UNDERGRADUATE RESEARCH SYMPOSIUM SU26

Cannon Chapel

Wednesday, July 29th, 5:00PM-7:00PM

Emory Student Center

Thursday, July 30th, 10:00AM-3:00PM

A celebration of research and scholarship

EMORY | Undergraduate Research Programs
Pathways Center

VISUAL ARTS AND MUSIC PREFORMANCES

TITLE: BEYOND RECOGNITION: EXPLORING EMOTION THROUGH ABSTRACTION

PRESENTER: JENNA BLACK

MENTOR: DR. AARON PUTT

PROGRAM: SURE- CREATIVE & PERFORMING ARTS



Beyond Recognition is a body of experimental artworks that explore abstraction as an act of attention and performance. Developed over the course of a summer spent almost entirely in the art studio, this project began with a simple question: Can abstract painting communicate emotion without relying on recognizable imagery? I initially approached each painting by choosing a specific emotion and attempting to express it through color, gesture, texture, and composition. As the project developed, however, my focus gradually shifted. Rather than asking whether I had successfully communicated a predetermined emotion, I became interested in what would happen if I assessed the painting formally before asking what it meant. By attending first to relationships of color, surface, gesture, rhythm, and material, I found that interpretation became less about confirming an intended meaning and more about discovering what the painting was already doing.

This shift emerged through continual experimentation in the studio, conversations during critiques and studio visits, and readings by artists and critics including Peter Halley and Harold Rosenberg. Working across monochromatic atmospheres, lyrical abstraction, and heavily textured surfaces, each series became a way of testing how different formal decisions shaped perception before representation. The monochromatic works explored whether color, transparency, and layered brushwork alone could create an emotional atmosphere. The lyrical abstractions examined how gesture and shape influence recognition, while the textured works emphasized materiality through plaster-like surfaces and palette knife application. Rather than beginning with interpretation, I learned to ask what these formal relationships were already communicating and how they invited certain responses before they suggested any fixed meaning.

Throughout this process, I found that my paintings repeatedly returned to bodily colors, raw surfaces, and traces of touch, despite never intentionally setting out to depict the body. Those recurring formal qualities suggested that meaning is not simply something an artist places into a painting, nor something a viewer uncovers afterward, but something that develops through sustained attention to the work itself. Peter Halley's writing challenged me to think about abstraction as inseparable from the ways we already organize and experience the world, while Harold Rosenberg's description of the canvas as "an arena in which to act" gave language to my experience of the studio as a space where painting became a form of performance rather than simply a means to create a finished object. Through this process, I also began to question whether it is ever possible to encounter a painting without bringing meaning into the experience. Even when we believe we are responding only to color, form, or material, we are already shaped by memory, association, and lived experience. Formal observation does not remove these meanings; instead, it allows us to become more aware of how they are formed. By the end of the project, I was no longer asking how to make a painting communicate a particular emotion, but how formal observation itself shapes interpretation. Before Recognition ultimately proposes abstraction as a practice of looking before naming, where meaning is not abandoned or predetermined, but gradually recognized through the act of making and sustained attention.

TITLE: **REINTERPRETING JOHANN SEBASTIAN BACH'S *THE WELL-TEMPERED CLAVIER* ON THE MODERN PIANO**

PRESENTER: **MATTHEW CHANG**

MENTOR: **DR. ELENA CHOLAKOVA**

PROGRAM: **SURE- CREATIVE & PERFORMING ARTS**

My work as a pianist and researcher this summer focused on Johann Sebastian Bach's The Well-Tempered Clavier (WTC), a keyboard work consisting of two volumes of preludes and fugues in all 24 major and minor keys. For the past five years, I have been fascinated by the rhythm, articulation, and interaction of the voices that constitute every piece in the WTC, as hearing the individual parts before listening to the entire polyphonic work is my favorite way to experience Bach's music. My primary goal was to reinterpret the WTC so that each voice could sound out clearly while also allowing the audience to perceive a broader structural melody or "compound voice." For inspiration, I drew on recordings by Glenn Gould, Sviatoslav Richter, András Schiff, Angela Hewitt, and Kimiko Ishizaka. However, my intent was not merely to imitate but to create an interpretation that I believe best conveys the music's architecture. The result was therefore almost always a synthesis of these artists' most effective choices.



TITLE: **EXPLORING APPLICATION OF IMPROVISATORY COMPONENTS FROM A 20TH CENTURY FANTASIE INTO A 19TH CENTURY FANTASIE**

PRESENTER: **KIMIKO DARCY**

MENTOR: **DR. ELENA CHOLAKOVA**

PROGRAM: **SURE- HUMANITIES**

I studied Robert Schumann's Fantasie in C major, Op. 17, 1st movement. Schumann composed this piece when he was forced to spend time apart from his soon-to-be wife, Clara, to express his passion for her, and to help raise money for a Beethoven monument in Bonn, Germany. My goal was to draw out the romantic passion from the Fantasie, while avoiding the sound of a carefully contrived execution of the piece; I worked towards making it sound spontaneous, as this genre of music is intended to sound. To achieve this goal, I closely listened to recordings of a 20th century Fantasie, Florence Price's Fantasie Negre No. 1 in E minor, where improvisatory elements feature prominently, much more so than in Schumann's. I was also inspired by recordings from pianists such as Maurizio Pollini, Yundi Li, Daniel Barenboim, and Murray Perahia, among others. My final performance is shaped by my own interpretation, created over the weeks studying the Schumann Fantasie while incorporating influences from other performers and Florence's Price's improvisatory style.

TITLE: UNRAVELING THE FABRIC OF ANTIQUITY: AN ONGOING EXPERIMENT IN ANCIENT WEAVING TECHNIQUE

PRESENTER: AVA REESE

MENTOR: DR. SANDRA BLAKELY

PROGRAM: SURE- HUMANITIES

Today, the general tedium, precision, and ubiquity of textile manufacture is fairly well understood by Classicists, but the messy (and virtually unrecorded) intricacies of the industry of textile manufacturing in the ancient Mediterranean have consistently proven difficult to piece together. As is made clear from both literary and iconographic sources, the textiles of the Roman artistic imagination varied widely; we see on Pompeiian frescoes both shimmering, transparent garments and heavy, rough cloaks. To move towards a more comprehensive understanding of the chaîne opératoire of the domestic (i.e. non-import) Roman textile industry, we must attempt to determine the limits of the warp-weighted loom, which was the predominant loom type until the 2nd century A.D. Experimental archaeology has proven invaluable in answering such questions. Landmark studies, such as that conducted by Linda Mårtensson et al. (2009) and the ongoing PENELOPE Project, have been critical in approximating the tools and techniques used in ancient weaving. Following similar methodology to both studies, particularly in my use of the optimal weight-to-thread ratios as determined by Mårtensson et al, this study consists of the warping and weaving of fabric with my best approximation of ancient techniques and tools. However, I diverge from those studies in my especial focus on the weight of the produced fabric. By weaving with increasingly finer thread, my hope is to eventually be able to produce garment-quality fabric on the warp-weighted loom. This experiment is one step of many towards the production of fine, even diaphanous, fabric on the ancient loom. Reproduction of this process, which is yet to be published, would be instrumental in progressing our understanding of the capability of the Roman weaver and, thus, refine our image of the textile industry at large.



TITLE: THE ROLE OF MUSIC IN EMOTIONAL COPING AMONG BLACK MEN

PRESENTER: JEREMIAH RICHARDSON

MENTOR: DR. CARL SUDDLER

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Mental Health challenges in men, specifically Black men, are often not spoken of in the Black community due to Black men having to be perceived as emotionally stoic individuals. It is a sensitive topic that has been approached by Black men reluctantly, causing them to be less likely than other groups to seek professional mental health care. Research has noted that evidence-based music therapy improves mood and reduces emotional distress. This qualitative phenomenological study will explore why Black men rely on music as a coping mechanism rather than seeking professional mental health care. Using this approach will allow me to conduct semi-structured interviews with Black men aged 18 and older, delving into their lived experiences and perceptions of mental health and music. Through this study, using the Emotion Regulation Theory and Help-Seeking Theory, relevant themes of traditional and societal masculine norms, emotional expression, cultural stigma, and the therapeutic role of music will be explored to better understand the lived experiences of Black men and their perceptions of professional mental health care. These findings can provide insight and understanding into relevant cultural approaches to mental health interventions for Black men, why they prefer music, and how music can be introduced through therapeutic approaches in the future.

Keywords: Black men, emotional regulation, music, mental health, coping mechanisms

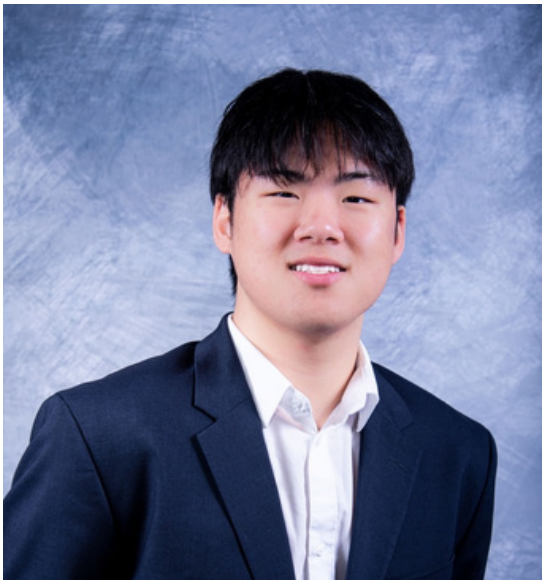
ORAL PRESENTATIONS

TITLE: **IDENTIFICATION AND VALIDATION OF PUTATIVE SUPPRESSORS OF RRP40-W195R (EXOSC3) IN THE RNA EXOSOME USING BUDDING YEAST**

PRESENTER: **KHUSHI AGARWAL**

MENTOR: **DR. ANITA CORBETT**

The RNA exosome is a highly conserved protein complex that processes and degrades RNA, making it essential for normal gene expression. The exosome is composed of 10 subunits; 3 cap subunits, 6 core subunits, and 1 catalytic subunit. In humans, mutations in RNA exosome genes cause rare neurodevelopmental disorders known as exosomopathies. The RNA exosome is highly conserved from yeast to humans, making the budding yeast Saccharomyces cerevisiae an effective model for studying disease-associated mutations. My project investigates whether we can use genetics to understand exosomopathy-associated mutations in the RNA exosome subunit Rrp40 (EXOSC3 homolog). I utilized temperature-sensitive yeast mutant rrp40-W195R strain to identify suppressors that restore growth. My suppressor screening identified 7 putative suppressor colonies of rrp40 mutant. I performed serial dilution growth assays to validate these putative suppressors. In the future, I plan to submit data for whole-genome sequencing to identify the genomic changes in these suppressors, and then reintroduce these mutations into the original rrp40 mutant strain to confirm their causal role. Identifying genetic suppressors of RNA exosome dysfunction will improve our understanding of how cells maintain RNA processing despite defects in essential cellular machinery. These findings may reveal conserved pathways that can be explored in future studies using human cell models and could provide insight into the molecular basis of exosomopathies and related neurodevelopmental disorders.



TITLE: DEVELOPMENT OF METABOLIC BIOMARKERS FOR PROGNOSTICATION IN DISORDERS OF CONSCIOUSNESS USING MAGNETIC RESONANCE SPECTROSCOPY

PRESENTER: JASON AHN

MENTOR: DR. CANDACE FLEISCHER

PROGRAM: SURE- BIOMEDICAL SCIENCES

Disorders of consciousness (DoC) are a spectrum of neurological conditions which include coma, unresponsive wakefulness syndrome (UWS), and the minimally conscious state (MCS). Typically following severe brain injury, DoC are characterized by prolonged impairment of arousal and awareness. Prognostication remains challenging because behavioral assessments alone may underestimate underlying brain function and have limited predictive value for emergence. Magnetic resonance spectroscopy (MRS) is a non-invasive technique that enables direct quantification of cerebral metabolites. The objective of this study is to determine the ability of MRS to identify potential biomarkers for prognosis and provide further information about brain activity. The final cohort included 25 patients diagnosed with either MCS or UWS who underwent 3T brain MRI, including single-voxel MRS of the brainstem and posterior cingulate cortex (PCC) using a point-resolved spectroscopy (PRESS) sequence. Coma Recovery Scale-Revised (CRS-R) scores were obtained clinically during patient care and were used to assess the level of consciousness. Metabolite concentrations were quantified using LCModel. The area under the receiver operating characteristic curve (AUROC) was calculated to assess the ability of clinical variables and individual MRS-derived metabolites to predict emergence from DoC. The metabolites with the highest individual AUROC from each voxel were used to generate a combined ROC curve. Emergence from DoC was determined within 6 months of injury. The combined model, including brainstem total creatine (tCr) and PCC glutamate, had the highest AUROC (0.96). This performance exceeded that of the CRS-R (AUROC = 0.69), suggesting that combining metabolic biomarkers from multiple regions may improve prognostication of emergence from disorders of consciousness beyond behavioral assessments alone. This work holds the potential to contribute to earlier and more accurate prognostication as well as better clinical decision-making regarding rehabilitation and goals of care.



TITLE: IN GOD'S HANDS: AN EXPLORATION OF FAITH PRACTICES AND POLITICAL DISSIDENCE IN BLACK CHURCHES OF ATLANTA

PRESENTER: CARLY AIKENS

MENTOR: DR. DEVAKA PREMAWARDHANA

PROGRAM: SURE- SOCIAL SCIENCES

This project examines how faith practices shape politicized survival and civic mobilization of Black churchgoers in Atlanta, GA in response to what philosopher Achille Mbembe calls necropolitics. Necropolitics emphasizes hegemony (dominance of an uninterrupted societal norm) through the death of the "other." My research focuses on three central questions. How do Black Christians imagine the future of a political machine predicated on their own dehumanization? What does faith-based hope mean for Progressive Black Christians in our political climate? How might the Southern Black Church aim to meaningfully disrupt the hostile Evangelical takeover of the American Right? My research methodology follows a two-pronged approach of ethnography and analysis of sermons. I plan to engage in one-on-one interviews with members of both congregations to gauge the trajectory of their personal political and faith journeys. This project will examine how hermeneutics (Biblical interpretation) is disseminated through the Black Church body and how the practice of homiletics (art of preaching) employed by Black preachers shapes the political ideals of the congregation. My sites of research are Big Bethel AME and Ebenezer Baptist Church. Ebenezer Baptist – "America's Freedom Church" – and Big Bethel AME – "the City Hall of Sweet Auburn" – are two of Atlanta's most invoked names in discussions of church-rooted activism. The pulpit of Ebenezer Baptist reflects generational Black political engagement, first served by Martin Luther King Jr. and now GA Sen. Raphael Warnock. Similarly, Big Bethel AME's roots are the oldest of any Black Church in Atlanta. My methodology will move beyond the sanctuary towards small group ministries (community outreach, worship/arts, and social action), prayer groups, and special church events to cover the breadth of experience the church provides. My intervention lies in understanding how faith-based hope manifests against authoritarianism and surveillance.



TITLE: CHARACTERIZING THE ANTIBODY REPERTOIRE AGAINST HUMAN SEASONAL INFLUENZA VIRUSES FOLLOWING THE OUTBREAK OF H5N1 IN DAIRY CATTLE

PRESENTER: ABBY ARROYO

MENTOR: DR. SEEMA LAKDAWALA

PROGRAM: SURE- BIOMEDICAL SCIENCES

In March 2024, avian-origin H5N1 influenza A virus (IAV) was detected in US dairy cattle for the first time. Since then, there have been 1,160 infected herds, and 71 human cases associated with exposure to these infected animals. Previous work has shown that infected cattle shed high viral titers in the milk but little to no virus in the respiratory tract. Given this novel host tropism, little is known about previous exposure histories of dairy cattle to influenza virus and how primary IAV infections shape susceptibility, immunity, and disease outcomes. To investigate prior cattle exposure to IAV, we obtained 253 sera samples from cows on a California dairy that recovered from a H5N1 outbreak. Samples were collected one year post the peak clinical phase and tested for antibodies against H5N1 HA protein by enzyme-linked immunosorbent assay (ELISA). 227 of the 253 (90%) samples tested were positive for anti-H5 antibodies suggesting most cows were infected with H5N1, including animals with no clinical signs. Given the high seroprevalence for anti-H5 antibodies, we next tested the sera samples for antibodies against H1N1, A/California/07/09, HA protein to determine potential susceptibility of cattle to human seasonal IAVs. We hypothesize that H1 HA-reactive antibodies will be detected due to prior human influenza exposure, as reported in other studies, or due to H5-H1 cross-reactivity. Of 90 samples tested against H1, 40 were positive for anti-H1 antibodies. This suggests that dairy cattle are potentially susceptible to human IAVs. Detection of anti-H1 antibodies against human seasonal influenza viruses would be significant because if cattle can host both H5N1 and human influenza viruses, reassortment could occur, increasing the risk of novel influenza strains. Overall, this work contributes to efforts to better understand cattle and human transmission dynamics, helping to inform public health risk assessment.



TITLE: RECLAMATION & EMPOWERMENT: BLACK WOMEN'S MULTIPLE RELIGIOUS ALLEGIANCES TO CONJURE AND CHRISTIANITY

PRESENTER: LANIAH BOWDERY

MENTOR: DR. KYRAH DANIELS

PROGRAM: SURE- HUMANITIES

Forms of religion, such as Christianity and Africana religions, are deeply intertwined with the lived experiences of Black women. The current literature notes that this phenomenon is evident when it comes to language, how Black women speak in the church about "juju" and dreams, and the interaction with spirits and ancestors. The integration can also be recognized in supposedly "secular" behaviors of the community, including the dances, food, and rhythms of certain songs. Observing this, I intend to explore the question of how is it that Christianity and Africana religions, which are both deeply ingrained in Black communities in the U.S., can co-exist so peacefully, yet so harmfully? Drawing from my previous experiences with ethnographic research, I am proposing a study of Black women's relationship to Africana religions and African-derived religions, specifically Ifá and Conjure. I plan to rely upon Yvonne Chireau's work on Conjure and Hoodoo (2003) and Tracey Hucks' concept of dual religious allegiance (2001), which both highlight Black people's plural religious experiences. My methods will involve media analysis of Black women's interactions with these religions in Eve's Bayou (1997). I will also engage in archival research, examining how Africana religious devotees explored these religions in the past. By researching Black women's relationships to Africana religions in the 21st century, this study can help to empower Black women to proudly reclaim their African heritage and identity, especially as they embrace multiple traditions.



TITLE: RECKONING WITH WHAT'S "REASONABLE": A CORPUS-LINGUISTIC APPROACH TO UNDERSTANDING THE CRIMINAL BURDEN OF PROOF

PRESENTER: NAYANTARA CHANDRASEKHAR

MENTOR: DR. MARJORIE PAK

PROGRAM: SURE- SOCIAL SCIENCES

The phrase beyond a reasonable doubt (BARD), the standard of proof in criminal trials, is key when reaching legal verdicts. But what does or does not constitute BARD is decided by lay jurors that have little to no experience with legal jargon. Courts generally rely on jury instructions to communicate legal jargon to jurors, but not all jury instructions include a definition of BARD (e.g. Green 2017), and those that do take very different approaches (Allen & Elliot-Smith 2025). Moreover, quantified definitions (e.g. '90% certainty') are not permitted to use quantities to define BARD, even though Kagehiro (1990) finds that quantified definitions are the only ones that result in a corresponding reduction in convictions. How do courts explain this "unknowable" standard in jury instructions within these boundaries?

I build on Allen & Elliot-Smith (2025) by examining criminal pattern jury instructions from 38 states. I show first why BARD is such a confusing phrase (composed of metaphor and a subjective term, "reasonable") that can be interpreted in several different ways. I then identify a number of recurring patterns in the way that these states explain BARD – for instance, many use repeated phrases like "firmly convinced" or "based upon reason and common sense." Strikingly, while no states refer to specific degrees of certainty, 75% of the states in my corpus use an implicit scale of reference upon which they place BARD by defining it negatively. For instance, Minnesota says, "It does not mean a fanciful or capricious doubt" (creating a lower limit), "nor does it mean beyond all possibility of doubt" (creating an upper limit). I find that by framing BARD negatively and as a function of juror reason, pattern jury instructions conceptualise it as a nonquantifiable but scalable entity.



TITLE: WIRED FOR WORK OR REWARD? THE ROLE OF THE ANTERIOR CINGULATE CORTEX IN SOCIAL FORAGING STRATEGIES IN MICE

PRESENTER: EMILY CHEN

MENTOR: DR. MALAVIKA MURUGAN

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Cooperative behavior is essential for survival in social species, which enables individuals to obtain resources efficiently and improve group survival. Nonetheless, little is known about how stable cooperative and exploitative social roles emerge and are maintained by neural circuits. Previously, our group developed a social foraging assay that identifies stable worker and parasite behavioral phenotypes in both male and female mice. In this shared-reward paradigm, workers perform most effortful actions to obtain rewards, whereas parasites obtain rewards with minimal effort. This assay provides a model for investigating the neural mechanisms underlying social contribution strategies. To further our understanding of how these contribution strategies emerge and stabilize at the neural level, we focused on the anterior cingulate cortex (ACC), a region known to play a key role in social decision-making and effort allocation. In this project, we aim to determine whether the ACC is necessary for cooperative effort in mice using optogenetic inhibition in a social foraging task. We focused on male mice as an initial step toward determining the causal role of ACC in social foraging behavior. We implemented optogenetic inhibition by expressing the inhibitory opsin GtACR in the ACC. For each trial, ACC inhibition began when a mouse nose-poked the choice port and continued until five seconds after reward delivery. Preliminary analyses suggest that ACC inhibition biases mice toward adopting the parasite role during social foraging, and that this behavioral phenotype persists after inhibition is removed. Overall, this work further clarifies the neural mechanisms and brain regions involved in the emergence and maintenance of social roles within groups. Understanding how neural circuits regulate cooperative and exploitative behaviors may provide broader insight into the neural basis of social organization and collective decision-making.

