition was developed in the form of the Cerebellar Neuropsychiatric Rating Scale (CNRS), previously validated in cerebellar diseases but not reported in CM1 patients. The CNRS is a 105-point survey that rates neurocognitive symptoms on a four-point Likert scale. Here we evaluate the utility of the CNRS to describe neurocognitive symptoms associated with CM1 by comparing these results against a well-validated neuropsychological battery. We then examine post-surgical changes in CNRS scores to evaluate the effect of decompression surgery on emotive and cognitive function in CM1 patients. Patients with CM1 considering surgical decompression were administered the CNRS questionnaire pre- (N=87)

and 8-24 months post-operatively (N=49). A subgroup (N=24) was administered a full neuropsychological battery pre-operatively (Wechsler Full Scale IQ, Digit Span, Coding; WRAML Finger Windows; DKEFS Trail Making; Verbal List Learning; Grooved Pegboard). Descriptive and correlative measures were computed. Pre- and post-operative scores were compared using a paired t-test. The results indicate a moderate correlation between the impairment detected by pre-operative CNRS scores and the standardized neuropsychological test battery (Spearman rank coefficient $\rho = 0.56$, $p=0.003$). This suggests that the CNRS could be a more concise alternative to screen for neuropsychological symptoms in CM1. The average CNRS composite score showed a statistically significant improvement, with a mean (SD) of 34.7 (±21.8) pre-op vs. 29.3 (±22.9) post-op, $p=0.014$. Of CNRS sub-domains, there was a statistically significant decrease in CNRS scores for attentional ($p=0.003$), emotional ($p=0.048$), and autism spectrum ($p=0.025$) domains, indicating that cognitive-affective dysregulation can be improved by decompression surgery.

Brianna Pham **Poster #F10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Suchitra Kamle, MMI (Molecular Microbiology & Immunology)

CHI3L1 regulation in EGFR non-small cell lung cancer proliferation, invasiveness, and drug resistance

Lung cancer is the leading cause of cancer deaths worldwide. Non-small cell lung cancer (NSCLC) accounts for approximately 75-80% of lung malignancies and adenocarcinoma is the most common type of lung cancer. Although the molecular pathogenesis of lung cancer has not been fully defined, the epidermal growth factor receptor (EGFR) is responsible for about 15-40% of lung adenocarcinomas in the US. EGFR (also called ErbB1 and Her1) is a transmembrane receptor tyrosine kinase (TK) that transduces signals which drive cell proliferation and differentiation. Multiple generations of tyrosine kinase inhibitors (TKIs) have been developed to treat NSCLC patients with EGFR mutations in exons encoding the tyrosine kinase domain (TKD). These tumors generally respond well to initial TKI treatment; however, most patients develop resistance to these drugs about one year after starting treatment. Several mechanisms have been implicated in this resistance including the accumulation of secondary mutations in exon 20, alterations in signaling downstream genes of EGFR, and the amplification of receptor-associated tyrosine kinases. However, other poorly defined pathways of TKI resistance, such as alterations in the levels of p53 and stemness factors, clearly exist. Surprisingly, the mechanisms that contribute to resistance to TKIs cannot be defined in approximately 50% of cases. Thus, therapies that are effective in these patients have not been defined. Chitinase 3-like-1 (CHI3L1), a prototypic protein, which is also called YKL-40, is a member of the 18 glycosyl hydrolase gene family. CHI3L1 is produced by a variety of cells including epithelial cells, macrophages, and tumor cells that inhibit cell death and innate immunity. Our studies suggest that CHI3L1 plays an important role in EGFR-mutant NSCLC. Specifically, these studies demonstrated that EGFR activation with its physiologic ligands such as EGF and TGF-a induces the production of CHI3L1 where CHI3L1, in turn, feeds back to stimulate the expression and accumulation of EGF, TGF-a, and EGFR. We also evaluated the effects of TKI inhibitor (gefitinib) on the production of CHI3L1, the effects of anti-CHI3L1 (FRG antibody), and TKI, alone and in combination on tumor progression on therapeutic resistance to TKIs in EGFR mutant NSCLC cells (A549, H1975).

Benjamin Schornstein **Poster #F11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Leigh Hochberg, Engineering

Restoring Upper-Limb Movement with an Integrated iBCI-Soft Robotics System

The BrainGate team and others have previously shown that people with long-standing tetraplegia can use a neural interface to control an anthropomorphic robotic arm for 3D reach and grasp movements. However, individuals with tetraplegia consistently rank restoring movement to their own limb as a priority. Combining intracortical BCI (iBCI) technology with functional electrical stimulation (FES) has been demonstrated for reanimating paralyzed limbs, but while proof of concept demonstrations have been successful, FES can require multiple surgeries and is not suitable for certain patient populations. The recent emergence of wearable soft robotics, coupled with iBCI technology, offers a promising alternative solution that addresses such challenges. Our goal is to design a wearable, textile-based, inflatable soft robotic arm (SRA) that directly restores mobility to the paralyzed arm, with the aim to provide a greater sense of embodiment. We have previously developed a soft robotic glove that enables hand extension, power grip, and precision grip by supplying compressed air to two air-tight bladders for each finger. While we have successfully demonstrated neural control of this glove for grasping movements, it remains unclear whether a neurally controlled soft robotic system can directly restore mobility to the upper arm for 3D reach and grasp movements. Here we present the development of a custom virtual environment to simulate control of an anthropomorphic limb. Using the virtual environment, we characterized information in cortical signals under open loop conditions, where the arm moves towards targets in a 3D workspace and the participant is asked to attempt the observed movements. This virtual research platform enables analysis of neural activity patterns, evaluation of linear and non-linear decoders, and customizable kinematics mimicking constraints of the soft robotic system and residual movements. In parallel, we have also developed a wearable soft exosuit to support shoulder elevation, including its necessary electromechanical control box. The work presented here demonstrates progress towards an iBCI-SRA system that can restore intuitive, flexible, functionally useful upper extremity movement for people with tetraplegia.

Lauren Chiu **Poster #F12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Tom Bartnikas, Pathology and Laboratory Medicine

The role of metal transport proteins in manganese and iron absorption

Manganese is a metal and dietary nutrient essential for multiple biological pathways including antioxidant defense and protein glycosylation. However, manganese levels must be regulated, as both excess and deficiency can be detrimental to health. Manganese excess can be caused by mutations in the Slc30a10 gene. The Slc30a10 protein regulates manganese levels in the body by exporting manganese from liver into bile and from intestinal enterocytes into the gastrointestinal tract. Knocking out intestinal Slc30a10 in mice leads to excess manganese in the body, because these enterocytes lack the transporters to export manganese for excretion. Unexpectedly, mice with whole body or intestinal Slc30a10 deficiency have increased manganese absorption. To identify the proteins responsible for increased manganese absorption, we looked at the transport protein ferroportin. Ferroportin exports iron from enterocytes into

the blood, but it has also been shown to export manganese. In order to upregulate ferroportin, we employed hemojuvelin (Hjv) deficient mice. Hjv is a key regulator of ferroportin expression, because Hjv deficiency leads to low levels of hepcidin, which binds and degrades ferroportin. The goal of this study was to determine how the manganese and iron metabolic pathways interact via ferroportin, which could potentially give insight into targeting conditions of iron or manganese excess or deficiency. In this study, we observed metal levels of mice with whole body Hjv deficiency and intestinal Slc30a10 deficiency. Manganese levels were significantly higher in the livers, brains, and bones of these mice, but iron, copper, and zinc levels were not affected. Our results suggest that ferroportin may be involved with increased manganese absorption in Slc30a10-deficient mice. This study will help us to better understand how the body regulates absorption of essential dietary nutrients.

Monica Ocitti **Poster #F13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Theresa Desrochers, Neuroscience

Using converging methods to classify neurons in monkey lateral prefrontal cortex (LPFC)

The prefrontal cortex (PFC) plays an important role in emotional regulation, and it has two general types of neurons - inhibitory interneurons and excitatory pyramidal neurons. In healthy brains, the functional ratio of excitatory events to inhibitory events remains fairly constant across different brain regions. However, over-inhibition/over-excitation in the PFC disrupts this ratio. This disruption has been linked to several neuropsychiatric disorders, including depression and anxiety.

To evaluate the distribution of excitatory and inhibitory neurons in primates, previous studies have used extracellular action potential (EAP) waveform classification to differentiate cell types. Using this method, researchers have identified that broader waveforms (longer durations) tend to be classed as putative excitatory cells, while narrower waveforms (shorter durations) are classed as putative inhibitory. Additionally, it has been found that at baseline, inhibitory cells (narrower waveforms) tend to have higher spontaneous firing than excitatory cells (broader waveforms). However, other studies have found that some putative excitatory cells share waveform characteristics with putative inhibitory cells and vice-versa; thus, relying purely on this method can lead to the misclassification of cells.

In this project, we will use the relationship between the width of the cell waveform and cell firing rate in conjunction with classic EAP waveform analysis to classify cells more accurately. We hypothesize that inhibitory neurons have narrow waveforms because inhibitory neurons have high firing rates. Based on this hypothesis, we will test our first prediction - a separation of two main cell clusters. One cluster having narrower widths and higher firing rates, and another cluster with broader widths and lower firing rates. Building on this prediction, we will test a second prediction - whether cells with high firing rates or narrow waveforms show quasi-inhibitory connections when looking at their cross-correlograms.

If these predictions are supported, these analyses will give insight into the structural balance between excitatory and inhibitory neurons as well as the functional - how the distribution of different types of excitatory cells and inhibitory cells (fast-spiking vs low-spiking) influence the functional excitatory-inhibitory ratio.

Anne Wang **Poster #F14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Joo-Hyun Song, CLPS; Sean O'Bryan, CLPS

History of motor precision predicts learning in new disrupted environments

Visuomotor learning is crucial to adapting to disruptions in new environments. When learning a new visuomotor mapping, people usually engage two possible strategies: explicit and implicit learning. Explicit learning recruits top-down mental strategies that can be easily switched on. Conversely, implicit learning is gradually refined through trial and error. Previous studies have established that spatial working memory and pupil diameter predict future motor performance. However, the impact of baseline reach precision prior to disruptions has not been studied. Baseline reach accuracy can be measured in both directional bias and absolute error. Therefore, our study investigated how baseline reach error and direction affect future reach accuracy in trials where a disruption is introduced. Furthermore, we examined how baseline reach precision is linked to explicit versus implicit learning strategies. We ran three visuomotor learning tasks where participants were instructed to reach to a target using a touch surface. In the first experiment, the participants were introduced to a novel 45° cursor rotation relative to their hand and had to learn to adjust to the new environment. In Experiment 2, the task was modified to inhibit the implicit learning system by introducing a delay to the endpoint feedback, meaning participants strongly relied on explicit learning. In Experiment 3, the task incorporated clamped feedback to disrupt the explicit learning system, encouraging participants to primarily recruit implicit learning. We found that people with high baseline reach precision were less sensitive to feedback perturbations in Experiments 1 and 3, where the implicit system is employed. Conversely, low baseline reach precision was correlated with greater learning and performance in Experiment 2, where the explicitly learning system is recruited. Furthermore, initial directional biases persisted in all experiments. Therefore, we conclude that people with precise baseline reaches rely more on their implicit motor system than their explicit cognitive system. These conclusions provide important implications for motor rehabilitation, prosthetics adaptation, and sports programs.

Daniel Zhu **Poster #F15**

Home Institution: Brown University

Summer Research Program: Undergraduate Research Assistant, Wands Lab

Faculty Mentor: Jack Wands, Medicine

Investigating Optimal Concentrations of Small Molecule Inhibitor for Targeting Aspartate Beta-Hydroxylase in Hepatocellular Carcinoma

Hepatocellular carcinoma (HCC) is the most common type of primary liver cancer and the second most common cause of cancer mortality worldwide. Aspartate β-hydroxylase (ASPH) is a type II transmembrane protein that plays an important role in the progression of HCC by regulating the tumor microenvironment and metastasis. ASPH has been identified as a promising therapeutic target due to its overexpression in human HCC tumor cells and not in healthy liver cells. Previous studies have demonstrated the effectiveness of small molecule inhibitors (SMI) targeting ASPH. It is therefore important to identify the optimal concentrations of SMI for suppressing excessive cell proliferation in HCC. FOCUS (Friendship of China and United States) cells were utilized for the experiments. The FOCUS cell line originates from a 63-year-old male patient with HCC. It was found to have a stable growth pattern in culture and maintained its malignant properties, making the cell line a useful model for studying HCC. Since the FOCUS cell line expresses ASPH, it is labeled as the wild-type (WT). An ASPH knock-out cell line acts as the negative control. To characterize growth in the ASPH knock-out and wild-type cell lines,

MTT assays, which measure cell viability and proliferation, were used to determine the optimal seeding density for cell growth in both cell lines. Further MTT assays with varying concentrations of SMI are in progress to identify the ideal concentration for inhibiting growth while not being toxic to normal cells. Similar to SMI, doxorubicin is a known therapeutic that disrupts the growth of cancer cells, but its effectiveness is lessened if the cells express ASPH. Therefore it would be interesting to investigate the impact of SMI on doxorubicin effectiveness. Future experiments will use MTT assays to determine how using both SMI and doxorubicin will influence cancer cell growth.

Lewis Nunez **Poster #F16**

Home Institution: Hunter College, CUNY

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Theresa Desrochers, Neuroscience

Investigating Neural Activity Patterns Underlying Abstract Sequences in Humans

Understanding complex patterns in daily life requires the ability to keep track of sequential information. Some types of sequences are “abstract” as they rely on a set of goals rather than the specific content in them. Instead of focusing on the specific items used, the brain must monitor the sequential information by keeping track of steps (e.g., slicing then spreading when making a sandwich). Despite the utility of abstract sequences, our understanding of the neural representations underlying them remains limited. Previous work identified that the rostrolateral prefrontal cortex (RLPFC) is necessary for abstract sequential monitoring in humans during a response task. In monkeys, it was demonstrated that dorsolateral prefrontal cortex (DLPFC) responds to abstract sequential changes during a no-report task. We tested the hypothesis that human RLPFC responds to sequence changes during a no-response abstract sequential task. We predict that neural activity patterns involved in monitoring sequential changes in humans will be similar to those observed in prior studies with monkeys. We conducted fMRI scans on 23 human participants who engaged in a no-report viewing task of abstract sequences that assesses changes in the number and rule of the sequences. Using univariate analyses, we identified brain regions active during certain conditions in the task similar to previous results in monkeys. Then, we employed region of interest (ROI) analyses to identify specific active regions during the task. Ultimately, exploring similarities in the neural mechanisms underlying the monitoring of abstract sequence contributes to broader understanding of how we keep track of sequential information.

Lily Yu **Poster #G1**

Home Institution: Brown University

Summer Research Program: Undergraduate Research Assistant in Tejal Desai's Lab

Faculty Mentor: Tejal Desai, Biomedical Engineering

Optimizing Nanoparticle-Based Gene Delivery System for Cancer Treatment

In the midst of recent research, nanoparticle delivery systems [NPDS] are exhibiting promising results. With the use of targeting ligands, nanoparticles more easily differentiate between cancerous and healthy cells. Additionally, nanoparticle biodistribution is greatly impacted by particle size, meaning that controlling particle size allows us to more precisely target local tumors. As such, NPDS have shown to improve many side effects of chemotherapy. NPDS are also widely applicable as they can deliver a wide variety of both

genes and drugs.
Amongst the many methods used to make polymeric nanoparticles, nanoprecipitation is advantageous due to its relative simplicity and versatility. Furthermore, the synthesized particles have a very small diameter, a well-defined size, and a narrow size distribution.
The nanoprecipitation method we used requires the organic phase to be injected into the aqueous phase while the aqueous phase is stirred on a stir plate. The aqueous phase consists of a surfactant and water solution while the organic phase consists of poly(lactic-co-glycolic acid) [PLGA] polymer dissolved in acetone. Once the organic phase is injected, the nanoparticles instantaneously form with a PLGA core and a surface layer of surfactant. After evaporating off the acetone, the nanoparticles are washed in a centrifugal filter tube [pore size: 300 kDa]. Initially, the filter tubes were placed in a centrifuge 4x60 minutes at 500 xg. Our data shows that washing the particles 2x30 minutes at 2000 xg achieves the same results.

Next, the effect of several factors on particle size were studied. For optimal cell uptake, nanoparticles must be 20-200 nanometers in diameter. Although this figure varies depending on the cell line and other environmental factors, minimal nanoparticle size remains critical to maximize cell uptake. To this end, several variables were tested to determine their effects on nanoparticle size: I) injection method II) syringe placement III) needle size. These findings can help guide and enhance the efficacy of future research carried out on polymeric nanoparticles prepared by the nanoprecipitation method.

Alexa Torres **Poster #G2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kristi Wharton, Molecular & Cell Biology

ALS Models: Can They Be Rescued with The Knockdown of These Genes?

Amyotrophic Lateral Sclerosis (ALS) is a neurodegenerative disease involving the degeneration of upper and lower motor neurons, which causes muscle weakness and eventual paralysis. Mutations in Fused in Sarcoma (FUS) and TAR DNA-binding Protein 43 (TDP-43) play major roles in those who have been diagnosed with familial ALS. Previous research identified DEAD-box RNA helicase belle (DDX3/bel) as a component of Stress Granules (SG), which are cytoplasmic structures that sequester RNAs and proteins during times of cellular stress. An increase in SGs has been associated with neurodegeneration. This project delves into the role bel plays in ALS neurodegeneration using two models of ALS in Drosophila melanogaster: 1) rough eyes result when human genes FUS or TDP43 genes carrying ALS patient mutations are expressed in the photoreceptor neurons using GMR-Gal4; and 2) the adult fly exhibits a shortened lifespan when a hTDP43 mutation is expressed in motor neurons (OK371-Gal4) beginning in adulthood. I used bel RNA interference (RNAi) to test if reducing bel levels modifies these Drosophila models of ALS. In addition to testing the knockdown of bel, I tested the knockdown of two other genes, a transcription factor encoded by Mothers against dpp (Mad), and Gustavus (Gus) in motor neurons for their effect on lifespan. Results from the GMR>FUSR521C and GMR>TDP43M337V eye degeneration assay indicate that the knockdown of bel dramatically rescued loss of pigmentation and ommatidial organization in the male and female models of FUS. bel knockdown also clearly rescued the TDP-43 model in males, while partially rescuing the female model. Analysis of this data may contribute to uncovering future gene therapy methods for ALS, as well as broadening the understanding of the roles of specific pathways in neurodegenerative diseases, respective to sex.

Austin Jacobson **Poster #G3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kristi Wharton, MCB

Investigation into Dph4 knockdown as a dominant modifier of TDP-43 and FUS familial-ALS phenotypes in Drosophila Melanogaster

Amyotrophic Lateral Sclerosis (ALS) is a progressive neurodegenerative disease characterized by motor neuron dysfunction and muscle atrophy. The disease is usually fatal within the first 3-5 years of patient diagnosis. ALS is also highly genetically diverse; among genes most commonly associated with the disease are TAR DNA Binding Protein (TDP-43), Fused in Sarcoma (FUS), and Chromosome 9 open reading frame 72 (C9orf72). Historically, the use of genetic screens has been used to delineate the effects of dominant modifiers on the phenotypes associated with ALS. By developing an adult onset motor neuron-specific model of human C9orf72-ALS characterized by hexanucleotide expansion (G4C2)49, a screen of 371 deficiency lines conducted by the Wharton lab successfully identified a handful of candidate suppressor genes for their ability to modify the lifespan defect phenotype found in C9-ALS. While many deficiencies have been shown to suppress the lifespan defects found in the model, most target genes within each deficiency have yet to be tested individually.
My research focuses on a target gene uncovered by the overlap of several chromosomal deficiencies that exhibited strong suppression of the C9-ALS model in our screen: Dph4. We assessed its ability to suppress the lifespan and eye degeneration phenotypes found in other fALS Drosophila models by using gene-specific knockdown via RNAi interference and insertions. Initial results reveal a significant suppression of the TDP-43 ALS lifespan phenotype after knockdown of Dph4 using an RNAi. I also investigated two other candidate suppressor genes identified in the screen, Tudor-SN and Sax, in order to better understand their modification of the lifespan phenotype. The mechanism by which Dph4 knockdown modifies TDP-43 ALS is poorly understood. As a next step, I plan to use immunohistochemistry in order to identify the relationship between Dph4 knockdown and apoptosis. Furthermore, I will use qPCR to quantify the changes in expression of genes involved in the Dph4 pathway. These assays will provide insight into the mechanistic role of Dph4 in ALS pathogenesis.

Smriti Vaidyanathan **Poster #G4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Erica Larschan, Dept of Molecular Biology, Cell Biology & Biochemistry

The Effect of CLAMP on the Dynamics of RNA-Binding Protein Condensates in Drosophila

RNA splicing is a vital process in gene regulation, particularly in sex-based genetic differentiation. Studying the underlying mechanisms of splicing can help us understand gene expression regulation between biological sexes, which is especially important during the highly conserved process of zygotic gene activation (ZGA). In this research, we explore the mechanisms that drive ZGA using the well-established Drosophila model. We identified CLAMP (chromatin-linked adaptor for male-specific lethal proteins) as a pioneer factor that plays a targeted, essential role in Drosophila ZGA. We hypothesize that CLAMP regulates splicing function via interactions with RNA binding proteins (RBPs) in spliceosomes. To test our hypothesis, we employed motif analysis of CLAMP binding sites through iCLIP

data, and identified two RBPs known to play essential roles in splicing—MLE and Hrp38—with target motifs within CLAMP-bound RNA. To investigate the influence of CLAMP on the dynamics of MLE and Hrp38 in males and females, we incorporated CLAMP mutant and wild-type male and female tissue culture models in our research, and used fluorescence microscopy and live-cell imaging techniques on third instar Drosophila larvae. From there, we obtained a series of comprehensive movies of the MLE and Hrp38 fluorescently tagged nuclear condensates. Subsequently, we developed a robust pipeline of image processing and correction, particle detection, tracking, and data analysis to quantitatively analyze the behavior of nuclear condensates under different conditions. Our preliminary results suggest distinct differences in the dynamics of MLE and Hrp38 nuclear condensates between CLAMP mutants and wild-type, as well as between female and male samples. To facilitate accessibility and utility, we aim to scale up the developed pipeline to run efficiently on Brown University's research computer cluster. In conclusion, by combining live-cell imaging and computational analysis, we gain a deeper understanding of the dynamics of RNA-binding proteins and their significance in gene regulation, offering potential avenues for future research in splicing mechanisms.

Alexander Gonzalez **Poster #G5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Alison DeLong, Molecular Biology, Cell Biology & Biochemistry

Hot Topic: Does Protein Phosphatase 2A Regulate Leaf Expansion Under Heat Stress?

The protein phosphatase 2A (PP2A) holoenzyme is a conserved regulatory hub that controls the phosphorylation status and activities of key cellular players in eukaryotes. The PP2A complex holds a scaffolding subunit (A), a regulatory subunit (B), and a catalytic subunit (C) bound together. The DeLong laboratory has found that a set of regulatory B subunits belonging to the B72 gene family controls leaf expansion in Arabidopsis thaliana. To learn more about the mechanism[s] through which PP2A contributes to leaf morphology, I conducted bioinformatic analysis on a list of differentially expressed genes (DEGs) identified in an RNAseq experiment that analyzed gene expression in developing leaves of b13, b1617-1, and b72-1 mutant plants. Using tools such as GO and Panther, I found DEGs that are upregulated and downregulated, as well as their biological and molecular function. Earlier experiments showed that b72 mutants exhibited a large leaf phenotype, demonstrating a connection between leaf expansion and the B72 subunit. A separate study found that Arabidopsis grown at higher temperatures exhibited decreased leaf area. Regulation of leaf expansion is an important agricultural trait in crop and seed yield. Furthermore, given the current rise in temperature in the world, understanding the connection between PP2A and heat stress responses in leaves is essential. Heat stress experiments will provide insight into PP2A’s potential significance in the temperature response in Arabidopsis leaves, and the bioinformatics analysis will give insight into mechanisms that control leaf expansion.

Liana Haigis **Poster #G6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Elizabeth Harrington, Medicine; Amy Princiotto, Research Staff

Investigating the Role of Inflammatory Extracellular Vesicles in Settings of Respiratory Distress

Traumatic injury is one of the leading causes of death for all age groups in the United States. The development of sepsis, acute respiratory distress syndrome (ARDS), and systemic inflammatory response all contribute to mortality among patients hospitalized for traumatic injury. These comorbidities often result in increased permeability of lung vasculature and subsequent pulmonary edema. Although pulmonary edema is a widely prevalent and severe condition, there remain few specific diagnostic or treatment methodologies. Extracellular vesicles (EVs) are small molecules derived from cell membranes that contain a variety of cargo, including proteins, DNA, and RNA, which are released and can be taken up by other cells. Trauma and sepsis have been shown to cause the release of EVs, as well as a variety of other pro-inflammatory molecules, which in turn can damage the lung endothelium and cause pulmonary edema. Previous work in the lab has demonstrated that EVs released by damaged lung endothelium (referred to as inflammatory EVs, or iEVs) affect naive endothelial cell (EC) barrier function and angiogenesis. In the current study, we further assessed the effect of the iEVs on naive EC function. EVs were collected from the media of EC monolayers that had been exposed to 1ug/ml lipopolysaccharide (iEVs) or PBS (vEVs) for 24h by centrifugation. The EVs were subsequently used on naive EC to assay migration and adhesion. Cell migration was assessed in human pulmonary microvascular ECs (HPMECs) treated with EVs by creating a scratch in a confluent cell monolayer, then quantifying the rate at which the ECs moved to fill in the wound in comparison to controls. Cell adhesion was assessed in HPMECs treated with EVs by allowing the cells to adhere to a plate for several hours, then quantifying the number of cells that successfully adhered to the surface in comparison to controls. These studies may lead to the identification of EVs as potential biomarkers and/or therapeutic targets.

Ainsley Bonin **Poster #G7**

Home Institution: Colby College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Amitai Shenhav, Cognitive, Linguistic, and Psychological Sciences

Expected Reward Modulates the Costs Associated with Adjustments of Cognitive Control

Cognitive control processes determine which information we process and how we process it. Adjustments in control are critical for adaptive behavior in changing environments, but they come at a cost. Recent work shows that performance on a control demanding task is impaired when participants have to frequently adjust their performance goals (e.g., perform accurately vs. fast). Goal switches demand adjustments in two control signals: processing efficiency (e.g., attention) and response caution, and these adjustments are costly. However, previous work on adjustment costs has not yet investigated whether they can be modulated by reward. In this project, we investigated whether the cost of adjusting control signals is increased in situations in which people are reinforced to implement those signals. To do this, we had 51 participants perform a Stroop task under two performance goals: accuracy or speed. We studied adjustment costs by comparing blocks that require control adjustments (e.g., adjusting from the speed to the accuracy goal) to blocks that did not. In addition, we modulated the expected reward (high vs. low) for performing under each of the two goals. Across blocks, participants could earn extra points for making more responses (speed) or more correct responses (accuracy). Our behavioral results replicated the finding that behavioral performance is changed when comparing varying to fixed blocks. In both reaction times and accuracy, the difference between speed and accuracy conditions was reduced in varying compared to fixed blocks. This finding suggests that there are control adjustment costs in situations in which people have to frequently adjust control signals. Further, our results show that these adjustment

costs are amplified when people are more incentivized to achieve each of the two performance goals. These findings provide preliminary evidence that rewards associated with performance goals modulate the costs associated with moving away from the current cognitive control state.