TITLE: THE ROLE OF SENSORY ORGANS IN OVIPOSITION PREFERENCE OF MONARCH BUTTERFLIES

PRESENTER: BRITNEY CHEN

MENTOR: DR. JAAP DE ROODE

PROGRAM: SURE- BIOMEDICAL SCIENCES

Female monarch butterflies (Danaus plexippus) use chemoreceptors on antennae and tarsi to detect chemical cues when evaluating host plants for oviposition. Although these sensory organs differ in sensitivity to specific compounds, their relative contributions to oviposition preferences and behavior remain unclear. This study investigates the roles of the antennae, fore-tarsi, and mid-tarsi in monarch butterflies' host-plant selection and oviposition behavior by blocking the chemoreceptors on each organ with nail polish. Monarch butterflies from five lineages are reared under standard conditions on A. incarnata. Mated females are assigned to one of five treatment groups: control (untreated), antennae blocked, fore-tarsi blocked, mid-tarsi blocked, or all three sensory organs blocked. Each female is placed in a separate cage with one A. incarnata plant and one A. linaria plant and is given a two-hour window for oviposition. Their plant choice and the number of eggs laid on each plant are recorded to analyze how impairment of different sensory organ functions affects their oviposition preferences. We hypothesize that blocking tarsal chemoreception will reduce females' ability to discriminate between the two host species, resulting in a weaker host-plant preference. The lack of chemical cues may also reduce oviposition frequency, and the effect may be significant when mid-tarsal or multiple regions are blocked. The effect of blocking antennae chemoreception is expected to be small due to sensory compensation by the tarsi. The specific effects of each treatment will be evaluated by comparing the results with natural host-plant preference observed in the control group. This study addresses a gap in current understanding of how monarch butterflies integrate sensory information to form oviposition preferences and tests the relative contribution of each sensory organ. The study also evaluates the effectiveness and limitations of an experimental approach of sensory blocking, providing methodological reference for similar studies.

TITLE: **FROM ARCHIVAL SILENCE TO PUBLIC HISTORY: THE CASE OF LATINX HISTORY IN AN ELITE SOUTHERN INSTITUTION**

PRESENTER: **ESTELA DE LEÓN CORDERO**

MENTOR: **DR. ILIANA YAMILETH RODRIGUEZ**

PROGRAM: **LGS SOAR- HUMANITIES**

Relations of power shape institutional archives, and in doing so influence whose histories become legible and memorialized. As an elite Southern institution, Emory University's archival and institutional materials reflect a relative scarcity of Latinx presence in the historical record. This project examines the possibilities of public history as a relational practice that can challenge institutional silences. By placing Michel-Rolph Trouillot's Silencing the Past (1995) in conversation with Arturo Escobar's concept of relationality (2024), I argue that community formation constitutes an ontological condition that precedes the archive and exceeds its representational capacities. To illustrate this argument, I searched for evidence of (1) Latinx organizing and community formation and (2) institutional recognition in Emory's recent past through archival records, investigating the production of Emory's history as an active production of space and memory. To interpret the forms of Latinx politics that emerge, the project draws on Cristina Beltrán's The Trouble with Unity (2010), which theorizes Latinidad as an ongoing site of political contestation. Ultimately, this research proposes an ethical and theoretical contribution to the Public Humanities by examining forms of collective life that resist the logics through which elite universities narrate and produce their institutional histories, and determine who is recognized or excluded within them.



TITLE: REGULATION OF PERIPHERAL IMMUNE CELLS BY COCAINE AND CBD CO-EXPOSURE AND IMPLICATIONS FOR REWARD-ADDICTION NEUROIMMUNE PATHWAYS

PRESENTER: JULIA DIETRICH

MENTOR: DR. RODNIE COLON ORTIZ

PROGRAM: SURE- BIOMEDICAL SCIENCES

Substance use disorders (SUDs) are a persisting global health concern, associated with addictive behaviors and chronic neuroinflammation. Emerging evidence suggests that peripheral blood mononuclear cells (PBMC), including monocytes and T-cells, contribute to neuroinflammation during SUDs by increasingly migrating across the blood-brain barrier (BBB). During this process, brain microvascular endothelial cells (BMVECs) use chemokine signaling to bind and recruit PBMC at the BBB, and this adhesion step, a critical checkpoint in immune cell trafficking, promotes diapedesis across the BBB. Previous work in our lab has suggested that commonly used substances, such as cocaine (COC) and cannabidiol (CBD), possess immunomodulatory properties that may alter PBMC recruitment at the BBB. However, the extent to which these compounds modulate immune cell interactions at the BBB and contribute to neuroinflammatory processes remains poorly understood. We hypothesized that COC increases monocyte, but not T-cell, adhesion to BMVECs, whereas CBD reduces immune cell adhesion. Furthermore, we predicted that combined COC and CBD treatment can neutralize their respective pro- and anti-inflammatory effects, restoring immune cell adhesion to basal non-inflammatory levels. To evaluate this, PBMCs were isolated from five healthy donors and treated with 10 µM COC, 1 µM CBD, combined10 µM COC and 1 µM CBD, or vehicle for 24 hours. PBMCs were then added to BMVEC cultures and incubated for one hour to allow adhesion. Afterward, nonadherent cells were removed using a wash, adherent cells were collected, and flow cytometry was performed to enumerate adherent cells. The findings of our study can be used to address a critical gap in understanding how COC and CBD regulate immune cell interactions at the BBB during SUD-associated neuroinflammation. Ultimately, this work aims to advance our understanding of the neuroimmune consequences of substance use and support the development of biologically informed approaches for addressing the growing global burden of SUDs.



TITLE: MAPPING THE PEACE MISSION: USING ARCGIS TO VISUALIZE HISTORICAL CORRESPONDENCE

PRESENTER: ELIZA DINENBERG

MENTOR: DR. FLORIAN POHL

PROGRAM: OXFORD- HUMANITIES

This project indexes the correspondence of the Father Divine archives located in Emory University's Stuart A. Rose Manuscript, Archives, and Rare Book Library. The collection and specifically the correspondence is a documentation of the influence and life of Father Divine and the Peace Mission, shedding valuable insight into where, for what, and who sought out Father Divine. My work is focused on indexing the archival correspondence, piloting a comprehensive digital index in order to improve the accessibility of the collection, and the preservation of the documents. The data was cleaned using OpenRefine and ArcGIS was used to create spatial visualizations. The project demonstrates how digital humanities tools can be used to not only preserve archival data but allow researchers to combine preservation and analysis, creating opportunities for interpreting historical archives. Integrating archival materials with digital tools allows this project to contribute to ongoing conversations of digital preservation and further access, showing how digital archives are able to support new forms of historical inquiry while also making collections more accessible for researchers within the Emory community.



TITLE: STIGMERGIC GRAPH MEMORY: AN ENVIRONMENT-AWARE APPROACH FOR MANY-TO-MANY MULTI-AGENT PICKUP AND DELIVERY

PRESENTER: ADITYA DUTTA

MENTOR: DR. JOON-SEOK KIM

PROGRAM: SURE- TECHNOLOGY, ENGINEERING, MATHEMATICS

Automated fulfillment warehouses must continuously assign and execute pickup-and-delivery work while avoiding congestion. In many-to-many Multi-Agent Pickup and Delivery (MAPD), a request specifies a stock-keeping unit rather than fixed endpoints, requiring the controller to select an agent, source, and destination before path planning. Existing graph-guidance methods primarily influence routing after goals are fixed, leaving endpoint instantiation uninformed by recent traffic. We introduce Stigmergic Graph Memory (SGM), a bounded, decaying memory layer that records recent execution signals on warehouse nodes and directed edges to rank feasible endpoints and route preferences without altering collision constraints or planner validity. Across paired request streams on five layouts, three load levels, and 25 seeds per condition, SGM outperforms two reconstructed many-to-many allocation baselines in all 15 map-load conditions, with paired throughput gains of 20.5-36.7%. These results show that recent execution memory can improve warehouse throughput by shaping which feasible goals enter the planner, not only how agents travel to already fixed goals.



TITLE: A CRITICAL ANALYSIS OF THE AIDS PANDEMIC IN MEXICO FROM THE 1980S TO THE 1990S

PRESENTER: BINNY FLORES

MENTOR: DR. ADRIANA CHIRA

PROGRAM: LGS SOAR- HUMANITIES

In the 1980s, the disease known as Acquired Immunodeficiency Syndrome (AIDS) shocked the world: while the disease spread and it quickly became associated with queer communities, treatment appeared to be beyond reach. Most scholarship, media coverage, and personal testimonies about how the disease impacted their loved ones and communities focus on its impact in the United States. This research project explores the Mexican government's preventative policies and how queer communities within the country responded to them and also developed their own policies. I explore this topic through a close study of campaign posters, pamphlets, newspaper coverage, and secondary sociological studies. I bring a unique lens to this question as both a researcher of Mexican descent in the U.S. and as queer.

As somebody who is both of the Mexican diaspora and queer, I was inclined to review any coverage of how AIDS impacted Mexico from the 1980s to the 1990s by looking at how the Mexican government enacted preventative spread policies, how Mexico's queer community took preventative measures within the community, AIDS awareness campaign pamphlets and posters, and which populations in Mexico were being infected with the disease. In my findings, my study concludes that (1) the Mexican government responded quicker to the pandemic; (2) in comparison to the United States, the most common path of transmission was through unprotected heterosexual intercourse rather than intravenous drug use or through soliciting sex workers; (3) in a signficant numbers of cases, Mexican men returning after Mexican men returning from the U.S. were carriers of the disease, which means that some of the conditions were outside the limits and control of the country and its government.

TITLE: **THE INDIAN WEST COAST IN A 14TH CENTURY CHINESE MARINER'S EYES: AN ANNOTATED TRANSLATION OF DAOYI ZHILUE**

PRESENTER: **MIYA FU**

MENTOR: **DR. ROXANI MARGARITI**

PROGRAM: **SURE- HUMANITIES**

The medieval West Indian Coast was one of the major hubs of maritime trade connecting the Indian Ocean world with other parts of the globe, and travelogues from 11th to 14th century provide vital evidence of this exchange. Wang Dayuan, a 14th-century mariner from Yuan China, recorded the places he visited during his voyages in a book titled Daoyi Zhilue. Despite the fact that Wang's contemporaries Ibn Battuta and Ma Huan – the latter sharing Wang's cultural background – have both been widely studied, few English-language scholarship engages with Wang's travelogue, and no reliable English translation of the work exists. This project produces an annotated translation of selected chapters of Daoyi Zhilue: it renders the original text from Classical Chinese into English, provides annotations to situate readers in the historical context, and references existing scholarly discussions of the text. During this process, Classical Chinese dictionaries and annotations by other scholars are consulted most frequently, and secondary sources on other topics are incorporated into the annotations whenever the text references a specific phenomenon or good. These chapters confirm the prosperity of world trade through evidence of goods such as pepper and horses, and offer observations on religious communities that existed in the 14th century. By providing a usable English translation of this Chinese text, this project sheds light on the significance of Daoyi Zhilue and fills a gap in English-language scholarship.



TITLE: COMPUTATIONAL DISCOVERY AND VALIDATION OF UBE2C INHIBITORS IN ATYPICAL TERATOID RHABDOID TUMORS

PRESENTER: MATTHEW GENTNER

MENTOR: DR. ANDREW HONG

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Atypical Teratoid Rhabdoid Tumor (ATRT) is a rare and aggressive pediatric brain cancer with poor survival prognosis and limited treatment options. Proteasome inhibitors show promise by inducing mitotic arrest through inhibition of UBE2C, an E2 enzyme partnering with the Anaphase-Promoting Complex. However, preliminary data suggest that resistance to proteasome inhibitors involve transcriptomic changes in members of the UBE2C pathway, but not UBE2C itself. UBE2C drives mitotic progression by ubiquitinating cyclin B1 and securin. UBE2C has remained undruggable for two decades due to its flat surface and structural homology within the E2 family; small peptides, PROTACs, and small molecules have yet to achieve selective inhibition. New computational methods for detecting targetable residues offer a promising path forward.

Using POOL/THEMATICS, we have identified Cys102 as UBE2C's dominant residue which is absent in E2 family members such as UBE2D3 and UBE2S. Foldseek reveals high structural conservation across eukaryotic lineages with variable Cys102 retention. SiteMap analysis yielded D-scores of 0.51-0.68 across sampled conformations which suggest that a covalent, reactivity-based targeting strategy may be favored over a conventional pocket-shape design. Together, these convergent lines of evidence identify Cys102 as a selective site warranting further investigation as a druggable target. An initial screen of 4,177 ligands (Enamine Anti-Cancer and FDA-Approved libraries) identified seven compounds for validation. Testing these in our parental and proteasome inhibitor resistant cell line model showed modest activity in 2 of the 7. Future work may incorporate covalent warheads and extended, partner-inclusive MD simulations toward a selective UBE2C inhibitor for ATRT.



TITLE: ONTOLOGICALLY ADRIFT: THE EXPLORATION OF AFRICAN AMERICAN COMPOSITION IN CHARLES JOHNSON'S MIDDLE PASSAGE

PRESENTER: B. HAYNES

MENTOR: JANERIA EASLEY

PROGRAM: LGS SOAR- HUMANITIES

By critically engaging with Charles Johnson's Middle Passage, it becomes clear that his protagonist, Rutherford Calhoun, is only able to operate as a accomplice for the Transatlantic Slave Trade as a result of natal alienation, the loss and distance from one's own history. While antebellum novels commonly examine protagonists that respond to the terrors of Slavery, Middle Passage offers a protagonist that accommodates that terror. This project is intended to advance understanding of African American ontology by proposing a theory that interconnects natal alienation, ethnocide, epistemicide, and bereavement. Via a close reading of the text, it indicates that through these losses, the innate wholeness of African American existence is revealed. As African Americans balance reinvention and defiance, the possibilities that lie in rejecting the perpetual victimization essential to Afropessimism and Black Nihilism could provide a solution to the perceived void of African American being.



TITLE: THE EFFECT OF INCREASING BROMATE CONCENTRATION ON THE GROUP BEHAVIOR OF BELOUSOV-ZHABOTINSKY (BZ) OSCILLATORS

PRESENTER: JENNIFER HE

MENTOR: DR. SIMBA NKOMO

PROGRAM: OXFORD- NATURAL AND PHYSICAL SCIENCES

The Belousov-Zhabotinsky (BZ) reaction is a chemical redox reaction commonly used for modeling oscillatory behavior found in various biological systems. Previously, studies on the heterogeneous BZ have focused on variables such as bead size that can affect BZ oscillatory behavior, yet little is known about the factor of solution composition on group dynamics. This project investigates the effect of bromate concentration in the BZ reaction on the emergence of group behavior of micro-oscillators. The experiment varied the concentration of bromate, a chemical species present in the BZ solution in which the micro-oscillators reside, and the number of micro-oscillators. The onset and the nature of collective behaviors were determined through image analysis in MATLAB. Results of this experiment showed an increase in wave activity as a function of increasing bromate concentration and the number of micro-oscillators. Increasing the number of micro-oscillators in the BZ solution resulted in more complex group oscillations. A similar pattern was observed with increasing bromate concentration. Thus, findings from this project can provide insight into the role of bromate concentration, an excitatory species, on group BZ oscillatory behavior. The results suggest that increasing the number of grouped micro-oscillators increases the concentration of excitatory species. This project offers a controllable, observable method for understanding collective behaviors such as quorum-sensing behavior in biological processes, like patterns related to neuronal firing and cell communication. Future studies involve using these results to understand the effect of temperature on the emergence of collective behavior.



TITLE: WATCHING ENZYMES WORK: TOWARD THE FIRST STRUCTURAL SNAPSHOTS OF SEROTONIN BIOSYNTHESIS IN ACTION

PRESENTER: DOMINIC KASSING

MENTOR: DR. KATHERINE DAVIS

PROGRAM: SURE- BIOMEDICAL SCIENCES

Serotonin regulates mood, sleep, digestion, and numerous other physiological processes, yet the mechanism underlying its biosynthesis remains incompletely understood. The first and rate-limiting step in serotonin production is catalyzed by tryptophan hydroxylase (TPH), an iron-dependent enzyme that converts tryptophan into 5-hydroxytryptophan using tetrahydrobiopterin (BH4) as a cofactor. The reaction proceeds through a series of high-energy intermediates, leading to a short-lived ferryl species (Fe(IV)=O) that has never been observed structurally in this class of enzymes. We use time-resolved X-ray crystallography to capture these intermediates. A major obstacle to characterizing these intermediates in this system is the inherent substrate inhibition in TPH1, the peripheral isoform of TPH. The same high concentrations of tryptophan necessary for crystallization produce an unproductive dead-end complex, preventing formation of the relevant ternary complex (the enzyme simultaneously bound to iron, BH4, and tryptophan in a reactive state). To overcome this, we generated a mutant variant of TPH1, denoted TPH1-5, that consists of five mutations reported to reduce substrate inhibition. We have successfully expressed, purified, and crystallized TPH1-5 on its own and co-crystallized with tryptophan and BH4, with hopes of solving the ternary structure. Crystals have been sent to a synchrotron, and diffraction data will be collected shortly. This work represents a critical step toward the first structural capture of the ferryl intermediate in an amino acid hydroxylase, with direct implications for understanding the chemical basis of serotonin biosynthesis and potential therapeutic targeting of this pathway.

TITLE: **MARKING AND DEFENDING YOUR TERRITORY: CONSTRUCTING AND COMPARING TWO SOCIAL DOMINANCE ASSAYS IN MICE**

PRESENTER: **JOSHUA KHO**

MENTOR: **DR. MALAVIKA MURUGAN**

PROGRAM: **BIOLOGY DEPARTMENT**

Understanding social dynamics, like social hierarchy and competition, and the neural substrates underlying them is foundational for developing and implementing treatments for neurological disorders in which social behavior goes awry, such as Alzheimer's disease and schizophrenia. Though researchers have developed various paradigms for exploring social dominance, there remains a need for replicable and reproducible implementations of these assays and clearer relationships between the different aspects of dominance they assess. We aimed to establish the use of two assays, the Urine Marking Assay (UMA) and Warm Spot Assay (WSA), to assess dominance within our lab. However, both the UMA and WSA assay lacked clear, accessible protocols for setting up and conducting these tests. Additionally, how the UMA and WSA may correlate with each other was unclear. Therefore, over this summer, we 1) created 3D-printed models to allow for easy replication of the UMA and WSA across research labs and 2) tested the correlation between dominance rankings determined by the UMA and WSA. Using our custom 3D-printed assays, we found that dominance rank as determined by the UMA correlated with the ranks from the WSA. Both the total and relative volume of urine deposited during the UMA correlated with the amount of time occupying the warm spot during the WSA. We have already begun applying these assays in new ways in the lab. Preliminary data suggests that the UMA ranks, but not the WSA ranks, predict social foraging phenotypes in a reward-related task in the lab, highlighting the insights that can come from assessing dominance via multiple avenues. The custom models built for this project will be made open-source, establishing this as a reproducible, accessible tool for determining dominance roles in a group of mice across labs.

TITLE: **REVOLUTION BY REDEMPTION: CHARLES DICKENS' CHARACTER DRIVEN APPROACH TO THE FRENCH REVOLUTION IN A TALE OF TWO CITIES**

PRESENTER: **NICOLAS LARA**

MENTOR: **DR. PAUL KELLEHER**

PROGRAM: **SURE- HUMANITIES**

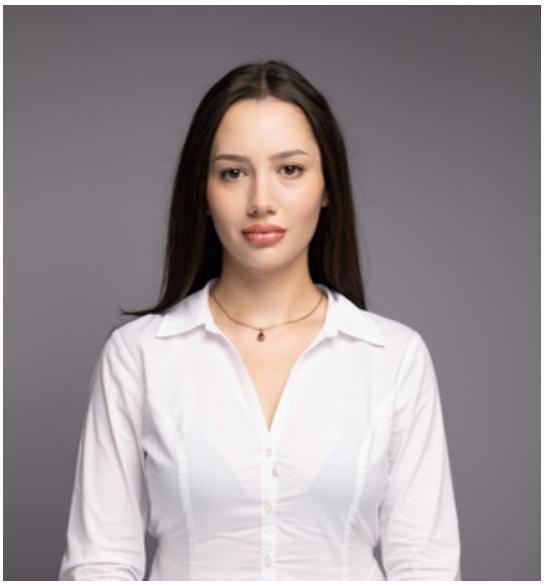
A Tale of Two Cities is one of Charles Dickens's most recognizable and studied works, in part because of its treatment of one of history's most politically controversial time periods: the French Revolution. It is therefore intriguing that one of the novel's principal attractors has also been the main point of contention in the scholarship surrounding it. Throughout the decades in which researchers have written about A Tale of Two Cities, a negative attitude emerged regarding the novel's approach to the complex history and politics of the French Revolution. George Orwell's "Charles Dickens" essay is often cited as a notable example of political criticism towards the novel. He wrote that while the novel recognized the Revolution as the product of the aristocracy's oppression of the French populace, Dickens appeared so taken by a "revolutionary terror" that he intensely portrayed its violence, while providing no satisfying alternative to counteract that same oppression he identified. Rather than extensively commenting on the French Revolution and its politics, A Tale of Two Cities devotes itself to the sentimental journeys of its characters, be it with the sacrifice of Sydney Carton, or the restoration of Dr. Manette, all packed with a consistently threaded theme of redemption through love, devotion and selflessness. Nevertheless, it is unclear whether these two notions, of historical commentary and character sentimentality, ought to be mutually exclusive. Orwell's essay provides an answer to such a question. Though the piece is often characterized as critical of Dickens, it contains within its less-excerpted sections a more favorable reading of the author's work. Orwell claims that all of Dickens's novels contain a form of critical social commentary expressed from a moralist lens, rather than a political one. The aim of this paper is therefore to apply Orwell's reading of Dickens's work to A Tale of Two Cities, in order to uncover the full extent of Dickens's moral critique of the French Revolution. Specifically, I will look at Dickens's work in characterization, and how the arcs he builds for his characters unveil his nuanced approach to revolutionary politics.

TITLE: HEGEMONY AND THE CONTEMPORARY EROTIC EXPERIENCE

PRESENTER: JOSEFINA LOGRIPPO

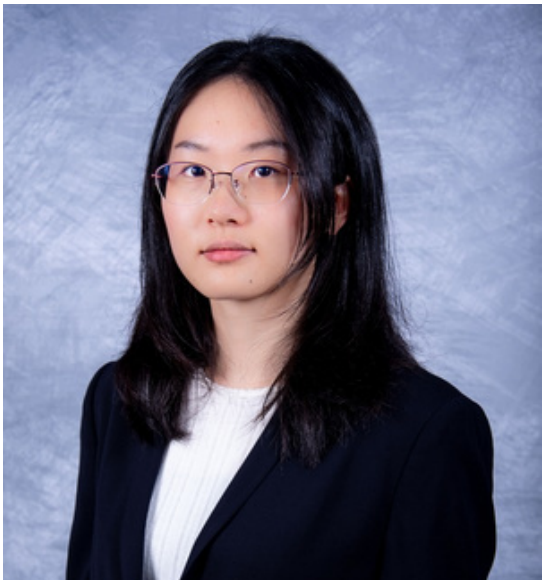
MENTOR: DR. ANGELA PORCARELLI

PROGRAM: SURE- HUMANITIES



Antonio Gramsci's observations on European cultural phenomena of the early 20th century in relation to power continue to be relevant in assessing how modern models of productivity and systems of social reproduction operate on a societal and subjective level. Numerous scholars have resorted to Gramsci in order to explain how contemporary social beliefs and interpersonal dynamics at times counter capitalist objectives or are shaped within capitalism to serve productive goals. Focusing on Antonio Gramsci's conceptualization of hegemony, as well as his writings on Americanism and Fordism, structure, superstructure, knowing, and feeling, my research analyses how the Italian philosopher's insights can be applied to further understand how the subject's 'eroticness' is manipulated and exploited in the age of digital capitalism. I argue that contemporary capitalist modes of production, particularly those of the digital sphere, have shaped the subject's erotic desire to fit a model of hyperproductivity and hyperconsumption that ultimately empties the erotic of its innate characteristics.

The following is a brief synopsis of how Gramsci's philosophical frameworks and theories fit a larger investigation project on how the erotic is materialized and manifested in contemporary capitalist societies.



TITLE: DROSOPHILA NEURAL CIRCUITS MEDIATING CROSS ORGAN SENSORY INTEGRATION

PRESENTER: VIOLA MING

MENTOR: DR. ANITA DEVINENI

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Daily food consumption relies on the brain's ability to integrate sensory information from multiple sources, such as vision, smell, and taste. Nonetheless, the mechanisms by which various types of input are merged in neural circuits to drive behavior remains unclear. It is known that flies primarily rely on gustatory signals from the leg and feeding organ (proboscis) to initiate feeding. Therefore, Drosophila melanogaster provides an ideal system to study these behavioral principles, as it has a well-mapped sugar feeding initiation circuit, and its complete connectome enables synaptic-resolution circuit mapping. To investigate the mechanisms underlying cross-organ integration of sugar signals in feeding, we propose three models for how flies may combine leg and proboscis taste inputs: (A) a gating model, in which proboscis input dominates feeding decisions; (B) a summation model, in which inputs from both organs accumulate to promote feeding; and (C) a comparison model, in which the leg signal sets an expectation for the proboscis response. To distinguish among these models, we measured feeding initiation and consumption behaviors to sucrose simultaneously presented to the legs and proboscis. We then mapped potential convergence from leg gustatory signals to the proboscis feeding initiation circuit using Drosophila brain connectome and recorded neuronal activity of potential convergence sites with in vivo calcium imaging. We found that feeding initiation is dominated by proboscis sugar input under concurrent stimuli on both organs, and leg gustatory receptor neurons have strong connections with the proboscis feeding initiation circuit. Interestingly, neuronal recordings of sugar gustatory neurons also suggested evidence for summation of inputs from both organs. These findings can reveal how the fly brain integrates concurrent gustatory signals to generate flexible feeding behaviors. Understanding these mechanisms may reveal conserved principles of multisensory integration and how brains transform sensory inputs into adaptive behavior.



TITLE: EVALUATING IN VITRO THERMAL RESPONSES OF HORIZONTALLY TRANSMITTED SYMBIONT STRAINS

PRESENTER: ALEX NUCKOLS

MENTOR: DR. PATRICK STILLSON

PROGRAM: MARC- BIOMEDICAL SCIENCES

Microbial symbionts in insect-microbe mutualisms are critical for host survival and fitness. However, symbioses are sensitive to external stressors. Understanding how a warming climate will impact these associations, therefore, is critical. Previous work on horizontally transmitted bug-Caballeronia bacterial symbionts has shown that different symbiont strains confer variable host outcomes under thermal stress, suggesting that environmental symbiont acquisition could be advantageous under shifting temperature regimes. However, it is unknown what specific bacterial thermal responses could impact microbial survival in the environment, which would be key to host acquisition. We interrogated in vitro thermal response mechanisms of heat-vulnerable and heat-resistant strains of Caballeronia by analyzing transcriptomic data of each strain at 24°C, 30°C, and 36°C, to identify pathways associated with the strains' different thermal tolerances. We found that both strains arrest growth at sub-optimal temperatures by repressing growth-associated genes and pathways, with the strongest repression at 24°C for the heat-resistant strain and 36°C for the heat-vulnerable strain. Additionally, we found that the heat-resistant strain is far more motile at all temperatures and represses motility at sub-optimal temperatures. Meanwhile, the heat-vulnerable strain shows strong induction of biofilm formation under thermal stress. These results are indicative of variable bacterial thermal response strategies for elevated temperature survival. Based on these in vitro results, we speculate that these responses may alter which symbionts are more available to insect hosts in the environment as temperatures continue to rise.

TITLE: **IRON & THE BOMI HILLS: LIBERIA, THE UNITED STATES, AND POSTWAR RESOURCE SOVEREIGNTY, 1944-1977**

PRESENTER: **CABOT POSTOL**

MENTOR: **DR. ADRIANA CHIRA**

PROGRAM: **SURE- HUMANITIES**



In 1946, Liberia's government and the American-owned Liberia Mining Company (LMC) ratified an agreement for the country's first iron mining concession. Located in the Bomi Hills, the mine was part of Liberia's "Open Door Policy," which sought to foster economic development through foreign investments and corporate concessions. This presentation focuses on labor and life within the LMC mining enclave. Using archival material, including periodicals and company records, I describe labor conditions, life, and conflict within the mine and its surroundings from the first shipment of ore in 1951 to the mine's closure in 1977. I outline how workers, government officials, and corporate executives used iron mining and the Bomi Hills' landscape to articulate competing distributional and temporal visions of development, making claims to natural resources and the extractive process.

TITLE: **ANALYZING CHANGES IN RETINAL METABOLIC FLUX IN A TRANSDUCIN-KNOCKOUT MOUSE MODEL**

PRESENTER: **YILIN QIAO**

MENTOR: **DR. DANIEL HASS**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**



Degeneration of retinal metabolism leads to degenerative retinal disease, yet uncertainty about the exact workings of retinal metabolism hampers development of novel metabolism-oriented therapeutic approaches. The unique neural organization of the retina, with a “dark current” being maintained through active ion transport in the absence of light, causes energy costs to fluctuate greatly in different environments. Previous studies have estimated dark-state retinal energy consumption at up to four times that of light-state. This total increase of energy demand is well-known, but how metabolic mechanisms shift to meet this demand remains unknown. Therefore, a better understanding of metabolic flux, both in stasis and flux, could enhance our understanding of the retina. Transducin knockout models--GNAT1 and GNAT2--in rods and cones respectively, sever signaling from photopigments to simulate a permanent dark-state. Electroretinograms of GNAT1KO mice confirmed the elimination of neural responses in the retina. Photospectrometric enzyme assays of media used to incubate GNAT retinas showed no significant difference across genotypes regarding consumption of extracellular glucose or release of lactate, instead emphasizing intracellular flux shifts. Retinas were incubated in 13C glucose media; tracing samples were collected at steady state and dynamic timepoints for LC-MS quantification. Steady state tests upheld glucose as the primary retinal fuel in either dark- or light-state; M+3 glucose signal was observed, implying a non-negligible level of gluconeogenesis. Activity of alternative metabolic pathways, such as pyruvate carboxylation, were suggested but not strongly supported by the ratio of M+2/M+3 Malate. Dynamic tests demonstrate timewise consumption of U-13c-labeled glucose strongly prefers aerobic glycolysis over the TCA. We acknowledge limited sample sizes and variability, though LC-MS of isotopologues concretely reveal that alternative glycolytic and glycogenic pathways are at play in the retina, opening up new questions about whether these pathways are conditional with light-state.



TITLE: ASSOCIATION BETWEEN STERNAL VIBRATION AND LOW-FREQUENCY HEART-RATE VARIABILITY TRAJECTORIES IN TRAUMA-EXPOSED ADULTS

PRESENTER: AMMAR RAZZAK

MENTOR: DR. NEGAR FANI

PROGRAM: SURE- BIOMEDICAL SCIENCES

Trauma exposure is a pervasive public health concern that is known to have lasting effects on both neural and physiological functioning. It is estimated that 70% of individuals worldwide will face a traumatic event in their lifetime, and 3.9% of those will develop post-traumatic stress disorder (PTSD)(1). PTSD is characterized by dysregulation in autonomic functioning, including heart rate variability (HRV), a well-established indicator of autonomic flexibility and regulation. Breath-focus mindfulness meditation augmented with sternal vibration is a promising novel non-invasive intervention for individuals with PTSD who have limited relief with extant therapies(2). We evaluated 189 adults with trauma exposure and elevated dissociation (74% female; aged 18-62), who were recruited to be part of an ongoing multi-site clinical trial testing the effect of vibration-augmented breath-focused mindfulness. Participants underwent up to eight mindfulness interventions over 4 weeks and were grouped by whether they received sternal vibration (n=100) or no vibration (n=89). A latent growth-curve model was used to estimate baseline low-frequency HRV (LF-HRV) and its linear change across visits, where vibration group was used as a predictor of latent intercept and latent slope, with covariates for age, biological sex, study site and race. We found that vibration resulted in a steeper increase in LF-HRV across interventions compared to no vibration ($\beta = 0.39$; $p = 0.031$). These findings suggest that repeated sternal-vibration augmentation may be associated with improved autonomic regulation over time in trauma-exposed adults; future research should determine whether these physiological changes translate to improved PTSD and dissociative symptoms or greater treatment engagement.

TITLE: UNRAVELING THE FABRIC OF ANTIQUITY: AN ONGOING EXPERIMENT IN ANCIENT WEAVING TECHNIQUE

PRESENTER: AVA REESE

MENTOR: DR. SANDRA BLAKELY

PROGRAM: SURE- HUMANITIES

Today, the general tedium, precision, and ubiquity of textile manufacture is fairly well understood by Classicists, but the messy (and virtually unrecorded) intricacies of the industry of textile manufacturing in the ancient Mediterranean have consistently proven difficult to piece together. As is made clear from both literary and iconographic sources, the textiles of the Roman artistic imagination varied widely; we see on Pompeiian frescoes both shimmering, transparent garments and heavy, rough cloaks. To move towards a more comprehensive understanding of the chaîne opératoire of the domestic (i.e. non-import) Roman textile industry, we must attempt to determine the limits of the warp-weighted loom, which was the predominant loom type until the 2nd century A.D. Experimental archaeology has proven invaluable in answering such questions. Landmark studies, such as that conducted by Linda Mårtensson et al. (2009) and the ongoing PENELOPE Project, have been critical in approximating the tools and techniques used in ancient weaving. Following similar methodology to both studies, particularly in my use of the optimal weight-to-thread ratios as determined by Mårtensson et al, this study consists of the warping and weaving of fabric with my best approximation of ancient techniques and tools. However, I diverge from those studies in my especial focus on the weight of the produced fabric. By weaving with increasingly finer thread, my hope is to eventually be able to produce garment-quality fabric on the warp-weighted loom. This experiment is one step of many towards the production of fine, even diaphanous, fabric on the ancient loom. Reproduction of this process, which is yet to be published, would be instrumental in progressing our understanding of the capability of the Roman weaver and, thus, refine our image of the textile industry at large.

TITLE: **CHARACTERIZING THE PROGRESSION OF ANTERIOR CRUCIATE LIGAMENT AUTOGRAFT MATURATION WITH MAGNETIC RESONANCE IMAGING: EFFECTS OF THE LATERAL EXTRA-ARTICULAR TENODESIS PROCEDURE**

PRESENTER: **TIM RICHTER**

MENTOR: **DR. JED DIEKFUSS**

Introduction: Anterior cruciate ligament (ACL) reconstruction (ACLR) using an autograft is standard for ACL rupture. Following ACLR, the autograft undergoes ligamentization, progressively remodeling to resemble the native ACL. The lateral extra-articular tenodesis (LET) procedure may improve knee stability, but its influence on graft maturation remains unclear. The purpose of this study was to characterize ACL autograft maturation for patients with and without LET using magnetic resonance imaging (MRI).

Methods: Twenty-seven participants (15.4 ± 1.4 years) undergoing primary ACLR, including nine who received concomitant LET, were evaluated. MRI was performed preoperatively on the contralateral knee and at 3-, 6-, and 12-months postoperatively on the ipsilateral knee. T2-weighted fat-saturated images were acquired, ACL and autograft structures (proximal, proximal-middle, distal-middle, and distal regions) were segmented using a semi-automated method, and signal intensity ratio (SIR) was calculated by normalizing SI to the posterior cruciate ligament. Linear mixed-effects models evaluated the effects of time, LET, and their interaction, with Bonferroni post hoc comparisons set a priori ($\alpha = 0.05$).

Results: No significant main effects of LET or time × LET interactions were observed for any region ($p > .05$). However, significant longitudinal changes in SIR were observed in the proximal, proximal-middle, and distal autograft regions (all $p \leq .05$). Compared with the preoperative native ACL, SIR was elevated at 3-, 6-, and 12-months in the proximal region, at 3- and 6-months in the proximal-middle region and was lower at 3- and 12-months in the distal region (all $p < .05$).

Significance: LET did not uniquely influence autograft SIR. However, postoperative SIR differed from the native ACL across regions and timepoints, indicating that graft maturation is spatially heterogeneous and may remain incomplete 12 months after ACLR. Future studies should determine whether autograft maturation patterns are associated with clinical outcomes and predictive of secondary ACL injury.

TITLE: **TARGETING MYC-DRIVEN OSTEOSARCOMA THROUGH TGF-B RECEPTOR INHIBITOR VACTOSERTIB**

PRESENTER: **DANIEL SUN**

MENTOR: **DR. JASON YUSTEIN**

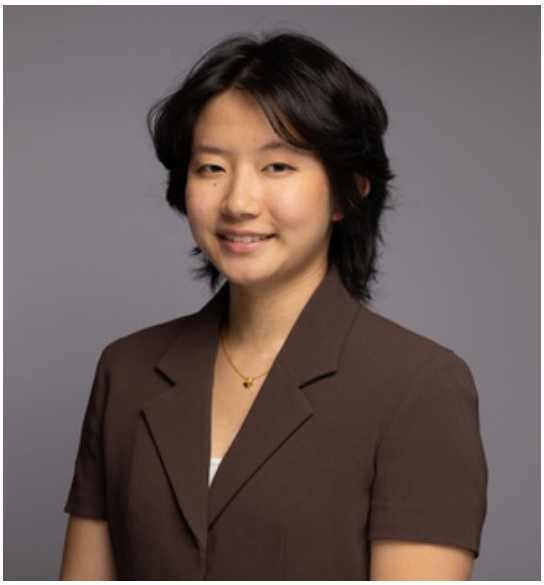
PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Osteosarcoma (OS) is the most common malignant bone tumor in children and adolescents, and it remains a leading cause of cancer-related mortality in this age group. Approximately 20–25% of OSs carry amplification of chromosome 8q24, which overexpresses the oncogene c-MYC, a driver of osteosarcoma growth. However, MYC remains a challenging therapeutic target due to the lack of suitable binding pockets. Activation of the TGF-β (transforming growth factor-β) pathway induces c-MYC expression and drives disease progression. Vactosertib, a selective inhibitor of the TGF-β type I receptor (ALK5), blocks TGF-β signaling and has demonstrated anti-tumor activity across different preclinical cancer models. Therefore, in this study, we aim to target upstream signaling pathways that sustain MYC expression and activity.

We evaluated the therapeutic effects of vactosertib across a panel of OS cell lines, including a murine MYC-high OS model. Cell viability assays were performed to determine vactosertib sensitivity. Cell proliferation was assessed over 72 hours following treatment with 1 μM vactosertib and normalized to the DMSO control. Cell migration was measured using a Transwell migration assay. To investigate the mechanisms of Vactosertib activity, we analyzed MYC-associated signaling changes by using Western blotting and quantitative reverse-transcription PCR.

Vactosertib showed anti-proliferative activity across the OS cell panel. Sensitivity did not correlate with MYC status, as responses remained similar among all groups. The most interesting result was inhibition of migration, suggesting that TGF-β signaling contributes strongly to the migratory behavior of these cells. At the molecular level, vactosertib reduced MYC transcript levels, and MYC protein expression was also decreased, although the suppression varied between cell lines.

These findings indicate that vactosertib has meaningful activity in murine OS. Future studies in in vivo models should determine whether response correlates with p-SMAD suppression, MYC pathway modulation, and validated MYC-status classification, and whether combination strategies improve therapeutic efficacy.



TITLE: GOUBIAN READER: CREATION OF AN INTERACTIVE CROCHET LITERACY APPLICATION TO ENHANCE PATTERN SENSE-MAKING

PRESENTER: MANDY SUN

MENTOR: DR. KRISTIN WILLIAMS

PROGRAM: SURE- TECHNOLOGY, ENGINEERING, MATHEMATICS

Video has become a dominant means to learn precise techniques and pattern notations for modern day crafts like crochet. Although videos provide step-by-step visual guidance on how to complete a project, they lack the precise language found in more advanced crochet patterns and can restrict or frustrate viewers with poor angling, lighting, and pacing. These challenges can cause users to plateau in their learning without having reading intuition for integrating pattern notations in both written and diagrammed formats. Although current technologies such as CrochetPARADE attempt to bridge the gap in creating and understanding crochet patterns by parsing, debugging, and rendering them, the complex, application-specific syntax and simplistic user interface are not readily accessible to beginner crafters. This research provides a craft-based user interface that augments the crochet learning experience by offering (1) translation between crochet languages and (2) interactive crochet graphs that offer step-by-step animations and precise notation implemented with CrochetPARADE logic. These features offer crocheters a digitized means of navigating crochet patterns at their own pace and with clear instructions in both pattern languages, enhancing a sense of agency in crafting by encouraging pattern literacy. This project will aim to answer the following questions: How can a craft-based user interface for crochet, a complex and variant handcraft, support agency over craft? How do crochet-beginners use 2D-animated instructions in a digital, craft-based user interface to learn to read written or diagrammed crochet patterns differently from a video?



TITLE: REASSESSING THE ISLAMIST ADVANTAGE: POLITICAL ISLAM AND ELECTORAL MOBILIZATION STRATEGIES IN ISRAEL

PRESENTER: THOMAS WAINWRIGHT

MENTOR: DR. COURTNEY FREER

PROGRAM: SURE- SOCIAL SCIENCES

The “Islamist advantage” thesis posits that political parties advocating for the use of political power to embed Islam in society have an electoral advantage over other political parties. Prior investigations of the mechanisms for this advantage have focused on states with relatively strong Muslim socio-political consciousness, while cases with competitive Islamist political parties but no Muslim majority are often overlooked. In this work, I use existing scholarly research to survey the electoral mobilization mechanisms employed by Islamists in Israel, a state with a Muslim minority and an electorally competitive Islamist political presence (i.e. the Islamic Movement). Preliminary findings suggest that Islamists in Israel provide social services (e.g. education, childcare, and transportation support) with a uniquely nationalist focus, contributing to their electoral success at a local level. This provision may contribute less to broad electoral support in Israel relative to previously studied cases due to the Islamic Movement's targeting of lower socioeconomic classes and their struggle to compete with Jewish ideological hegemony. Results provide empirical support for Cammett and Jones Luong’s contention that several mechanisms work in tandem to produce an electoral advantage for Islamist political parties. Results also demand an increased consideration of Islamists’ ability to cultivate a reputational advantage or the exceptionalism of that advantage when competing in religiously pluralist or ideologically inhospitable settings.