Kaleb Zuckerman **Poster #G8**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jeff Bailey, Pathology, laboratory medicine

Selective whole genome amplification for improved malaria and pathogen sequencing

Malaria remains one of the most life-threatening infectious diseases worldwide, yet efforts to decrease mortality in recent years have stalled due to the rapid development of drug and insecticide resistance in the parasite. Close monitoring of antimalarial drug's resistance is key to informing control strategies, but isolating the malaria genome from blood samples for study or testing is extremely challenging due to the low parasitemia in many cases and the small size of the malaria genome compared to the human. Selective whole genome amplification (sWGA) could be the cost effective and efficient method needed to isolate the malarial genome for study and testing, using a pool of primers that target the malarial genome while "ignoring" the human. A new software was designed that improved on two older versions of sWGA pipelines, picking out common motifs in a provided target genome and ensuring that those kmers would effectively cover the target genome, returning a final primer pool that would selectively amplify the target. The software has proven to be very effective for Plasmodium Falciparum, giving nearly 98% of reads mapping to malaria when amplifying from a dried blood spot (DBS) with 80% 1x coverage of the genome and a mean coverage of 6x. This outperforms the previous softwares and the currently accepted primer pool for P. Falciparum by a large margin, and is very promising for a cost-effective and more efficient way to isolate and test for the malaria genome. In addition this pipeline could be extended to test for other diseases that reside in the blood as well.

Chandler Zhu **Poster #G9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Peng Zhang, Department of Medicine

Using HyPer7 to study Mitochondrial Morphology and Oxidative Stress in Adult Rat Cardiac Fibroblasts

Background: Cardiac fibroblasts activate myofibroblasts in response to injury. Persistent existence of myofibroblasts in myocardium often leads to myocardial fibrosis and cardiac dysfunction. Mitochondria are important organelles in all kinds of cells, including fibroblasts. A few studies suggest that fibroblast activation and fibrosis are associated with increased mitochondrial fragmentation and altered oxidative stress in fibroblasts, but the mechanisms remain unclear. One of the reasons is due to lack of sensitive approaches to measure mitochondrial morphology and reactive oxygen species (ROS) levels in live cells and in a real-time manner. Recently, HyPer7 was developed as a novel mitochondrial-targeted ultrasensitive, ultrafast, and pH-stable ratiometric biosensor. The goal of this study is to determine whether HyPer7 can be used as a novel biosensor to study mitochondrial morphology and oxidative

stress in adult rat cardiac fibroblasts (ARCF).
Methods: ARCF were isolated from adult SD rats and passage 1 ARCF were used for the experiments. After starving overnight, ARCF were treated with or without transforming growth factor-β (TGF-β, a well-known profibrotic agonist) for 48 hours together with HyPer7 expression via adenoviral vectors. Mitochondrial morphology and ROS were then recorded using confocal microscopy with Z-Stack and ratiometric fluorescence, respectively. For mitochondrial morphology, aspect ratio (AR) and form factor (FF) were measured. Minimum and maximum ROS values were determined by sequentially adding dithiothreitol and hydrogen peroxide. ImageJ was used to analyze the data.
Results: TGF-β treatment activated ARCF in culture, suggested by increased α-smooth muscle actin expression and collagen production. TGF-β treatment leads to smaller mitochondria in comparison to untreated ARCF (Treated vs. untreated; AR: 2.04±0.94 vs. 2.37±1.2, $p<0.01$; FF: 1.65±0.96 vs. 2.29±2.2, $p<0.01$; Area: 0.0023±0.0019 vs. 0.0039±0.0047 , $p<0.01$). Basal ROS is also significantly higher in TGF-β-treated cells compared to control (11.8% vs. 2.27%, $p<0.01$).
Conclusions: Our findings show that TGF-β-induced fibroblast activation is associated with significant mitochondrial fragmentation and increased in ARCF. HyPer7 can serve as a sensitive biosensor to assess the alterations of mitochondrial morphology and oxidative stress in ARCF. This study forms the foundation for us to subsequently delineate the mechanisms underlying mitochondrial dysfunction in ARCF.

Wyatt Ploot **Poster #G10**

Home Institution: University of Montana

Summer Research Program: Visiting scholar

Faculty Mentor: Karla Kaun, Neuroscience

Visualizing Glutamate Response in Dual-transmission Target Neurons Utilizing Two-photon Microscopy

Dual neurotransmission, the release of more than one small-molecule, neuromodulator, or neuropeptide transmitter from a single neuron, has the potential to transform our understanding of how neurons, circuits, and networks transmit and compute information. Throughout the nervous system, examples of neurotransmitter colocalization are growing, indicating this is an important fundamental mechanism by which a significant number of neurons communicate. Understanding whether neurons use their “bilingual” ability to transmit information with one neurotransmitter to a downstream target or both neurotransmitters is a critical question to understanding network and brain function. In the powerful genetic model *Drosophila melanogaster*, the Mushroom Body Output Neuron 11 (MBON11) is a major postsynaptic target of the glutamate and octopamine (OA) releasing neuron Ventral Paired Medial 4 (VPM4). Increased OA or glutamate signaling from VPM4 results in high intensity male aggression including boxing and wrestling[1]. Manipulating MBON11 activity including changing GABA release also increases male aggression. The goal of this project is to understand if both OA and glutamate signaling to MBON11 are required to regulate aggression circuity output. To verify if MBON11 is capable of receiving glutamatergic input, the Gal4-UAS gene driving system was used to express the intensity-based glutamate sensing fluorescent reporter (iGluSnFR) in MBON11. iGluSnFR is a GFP based glutamate sensor with high spatial and temporal resolution. Two-photon microscopy was utilized to image glutamate responsivity in dendritic arborizations of MBON11. In vivo imaging verifies that MBON11 receives glutamatergic input and provides promising preliminary results for further functional imaging of this neuronal pathway.

Zane Darden **Poster #G11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mark Johnson, Department of Molecular, Cellular Biology, and Biochemistry

Promoting Pollen Persistence: Is HSP101 necessary and sufficient to confer thermotolerant pollen tube growth Tomato?

As the human population and global temperatures continue to increase, the threat of food shortages has reached historic highs due to the negative effects of high temperatures on crop sexual reproduction. Plant reproduction starts with pollen landing on the stigma, forming a pollen tube that extends toward and then fertilizes the ovary, which develops to yield fruit and seeds. Pollen function has been identified as a particularly vulnerable aspect of crop productivity, as heat stress can easily induce male sterility, leading to low fertilization rates and fruit yield due to the pollen's reduced fitness at high temperature. Heat shock proteins (HSPs) are a class of proteins that function to mitigate this temperature stress, employing a variety of cellular mechanisms to buffer the effects of heat stress on the molecular level. Through RNA sequencing of heat-stressed pollen tubes from various tomato cultivars, we have identified a particular heat stress protein (HSP101) as being the first to act and significantly overexpressed at elevated temperatures in thermotolerant lines. While HSP101 has been identified as a protein refolding chaperone and a signaling protein for protein degradation in other tissues, its role in pollen function under heat stress remains largely unexplored. In our research, we aim to investigate the significance of HSP101 in pollen function under elevated temperatures by 1) testing if HSP101 is essential for pollen function in high-temperature conditions, 2) if HSP101 is sufficient to confer thermotolerance to thermosensitive pollen tubes, and 3) monitoring the abundance and localization of HSP101 change in response to heat stress in growing pollen tubes. Utilizing Golden Braid and Green Gate cloning strategies, we have designed a transgenic approach to reach each goal: 1) a CRISPR-CAS9-mediated HSP101 knockout, 2) an HSP101 overexpression line, and 3) HSP101-GFP fusion. We seek to understand HSP101's activity, signaling pathways, and effects on pollen tube resilience in thermotolerant cultivars to contribute to efforts to generate crop varieties that continue to produce fruit at high temperatures.

Sacha Sides **Poster #G12**

Home Institution: University of Florida

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Elizabeth Brainerd, Ecology, Evolution and Organismal Biology

New Developments in Micro-XROMM to Assess Mastication in Mice

X-ray Reconstruction of Moving Morphology (XROMM) uses marker-based X-ray motion tracking combined with CT reconstruction to visualize in-vivo skeletal motion in 3-Dimensional space. XROMM's utility has been limited primarily by size, with smaller animals requiring increasingly specific accommodations to achieve high-quality imaging during fluoroscopic capture. These size constraints present challenges both on the technological side— with smaller animals necessitating a micro-fluoroscopy machine to allow image and light amplification without sacrificing resolution— and also on the methodological side of requiring minimally-invasive microsurgical implantations of trackable, radio-opaque tantalum marker beads in fixed landmarks.

We describe the development of the first microXROMM study and its early application in analyzing hemimandibular kinematics during mastication in Mus musculus. Modern evolutionary theory suggests that much of mammal diversity can be attributed to early adaptive radiation of rodents, making mice a model organism for studying mammalian evolution. Mouse cranial morphology prevents simultaneous incisal and molar occlusion, resulting in a bimodal system of food acquisition and propalinal mastication that has been difficult to quantify biomechanically. We explored this system by implanting 0.25 mm tantalum markers in the cranium and hemimandibles of mice, and utilized the videofluoroscopy machines in the Keck Research Laboratory to record quantifiable biomechanical data with a minimally invasive setup. This reveals micro-movements of small animals that previously had to be measured by proxy. This project reports defined steps in new microXROMM protocols that can be applied across taxa, overcoming a limit that has prevented the progression of in-vivo kinematic assessments in smaller organisms.

Camille Donoho **Poster #G13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Alexander Fleischmann, Neuroscience; Jason Ritt, Neuroscience

A novel task exploring olfactory-spatial association in the lateral entorhinal cortex of freely-moving mice

Recalling past sensory information is critical in generating and navigating cognitive maps of the external world. The lateral entorhinal cortex (LEC) likely acts as a neural substrate for sensory-spatial associative activity due to significant connectivity with the hippocampus and sensory cortices. Likewise, we seek to identify neuronal populations in LEC that encode spatial, olfactory, and odor-spatial conjunctive information.
We use Inscopix mini-endoscopes to record fluorescence in the LEC of freely moving mice during a complex behavioral task consisting of both allocentric and egocentric spatial contexts. To set up the dual condition system, we employ a diamond arena split down the middle by a transparent wall. The mouse initially learns to navigate to a cue port on the active side and receive a reward at a spatially dissociated reward port dependent on odor identity dispensed at the cue port. After the mouse has learned the initial task, the mouse completes the task on the other side of the wall using one of two randomly assigned decision policies: egocentric, a “Go-Left, Go-Right” task that mirrors that of the initial task, or allocentric, a “Go-East, Go-West” task that preserves the odor-space association in absolute space. Preliminary results suggest that mice can successfully perform the egocentric version of the task. Ongoing work aims to integrate calcium imaging data with videographic pose estimation analyses to effectively combine spatial information with odor and neural data.

Colm Ryan **Poster #G14**

Home Institution: Trinity College Dublin, Ireland

Summer Research Program: J1 International Research Exchange

Faculty Mentor: Emilia Huerta-Sanchez, Department of Ecology, Evolution and Organismal Biology

Remnants of Ancient Human DNA: Neanderthal and Denisovan Introgression in Modern Functional Genes

Archaeological and genetic data shows that anatomically modern humans (AMH) and other extinct hominin, such as Neanderthals and Denisovans, interbred intermittently after their separation into subspecies. As a result, tracts of ancient DNA survive from this introgression in AMH, particularly in non-African populations. Surviving tracts vary between selection-neutral DNA sequences, evolving neutrally with negligible impact on fitness; and selection-positive DNA sequences, which provide some advantage over their AMH homologues and are positively selected for. Selection-negative DNA is quickly purged from the genome, and is assumed to not have survived to modern populations.

However, much remains unknown about these introgressed tracts: for example, which are undergoing neutral evolution, and what advantage is given by those undergoing positive selection. Functional genes, which usually undergo strong negative-selection during introgression, provides a great place to search for outlier genes which have been positively selected for. Hence, this exploratory research project compares functional genes from participants in the 1000 Genomes Project with their homologues in reconstructed genomes of the Altai Mountain Neanderthal, Vindija Cave Neanderthal, and Denisovan genomes. The comparison is performed via a combination of Python coding in Jupyter Notebook, and the use of the supercomputer Oscar.

The aim is to identify candidate genes which show signs of strong positive selection in either the general population, specific superpopulations or populations, or in a sex-specific population. Genes which show no introgression whatsoever (in “introgression deserts”) have also been identified in this research project. These candidate genes can then serve as the launching point for future research into the potential reasons for each one’s positive or negative selection.

Anusha Srinivasan **Poster #G15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Elizabeth Chen, Brown Center for Biomedical Informatics

Characterizing Pediatric Anxiety and Depression in the All of Us Research Program

The All of Us Research Program is dedicated to collecting electronic health records, surveys, and biosamples data representing the diversity of the US population, with particular focus on recruiting participants from groups typically underrepresented in biomedical research. It is important to understand how data from the program has been used in order to use the database most effectively in the future. A literature review was conducted to understand what populations have been studied using the All of Us Researcher Workbench, what methodologies have been used, and what gaps may exist to inform future studies. The review identified 106 articles in PubMed published between 2021 and 2023, which analyzed All of Us data. These studies covered a wide range of topics, including dermatological conditions, stroke, glaucoma, and other conditions. Certain studies also focused on particular sociodemographic groups such as Black and Hispanic patients or disparities between groups, while others sought to identify comorbidities for particular conditions. The literature review revealed that despite the increasing prevalence of pediatric anxiety and depression, the All of Us Research Program has not yet been used to characterize this population. Studies have shown that racial and gender minorities may be at increased risk for these mental health disorders. Therefore, data from All of Us could help with better understanding which groups are most at risk for developing anxiety or depression and what comorbidities may be associated with these conditions. As part of a preliminary study, demographics and comorbidities for pediatric anxiety and depression are being analyzed using the All of Us Researcher Workbench. The prevalence of anxiety and depression in the pediatric population will be calculated and odds ratios will be used to assess relative risk by gender and race. All of Us data will also be used to identify comorbidities.

Overall, the findings from this study have the potential to advance our understanding of pediatric anxiety and depression within underrepresented populations, providing insight to inform targeted interventions and improve healthcare outcomes.

Anel Zhussubali **Poster #G16**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Joo-Hyun Song, CLPS

Dual-task interference enhances implicit learning in visuomotor adaptation

Prior research in sensorimotor learning has established a relationship between spatial working memory capacity (WMc) and visuomotor adaptation (VMA), which is the ability of individuals to adjust their sensory input-output mappings to an unexpected change in the environment. VMA typically involves both explicit and implicit learning processes: explicit learning is intentional learning that involves top-down control and strategies, such as working memory, while implicit learning occurs without a conscious awareness of learning and relies on motor error feedback mechanisms.The relationship between spatial WMc and VMA prompted us to design a dual (simultaneous) task, where a visuomotor rotation task is introduced in the delay phase of a spatial working memory task. Participants were asked to memorize a display of dots, and following a 45-degree rotated reach movement towards the target, make a memory response. We hypothesized that visuomotor rotation would draw upon similar explicit cognitive resources to the WMc task, and may compel participants to rely more on implicit learning for the visuomotor transformation. Our results supported this hypothesis. We found that reach error continued to decrease throughout early and late learning trials, instead of decreasing in early learning and then plateauing in late learning as was observed in our previous study. We also observed a greater reach aftereffect associated with the WMc dual task – participants had difficulty re-adapting to no rotation in the washout phase of the reach task, which more strongly suggests the presence of implicit learning. Our results suggest that spatial working memory capacity may demand cognitive control resources that interfere with explicit elements in visuomotor adaptation, leading to higher involvement of implicit learning and improved performance in visuomotor adaptation tasks. Therefore, participants can adapt to high cognitive demand interference by increasing their dependence on the implicit learning system.

Lisa Duan **Poster #H1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Wael Asaad, Neuroscience

Categorization of Emotionally Ambiguous Faces

The ability to process ambiguous facial affect is crucial for complex social interactions. Previous research has identified brain regions, such as the fusiform gyrus and amygdala, where facial expression is encoded. However, the behavioral patterns and neurophysiological signals underlying the categorization of emotionally ambiguous faces are not well understood. While studies have employed two-alternative forced-choice tasks (i.e., participants are shown an ambiguous face and must choose either "Happy" or "Sad"), PCA analyses have shown that emotions are not encoded in a binary fashion. To address this gap, we designed a novel task where participants use a joystick to place faces in a 2D parametric space,

with axes representing the happy-sad and angry-afraid morphs. These faces were either unambiguous (unambiguously happy, fearful, sad, angry, and neutral) or graded morphs (i.e. 20% happy/sad 80% angry) between the pairs specified above. Results indicate that participants rate anger and happiness more accurately than fear and sadness at all morph percentages. Additionally, anger and happiness are consistently perceived to be more intense than fear and sadness even if the morph percentage is the same, measured by a joystick selection farther out from the theoretical midpoint. Notably, when the expression is maximally ambiguous (50% one emotion/50% another emotion), categorization accuracy significantly decreases and reaction time is longer compared to both neutral and less ambiguous conditions. These findings may help elucidate the best locations for stimulation therapy, which aim to bias one's emotional perception towards a more positive valence in mood disorders such as depression. Concurrent sEEG studies in neurosurgical patients will characterize how emotional-decision making is reflected in neuronal firing patterns.

Henry Zheng **Poster #H2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ruth Colwill, CLPS

Zebrafish Larvae as a Model for Behavioral Abnormalities Induced by Anthropogenic Pollutants

Many anthropogenic pollutants are under scrutiny due to potential links to clinical disorders. Zebrafish (Danio rerio) are an increasingly popular model animal for studying the effects of these substances on learning and behavior, in part due to close parallels between the genomes of zebrafish and humans. In this study, we investigate the impact of microplastics (MPs) on zebrafish locomotor behavior. MPs are small plastic particles that are typically characterized as between 1 μm and 5 mm in length. MPs have recently generated concerns due to their ubiquitous presence in the biosphere, especially aquatic ecosystems, and their potential to accumulate in tissues of living organisms. In our experiment, wild-type zebrafish embryos were exposed to polystyrene MPs of 1 μm in diameter at sublethal concentrations of 100 μg/L and 1000 μg/L. It has been demonstrated that zebrafish larvae ingest MPs of this size, which subsequently can enter tissue. At 120 hrs post fertilization, the zebrafish larvae were rinsed and then evaluated using the alternating light-dark assay. In this assay, the larvae underwent 10 min in light conditions followed by 10 min in dark conditions continuously for 3 light-dark cycles. Total distance moved by the larvae was tracked in 1 sec time blocks using the Zantiks MWP system. Control larvae typically exhibited higher locomotion in the dark compared to the light, and notable startle responses were observed between transitions from light to dark. It was hypothesized that MPs would impede neurotransmission by inhibiting breakdown of acetylcholine, leading to decreased sensitivity in response to changes in brightness. Preliminary results indicated potential suppression of activity in dark conditions with exposure to MPs. These findings would warrant further investigation into potential neurotoxic effects induced by MPs, especially since the mechanisms governing these effects are largely unknown. In addition, synergistic toxicity between MPs and other environmental pollutants should be considered to better understand how MPs act as an interface for adsorption. Temperature manipulations can potentially illustrate the trend of ocean warming and the impact this has on aquatic wildlife.

Liam O'Connor **Poster #H3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Carlos Vargas-Irwin, Neuroscience

Using Deep Learning to Predict Neuronal Activity in Primate Motor Cortex

We aim to examine how information is represented in the motor cortex of primates. An adult rhesus macaque was trained to perform a cued grasping task for juice rewards. The task consisted of grasping and pulling objects affording either a power or pinch grip. The objects were presented at four different spatial positions and two orientations (horizontal or vertical). The experimental layout, trial, and holds were recorded by the apparatus. 87 individual M1 neurons were also recorded using a chronically implanted multielectrode array. Five video streams were recorded from different angles, including eye tracking, and were synched with the neural and task data. DeepLabCut (DLC) was used to approximate three-dimensional (kinematic) joint positions. These data were then analyzed using various regression models (linear regression, multi-layer perceptron (MLP), convolutional neural network (CNN)) to predict smoothed single unit firing rates and trained on various input features, namely kinematic tracking, raw video data, combined kinematic and video data, movement directions, and speeds. Greater performance on the combined video and kinematic data than just kinematic tracking indicates the presence of contextual information encoded in motor cortex in addition to information directly related to movement output. The varied performance of individual neurons under restricted input conditions suggests the relevance of different features of the input space to different neurons.

Julien Song **Poster #H4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jeremy Warner, Medicine; Sanjay Mishra, Medicine

Determining the Representativeness of COVID-19 & Cancer Consortium (CCC19) Participating Institutions Across the United States of America

The COVID-19 and Cancer Consortium (CCC19) is a voluntary collective of cancer centers in North America that compile, analyze, and disseminate data on cancer patients who have been diagnosed with COVID-19. Many of these centers have been acknowledged by the National Cancer Institute (NCI) for distinguished research efforts in cancer prevention, diagnosis and treatment. This project aims to superimpose the geographical distribution of CCC19 participating institutions with the incidence rates of cancer and COVID-19 cases within each state. Due to HIPAA restrictions, patient residence is captured only at the state level. The project also strives to portray catchment areas for the average driving time and population of patients served at each participating institution.

All CCC19 participating institutions are listed on the CCC19 website. Incidence data has been collected from the Centers for Disease Control and Prevention (CDC)'s public datasets. The cancer incidence rates per state represent the average number of reported cases per 100,000 people as of the year 2020, while those for COVID-19 do so for data as of June, 2023. Catchment data was computed using the service area calculator of ArcGIS, with driving times calculated in durations of 0 to 30, 15 to 30, and 60 to 120 minutes. Site addresses were geocoded using the SUNGEO wrapper for OpenStreetMap's API. Catchment populations were determined via 2020 decennial census tract data through the TidyCensus R package. The final map was rendered in RStudio using the Leaflet R package.

It can be inferred that CCC19 site locations are generally representative of the distribution of cancer and COVID-19 incidence, although some high incidence states are not represented. CCC19 sites tend to be more frequent in areas with higher COVID-19 case rates. The map is also predictive of the correlation that catchment areas are greater in size, population, and driving time for areas with higher densities of NCI-designated sites. Once finalized, The map is to be made publicly available through its integration into a CCC19 Shiny Web App, which would enable users–both healthcare staff and the general public–to interact with the map through a web browser and view customized results.

Elaine Wang **Poster #H5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jeremy Warner, Center for Cancer Bioinformatics and Data Science

Cancer Center Catchment Analysis: A Geographic Information System (GIS) Shiny App with Advanced Backend and User-Friendly Web Interface

HemOnc.org is a website that provides medical information and resources related to Hematology-Oncology, which is the branch of medicine that deals with the diagnosis and treatment of blood disorders and cancers. The website is designed to be a valuable resource for healthcare professionals, including physicians, oncologists, hematologists, nurses, medical students, and patients seeking information about various hematological and oncological conditions. The primary objective is to allow providers to refer to the primary literature quickly, review notes from themselves and their peers, and share useful resources. HemOnc.org offers a wide range of content, including clinical guidelines, research articles, case studies, drug information, and educational materials. It aims to keep healthcare professionals updated with the latest advancements, treatment options, and best practices in the field.

Determining the catchment areas of cancer centers is crucial for healthcare planning and accessibility. To address this need, we present a Geographic Information System (GIS) Shiny App that leverages backend technology and offers an intuitive web-based user interface. The catchment areas are calculated using ArcGIS, and the catchment area populations were determined using the 2020 decennial census data and the tidy-census R package. The app enables users to efficiently assess travel times that are variable by region and time of day to nearby cancer centers, facilitating better resource allocation and patient care. Our backend algorithms incorporate sophisticated routing and distance calculations, ensuring accurate and real-time results. The user-friendly web interface allows for seamless data input, dynamic visualization of catchment areas, and interactive exploration of results. This novel GIS Shiny App aims to empower healthcare professionals and policymakers in making informed decisions to enhance cancer care accessibility nationwide.

Ofubofu Cairns **Poster #H6**

Home Institution: Swarthmore College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Thomas Roberts, Ecology, Evolution and Organismal Biology

Leg Jiggling - A Model For Understanding Biological Spring-Mass Systems

Cyclic motion is a recurring theme across diverse biological movements. Some cyclic motions utilize elastic structures to drive motion, such as tendons, and are governed by the physical rules of spring-mass systems. A simple biological model could be beneficial for understanding how these physical and physiological principles interact. We used leg jiggling as our model, investigating its rhythmicity with force and displacement transducers. Preliminary data show that individuals exhibit consistent preferred leg jiggling frequencies. When tasked with changing their leg jiggling frequencies, individuals successfully jiggled at frequencies lower and higher than their baseline but were unable to move at intermediate frequencies closer to their preferred frequency. Leg jiggling frequency also increased with mass which could be the result of increased leg stiffness. Through this work, leg jiggling has shown itself to be an effective and efficient model for understanding more complex physical and physiological interactions in biological cyclic motion.

Zain Peerbhoy **Poster #H7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Carlos Aizenman, Neuroscience

EFFECTS OF AMPA ANTAGONISTS ON XENOPUS TADPOLE MOTILITY AND ANALYSIS OF RECOVERY TIMES

The following study aimed to determine the effect of three different AMPA antagonists- GYKI, Philanthrotoxin (PHTX) and N-Acetylspermine (NASPM) on xenopus motility. Furthermore it aimed to ascertain if there was a presynaptic homeostatic mechanism at play to compensate for AMPA receptor blockage. Prior research has showed levels of synaptic input change during development and with changes in the sensory environment. Homeostatic plasticity serves as an adaptive response to keep sensory processing within a specific dynamic range. Whilst longer term, postsynaptic homeostatic adaptation has been observed occurring after days of sensory alteration this project aimed to ascertain if there was a quicker homeostatic plasticity which may occur via presynaptic changes. The study showed that GYKI decreased swimming motility and led to no recovery in swimming behaviour. Whereas the NASPM and PHTX showed an increased response to startle stimuli, higher swimming motility and signs of recovery. Overall, the data Indicated increased motility when NASPM and PHTX AMPA antagonists were used thus indicating there may be homeostatic presynaptic plasticity mechanisms in place to compensate for AMPA receptor blockage.

Adriana Ramirez Marrero **Poster #H8**

Home Institution: University of Puerto Rico at Cayey

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Alfred Ayala, Division of Surgical Research; Chyna Gray, Division of Surgical Research

Immune checkpoint protein, VISTA, regulates neutrophil abundance in murine sepsis

Sepsis is a “life-threatening organ failure caused by the dysregulated host response to an infection”. It affects 1.7 million adults annually, is responsible for 35% of in-hospital deaths, and costs over $24 billion in treatment. Neutrophils are a type of leukocyte that help fight infection. They can engulf pathogens and release neutrophil extracellular traps to kill them. During sepsis, their ability to fight infection may be

impaired and contribute to sepsis pathology. Immune checkpoint protein, V-domain immunoglobulin suppressor of T cell activation (VISTA), is expressed on neutrophils and can be used to strategically target during sepsis. Our laboratory found that VISTA mediated survival and decreased proinflammatory cytokine concentration in experimental murine sepsis. Based on this work, and the known role of neutrophils in sepsis pathology, we hypothesized that VISTA expression regulates neutrophil abundance in murine sepsis. To test this, we induced sepsis in wild-type (WT) and VISTA-deficient (VISTA-/-) mice and measured neutrophil abundance in the peritoneum using flow cytometry. We found that neutrophil frequency and absolute cell count were higher in the VISTA -/- mice while the frequency of neutrophil progenitors was higher in WT mice post CLP. WT mice also exhibited an increase in VISTA+ neutrophil count post CLP. Neutrophils have shown to be dysfunctional and contribute to sepsis pathology. Understanding the precise processes by which neutrophils contribute to sepsis pathogenesis could lead to the development of new diagnostic tools for early detection and evaluation of risk.

Dana Vargas Solivan **Poster #H9**

Home Institution: University of Puerto Rico, Mayagüez

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Sheldon Holder, Department of Pathology and Medicine; Kim Seymour, Department of Pathology and Medicine

Targeting the Pathway for PIM1 Expression in Breast Cell Carcinoma

Breast cancer is the second leading cause of cancer-related deaths in women, with 297,790 cases estimated to occur in 2023 in the US. In addition, there is an unmet need to identify targeted therapies for Triple Negative Breast Cancer (TNBC), a more aggressive and metastatic subtype that lacks the hormone receptors ER, PR, and HER2. For TNBC the standard treatment is chemotherapy, and the median survival rate is only 13 months. Recent research has shown that PIM1, a serine/threonine kinase downstream to the JAK/STAT pathway has the capacity to promote different types of cancers, including breast cancer via cell growth, preventing apoptosis, and conferring treatment resistance. However, the mechanism by which PIM1 expression is regulated in breast cancer cells remains unknown. Due to past studies, we hypothesized PIM1 expression is contingent to the IL-6/JAK/STAT signaling pathway. To identify the expression of PIM1 and compare this to initial IL-6 signaling, we completed Western Blots and ELISA assays on untreated cells and cells with treatments that block the hypothesized pathway. To further comprehend the effects on PIM1 after blocking this pathway we also carried out a scratch assay. Given preliminary data, we expect to find PIM1 expression levels correlated with IL-6 measures. Understanding how this protein is expressed in breast cell carcinoma could lead to targeted therapies that may be more efficient in metastatic breast cancers and increase current patient survival rates.

Jacqueline Lopez **Poster #H10**

Home Institution: University of Texas at El Paso

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Christopher de Graffenried, Molecular Microbiology and Immunology

Development of an Inducible Protein Degron System in Trypanosoma brucei and Trypanosoma cruzi to Facilitate Study of Essential Genes

Trypanosomatids are flagellated protozoan parasites responsible for important diseases, including African trypanosomiasis (Trypanosoma brucei) and American trypanosomiasis (T. cruzi). These diseases are insect-borne and are considered a neglected public health problem worldwide. There is no effective vaccine for either disease, and treatment options are limited. Understanding parasite biology is essential for finding vaccine candidates and drug treatments. Often, the best drug target candidates are proteins that are essential to parasite survival. Research in T. brucei has benefited from RNA interference (RNAi) and tetracycline-inducible expression, which combined can produce inducible knockdown (iKD) of essential genes. However, the lack of iKD techniques for T. cruzi has made it challenging to investigate essential genes. To overcome this limitation, we have adapted an inducible protein degron system known as the SMASh-tag to T. brucei and T. cruzi. In this system, the gene of interest is tagged with a viral protease and linked to a degron domain. Without the viral protease inhibitor, the modified protease self-cleaves from the protein of interest, producing the native protein. When a protease inhibitor is added, the process of self-cleavage is blocked, causing the degradation of the modified protein. We demonstrate that this system works on YFP expressed in the parasites. Using homologous recombination in T. brucei and CRISPR/Cas9 editing in T. cruzi, we introduced the SMASh-tag to the N-terminus of Centrin2 and PLK, respectively. These two genes are essential and well characterized, which will allow us to validate the utility of the SMASh-tag system as an iKD tool.

Min Sung Kim **Poster #H11**

Home Institution: Brown University

Summer Research Program: Summer Research Assistantship in Biomedical Sciences

Faculty Mentor: Gary Wessel, MCB; Nathalie Oulhen, MCB

Estrogen is awesome

Sex steroids are essential in reproductive systems, having an involvement in development of secondary sexual characteristics, gonadal maturation, germ cell proliferation, and sexual behavior to name a few. In women, estrogen regulates the reproductive system along with neuroendocrine, skeletal, adipose, and cardiovascular systems. In contrast to humans who are born with a finite pool of oocytes, Echinoderms such as sea urchins and sea stars have the ability to constantly produce new oocytes throughout their lifespan. This phenomenon implies the existence of stem cells for eggs that are constantly replicating and developing. This continuous pool of new oocytes must require continual regulation by interaction with the gonadal somatic cells likely through intercellular signaling mechanisms. We are testing the hypothesis that echinoderms, which are invertebrates, may use an estrogenic signaling mechanism to regulate long-term stem cell function for oocyte development. First, we find that the genomes of sea urchins and sea stars have expressed genes in their ovaries required for estrogen biosynthesis. Second, we have conducted an estrogen challenge on ovary explants followed by RNA-seq experiments to test if exogenous estrogen can alter gene expression in this tissue. Preliminary data shows that estrogen affects the RNA expression of multiple genes in the ovary of the sea urchin Lytechinus variegatus. Here, I report tests on the effect of the estrogen on different stages of ovary maturation. To carry out this experiment, ovary cultures from different stages of maturation and from different Echinoderms (sea urchins and sea stars) were treated with estrogen and gene expression of potential estrogen responsive genes was tested by qPCR. Our results indicate that estrogen reduces the expression of genes specifically involved in hormonal regulation (such as wwox) and increases genes regulating the Wnt pathway (such as Wif). We will next determine what cells are responsible for this response, and how they may interact with the germ line. Excellent genomic resources are available for multiple Echinoderms making them great model organisms to study their ovarian gene expression.

Chris Ma **Poster #H12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Qian Chen, Orthopedic Department

Delivery of Antisense Oligonucleotides Across the Blood-Brain Barrier via Nanopieces in a Neurodegenerative Mouse Model

The blood-brain barrier (BBB) is a protective endothelial membrane that regulates the transport of ions, nutrients, and waste products between the bloodstream and the brain's neural tissue. Disruptions to the BBB can result in an influx of blood-derived debris, leading to neurodegeneration. Given the critical role of the BBB in restricting the entry of therapeutic agents to the brain, an Alzheimer's disease (AD) model serves as a valuable representation of a compromised BBB. Antisense oligonucleotides (ASOs), which effectively suppress gene expression at the post-transcriptional level, hold promise for the treatment of AD and other neurological disorders. However, the BBB restricts the entry of polar and negatively charged molecules like ASOs, limiting their therapeutic potential. Current delivery approaches require invasive intrathecal or intracranial injections, highlighting the need for a clinically advantageous intravenous (IV) administration method. This project aimed to address the challenge of efficient ASO delivery to the brain by exploring the potential of nanopieces (NPs), an emerging technology utilizing bundled Janus base nanotubes (JBNTs), as delivery vehicles. Crucially, NPs can effectively encapsulate nucleic acid cargo while minimizing negative charge and ensuring safe degradation. To evaluate the effectiveness of NP/ASO treatment, we investigated the time-dependent distribution and knockdown of MALAT1, a ubiquitously expressed segment of noncoding RNA, in the hippocampus region of the mouse brain. The NP/ASO treatment was prepared and injected intravenously into mice. The mice were then sacrificed, and tissue from the hippocampus region was analyzed using qPCR to determine RNA concentration levels. By assessing the knockdown efficiency of MALAT1 in the hippocampus, we gained insights into the potential of NP-mediated ASO delivery for AD therapy. The findings from this study contributed to our understanding of the therapeutic utility of NPs and their ability to overcome the limitations imposed by the BBB. This research project sought to explore the application of NPs as delivery vehicles for ASOs in the treatment of AD. The investigation of MALAT1 knockdown in the hippocampus following intravenous NP/ASO administration provided valuable insights into the potential of this novel approach for AD therapy, offering a promising avenue for future clinical advancements.

Alexa Ryan **Poster #H13**

Home Institution: Howard University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Craig Lefort, Division of Surgical Research

“Don’t Eat Me”:The Effects of Ectopic Overexpression of CD47 in Neutrophil Progenitors

In today's medical world, a common treatment for those with blood cancers and immune deficiency disorders is a hematopoietic stem cell transplant (HSCT). Patients often undergo chemotherapy to eradicate their immune system in order to prevent rejection of transplanted cells and allow engraftment of donor HSCs. One complication of this treatment is neutropenia during the first few weeks post transplant, leading to an increased amount of infections. Previous studies in our lab showed that HoxB8-conditional neutrophil progenitors can successfully engraft into naïve, unconditioned mice and rapidly differentiate

into mature neutrophils, suggesting their potential use as an adjunct cell therapy with HSCT. However, their engraftment can only be seen in C57BL/6J mice, the strain in which the HoxB8-conditional progenitors were derived, while engraftment was unsuccessful in Balb/c mice. We want to determine if engraftment is possible in other mouse strains if CD47, a protein expressed on the HoxB8-conditional progenitors, was ectopically overexpressed. CD47, considered the “Don’t eat me” signal, interacts with macrophages to avoid phagocytosis when transplanted progenitors migrate to the bone marrow. Mice will be injected with the HoxB8-conditional progenitors in which CD47 is overexpressed, and bone marrow will be collected for analysis using flow cytometry. We expect that overexpressing CD47 will allow the HoxB8-conditional progenitors to avoid phagocytosis and achieve successful engraftment in recipient naïve mice. We also anticipate that there will be an optimal level of expression of CD47 that yields the most amount of donor cells in mice. If this proves to be true, researchers can develop a HSCT that can reduce the duration of neutropenia and limit post transplant infections in these patients.

Valentin Kirilenko **Poster #H14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Nicolas Fawzi, Molecular Biology, Cell Biology and Biochemistry

Probing the Phase Separation and Hydrodynamic Properties of FUS LC and RGG Domains

The RNA-binding protein Fused in Sarcoma (FUS) participates in the formation of functional biomolecular condensates through the process of liquid-liquid phase separation (LLPS). The molecular level details driving phase separation are poorly understood; however, mutations in the low-complexity (LC) domain have been causally linked to neurodegenerative diseases including frontotemporal dementia (FTD) and amyotrophic lateral sclerosis (ALS). Thus, studying the phase separation of FUS deepens not only the understanding of LLPS as a mechanism of self-assembly, but also advances our understanding of these neurodegenerative diseases. The two primary factors determining phase separation are the intermolecular interactions of residues and the hydration of the protein monomers - in other words, how favorably does the protein interact with itself compared to with water. Here, we study numerous mutants of FUS LC to determine how the removal of tyrosines impacts both hydrodynamic properties and phase separation. We found that while phase separation was greatly affected, the hydrodynamic properties such as diffusion were not. We also studied the partitioning of peptides modeling the RGG domain to determine the role of glycine in phase separation. The results demonstrate that the peptides were either more hydrophobic or more flexible than the RGG domains. Lastly, we studied the hydrophobicity and hydrodynamic radius of numerous diols to explore the mechanism by which diols disrupt phase separation.

SUMMER RESEARCH SYMPOSIUM POSTERS

Friday, August 4th

Physical Sciences and Social Sciences

Physical Sciences

Ethan Bove; Michael Cho; Lisa Baek; Xingyi Zhang **Poster #A1**

Home Institution: Brown University; Stanford University; Carleton College

Summer Research Program: Institute for Computational and Experimental Research in Mathematics (ICERM)

Faculty Mentor: Jessica Sorrells, Mathematics; Cory Johnson, Mathematics

Optimal Constructions for DNA Self-Assembly of k-Regular Graphs

Within biology, it is of interest to construct DNA complexes of a certain shape. These complexes can be represented abstractly in the language of graph theory, where edges are understood to be strands of DNA joined at junctions, represented by vertices. Because guided construction of such structures is inefficient, design strategies for DNA self-assembly are desirable. Branched DNA molecules are referred to as tiles, each consisting of flexible unpaired cohesive ends with the ability to form bond-edges. We thus consider the minimum number of tiles and bond-edge types to construct a graph G (corresponding to a DNA target structure) without allowing the formation of smaller graphs, or non-isomorphic graphs of the same size. In this paper, we specifically investigate the case where G is k-regular.

We introduce the concept of (un)swappable graphs, using the property to establish lower bounds on bond-edge and tile types in the unswappable case. We also introduce a method of generating upper bounds using a vertex-cover model. We apply both of these methods to prove new bounds on a number of regular families, including crown graphs, prism graphs, Kneser graphs, Johnson graphs, Antiprism Graphs and Archimedean solid graphs.

Grace Bielefeldt; Iris Horng; Holly Luebsen; Mitchell VonEschen; **Poster #A2**

Home Institution: St. Olaf College, University of Pennsylvania, University of Texas at Austin, Lawrence University

Summer Research Program: Institute for Computational and Experimental Research in Mathematics (ICERM)

Faculty Mentor: Leyda Almodóvar Velázquez, Mathematics; Cory Johnson, Mathematics

Algorithmic Generation of DNA Self-Assembly Graphs

With recent advancements in the field of nanotechnology, there has been increasing interest in self-assembling nanostructures. These are constructed through the process of branched junction DNA molecules bonding with each other without external guidance. Using a flexible tile-based model, we

represent molecules as vertices of a graph and cohesive ends of DNA strands as complementary half-edges allowing the molecules to bond with each other. Due to the unpredictability of DNA self-assembly in a laboratory setting and the risk of undesirable products being incidentally constructed, predicting what structures can be produced from a given list of components, referred to as a “pot of tiles,” is useful but has been proven NP-hard. Our project introduces an algorithm to computationally generate and visualize at least one valid graph given a pot of tiles. By adjusting a number of construction parameters, we can produce graphs of various orders and proportions of tiles.

Toby Anderson; Olivia Greinke; Luis Santori; Iskandar Nazhar **Poster #A3**

Home Institution: Harvey Mudd College, Transylvania University, University of Massachusetts Amherst, University of Florida

Summer Research Program: Institute for Computational and Experimental Research in Mathematics (ICERM)

Faculty Mentor: Amanda Harsy, Mathematics; Cory Johnson, Mathematics

Relationships in the Flexible Tile Model of DNA Self Assembly

DNA self-assembly is an emerging area of study within the field of biology and nanotechnology with applications in targeted drug delivery, biomolecular computing, and biosensing. Branched molecules of DNA bond to each other with complementary strands of base pairs to form a target nanostructure. Using a flexible tile model, these structures can be modeled mathematically as graphs that are constructed from vertices with extending half-edges. These vertices are referred to as tiles, and their extending half-edges are labeled with bond-edge types that represent different extending sequences of DNA base pairs.

Most mathematical research using the flexible tile model seeks to find optimal constructions for various graphs and graph families in an effort to maximize laboratory efficiency within three scenarios of increasing restriction. Our research focuses on searching for underlying relationships between the minimum number of bond-edge types and tile types needed to construct a graph across these scenarios. Building on previous work, we explore a variety of low-order graphs and present optimal constructions for all graphs of order five and below in all scenarios. In addition, we present results for various lattice graphs, particularly hexagonal lattices, and web graphs.

Fausto Navarro; Luca Grossman; Jacob Ashworth **Poster #A4**

Home Institution: Johns Hopkins University

Summer Research Program: Institute for Computational and Experimental Research in Mathematics (ICERM)

Faculty Mentor: Jessica Sorrells, Mathematics; Cory Johnson, Mathematics

Algorithmic Pot Generation

Recent advancements in microbiology have motivated the study of the production of nanostructures with applications such as biomedical computing and molecular robotics. One way to construct these structures is to allow bonding of branched DNA molecules with complementary cohesive ends. One practical question is: given a target nanostructure, what is the optimal set of DNA molecules that can assemble such a structure? We use a flexible-tile graph theoretic model to develop several algorithmic approaches,

including a linear programming approach. These approaches take a target undirected graph as an input and output an optimal collection of component building blocks which construct the desired structure. In addition, we present several tools for characterizing the structure of the solution space.

Tanner Diring; Kiera Fullick; Jayna Rybner **Poster #A5**

Home Institution: University of Wisconsin - Madison, Brown University, University of Southern California

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kenneth Breuer, Engineering

Aerodynamic Tail Effects Developed in Robotic Flapping Flight Wake

Bird flight continues to be of interest in the world of fluid dynamics and flight due to its potentially innovative applications within the world of machine flight. While the aerodynamics of bird wings have been studied extensively, the effects of a pitching or rolling tail in flapping flight and how these movements can be advantageous to bird flight has had little attention. We are aiming to quantify the aerodynamic tail effects and forces on a wing-flapping robot operating within a wind tunnel which acts as a simulated flying environment. By varying the spread, pitch, and roll of a fabricated tail, we will be able to isolate the aerodynamic forces present on the robot, which in turn will help to eventually answer the question of how birds generally use their tails in flapping flight. This knowledge and documentation of the acting aerodynamic forces on bird tails can help achieve higher maneuverability, stability, and efficiency of drones or ornithopter applications.

Yilin Xie; Zachary Brown; Marcus Lewis; Joseph Militello **Poster #A6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Chemistry

Controlling the Dimensions and Uniformity of Magnetic Nanoparticles for Environmental and Biological Applications

Magnetic fields can be used to image, move, and heat matter at the very smallest of length scales. Traditionally, these capabilities cannot be easily applied to non-magnetic biological and environmental systems. If magnetic nanoparticles are incorporated into these materials, however, they can render these organic materials magnetic and enable novel applications in areas such as MRI imaging and water treatment. To accomplish this requires magnetic nanoparticles that are highly uniform, very small (nanometer scale dimension), and of tunable dimension. In some examples it may be better to work with very small magnetic nanoparticles while in others larger materials are required. The objective of this project is to understand and control the dimensions of these small and highly crystalline magnetic particles.

The synthetic procedure used relies on the thermal decomposition of iron carboxylates at high temperatures to produce iron oxide (Fe3O4 or magnetite). While this approach has been used for over a decade by hundreds of research groups to make magnetic nanoparticles, much of its underlying chemistry remains a mystery. For example, why does this approach result in such uniform nanoparticles which, over certain size ranges, can have size distributions under 10% on the diameter? How can we extend this chemistry to forming magnetic nanoparticles of larger dimensions which are particularly

relevant for applications that use magnetic nanoparticles to move larger objects in magnetic fields? Classical models of crystal growth that describe discrete nucleation and growth stages are not sufficient for answering these questions. We hypothesize that the iron carboxylates form an intermediate condensed phase prior to their crystallization into Fe3O4. These inverse micelles consist of polar head groups(carboxylates) coordinating iron surrounded by the hydrophobic longer chain hydrocarbon. We expect that increasing the amount of iron relative to carboxylate should yield larger particles similar to room temperature inverse micelles. Moreover, we also expect that below a threshold level of carboxylate the reaction would not yield nanoparticles as there would not be sufficient surfactant. These hypotheses are evaluated in systematic experiments that probe how these parameters influence the dimensions and quality of the resulting magnetic nanoparticles.

Alice Min; Robayet Hossain; Narek Harutyunyan; Hammad Izhar **Poster #A7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Nora Ayanian, Computer Science, Engineering

Advancements in Multi-Robot Systems: Enhancing the Crazyflie Drone Platform, Testing MAPF implementation, Creating Drone Art, and Integrating JARVIS

The Automatic Coordination of Teams (ACT) Lab spearheads cutting-edge research in the realm of multi-robot systems, with a specific focus on the innovative Crazyflie drone platform. We present a comprehensive overview of the ongoing efforts within the lab, showcasing implementations of drone construction, motion capture, MAPF, artificial intelligence integration, and interactive LED dancing.

The careful planning and ongoing improvement of the Crazyflie drone system are one of the main contributions of this effort. Work has been done to improve the construction process, including intricate machining, soldering, and circuitry replacement to ensure the longevity and operational efficiency of the drones. Innovative methods have also been developed to enhance drone recordings and long-exposure photos, utilizing the strategic coverage of specific drone limbs to reduce interference and produce better footage.

Within the scope of the MAPF planning research, a significant aspect has been devoted to implementing a small-scale robot system, identifying and resolving planning issues while operating with real-time commands. The project has used ROS, optimal planning algorithms, and the VICON motion capture system to navigate drones within a 3D grid environment, creating smooth trajectories and offering spontaneous replanning. The resulting program offers proof of validity of MAPF planning on ACT Lab's CrazySwarm's system.

Regarding multi-drone art, this project involves designing and optimizing a custom-built drone for controlled paint application on canvas. Using Fusion 360, specialized mechanical components were created, enabling precise paint dispersion. The drone's firmware was fine-tuned to ensure smooth operation and accurate paint-spreading, producing artistic creations. A dynamic LED dance performance was developed using the drone, responding to sound frequencies. Through sound analysis, the drone's LED colors changed in sync with music pitch, creating captivating visual effects during choreographed movements. The project merges technology and art to deliver an immersive and engaging experience.

As a complementary endeavor, the lab has also embarked on the development of a groundbreaking JARVIS as an advanced AI chat using the Llama 2 large language model published by Meta AI. This

enables voice-activated drone control through an Amazon Alexa device to navigate drones along predefined paths, and interact with JARVIS.

Catherine Jacobs; Amelia Julian; Katelyn Buck **Poster #A8**

Home Institution: Wellesley College, Plymouth State University, and The University of Texas at Austin.

Summer Research Program: Institute for Computational and Experimental Research in Mathematics (ICERM)

Faculty Mentor: Cory Johnson, Mathematics, California State University, San Bernardino; Amanda Harsy, Mathematics, Lewis University

Multi-Dimensional Graphs Modeling Self-Assembling DNA Nanostructures

Employing tools from graph theory and linear algebra, we model the biological process of the creation of nanostructures from self-assembling DNA complexes. We represent k-armed branch junction molecules with tiles which are vertices in a graph with half-edges. The half-edges depict the cohesive-end types of a DNA strand. We aim to determine the minimum number of tiles and cohesive-end types necessary to form the complete complex of a given multi-dimensional graph structure. The problem of modeling DNA self-assembly is particularly challenging when considering graph families which change in multiple dimensions. In this research, we present the minimum number of tiles and cohesive-end types necessary to create the stacked book graphs, the square lattice graphs, and the Mongolian tent graphs, under different laboratory constraints.

Doh Hyun (Dennis) Kim; Matthew McKee **Poster #A9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jay X Tang, Physics; Peter Belenky, Molecular Microbiology & Immunology

Swarming motility of Enterobacter sp. SM3

The bacterial swarming phenotype is defined as the collective motion of bacteria on a solid surface. Swarming is typically quantified by the growth rate of the area covered on an agar plate. The swarming motility is thought to have a correlation with flagellation and the length of the bacteria. Specifically, the more flagella per cell and the longer the bacteria, the better swarming behavior they exhibit. Here, we study Enterobacter sp. SM3, which is found to have the swarming phenotype. Reduction of inflammatory symptoms in mice with irritable bowel disease had been reported after ingesting swarming SM3 (De et al., Gastroenterology, 2021). We aimed to create hyper-swarming mutants of SM3 and study the genotype involved in the expression of the hyper-swarming phenotype. To achieve this goal, we created a genetically homogeneous colony of the original SM3, SM3A. Patches from the swarm front of the growing SM3A colony were collected and inoculated on another 0.5% agar plate. At the end of five or six repeats of the colony spread cycle, considered to be five or six passages, a patch was picked from the swarm front, diluted, and observed under an optical microscope. It was found that these final SM3 variants collected at the swarm front were on average 2-3 times longer compared to the average length of the original SM3 at ~1.5 μm. We identify these longer SM3 mutants as hyper-swarmers and name them “Swarmium”. Their DNA sequences will be assessed in the near future to determine the correlations between genotype and swarm motility.

Work Cited:
De, Arpan et al. “Bacterial Swarmers Enriched During Intestinal Stress Ameliorate Damage.” Gastroenterology vol. 161,1 (2021): 211-224. doi:10.1053/j.gastro.2021.03.017

Mikayla Walsh; Peter Zhu **Poster #A10**

Home Institution: Brown University

Summer Research Program: Integrative Initiative: Sex, Aging, Genomics, and Evolution (IISAGE)

Faculty Mentor: Ritambhara Singh, Computer Science

Analyzing Sex-specific Aging Differences using Machine Learning

Sex-specific differences in aging have been observed across a variety of species. Researchers work to find an explanation for why these sex-specific differences occur. One hypothesis suggests that the cellular processes and gene interaction might play a role in these differences. In order to further explore this idea, we used single cell RNA sequencing data in the heads of fruit flies to take a closer look at the relationship between these genes and cells. We use a graph convolutional network to predict sex and age from this set of scRNA-seq data. We trained one model on all of the cells for one age group and aimed to predict sex and we trained another model on a subset of the cells for one sex and aimed to predict age. Our goal was to determine if there was a correlation between sex and age using scRNA-seq data from fruit flies.

Faith Kim; Vatsal Vemuri **Poster #A11**
Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brenda Rubenstein, Chemistry

Unraveling a Cancer Drug’s Unbinding Pathway with Molecular Dynamics Simulations

In recent years, molecular dynamics (MD) simulations have had dramatic impacts on the power to understand complex physical and biological systems, including human health and disease. In contrast with other methods for predicting dynamics, MD simulations maintain high accuracy with full atomistic detail, allowing for the discovery of biochemical mechanisms and pathways. Along these lines, MD has served as a powerful method for predicting how protein mutations can affect drug efficacy. In this work, we use MD to study how mutations affect the ability to drug Abl1 kinase, an important cellular “switch” for key signaling pathways that can drive oncogenesis. Abl1 is a common and effective target for kinase inhibitor drugs such as Ponatinib, which is a highly potent treatment for chronic myeloid leukemia (CML) and Philadelphia chromosome–positive (Ph+) acute lymphoblastic leukemia (ALL). In particular, we examine how the F382V and F382L mutants of Ab1 kinase alter the residence times for Ponatinib, using MD simulations and related statistical analyses to provide a detailed explanation of the conformational changes and resultant unbinding mechanisms. This work demonstrates the ability of MD simulations to generate mechanistic insights into the design of drugs that can have substantial impacts on human disease.