TITLE: BROADENING ACCESS TO AGENT-BASED MODELING THROUGH A NO-CODE STEERING BEHAVIOR SIMULATION PLATFORM

PRESENTER: KEVIN WANG

MENTOR: DR. HAI LE

PROGRAM: OXFORD- TECHNOLOGY, ENGINEERING, MATHEMATICS

Agent-based modeling (ABM) can provide a powerful approach for investigating how individual-level behavioral rules result in group-level emergent patterns, such as disaster response and opinion polarization. However, many existing simulation frameworks require programming proficiency, specific hardware, or software installation, creating barriers for users without computational backgrounds. This project addresses these challenges with a cloud-based simulation of WebApp requiring no installation and minimal programming background, allowing users to focus on scenario design rather than technical setup.

Developed using React, a JavaScript library supporting modular interface design, the WebApp presented here includes a simulation canvas and control panel for creating, editing, and deleting entities, currently agents and obstacles, where agents may represent people in an evacuation scenario. Users define behavior rules by selecting a target property, such as speed, heading, or position, referenced to the agent itself or a neighbor, with an offset modifying the property relative to that reference. Filters determine which entities influence a behavior based on properties such as distance or relative bearing, for example allowing an agent to follow its nearest neighbor.

Preliminary testing has revealed two problems: (1) a group of agents in a snake-shaped line briefly lost formation while warping, the process by which agents cross a canvas boundary and reappear on the opposite side; (2) agents often oscillated during avoidance, turning back and forth when a relative-bearing filter was used since the framework gives equal influence to behaviors sharing a target property. These findings identified areas requiring further refinement, motivating a planned activation component described below.

Lowering the technical threshold for ABM shifts attention from software setup toward scenario design and interpretation. In the next phase, we will investigate how evacuation time varies with exit placement, obstacle configuration, and agent density. Planned development also includes an activation component that will dynamically weight concurrent behaviors that share a target property according to changing environmental conditions, letting the most appropriate behavior take priority and reducing oscillation.



TITLE: POLITICAL PROXIMITY AND CORPORATE GOVERNANCE IN CHINESE ENTERPRISES: DOES DISTANCE TO BEIJING MATTER?

PRESENTER: ANDREW WANG

MENTOR: DR. DANIEL LUDWINSKI

PROGRAM: OXFORD- SOCIAL SCIENCES

China's vast territory and population make it impossible for the Central Government to completely centralize power into the hand of the Central Government. The Chinese government's fiscal decentralization system grants local governments substantial discretion. While this topic has primarily beens studied in the context of politics and local economy, whether such independence also applies to the enterprises is left unexamined. Focusing on all companies in Chinese A-share, this project studies whether an enterprise's governance outcome differs based on its proximity to The State Council, based on the hypothesis that decreased proximity grants higher independence, and if this proximity effect is moderated by Chinese Communist Party embeddedness in the firm. Governance outcome is measured along two dimensions: an enterprise's likelihood to violate regulations and its internal control level. This study finds that enterprises farther away from The State Council are more likely to violate regulations in a year, with an interquartile increase in distance corresponding to a 6.2% relative increase in violation probability, and exhibit a lower internal control level, though this second effect is economically modest. While party embeddedness initially appears to reduce violation likelihood in the full sample, this effect disappears entirely once firm ownership type is controlled for, indicating that it reflects systematic differences between SOEs and private firms. This study finds no evidence that distance moderates the effect of party embeddedness on either governance outcome, nor that the distance effect itself differs between SOEs and non-SOEs.



TITLE: SECULARIZATION AS CONCEPTUAL CHANGE: WHAT A CENTURY OF IRISH PARLIAMENTARY LANGUAGE REVEALS ABOUT THE MODERN STATE

PRESENTER: LITONG WANG

MENTOR: DR. JO GULDI

PROGRAM: SURE- HUMANITIES

Between 1922 and 2025 the word dignity never left Irish parliamentary speech: its frequency is essentially flat across the century. What changed is its meaning.

Historians read Irish secularization institutionally – the Catholic Church's control of welfare, health and education passing to the state – while constitutional scholars dispute whether the dignity written into the 1937 Constitution was a religiously-inspired concept or a plural one. Both arguments rest on institutions and drafting memoranda; neither reads the century of parliamentary usage that followed. Can that usage be measured, and what does it show? This paper sets out to measure it, testing the expectation that dignity travelled with the secularizing vocabulary of the welfare state.

Reading the full bicameral Oireachtas record (Dáil and Seanad, 1922–2025)as a Critical Search, it chains five exhibits: collocates, a distant-reading timeline, a word-embedding Axis of Secularization, keyword collocates, and clustering, each grounded in close reading of the floor.

Two findings emerge. The vocabulary of social provision (human, welfare, housing, poverty, labour) migrates measurably from church-state language toward the language of rights, beyond baseline drift; human is the largest mover (+0.55). But dignity does not ride that axis. Across the century its company is never distinctively religious but secular-moral throughout; what moves is the basis of the standing it confers, from the honour of an office to the rights and care owed a person – a shift legible on the floor from de Valera (1931) to Chochinov (2023).

The project thus confirms the historians on provision and complicates them on dignity, adjudicating the 1937 dispute by showing that the religious root does not govern the word's legislative life. It supplies the instrument the secularization literature implied but never built: church-to-secular transition measured directly from the language of parliament.

TITLE: **OPTIMIZATION OF CHROMATIN IMMUNOPRECIPITATION SEQUENCING FOR PROFILING OF TRANSCRIPTION FACTOR-MEDIATED REGULATION OF GENE EXPRESSION THROUGH EPIGENETIC MODULATIONS**

PRESENTER: **ARBA ZHAO**

MENTOR: **DR. YOUNGMIN HAN**

The understanding of epigenetic mechanisms behind cardiovascular cell reprogramming from other cell types requires the mapping of significant associations of key transcription coactivators, notably the myocardin gene (MYOCD), and their association with local and global chromatin environments. However, Chromatin immunoprecipitation (ChIP) assays have traditionally been known to be prone to suffering from loss of transient protein-DNA interactions as well as high background noise. To be able to decode the reprogramming regulatory pathways comprehensively, this study aims to systematically optimize an approach that maximizes nucleosome complex purity and specificity, as well as effectively monitors associations between MYOCD and specific histone modifications. In order to balance the capture of transient physical interactions with assay specificity, we will comparatively evaluate crosslinking techniques using paraformaldehyde (PFA) against dithiobis(succinimidylpropionate) (DSP) reagents. Further, the protocol will seek to optimize chromatin shearing techniques by comparing the shearing efficacy of sonication against enzymatic digestion (MNase) techniques. Downstream immunoprecipitation will target FLAG-tagged MYOCD alongside highly specific monoclonal antibodies for histone markers such as H3K4me3, H3K27me3, H3K27ac, and H3K9ac. As high-quality ChIP sequencing for global genomes relies entirely on the purity of the input nucleosome complex, an optimized immunoprecipitation pipeline that yields refined cross-linking while preserving target complex integrity is absolutely crucial. By generating high-resolution global genome datasets, this study will move beyond localized interactions of epigenetic factors and instead reveal epigenetic landscapes controlled by MYOCD. Ultimately, this sequencing will provide a foundational epigenetic map to inform cellular reprogramming mechanisms for cardiovascular regeneration techniques.

TITLE: **PIECEWISE-STATIONARY TEMPORAL AUTOENCODERS FOR CAUSAL INFERENCE IN MULTIVARIATE TIME SERIES**

PRESENTER: **JASMINE ZHOU**

MENTOR: **DR. GORDON BERMAN**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Time series data are ubiquitous across scientific disciplines. Interactions among parts of a complex system can appear, disappear, or reverse over time, and understanding when and how these interactions occur is critical for assessing causality in dynamical systems. Classic causal-inference methods often rely on assumptions of linearity, stationarity, and separability. Temporal Autoencoders for Causal Inference (TACI; Calderon & Berman, 2024) was developed to detect time-varying, nonlinear causal relationships using a Comparative Surrogate Granger Index (CSGI) computed by temporal convolutional autoencoders. However, TACI trains four networks for each variable pair, does not test whether detected relationships are stronger than expected by chance, and can produce non-zero CSGI values even when no true directional coupling is present. To address these limitations, we present Piecewise-Stationary Temporal Autoencoders for Causal Inference (psTACI), a reimplementation of TACI built on three core components: (i) a single shared temporal-convolutional predictor trained using three versions of the input data, including surrogate inputs that remove directional information; (ii) a variance-stable directed predictive information index, ΔI, reported alongside CSGI; and (iii) statistical significance testing against time-shifted surrogate data controlled at a false-discovery rate < 0.05 by the Benjamini–Hochberg procedure. Across synthetic static and time-varying bivariate systems, psTACI recovered the causal-inference performance of TACI while reducing runtime by an average of 2.3x. On the static coupled-Henon benchmark, psTACI suppressed the spurious reverse-direction null score by ~13x and improved the separation between true and false directions from 7× to 33×. These results indicate that a shared-predictor architecture and variance-stable scoring can improve computational efficiency without sacrificing sensitivity to time-varying interactions. By combining scalable inference with statistical testing, psTACI provides a more reliable framework for determining when and in which direction nonlinear interactions occur in complex dynamical systems.

TITLE: MUSHROOMS AND MINDFULNESS: A PROJECT ON HARM ASSESSMENT IN PSYCHEDELIC AND MEDITATION RESEARCH

PRESENTER: RICHARD ZHU

MENTOR: DR. ALI ZARRABI

PROGRAM: SURE- SOCIAL SCIENCES



In recent years, clinical studies exploring the therapeutic benefits of consciousness-altering practices have expanded considerably, showing that these practices can influence multiple dimensions of human experience beyond symptom reduction alone, including affective, cognitive, perceptual, sense of self, somatic, and social functioning (Britton et al., 2021). While psychedelic therapy and meditation can induce powerful alterations in consciousness, they are not fully captured by conventional methods of harm assessment. My project compares the strengths and limitations of three emerging approaches to assessing adverse effects in clinical psychedelic and meditative experiences. The three assessments I examine are the Varieties of Contemplative Experience (VCE) framework and its accompanying Meditation Experiences Interview (MedEx-I), the Swiss Psychedelic Side Effects Inventory (SPSI), and the Psychedelic-Assisted Therapies Adverse Events (PAT-AE) framework. These three approaches differ in their primary focus. VCE and MedEx-I characterize meditation-related adverse effects through a structured interview, emphasizing that whether a participant's experience is harmful is dependent on a multitude of contextual factors, such as practice intensity, duration, and teacher and community support. SPSI offers a structured questionnaire that focuses on the consistency of psychedelic-specific symptom reporting, creating a precise list of relevant side-effects to examine. PAT-AE proposes a comprehensive framework for identifying, interpreting, and then monitoring adverse events, highlighting the importance of multidimensional questioning through all stages of a clinical trial. Despite these differences, common themes include emphasized multidimensional assessment, context-dependent analysis of symptoms, and the use of targeted and open-ended questions to assist in active monitoring of adverse experiences. Together, these assessments reveal the importance of multidimensional and context-specific harm assessment, illustrating different approaches to improve adverse event frameworks.

POSTER PRESENTATIONS



TITLE: MAPPING CKD MYOPATHY WITH QUANTITATIVE MRI: NOVEL MUSCLE INFLAMMATION AND FAT INFILTRATION BIOMARKERS

PRESENTER: SAKETH AGAVA

MENTOR: DR. JINHEE JEONG

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Uremic myopathy is a major complication of chronic kidney disease (CKD) characterized by skeletal muscle atrophy and fat infiltration. This cross-sectional pilot study aimed to characterize novel quantitative magnetic resonance imaging (qMRI) metrics for uremic myopathy by mapping their regional distribution and clinical associations, and to compare them between CKD and controls. We acquired multi-echo Dixon and structural 3T MRI sequences of the mid-thigh from 25 patients with CKD Stage III-IV and 6 age-matched controls. Custom MATLAB pipelines extracted T2 water relaxation time, as an index of muscle inflammation, and proton density fat fraction (PDFF) from 12 manually segmented thigh muscle regions. qMRI biomarkers were tested for their associations with clinical outcomes, including bioimpedance-derived body composition and the extracellular-to-total body water (ECW/TBW) in CKD, and group differences with controls.

T2 and PDFF demonstrated muscle-specific regional patterns rather than uniform values across the thigh. Between-subject variability of T2 was comparable to within-subject variability, indicating that regional muscle differences contribute substantially to the total observed variance. Elevated T2 was significantly associated with worsening glycemic status and ECW/TBW, establishing a dynamic metabolic-hydration axis. PDFF was significantly associated with total body adiposity and age, reflecting chronic compositional remodeling. Neither biomarker correlated with estimated glomerular filtration rate. There were no significant differences between T2 and PDFF between patients with CKD and controls.

Together, T2 water and PDFF provide independent, complementary biomarkers that distinguish current physiological muscle state from chronic structural remodeling, potentially improving the assessment of disease progression and guiding future targeted therapeutic interventions.



TITLE: SUPPORTING THE SUPPORTERS: A QUALITATIVE STUDY ON STRATEGIES TO FACILITATE SEXUAL HEALTH CONVERSATIONS WITH ADOLESCENTS AND YOUNG ADULTS IN THE SOUTHERN UNITED STATES

PRESENTER: MARIA ANTONIO GOMEZ

MENTOR: DR. SAMANTHAHILL

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Sexually transmitted infection (STIs) incidence is highest in adolescent and young adults (AYAs) compared to other age groups, with Black AYAs, especially those residing in the Southern United States being disproportionately overburdened. Studies have utilized support persons to influence positive sexual health outcomes among AYAs; however, as the technological landscape continues to grow, interventions that combine support persons and technology have great potential. This study explores adult support persons' attitudes towards engaging in sexual health conversations with Black AYAs and how mobile health apps (mHealth) can facilitate those conversations.

In-depth interviews (IDIs) and focus groups (FGs) were grounded in Social Cognitive Theory and Social Supports and Social Networks theory to explore support person knowledge, attitudes, and perspectives engaging with AYAs through technology. Inclusion criteria were adults aged 22 years of age and older self-reporting supporting Alabama Black AYAs ages 14-21. Transcripts were analyzed using inductive and deductive coding via rapid qualitative analysis in Excel.

Thirty-six support persons completed 23 IDIs and two FGs. Support persons had a mean age of 42 years, were 87% women and 100% Black, with 57% residing in urban areas, and 78% reporting supporting more than one youth. Transcribed IDIs and FGs revealed major themes including that 1) trust and relatability between the support person and AYAs shape sexual health conversations, 2) support persons express the need for confidence, preparation, and accurate health information before speaking with AYAs, and 3) technology can strengthen sexual health conversations between AYAs and support persons. Features support persons desired were 24-7 support, preview pane, and credible information sources.

This study revealed support persons are willing to help AYAs navigate their sexual health through mHealth. Next steps are adapting and piloting an mHealth app based on these findings. Future endeavors can work to improve accessibility and usability of the mHealth application.

TITLE: EVOLUTIONARY CONSERVATION OF HISTONE GENE REGULATION BETWEEN DROSOPHILA SISTER SPECIES

PRESENTER: SALAAM AWAD

MENTOR: DR. LEILA RIEDER

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Histone proteins, which compact and organize DNA in the nucleus, are some of the most conserved proteins across eukaryotes despite having vast differences in their cis-regulatory elements and genomic organization. How eukaryotic organisms can maintain similar histone gene regulation with differences in regulatory elements remains largely unexplored.

Drosophila melanogaster is a prominent model for histone gene regulation, hosting a histone locus of ~100 tandemly repeated histone gene arrays. Its sister species, D. simulans, has a similar histone locus organization and shares the histone gene regulatory proteins CLAMP and Mxc, responsible for binding histone gene promoters and forming the Histone Locus Body (HLB). However, D. melanogaster and D. simulans histone genes have wildly diverged promoters. The goal of my research is to determine if histone regulatory proteins co-evolve with regulatory sequence. I will examine how each species' regulatory proteins interact with both regulatory sequences in vivo using D. melanogaster and D. simulans hybrids.

I compared the Mxc and CLAMP protein sequences between species. The CLAMP protein sequences are highly conserved. I hypothesize that in vivo, D. melanogaster and D. simulans CLAMP can bind the histone regulatory sequence of both species. However, the Mxc protein sequences have dramatic differences in the domains required for Mxc self-interaction and HLB formation. I hypothesize that Mxc will form exclusive, species-specific, condensates with their associated species' histone genes.

To test whether Mxc and CLAMP have co-evolved with regulatory sequence, I crossed D. melanogaster with D. simulans to create hybrids carrying both species' histone loci. I visualized the regulatory proteins using immunofluorescent staining on polytene chromosomes. To determine which species' histone genes are expressed in hybrids, I am using droplet digital PCR and Taqman probes specific to each species' Histone 3 (H3) gene. These experiments will show whether regulatory proteins between sister species co-evolve with regulatory sequences.



TITLE: PHYSIOLOGICAL IMPACTS OF RACIAL DISCRIMINATION: EVIDENCE FROM LONGITUDINAL ECOLOGICAL ASSESSMENTS IN BLACK AMERICANS

PRESENTER: HILARY BARKEY

MENTOR: DR. NEGAR FANI

PROGRAM: SURE- BIOMEDICAL SCIENCES

Racial discrimination (RD) is a pervasive stressor that affects the majority of Black Americans across various facets of their lives. Exposure to RD is associated with autonomic dysregulation, measured by changes in average heart rate (HR), as well as psychiatric and physical illnesses including hypertension, symptoms of post-traumatic stress disorder, depression, and cardiovascular disease. Despite new research surrounding the impacts of RD, previous work has only examined the physiological impacts of race-related stressors (RRS) in isolation, and not how they may function relative to otherwise stressful experiences. As such, I examined the physiological differences underlying RRS and non-race-related stressors (NRRS) within Black Americans, as measured by HR, to get a more complete picture of the specific impact of RD compared to other types of stress. Data were collected from a sample of 46 self-identified Black/African-American individuals between the ages of 18 and 65 (average age=35.83 years). Participants wore a Fitbit for 1 month to collect physiological data, while using an app called Fabla to document the details of their RRS and NRRS in real time. Responses were then compared to participants' average HR during the stressors through statistical processing (ANOVAs with Tukey post-hoc contrasts, t-tests, and Pearson correlations) in SPSS. I found no difference in overall HR between RRS and NRRS, but I did find significant HR differences between coping strategies utilized across RRS and NRRS, as well as within NRRS specifically. HR did not vary between any coping mechanisms for RRS. These findings suggest that there are unique physiological impacts of RRS as compared to NRRS, where RRS may be more difficult to "overcome" than NRRS. Moving forward, we plan to compare all stressor and HR data to participants' fMRI imaging to further examine the interaction between HR, stressor type, and neural activation patterns.

TITLE: **EVALUATING THE RELATIONSHIP BETWEEN BRAIN METABOLITES, AGE, AND SEX IN PATIENTS WITH LONG COVID USING MAGNETIC RESONANCE SPECTROSCOPY**

PRESENTER: **JENNIFER BELTRAN**

MENTOR: **DR. VINCENT MARCONI**

PROGRAM: **INSPIRE- BIOMEDICAL SCIENCES**

Background

Post-acute sequelae of SARS-CoV-2 infection (PASC), or Long COVID (LC), has reduced the quality of life for millions of Americans, disproportionately affecting women and older adults. Magnetic Resonance Spectroscopy (MRS) studies have reported neurometabolic changes in LC patients compared to healthy controls, such as reduced N-acetyl aspartate (NAA) and glutamate (Glu) in the posterior cingulate cortex (PCC). This region is among the brain's most metabolically active, with changes being linked to cognitive impairment and mood dysregulation. Sex and age are rarely examined as variables of interest in these studies, so whether these neurometabolic changes vary meaningfully by sex or age remains unclear. This study aims to characterize MRS metabolite concentrations by age and sex in an LC cohort.

Methods

24 LC patients, 66.7% female (median age 54, IQR 37.5-60.5), underwent brain proton MRS at 3T to assess neurometabolic concentrations in the PCC, calculated as ratios relative to total creatine (tCr): Glu, myo-inositol (Ins), total choline (tCho), total NAA (tNAA), and glutamate + glutamine (Glx). Associations were assessed using linear regressions and Welch's t-tests.

Results

Age was significantly associated with declines in Glu/tCr, tNAA/tCr, and Glx/tCr (all $P<0.001$). When stratified by sex, this decline remained significant in females but not in males. Ins/tCr and tCho/tCr showed no significant age association in either sex. Independent of age, females showed significantly lower tCho/tCr than males, with no significant differences in other metabolites.

Conclusion

Our findings suggest LC may disproportionately alter Glu/tCr, Glx/tCr, and tNAA/tCr in the PCC in older females, along with females showing lower tCho/tCr than males overall. These changes may reflect reduced neuronal integrity, membrane turnover, and glutamatergic signaling. These factors may contribute to the worse LC symptomatology reported in women. Future studies should include larger samples to examine whether these neurometabolic differences predict symptom severity or treatment responses based on sex and age.