Xavier Lee **Poster #A12**

Home Institution: Brown University

Summer Research Program: Summer Research

Faculty Mentor: David Borton, Engineering

Development of Evaluation System for Closed-Loop Neuromodulation Accelerator Platform

The development of implantable neurotechnology is throttled by the pacing disconnect between clinical studies and benchtop demonstrations. The subcomponents of implantable systems advance concurrently with the overarching systems themselves, but verifying that system redesigns, the integration of new manufacturer devices, and different electrical components meet safety requirements before clinical studies begin can often be impossible due to time and cost. Retaining system modularity throughout the development process would alleviate the described bottleneck by permitting users to design, evaluate, and iterate on a single hardware platform, removing the extensive PCB design process from the equation. A real-time, cross-development platform (xDev) is proposed to realize this goal. The xDev platform would simplify the design process for translational devices to a benchtop, software-controlled sandbox relying on a real-time QNX operating system to manage device connectivity and programming, neural stimulation and recording, and a safety watchdog for emergency disconnect. The system will run on a BeagleBone Black controlling four crosspoint switches (AD75019), providing 26 input and output lines.
An Arduino-based system was developed to first validate the feasibility of the xDev platform. PCBs managing our crosspoint arrays were designed to be connected in series, either with other evaluation boards or external modules designed in-house. This system enables us to investigate how devices might be affected by the introduction of the xDev platform into the signal chain. Hardware has been both designed and manufactured, and software has been created to control the evaluation platform.
We are currently assessing the frequency response of different traces and the effects of crosstalk. Once frequency responses have been characterized, we can computationally remove systemic noise to improve signal quality. The xDev platform will then manage a real-time neuromodulation system consisting of a horizon active spinal electrode array (ovine spinal cord, dorsal aspect), a component-level neural recorder, and an external spinal stimulation device. Success metrics include successful device configuration, no loss of data packets, and continuous stimulation according to parameters defined by the closed-loop controller. For analog traces, we verify that xDev will not introduce significant noise into the signal chain by recording both inputs and outputs for comparison.

Aidan Hennessey **Poster #A13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Richard Schwartz, Mathematics

Tripod Nim

The ancient game of nim is played by two players who take turns removing coins from heaps according to some basic rules. In particular, each turn a player must remove some number of coins from any one heap. This can include anything from taking a single coin to removing an entire heap. The player who removes the last coin wins. The full analysis of this game has been known for over 100 years, but slight variations of its rules often produce difficult and interesting theory.
Because these games are impartial combinatorial games, every position either has a winning strategy for the Next player (an N position) or the Previous player (a P position). Analysis consists of determining which positions in a game are N positions and which are P positions.

This project focuses on a variant we name tree-nim, and a special case of tree-nim called tripod nim. In tripod nim, there are 4 nim heaps, one of which (the center) can only be taken from once two other heaps (leaves) are fully extinguished.
I show that, fixing the center and 2 leaves, there is exactly 1 value of the remaining heap which makes it a P position. Additionally, fixing the center and one leaf, and letting the value of the second leaf take variable value n, the value of the third leaf needed to make a P position is an arithmetico-periodic function of n. Comparable results can be shown for larger classes of impartial combinatorial games. I also give full analyses of positions in which the center is one less than a power of 2. In these cases, the game is nearly identical to traditional nim with 3 heaps.

Matthew Fang **Poster #A14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brian Sheldon, Materials Science and Engineering

Residual Stress Analysis of Ion-Exchanged LLZTO via X-Ray Diffraction

Ion exchange is a thermally activated interdiffusion process that is commonly used to strengthen the surface of glass. During glass ion exchange, alkali ions near the surface of the glass are exchanged with larger ions of equal charge from a molten salt solution. The ion replacement occurs at the same molecular site, resulting in residual compressive stress but no major changes in network structure. It has been suggested recently through modeling and experimental efforts that the concept of ion exchange may be applied to Li6.5La3Zr1.5Ta0.5O12 (LLZTO) to hinder Li filament growth and thus improve its critical current density (CCD), the current level at which Li filament growth causes cell failure. In this study, ion exchanged LLZTO fragments are analyzed using X-ray diffraction (XRD) and the sin2Ψ method to determine the magnitude of residual compressive stress induced by ion exchange. Compressive stress measurements up to ~1.7 GPa were recorded but non-linear d-spacing vs. sin2Ψ plots indicated inhomogeneous stress distributions. Alterations were made to the XRD stress analysis method to increase accuracy. An approximation of the effective X-ray penetration depth in analyzed LLZTO samples was thus calculated to better understand collected data. The CCD of ion exchanged LLZTO was increased to ~1.0 mA·cm-2 from a baseline of ~0.4 mA·cm-2, showing a correlation between surface compressive stress and CCD.

Yizhong Hu **Poster #A15**

Home Institution: Brown University

Summer Research Program: Statistical Mechanics on Random Graphs

Faculty Mentor: Kavita Ramanan, Department of Applied Mathematics

Annealed Pressure of Sparse Random Regular Graphs

The Ising model, initially introduced in the early 1900s to study magnetization in statistical mechanics, has since become a versatile tool applied in various fields like social sciences, genetics, and combinatorics. It assigns probabilities to configurations of 1's and -1's, representing dipole spins, on a graph or network. In

the ferromagnetic model, neighboring 1's are favored, while in the antiferromagnetic model, opposite signs are preferred. Over time, the Ising model has been extended from the traditional d-dimensional lattice to more general network or graph structures.

In this study, we explore the Ising model on random graph geometries as the number of particles approaches infinity. Our focus is on a quantity called the 'annealed pressure,' which helps us understand key aspects of the model, such as the limiting magnetization. To do this, we employ a large deviation approximation and express the annealed pressure as an optimization problem. Through numerical and analytical techniques, we investigate the Ising model on random regular graphs and random regular bipartite graphs. In particular, we establish a link with a quantity referred to as the 'Bethe prediction' through a certain cavity equation, proving that the Bethe prediction is equivalent to the annealed pressure in specific statistical physics models. We also demonstrate the method's applicability to other statistical physics models on random graphs, such as the Hardcore model. Our research contributes to a deeper understanding of statistical physics and optimization theory, particularly in the context of complex systems on random graph structures.

Cameron Goodreau **Poster #A16**

Home Institution: Brown University

Summer Research Program: Space Grant/NASA

Faculty Mentor: Yongsong Huang, Geochemistry

Advancements in the Extraction of Volatile Organic Compounds from Carbonaceous Extraterrestrial Materials

The identification of organic compounds in meteorite and asteroid analysis provides information about how and where these compounds originate, along with evidence towards galaxy, solar system, and planet formation. The previous research focuses on analyzing individual groups of organic compounds, using large amounts of sample mass and techniques that can eliminate other groups. We have instead come up with an optimized method for analyzing monocarboxylic acids within carbonaceous meteorites, along with aldehyde, ketone, alcohol, and sulfur-compound based low molecular weight organic material. The method utilizes fumigation of the sample with gaseous HCl to release acids and low temperature desorption analysis, identifying organic compounds that were not present in non-acidified samples or a result of pyrolysis of insoluble organic matter at high temperatures. The optimized method was concluded to be an acidification of the sample at 50°C and thermal desorption at 150°C.

Rio Aguina-Kang **Poster #A17**

Home Institution: University of California, San Diego
Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Daniel Ritchie, Computer Science

OVoSS3D: Towards Open Vocabulary 3D Scene Synthesis using LLM-guided Constraint Satisfaction

Recent advancements have showcased the potential of deep generative models in generating 3D scenes. However, these existing methods often suffer from limited diversity, input specificity, or output consistency.

We propose OVoSS3D, a novel approach that leverages large language models (LLMs) for open vocabulary 3D scene synthesis. By leveraging the commonsense knowledge embedded within LLMs, our system enables flexible and diverse natural language specifications as input, eliminating the need for 3D training data required by current state-of-the-art generative models. To translate the symbolic world knowledge of LLMs into 3D spatial data, we prompt the LLM to generate programs in a domain-specific language (DSL), which describe 3D scenes through a set of object descriptions and constraint functions. These descriptions are used to retrieve objects from the Objaverse dataset using CLIP's image-text embedding space and constraint functions are subsequently optimized to generate the complete scene. Our results highlight the ability of OVoSS3D to synthesize scenes that surpass the limitations of existing generative models. This research contributes to the advancement of flexible and diverse 3D scene synthesis and opens up new possibilities for creative expression and virtual world design.

Marlena Brown **Poster #B1**

Home Institution: Brown University

Summer Research Program: Undergraduate Research Assistant

Faculty Mentor: Kim Cobb, Institute at Brown for Environment and Society, Geochemistry

Early 19th-century coral records the transition into the industrial period in the central tropical Pacific

Quantifying past climate in the tropical Pacific is vital to understanding the modern global climate and the impacts of climate change. The Pacific is a key region, as it comprises nearly a third of the Earth's surface and contains the El Niño-Southern Oscillation, a recurring climate pattern that is a major source of global climate variability. The 19th century is particularly important, as it contains the unclear transition from the "pre-industrial" period, before the onset of anthropogenic warming, into the industrial period. Yet instrumental data remains extremely sparse. To help form a more robust picture of early industrialization, I use corals as a climate record to quantify ocean conditions in the central tropical Pacific during the 19th century. Here, I measure the ratio of oxygen isotopes (δ18O) in a short (decades-long) fossil coral from Kiritimati Island (2°N, 157°W), dated to 1810 CE. The δ18O data reveals combined temperature and salinity information about the ocean at Kiritimati during the early 1800s. In the longer term, I plan to perform Sr/Ca analysis to distinguish and more precisely quantify temperature and salinity signals. I also plan on additional U/Th dating to link δ18O signals to dates at high resolution, allowing me to pinpoint climate variance on a yearly timescale. The coral will become part of a longer, ensemble δ18O reconstruction of environmental conditions at Kiritimati during the entire 19th century, combining six to seven short coral records to clarify the early decades of climate change in this critical region.

Joan Graniela **Poster #B2**

Home Institution: University of Puerto Rico - Mayaguez Campus

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Roberto Zenit, Engineering

Deformation and Velocity of Bubbles in Viscous and Viscoelastic Fluids

The motion of gas bubbles in liquids has a significant impact on many environmental and industrial

processes. This research analyzes the velocity and shape of air bubbles moving steadily due to buoyancy, for a range of bubble diameter in Newtonian and Non-Newtonian fluids. To establish these relationships, an experimental arrangement was designed where individual air bubbles are formed, once at a time, introduced into a viscous fluid. The bubble is released to reach its terminal speed, then its speed and shape are captured by a high-speed camera. This experiment is repeated multiple times, increasing the volume of air in the bubble. Subsequently, the fluid was replaced with a viscoelastic fluid. Direct comparisons of the bubble behavior in different fluid properties were obtained. The average speed and deformation increase with the bubble volume in both viscous and viscoelastic fluids. We discuss the differences between the two cases.

Presley Hernandez **Poster #B3**

Home Institution: CUNY Hunter College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: James Russell, Department of Earth, Environmental, and Planetary Sciences

Analyzing PAH Concentrations in Soils to Improve Reconstructions of Savanna Fires

Today, savanna fires are responsible for 80% of burned areas globally, but it is difficult to predict how these fires may change in the future. To better understand how wildfires will respond to climate change, scientists reconstruct changes in savanna fire occurrence on long timescales using chemical indicators. To do so, we must understand what conditions control the concentrations and distributions of these fire chemicals in savannas. We used soil samples from Kruger National Park in Africa where managers have conducted controlled fire experiments for the last 69 years to test how fire compounds are preserved in soils with a known fire history. I analyzed the fire chemicals' concentrations in soils from plots before and after burns (pre- and post-burn) in addition to control plots that have not burned for decades. We expect to see the highest concentrations of fire indicators in post-burn plots, next highest in pre-burn plots, and lowest in control plots. We also expect that the concentrations and distributions of chemicals in post-burn samples will vary depending on the differences in fire conditions such as fuel load, fire temperature, windspeed. My work will improve interpretations of fire reconstructions and thereby, wildfire dynamics.

Gabrielle Rose **Poster #B4**

Home Institution: Wellesley College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Karen Fischer, Department of Earth, Environmental, and Planetary Sciences

Evidence for Active Volcanoes in West Antarctica

Volcanoes are thought to be prevalent throughout Western Antarctica, yet little is known about which of these potential volcanoes are active due to the thick layer of ice covering the continent. This work focuses on determining the locations of active volcanoes in West Antarctica, specifically Ellsworth Land. Using data requested from the Incorporated Research Institutions for Seismology (IRIS), we analyzed seismic waveforms recorded by stations near potential volcanoes. Using initial event locations from Peña Castro et al. (2022), we calculated differential travel times between events at each station using cross-correlation and used these times to relocate the events with the GrowClust algorithm (Trugman and Shearer, 2017).

Initial relocations show events beneath volcanoes that are consistent with volcanic activity. This research is especially important because the ice mass of the continent has changed significantly as a result of ongoing global warming. Findings will help us understand how much heat is going into the ice, which is crucial information in regard to climate change as it can ultimately help improve models on ice sheet melting and sea level rise.

Jiashu Huang **Poster #B5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Greg Landsberg, Physics; Marko Stamenkovic, Physics

Probing New Physics with a Top Quark; Feasibility for a Mass Measurement of the Top using t -> b W Z Channel

The mass of the top quark plays a crucial role in our understanding of the fundamental properties of the universe. In this research, we explore the feasibility of measuring the mass of the top quark through a rare channel of decay, namely, the decay of the top quark into a bottom quark, a W boson, and a Z boson (t -> b W Z). This particular decay mode is kinematically constrained, making it highly sensitive to the mass of the top quark. By reconstructing the top mass from the decay products, we employ a kinematic fit technique to optimize the accuracy of the measurement. This study aims to provide valuable insights into the mass of the top quark, which in turn contributes to our understanding of the universe's stability and potential new physics phenomena.

Jacob Stifelman **Poster #B6**

Home Institution: Brown University

Summer Research Program: Undergraduate Research Assistant - Computer Science

Faculty Mentor: Ritambhara Singh, Computer Science

Evaluation of Explainability Methods on Single-Cell Classification Tasks Using Graph Neural Networks

Single Cell sequencing data has created new methods in using Graph Neural Networks(GNNs) to classify cells. Specifically, these developments have helped find new explanations that reveal underlying cellular mechanisms for GNNs. While some work has been done into the reliability of these explanations on synthetic datasets, there is a lack of research on the reliability of these explanations on real world datasets.

This project evaluates a graph neural network explanation method, GNNExplainer, on real world datasets with known ground truth networks. A GNN model is then trained using these datasets with both the ground truth and simulated gene regulatory networks using the grnboost2 algorithm, as well as ATAC-Seq data. Afterwards, the explanations are evaluated using fidelity, sparsity and precision and recall metrics.

Similar to as seen with synthetic datasets, we hope that GNNExplainer will continue to adequately evaluate the reliability of explanation models.

Anna Chung **Poster #B7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Ming Xian, Department of Chemistry

Inhibition of Papain by Sulfane Sulfur Species

Sulfane sulfur species, such as polysulfides (RSnR) and hydrogen persulfides (H2Sn), are involved in sulfur-mediated redox signaling, thereby playing an important role in regulating the physiological and pathological functions of biological systems. The major mechanism by which these molecules regulate these processes is through the posttranslational modification (PTM) of free cysteines in proteins (Cys-SH). Sulfane sulfur species can interact with the sulfhydryl group of cysteines to form persulfides (-SSH) in a process known as persulfidation. However, the consequences of this PTM on protein activity requires further examination. Therefore, this study aimed to elucidate the effects of different sulfane sulfurs on protein activity using papain, a cysteine protease. In this study, papain was treated with the following sulfane sulfurs: sodium disulfide (Na2S2), N-acetylcysteine tetrasulfide (NAC-S4-NAC), glucose tetrasulfide (Glc-S4-Glc) and diallyl trisulfide (DATS). The inhibitory effects of these compounds on papain activity were examined by determining the kinetic parameters for enzyme inactivation upon incubation with each sulfane sulfur. The effects of persulfidation on enzymatic activity could then be observed and compared to that of other PTMs on protein thiols, such as S-nitrosylation. Additionally, we explored methods to effectively and specifically recover protein activity after persulfidation to differentiate persulfidation from other PTMs.

Adam Gendreau **Poster #B8**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Meredith Hastings, DEEPS

Investigating Potential Causes of Intra-Urban Air Quality Variation via The Breathe Providence Network

Hyperlocal air monitoring offers insights into intra-urban pollutant variation, which can occur on a finer scale than is captured by current government-operated sensors. Through the Breathe Providence network, located in Providence, RI, differences in pollutant concentrations can be observed at a neighborhood-level. Poor air quality in urban locations is often correlated with vehicular traffic, which produces carbon monoxide (CO) through combustion processes. Two sensors in the Breathe Providence network, located at the Zuccolo Recreation Center and the United Way of Rhode Island, demonstrate a notable disparity in their CO measurements (a 20% difference in the mean CO concentration), despite being equidistant from the Route 6 Highway and less than 1 kilometer apart. This project investigates various potential drivers of this disparity such as vegetation, elevation, proximity to surrounding point-source emission sites, prevailing wind direction and speeds, and microclimatic conditions. Analysis indicates that vegetation and street canyon conditions are a possible explanation for the difference, conveying the importance of the surrounding microclimate of each sensor. This work showcases the need for hyperlocal monitoring projects in urban settings as they can uncover surprising intra-urban pollution variability and show the powerful effects of urban microclimates on pollutant concentration.

Niyanta Nepal **Poster #B9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anita Shukla, Biomedical Engineering; Akram Abbasi, Biomedical Engineering

SERS-based Hydrogel Sensor for Rapid Detection of Antibiotic-Resistant Bacteria

β-lactam antibiotics play a crucial role in treating infections, but as antibiotic drug resistance increases, new detection methods to determine β-lactam antibiotic resistance must be considered. Surface Enhanced Raman Spectroscopy (SERS) detects biomolecules at low concentrations by amplifying Raman signals with plasmonic nanoparticles (eg., gold). β-lactam antibiotics undergo hydrolysis of their β-lactam ring by β-lactamases, rendering them ineffective. CENTA, a commercially available non-antibiotic cephalosporin, undergoes the process of hydrolysis with β-lactamases resulting in the release of a sulfur-containing leaving group. This leaving group can chemically bond to gold nanoparticles (AuNP), and leveraging this mechanism, an alginate-based hydrogel sensor can be loaded with AuNP to act as a SERS substrate to enable sensitive detection of β-lactamase-producing bacteria.

The alginate hydrogel matrix was synthesized by dissolving 2.5% (w/v) alginate in 2-(N-morpholino)ethanesulfonic-acid (MES), and adding adipic-acid-dihydrazide (AAD), hydroxybenzotriazole (HOBt), and 1-ethyl-3-(-3-dimethylaminopropyl)-carbodiimide-hydrochloride (EDC). Absorbance testing was carried out for each step of the hydrogel synthesis process, confirming that AuNP formation occurred once HAuCl4 interacted with the MES solution. We then determined the characteristics of the hydrogel sensor that yielded the highest intensity Raman signal by varying thickness, (1.2, 2.4, or 3.6 mm) and AuNP concentration (1, 2, 3, 5, and 10 mM). We used aminobenzenethiol (ATP), as the model for the sulfur-containing leaving group that would release from CENTA to compare the detection performance of each sensor. ATP has Raman peaks at 1080 cm-1 and 1586 cm-1 describing C-H stretching and in-plane stretching of the benzene ring, respectively.

Our preliminary data demonstrated a 1.2 mm thickness, 2mM AuNP hydrogel results in a Raman intensity of ~271 compared to the intensity of the 1.2 mm / 1 mM AuNP and 2.4 mm/ 2mM AuNP hydrogels, which for C-H stretching, gave a signal intensity of ~258 and ~68, respectively. The next steps include optimizing the hydrogel to detect low concentrations of β-lactamases when combined with CENTA and then integrating CENTA into the hydrogel matrix. This work has the potential to allow for more accurate identification of resistant infections due to β-lactamases, improving treatment decisions.

Emma Hagenaars **Poster #B10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anubhav Tripathi, Biomedical Engineering

Portable Electronic Device for High-Throughput Dried Blood Spot Processing at the Point of Care

Dried blood spots (DBS) are stored blood samples used for genetic testing and other analyses. In order to extract nucleic acids from DBS, one must follow extensive protocols requiring specialized equipment and manual preparation. Electrokinetic phenomena can be used to manipulate particles within a fluid using an applied electric field. Herein, a novel method that applies electrophoresis, an electrokinetic mechanism based on charged particle manipulation, is used for the extraction of negatively charged genomic DNA

(gDNA) from DBS. The Electro-DBS method results in enhanced diffusion and elution times of the gDNA and decreases extraction time from 40 minutes to 1 minute. After testing various voltages, frequencies, and waveforms, the optimal processing parameters appear to be 100 Hz at 2 V square wave. A device for high-throughput Electro-DBS was developed, enabling co-extraction of up to 20 DBS concurrently with variable parameters. Ultimately, this compact, portable, and low cost device eliminates the requirement for dependence on manual, time-consuming protocols that rely on additional equipment for heat, mechanical agitation, and purification steps. As DBS are commonly used in resource-limited environments, this represents an excellent point-of-care diagnostic tool.

Zeno Chen **Poster #B11**

Home Institution: Brown University

Summer Research Program: UConn Physics Research Internship

Faculty Mentor: Richard Jones, Physics

Achieving UltraShort Pulse Laser by the Modulation of the Speed of Light with a Pockels Crystal

An ultrashort pulse laser is currently achieved by active or passive modulation techniques which work using methods of light attenuation within the laser cavity. The laser pulse width is determined by the switching time of the modulator, which will limit the pulse width based on the physical limit of the active modulation or the saturation time of the passive modulator. In this paper, a new technique based on the theory of the parametric instability of the wave equation is proposed to achieve an ultrashort-pulse high-energy laser with controlled pulse width. The premise of the theory is to modulate the speed of the photons at a designated frequency by an electro-optical modulator in a laser cavity, which will result in all photons converging together to form an ultrashort pulse, and whose width can be controlled by the convergence duration. While the method does rely on an electro-optical modulator such as a Pockels Cell, it is fundamentally different from Q-Switching and active mode-locking, in the sense that there is no attenuation of the light waves nor loss of energy. In theory, its energy intensity is only limited by the gain medium and fundamental limits.

Noah Whelpley **Poster #B12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brenda Rubenstein, Chemistry

Calculating Transition States Using the Surrogate Hessian-Accelerated Line Search with Quantum Monte Carlo Methods

Current stochastic modelling methods such as Diffusion Quantum Monte Carlo (DMC) are able to predict very accurate transition state structures but are computationally expensive. The Surrogate Hessian Accelerated Parallel Line-search is a recently-developed algorithm used to achieve the accuracy of advanced stochastic methods with less computational expense. It calculates an approximate Hessian matrix and potential energy surface (PES) using a surrogate theory, such as Density Functional Theory (DFT), then uses this to inform and accelerate a line search in the high-accuracy theory. In this research, we investigate the use of this method to calculate high-accuracy transition state (TS) structural and energetic information. We focus on simple conformation-change reactions as a proof of concept, such as ammonia inversion and cyclohexane chair/boat swapping. We plan to demonstrate this method's

effectiveness on traditionally difficult transition state calculations, such as heterogeneous catalytic reactions with highly correlated transition states. In order to effectively use this method on more complex systems, we are developing a general-use automated pipeline to create structural parameterizations for input to the method using the vibrational modes of a given molecular system. Thus far, we have used this method to successfully calculate a highly accurate and precise transition state for the ammonia inversion reaction. This research aims to significantly reduce the computational cost of determining accurate and precise transition state structures, in particular for systems which cause challenges when using non-hybrid methods

Lucas Chan **Poster #B13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brad Marston, Brown Physics Department

Applying Quantum Computation to Collect the Statistics of Nonlinear Dynamical Systems

Nonlinear dynamical systems can be understood through their statistics. Solving the linear Fokker-Planck Equation (FPE) for these systems is a direct and efficient method of collecting their statistics. We study the efficacy of quantum computers in this process. We first classically implement a novel procedure introduced by Andre N. Souza (2023) to dimensionally reduce the FPE operator. The procedure requires the use of a partitioning strategy or algorithm that partitions the nonlinear dynamical systems in state space. We explore the utility of fixed points as well as K-means clustering in accomplishing this partitioning. After completing Souza's procedure, we use the resulting dimensionally-reduced FPE operator as a parameter for Quantum Phase Estimation (QPE). Using QPE, we obtain the zero mode of the FPE operator, which corresponds to its steady-state distribution. We then proceed with the method described by Souza (2023) to calculate observables of interest. This process was applied to the Lorenz Attractor, the Rossler Attractor, and the Henon-Heiles Attractor.

Anjali Shah **Poster #B14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Timothy Herbert, DEEPS, Kristin Kimble, DEEPS

Revisiting the benthic foraminifera d18O record in the Eastern Equatorial Pacific

Benthic foraminifera are single celled organisms living at the bottom of the ocean that record surrounding ocean conditions in their shells; more specifically, they provide crucial information regarding oceanic δ 18 -Oxygen (δ18O) levels over timescales of thousands of years; 18O is more prevalent in the water during global ice ages due to the sequestration of the alternative, 16O, in glacial ice caps. Thus, δ18O is an essential proxy for global ice cover and deciphering Earth's past ice ages. Here we show significant deviation from a previously derived equatorial Pacific δ18O record by Shackleton et. al 1995, with samples from the same site (ODP 846) and time period (5 to 6 million years ago). The most notable discrepancy exists at about 5.5 million years ago; Shackleton et. al 1995 showed a sharp temperature increase whereas our data show the onset of slower warming, which corroborates with U1338, another equatorial Pacific record. Additionally, the Shackleton record exhibits a dominant spectral frequency at

41kyr while the Brown record is most dominant at 23kyr. This difference in spectral dominance indicates that the two records may diverge in their portrayal of connection between orbital variation and glacial cycles. Furthermore, Shackleton et. al 1995 created a widely accepted δ18O record, and the differences presented could have important implications for sea surface temperature and δ 18 O records surrounding the late Miocene and Pliocene.

Mageean Brown **Poster #B15**

Home Institution: Brown University

Summer Research Program: Research with the Wilhelmus Lab

Faculty Mentor: Monica M. Wilhelmus, Engineering

Appendage Cupping and Hydrodynamics of a Shrimp-inspired Model

Shrimp can adapt to their environment through dynamic morphology, contributing to their remarkable maneuverability and efficiency during swimming. Integral to this morphological adaptability of shrimp is the cupping of leg appendages (pleopods) during their power and recovery stroke. Cupping occurs through the change in the cupping angle between each endopodite and exopodite pair that make up a pleopod. This cupping angle contributes to the actuation of the exopodite to spread outward (abduction) during the power stroke and to move inward (adduction) during the recovery stroke. Previous studies have given insight into these pleopod kinematics. However, the optimal angle of pleopod cupping for different swimming modes and hydrodynamic conditions still needs to be explored. Here, we use biological studies of shrimp to guide the design of a robotic pleopod, which we leveraged to investigate the hydrodynamics of pleopod cupping. We examine the vortex generation across a range of cupping angle configurations through Particle Image Velocimetry (PIV) experiments. Implementing the optimal cupping angle will ensure the maneuverability of future underwater metachronal robots under different environmental conditions.

Anneke Wernerfelt **Poster #B16**

Home Institution: Haverford College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Stefanie Tellex, Computer Science

A Dataset of Natural Language Commands for Robotic Tasks

A longstanding goal in robotics research is having competent robot assistants that understand natural language (NL) commands for everyday tasks. In existing work, robots convert temporal commands to linear temporal logic (LTL) expressions, a form of logic which uses temporal operators. They use learned reasoning skills to carry out sequential tasks where the location of the target object is unknown. However, there's a lack of comprehensive datasets to train robots on long-horizon temporal tasks which rely on temporal and spatial reasoning; existing datasets do not combine navigation, manipulation, and perception skills all together, and also lack diversity in the types of environments they use. In this study, we compile NL commands annotated to LTL representing a range of complex tasks that users might ask a robot. We began with a pilot study that uses navigation in the lab environment. We plan to collect more data in a wide range of real and simulated environments in order to expand the settings in which robotic

assistants can thrive. We hope this work will lead to better reasoning ability in robots for executing a broader range of tasks.

Sofia Juliani **Poster #B17**

Home Institution: Rutgers University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Stefanie Tellex, Computer Science

A Dataset of Robotic Task Execution of Natural Language and Vision

Natural language (NL) is an intuitive way for humans to collaborate with robots, in environments like the home or workplace. Existing models follow NL commands to navigate to a landmark, with high accuracy. However, more datasets are needed to train a robot to execute tasks by utilizing manipulation and perception skills in addition to navigation. Here, we demonstrate how robots can use these three skills to complete tasks. Our approach grounds NL commands to linear temporal logic (LTL) expressions, which represent temporal tasks. We will create a new dataset of free-form NL utterances from participants, paired with corresponding LTL translations, so that the model can learn to convert NL instructions to LTL expressions. We will first train our model in a real-world lab setting and then in multiple simulated environments, including factory and home settings, to increase the variety of NL commands in our dataset. With this new dataset, we hope to enable personal robots to achieve a wider range of tasks in diverse environments.

Ian Bartlett **Poster #C1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jerome Robinson, Chemistry

Capturing Snapshots of Lanthanide Oxygen Cycling With Well-Defined Molecular Species

The chemistry of the lanthanide series is an ocean of the unknown. While some lanthanide complexes see common utilization in day-to-day life, such as ceria in catalytic converters, most have yet to be explored in-depth in a laboratory setting. Little research has been done on if other f-block metals react with oxygen similarly to ceria. While they might not be useful in similar settings due to their sensitivity, the advancement in our understanding of f-block chemistry could be a vital stepping stone for future research and industry.
Our project focuses on the study of oxygen gas binding to these lanthanide metal centers. We hope to synthesize and characterize superoxo metal compounds and compare reaction rates and further reactivity. One challenge to this is the stabilization of these compounds - at each stage in the synthesis, a different environment is required to ensure the purity of the compounds. We work in a positive-pressure glovebox and under a Schlenk line to ensure control of the atmosphere.
The initial thought behind the project was that the reaction rate of the oxygen binding would relate to the reductive power of the metal center. Lanthanides are known for their strong reducing power in the divalent state, which is the state the metal centers are in prior to oxygen binding. However, so far, we have found that the trend for binding rates follows the ionic radius of the metals, which is the opposite of the reductive power trends. This outcome is a unique discovery in the field of f-block chemistry and we hope to continue to gather data and study this abnormality.

Lucca Paris **Poster #C2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Stephon Alexander, Physics; Tucker Manton, Physics

Simulating Gravitational Wave Mediated Particle Production in a Post-Inflation Early Universe

Very shortly after inflation, in which the early universe expanded exponentially due to a permeating field known as the inflaton, said field is thought to have dumped its remaining energy into accompanying matter fields as it oscillated around its potential minimum. This in turn excited said fields, producing particles in a process known as preheating. While most models of this process assume a direct coupling between the inflaton and Standard Model matter fields, nothing prevents the gravitational field, in the form of gravitational waves, from acting as a mediating agent. This would involve gravity itself coupling to the inflaton and the matter fields. The energy released by the inflaton field would induce oscillations in the gravitational waves. In turn, said oscillations would bring about a state of resonance within the matter fields in a process known as parametric resonance, prompting particle production. Recently, work has been done to derive the equations of evolution for the gravitational and matter fields during this proposed process. However, once derived, such equations are fairly complex and do not lend themselves to being solved analytically. Therefore, this work involved taking such equations and creating code to extract the relevant numerical solutions, in turn simulating particle production during this process of gravitational-wave mediated preheating. Specifically, said production was simulated for both spin-1 and spin-½ particles.

Masarrah Abdur-Rahman **Poster #C3**

Home Institution: Brooklyn College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Roberto Zenit, Engineering

Splashing Behavior of Viscoelastic Droplets

Splash images are one of the most iconic and familiar scientific photographs. By studying the splashing of fluids not only can we gain a better understanding of the physics of liquid collisions but we can also produce aesthetically pleasing images. The objective of this project is to capture the splashing behavior of fluids of varying viscoelastic and non-Newtonian characteristics. Using an Arduino microprocessor, we release droplets onto a thin pool of the same fluid. We control droplet size with a peristaltic pump and trigger the camera and flash to go off at specific times, therefore capturing the splashing behavior at a defined moment. The Reynolds number, which is a ratio of the inertial forces and the viscous forces, and the Weber number, the ratio of the fluid's inertia and surface tension, are the two dimensionless numbers that characterize the splash. Depending on these two values we produce different types of splashes including microdroplet formation, crown splashes, and combinations of the two. For experiments conducted with viscoelastic fluids, the splashes had new features that are contrastingly different from those observed in Newtonian liquids. In addition to the scientific knowledge gained while observing these splashes, aesthetically pleasing images were produced.

Lia Lubit **Poster #C4**

Home Institution: Brown University

Summer Research Program: Space Grant/NASA, SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Stephon Alexander, Physics

Axion Dark Matter and Parametric Resonance Production of Photons

Axions and axion-like particles are CP-odd dark matter candidates. When coupled to photons, axions can lead to parametric resonance production of photons. We investigate two axion theories and their impacts on photon mode functions. Our first theory is a simple one-axion theory in which the axion couples to photons and fermions. Our second theory involves a pathway to axion-like particles through a dark copy of the Standard Model. In this model, dark quark masses are much lower than in the Standard Model, and the dark QCD scale is much higher. In this situation, axion-like particles arise as composite degrees of freedom, akin to pions. We name dark pions with masses within the axion mass range 'π-axions.' For each of our two theories, we begin with a Lagrangian, work through the equations of motion, and then employ a Fourier transform to determine the photon mode function. From these mode functions we hope to predict signatures of photon-axion interactions that can be compared with observational data, allowing scientists to assess the accuracy of these axion theories.

Avi Trost **Poster #C5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Stephen Bach, Computer Science

Task Generation for Domain Adaptation of Instruction-Tuned Language Models

Instruction tuned language models are able to generalize to new tasks as a result of fine tuning a model on a multitude of different tasks through instructions framed with natural language. While the models achieve good performance on held-out tasks, it is unclear how to best adapt them to a new domain in a zero-shot setting. We explore this research problem of adapting instruction tuned language models to new domains. We show that naively fine-tuning on text from a new domain is insufficient to achieving domain adaptation; this process incurs catastrophic forgetting of benefits gained from the instruction tuning process. We propose a method to overcome this issue, showing that currently available general-domain large language models are able to synthetically generate tasks in an arbitrary domain given domain-specific text. We empirically show that language models fine-tuned on this synthetic data can improve performance on downstream tasks within that domain without the need for labeled data.

Adnan Aldabbagh **Poster #C6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Derek Stein, Physics

On the Energetics and Kinetics of Ion Evaporation from a Nanopore source

Ion evaporation is a process by which ions leave a fluid meniscus with the assistance of an applied electric field. We are inspecting this phenomenon for application in protein sequencing. After evaporating from a meniscus, amino acids' mass-to-charge ratio is determined by mass spectrometry. A challenge with ion evaporation is that the emitted ions are often bound to solvent molecules. These clusters of amino acids and solvents, called hydration states, alter the measurement of the mass-to-charge ratio. We experimentally probe the influence of the solution's temperature and pH as well as the voltage applied on the evaporation of the amino acids. We present mass spectra that indicate that higher temperatures increase the general current of emission while decreasing the emission of more massive hydration states. In addition, increasing the voltage applied has an effect as to increase the emission of amino acids relative to other, lighter ions.

Isabella Lizalda **Poster #C7**

Home Institution: Florida State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Blake Hodgin, Earth, Environment and Planetary Sciences

Testing covariation of the Shuram isotope excursion in inorganic and organic carbon

Carbon isotope excursions generally reflect major environmental perturbations, with most excursions reflecting major inputs or outputs of carbon associated with extinction and climate change. Carbon isotope excursions are also presumed to reflect organic carbon burial with associated changes in Earth's oxygen budget, thus also potentially giving insight into the history of oxygenation required for metazoan evolution. The Ediacaran Shuram carbon isotope excursion is the largest in Earth history, closely associated with the rise of the first metazoans and a less rise in oxygen. Although it has been observed in many different parts of the world, there is still uncertainty as to what caused it and if unique carbon cycling processes drove it.

We are studying and characterizing rock samples from Peru, where the Shuram excursion has been observed, by measuring their organic carbon composition. More specifically, how organic and inorganic carbon values differ within the excursion.

Zharia Hill **Poster #C8**

Home Institution: Penn State University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Timothy Herbert, DEEPS

Exploring an Enigmatic Glaciation during a Geologically Warm Period

The Pliocene is the key to understanding what is in store for humanity. Global temperatures are projected to rise by between 1.2°C and 4.1°C. Similarly, the Pliocene had mean annual surface temperature around 1.8°C and 3.6°C warmer than preindustrial temperatures. Additionally, the Pliocene was the last time Earth had high carbon dioxide levels.
During this geologically warm period 3.3 million years ago, there was a glacial event that lasted fifty

thousand years, the MIS M2 glaciation. This glaciation was a disruption that began and ended under enigmatic terms. During the MIS M2 event, sea levels fell and ice sheets began to build up.
Using alkenones, long-chain unsaturated methyl and ethyl n-ketones produced by very few ancient phytoplankton, we can reconstruct and map ancient sea surface temperatures. Sea surface temperature patterns are noteworthy for climate monitoring. Alkenones are found in deep sea ocean sediments. The two locations of deep ocean sediment come from sites ODP 1021 and ODP 958. Site ODP 1021 is located off the coast of California and ODP 958 is located off the coast of West Africa.Through gas chromatography-mass spectrometry, we are able to detect alkenones with a very small amount of sediment. The alkenone unsaturation index (Uk'37) is the biomarker for sea surface temperature.
Our reconstructed sea surface temperature records capture the rapid onset and termination of the M2 glacial event at both ODP Sites. The sea surface temperature records from these sites will be part of a global compilation illustrating the M2 glacial event worldwide.

Jasper Lincoln **Poster #C9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brenda Rubenstein, Chemistry and Physics

Machine Learning Microsolvation Models

The field of chemistry is dominated by reactions which occur in solvents1. While modern quantum chemical methods boast experimental accuracies for small molecules in vacuum, current methods for predicting reaction free energies and mechanisms in solution lag far behind. Current techniques for describing solvation either employ an approximate polarizable continuum that surrounds the solute and assumes a passive role in the reaction, explicit methods which surround a solute molecule with multiple physical shells of solvent molecules, or microsolvation techniques that include a few explicit solvent molecules key to the progress of the reaction surrounded by a polarizable continuum. Microsolvation methods stand out among these techniques because they provide high accuracy at a relatively affordable computational cost. However, it can be challenging to determine: the optimal number of explicit solvent molecules and the optimal positions for these molecules during the course of a reaction. While chemical intuition can be of guidance, automated techniques are needed to address these challenges in a high-throughput fashion. In this ongoing research, we propose both machine learning and Monte Carlo models to map outputs of implicit continuum calculations onto microsolvation calculation outputs. To determine the optimal positions and number of explicit solvent molecules, Monte Carlo sampling of the number and position of solvent molecules around a solute is first employed. The lowest energy points, within 2 kcal/mol of each other, are then selected and assigned a weight inversely proportional to their energy, for later machine model training. These points are then used as initial parameters for molecular dynamics (MD) simulations of well studied reactions where the solvent participates in the reaction such as the Baylis Hilman reaction. Similarly, MD simulations will be run within fully implicit systems for the same reactions. With the generated data from both batches of simulations, a machine learning neural network model will be trained on the difference between them, which will be able to map implicit calculations onto explicit observables. Ultimately, this trained model may be used to translate cheap implicit calculations into accurate microsolvated outputs within the chemical reaction space the model has been trained.

Nina Hernandez **Poster #C10**

Home Institution: Smith College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Anita Shukla, Engineering

Chemical synthesis of a photopolymerizable β-lactamase responsive crosslinker for microneedle fabrication

Biofilm bacteria are three-dimensional microbe communities that have an increased resistance against antibiotics due to the formation of a protective barrier known as extracellular polymeric substances (EPS). Biofilms exhibit numerous antimicrobial resistance mechanisms, among them the production of antibiotic inactivating enzymes, such as β-lactamases (βLs). βLs hydrolyze many first line antibiotics that contain a β-lactam ring such as cephalosporins and penicillins. This project aims to chemically synthesize a photopolymerizable diacrylate terminated βL-responsive crosslinker for developing biomaterials, which include microneedles (MNs). The usage of free radical photopolymerization in biomaterials has many advantages, most notably being simple and time efficient. The β-lactam containing crosslinker will be used to fabricate a MN patch that hydrolyzes and separates in the presence of βLs, resulting in the degradation of the hydrogel MNs. Here we demonstrate the development towards βL-responsive MN patches by synthesizing and purifying the βL-responsive crosslinker in three chemical steps: 1) nucleophilic-electrophilic addition (SN2 reaction), 2) condensation reaction, 3) deprotection. The time of purification was decreased for compound 1 and the average yield was increased from 30% to 80%. Different reaction solvents were explored in compound 2, using acetonitrile instead of dimethylformamide. Additionally, different purification strategies were explored for compound 3, which includes a wash in a nonpolar solvent. All compounds were analyzed and confirmed using proton nuclear magnetic resonance (1H-NMR). This βL-responsive photopolymerizable crosslinker has the potential to be used as a key component in bacteria-responsive drug-delivery biomaterials for a more controlled and localized antimicrobial release to fight against bacterial biofilm infections.

Kailee Tanaka **Poster #C11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anita Shukla, Department of Engineering

Evaluating the drug delivery capacity of biological allograft bone implants

Vertebral compression fractures are the most common fractures in osteoporosis patients, impacting 1.5 million individuals annually, who require both surgical treatment for the vertebral fracture and therapeutic treatment for osteoporosis. However, the current osteoporosis treatments necessitate frequent subcutaneous drug injections which are often subject to delays, leading to subsequent fractures. To address these challenges, a proprietary biological allograft bone implant has emerged as a novel and effective clinical solution. It is hypothesized that incorporating therapeutic agents into these implants could significantly enhance the efficacy by providing intraosseous drug elution, enabling treatment of the underlying disease.
Here, we evaluated whether these bone implants have the capacity to be used as a drug delivery system. We investigated the drug loading capacity and drug release behavior of the biological allograft bone

implants using two fluorescent molecules, rhodamine B (hydrophilic) and pyrene (hydrophobic). These model drugs were loaded into the implants by rehydrating implants in a drug containing saline solution. The saline solution was sampled at predetermined time points to analyze the amount of drug loaded into each implant. We also examined the drug release profile by incubating drug-loaded implants in saline at 37℃ and monitoring drug concentration in solution over time. Loading and release of each drug were analyzed using fluorescence intensity measurements of the saline. The effect of different parameters including rehydration time, shaking speed, and temperature on drug loading and release were also studied.
Our results demonstrated that biological allograft bone implants are capable of being loaded with the model drugs examined. Approximately 43% (w/w) of rhodamine B and 90% (w/w) of pyrene, respectively, were loaded into the implants. Approximately 17% of loaded rhodamine B was released from the implants over the first 24 hours, whereas the amount of pyrene released over the same time was lower than detection limit. Our results suggest that the hydrophilicity of the drug plays an important role in drug loading and release of biological allograft bone implants. These results demonstrate the potential of the allograft bone implants to be used as a drug delivery system to potentially provide treatment of osteoporosis.

Uri Dickman **Poster #C12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Matthias Kuehne, Physics

Specific Heat of Nano-Confined Fluids

The physico-chemical properties of fluids under nano-confinement are distinct from their bulk and important for an array of industrial and natural processes. In particular the characteristics of different water phases in single digit nanopores, or pores with size < 10 nm, are not fully understood. Carbon nanotubes are a prime model system in this space, and this project explores their use as testbeds for the thermodynamics of fluids confined in their interior. Specifically, we investigate the thermal response and specific heat of water in an isolated CNT using a mathematical approach based on diffusive heat transfer as well as molecular dynamics simulations.

The first is a numerical approach, in which we looked at the simplest possible system – an infinite cylinder with fixed temperature at the radius. Using the transient radial heat equation, we modeled a cylinder filled with a bulk fluid and used the finite difference method to solve it, achieving a root mean squared error below 0.1 for large time. The other approach was to model the molecular interactions directly using the Molecular Dynamics software LAMMPS. By placing a bulk of water inside a small carbon nanotube with periodic boundary conditions in z, we were able to model the molecular interactions between the water molecules and their container, and extract the specific heat using the fluctuations in the potential energy.

The numerical results indicate fast radial thermal equilibration, suggesting that a transient electrothermal technique may be deployed to measure the specific heat of water in an isolated carbon nanotube even in the presence of a finite thermal boundary (Kapitza) resistance. We discuss design rules for this method, whose implementation would allow for the detailed thermodynamic characterization of water and other fluids under extreme nano-confinement that is currently missing.

Andy Zhu **Poster #C13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jacob Rosenstein, School of Engineering; Brenda Rubenstein, Chemistry Dept.

Secure Transmission of Secret Messages in the Molecules on Everyday Objects

Steganography is the practice of concealing information within an innocuous-seeming cover medium. Unlike cryptography, the primary goal of steganography is to conceal the existence of a message. The small size and ubiquity of chemicals makes them an appealing medium for steganography. To ensure secrecy, it is necessary for steganographic media ("stego-objects") to resemble non-steganographic media ("cover-objects"), as quantified by relative entropy. It is therefore important to understand distributions of chemicals on cover-objects. In this project, we propose using a Potts model to estimate chemical distributions on cover-objects. Using our model, we propose a method for encoding messages to match the cover-object distribution so that stego-objects are statistically indistinguishable from cover-objects in our model.

Alicia Chandler **Poster #C14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Chemistry

Separating Bacteria Engineered to Bioaccumulate Arsenic from Drinking Water Using Microfiltration

Arsenic contamination of drinking water elevates cancer risk and is an ongoing public health concern; both the World Health Organization and the US Environmental Protection Agency have set limits for arsenic in drinking water to 10 ppb—among the lowest of any water contaminant. Millions of people worldwide are exposed to arsenic in their drinking water. In the Northeastern US the problem is acute in rural communities that rely on private wells. These populations often lack the resources to test their well water for arsenic—much less to install and maintain the specialized filters currently recommended for removing arsenic. Commercially available filtration technologies vary substantially in performance depending on local water conditions and still demand large amounts of energy and materials. Thus, there is a need for novel approaches to remove trace levels of arsenic from drinking water using technology and materials that are renewable, inexpensive, and reliable.

We constructed a living filter system that utilizes genetically modified bacteria to remove arsenic from drinking water. Our engineered E. coli selectively adsorb arsenic by expressing a novel protein that has strong and specific arsenic interactions. These living filters can predictably remove arsenic no matter the specific composition of the input water. However, once the engineered bacteria bioaccumulate arsenic, they must be removed from treated water. A living filter system will require microfilters to ensure no bacterial contamination is breaking through into produced water. These filters are substantially cheaper and more reliable than filters designed to remove the molecular forms of arsenic in water (arsenite and arsenate). Hollow fiber filters sold commercially for consumer use can remove bacteria from our living filters and produce water that meets EPA drinking water standards as measured by agar streak plates and qPCR methods. We also evaluated commercial hollow fiber microfilters to determine their load capacity and the effectiveness of cleaning procedures that permit filter reuse. This experimental

information is used in a model that projects the economic cost and efficiency of different use cases for living filters that rely on commercial hollow fiber filters for the secondary treatment of water cleaned by living filters.

Daniel Zhang **Poster #C15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Victor Tsai, Department of Earth, Environmental & Planetary Sciences

Improving the Interpretability of Tomographic Images of Subduction Zones Using Geologically Motivated Parametrizations

Geologic tomography is important because it allows geologists to study the interior of the Earth indirectly, which is otherwise inaccessible due to inhospitable conditions. Understanding this area is essential to understanding Earth's internal dynamics. Current geologic tomography is fraught with issues primarily related to the lack of high-resolution and frequent data from seismic waves and stations, making high-resolution imaging of this area of the Earth difficult. The current approach parametrizes the problem into many pixels and solves for the desired parameter inside these discretized locations. Due to the scarcity of data, image smoothing is inevitable, leading to the inability to resolve the structures which are thought to be present.

Geologic parametrization attempts to resolve the scarcity of data by decreasing the number of parameters required to be solved. This is accomplished by understanding Earth's structure at the location of interest. This project seeks to parameterize a subduction zone into the most important constituents, such as the oceanic lithosphere seismic velocity, oceanic mantle seismic velocity, angle and rate of subduction, and age of the subducting plate. It also incorporates results such as the temperature dependence of seismic velocity in the crust and mantle. One can determine these parameters when knowing the geologic geometry of the system. Using these geologically significant parameters allows for significantly fewer degrees of freedom, which helps solve the issue of the scarcity of available data.

This project also aims to increase the accuracy of the subduction zone model by incorporating more precise and accurate additions to the model, such as diapirs resulting from flux melting of the subducting oceanic lithosphere, thermal contraction of the oceanic lithosphere, and velocity gradients following the geotherm for the oceanic and continental lithosphere. Also present are heat conduction problems with the heating and cooling of the subducting plate and mantle wedge, respectively. By adding these additional factors, the model approaches a more accurate representation of the current consensus of a subduction zone, and aims to resolve these features at a higher resolution.

Dylan Hu **Poster #C16**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Srinath Sridhar, Computer Science

Low-Shot Hierarchical Part Segmentation for Neural Radiance Fields via Large Open-world Models

Recently, large open-world models for segmentation have emerged and demonstrate impressive results

for 2D images. Importantly, flexible prompting for these models enables control over granularity in segmentation. Applying the knowledge of these models in 3D through the training of neural fields enables multi-view consistent volumetric segmentation for tasks like extracting an object from its background. However, the ability to automatically decompose an object into its part hierarchy would further enable tasks in robotics, scene understanding, and virtual and augmented reality. In this work, we demonstrate the presence of hierarchical structure in the feature embeddings of these 2D segmentation models and propose a novel method for incorporating that information during decoding in order to enable hierarchical part-level segmentation of objects in 3D.

Pamil Tamelessio **Poster #C17**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Department of Chemistry; Jingge Chen, Department of Chemistry

Using magnetic nanoparticles to increase filterability in living filters

Groundwater contamination by arsenic is a significant problem for our planet– more than 140 million people worldwide are exposed to arsenic levels above the 10 ug/L recommended by the World Health Organization in their drinking water. Its known health hazards and its widespread prevalence in drinking water have placed arsenic at the top of the US priority list of toxic substances for over a decade. New evidence suggests that the neurological development of young children is particularly sensitive to the adverse effects of arsenic, and there is growing evidence that suggests routes of arsenic exposure can also include common beverages. According to the National Academy of Sciences, an Arsenic level of just 1 ppb (0.001 mg of Arsenic per Liter) in tap water has a cancer risk of 1 in 10,000 people who consume just 2 liters of this water per day.

However, the detection and removal of trace levels of toxic Arsenic from water utilizing safe and abundant components is an unreliable and expensive endeavor. Currently, conventional remediation techniques such as coagulation/filtration or lime softening in conjunction with traditional chemical treatments are unable to remove trace—but still highly toxic—levels of heavy metals and metalloids. Additionally, Arsenic contamination is an issue that disproportionately affects low-income populations. One possible solution to this problem is the recent development of nanomaterials used for heavy metal remediation due to their high adsorption capacities and affinities to heavy metals, particularly iron oxide nanoparticles, which stand out due to their ability to be efficiently removed from water using magnetic separation. However, the selectivity of these nanomaterials poses concern as it is very difficult to discern toxic metals from safe water constituents. As a result, this project aims to utilize bacteria and their genetic components, particularly bacterial metalloproteins, which can effectively bind to their specific metal cofactors. In particular, we plan to combine the efficiency of the bacterial metalloproteins with the efficiency of magnetic nanoparticle separation in an effort to design a living filter that can effectively remove Arsenic from contaminated waters.

Evan Ren **Poster #D1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kareen Coulombe, Biomedical Engineering

Endothelial cell lining of patterned vessels in engineered human myocardium to facilitate

perfusion and integration in a post-infarct heart

In the US, someone experiences a heart attack once every 40 seconds. Given the long-term complications associated with the post-infarct heart, including disrupted blood flow and scarring that interferes with the heart's contractility, current research focuses on replacing lost cardiomyocytes through the delivery of human induced pluripotent stem cell-derived cardiomyocytes. One method of delivering cells includes encapsulation in a collagen scaffold to produce engineered human myocardium (EHM). Research has shown that incorporating human umbilical vein endothelial cells (HUVECs) in pre-patterned EHMs facilitates tissue perfusion and recognition by the host heart via inosculation. Developing endothelialized channels requires manual threading of sacrificial (to be later removed) gelatin-alginate fibers through a polymer tissue mold. This is followed by careful coating with a gelatin-alginate-collagen (GAC) gel containing HUVECs. This project introduces a 3D-printed frame to guide consistent fiber placement and develops a more consistent and compliant GAC coating gel. Once coated, fibers were cast in a collagen scaffold, allowed to set, and the alginate uncrosslinked to produce a patent, endothelialized channel. The hydrogels were then connected to an advanced bioreactor with a peristaltic pump for perfusion and to study the endothelial cell barrier function through diffusion measurements. Increasing the concentration of gelatin from 2.5% to 5% in the fiber-producing crosslinking solution was unable to simplify the HUVEC coating process. Though initial experiments suggest comparable fiber diameters (426 μm vs 439 μm, respectively), subsequent trials revealed a greater prevalence of abnormal fiber formation and fragility associated with the higher gelatin concentration. However, it was found that changing the collagen concentration from 4 mg/mL to either 8 mg/mL or 2 mg/mL in the coating solution decreased the number of abnormal nodal formations during coating while maintaining the gelation properties of the coating gel. Fiber patterns in the hydrogel were varied to ensure the success of perfusion with increased vascularization. Diffusion analysis used hydrogels with one longitudinal channel to allow channel-specific measurements. These results facilitate the development of a consistent and effective coating protocol and will guide future studies on the impacts of hemodynamic shear stress on the maintenance of implanted myocardial tissues.