TITLE: EXAMINING THE INTERGENERATIONAL EFFECTS OF LARVAL NUTRITIONAL STRESS ON FITNESS AND REPRODUCTIVE TRAITS IN WALBB-INFECTED AEDES AEGYPTI MOSQUITOES

PRESENTER: AMANDA BENNEH

MENTOR: DR. GONZALO VAZQUEZ PROKOPEC

PROGRAM: INSPIRE- NATURAL AND PHYSICAL SCIENCES

The female Aedes aegypti mosquito transmits several viral diseases, including Zika, dengue, and yellow fever, posing a major global health threat. Wolbachia pipientis (wAlbB), an intracellular bacterium that infects mosquito reproductive tissues and induces cytoplasmic incompatibility (CI), has emerged as a promising vector control strategy for suppressing wild mosquito populations. Previous studies have demonstrated that environmental stressors such as temperature and larval density can influence the fitness and reproductive traits of Wolbachia-infected mosquitoes. However, it remains unclear whether nutritional stress experienced during larval development has intergenerational effects on the fitness of wAlbB-infected mosquitoes and their offspring. To establish a baseline for future intergenerational studies, we modeled larval nutritional stress in wAlbB-infected Ae. aegypti and assessed its effects by measuring time to pupation, adult morphology, and egg hatch rate. Baseline data confirmed wAlbB infection and CI through individual cross assays. Results revealed a dose-dependent increase in time to pupation and altered adult morphology with decreasing nutritional availability, with the 1/5 food treatment exhibiting the greatest developmental delay. Future studies will investigate transgenerational effects across subsequent generations and determine whether Wolbachia alters mosquito metabolic pathways. This work contributes to ongoing global vector control efforts by improving our understanding of how larval nutritional stress may influence the long-term performance and reproductive success of wAlbB-based mosquito control programs under fluctuating environmental conditions.



TITLE: NEW COMBINATIONS TO ENHANCE AN ESTABLISHED THERAPY FOR MEDULLOBLASTOMA: ADDING A NOVEL SHMT2 INHIBITOR

PRESENTER: KAYLAH BENTON

MENTOR: DR. CYNTHIA WINHAM

PROGRAM: LGS SOAR- RBIOMEDICAL SCIENCES

Methotrexate (MTX) , which targets folate metabolism, is a commonly used chemotherapeutic agent in the treatment of infant medulloblastoma (MB). MTX often induces initial tumor regression but poses risk of neurotoxicity and fails in some patients. This study investigates a new approach to antifolate therapy, using POx-SHIN2, a nanoparticle-formulated inhibitor of serine hydroxymethyltransferase (SHMT1/2). SHMT1/2 operate downstream of the MTX target DHFR in the folate pathway. We hypothesize that simultaneous inhibition at multiple points in folate metabolism will enhance metabolic stress and improve anti-tumor efficacy in MB. I modeled anti-folate therapy in vivo using Gfap-Cre/SmoM2 (G-Smo) mice, which develop endogenous medulloblastoma early in life. To determine if POx-SHIN2 enhances MTX therapy, I assigned G-Smo mice to treatment with MTX alone, POx-SHIN2 alone, or the combination and compared to saline-treated controls. Treatments were administered according to previously determined optimized schedules for ICV 4 mg/kg POx-SHIN2, and IP 5 mg/kg MTX with 5 mg/kg folinic acid rescue at 16 and 20 hours. I assessed pharmacodynamic effects by comparing expression of folate pathway enzymes SHMT1, SHMT2, and TYMS, and integrating with markers of proliferation, DNA damage, and cell death. The combination regimen demonstrated no observable toxicity. Western blot analyses showed that MTX decreased SHMT1&2, while POx-SHIN2 increased SHMT2 at 48 hours after treatment, consistent with a compensatory up-regulation. The combination durably uppressed TYMS expression, which remained low 4 days after treatment. Additional studies of proliferation and progression-free survival are ongoing. This study establishes a preclinical platform to evaluate a new antifolate therapy for MB. By inhibiting both DHFR and SHMT1/2, the MTX and POx-SHIN2 combination may produce more profound disruption than single-agent therapy. Ongoing analyses will determine whether this approach enhances anti-tumor efficacy and provides a rationale for this combination of antifolate strategies for MB.

TITLE: TRANSFORMING THE LANDSCAPE OF ABORTION CARE: DEMOGRAPHICS AND TRENDS OF A MISCARRIAGE AND ABORTION HOTLINE RESOURCE

PRESENTER: SADIE BERG

MENTOR: DR. WHITNEY RICE

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Background: In an increasingly restrictive abortion policy landscape, individuals seeking abortion and miscarriage care face more questions, greater obstacles, and fewer resources. Self-managed medication abortion, in combination with telehealth care, is an important access avenue for those managing their abortions and miscarriages. The Miscarriage and Abortion Hotline (M+A Hotline) provides support for individuals experiencing these health events.

Objective: This study provides preliminary descriptive analyses of M+A Hotline call data, evaluating the demographics, trends, and evolving needs of callers from September 2025 to March 2026.

Methods: De-identified call reports, originally completed by Hotline volunteers, were extracted from Signal and coded into quantitative variables in Excel. Variables included date, location, reason for calling, gestational duration, resources provided, medication information, and more. Data were analyzed to reveal descriptive information about the call period.

Results: Preliminary results from 2,036 calls revealed higher rates of calls in states with restrictive policy environments and/or limited reproductive health providers. These states include Louisiana (11.44 calls per 100,000 people of reproductive age), Wyoming (7.26), Mississippi (7.50), and Arkansas (7.14). Ninety-two percent (n=1,871) of calls focused on abortion, 3% (n=70) on miscarriage, 1% (n=29) on other reproductive health concerns, and 3% (n=67) on unknown topics. Twenty-one percent (n=415) of callers received help sourcing abortion pills, 29% (n=580) received symptom counseling, 42% (n=848) received informational support and help with dosing, 4% (n=87) received instructions for confirming abortion, 1% (n=23) received emotional support, and 3% (n=52) received unknown aid.

Implications: Resources like M+A Hotline effectively respond to gaps left by restrictive policy climates around the United States. By offering informational and emotional support to people at all stages of gestation and addressing concerns outside of the clinical context, communities may receive holistic care throughout the timeline of pregnancy termination.

TITLE: **THE IMPACT OF THE INTRACELLULAR INTERACTION BETWEEN RNA-BINDING PROTEIN NF90 AND THE PYRUVATE DEHYDROGENASE COMPLEX ON PROSTATE CANCER CELL GROWTH**

PRESENTER: **NATALIE BOORJIAN**

MENTOR: **DR. JINDAN YU**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Background: Prostate cancer is the second leading cause of cancer death amongst men and, while highly curable when detected early, metastatic prostate cancer remains lethal. Initial therapy for metastatic disease is with androgen deprivation; however, response rates to this treatment are time-limited, and patients then develop what has been designated as castration-resistant prostate cancer (CRPC). Preliminary data has demonstrated a novel interaction between PDC and NF90 in nucleus which fuels histone acetylation and could, therefore, be a potential target in slowing prostate cancer progression. Our hypothesis is that the interaction of NF90 and PDC is required for prostate cancer progression. Thus, targeting this interaction will slow the progression of cancer.

Methods: We cultured LnCP prostate cancer cells and performed shRNA-mediated knockdown of NF90 and key components of the PDC, including PDHA1 and DLAT. We then performed western blot analysis to examine the effects of NF90 and PDC knockdown on the expression of cell cycle regulatory proteins, including AURKA.

Results: Western blot results have confirmed proper knock down efficiency of target proteins. Subsequently, additional western blot data has demonstrated that knocking down specific PDC protein components including PDHA1 and DLAT or NF-90 reduced the expression of AURKA.

Conclusion:Our results demonstrate that the NF90 and the PDC complex (PDHA1/DLAT) positively regulate AURKA expression in prostate cancer cells. The results support a functional role for the NF90–PDC axis in regulating cell cycle–associated proteins in prostate cancer. Future studies will identify genome-wide target genes regulated by NF90 and the PDC using RNA-seq. We will also determine the impact of NF-90-PDC knockdown on cell proliferation, cell migration, and apoptosis.



TITLE: INVESTIGATING EIF3 AND FAS1 CO-PURIFICATION IN CANDIDA ALBICANS

PRESENTER: SHA'MYIA BURGESS

MENTOR: DR. SOHAIL KHOSHNEVIS

PROGRAM: INSPIRE- BIOMEDICAL SCIENCES

Candida albicans is a commensal fungus commonly found on the skin and within the gastrointestinal and reproductive tracts. Although it is normally harmless, C. albicans can become pathogenic when the immune system is weakened, the normal microbiome is disrupted, or protective tissue barriers are damaged, leading to infections collectively known as candidiasis. The ability of C. albicans to grow and adapt depends on coordination between protein production and cellular metabolism; however, the relationship between these pathways remains unclear.

This study focused on two essential cellular components: eukaryotic translation initiation factor 3 (eIF3), a protein complex required to initiate protein synthesis, and FAS1, a subunit of fatty acid synthase that is necessary for fatty acid production. These factors were selected because protein synthesis and lipid metabolism are both required for cellular growth and adaptation, yet it is unknown whether eIF3 physically associates with FAS1 in C. albicans. Identifying such an association could reveal a mechanism through which protein production is coordinated with the metabolic needs of the cell.

A FAS1 DNA construct was amplified using polymerase chain reaction, and agarose gel electrophoresis was used to evaluate the approximate size of the amplified product. Spectrophotometry was used to measure DNA concentration and yeast cell density. The DNA was then purified, concentrated through ethanol precipitation, and transformed into C. albicans. Hygromycin selection produced resistant colonies that may contain the construct. Additional screening is required to confirm proper genomic integration, followed by protein purification experiments to determine whether eIF3 co-purifies with FAS1. This work provides the foundation for investigating how translation and fatty acid metabolism may be coordinated in C. albicans and how this relationship may contribute to fungal growth, adaptation, and pathogenicity.

TITLE: A NOVEL METHOD FOR PROFILING BCL-2 FAMILY INTERACTIONS IN BIM-MUTANT MYELOMA

PRESENTER: CHLOE BUSRACAMWONGS

MENTOR: DR. JANGHEE WOO

Interactions among BCL-2-family proteins help determine whether cancer cells survive or undergo apoptosis. The pro-apoptotic protein BIM can bind anti-apoptotic proteins such as BCL-2, BCL-xL, and MCL-1, and phosphorylation may alter these interactions. This project applies a single-molecule pull-down and co-immunoprecipitation platform to compare BIM binding across five related models derived from KMS12PE, a human multiple myeloma cell line established in 1987 from the pleural effusion of a 64-year-old patient. The models include the parental line, two independent BIM S94E phosphomimetic clones, and two independent BIM S94A phospho-null clones.

The mutant lines were generated by CRISPR-mediated editing of serine 94 in BIM, encoded by BCL2L11. In S94E cells, serine is replaced by glutamic acid to model some effects of persistent phosphorylation. In S94A cells, serine is replaced by alanine, preventing phosphorylation at this position. Cell lysates from the parental line, S94E clones, and S94A clones were analyzed using Proteina PathFinder microchips. Capture antibodies immobilized BCL-2, BCL-xL, or MCL-1 on the chip surface, while associated BIM was detected using a BIM-specific antibody and fluorescent secondary antibody. Mild GDN-based lysis was used to help preserve native protein complexes. Parallel assays measured total anti-apoptotic protein abundance and available BIM-BH3 binding capacity.

The Proteina imaging system detects fluorescent events at multiple positions within each well and converts them into digital measurements of captured proteins or protein complexes. Serially diluted positive controls generate calibration curves, while negative controls estimate nonspecific background. The software reports direct spot counts at lower signal densities and intensity-derived extrapolated counts when signals become too dense to resolve individually.

This platform provides a low-sample, quantitative approach for comparing BIM interactions among wild-type, S94E, and S94A cells. Its higher-resolution output may reveal differences in protein-complex formation that are difficult to distinguish using conventional co-immunoprecipitation.



TITLE: CHARACTERIZATION OF REPLICATION STRESS RESPONSES USING BLOCK-ID

PRESENTER: CAMILA CARDOZO

MENTOR: DR. KYLE MILLER

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Genome instability, including by replication stress, is a hallmark of cancer, fueling cancer cell mutations that enable carcinogenesis. Cancer cells, however, must maintain fitness in the presence of replication stress. This cancer cell vulnerability is currently being explored as a therapeutic target through targeting replication pathways. A deeper understanding of proteins involved in replication stress responses in cancer cells is needed to identify new targets and mechanisms of replication stress targeting. The Miller lab has developed Biotinylation of Lac Operator array RepliCation Stress Protein NetworK Identification, or BLOCK-ID, which creates a site-specific replication fork block using the LacR and LacO array system. Using LacR-BirA, recruited proteins to the block are biotinylated and identified by BioID mass spectrometry approaches. A BLOCK-ID cell line was stablished in osteosarcoma cancer cell line U2OS to study Alternative Lengthening of Telomeres (ALT+). As most cancer cell lines are telomerase-positive, we aimed to establish an additional BLOCK-ID cancer cell line using ALT- HeLa cells. Using LacO array containing HeLa cells, we transfected BirA-LacR and looked for signals associated with replication stress and DNA breaks. Using immunofluorescence and confocal microscopy, we analyzed the formation of the DNA damage signals, RPA, pATR-S428, BRCA1, and γH2AX-S139 at the LacR-LacO replication fork block. Our analysis showed that compared to U2OS, HeLa cells showed significantly less colocalization of these proteins after 24 hours at the site of the block. Colocalization in HeLa cells increased after 48 hours, with RPA notably increased from 10% to 46%, though still lower than in U2OS, suggesting that this system may require increased LacR expression times to fully block replication. Future studies will enlist BLOCK-ID Biotinylation-MS to identify proteins associated with blocked forks in this cell line, which will help identify conserved proteins and unique candidates involved in the replication stress responses in human cancer cells.

TITLE: **EFFORTS TOWARD TOTAL SYNTHESIS OF PINOCICOLINS**

PRESENTER: **GIA CHAMBERS**

MENTOR: **DR. ELISE BEZOLD**

PROGRAM: **CCC- NATURAL AND PHYSICAL SCIENCES**

As antibiotic resistance continues to present an escalating threat to public health, the need for new antibiotics is dire. Isonitrile natural products present a promising class of novel therapeutics, as these natural products can act as chalkophores that bind copper and starve bacteria. We aim to synthesize Pinocicolin A, an isonitrile natural product that may exhibit copper-dependent binding in gram-positive Staphylococcus aureus. Herein, we describe efforts toward the synthesis of Pinocicolin A. Once accessed, we will perform structure-activity-relationship studies to understand which structural characteristics are necessary for biological activity.

TITLE: **DETERMINING LIFE-STAGE TRENDS OF RESPIRATORY PATHOGENS IN WILD CHIMPANZEES THROUGHOUT GOMBE NATIONAL PARK.**

PRESENTER: **AMBER CHEUNG**

MENTOR: **DR. THOMAS GILLESPIE**

PROGRAM: **SURE- NATURAL AND PHYSICAL SCIENCES**

Respiratory infectious diseases are a leading cause of mortality in wild chimpanzees and pose an increasing threat as human-wildlife interactions intensify. In Gombe National Park (GNP), Tanzania, where chimpanzees live in close proximity to humans and livestock, understanding factors that influence disease susceptibility is critical for both conservation and public health. Although increased disease risk in young children and older individuals has been well-documented in humans and has been suggested in chimpanzees, few studies have directly examined how respiratory pathogen prevalence varies across chimpanzee life stages. This study will investigate age-related trends in respiratory pathogen detection and coinfection in wild chimpanzees using 287 fecal samples collected from identified individuals in GNP between 2012 and 2020. DNA and RNA will be extracted from fecal samples and screened for Streptococcus pneumoniae (S. pneumoniae), respiratory syncytial virus (RSV), and Influenza A (Flu A) using conventional PCR. Infection and coinfection prevalence will be compared across three life stages—sexually immature, adult, and older adult—using generalized linear mixed models while accounting for factors including sex, community, year, and season. Of the three respiratory pathogens, S. pneumoniae had the highest prevalence (3.48%). By identifying life-stage patterns of respiratory disease susceptibility, this research will improve understanding of disease transmission dynamics in endangered chimpanzee populations and help identify individuals at greater risk during outbreaks. The findings will support the Gombe Ecosystem Health Project's efforts to strengthen disease surveillance and conservation strategies while contributing to broader One Health research on the interconnected health of wildlife, humans, and ecosystems.



TITLE: LONGITUDINAL ANALYSIS OF COVID-19 ANTIBODY LEVELS IN PATIENTS WITH PERSISTENT SYMPTOMS AND RECOVERED CONTROLS

PRESENTER: KYNDALL COKER

MENTOR: DR. ZANTHIA WILEY

PROGRAM: INSPIRE- BIOMEDICAL SCIENCES

COVID-19 has affected millions of people worldwide since 2020, and a significant subset of patients experience Long COVID, with symptoms that persist long after the initial infection. The biological mechanisms behind why some patients recover fully while others develop prolonged illness remain poorly understood. This study aims to compare antibody responses to SARS-CoV-2 between COVID-19 patients who developed persistent symptoms and those who recovered fully with no ongoing symptoms and no breakthrough infection. The study includes 15 participants with persistent symptoms and 15 fully recovered controls, matched one to one by age and sex to control for demographic variables that could influence immunological findings. IgG antibody levels to three SARS-CoV-2 targets, including the receptor binding domain, spike protein, and nucleocapsid protein, were measured in AU/mL on a log scale across longitudinal blood samples collected over six years of follow up visits from 2020 to 2026. Although there was no statistically significant difference in the magnitude of antibodies between Long COVID patients and controls, there was a consistent trend over time of higher antibody levels in individuals with long COVID. This research aims to improve understanding of immunological factors associated with Long COVID.

TITLE: **XINVESTIGATING THE ROLE OF FGFR3 INHIBITION ON PROSTATE CANCER**

PRESENTER: **ELIZABETH CORTES**

MENTOR: **DR. CARLOS MORENO**

PROGRAM: **LGS SOAR- BIOMEDICAL SCIENCES**



Prostate cancer (PCa) accounts for one of every five cancer diagnoses in males within the United States, and African American (AA) men diagnosed with prostate cancer have double the mortality risk compared to European Americans (EA). However, the exact cause for the increased mortality risk is not clear. To address this, preliminary studies in our lab have shown that PCa tumors from AA men are enriched with genes related to oxidative phosphorylation (OXPHOS) compared to those of EA men. Moreover, prior evidence has suggested that an alternatively spliced variant of FGFR3 - a fibroblast growth factor tyrosine kinase receptor that activates OXPHOS along with PI3K/AKT, STAT, RAS/MAPK, and ERK signaling pathways - is preferentially expressed in PCa tumors of AA males, driving the cancer to be more aggressive and treatment-resistant. Because of its relationship to OXPHOS and its differential expression between AA and EA males, we are investigating the effects of FGFR3 inhibition in PCa cell models. We treated an AA PCa cell line (RC77T/E) and an EA PCa cell line (22Rv1) with infigratinib, a selective inhibitor for FGFR1-3. We conducted MTT and apoptosis assays to detect the effects of infigratinib on cell death and viability in PCa cell lines, as well as Western Blots to detect protein expression and activity. The results of our study found that infigratinib did not have a significant effect on cell viability and apoptosis in these cell lines. Further experiments are needed to understand why the drug had no observable effect on viability or apoptosis.



TITLE: EFFECT OF BLOOD PRESSURE MEDICATION ON URINARY NA/K RATIO: ROLE OF INTRARENAL ACTIVATION

PRESENTER: AYELEN CRUZ

MENTOR: DR. CESAR ROMERO

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Hypertension is the main risk factor for cardiovascular disease. In salt-sensitive hypertension, increased sodium intake raises blood pressure (BP) and suppresses the Renin-Angiotensin System (RAS) due to volume expansion. Urinary sodium-to-potassium (Na/K) ratio is a marker of sodium intake. Whether antihypertensive medications alter Na/K ratio independently of sodium intake remains unclear. Liddle Syndrome mice, a salt-sensitive model characterized by a genetic gain-in-function of ENaC, and WT mice control were fed normal (0.4% NaCl) and high salt (4% NaCl) diets. We determined the effect of Enalapril, Hydrochlorothiazide, and Amlodipine on urinary Na/K ratio and BP on day 1 and 8. Angiotensinogen expression was assessed in the urine, kidney, and liver by western blots. On a normal-salt diet, urinary Na/K (0.7± 0.1) was similar for WT and Liddle mice ($p=0.69$). High salt diets increased Na/K (3.9±0.5) for both genotypes ($p<0.001$) but induced hypertension only in Liddle mice. Hydrochlorothiazide and enalapril, despite the expected suppression of systemic RAS, reduced Na/K on day 8 ($p<0.01$). Only Amlodipine decreased BP ($p=0.02$) but did not affect Na/K. Combined treatments decreased Na/K, however only enalapril with amlodipine on day 8 was statistically significant ($p=0.03$). High-salt diet increased angiotensinogen expression in the kidney and urine (both $p<0.01$), but not in the liver. In conclusion, RAS inhibitors and diuretics decrease Na/K ratio in Liddle mice without modifying BP which suggests increased distal delivery of sodium. On the contrary, Amlodipine does not affect Na/K ratio but does decrease BP. High salt diet increases tissue specific RAS activation in Liddle mice.