Gabriel Traietti **Poster #D2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: James Russell, Department of Earth Environment and Planetary Science; Meredith Parish, Department of Earth Environment and Planetary Science

A Middle Pleistocene Hydroclimate Record of Terrestrial Indonesia

Building records of past hydroclimate changes in a region is vital in supporting an increased understanding of the workings of changing climatic patterns. The Indo-Pacific Warm Pool (IPWP), an oceanic region around the Indonesian archipelago and Oceania which continuously has a high sea surface temperature, is the largest driver of atmospheric convection, and therefore deeply affects Earth's whole climate system. Differing climactic proxy records from the region have yet to make a strong consensus on which, if any, orbital scale forces cause climate boundary conditions and variations in the region. The purpose of this broader study is to build a long term (~1.1 ma), high resolution (~2 kyr) terrestrial hydroclimate record using brGDGT and n-alkane proxies from a sediment stack of Lake Towuti, Indonesia. It is the hope that this ~300 kyr temperature record from 830 kyr BP to ~1.1 ma PB will extend the record to understand how the Mid-Pleistocene Transition affected IPWP climate. Furthermore, this record may aid in identifying the important climate forcings in the IPWP, aiding in an improved understanding of the future hydroclimate variability of this region.

Eric Sorge **Poster #D3**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Chemistry, Engineering; Megan Kizer, Chemistry

Whole-Cell Biosensing and Remediation of Arsenic Using E. Coli: Towards Sustainable Materials for Water Treatment

The World Health Organization (WHO) identifies arsenic, a common element in the Earth's crust, as a carcinogenic toxin. Exposure limits in drinking water are set as low as 10 ppb. Arsenic's prevalence in groundwater occurs naturally but is exacerbated by anthropogenic activities, affecting millions of people around the world – particularly those in rural areas. Preventing human exposure to arsenic with accessible, inexpensive, and sustainable technology is crucial. In contrast to conventional strategies employing expensive and cumbersome inorganic sorbents, we focus on a strategy for removing and detecting arsenic in drinking water that exploits engineered bacteria for both bioaccumulation and whole-cell biosensing. A gene coding for a chimeric protein with two different arsenic binding domains was transfected into wild type E. coli; the resulting microbes can reduce arsenic concentrations in water samples containing up to 500 ppb to our instrument detection limit (~ 10 ppt) within 60 minutes. While the dry-weight sorption capacity of these "living sorbents" is less than that of their commercial counterparts, their arsenic affinity and selectivity is much greater. As a result, it is possible to reduce even very low levels of arsenic to acceptable levels using reasonable sorbent loadings.

We investigate strategies for engineering these organisms further to detect arsenic through optical reporters, providing an important integrated solution to the problem of arsenic in drinking water. Environmental arsenite binds to the ArsR transcription regulator, a protein that is central to the function of both the native ars operon and the arsenic bioaccumulation described earlier. This same protein, and the operon it interacts with, can be leveraged to up-regulate a reporter protein such as green fluorescent protein (GFP). Whole-cell biosensors should indicate the presence of arsenic at the extremely low levels relevant to meeting global exposure standards, on the order of ppb. Such sensitivity can be achieved through genetic signal amplification strategies such as the use of engineered positive feedback or the application of multiple optical reporters. Combining whole-cell biosensing with bioremediation capabilities will allow for the simultaneous detection and sequestration of arsenic by biological means, contributing to the creation of a novel and renewable water treatment system.

Lana Yang-Maccini **Poster #D4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mauro Rodriguez, Engineering

Reduced-order model of a wave-induced gas cylinder collapse

Exposure to heterogeneous environments (e.g. pressure waves) may lead to the asymmetric collapse of a gas-filled bubble or cylinder in liquid, which results in a weaker shock wave that propagates outwards. The bubble's morphology during collapse, found by solving the Navier-Stokes equations, is non-trivial. We use potential flow theory and limited morphology data to develop a reduced-order, potential flow theory-informed model of a wave-induced two-dimensional gas-filled cylinder collapse in soft gel. We consider a potential flow composed of a wave, sink, and vortex doublet flow. We can determine the

time-dependent strengths of each of these basic potential flows using the velocity field surrounding the collapse or reconstruct the wave and sink flow using only bubble interface morphology. For the doublet flow, we use spherical harmonic modes up to the tenth mode to estimate strength. The resultant doublet and source strengths compare well with those obtained from the velocity field approach, which will be presented.

Mayayi Izzo **Poster #D5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Anita Shukla, Engineering

Polymyxin B-modified Liposomes for Active Targeting and Treatment of P. aeruginosa Infections

The rise of antibacterial resistance is an urgent threat to global health. Gram-negative bacteria are increasingly resistant to multiple antibiotics, with Pseudomonas aeruginosa being one of three "highest priority" pathogens, according to the World Health Organization. There is an urgent need to develop novel drug delivery methods to target P. aeruginosa infections and enhance the treatment efficacy of existing antibiotics. Liposomes are lipid-based nanoparticles that can encapsulate both hydrophobic and hydrophilic drugs. Liposomes can be functionalized with surface ligands for enhanced drug delivery via active targeting of bacteria. Polymyxin B is a polypeptide antibiotic that has a high affinity for lipid A of lipopolysaccharide, which is found in the outer membrane of Gram-negative bacteria, including P. aeruginosa. Here, we developed PMB-modified liposomes (PMB-Lipo) to target P. aeruginosa infections and increase the quantity of antibiotic delivered to the infection site.

First, PMB was covalently conjugated to the lipid 1,2-distearoyl-sn-glycero-3-phosphoethanolamine-N-[acetyl-(polyethylene glycol)-2000-O-acetic acid] (DSPE-PEG2000-COOH) via EDC-mediated amide formation. Successful conjugation was confirmed via nuclear magnetic resonance (NMR) spectroscopy. The DSPE-PEG2000-PMB conjugate was then incorporated into hydrogenated soy phosphatidylcholine (HSPC) liposomes as the targeting ligand. Unmodified HSPC liposomes (Lipo) were prepared as the control group. Both Lipo and PMB-Lipo were tagged with rhodamine B, a fluorescent molecule, causing the liposomes to fluoresce red. Lipo and PMB-Lipo exhibited a hydrodynamic diameter of ~116 and ~104 nm, respectively. Additionally, the in vitro targeting and antibacterial activities of PMB-Lipo were assessed against P. aeruginosa PA01 via fluorescence spectroscopy and microdilution assays. Lipo and PMB-Lipo were incubated with PA01 and the mixtures were centrifuged to get a pellet of bacteria with bound liposomes. Our preliminary data showed enhanced binding of PMB-Lipo to PA01 compared to Lipo, where the fluorescence of rhodamine B was a measure of liposomes localized to the PA01 in the resuspended pellet. The pellet of PMB-Lipo in PA01 exhibited 32% more fluorescence intensity than that of Lipo. Our results showed that these PMB-Lipo have the potential to increase targeting of antibacterial liposomes to P. aeruginosa for enhanced elimination of these infections.

Anaya Kaul **Poster #D6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kareen Coulombe, Engineering

Designing an endothelial cell-compatible hydrogel for 3D coaxial bioprinting of patterned vasculature in engineered cardiac tissue

As heart disease is the leading cause of death in the U.S., therapeutics to treat patients post-myocardial infarction are increasingly vital to recover cardiac function and prevent the progression of heart failure. One type of treatment to improve heart function provides new cardiomyocytes to replace affected regions either through cell injections into the myocardium or tissue patches implanted onto the surface of the heart. However, these tissues lack vasculature which prevents the delivery of oxygen and nutrients to the new cardiomyocytes to assist in their survival and engraftment with host tissues. Pre-perfused patterned vasculature has been shown to improve engineered cardiac tissue survival and integration, but previous methodology of coating sacrificial hydrogel fibers with endothelial cells (ECs) to be implanted in cardiomyocyte tissue can be laborious as well as limiting to engineering geometric complexity to mimic native vessels in designed vasculature. 3D core-shell bioprinting allows for more customization of vasculature to increase its complexity. It also eliminates the need to coat or seed endothelial cells in hydrogels as they are extruded from the outer needle within the shell gel with a sacrificial gel in the core, allowing the engineering of a hollow channel surrounded by ECs. To establish a compatible EC-containing shell hydrogel for printing, mechanical properties and cell viability in three candidate hydrogels were assessed. Alginate was chosen for its biocompatibility, ability to increase stiffness, and biodegradability, gelatin for its cell-attachment capabilities, and fibrinogen for its role in cell viability. The hydrogels tested were 10% (w/v) gelatin 0.5% (w/v) alginate (GA), GA with 1% (w/v) fibrinogen (GAF), and GAF with 0.2% (w/v) thrombin (GAFT). All gels were cross-linked with calcium chloride at varying concentrations and durations to evaluate mechanical properties while maintaining cell viability to optimize stiffness and print fidelity. Identification of promising bio-inks to create endothelial-lined channels in engineered cardiac tissues for improved cardiac function has the potential to allow for the consistent creation of patterned perfusable vascular networks with complex geometry in tissue engineering applications, leading to better engraftment and integration with host tissues.

Isaiah Olds-Campanile **Poster #D7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Blake Hodgin, Department of Earth, Environmental, and Planetary Sciences

Implications of a Glacial Re-Advance on Block Island

Glacial advances tend to erase the record of previous glaciations, making it difficult to decipher ice sheet extent and sea level before the Last Glacial Maximum (LGM). Block Island is composed primarily of glacial deposits that could provide insight into pre-LGM ice extent. The glacial sediments on Block Island are typically categorized into two units: the 18-25 Ka Upper Drift and the Lower Drift which is of unknown age but believed to have been deposited between 150-25 Ka. The lower drift has been heavily deformed by the advance of the Laurentide ice sheet, suggesting that it was deposited prior to LGM, and its exact age has various implications. If the Laurentide ice sheet reached Block Island pre-LGM, it could explain an earlier emergence of the Bering Strait and the timing of human migration across it into North America.

This scenario would be consistent with recently documented occurrences of humans in North America ~30 Ka, which is thousands of years earlier than previously established. To investigate the timing of pre-LGM ice extent on Block Island, we collected samples to be used for luminescence and radiocarbon dating and examined the stratigraphy and deformation of the Lower Drift. The new dates could help to inform the history of ice sheet extent and sea level change in the context of human migration.

Devynn Wilderman **Poster #D8**

Home Institution: Amherst College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Colleen Dalton, Earth, Environmental, and Planetary Sciences

Inferring mantle flow patters beneath Iceland from the phase velocity of Rayleigh and Love waves

Iceland sits directly on top of both a mantle plume and a spreading ridge, making it a tectonically complex and unique location. Plumes and ridges involve different patterns of flow in the mantle, and how plume-ridge interaction changes those flow patterns remains an open question. In this work we investigate seismic anisotropy in the upper mantle beneath Iceland by measuring and mapping the phase velocities of Rayleigh and Love waves generated by 162 distant earthquakes and recorded at 33 seismic stations in Iceland. Olivine crystals align in the direction of mantle flow, and this alignment causes anisotropy in the speeds of seismic waves. Rayleigh waves are sped up by vertically oriented olivines, whereas Love waves are sped up by horizontally oriented olivines. We measure Rayleigh and Love wave travel times using waveform cross-correlation and consider two methods to calculate the phase velocities; the first converts the change in time of the waves (dt) into single-station travel times, interpolates the surface of those times, and takes the gradient of the surface to compute the Rayleigh wave phase velocity (cR). The other method uses the dt values to directly solve for the velocity maps. The median phase velocities from method 1 yield notably more accurate results compared to the mean velocities, due to the mean's sensitivity to outliers. We find that there are inconsistencies between the phase velocity maps generated by each method, especially at periods beyond 84s.

Damir Kulzhanov **Poster #D9**

Home Institution: Brown University

Summer Research Program: Michael Frank's Lab

Faculty Mentor: Michael Frank, Cognitive, Linguistic & Psychological Sciences

Navigating sequential environments using biologically informed learning algorithms

Reinforcement learning (RL) in computer science characterizes how an agent learns and makes decisions through trial-and-error in its environment to maximize reward. It is highly impactful both in CS applications and in the field of behavioral neuroscience, where dopamine neurons are thought to convey "reward prediction error" signals, which drive learning in RL algorithms. Here, I explore how a biologically informed algorithm (OpAL*) and a classic RL algorithm (actor-critic) behave in a sequential grid navigation task (i.e. grid world). OpAL* is a biologically-inspired computational model that incorporates the dynamics of dopamine in the opponent reward pathways (D1/D2) in a standard 'actor-critic' architecture (Jaskir & Frank, 2023; Collins & Frank, 2016). In contrast to OpAL*, standard RL algorithms demonstrate

decreased performance in simple environments when rewards are infrequent (“lean environment”) relative to when reward is frequent (“rich environment”). Here, we explore whether this asymmetry holds in more complex sequential grid worlds.

Maxwell Ferguson **Poster #D10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Timothy Herbert, Earth, Environmental and Planetary Sciences; Kristin Kimble, Earth, Environmental and Planetary Sciences

Paleoclimate analysis of Pliocene tropical Pacific Ocean using planktonic foraminifera

Marine sediments can provide detailed information for reconstructing paleoclimate records and understanding climate behavior. Fossilized calcium-carbonate structures produced by single-celled organisms called foraminifera (or “forams”) record stable isotopes of oxygen and carbon and can be found in ocean sediments. This project concerns two species of surface and sub-surface dwelling foraminifera, referred to as “planktonic” forams, from the Pliocene (3.0 – 3.6 million years ago). N. dutertrei live at thermocline depth (the boundary between warm and cold water in the ocean), and T. sacculifer live at the ocean surface. Forams from two ocean drilling sites in the eastern equatorial Pacific (EEP), sites 846B and 1338B, are analyzed to examine variability in sea surface temperature (SST) and thermocline depth. The forams are picked from sediment samples and prepared for the isotope ratio mass spectrometer (IRMS). The IRMS outputs values regarding the ratio of δ 18O in each foram (δ18O is the relative abundance of 18O and 16O isotopes). A higher δ18O indicates colder ocean temperature (this value should decrease with depth). Furthermore, a large difference in δ18O values between the two species correlates to a shallow thermocline, and a small difference in δ18O to a deeper thermocline. Using the values generated for many Pliocene samples, the variability of thermocline depth and SST in the tropical Pacific Ocean can be studied. This data is compared to other EEP and global paleoclimate data from the Pliocene for analysis, including alkenone-derived SST and Earth’s obliquity cycles. Further data collection for this project will build a more complete picture of SST and thermocline depth evolution during the Pliocene, a time of similar atmospheric carbon dioxide levels to modern day, but much warmer global temperatures. Site 846 and 1338 are specifically important as they exist in a highly productive area of the Pacific Ocean where upwelling occurs. This region is heavily relied upon for multiple countries’ economic stability. Therefore, understanding the evolution of SST and thermocline depth in the EEP is incredibly important and could help inform decisions regarding climate change in the tropical Pacific.

Chandler Stevenson **Poster #D11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kimani Toussaint, School of Engineering

Signal Processing and Optimization Techniques for Enhanced Physiological Monitoring

We present a comprehensive exploration of innovative methodologies for physiological monitoring through advanced signal processing techniques. The physiological measure of interest was the heart rate, which was obtained through photoplethysmography (PPG), a low-cost optical technique that assesses the volumetric changes in the cardiovascular system. For these experiments, infrared light generated from a

femtosecond laser was shone through the finger and the transmitted light was captured by a detector in the form of a camera and a photodiode. Gaussian and Bessel Beams were tested in multiple trials for their efficacy in pulse oximetry. The time-varying signal obtained from both beams was analyzed using the Fast Fourier Transform (FFT) technique.

An optimized data partitioning method was developed which illustrated the FFT of a calculated window size as a viable approximation of the full dataset; this has significant implications for the design of compact pulse oximeter setups due to its ability to determine the number of samples of a signal it takes to allow for accurate computation. Next, a comparative analysis of noise-reducing digital filters, including Chebyshev, Elliptic, and Butterworth, was undertaken, yielding the Butterworth II filter as the optimum choice due to its performance in preserving PPG signal amplitude, attributable to its ripple-free passband. Cross-correlation was leveraged as a powerful tool for assessing the consistency between the frequency-dependent Fourier Transform and the quasi-periodic time-dependent PPG signal. This validated the robustness of assessing signal similarity across variable readings. This cross-correlation lends itself to a parity peak prediction algorithm (PPPA) that allows users to understand the quality of the signal being processed in real-time. This quality, known as the Signal Quality Index (SQI), was calculated as a function of observed and expected PPG peaks in tandem with the auto-correlation of the PPG data. From here, an algorithm for PPG data flooring was also developed. Lastly, a novel technique was created for peak and trough detection within PPG signals, enabling accurate calculation of heart rate and its variability within a fixed sampling window.

Tyler Lane **Poster #D12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Eric Larson, Mathematics

Towards the Integral Chow Ring of the Moduli Stack of Stable Hyperelliptic Curves of Genus 3

Some of the most natural and interesting questions in algebraic geometry are enumerative in nature. When dealing with an enumerative problem, one considers a certain type object and sets out to compute the number of those which satisfy some specified conditions. Intersection theory is a powerful tool for answering these sorts of questions. Indeed, a common approach to answering them is to construct a moduli space which parameterizes all of our objects, including those which might not satisfy the additional conditions conditions; compute its Chow ring, which captures the space's intersection-theoretic data; and use intersection theory to finish solving our problem. The issue is that even for relatively simple objects, such as algebraic curves, our moduli spaces and their intersection theory are quite complicated. In fact, it wasn't until 2019 that the integral Chow ring of the moduli stack of stable curves of genus 2 was computed by Eric Larson. A natural next step is to look at curves of genus 3. In this case, we can split the moduli stack into two pieces, the hyperelliptic locus, and its complement. The aim of this work is to compute the integral Chow ring of the hyperelliptic locus.

Zachery Gottshall **Poster #D13**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Brenda Rubenstein, Chemistry

Modeling Entanglement Among Fermions

Quantum computers offer the possibility of solving problems in areas such as physics, chemistry, and cryptography that are thought to be intractable by classical means. Despite their potential, building a quantum device capable of outperforming the best classical hardware and algorithms to a useful effect remains an elusive goal. The ideal quantum architecture involves qubits, or basic units of quantum information, that are strongly entangled. While many different types of qubits have been developed, our group is particularly interested in qubits composed of spin bearing molecules. These qubits offer the advantage of properties that can be tuned through edits to their chemical structure, and the possibility of integration into a chemical lattice, which would provide a systematic means of scaling the architecture. However, understanding how entanglement occurs within the qubit itself is an important step for determining its suitability as a quantum information processor. This requires a model of the electrons within the qubit, which can be quite computationally expensive for large molecules. The purpose of this project is to investigate tractable means for modeling this entanglement. To that effect, I have used QuTip, a library designed as a computational tool for quantum simulations, to compute the Hamiltonian for the Hubbard Model, from which a measure of entanglement can be derived. Future steps involve expanding these computational techniques to a model that more accurately captures the molecular structure, and implementing new algorithms that reduce the computing cost further and increase the size of the system that can be modeled.

Gannon Lemaster **Poster #D14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kimani Toussaint, ENGN

A Multifaceted Approach to Improving Physiological Monitoring Enabled by Polarization Optics

The pulse oximeter was developed to be used as a non-invasive alternative to the arterial blood gas analysis, a medical monitoring method that measures arterial blood oxygen saturation (SaO2), the percentage of oxyhemoglobin within arterial blood. Standard pulse oximetry is most commonly based on photoplethysmography (PPG), an optical technique used to quantify blood volume changes in the target microvascular tissue and monitor peripheral oxygen saturation (SpO2) using two wavelengths of light. However, factors such as low perfusion, temperature, skin pigmentation, and internal carbon monoxide levels can affect absorption and scattering rates, leading to errors in readings. A polarization-based approach, specifically using a radially polarized vector beam, is particularly promising in increasing the accuracy of pulse oximetry. This project introduces a mechanical and electrical framework for a highly customizable, modular, and miniaturized pulse oximeter design. Additionally, analysis tools for a modified Monte Carlo simulation have been developed to model optical transport in turbid media for the validation of the proposed theoretical model.

Ben Radick **Poster #D15**

Home Institution: Cambridge, UK

Summer Research Program: Churchill College exchange program

Faculty Mentor: Richard Stratt, Chemistry; Brenda Rubenstein, Chemistry

Modelling slow diffusion in supercooled liquids as a lattice percolation problem

Super-cooled liquids exhibit unusually slow diffusion – I am working in a research group aiming to explain this phenomenon. The group views the slow diffusion as being due to the large, winding nature of the geodesic between states through the 'potential energy landscape' at low temperature. This perspective differs from the Arrhenius equation, which assumes rates are only dependent on the largest energy barrier between states, not the topology of the paths between them. The group has made progress by considering how the diffusion constant D depends on the length of the geodesic g. Further improvements could be made by considering the effect on D of there existing multiple paths between states, and probing the nature of these paths (e.g., how narrow/wide they become); I have been attempting to study this effect by drawing an analogy with electrical circuits as there already exists machinery for understanding the effect of multiple paths on conductivity, namely Kirchhoff's and Ohm's laws. I have considered a 2D square lattice, with edges representing resistors, in which only a fraction p of edges remains, chosen at random to induce disorder. This 'lattice percolation problem' lends itself to computer simulations, and this is how I am approaching my research. It is well known that on an infinite grid, there is a percolation transition p = pc below which there exists no infinite connected subgraph, meaning no long-range conductivity. Slow diffusion corresponds to being just above the percolation transition point. Computationally, calculating resistance is too inefficient to be helpful on large grids. Aided by a supercomputer, I am trying to find more efficient ways to gain insight about a graph's resistances that can be scaled, and determine what information is best to extract. For example, if most of a path's resistance arises from a single small region of the graph, computation could be greatly reduced by first identifying such regions, and only carrying out calculations there.

Anna Novatney **Poster #D16**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Karen Fischer, Earth, Environmental, and Planetary Sciences

Finding Earthquake Faults in Nicaragua with High Accuracy Earthquake Relocation

Nicaragua, situated on a complex system of faults within the Caribbean tectonic plate, has a history of devastating earthquakes due the subducting Cocos plate. These faults are primarily oriented to the northeast. However, the 2014 Lake Managua earthquake presented an exceptional case, occurring on a northwest fault and followed by volcanic activity and two smaller earthquakes in 2016. The fault plane responsible for the 2016 earthquake, near San Cristobal volcano, is not well understood. In this project, we aim to enhance the understanding of the 2014 and 2016 earthquake faults, along with their relationships to neighboring volcanoes, through high accuracy relocation of their aftershocks. Aftershocks typically cluster along the same fault plane, thus offering valuable information to delineate the primary event fault plane accurately. Leveraging new seismic waveform data from INETER and utilizing relative travel-times, we have improved the locations of the aftershocks, thereby determining the dimensions and orientations of the fault planes. Additionally, our analyses explore the temporal history of aftershocks to determine which portions of the fault planes broke first, how different fault planes interacted with each

other, and how they related to Momotombo volcano. Furthermore, we have examined other active faults in the region, including the nearby fault associated with the 1972 Managua earthquake. These results significantly better constraints on the locations, orientations, and extents of the 2014 and 2016 earthquake faults, shedding light on their behavior in relation to adjacent volcanic activity.

Ryan Doherty **Poster #D17**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vicki Colvin, Chemistry

Nanoparticle Accelerants for FUS- LC Liquid-Liquid Phase Separation

Biomolecular condensates, also known as membrane-less organelles, play a critical role in cellular organization, and their dysregulation has been linked to multiple disorders including neurodegenerative diseases and cancers. They form through a liquid-liquid phase separation process (LLPS) that occurs when LLPS-forming proteins demix into higher concentration and lower concentration phases within a cell. Understanding what triggers LLPS formation and the role that protein structure may play remains an active area of research. Previous studies have shown that some small molecules and polymers may promote LLPS paving the way for generating druggable targets for this important class of biomolecules. This study evaluates whether nanoparticles can serve as accelerants for this biological process ex-situ.

Gold nanoparticles coated with polyethylene glycol (PEG) have previously been shown to be crowding agents able to accelerate protein-protein interactions during crystallization processes. Given that crystallization requires a liquid-liquid phase separation (LLPS) step, we expected that these same materials would also accelerate the LLPS of candidate proteins. Au-PEG nanoparticle conjugates (AuNP-PEG) also can expand the set of conditions that allow for protein-protein interactions to occur.

This study looks to understand how the inorganic core diameter of AuNP-PEG and the PEG chain length — both important variables in designing agents that are efficient accelerants — can change the rate of liquid-liquid phase separation (LLPS) and the properties of condensates. Such design of the organic-inorganic interface allows us to create better tools to promote LLPS. AuNP-PEG of various core diameters was prepared and functionalized with varying chain lengths of polymers from 1,000 to 40,000 molecular weight. Optical microscopy was used to evaluate the kinetics of LLPS in addition to other spectroscopic tools. We also analyzed biomolecular condensate diameter, density, and other material properties.

Materials that accelerate the liquid-liquid phase separation (LLPS) should also promote LLPS under less extreme solution phase conditions. In the presence of accelerants, this phase space should be expanded. A screening procedure was performed at various protein and salt concentrations to determine if the presence of AuNP-PEG would induce LLPS in more diverse conditions. A phase map was developed to understand this expanded range of phase separation.

Jack Kolman **Poster #E1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Roberto Zenit, School of Engineering

Experimental Demonstration of Reciprocal Swimming at Intermediate Reynolds Numbers

We examine a swimmer containing two rigid spheres that oscillate periodically along a common axis, experimentally proving that a reciprocal motion swimmer can swim in an intermediate Reynolds number fluid. We construct a version of this robot, which consists of two resin printed hollow spheres, controlled by an arduino connected to an IR sensor for remote control. An aluminum shaft connects the smaller sphere to a 3D printed motor-linkage system in the larger sphere. We also explore the feasibility of large scale Particle Shadow Velocimetry (PSV) as a cheaper and simpler alternative to Particle Image Velocimetry (PIV). PSV uses an LED in line with the camera (as opposed to a laser sheet normal to the camera line of sight like in PIV), allowing the camera to see the shadows of tracer particles in the fluid. This makes non-intrusive optical flow analysis more accessible, as the expensive lasers and optics used in PIV are not necessary.

Arnav Singhal **Poster #E2**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Richard Stratt, Chemistry

A Bare-bones Approach to Modeling Polymer Folding and Misfolding

Proteins are considered heteropolymers, meaning they are made up of a linear chain of distinct “pieces” (amino acids). Understanding how they fold in a solvated environment dictates their function, particularly for those acting as enzymes. However, rather than having one specific energetically-preferred conformation, some proteins are “inherently disordered,” meaning they have multiple possible shapes at relatively similar energy costs. This can lead to folding incorrectly, or “misfolding”, which causes proteins to fail in their functions and can lead to diseases.

We attempt to model these proteins in the simplest possible manner while still achieving these results of folding and misfolding. For example, we treat amino acids and the water solvent they are in–all molecules made up of many atoms–each as single atoms with relatively simple interactions between them. This bare-bones approach will allow us to see through the potentially confounding factors found in the vast amount of information encoded by the complex structures of amino acids in water, exposing the fundamental nature and reasons for how and why polymers, including proteins, fold and misfold more generally.

To begin, we attempt to form structures by adjusting the parameters of a standard Lennard-Jones model and assess the model’s success by running it through a simulation and seeing the polymer’s “closeness” to our goal evolve over time, with the eventual goal of being able to create structures that fold and misfold, so that we can see and analyze the pathways taken in both cases. Picking which structures to attempt to create and how readily they are formed also informs us as to what kinds of structures and substructures are possible, giving us vocabulary and categorization.

Daniel Graves **Poster #E3**

Home Institution: Brown University

Summer Research Program: IBES internship program

Faculty Mentor: Dawn King, Institute at Brown for Environment and Society

Conservation of Rhode Island Watersheds and the Human Value of Conservation

When evaluating conservation plans and strategies, considering the direct value of ecosystem services to humans is essential. Providing natural filtration of water is one of those services. In Rhode Island, most drinking water comes from surface reservoirs, ponds, and lakes. In this project, I analyze the extent of land conservation within the watersheds of drinking water sources throughout the state. I also calculate the proportion of riparian area conserved and the extent of wetland conservation within each watershed. Based on the current extent of conservation and water usage rates across the state, I highlight the most impactful conservation areas currently and recommend areas to target for future conservation.

Shuah Yu **Poster #E4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Charles Zuker, Neuroscience

Investigating the Neural Substrates of Neurohormones Involved in Feeding

The neural mechanisms of feeding offer important implications in treating health issues such as obesity and eating disorders; yet they are poorly understood. Thus, we investigated the neural basis of several neurohormones that may mediate feeding in mice. Using the immediate early gene FOS as a proxy for neural activity, we found that certain neurohormones induced strong bilateral activation of the parabrachial nucleus (PBN) and paraventricular hypothalamus (PVH). The PVH and PBN have been previously implicated to be key players in modulating energy expenditure as well as satiety and reward responses.

Shreyas Waghe **Poster #E5**

Home Institution: University of Massachusetts Amherst

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Chen Sun, Computer Science

Generative Modeling using Diffusion: From the Ground-Up

Given a set of samples from some process, the task of a generative model is to approximate the actual distribution of data generated from this process. Once learnt, this distribution is sampled to produce novel data instances. For example, given a set of images of cats, generative models can generate more pictures of cats. This project focuses on Diffusion Models as a framework for flexible generative modeling and its applications.

Diffusion Models model a complex generative process as stepwise denoising of random data, where each step is a reversible (de)noisification with some restrictive assumptions. Thus, starting with an initial sample from a standard probabilistic distribution, Diffusion models can generate meaningful results by applying a number of denoisifying steps to the sample.

Diffusion Models have an interpretation through energy-based and score-based models as well - where the models approximate and learn the probability distribution underpinning the generative process through estimating log gradients (score) of the distribution. Here, generating results from the Diffusion model is equivalent to random sampling from around the modes of the approximated distribution through a process known as Langevin dynamics.

Diffusion Models have found widespread application in several complex machine learning tasks – image generation (Stable Diffusion, Imagen), image reconstruction, image inpainting, reinforcement learning (Decision-Diffuser), Black Box Optimization etc. This success is strengthened by Diffusion Models outperforming GANs, the previous state-of-the-art, in image synthesis. This project builds up to these applications by studying generative models from the ground up through the fundamentals of Deep Learning, Variational Auto-Encoders, Conditional Auto-Encoders, Score Networks, Conditional Score Networks and the interplay between these interpretations of Diffusion Models.

Jacob Koster **Poster #E6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Edith Mathiowitz, Pathology and Laboratory Medicine

Investigation of Mesophase Induction in Varying PLGA/PCL Polymer Blends

Polymeric biomaterials, particularly polylactic-co-glycolic acid (PLGA) and polycaprolactone (PCL), have shown significant promise in a variety of biomedical applications due to their tunable properties and biodegradability. The phase behavior of polymer blends plays a critical role in determining their physical properties and utility in biomedical applications. This study focuses on investigating the impact of various PLGA/PCL blend ratios on the induction of mesophase under a set thermal and pressure treatment protocol.

A series of PLGA/PCL blends with different mass ratios were prepared and subjected to either two distinct pressing stages or only the first pressing stage. The first stage involved applying 10,000 pounds for 15 minutes. In the second stage, the samples were pressed at 50°C under 20,000 pounds for 10 minutes, followed by a 5 minute cooling period.

Characterization of the resulting mesophases was carried out using polarized light microscopy (PLM) and 2D x-ray diffraction (XRD) employing a D8 Bruker Diffractometer. PLM allowed for the visual assessment of mesophase formation, while the XRD provided details on the blend's crystalline structure.

The results of this research could have implications for the optimization of polymer blends in the context of drug delivery, tissue engineering, and bio-compatible implant fabrication. A better understanding of mesophase induction in PLGA and PCL blends not only contributes to the fundamental knowledge of polymer blend behavior but also expands the design parameters for fabricating advanced biodegradable

polymer-based devices. Further studies should be conducted to better understand the factors leading to the induction of mesophase and the impact of a larger library of polymers on mesophase induction.

Social Science

Mina Sarmas; Kenneth Kang **Poster #E7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Melissa Palma, Family Medicine

TayoHelp.com: Culturally Tailored Health Education and Community Based Participatory Research for Filipino Americans

Filipinx/a/o Americans have high CVD prevalence and mortality. The National Heart, Lung, and Blood Institute (NHLBI) The Heart Truth® Healthy Heart, Healthy Family (HHHF) curriculum, created in 2008, provides culturally-tailored heart health education materials for Filipinx/a/os. FYLPRO Tayo evaluated individual and community perceptions of heart health and the quality, accessibility, and perceived value of knowledge/behavior change from HHHF materials. Qualitative focus groups and online surveys queried: community health workers, health professionals, and caregivers and community members who self-identified as Filipinx/a/o American living in the U.S. Recommendations to improve cultural relevance included translating handouts into local languages (Ilokano, Bisaya), increasing intergenerational representation, updating medical knowledge, addressing structural factors/social determinants of health affecting Filipinx/a/o American communities, and incorporating multimedia content to improve outreach. Culturally-tailored information and outreach is critical in supporting heart health in Filipinx/a/o American communities

Sima Raha; Anahis Luna **Poster #E8 & #E9**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Kevin Escudero, Sociology; Rachel Freeman-Wong,

Immigrant Student Research Project (ISRP)

The Immigrant Student Research Project (ISRP) is a comprehensive inquiry into the educational needs and experiences of immigrant students in the American educational system, particularly in graduate school programs. It is essential to address the particular difficulties experienced by immigrant students and to create effective strategies to support their academic performance in light of the growing diversity and complexity of the United States' immigrant community. An overview of the ISRP, this abstract summarizes its goals, methods, challenges encountered, and ramifications.

The ISRP's main goal is to provide an in-depth overview of immigrant students' educational experiences through a national survey. To gather a variety of viewpoints, the study will combine an online survey with

follow-up qualitative interviews. The group being studied comprises immigrant students with a range of backgrounds, including various immigration statuses, countries of birth, and levels of English language ability. Our presentation will include a discussion of challenges while doing this study related to community outreach, categorizing students' immigration statuses, and its method.
Ramifications of the Immigrant Student Research Project for universities, educators, policymakers, and scholars involved in immigrant student education, are crucial. Institutions of higher education can build inclusive learning environments to support the academic achievement and overall well-being of immigrant students by addressing issues and recommendations that will be discovered in this project to enhance immigrant students' educational and professional experiences.

In conclusion, the Immigrant Students Project will offer significant insightful data about the needs and experiences of immigrant students within the American educational system as we are currently working to finalize and field the national survey. Considering graduate students' immigration statuses via this project, we have been working to create more opportunities and an equal educational environment so that immigrant students could thrive academically successfully and succeed in their professional life to contribute more to the country.

Christine Alcindor; Daliza Reinoso **Poster #E10**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Laura Stroud, Department of Psychiatry and Human Behavior; Zoe Mollicone, Department of Psychiatry and Human Behavior

Impact of Maternal Prenatal Smoking on Fetal Neurobehavioral Development Insights from Fetal Behavioral Coding

Our research project aims to investigate the impact of maternal smoking during pregnancy on fetal neurobehavioral development by utilizing the Fetal Neurobehavior Coding System. Maternal smoking during pregnancy has been associated with adverse outcomes in both maternal and fetal health, making it a critical public health concern.

The Fetal Neurobehavior Coding System (FENS) is a standardized tool used to assess and quantify fetal neurobehavioral responses to external stimuli during different stages of pregnancy (Salisbury, Fallone, & Lester, 2005). The FENS provides a systematic and objective method of observing and analyzing fetal movements, reflexes, and behavioral reactions to various stimuli during ultrasound examinations.

The FENS allows researchers and healthcare professionals to gain insights into the developing fetal nervous system's functionality and responsiveness. By evaluating specific neurobehavioral patterns, the FENS helps identify potential abnormalities or deviations in fetal neurodevelopment.

The focus of our research project is to explain how the FENS works and how the FENS is used to conduct fetal neurobehavioral assessments and observe fetal responses to mild external stimuli. We also want to explain the intricacies of the FENS scoring criteria and how this coding helps to characterize fetal movements, reflexes, and reactions to stimuli.

Data analysis will involve examining the relationship between maternal smoking and fetal neurobehavioral development, as indicated by the FENS scores. It is hoped that the results of this research will contribute to a deeper understanding of the impact of maternal smoking on fetal neurodevelopment. By shedding light on the specific effects of smoking on the developing fetal nervous system, the findings may inform

targeted interventions and raise awareness among pregnant women and healthcare providers about the risks of smoking during pregnancy.

In conclusion, our research project will examine the ways the Fetal Neurobehavior Coding System (FENS) investigates the relationship between maternal smoking and fetal neurobehavioral development. These findings are crucial because they have the potential to contribute significantly to maternal and child health in the future.

Britney De Leon; Jerry Quan **Poster #E11 & #E12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Suzanne Colby, Behavioral and Decision Sciences

Alcohol in the Media: An investigation of Adolescent Exposure to Alcohol Content in Social Media and Entertainment Media

This abstract presents a research study focused on investigating the extent and nature of adolescent exposure to alcohol content in popular social media platforms as well as general entertainment media.

This study employs a Smartphone app to enable adolescent participants to monitor and report their daily exposure to alcohol content in any form of traditional or digital media. Our UTRA project focuses on depictions of alcohol within music, through uploading images and text descriptions of what they are hearing. Participants' text and image uploads go through a coding process that assesses the sentiment, depiction, degree of usage, and positive/negative associations of alcohol.

In this poster, we will present preliminary results of our coding project. We will examine the common trends of songs that have been reported to date as well as the most commonly reported songs and artists. Additionally, we will delve into the number and percentage of lyrics retrieved while using the coding system we developed for analyzing the lyrics.

In conclusion, this research contributes to the larger literature in the area of adolescent exposure to alcohol content in media, shedding light on the prevalence and characteristics of alcohol-related messages within music on social media platforms and entertainment media. By gaining insights into the influence of such content on teenagers, investigators will aim to develop literacy programs that empower adolescents to make informed decisions and navigate media in a healthier manner. The strengths of this research lie in its innovative use of technology and participant-driven data collection, which provide a comprehensive view of the issue, and we believe our findings will have practical implications for promoting media literacy and positively influencing adolescent behavior.

Kayla Robinson **Poster #E13**

Home Institution: Emory University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Malabika Sarker, School of Public Health

What influences COVID-19 vaccination among school students in Bangladesh; A cross-sectional study

The COVID-19 pandemic presented unprecedented challenges, especially to nations without a history of large-scale healthcare crises. Bangladesh, a small country with no experience mitigating pandemics, struggled to flatten the curve while restoring normalcy.
The COVID-19 pandemic disrupted Bangladesh's educational systems, affecting over 37 million children for 18 months. Implementing preventive measures such as mask-wearing, physical distancing, and handwashing effectively reduced COVID-19 transmission rates in Bangladesh and served as potential models for other South Asian countries. However, significant challenges, including limited healthcare infrastructure, comorbidities among patients, and low recovery rates, hampered the initial response. Researchers played a vital role in public health efforts by conducting surveys to gauge general knowledge about COVID-19 prevention protocols and prevention methods, focusing on educating the public, but few studies involved schoolchildren.
Despite extensive research on university students, parents, and healthcare workers, little is known about what influences their participation in Covid vaccination. Challenges faced by children in accessing vaccines, including issues related to registration, lack of information, and skepticism surrounding specific vaccines, warrant a closer examination. There were notable gaps in knowledge between households whose children attended religious schools versus households where children attended secular schools. This study investigates factors associated with school children toward COVID-19 prevention protocols and vaccination in Bangladesh.
Our findings indicate a significant trend between parent and student vaccination among school children of both faith-based and secular schools. Addressing the gap in school childrens' public health knowledge is an efficient way to know if the information is relayed correctly.

Angel Barraza Estrada **Poster #E14**
Home Institution: Pitzer College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Andrea Flores, Anthropology of Education; Katherine A. Mason, Anthropology

Unmasking Covid-19's Impact on First-Gen Students' Educational Journeys

The Covid-19 pandemic has posed numerous challenges for students worldwide, even more so to those from historically marginalized groups. First-generation college students (FGCS), as pioneers in their families entering academic spaces, already encounter challenges when navigating these environments. The COVID-19 pandemic further compounded their existing stressors, leading to unemployment, food insecurity, and restricted access to academic resources and spaces (virtually and physically). Consequently, FGCS are compelled to shift their focus from academic pursuits to managing these additional burdens. The primary objective of this study is to shed light on the different strategies employed by FGCS in overcoming the educational challenges brought about by the pandemic. Through the Pandemic Journaling Project (PJP), FGCS are provided with a virtual platform to share their firsthand experiences of the COVID-19 pandemic through journaling, dyadic interviews, and one-on-one interviews. The data collected for this study exclusively comes from the PJP, incorporating monthly journal entries and one-on-one interviews from two FGCS participants. By examining the experiences of two FGCS we attempt to answer the question: Considering the existing impact of COVID-19 on FGCS' schooling and education, what strategies have FGCS developed in response to the pandemic? Though the results are preliminary, various stories that were shared with the PJP researchers show first hand FGCS student's resiliency and adaptability in their approaches to learning while facing the COVID-19 pandemic.

Aseel Rafat **Poster #E15**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Karin Arsenault, Public Health and Community Service

The Simulation Empathy Project: Enhancing Dental Education and Practice for Older Adults

The World Health Organization reported that in 2020 over one billion adults in the world were aged 60 years and over, with that number expected to double by the year 2050. As the age of the global population continuously rises, there is an increasing need for geriatric dental care. Nevertheless, dental training in geriatric dentistry is limited, thus creating a deficiency in the knowledge necessary to optimal care and empathy for the challenges older adults face. These challenges have been well defined in scientific literature as age-related changes in the dexterity, making it difficult to perform tasks such as brushing, reduced visual acuity and higher risk of cataracts, as well as an increased prevalence in hearing loss.

This study aims to simulate these changes through the use of an aging suit, which highlights physical and sensory aging. The literature strongly supports that immersive simulations can enhance empathy and improve clinical skills among healthcare workers. By using the aging simulation, dental students at the Tufts University School of Dental Medicine will receive a unique and immersive learning experience that enhances their empathy and communication skills towards older adults, while filling a critical gap in their knowledge.

This study uses a comprehensive curriculum that includes an asynchronous learning module, as well as pre- and post-surveys to assess the impact of the simulation on empathy and person-centered care in geriatric dentistry. Thus far a pilot study has been taking place since April of 2023, with students using simulated aging tools before the upcoming purchase of the aging suits. Many students have reported a tremendous positive impact on their empathy and clinical care as a result of the aging simulation present in their geriatric rotation.

By promoting inclusivity and better understanding of the needs of the elderly population, this project has the potential to improve the quality of dental care for older adults, ultimately leading to better overall health outcomes. Moreover, it aims to promote a more empathetic and person-centered approach to care, addressing ageism and ableism, and improving the quality of dental care for older adults and individuals with special needs.

Day Baez **Poster #E16**

Home Institution: Connecticut College

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Thomas Bayer, Department of Medicine at Alpert Medical School - Geriatrics and Palliative Medicine

"Unlocking the Link between Limited English Proficiency and Dementia Diagnosis: An Age of Immigration Perspective”

Title: "Unlocking the Link between Limited English Proficiency and Dementia Diagnosis: An Age of

Immigration Perspective”

Authors: Day Baez, Thomas Bayer MD, ScM

Institutions: Connecticut College, New London, CT, Alpert Medical School of Brown University, Providence, RI

Objectives: This study investigates the association between Limited English Proficiency (LEP) and dementia diagnosis in people within their age of immigration. Not receiving a diagnosis of dementia because of barriers can have significant harmful effects, such as: missed opportunities for appropriate care, increased caregiver burden, and potential negative consequences for the overall well-being of individuals and their families.

Methods: Data was drawn from round 5, in the year 2017 of the National Health and Aging Trends Study (NHATS). We included participants who had immigrated to the United States. A generalized linear model was performed and used with the family Gaussian and the link “identity”.

Results: Our weighted analytic sample represented 4,888,904 individuals. 10,781 (17%) of people who immigrated young and had LEP were diagnosed with dementia and 99,037 (7.8%) of people who immigrated old and had LEP were diagnosed with dementia. In contrast, 25,230 (97%) of people who immigrated young and do not have LEP were diagnosed with dementia and 1,069,078 (98%) of people who immigrated old and do not have LEP were diagnosed with dementia.

Conclusions: In this retrospective study, it was found that the rate of dementia diagnosis was lower in persons with LEP. It is unclear whether this represents a difference in health status or a difference in health care delivery for people with LEP. It is crucial to implement ways to reduce language barriers within healthcare when it comes to diagnosing patients.

Sofia Gerlein **Poster #E17**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Mascha van't Wout-Frank, Department of Psychiatry

Developing an accessible method to individualize transcranial direct current stimulation for optimal application

Transcranial direct current stimulation (tDCS) is a noninvasive brain stimulation technique that is being tested as an affordable, accessible treatment for psychiatric disorders, including posttraumatic stress disorder (PTSD). tDCS involves the application of a low level electrical current to change the likelihood of neuronal firing, and shows promise in modulating cognitive processes relevant to PTSD. However, the effects of tDCS vary drastically per individual, contributing not only to skepticism about tDCS as a neuromodulatory technique but also our inability to assess tDCS effectiveness. This variability can be attributed to the fact that the intensity of stimulation for tDCS is typically a fixed current (between 1-2mA), yet individual neuroanatomy does affect the current flow for the electrical fields generated in the brain by tDCS. This causes unpredictable, inter-individual differences in the amount of voltage gradient reaching the brain region(s) modulated by tDCS, resulting in large dosage variations of applied current. While it is possible to individualize tDCS dosage by MRI scanning each participant, calculating the electrical fields generated by tDCS, and reverse calculating the needed stimulation intensity, requiring MRI scans substantially reduces the cost effectiveness of tDCS and is inaccessible for many clinics. A possible

solution to this issue is the creation of guidelines dependent on accessible variables that can allow for individualizing tDCS intensity without the use of MRI scans. The current project aims to test if two easily accessible variables, sex-assigned-at-birth and age, affect the electrical field induced by tDCS. By pulling a large number of MRI scans from open access databases and running them through the ROAST (Realistic volumetric-approach to simulate transcranial electric stimulation) pipeline, we can reverse calculate the needed stimulation intensity for a large sample size, as well as a include variety in sex and age. With this data, we hope to develop guidelines of stimulation based on the differences of tDCS intensity for different age groups and sex-assigned-at-birth.

Rachel Gunderson **Poster #F1**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Portia Cornell, Health Services, Policy, and Practice

State-level Description of Medicaid Policy and Access to Licensed Assisted Living Care for Low-Income Adults

This project aims to investigate the funding and regulation of assisted living for low-income older adults who require assistance with their care needs. Many older adults who cannot live independently rely on assisted living or residential care for support. As a result, a growing percentage of Medicaid funds are being allocated to care in assisted living settings. However, unlike nursing homes, assisted living is not regulated or funded on the federal level, resulting in significant heterogeneity in coverage among states. States license assisted living facilities individually and finance care through different mechanisms such as Medicaid state plan amendments and waivers. States offer different levels of licenses for assisted living facilities that regulate the care and oversight that can be provided. However, in some states, not all licenses are eligible for state plan or waiver coverage. Due to this variation, coverage for assisted living is not well-documented on the licensed setting level. National studies typically analyze Medicaid funding at the state level, without distinguishing among different types of assisted living license types, which can vary greatly even within states.

This research seeks to address the limited understanding of Medicaid-funded assisted living on the licensed setting level. We describe the types of Medicaid waivers and amendments that states use to fund care in assisted living and identify the characteristics of individuals who have access to these funds (i.e., dual enrollment in Medicare and Medicaid, demographics, and chronic conditions). Additionally, using previously identified health services types for each license, we connect access to Medicaid funding with the type of care and level of oversight provided for each license type. This study aims to provide valuable insights into how various approaches to Medicaid-funded assisted living impact the quality and accessibility of care. This work will be beneficial for future research to evaluate the effectiveness of different funding strategies to ensure that vulnerable populations receive appropriate and effective care in assisted living facilities.

Sylvia E **Poster #F2**

Home Institution: University of Illinois Urbana Champaign

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Roman Feiman, Cognitive, Linguistic, and Psychological Sciences; Ellie Pavlick, Computer Science

The (And)venture Begins: Expl(or)ing How Thirty to Thirty-Six-Month-Olds Gain Comprehension of "And" & "Or"

While we intuitively understand that children comprehend words like 'fish,' 'blue,' and 'car' by relating words and sensory experiences, it is more difficult to understand how they comprehend logical connectives such as 'and' and 'or,' whose meanings are not concrete objects or events that can be directly sensed. Prior research has established that 30 - 36 month-olds understand the difference between 'and,' and 'or' between noun phrases. We do not know whether they have learned specifically how to use "and" and "or" to coordinate nouns, or if they understand the full, general meanings of these words. We investigate whether 30 to 36 month-olds' performance on comprehension-based tasks involving "and" and "or" support an item-based or abstractionist explanation for how children comprehend logical connectives. If an item-based explanation is correct, then children should understand how "and" and "or" co-ordinate nouns before they understand how those words coordinate adjectives. This is because "and" appears between noun phrases more frequently than between adjectives. When a type of phrase is encountered more frequently, it is grasped more rapidly. If an abstractionist view is correct, children should understand "and" and "or" between nouns and adjectives at the same time. Our corpus analysis of parent-child dialogues from the CHILDES database finds that children under 36 months of age are more frequently exposed to "and" and "or" between two nouns than two adjectives. Therefore, we predict that if an item-based view is correct, 30 to 36 month-olds should make errors in comprehension tasks involving two adjectives at a higher rate than tasks with two nouns. If an abstractionist view is correct, then errors involving two adjectives or two nouns should occur at the same rate.

Suha Khan **Poster #F3**

Home Institution: Cornell University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Jennifer Primack, Psychiatry and Human Behavior

Unveiling the Dangers of Masculinity: Are Gender Norms Contributing to a Higher Rate of Suicide in Men Compared to Women?

Why do men die of suicide 3.90x more frequently than women, when women are 1.9x more likely to attempt suicide? Is it due to the lethal means through which men attempt suicide with? In this paper, we will conduct a literature review to understand this trend, looking at 40 articles from 2010 - 2023. Suicide is currently the 11th leading cause of death, and is a public health issue for both men and women. Men using fatal means for suicide may be influenced by masculine gender norms including self-reliance and aggression. However, since women attempt more frequently, reviews often don't take a deeper look at discussing masculine gender norm adherence and how that can contribute to the higher mortality rate in men. Also, previous reviews rarely provide a holistic overview regarding socio-demographic factors and their affect on male suicide. We'll conduct our review through databases such as PubMed and MEDLINE,

using key terms such as “gender differences in suicide behavior”, “men and suicide”, and “masculinity and suicide”. Using this information, we’ll summarize what risk factors are contributing to men dying at higher rates through suicide. Secondly, we will look at masculine norm adherence and how it might impact suicidal ideation/behaviors in men. We’ll highlight a few ways in which intersectionality affects this relationship. This includes demographic factors such as age, race, gender, and ethnicity. Afterwards, we will discuss what implications for clinical intervention or prevention strategies these articles point to and what needs to be further looked into for future research.

Joshua Benzon **Poster #F4**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Daphna Buchsbaum, Cognitive Linguistic & Psychological Sciences (CLPS)

Web Experiment Design in Cognitive Developmental Research

This web application and an animation storyboard facilitated by the presence of Robbie the Robot provides a novel approach to improve children's learning experiences. One approach to enhance children's understanding of mathematical functions is by building a web application featuring a storyline of apple growth over time. The narrative consists of 15 bars, each representing the growth of apples and revealing distinct patterns of mathematical functions. Researchers can tailor the curriculum by selecting trial types, functions, and sample sizes through an interactive user interface.

Additionally, this app offers three trial rounds: a practice trial with one bar, where users can interactively reveal apples; a sample trial with all 15 bars and its hidden apples, where users can select which bars to sample from; and a predict trial, where users can guess the number of apples that align with the chosen function based on their previously sampled bars or a preset representation. The difference between the guessed and actual apples (the error) is calculated to assess their understanding. Furthermore, to enhance the experimental preface for children, animated short clips of a cartoon robot named Robbie were incorporated. These clips, featuring simple gestures and emotional expressions, create scenarios that children can watch, effectively priming them for future experiments.

Samira Lakhiani **Poster #F5**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: David Badre, Cognitive, Linguistic, and Psychological Sciences; Apoorva Bhandari, Cognitive, Linguistic, and Psychological Sciences

Examining Post-error Cognitive Control in Multitasking and Task Switching

Our study’s overall goal is to employ fMRI techniques to determine how neural geometries are reshaped as a result of multitasking practice. We ran a behavioral pilot that introduced participants (N=17) to 3 different, simple categorization tasks and then measured their ability to switch between them and carry out two of them concurrently. Here, we investigate post-error slowing, a phenomenon that exhibits slower response times following an error that reflects an increase in caution. We examine how this phenomenon influences multitasking and task switching behavior and how this influence changes with practice. Characterizing the influences of post-error slowing on multi-tasking is significant to our study as they will

likely inform hypotheses about the neural changes that occur with multitasking practice, which we hope to test in the fMRI phase of the experiment. These behavioral analyses are a stepping stone to understanding the capacity of the brain to multitask and task switch in our everyday lives.