TITLE: TARGETING THE JAK/STAT PATHWAY IN EPILEPSY

PRESENTER: GRACIE DATERS

MENTOR: DR. NICHOLAS VARVEL

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Epilepsy is a chronic neurological disorder characterized by recurrent, unprovoked seizures, affecting over 50 million people worldwide. Current epilepsy medications primarily treat the seizures, with approximately one-third of patients remaining unresponsive to treatment. No approved therapy can modify disease progression by preventing spontaneous seizures or reversing the associated cognitive impairments. Previous studies have implicated the activation of the Janus kinase/signal transducer and activator of transcription (JAK/STAT) signaling pathway, particularly through its role in promoting neuroinflammation, in epileptogenesis following status epilepticus (SE). Following an epileptogenic insult, the JAK/STAT pathway is rapidly activated, undergoes a transient period of suppression, and is subsequently reactivated during epileptogenesis. Prior work demonstrated that treatment with the FDA-approved JAK inhibitor, tofacitinib, during this second-wave activation improved disease outcomes in a mouse model of pilocarpine-induced SE. However, tofacitinib has limited brain permeability and is a p-glycoprotein (P-gp) substrate, leading to rapid brain clearance via these efflux transporters. This raises the question of whether further disease improvement could be observed by administering a JAK inhibitor with greater brain permeability than tofacitinib.

In the present study, a novel brain-penetrant JAK1-selective inhibitor was administered to adult male C57BL/6 mice via intraperitoneal (IP) injection following pilocarpine-induced SE. The goal was to more effectively target activated JAK1/STAT3 signaling within the brain. Fluoro-Jade staining was used to quantify neurodegeneration, while Western blot analysis was performed to measure phosphorylated JAK1 and STAT3 protein levels in the cortex and hippocampus as indicators of pathway activation. Data collection and analysis are ongoing. If enhanced brain penetration results in greater inhibition of JAK1 signaling and reduced neuronal degeneration, these findings would further support JAK1-mediated neuroinflammation as a therapeutic target for disease modification in epilepsy. Ultimately, this work may contribute to the development of treatments that address the underlying mechanisms of epileptogenesis rather than solely suppressing seizures.



TITLE: THEORETICAL PREDICTION OF LOW-LYING ELECTRONIC STATES & PROPERTIES OF LINEAR BERYLLIUM DIOXIDE

PRESENTER: ASHLEY DAVIDSON

MENTOR: DR. FRANCESCO EVANGELISTA

PROGRAM: CCC- NATURAL AND PHYSICAL SCIENCES

Beryllium containing compounds are generally underrepresented in experimental literature due to toxicity concerns. Therefore, known information on beryllium oxides is mostly derived from computational data. In this work, OBeO is considered for its unique electronic structure and bonding properties. Linear OBeO is an open-shell molecule which exhibits a strong multireference character, with many low-lying singlet and triplet states near the ground state of the neutral molecule. To study these states, DFT methods were used with the PSI4 programming package to generate orbitals and gain insight for an initial guess of active space for further calculations. Due to this system's highly correlated nature, we employ multireference CASSCF using the Forte2 programming package to calculate equilibrium bond lengths and energies with corresponding potential energy curves, as well as ionization potentials and spectroscopic constants.



TITLE: **SECRET TUNNELS: EXPLORING PROMISCUITY OF HEME TRANSPORTERS IN THE ASSEMBLY OF ARTIFICIAL METALLOENZYMES**

PRESENTER: **DANIEL DENG**

MENTOR: **DR. KATHERINE DAVIS**

PROGRAM: **CCC- NATURAL AND PHYSICAL SCIENCES**

Enzymes have historically been prized as biocatalysts due to their high reaction selectivities. Recently, many efforts have been made on the development of artificial metalloenzymes (ArMs), in which an enzyme's native cofactor is substituted for a non-natural one, allowing for previously inaccessible reaction pathways. Two common challenges encountered during the development of ArMs include the means and assessment of cofactor incorporation, as well as the possibility of undesired incorporation of environmentally-abundant metals. Using a combination of computational and experimental methods, we explore the promiscuous activity of a heme transporter, in order to bring a variety of cobalt catalysts into E. Coli cells. Additionally, we use X-ray absorption spectroscopy to probe the respective quantities of iron and cobalt in assembled ArMs. Overall, this work has the potential to expand the scope of available cofactors and incorporation methods in future ArMs.



TITLE: INVESTIGATING DIFFERENTIAL DESAT1 GENE EXPRESSION ACROSS SOCIAL ENVIRONMENTS IN DROSOPHILA MELANOGASTER

PRESENTER: SHREYA DESHPANDE

MENTOR: DR. EMILY MCLEAN

PROGRAM: OXFORD- BIOMEDICAL SCIENCES

Phenotypic variation, defined by observable differences among organisms in physiology and behavior, reflects the combined effects of an organism's own genotype and the genotypes of individuals it interacts with in its immediate social environment. The latter influence is termed an indirect genetic effect (IGE). Although IGEs have been documented across diverse taxa, the molecular mechanisms that mediate social experiences to “get under the skin,” as previously termed, and produce stable phenotypic change remain unclear. This study uses the model organism Drosophila melanogaster to examine how variation in the genotypic composition of a fly's social group alters expression of the desaturase gene desat1. This gene is significant due to its role in pheromone production and biosynthesis of cuticular hydrocarbons (CHCs), waxy substances that facilitate social interaction in Drosophila melanogaster. Because CHCs are genetically determined chemical cues guiding courtship and aggression, it has been previously hypothesized that desat1 may be a strong molecular link between social partner genotypes and resultant behavioral phenotypes. To examine this, flies of two genotypes (27896 and 13129) were reared in isolation. As adults, 27896 females were placed into social environments containing males of either the identical genotype (27896), a different genotype (13129), or a blend of both, creating homogeneous and heterogeneous compositions while holding female genotypes constant. Following a four day social exposure period, we extracted RNA from focal male flies and quantified desat1 expression using qPCR to assess whether varying genotypic composition of social partners alters expression of this CHC pathway gene. Our approach can be used to identify genes with social environment genetic composition-sensitive expressions. Since IGEs are known to influence the pace and direction of evolutionary responses to selection, identifying these transcriptional targets will provide insight into the molecular mechanisms through which social interactions shape adaptive evolution.



TITLE: TESTING VASOACTIVE INTESTINAL PEPTIDE (VIP) ANTAGONISM IN A SUBCUTANEOUS ACUTE MYELOID LEUKEMIA (AML) MOUSE MODEL

PRESENTER: DAVID DONG

MENTOR: DR. EDMUND WALLER

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Nearly half a million people in the United States are living with or in remission from leukemia. Programmed cell death protein 1 (PD-1) acts as a brake on T-cell activity, but anti-PD-1 treatment has historically shown limited effectiveness in acute myeloid leukemia (AML). CAMV-01 is a vasoactive intestinal peptide (VIP) receptor antagonist that targets another pathway that may suppress T-cell responses. This study used a subcutaneous C1498 AML mouse model to test CAMV-01 and anti-PD-1 alone and in combination, while developing a model that could later be adapted for central nervous system (CNS) leukemia studies. We predicted that CAMV-01 would reduce tumor burden more than anti-PD-1 alone and that combination treatment would produce the lowest tumor burden and longest survival.

Forty B6 mice were injected subcutaneously with C1498 leukemia cells and divided into four groups: no treatment, anti-PD-1, CAMV-01, or combination treatment. Tumor volume, body weight, activity, ulceration, and necrosis were monitored to evaluate intravenous treatment effects. Blood collected before and after treatment was analyzed by flow cytometry to identify leukemia cells and circulating T-cell populations.

C1498 cells were detected in the blood one week after inoculation, supporting intravenous treatment in this model. Untreated mice had the largest tumors and lowest survival. Anti-PD-1-treated mice had the smallest tumors and second-highest survival. CAMV-01 alone produced variable tumor growth and did not show the predicted improvement in tumor control or survival. The combination group had the highest survival, although tumor growth was similar to CAMV-01 alone. Treated groups also showed more ulceration and necrosis than untreated mice. Uniform Manifold Approximation and Projection (UMAP) analysis suggested differences in T-cell populations across treatment groups and over time.

Future work will include statistical analysis, tumor histology, in vivo imaging system (IVIS) bioluminescence imaging, and tumor-tissue flow cytometry before adapting the model for CNS leukemia studies.

TITLE: UNDERSTANDING DLL3 HETEROGENEITY IN HIGH-GRADE NEUROENDOCRINE TUMORS

PRESENTER: BANKE FALEBITA

MENTOR: DR. MENG ZHANG

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES



Prostate cancer is the second most common cancer in men. It predominantly affects men over 60 years old, more specifically, of African ancestry, as they have double the risk of carrying a more aggressive disease.

High-grade neuroendocrine tumors (NETs) consist of small cell lung cancer (SCLC) and neuroendocrine prostate cancer (NEPC). DLL3, a delta-like ligand, is a Notch inhibitory ligand that is overexpressed in SCLC and NEPC. In castration-resistant neuroendocrine prostate cancer (CRNEPC), DLL3 is highly enriched in the majority of CRNEPC while minimally expressed in benign prostate tissue. The tumor-specificity of DLL3 makes it an ideal therapeutic target and a DLL3 targeting T-cell engager, tarlatamab, was recently FDA approved for treating advanced-stage SCLC. However, all DLL3-targeted therapies face the challenge of substantial intra- and inter-tumoral heterogeneity of DLL3. Therefore, we aimed to assess DLL3 levels in SCLC and NEPC cell line models.

A NEPC cell line (LuNE), and two SCLC cell lines (H1048 and CORL279) were cultured under standard conditions, and baseline protein lysates were collected to assess DLL3 expression. After SDS-PAGE, proteins were transferred onto a PVDF membrane. The membrane was cut, blocked, and incubated in its respective antibody (DLL3 and GAPDH). GAPDH served as a loading control to ensure the amount of total proteins loaded onto the gel was equal.

Western Blot analysis revealed that H1048, LuNE, and CORL279 have differing DLL3 expressions. H1048 no longer served as our positive control due to minimal expression of DLL3. DLL3 expression was highest in CORL279, with GAPDH serving as the loading control.
Together, this data shows that DLL3 is expressed differently in LuNE, CORL279, and H1048, suggesting DLL3 expression is heterogenous across different cell lines. Future studies include testing additional NEPC cell lines to determine the reproducibility of DLL3 expression in our cell lines and controls.



TITLE: INDIVIDUAL DIFFERENCES IN CONTEXTUALIZED CONDITIONING RESPONSES AND COGNITIVE TASK PERFORMANCE IN ADULT FEMALE RHESUS MACAQUES

PRESENTER: TAYLOR FLAGG

MENTOR: DR. MAR SANCHEZ

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Individual differences in cognitive task performance are often attributed to variation in cognitive ability, yet behavioral engagement, motivation, and responses to the testing environment may also contribute to observed performance. The Contextualized Conditioning Response (CCR) framework proposes that demographic, social, temperamental, biological, and neurobiological factors influence cognitive performance through context-dependent behavioral responses expressed during cognitive testing. The present study examines the temperamental component of this framework. Using data collected during the first year of a seven-year longitudinal study at the Emory National Biomedical Research Center Field Station, we integrated demographic, social, and temperamental measures with behavioral data collected during the Intra-/Extra-Dimensional Set-Shifting Task (ID/ED). We then conducted a series of pathway-specific hierarchical regression analyses to evaluate whether demographic and baseline temperamental characteristics predicted trait-specific contextualized conditioning responses (timidity, curiosity, and aggression) during cognitive testing, and whether these contextualized responses subsequently predicted habituation beyond baseline temperament. Preliminary findings demonstrated the strongest support for the hypothesized timidity pathway, whereas curiosity showed partial support and the hypothesized aggression pathway received little support. These findings suggest that temperamental traits differ in the extent to which they generalize across behavioral contexts, highlighting the importance of considering context-dependent expressions of temperament when constructing, validating, and interpreting behavioral measures in nonhuman primates.

TITLE: ELUCIDATING THE LINK BETWEEN HIV RESERVOIR SIZE AND NON-AIDS COMORBIDITY BURDEN IN PEOPLE WITH HIV IN ATLANTA, GEORGIA

PRESENTER: KYLIE FLORES

MENTOR: DR. CECILE LAHIRI

PROGRAM: INSPIRE- BIOMEDICAL SCIENCES

'Despite effective antiretroviral therapy (ART), human immunodeficiency virus (HIV) persists in peripheral blood mononuclear cell (PBMCs) and gut tissue reservoirs, which may contribute to ongoing immune dysfunction. Persons with HIV (PWH) have an increased burden of non-AIDS comorbidities (NACM) compared to persons without HIV. This study investigated whether HIV reservoir size is associated with NACM burden in PWH.

We leveraged baseline data from the Gut Reservoir Study baseline to investigate the relationship between HIV reservoir size and NACM burden in PWH. Eligibility criteria included 1) ≥ 40 years old; 2) on ART for ≥ 2 years; 3) HIV viral load <200 cop/mL within the last 6 months; and 4) no history of cardiovascular disease. Comorbidity data were collected via questionnaires. Participants underwent venipuncture and rigid sigmoidoscopy for PBMC and rectal tissue collection, respectively. HIV reservoir was measured as total, intact, defective 3', and defective 5' proviruses per 10^6 CD4 T cells. NACM burden outcome was defined as the sum of the presence of nine NACM: diabetes, hypertension, dyslipidemia, cancer, or liver, bone, kidney, lung, or psychiatric disease. Separate linear regression models assessed the association of each viral reservoir measure on NACM burden, overall and stratified by sex, adjusting for age, BMI, and smoking. We included N=112 participants with either PBMC or gut reservoir data. Fifty-five percent were women; mean age was 56.1 years (SD = 7.9); 85% were Black/African American; 53% had undetectable viral loads; mean CD4 cell count was 697 cells/mm^3 (SD = 345); 51% had at least 3 NACM. Linear regression models showed no significant association between any PBMC or gut HIV reservoir measures and NACM burden (all p-values > 0.05). Our data currently show no clear association between HIV reservoir size and NACM burden. Small sample size (N=112) could explain the lack of a significant association. Further modeling analyses will consider whether HIV reservoir exposure should be examined as a categorical variable rather than a continuous variable.



TITLE: MECHANISTIC INSIGHTS INTO THE NOVEL ROLE OF THE PUA-LIKE DOMAIN OF RSMF METHYLTRANSFERASE IN RIBOSOMAL PROTEIN S12 RECOGNITION

PRESENTER: COLLIN FRANCE

MENTOR: DR. GRAEME CONN

PROGRAM: INSPIRE- NATURAL AND PHYSICAL SCIENCES

RsmF is a bacterial 16S rRNA methyltransferase that modifies the C1407 nucleotide in the decoding center of the 30S ribosomal subunit, a region essential for accurate protein synthesis and antibiotic binding. RsmF-mediated methylation of C1407 to form m5C1407 has been shown to influence Escherichia coli susceptibility to a widely used class of antibiotics, aminoglycosides, and to promote bacterial survival under host immune system-induced stress. Therefore, an understanding of how RsmF recognizes the 30S subunit may provide insight into the molecular mechanisms governing ribosome modification, antibiotic susceptibility, and bacterial stress adaptation. To address this, our lab is currently determining a cryo-EM structure of the RsmF–30S complex, which shows that the enzyme's PUA-like domain, which directly interacts with ribosomal protein S12 domain, is traditionally associated with RNA binding. To investigate the functional significance of this protein–protein interface, we examined a combination of specific amino acid residues in the PUA domain that formed a contiguous surface to interact with the S12 using biochemical approaches. Specifically, we used site-directed mutagenesis to generate RsmF variants, including R426A, R426A/R428A, R428A/Y431A, R459A, D471A, and [R426A/R428A]/Y431A. Recombinant enzymes were expressed and evaluated using in vitro methyltransferase activity assays with {3H}-S-adenosyl-L-methionine (SAM) as the methyl donor and E. coli 30S subunit as the substrate. Preliminary results demonstrated that the R426A/R428A mutant retained only approximately 30% methyltransferase activity, the R428A/Y431A retained activity comparable to the wild-type, and the R426A/R428A/Y431A retained <10% activity indicating that these residues play an important role in mediating the interaction between RsmF and its 30S subunit substrate domain. The remaining RsmF mutants are currently undergoing validation and activity analysis to underpin their role in 30S subunit recognition. Together, these studies will establish the mechanistic role of the PUA-like domain in RsmF function and may provide insight into mechanisms that influence bacterial susceptibility to ribosome-targeting antibiotics and stress.



TITLE: IMMOBILIZATION OF VANADIUM-DEPENDENT HALOPEROXIDASE ENZYMES FOR SUSTAINABLE ENZYMATIC HALOGENATIONS

PRESENTER: MAXINE FRASER

MENTOR: DR. KYLE BIEGASIEWICZ AND DR. ABIGAIL HALLORAN

PROGRAM: CCC- NATURAL AND PHYSICAL SCIENCES

Vanadium-dependent haloperoxidase (VHPO) enzymes are attractive biocatalysts for selective halogenation reactions but their reactivity is largely underexplored on immobilized resin. Here, we report the first immobilization of the vanadium-dependent bromoperoxidase from Corallina pilulifera (CpVBPO) on polymethyl acrylate ReliZyme™ supports. Two functionalized resins were evaluated, with iminodiacetic acid (IDA) beads emerging as the most effective support, enabling high catalytic activity and reuse over multiple cycles without loss of performance. Preparation of gram-quantities of immobilized CpVBPO demonstrated that the beads remained catalytically competent after drying and handling, and the system performed comparably to the free enzyme in bromination reactions. These results establish ReliZyme™ IDA supports as a robust and scalable platform for CpVBPO immobilization, advancing the practical deployment of VHPOs as reusable and sustainable biocatalysts.



TITLE: BILE ACID SIGNALING SHAPES PROVIRAL AND ANTIVIRAL PROGRAMS IN HIV PERSISTENCE

PRESENTER: ALBERT GAO

MENTOR: DR. RAFICK-PIERRE SEKALY

PROGRAM: SURE- BIOMEDICAL SCIENCES

Introduction. People living with HIV (PLWH) continue to harbor HIV in tissue-resident CD4+ T cells despite effective antiretroviral therapy, experiencing chronic inflammation and immune dysfunction. Gut dysbiosis and microbe-derived bile acids have been linked to long-term immune dysfunction, but how bile acid signaling shapes proviral and antiviral programs in gut-resident immune cells remains poorly defined.

Methodological Approach. We combined genome-wide CRISPR knockout screening in primary CD4+ T cells to identify bile acid-related HIV host factors, DOGMA-seq (joint transcriptome/chromatin profiling) of gut CD4+ T cells from PLWH to localize bile acid receptor programs relative to HIV-DNA+ cells, and two in vitro assays: stimulation of blood CD4+ T cells with cholic acid (CA) and glycocholic acid (GCA) before HIV infection, and a trained-immunity co-culture assay testing glycochenodeoxycholic acid (GCDCA) on β-glucan-trained monocytes co-cultured with CD4+ T cells before HIV challenge. Infection was quantified by intracellular p24 flow cytometry.

Results. Genome-wide CRISPR screens identified two opposing bile acid-related host factor pathways: a constitutive androstane receptor (CAR/NR1I3) pathway associated with HIV permissiveness, and a bile acid-sensing pathway associated with HIV restriction, showing bile acid signaling is embedded within host networks controlling HIV susceptibility. Likewise, DOGMA-seq showed HIV-DNA+ gut CD4+ T cells were enriched for FXR/PPAR-associated proviral programs, while VDR- and interferon-associated antiviral programs marked restrictive, reservoir-depleted states. CD4+ T cells stimulated with CA or GCA before infection showed significantly increased p24 expression relative to unstimulated controls, demonstrating select bile acids causally enhance HIV infection. Conversely, GCDCA-trained monocytes co-cultured with CD4+ T cells showed heightened cytokine responses and significantly reduced subsequent HIV infection, indicating GCDCA establishes an antiviral state.

Conclusions. Bile acids act as opposing proviral and antiviral determinants of HIV reservoir size, and engaging specific antiviral bile acid receptors can confer protection against infection, nominating them as targets for reservoir-reducing interventions.

TITLE: TARGETING STAT3 IN PTPN11-MUTATED JUVENILE MYELOMONOCYTIC LEUKEMIA

PRESENTER: CARLY HARRIS

MENTOR: DR. PENG ZHAO

PROGRAM: XSURE- BIOMEDICAL SCIENCES



Background: Juvenile myelomonocytic leukemia (JMML) is an aggressive pediatric myeloproliferative neoplasm with a relapse rate of approximately 40% post-transplant.

Approximately 35% of JMML are caused by a gain-of-function mutation in PTPN11, which encodes the protein tyrosine phosphatase SHP2 and promotes hyperactive Ras-MAPK signaling. In a Ptpn11E76K/+ mutant mouse model, we previously observed reduced Stat3 phosphorylation in leukemic stem cells (LSCs), implicating Stat3 signaling as a potential therapeutic target in Ptpn11-mutated JMML. Stat3 deletion in Ptpn11E76K/+ mutant mice also decreased the LSC pool and induced synthetic lethality, supporting the rationale for testing whether pharmacologic Stat3 inhibition can exploit this vulnerability in Ptpn11-mutated LSCs.

We aim to explore this therapeutic vulnerability through a series of experiments utilizing control Ptpn11+/+/VavCre hematopoietic cells isolated from mice, knock-in Ptpn11E76K/+/Vav-Cre mice LSCs, and FDA-approved Stat3 inhibitors Atovaquone and Pyrimethamine.

Methods: To evaluate the effects of Stat3 inhibition, lineage-negative (Lin−) cells were isolated from mouse bone marrow using a Lineage Cell Depletion Kit and LS magnetic columns. Lin- cells were cultured in vitro for 4 days in StemSpan medium supplemented with mSCF, mTPO, and mFLT3L, with varying concentrations of Atovaquone and Pyrimethamine. Myeloid proliferation and apoptosis were analyzed using flow cytometry. Colony-forming unit granulocyte-macrophage (CFU-GM) assays were performed to assess myeloid proliferation

Results: Western blot confirmed reduced Stat3 phosphorylation in Ptpn11E76K/+/Vav-Cre Lin- cells. Treatment with Atovaquone reduced both the size and number of colonies in CFU-GM assays, suggesting inhibited myeloid differentiation. In vitro culture of Ptpn11E76K/+/Vav-Cre cells showed enhanced myeloid differentiation in the vehicle-treated group, and reduced differentiation following Atovaquone and Pyrimethamine treatment compared to Ptpn11+/+/Vav-Cre. These findings suggest that Ptpn11E76K/+/Vav-Cre cells exhibit greater sensitivity to Stat3 inhibition than Ptpn11+/+/Vav-Cre cells. Apoptosis assays revealed more apoptotic cells in Ptpn11E76K/+/Vav-Cre compared to Ptpn11+/+/Vav-Cre cells after Stat3 inhibitor exposure.

Conclusion:
This preliminary data supports the hypothesis that Ptpn11E76K/+/VavCre mutant LSCs are more sensitive to pharmacological inhibition of Stat3, supporting Stat3 as a promising therapeutic target in JMML.

TITLE: **ENCODING THE PRICKE OF CONSCIENCE**

PRESENTER: **CAMERON HART**

MENTOR: **DR. JIM MOREY**

PROGRAM: **SURE- HUMANITIES**



This project examines a section of the early fourteenth-century poem The Pricke of Conscience, focusing on the connections between approximately ninety-six of its surviving 120 manuscripts. The project ultimately aims to create a user-friendly digital research database that allows scholars to explore the manuscripts. The website will also later include photographs of the stained-glass window associated with the poem and Henry Johnston's 1672 sketches documenting the window before its later reconstruction. As the project developed, its methodology shifted from the simple creation of a website to the implementation of digital humanities tools using the Textual Encoding Initiative (TEI). By encoding the poem in TEI XML and developing supporting JavaScript to display the encoded manuscripts, I designed an interactive comparison tool that can be embedded into the project's final digital platform. This tool allows researchers to select one witness as the base text and then choose one line to compare either to all of the other versions or to select versions. To prepare the manuscripts for comparison, I standardized line numbering, established a base text, and created a canonical alignment across all ninety-six manuscript witnesses. These datasets guided the TEI encoding process and gave me the foundation for the comparison tool, allowing users to examine, compare, and analyze textual variation across the manuscript tradition. This tool highlights how digital humanities tools like TEI can support medieval studies by making these manuscripts more accessible and allowing researchers to compare and contrast textual variation across all ninety-six witnesses.



TITLE: ULTRA-HIGH-MOLECULAR-WEIGHT RECYCLABLE MUCONATE–ISOPRENE COPOLYMERS FOR RECYCLABLE ELASTOMER PLATFORMS

PRESENTER: PATRICK HERRERA

MENTOR: DR. LETIAN DOU

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Renowned for their exceptional mechanical performance, conventional elastomers remain a formidable challenge to recycle because of their chemically robust carbon–carbon backbones and permanent crosslinked networks. Here, we present a family of ultra-high-molecular-weight muconate–isoprene copolymers that leverage entanglement-driven mechanical reinforcement and intrinsically depolymerizable backbone linkages to enable recyclable rubber materials synthesized under additive- and solvent-free conditions. Electronic effects promote a preferred alternating arrangement of muconate and isoprene, creating strategically placed weak links while suppressing unwanted muconate-to-muconate incorporation. Polymerization conditions, including monomer composition and reaction temperature, provide access to ultra-high molecular weights exceeding 1.6 MDa while maintaining controlled dispersity. Mechanical testing demonstrates that the uncrosslinked materials exhibit rubber-like behavior, with subsequent minimal crosslinking providing additional reinforcement while preserving the underlying entanglement-dominated network, achieving maximum tensile stresses exceeding 10 MPa at strains above 1200%. Thermal depolymerization experiments recover up to approximately 72% of the theoretical isoprene content under simple laboratory conditions, suggesting that polymer sequence can strongly influence monomer recovery. Ongoing solid-state NMR and X-ray scattering studies aim to better understand how molecular structure and network organization give rise to the observed mechanical properties. Collectively, this work establishes a strategy for designing recyclable elastomer platforms in which polymer sequence, molecular weight, and network architecture are jointly engineered to balance mechanical performance with chemical circularity, providing a foundation for future sustainable elastomers, stretchable technologies, and advanced copolymeric materials.

TITLE: **LEVERAGING SUNTHETICS AI TO DEVELOP FE AND NI CATALYZED ARYL AMINOMETHYLATION**

PRESENTER: **ARIANA HRIHORISAN**

MENTOR: **DR. HANNAH FORD**

Emerging technologies, like machine learning (ML), have allowed for expanded data modeling and increased rates of reaction optimization. C-H functionalization is an important transformation due to the ability to directly construct key C-C bonds from C-H coupling parters. One example of this type of reactivity is aryl aminomethylation which constructs a C(sp2)-C(sp3) bond commonly found in pharmaceuticals. This method employs two earth-abundant metal catalysts, Fe and Ni, and light irradiation, enhancing the sustainability and affordability of this method. By employing Sunthetics AI, a user-friendly ML platform designed for chemical synthesis, we aim to rapidly optimize Fe and Ni aryl aminomethylation. First, we used the Design of Experiments feature to generate initial reaction yield inputs. The Design of Experiments varied the metal precursors, ligands, catalyst loadings, and reaction solvent. Product yield, starting material consumption and side product distribution were determined using GC-MS analysis. From these findings, we used Sunthetics AI to model the data inputs and outputs, and generate suggested optimal data points. We also obtained the variable importance readings from the ML model, indicating which variables were most important for optimal input determination. Future research will utilize these outputs to create a second iteration ML model, ultimately guiding the optimization of aryl aminomethylation using light-driven earth abundant metal catalysis.



TITLE: DECODING THE RENAL LANDSCAPE: A HISTOLOGIC INVESTIGATION OF SICKLE CELL-ASSOCIATED NEPHROPATHIES

PRESENTER: BRIANNA JORDAN

MENTOR: DR. ANDREW HONG

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Sickle cell disease (SCD) and sickle cell trait (SCT) are associated with renal complications that can significantly impair kidney function. However, the mechanisms underlying the development and progression associated nephropathies, particularly in individuals with SCT, remain poorly understood. Using the humanized Townes mouse model, we investigated renal structural changes associated with sickle hemoglobin by comparing wild-type (HbAA), sickle cell trait (HbAS), and sickle cell disease (HbSS) mice.

To evaluate renal disease progression, we collected kidneys from male Townes HbAA, HbAS, and HbSS mice at 8, 16, and 26 weeks of age. Tissues were processed and stained with hematoxylin and eosin (H&E), and imaged at 10× magnification. Using Fiji (ImageJ), we quantified glomerular (area and circularity) and tubular (area and diameter) within cortical and medullary regions for genotypic differences.

Histological analysis revealed progressive renal remodeling across genotypes. At 26 weeks, the mean glomerular area measured 3012.10 μm^2 in HbAA mice, 3971.40 μm^2 in HbAS mice, and 5355.88 μm^2 in HbSS mice, demonstrating increasing glomerular enlargement with sickle genotype. Decreases in tubular area and diameter across the cortex and medulla, consistent with progressive nephron remodeling and tubular atrophy.

These preliminary findings demonstrate that presence of at least a single sickle allele promotes progressive renal remodeling. Further, these results provide the foundation for investigating renal segment-specific mechanisms that drive nephron injury, particularly in the SCT population. In the future, complementary functional and transcriptomic evaluation can provide insight into therapeutic strategies to slow or prevent the development of associated nephropathies.



TITLE: DISCOVERY, CHARACTERIZATION, AND VALIDATION OF IFI44 AS A KEY HEPATOCYTE ISG RESTRICTING HEPATITIS B VIRUS INFECTION

PRESENTER: KIRIN KARVER

MENTOR: DR. LEFTERIS MICHAILIDIS

PROGRAM: SURE- BIOMEDICAL SCIENCES

Hepatitis B virus (HBV) chronically infects over 250 million people worldwide and remains a major cause of liver-related morbidity and mortality. Although nucleos(t)ide analogs and interferon-alpha (IFNα) treatments are available to attempt viral suppression, a functional cure is rarely achieved. Because IFNα acts largely through the induction of interferon-stimulated genes (ISGs), identifying hepatocyte ISGs with robust anti-HBV activity is critical for improving therapeutic efficacies. To identify hepatic antiviral ISGs, we performed RNA sequencing on IFNα-treated mouse-passaged primary human hepatocytes (mpPHHs) isolated from humanized mice with chimeric human livers. This comparative transcriptomic analysis identified approximately 100 ISGs consistently and strongly induced across both systems. A targeted CRISPR-Cas9 knockout screen in HepG2-NTCP cells then assessed their functional impact on HBV. Among the top hits, IFI44 emerged as a potent restriction factor, its knockout markedly increasing HBV infection in the presence of IFNα - consistent with an independent ISG overexpression screen that flagged IFI44 and its paralog IFI44L as candidate antiviral effectors. While IFI44 has previously been linked to responses against several RNA viruses (including hepatitis C virus [HCV], human immunodeficiency virus [HIV], Dengue virus, Influenza A virus), its role in HBV has not yet been reported. Single-cell knockout clones of IFI44 and IFI44L in HepG2-NTCP cells confirmed the screenresults, showing enhanced IFNα-stimulated HBV replication, most pronounced in IFI44-deficient cells. RNAscope in situ hybridization independently corroborated these findings, revealing a higher proportion of infected cells and increased viral RNA in IFI44 knockout cultures. To localize the block within the viral life cycle, we used the HepDe19 system, which bypasses receptor-mediated entry. From this, we observed that IFI44 lost its restrictive activity in this setting, indicating that it acts at an early-entry step. Together, these findings establish IFI44 as a robust IFN-induced, post-entry restriction factor against HBV. Ongoing studies aim to define its molecular mechanism and evaluate its therapeutic potential for people living with chronic HBV.



TITLE: KINOME PROFILING IN HUMAN VESTIBULAR SCHWANNOMA

PRESENTER: OMAR KHATRI

MENTOR: XDR. RENEE READ

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Vestibular schwannoma (VS) is a benign tumor arising from Schwann cells of the vestibulocochlear nerve. It accounts for 8% of intercranial tumors, with an annual incidence of 3 to 5 cases in every 100,000 people. VS can cause debilitating symptoms, including hearing loss, cranial neuropathies, and, in severe cases, brainstem compression and hydrocephalus. Current treatments, including surgical resection and radiotherapy, can effectively control tumor growth but may lead to neurologic complications. Limitations highlight the need for mechanism-based non-invasive pharmacologic therapies that preserve neurological function while limiting tumor progression. Molecular profiling has revealed that VS is associated with loss-of-function mutations in the NF2 gene, resulting in multiple dysregulated signaling pathways. Kinases are essential signaling components that relay signal transduction. Receptor tyrosine kinase inhibitors have been evaluated in clinical trials, but show limited efficacy in VS. This may reflect an incomplete understanding of the pathways involved in VS pathology, as agents targeting kinases in downstream signaling, such as brigatinib, have shown promise. Therefore, we hypothesize that analyzing the VS kinome will provide a more comprehensive understanding of the pathways driving VS development and lead to the identification of novel therapeutic targets. To investigate this, we utilized the SureQuant method, which involved using a library of stable isotopically labeled peptides targeting >300 kinases and kinase-associated proteins to characterize their protein abundance in patient-derived VS tissue to identify alterations in signaling networks. Furthermore, we are using publicly available scRNA-seq datasets from human VS to survey the transcriptional expression of these kinases across cell types, analyzing their distribution in tumor cells and in its microenvironment. We plan to validate tumor-associated kinases using immunohistochemistry and additional multi-omic techniques. These studies aim to improve understanding of the molecular mechanisms underlying VS maintenance and progression, and may inform the development of improved targeted therapeutic approaches for VS.

TITLE: **HETERORESISTANCE EXPLAINS THE CEFAZOLIN INOCULUM EFFECT IN METHICILLIN-SUSCEPTIBLE STAPHYLOCOCCUS AUREUS**

PRESENTER: **MADISON KNAVEL**

MENTOR: **DR. DAVID WEISS**

PROGRAM: **INSPIRE- BIOMEDICAL SCIENCES**

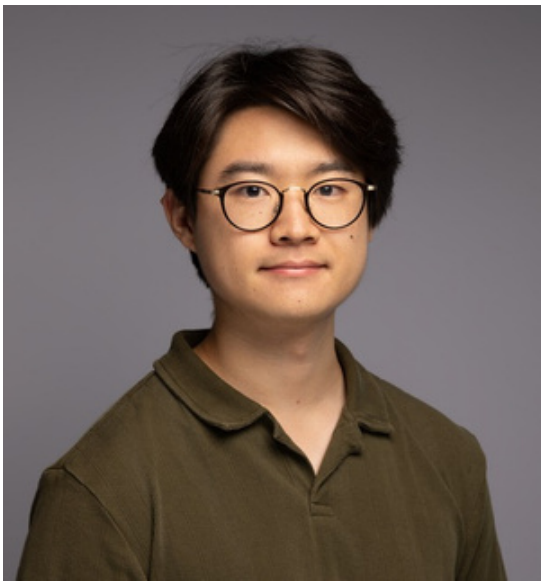
Antimicrobial resistance (AMR) is a major public health concern, causing about 1.14 million deaths globally in 2021 alone. Cefazolin is a first-generation cephalosporin class of antibiotic commonly used to treat methicillin-susceptible Staphylococcus aureus (MSSA) infections worldwide. However, MSSA isolates often identified as susceptible at lower bacterial densities have an increased minimum inhibitory concentration (MIC) against cefazolin at higher inoculum in vitro. This phenomenon is known as the cefazolin inoculum effect (CzIE) and has been associated with treatment failure in patients with MSSA infections treated with cefazolin; however, the mechanisms underlying the CzIE remain largely unknown. Heteroresistance, in which a seemingly susceptible strain harbors a small resistant subpopulation, can also cause treatment failure. We hypothesized that heteroresistance may cause the CzIE. This study is aimed at investigating the association between the CzIE and heteroresistance using a cohort of 127 MSSA samples collected from patients at Emory-affiliated hospitals in 2026. Samples were screened for heteroresistance to cefazolin using Population Analysis Profile (PAP) and were identified as heteroresistant (HR) if a minority subpopulation of cells greater than 1 in 10^7 survived beyond the Cefazolin breakpoint of 16µL/mL. CzIE testing was performed using broth microdilution assays at standard inoculum and high inoculum. Samples were identified as positive for the inoculum effect if the minimum inhibitory concentration (MIC) increased from a susceptible range of ≤ 8 µg/mL to a resistant range of ≥ 16 µg/mL at high inoculum. 31/127 isolates were identified as HR, and 18/127 isolates were identified as positive for the inoculum effect. All HR isolates exhibited the inoculum effect. These findings support the association between heteroresistance and the CzIE and expand our understanding of the mechanisms underpinning the CzIE, which may facilitate more accurate diagnosis and effective selection of antibiotic therapy.

TITLE: **HARNESSING NITROGEN DELETION FOR THE SYNTHESIS OF STRAINED COMPOUNDS**

PRESENTER: **YUKI KOBAYASHI**

MENTOR: **DR. MINGJI DAI**

PROGRAM: **CCC- NATURAL AND PHYSICAL SCIENCES**



Synthesis of strained compounds has been a major challenge in organic synthesis due to the difficulty in forming distorted carbon skeletons. Skeletal editing has become an increasingly popular strategy to address this issue in total synthesis as they have potential to greatly diversify ways to make natural products. One such skeletal editing approach is called nitrogen deletion, in which a nitrogen atom is removed from a molecule to make a new carbon framework.

During this summer, this project investigated whether it is possible to construct two targets using nitrogen deletion. Bielschowskysin, a natural product that features toxicity against cancer cells, contains a highly strained four member ring and has been a molecule that has not been synthesized chemically yet. Model studies on a simpler version of the compound have been conducted to see if the nitrogen deletion strategy is viable. Cubane, a highly strained molecule that has large potential applications in pharmaceutical chemistry, can serve as a replacement for benzene rings but remains difficult to synthesize because of its unusual three-dimensional structure. A synthetic route using nitrogen deletion was explored during this project.

Although the target precursors have not yet been obtained, this work highlights the synthetic challenges associated with constructing highly strained frameworks and establishes a foundation for applying skeletal editing strategies to their synthesis.



TITLE: CONSTRUCTING CRIMINALITY: EVALUATING THE ROLE OF THE MEDIA IN THE CASE OF THE MENENDEZ BROTHERS

PRESENTER: SYLVIE LANDMAN

MENTOR: DR. JULIA TULKE

PROGRAM: SURE- HUMANITIES

On August 20, 1989, Lyle and Erik Menendez shot and killed their wealthy parents, José and Kitty Menendez, in the family's Beverly Hills home. The trial that followed in the early 1990s became one of the first major criminal trials to be broadcast in its entirety on Court TV, expanding public access to the proceedings and intensifying media coverage of the case. The varying media depictions of the case fueled debate over the brothers' claims of childhood abuse and their role in explaining the killings. The trial's extensive media exposure and the central role of those abuse claims make it a particularly meaningful case for examining how media representations of trauma and abuse are constructed. This summer, I examined these representations by evaluating 258 Los Angeles Times headlines published throughout the brothers' first trial, from its beginning in July 1993 to its conclusion in January 1994. Using linguistic analysis, I examined how evaluative language and other linguistic choices influenced the neutrality of newspaper headlines. This analysis led to the development of a six-point neutrality scale that captured varying degrees of neutrality. Application of the neutrality scale revealed variation in neutrality across individual months of the trial, as well as across its major stages. Headlines describing the same courtroom events frequently occupied different positions on the neutrality scale despite reporting on the same proceedings. Rather than becoming consistently less neutral, headlines became increasingly varied as competing narratives emerged throughout the trial. The least neutral headlines revealed recurring patterns of evaluative language and selective emphasis that moved beyond straightforward reporting to construct representations of the trial. This provides the methodological foundation for the broader thesis, which will examine how media representations of trauma and abuse have evolved from coverage of the original trial to contemporary true crime media.

TITLE: **THE INTERSECTION OF HUNGER AND HEALTH: AN EXPLORATION OF FOOD INSECURITY, MENTAL HEALTH, AND CARE ENGAGEMENT AMONG BLACK SEXUAL MINORITY MEN IN ATLANTA, GA**

PRESENTER: **SOLEIL LAROCHE**

MENTOR: **DR. SOPHIA HUSSEN**

PROGRAM: **INSPIRE- SOCIAL SCIENCES**

Introduction: Black sexual minority men living with HIV face many health disparities fueled by multifaceted inequalities. Previous literature reflects that barriers like food insecurity can compromise HIV care engagement and medical adherence. Additionally, anxiety and depression are highly prevalent obstacles, but the intersecting associations of mental health, food insecurity, and clinical HIV care are understudied. This study explores the prevalence of food insecurity and its associations with mental health outcomes and care adherence among 246 BSSM living with HIV in Atlanta, Georgia.

Methods: This exploration used baseline data from 246 participants in the HIStory study. Food insecurity was scaled using the U.S. Household Food Security Survey Module. Outcomes included anxiety (GAD-7), depression (CES-D), past-year mental health utilization, and missing ≥3 ART doses in the past month. Linear and modified Poisson regressions estimated crude and adjusted associations, controlling for age ($p<0.05$).

Results: Food insecurity was prevalent at 77.1% (22.4% low; 54.7% very low). Participants faced high clinical depression risk (75.5%) and elevated anxiety (48.0%), yet 70.5% received no past-year mental health care. Missing ≥5 monthly medication doses was reported by 25.3%. Age-adjusted models showed food-insecure participants had higher anxiety ($\beta=4.33$, $p<0.0001$) and depression scores ($\beta=10.11$, $p<0.0001$). Food insecurity was associated with 1.80 times higher adjusted odds of missing ≥3 medication doses (aOR = 1.80, 95% CI: 0.94–3.45, $p=0.62$).

Conclusion: This analysis trends in the position that food insecurity is a highly prevalent burden associated with adverse health outcomes and clinical care barriers. By analyzing how food insecurity relates to anxiety, depression, and HIV medication adherence, this work highlights that ensuring patients are food secure is a medical necessity and a crucial step toward achieving true health equity.