Jadyn Ligoo **Poster #F6**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Jessie Trudeau, Center for Philosophy, Politics, and Economics

Hey you in the blue uniform! A spatial exploration of extra-judicial killings in Nairobi (2020-2021)

Kenya's capital city Nairobi has consistently maintained the highest rate of police violence in the country and in 2017, was reported to have the highest rate of extrajudicial killings of civilians in the country. Everyday encounters with the police are wrought with a combination of fear, disbelief and loaded with dismay at the normalcy of the situation. Arguably, a gap in mapping extrajudicial killings has undermined the public's ability to understand and interrogate the disproportionate spread of extrajudicial killings which, in the public psyche (especially for working class Kenyans), has normalized the act and its extent into near oblivion. However, responses such as community organizing by civil society and community protests serve as an attestation to the manipulation of power by men and women in blue uniforms. I worked to create a map that visually demonstrates the rationalization and state mobilization of violence on a more micro scale by geographically situating extra-judicial killings within the context of a city, examining how violence has been conceptualized, practiced, and legitimized.

The project visually demonstrates the ways in which Kenya's national government has mobilized violence through varied police bodies to systematically kill its poorest residents while simultaneously asserting their exclusion from the Kenyan state. The relationship between targets of police violence and the police bodies has proven to be one impossible to analyze without consideration of the role that structural poverty has played, effectively creating peripheral citizenship that has led to a disregard for the loss of life caused by the police in blue uniforms.

Danielle Whisnant **Poster #F7**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Lauren Micalizzi, Public Health: Center for Alcohol and Addiction Studies

Associations Between Perceived Harms of Cannabis Use and Demographic Characteristics

The prevalence of adult cannabis use has increased with the progressive national legalization of cannabis. While the true harms of cannabis use have not changed, perceived harms have steadily declined as availability of cannabis increases. Prenatal cannabis use is also increasing in prevalence, yet perceptions of the harms of prenatal use of cannabis remain underexplored. No literature examines how the perceived harm of general cannabis use compares to perceived harms of prenatal use, nor how these perceptions relate to perceived harm of the prenatal use of other substances. Moreover, individual characteristics may be associated with perceived harms of cannabis use. Understanding if/how these perceptions vary demographically and covary with one another is vital to inform drug policy. This study utilizes data from N=142 individuals who participated in a national study of cannabis risk perception.

Participants self-reported their demographics, substance use history (i.e., yes/no to past year use of cannabis), and responded to nine items (ranging from 1= strongly agree to 5 = strongly disagree) of the perceived harm of cannabis, and the prenatal use of other drugs (nicotine/tobacco, alcohol, and other illicit drugs). We first explored descriptive information (i.e., means, SDs), and calculated bivariate correlations among the perceived harms items. Correlational analyses were used to explore the association between age and the perceived harms items; an ANOVA was conducted to explore the association between past-year cannabis use and perceived harms of general use. The mean for perceived harm of general cannabis use was quite low (M=2.45, SD= 1.218). Perceived harm of prenatal cannabis use (M=3.43, SD= 1.330), was higher than perceived harm of general cannabis use, but lower than perceived harm of prenatal use of other drugs (nicotine/tobacco M=4.69, SD= .751, alcohol M=4.74, SD= .690, other drugs M=4.81, SD= .696). Correlational analyses indicated that the perception of cannabis use as generally harmful did not correlate with perceiving the prenatal use of other substances as harmful, however, perceived harm of cannabis use generally was positively associated with perceived harm of cannabis use in pregnancy; r=.492, p<.001). Perceptions were not correlated with age. Those who used cannabis in the past twelve months perceived harm of cannabis use as significantly lower than those who did not use cannabis in the past twelve months ($F(1, 78) = 19.310$, $p < .001$).

Eden Wolde **Poster #F8**

Home Institution: University of Nevada, Las Vegas

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Andrea Flores, Education; Kate Mason, Anthropology

The First-Gen Prophecy: Students' Experiences with Career Planning in the Midst of COVID-19 Pandemic

Students whose parents have not completed a college degree (Associate, Bachelor, or equivalent) are considered First-Generation College Students (FGCS). As the first in their families to explore the novel higher educational landscape, FGCS shoulder a familial responsibility to excel in an educational system dominated by racialized and socio-economic stratification. They do so, hoping their individual degrees and professional pathways lead to collective upward mobility for their families and communities. As a result of the COVID-19 pandemic and its lingering effects, FGCS has experienced increased difficulties pursuing a college degree and choosing a career path that may enable these hoped-for outcomes. This presentation aims to answer the questions: How has FGCS ' career planning changed during the COVID-19 pandemic? What factors influence their decisions? I examine case studies from the Pandemic Journaling Project (PJP) of FGCS career pathways and what factors impacted their decision-making, including the COVID-19 pandemic. Through the Pandemic Journaling Project (PJP), FGCS and their parents share their experiences and feelings during the COVID-19 pandemic by self-submitting journals and participating in ethnographic interviews. The motivations to pursue a career pathway, how FGCS determines it, and how it relates to their status as barrier-breakers in their families will be explored in-depth in this poster presentation. Accordingly, this case-study analysis of the PJP illuminates and conceptualizes how FGCS navigated the pandemic while living up to familial expectations of degree attainment and career prosperity, like fulfilling a prophecy.

Paloma Lucero-Hancock **Poster #F9**

Home Institution: Johns Hopkins University

Summer Research Program: Leadership Alliance-Summer Research Early Identification Program (SR-EIP)

Faculty Mentor: Alicia Cohen, Public Health

Understanding Healthcare Inequities: Patient Experience in Disclosing Racial and Ethnic Demographics

Background: Systemic and structural racism is deeply embedded within many sectors of our society, notably the health sector, where less visible discriminatory medical encounters persist. Recent discourse surrounding healthcare issues has revealed an association between incomplete data and racial and ethnic inequities. Without measurements of disparities in care based on race and/or ethnicity, inequities will persist.

Objective: To understand the state of literature on the completeness and accuracy of racial and ethnic data and to explore reasons why patients may decline to provide their racial and/or ethnic information.

Methods: This scoping literature review included literature from PubMed published between October 2005 and April 2022. Additional studies were screened by reference searches and research experts. Included studies were based in the U.S and were integrated into the healthcare system.

Evidence Synthesis: Screening of 3,452 articles identified 20 studies of relevance. Studies reported that primary reasons why patients may decline to provide their information are the following: lack of trust in providers, lack of survey variability, and ineffective patient-provider communication. One study reported limitations of the OMB operationalization of race and ethnicity and its failure to capture diverse experiences of racialization.

Conclusions: Lack of trust and concern about provider behavior has led to higher item missingness on race and ethnicity surveys: suggesting that current data collection practices lack effective communication and understanding of patient experiences. By addressing the limitations of current measurements, healthcare providers can make substantial progress in achieving health equity in the U.S.

Kathryn Farber **Poster # F10**

Home Institution: University of San Francisco

Summer Research Program: The Leadership Alliance

Faculty Mentor: Meredith Hastings, Department of Earth Environmental and Planetary Sciences (DEEPS)

Unveiling the Local Impact of Wildfire Pollution Events Using the Breathe Providence Network

Exposure to poor air quality is a significant determinant of respiratory health issues with a disproportionate impact on underrepresented communities. Due to the spatial resolution limitations of higher-cost federal monitoring systems, ‘hyperlocal’ low-cost sensor networks have gained traction as a tool to assess air quality disparities among neighborhoods. However, these sensor networks' full utility

and effectiveness are still being determined. This research project aims to utilize the hyperlocal, low-cost Breathe Providence air quality monitoring network located in Providence, RI, to investigate the impacts of the natural air quality events in a case study of the transported smoke from Canadian wildfires, focusing on particulate matter 2.5. This study focuses on analyzing the data collected from May 5st to June 13th by the Breathe Providence network, focusing on particulate matter ($PM_{2.5}$), and meteorological conditions. The research methodology utilizes open-source code and statistical analysis techniques to analyze the air quality data in conjunction with meteorological data. The goal is to assess air pollution's temporal and spatial patterns during typical air quality conditions and how the spread of pollutants from Canadian wildfires enhanced pollution concentrations due to meteorological conditions. We show the levels of pollutants to be similar across the network during the pollution events and investigate local implications. These findings can contribute to developing targeted interventions and policies to mitigate the negative impacts of these events, promote public awareness, and inform decision-making processes regarding air quality management and public health.

Margherita Rampichini **Poster # F11**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Maria Guglielmo, Brown Alpert Department of Neurosurgery

Short-Term Pain Outcomes and Pain Medication Utilization Among Urine Toxicology-Identified Opioid and Marijuana Users Following Elective Spine Surgery

Chronic back pain is a common condition across the world and elective spinal surgery is commonly used for elderly patients. Postoperative pain is a measure that can be used to quantify the success of surgery. This measure can be influenced by preoperative substance use, often underreported due to social stigma. Our study used urine toxicology-identified preoperative opioid and marijuana use to measure the impact of substance use on postoperative pain outcomes and pain medication use following elective spinal surgery. We recruited 111 patients (mean age 58 years, 59% female) undergoing surgery between September 2020 and May 2022. We collected demographic information, urine toxicology, VAS, and pain medication regimen data. Comparisons between self-reported and urine toxicology-identified substance use, pre-and post-operative VAS ratings, and postoperative pain medication use were calculated using statistical analysis and were adjusted for age, sex, and race. Relative to patient reports, our urine toxicology overestimated drug use (47% vs 16%, p<0.001) and underestimated alcohol use at the preoperative baseline. At the two-week postoperative mark, participants on preoperative opioids, as determined by the urine toxicology, reported no significant improvements in pain from the baseline, but non-users did. Participants on preoperative opioids also had worse postoperative VAS and were more reliant on opioid medications. However, participants on preoperative marijuana reported similar improvements in pain from baseline, similar postoperative pain, and similar postoperative reliance on opioid medications. Overall, preoperative opioid use was associated with poorer postoperative pain relief and persistent reliance on postoperative opioids for pain management following elective spinal surgery. In contrast, preoperative marijuana use didn’t worsen postoperative outcomes. Therefore, preoperative marijuana should not be a reason to delay or be a contraindication to elective spinal surgery.

Karolina Palac **Poster #F12**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Vikas Srivastava, Biomedical Engineering

Polymeric Gel Brain Tissue Surrogates for Studying TBI

A challenging issue within biomedical research is the inability to recapitulate the in vivo conditions of the body in studies performed in vitro. Commonly, this problem is generalized more towards the unique chemistries of biological environments that are difficult to replicate. The mechanical properties of the extracellular matrix are also important to reproduce experimentally. We aim to mimic tissues' appropriate mechanical properties by using polymeric gels as surrogate materials. The prevalence of traumatic brain injury (TBI) and its cause directly result from mechanical forces applied to the brain, making it a desirable tissue to investigate using suitable gel surrogates. Additionally, there exists a research gap in relating the continuum scale mechanical damage experienced by the tissue to the local loss of cell function experienced during impact. The two key objectives of the research project are: (i). study and characterize the mechanical properties of brain tissue mimicking materials at quasistatic and high strain rates, and (ii). determine the effect of applied mechanical loading on the function and expression of brain cell populations using in-vitro methods.

Anna Li **Poster #F13**

Home Institution: University of Rhode Island

Summer Research Program: MARC U*STAR

Faculty Mentor: Anita Shukla, School of Engineering; Alec McCall, School of Engineering

Development of β-lactamase responsive microneedles for treatment of diabetic foot ulcer bacterial biofilm infections

Individuals with diabetic foot ulcers (DFUs) can develop infections and 60% of those infections are associated with biofilm formation. Biofilms are three-dimensional microbial communities embedded within a matrix of extracellular polymeric substances (EPS). Bacterial biofilms exhibit various antibiotic-resistant mechanisms, such as the secretion of β-lactamases (βLs) which inactivate many first-line β-lactam antibiotics via hydrolysis. The EPS barrier limits the effectiveness of current topical and systemic treatments, often resulting in low drug bioavailability at the site of infection and a higher risk of antibiotic resistance. Antibiotic-loaded microneedle (MN) patches offer an alternative to biofilm infection treatments by using miniaturized needles (<1 mm in height) to puncture the EPS, releasing an antibacterial cargo into the biofilm. To overcome antibiotic resistance, we developed a βL-responsive MN patch containing a βL-responsive crosslinker that can undergo free radical photopolymerization and degrade in the presence of βLs. The MNs will be compared to a non-responsive formulation using poly(ethylene glycol) diacrylate as the crosslinker. Mechanical stability was determined through compression testing and in vitro puncture studies with non-responsive MNs formulated with and without fluorescent nanoparticles as a drug cargo model. At a pre-load of 0.1 N, the compression testing results indicated an exponential increase in compression force at a displacement of ~0.3 mm of the non-responsive MNs. Puncture studies indicated that non-responsive MNs punctured through 2 parafilm layers, with a 47% decrease in holes created between the first and second layers. Scanning electron microscopy and confocal microscopy confirmed MN formation and deformation of MNs due to mechanical stress. Current work is using similar approaches to characterize the βL-responsive MNs.

Grace Ma **Poster #F14**

Home Institution: Brown University

Summer Research Program: SPRINT Undergraduate Teaching and Research Awards (UTRA)

Faculty Mentor: Yongsong Huang, Earth, Environmental, and Planetary Sciences

Development of a GC-MS Data Processing Pipeline for Automatic Identification of Unknown Compounds

Analysis of unknown organic compounds in a sample is crucial for answering many of the questions in chemistry, biology, medical, environmental and space sciences. For instance, identifying the organic chemistry of the asteroid Bennu could provide important context for the origin of life on Earth, as scientists theorize that organic material from this asteroid could have been a part of the primordial soup. To perform a chemical analysis of the asteroid, samples will be put through a GC-MS — a machine that combines gas chromatography (GC) for the separation of compounds and mass spectrometry (MS) to determine their chemical structure. However, the conventional identification process for GC-MS data is often tedious and can produce inaccurate results due to noise and limitations with software. To address this issue, a data processing method was developed to facilitate better identification by reducing noise and machine calculation error. The method works by identifying baselines for each ion chromatogram and subtracting it from the data, as well as normalizing erroneous mass calculations by the machine. Additionally, a neural network was employed to automatically identify peaks in the chromatogram, reducing the potential for human error in visual perception. Next, an algorithm to match mass spectra to an existing library will be developed, allowing for the automatic identification of compounds, and this will be integrated into a graphical user interface (GUI) for ease of use.

Robert Guterl **Poster #F15**

Home Institution: Brown University

Summer Research Program: Royce Fellowship

Faculty Mentor: Elena Shih, Sociology; Baylor Fox-Kemper, Professor of Earth, Environmental, and Planetary Sciences

Urban Tree Canopy, Greenspaces, and the Climate Crisis in Providence

My project is a community-engaged research project that aims to explore the potential impact of increasing urban tree canopy and green spaces on climate resilience and equity in Providence. The project focuses on understanding the current state of the city's park system, analyzing the distribution of urban tree canopy, and examining the effects of these green spaces on biodiversity and environmental conditions.

The research project will begin with a comprehensive review of relevant literature on urban tree canopy, green spaces, and their role in climate change mitigation and adaptation. It will also include a thorough analysis of the city's zoning and land use regulations, as these policies play a crucial role in shaping the development and distribution of green spaces within the city.

Fieldwork will be conducted to gather data on the current state of the city's park system, including the location, size, and accessibility of green spaces, as well as the demographics of communities surrounding these areas. Surveys and interviews with local stakeholders, community members, and representatives from organizations involved in park management and environmental advocacy will provide insights into

the challenges and opportunities for promoting biodiversity and equity in the city's green zones.

The research will also involve comparisons with cities that have similar demographics to Providence and have successfully implemented green infrastructure and tree planting initiatives. By examining best practices and success stories from other cities, the project aims to provide actionable recommendations for enhancing Providence's green spaces and urban tree canopy to address climate change and support the needs of marginalized communities.

The ultimate goal of this research project is to create a comprehensive report that can be shared with city planners, policymakers, and community stakeholders. The report will offer evidence-based insights and policy recommendations to guide future development and investment in green infrastructure, taking into account the importance of equitable distribution of green spaces across all neighborhoods in Providence. By promoting biodiversity and climate resilience through the expansion and enhancement of urban tree canopy and green zones, the project seeks to foster a more sustainable and inclusive city for all residents.

Emilio Allan **Poster #F16**

Home Institution: University of Florida

Summer Research Program: SR-EIP

Faculty Mentor: Yan Liang, Department of Earth, Environmental, and Planetary Sciences

Geothermometry and Petrology of Martian Meteorite LAR12095

Despite numerous robotic missions to the planet, Martian meteorites remain the only source of in-depth petrologic analysis of Martian igneous rocks. 262 of such meteorites have been collected, broadly falling into 3 categories - shergottites, nakhlites, and chassignites, ranging from mafic to ultramafic in composition – providing us a window into the conditions of the Martian mantle. We focused on the meteorite Larkman Nunatak 12095, discovered in Antarctica in 2012. LAR12095 is an olivine-phyric shergottite, consisting of coarse-grained olivine (Fo_{70} - Fo_{58}) in a matrix of finer-grained pyroxene, olivine, feldspar (shocked into maskylenite), and spinel. Following the olivine-spinel Al_2O_3 equilibrium geothermometer developed by Wan and Coogan (Wan 2008), we analyzed the composition of olivine phenocrysts and their associated chromite-spinel grains using an electron probe microanalyzer (EPMA) to determine the crystallization history and olivine-spinel equilibrium temperature as a proxy for the olivine liquidus. Our findings were consistent with current petrogenetic models of olivine-phyric shergottite formation from an evolving magma temperature and chemical composition (Udry et al. 2020). Three “generations” of olivine represent fractional crystallization and emplacement between a lower crustal magma chamber at ~1300 °C at 1 GPa (Dunham et al. 2019), a near-surface volcanic magma chamber at ~1000 °C, and eruption onto the Martian surface at 880 °C.

Thursday, August 3rd, 2023

Name	Poster #
Hannah Stoch; Happy Jara	#A1
Kate Choi; Brynne Miller	#A2
Ashley Zarco	#A3
Jean Wanlass	#A4
Alexandra Floru	#A5
Da-Young Kim; Ethan Register	#A6
Cara Kaminski; Jessica Hooper; Max Newman; Eloise Gacetta; Ian Wright	#A7
Rainy Wortelboer; Christopher Liu; Samantha Chon; Alex Hernandez-Manriquez; Joseph Suh	#A8
Nellely Lopez-Mendez; Harper Liang	#A9
Jack Blocker; Olivia Maule; Jacob Lerman	#A10 & #A11
Lizi Zhang; Lucy Anderson	#A12
Mason Romantic; Octavia Rowe	#A13
Nate Nigrin; Sanyu Rajakumar; Zining Chen	#A14
Elisa Dong; Ayla Taylor-Robichaud; Brown Bulloch	#A15
Celia Johnson; Cassandra Travis	#A16
Mareesa Islam; Noah Medina	#B1
Victoria El-Khoury; Sara Santacruz	#B2
Bryce Okihiro; Yahir Oseguera	#B3
Camilla Regalia	#B4
Melissa Aldana	#B5
Amber Wang	#B6
Ju-Woo Nho	#B7
David Okoh	#B8
Jordan Feldman	#B9

Kenia Sanchez	#B10
Conenicus Weeden	#B11
Pranav Gundrala	#B12
Adrian Lin	#B13
Colin Baker	#B14
Justin Currie	#B15
Miauaxochitl Haskie	#B16
Blaire Williams	#C1
Tsunami Núñez-Irizarry	#C2
Samir Samadov	#C3
Tayler Leonard	#C4
Ian Joe	#C5
Hassan Alemara	#C6
Timothy Reiad	#C7
Rosa Rijo Benitez	#C8
Victoria Chen	#C9
Charles Finch Stowers	#C10
Flavia Maria Galeazzi	#C11
Mallory Tucker	#C12
Rolake Feyisetan	#C13
Kanny Barry	#C14
Hoon Hee Ryan Rhew	#C15
Rachel Kaniuk	#C16
Samara Cummings	#D1
Nicole Melendez	#D2
Aleah Davidsen	#D3
Joanne Lee	#D4

Brandon Ulin	#D5
Dan Bernstein	#D6
Mary Avella	#D7
Ava Nemerovski	#D8
Chloe Kim	#D9
Lily Zhou	#D10
Mya Collins	#D11
Jonathan Li	#D12
Elena Pearson	#D13
Nicole Dennis Talley	#D14
Avi Lukacher	#D15
CJ Abeshaus	#D16
Jaden Zhang	#E1
Byron Butaney	#E2
Nishitha Chaayanath	#E3
Maliha Tasnim	#E4
Jared Chung	#E5
Nova Dea	#E6
Will Malloy	#E7
Andres Filizzola	#E8
Justin Moustouka	#E9
Anna Shlimak	#E10
Bryanna Vilnaigre	#E11
Barron Clancy	#E12
Kareena Sandhu	#E13
Annika Coleman	#E14
Yihuan Dong	#E15

Meher Sandhu	#E16
Kristine Yang	#F1
Evan MacLure	#F2
Jasmine Xi	#F3
Tarrin Dewberry	#F4
Giordana Serretta Fiorentino	#F5
Sai Chamarthi	#F6
Markelle Worrell	#F7
Halle Nwanne	#F8
Lella Wirth	#F9
Brianna Pham	#F10
Benjamin Schornstein	#F11
Lauren Chiu	#F12
Monica Ocitti	#F13
Anne Wang	#F14
Daniel Zhu	#F15
Lewis Nunez	#F16
Lily Yu	#G1
Alexa Torres	#G2
Austin Jacobson	#G3
Smriti Vaidyanathan	#G4
Alexander Gonzalez	#G5
Liana Haigis	#G6
Ainsley Bonin	#G7
Kaleb Zuckerman	#G8
Chandler Zhu	#G9
Wyatt Ploot	#G10

Zane Darden	#G11
Sacha Sides	#G12
Camille Donoho	#G13
Colm Ryan	#G14
Anusha Srinivasan	#G15
Anel Zhussubali	#G16
Lisa Duan	#H1
Henry Zheng	#H2
Liam O'Connor	#H3
Julien Song	#H4
Elaine Wang	#H5
Ofubofu Cairns	#H6
Zain Peerbhoy	#H7
Adriana Ramirez Marrero	#H8
Dana Vargas Solivan	#H9
Jacqueline Lopez	#H10
Min Sung Kim	#H11
Chris Ma	#H12
Alexa Ryan	#H13
Valentin Kirilenko	#H14

Friday, August 4th, 2023

Name	Poster #
Ethan Bove; Michael Cho; Lisa Baek; Xingyi Zhang	#A1
Grace Bielefeldt; Iris Horng; Mitchell VonEschen; Holly Luebsen	#A2
Toby Anderson; Olivia Greinke; Luis Santori; Iskandar Nazhar	#A3
Fausto Navarro; Luca Grossman; Jacob Ashworth	#A4
Tanner Diring; Kiera Fullick; Jayna Rybner	#A5
Yilin Xie; Zachary Brown; Marcus Lewis; Joseph Militello	#A6
Alice Min; Robayet Hossain; Narek Harutyunyan; Hammad Izhar	#A7
Catherine Jacobs; Amelia Julian; Katelyn Buck	#A8
Doh Hyun (Dennis) Kim; Matthew McKee	#A9
Mikayla Walsh; Peter Zhu	#A10
Faith Kim; Vatsal Vemuri	#A11
Xavier Lee	#A12
Aidan Hennessey	#A13
Matthew Fang	#A14
Yizhong Hu	#A15
Cameron Goodreau	#A16
Rio Aguina-Kang	#A17
Marlena Brown	#B1
Joan Graniela	#B2
Presley Hernandez	#B3
Gabrielle Rose	#B4
Jiashu Huang	#B5
Jacob Stifelman	#B6

Anna Chung	#B7
Adam Gendreau	#B8
Niyanta Nepal	#B9
Emma Hagenaars	#B10
Zeno Chen	#B11
Noah Whelpley	#B12
Lucas Chan	#B13
Anjali Shah	#B14
Mageean Brown	#B15
Anneke Wernerfelt	#B16
Sofia Juliani	#B17
Ian Bartlett	#C1
Lucca Paris	#C2
Masarrah Abdur-Rahman	#C3
Lia Lubit	#C4
Avi Trost	#C5
Adnan Aldabbagh	#C6
Isabella Lizalda	#C7
Zharia Hill	#C8
Jasper Lincoln	#C9
Nina Hernandez	#C10
Kailee Tanaka	#C11
Uri Dickman	#C12
Andy Zhu	#C13
Alicia Chandler	#C14
Daniel Zhang	#C15
Dylan Hu	#C16

Pamil Tamelessio	#C17
Evan Ren	#D1
Gabriel Traietti	#D2
Eric Sorge	#D3
Lana Yang-Maccini	#D4
Mayayi Izzo	#D5
Anaya Kaul	#D6
Isaiah Olds-Campanile	#D7
Devynn Wilderman	#D8
Damir Kulzhanov	#D9
Maxwell Ferguson	#D10
Chandler Stevenson	#D11
Tyler Lane	#D12
Zachery Gottshall	#D13
Gannon Lemaster	#D14
Ben Radick	#D15
Anna Novatney	#D16
Ryan Doherty	#D17
Jack Kolman	#E1
Arnav Singhal	#E2
Daniel Graves	#E3
Shuah Yu	#E4
Shreyas Waghe	#E5
Jacob Koster	#E6
Mina Sarmas; Kenneth Kang	#E7
Sima Raha; Anahis Luna	#E8 & #E9
Christine Alcindor; Daliza Reinoso	#E10

Britney De Leon; Jerry Quan	#E11 & #E12
Kayla Robinson	#E13
Angel Barraza Estrada	#E14
Aseel Rafat	#E15
Day Baez	#E16
Sofia Gerlein	#E17
Rachel Gunderson	#F1
Sylvia E	#F2
Suha Khan	#F3
Joshua Benzon	#F4
Samira Lakhiani	#F5
Jadyn Ligoo	#F6
Danielle Whisnant	#F7
Eden Wolde	#F8
Paloma Lucero-Hancock	#F9
Kathryn Farber	#F10
Margherita Rampichini	#F11
Karolina Palac	#F12
Anna Li	#F13
Grace Ma	#F14
Robert Guterl	#F15
Emilio Allan	#F16

SUMMER RESEARCH PROGRAMS REPRESENTED

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- Summer Research Assistantship in Biomedical Sciences
- Summer Undergraduate Research Assistant in MCB
- UConn Physics Research Internship
- Undergraduate Research Assistant - Computer Science
- Undergraduate Research Assistant in Michael Frank's Lab
- Undergraduate Research Assistant in Ritambhara Singh group, CCMB
- Undergraduate Research Assistant in Tejal Desai's Lab
- Undergraduate Research Assistant in Wharton Laboratory
- Undergraduate Research Assistant in Wilhelmus Lab

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- Brown University
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- Carleton College
- Colby College
- Colorado State University
- Connecticut College
- Cornell University
- Emory University
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