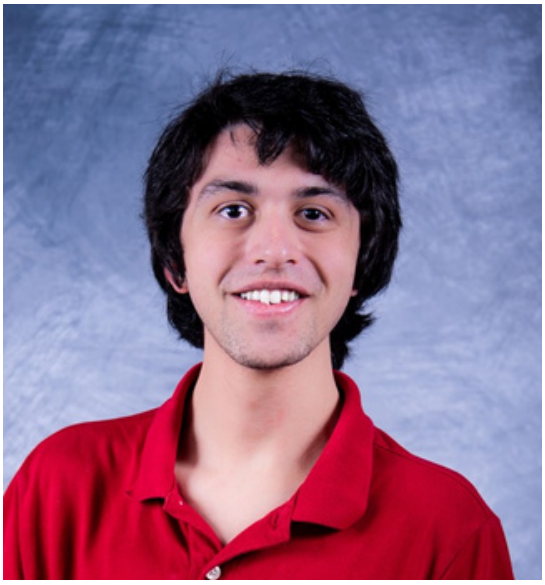
TITLE: PROGRESS TOWARDS CONVERGENT SYNTHESIS OF CREMIMYCIN

PRESENTER: PHILL LEE

MENTOR: DR. BILL WUEST

Antimicrobial resistance is an ongoing global crisis, with an estimated 4.71 million deaths associated with antimicrobial-resistant bacteria in 2021. Among resistant pathogens, methicillin-resistant Staphylococcus aureus (MRSA) is a major clinical concern, highlighting the urgent need to develop novel antibiotics. Cremimycin is a 19-membered macrocyclic lactam produced by Streptomyces sp. MJ635-86F5 that exhibits antimicrobial activity against a range of Gram-positive bacteria, including MRSA. Cremimycin was first reported in 1998, but the three-dimensional arrangements around its four stereocenters remain undefined. This project aims to determine the stereochemistry of cremimycin and evaluate how differences in its three-dimensional structure affect antimicrobial activity.

Here, we describe our progress toward the total synthesis of cremimycin. A convergent synthetic route was designed in which five smaller molecular fragments, each synthesized with defined stereochemistry, are assembled through five key reactions. To date, one of the five fragments has been synthesized, two are nearing completion, and synthesis of the remaining two is ongoing. Once assembled, the resulting synthetic stereoisomers will be compared with natural cremimycin to determine its three-dimensional structure and tested for antimicrobial activity.



TITLE: **DEVELOPING A DARK-QUENCHED FÖRSTER RESONANCE ENERGY TRANSFER (FRET) TENSION SENSOR: EXPRESSION-NORMALIZED SIGNAL WITHOUT BLEED-THROUGH CORRECTION**

PRESENTER: **ELI LEWIS**

MENTOR: **DR. KHALID SALAITA**

PROGRAM: **SURE- NATURAL AND PHYSICAL SCIENCES**

Cells under the microscope move and change shape. Proteins are the molecular machines that create this motion by generating piconewton (pN) forces: 1 pN is one ten-billionth the weight of a paper clip. Despite their size, pN forces drive biological processes, including migration, differentiation, and immune responses. Genetically encoded tension sensors (GETSs) are constructs inserted into native force-active proteins to report the forces they transmit. Traditional GETSs use a Förster resonance energy transfer (FRET)-based reporting system, with donor and acceptor fluorescent proteins (FPs) flanking a spring-like or coiled-coil element. FRET is the distance-dependent transfer of energy between two molecules: the donor is excited by light, but rather than re-emitting that energy as light, it transfers it to a nearby acceptor molecule, which fluoresces at its own wavelength. Like a macroscopic spring, the GETS, when stretched, exerts a restoring force proportional to its displacement from rest. Because stretching changes the distance between the FPs, it changes FRET efficiency; since efficiency is proportional to that distance, light emission reveals how far the sensor stretched, allowing the force to be calculated. A limitation of traditional FP pairs is that calculating FRET requires identifying and subtracting two confounding signals from the FRET readout: donor bleed-through (donor emission that falls within the acceptor's emission spectrum) and acceptor cross-excitation (acceptor fluorescence excited directly by the donor's wavelength). Additionally, the FRET index is sensitive to experimental conditions, making it variable and difficult to standardize. We address these issues by developing a GETS using an mRuby2–ShadowR FRET pair, ShadowR being a light-absorbing chromoprotein, with an added TagBFP for ratiometric measurements. We validate this construct's design, inserted into the native protein vinculin, through AlphaFold 3 modeling and live-cell FLIM-FRET measurements. Beyond demonstrating our design's functionality, we hope to further optimize our epifluorescence microscopy to obtain valid force readings.

TITLE: **BRAIN WAVE ACTIVITY DURING WALKING AND TURNING IN PEOPLE WITH PARKINSON'S DISEASE AND DEEP BRAIN STIMULATION**

PRESENTER: **TINA LI**

MENTOR: **DR. ARYAMAN GALA**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Parkinson's disease (PD) is a progressive neurodegenerative disorder characterized by bradykinesia, rigidity, tremor, and gait impairment. Turning impairment is a major contributor to falls, freezing of gait, and reduced mobility. Although deep brain stimulation (DBS) improves many motor symptoms, its effects on gait are variable, and turning remains understudied. Oscillatory activity measured using local field potentials (LFPs), particularly beta-band activity, is associated with PD symptom severity; however, activity during turning is poorly understood and may show a distinct signature because turning is dynamic and asymmetric. This study aims to (1) compare turning performance between DBS ON and OFF conditions; (2) characterize subthalamic nucleus (STN) and internal globus pallidus (GPi) oscillatory activity during turning and its associations with turning performance and DBS outcomes; and (3) determine whether the more affected side (MAS) provides a more sensitive neural biomarker than bilateral or less affected side recordings.

We analyzed 21 individuals with PD implanted with sensing-enabled DBS systems under DBS OFF and ON conditions. Participants completed 60 seconds of sitting, 30 seconds of standing, and four self-paced walking trials on a 6-m pressure-sensitive gait mat, turning twice in each direction. Turn time and step count were the primary outcomes. LFPs were recorded during sitting, standing, and turning, and spectral analyses quantified low-beta (13–20 Hz), high-beta (20–30 Hz), and gamma (40–90 Hz) power. We hypothesized that DBS would decrease turn time and step count, suppress beta activity during turning, and that MAS recordings would show stronger associations with turning outcomes. This work aims to identify objective biomarkers to guide individualized DBS programming and improve mobility and fall prevention in PD.

TITLE: **CHARACTERIZING THE EFFECT OF PATHOGENIC PHF14 G461E MUTATION ON ITS INTERACTION WITH TCF20 USING CO-IMMUNOPRECIPITATION**

PRESENTER: **ICEY LI**

MENTOR: **DR. JIAN ZHOU**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Autism spectrum disorder (ASD) is a neurodevelopmental disorder (NDD) characterized by deficits in social interaction, communication, and restricted or repetitive behaviors. Previous studies have identified a novel chromatin regulatory complex composed of methyl-CpG binding protein 2 (MeCP2), plant homeodomain finger protein 14 (PHF14), and transcription factor 20 (TCF20). Prior work from our laboratory has demonstrated that two missense mutations (C322G, L428R) in the human PHF14 gene disrupt protein-protein interactions within the MeCP2–PHF14–TCF20 complex, leading to impairment in brain development and typical NDD phenotypes.

Recently, we identified a missense variant, PHF14-G461E, in a patient with NDD. G461E maps into the PHD–zinc knuckle–PHD (PZP) module of PHF14, a region required for the PHF14–TCF20 interaction. However, how PHF14-G461E perturbs the interaction between TCF20 and MeCP2 remains unknown, and how its severity compares with previously characterized pathogenic variants has not been assessed. The goal of this study is to determine how PHF14-G461E affects the recruitment and interactions of the regulatory complex, and to position its effect relative to the known pathogenic variants C322G and L428R. We hypothesize that PHF14-G461E compromises the protein-protein interactions in complex formation and function, leading to dysfunction in chromatin regulation and neurodevelopment.

To test this, we introduced the G461E substitution into PHF14 by site-directed mutagenesis and verified the construct by Whole Plasmid Sequencing (WPS). We transiently expressed wild-type (WT) PHF14 and the G461E, C322G, and L428R variants in HEK293T cells and assessed their association with TCF20 by co-immunoprecipitation and Western blot, using PCNA as a control.

Consistent with prior work, the two previously characterized variants reduced TCF20 binding relative to WT, with PHF14-C322G causing the most severe loss and PHF14-L428R an intermediate reduction. On this scale, PHF14-G461E reduced TCF20 binding to a level comparable to PHF14-L428R, placing it in the intermediate severity range. PCNA levels remained unchanged across all conditions, consistent with equal loading. These findings identify G461E as a third PHF14 variant that impairs TCF20 recruitment in the MeCP2–PHF14–TCF20 complex, revealing graded severity across variants. This severity gradient refines the molecular mechanism linking PHF14 mutations to NDDs and provides a blueprint for future diagnostic or therapeutic approaches.

TITLE: **INTEGRATIVE BIOENERGETIC PROFILING AND RESCUE OF MITOCHONDRIAL DYSFUNCTION IN CDKL5 DEFICIENCY DISORDER**

PRESENTER: **ELIANA LIPORACE**

MENTOR: **DR. VICTOR FAUNDEZ**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**



CDKL5 Deficiency Disorder (CDD) is a severe neurodevelopmental disorder caused by mutations in the CDKL5 gene, characterized by early-onset epilepsy, intellectual disability, and motor impairments. While CDD shares clinical features with Rett syndrome (RTT, MECP2-linked), its molecular underpinnings are distinct. Mass spectrometry (MS) of cerebrospinal fluid (CSF) from Cdkl5-/y and Mecp2-/y mice revealed divergent metabolic pathologies: CDD CSF exhibited enrichment in mitochondrial inner membrane pathways (GO:0005743, p = 7.5e-38), marked by downregulated respiratory complex I subunits (Ndufa12, Ndufs4) and solute carriers (Slc25a11, Slc25a18). In contrast, RTT CSF proteomes implicated synaptic vesicle cycling (GO:0016079) and fatty acid oxidation (Acadm, Cpt1a), with no overlap in CDD-specific mitochondrial signatures. To investigate these metabolic disruptions, we analyzed CDKL5 knockout Hap1 cells (KO1: exon 6 22bp deletion; KO9: exon 5 10bp deletion) using Seahorse XF assays. Under glucose, KO cells showed elevated basal respiration (+42%, $p<0.01$) but impaired maximal respiration (-42%) and ATP production (-40%), alongside increased proton leak (+67%). Glutamine supplementation partially rescued ATP synthesis (KO1: +28%, KO9: +32%) but failed to restore maximal respiration, reflecting compensatory reliance on anaplerosis. Proteomics linked this to downregulated mitochondrial pyruvate carriers (MPC1/2, 2.1-fold, $p<0.05$) and upregulated glutaminolysis (Gls1, 1.8-fold), highlighting CDD's substrate prioritization defects. These findings establish CDD as a disorder of mitochondrial substrate shuttling, driven by complex I dysfunction and metabolic inflexibility. Future studies will target mitochondrial carrier system (MCS) redundancy, testing alternative fuels (e.g., fatty acids, ketones) and pharmacological MPC reactivation to restore bioenergetic homeostasis. By delineating CDD-specific pathways distinct from RTT, this work advances precision therapeutic strategies for neurodevelopmental disorders.

TITLE: THERAPEUTIC TARGETING OF TP53-MUTANT ACUTE MYELOID LEUKEMIA

PRESENTER: MICHELLE LU

MENTOR: DR. KIRANJ CHAUDAGAR

Background: TP53-mutant acute myeloid leukemia (AML) is associated with dismal clinical outcomes, with median survival of less than six months due to rapid development of resistance to chemotherapy and venetoclax/azacitidine (VEN/AZA). Current immunotherapeutic strategies targeting PD-1 or CD47 have shown limited efficacy, highlighting the need to identify alternative immune checkpoints that regulate leukemia persistence.

Methods: We investigated the role of vasoactive intestinal peptide (VIP) signaling in TP53-mutant AML using patient-derived datasets, primary AML specimens, TP53-isogenic leukemia cell lines using CRISPR-engineered models, flow cytometry, ELISA, and macrophage phagocytosis assays. Therapeutic efficacy was evaluated using ANT308, a first-in-class VPAC antagonist, alone and in combination with VEN/AZA or cytarabine.

Results: Bioinformatic and experimental analyses identified VIP as a previously unrecognized immune checkpoint selectively enriched in TP53-mutant AML. Leukemic blasts were the primary source of VIP, and both TP53 loss and therapeutic exposure further increased VIP secretion, establishing a therapy-amplified immunosuppressive program. VIP signaling through VPAC1 suppressed macrophage-mediated phagocytosis, thereby may be impairing adaptive immune priming. Pharmacologic blockade of VPAC signaling with ANT308 restored macrophage phagocytosis, enhanced pro-inflammatory activation, and promoted durable anti-leukemia immunity. ANT308 improved responses to VEN/AZA and cytarabine in therapy-resistant models. Mechanistic studies further revealed dynamic VIP-associated leukemia cell states that facilitate immune evasion and persistence under therapeutic pressure, suggesting that VIP functions as a central regulator of adaptive therapy resistance rather than simply promoting proliferation.

Conclusions: These findings identify the VIP-VPAC1 axis as a macrophage-centered immune checkpoint that drives persistence and relapse in TP53-mutant AML. Therapeutic inhibition of VPAC signaling restores innate and adaptive anti-leukemia immunity while sensitizing resistant leukemia to standard therapies. This work establishes a novel immunotherapeutic paradigm for eliminating persistent leukemia cells and provides a strong rationale for clinical development of VPAC antagonists, alone, or in combination with VEN/AZA or cytarabine, for patients with high-risk TP53-mutant AML.



TITLE: EFFECT OF AMYOTROPHIC LATERAL SCLEROSIS (ALS) ON NEURON POPULATIONS IN THE RED NUCLEUS AND MOTOR CORTEX

PRESENTER: EHSAAS MADAN

MENTOR: DR. NICHOLAS BOULIS

PROGRAM: SURE- BIOMEDICAL SCIENCES

To study this, rats were injected with a virus called AAV2.retro, which travels backward along nerve connections from a single injection site and can reach nerve cells in multiple brain regions at once. Brain tissue from wild-type, early-stage, and late-stage disease rats was stained to reveal virus-labeled nerve cells, and cell counts in the motor cortex and red nucleus were measured using an unbiased microscopy technique called stereology.

Red nucleus cell counts declined steadily as disease progressed, dropping to roughly 30 percent of healthy levels by late-stage disease, regardless of whether that side had received additional treatment. Motor cortex counts showed a related but more complex pattern, with treated and untreated sides diverging over time rather than declining together.

These findings suggest the red nucleus is affected by ALS in a pattern similar to already established regions, and that a single AAV2.retro injection may be able to reach it alongside the motor cortex and spinal cord. This positions the red nucleus as a promising additional target for future ALS gene therapies, and highlights the need for larger studies to confirm these early trends.

TITLE: DOES THE PAVLOVIAN-INSTRUMENTAL CONFLICT EXTEND TO COGNITIVE ACTIONS?

PRESENTER: PRANAVI MARELLA

MENTOR: DR. PETER HITCHCOCK

PROGRAM: SURE- SOCIAL SCIENCES



The Pavlovian-Instrumental Conflict (PIC) describes the tendency to learn better when individuals must approach to gain reward and withdraw to avoid punishment than vice versa. While this effect is typically attributed to overt motor actions providing evolutionary advantage, studying similar biases for abstract cognitive operations is essential to understand whether reward-driven behavior is rooted solely in action or in thought as well. The Cognitive Actions Task developed by Hitchcock and Frank required participants to choose whether to add or subtract the two numbers above and below a fractal image based on probabilistic feedback. In the original study, PIC produced an interaction between reward-seeking behavior and reinforcement learning in the cognitive condition, with addition representing approach and subtraction representing withdrawal. Specifically, participants showed higher accuracy during the learning phase in the addition/reward and subtraction/punishment conditions relative to the addition/punishment and subtraction/reward conditions. This effect, however, did not persist in the test phase, likely due to a ceiling effect caused by strong feedback and prolonged learning that allowed participants to fully master the task. This study will use the Cognitive Actions Task as a template to better display the level of influence PIC has in a cognitive setting. The learning phase will have reduced feedback contingencies and more complex cognitive operations (double-digit addition/subtraction) to prevent overlearning in the test phase. This study is expected to reveal clearer PIC effects, with participants demonstrating higher accuracy when cognitive actions align with approach/reward and withdrawal/punishment, and measurable interference when they conflict.

TITLE: **A GRACE LIBRARY SCREEN OF METHYLTRANSFERASES IDENTIFIES SPB1 AS A POTENTIAL TARGET OF SINEFUNGIN IN CANDIDA ALBICANS**

PRESENTER: **OM MEHTA**

MENTOR: **XDR. SOHAIL KHOSHNEVIS**

Candida albicans is a commensal yeast that resides in the human gut, mouth and other mucosal surfaces that can become pathogenic when one's immune system is suppressed. C. albicans is the leading cause of fungal infections in humans and does this by invading deep tissues and organs. Its ability to do so is attributed to its morphological transition from single budding yeast cells to filamentous hyphae that eventually make up invasive biofilms. Sinefungin, a pan-inhibitor of SAM-dependent methyltransferases, has been shown to impair hyphal formation, adhesion and biofilm development in C. albicans. The transition from yeast to hyphae is tightly controlled by multiple regulatory pathways and while the transcriptional regulation of hyphal induction has been extensively studied, post transcriptional regulation remains less explored. We identified Spb1, a SAM-dependant rRNA methyltransferase that plays a key role in rRNA modification and in the biogenesis of the 60S ribosomal subunit, as a potential target of Sinefungin. Identifying regulatory nodes offers a promising alternative to conventional antifungal treatments that usually target the cell wall or cell membrane. Understanding the basis of Spb1's function in C. albicans and its sensitivity to Sinefungin could uncover novel therapeutic strategies while minimizing antifungal resistance.

TITLE: **URINE ALBUMIN CREATININE RATIOS IN MIGRANT FARMWORKERS**

PRESENTER: **SAMMY MENDEZ**

MENTOR: **DR. ROXANA CHICAS**

PROGRAM: **SUPERR- BIOMEDICAL SCIENCES**

Migrant farmworkers labor in poor working conditions, including a lack of access to shade, poor hydration, and intense heat. While previous cross-shift studies have shown an acute decline in kidney function over a typical workday, the exact mechanism underlying the injury remains unknown. This study aims to understand this mechanism by analyzing renal biomarkers including urine Albumin-to-Creatinine Ratios (uACR), estimated Glomerular Filtration Rates (eGFR), and hydration levels.

In Spring 2026, we collected data from 110 participants, including urine, blood, and demographic information. Paired within-worker analyses compared pre- to post-shift values. Cross-shift acute kidney injury (AKI) followed KDIGO creatinine criteria or a 25 percent eGFR decline.

Results indicated that cross-shift changes in eGFR did not correlate with hemoconcentration. Similarly, changes in eGFR also did not correlate with post-shift hydration status. The single strong correlation was between uACR and urine specific gravity. However, this change reflected the urine-creatinine denominator, not the albumin numerator, which would indicate glomerular injury, and thus was not inferred as a biological effect.

The drop in kidney function does not appear to be glomerular since auACR remained normal. Furthermore, this decline does not mirror a pre-renal or dehydration-driven pattern, since hemoconcentration did not significantly correlate with the drop in eGFR. This injury is most consistent with subclinical tubular or functional injury, aligning with prior evidence pointing to proximal tubule and oxidative-stress pathways.

TITLE: **INFLUENCE OF MESO- ARYL GROUP VARIATION ON THE OPTICAL PROPERTIES OF DIPYRRINS**

PRESENTER: **ETHAN MILLER**

MENTOR: **DR. AUSTIN SCHARF**

PROGRAM: **OXFORD- NATURAL AND PHYSICAL SCIENCES**

Fluorescent and phosphorescent molecules are widely used as tracer molecules in biological imaging applications. Dipyrrins have been known to exhibit unique optical properties due to their large conjugated systems. Dipyrrins consist of two pyrrole rings connected by a methyne bridge. Dipyrrins are commonly known as half-porphyrins. Porphyrins are macrocyclic molecules containing four interconnected modified pyrroles; for example, a common porphyrin is heme. Variation of the meso- aryl group has not been studied in 1,9-bis(adamantyl) dipyrrins. In response to this, a series of 1,9-bis(adamantyl) dipyrrins with varying meso-aryl groups have been synthesized to investigate the role of free rotation about the C-C bond at the dipyrrin meso position, extension of the π system, and electron-donating or -withdrawing capacity of the meso-aryl group on the optical properties of 1,9-bis(adamantyl) dipyrrins. Their UV-visible and fluorescence spectra have been obtained, and we describe the influence of meso-aryl variation on the optical properties of 1,9-bis(adamantyl) dipyrrins. Our results lead to progress to synthesize a paramagnetic dipyrrin that exhibits near IR phosphorescence emission. Near-IR phosphorescent molecules hold significance as tracer molecules for biological imaging applications.

TITLE: **SYNTHESIS AND INVESTIGATION OF MESO-SUBSTITUTED DIPPYRIN COMPOUNDS AND THEIR OPTICAL PROPERTIES**

PRESENTER: **ETHAN MILLER**

MENTOR: **DR. AUSTIN SCHARF**

Fluorescent and phosphorescent molecules have diverse usage in the fields of medicinal chemistry and biology as molecular indicators, and maximizing their optical properties is crucial for their function as tagging molecules. Dippyrin complexes (such as BODIPY) are often used as such fluorescent indicators due to their intense optical properties, and substantial paramagnetism when complexed with metals such as lithium. If one such Dippyrin may be altered to the point of absorbing infrared light, then there are interesting implications for a new methodology of a medicinal dye that requires no invasive procedures nor X-ray exposure. A series of meso-substituted dippyrin complexes differing in rotational freedom, π-conjugation, and electronegative properties have been synthesized and their optical properties have been recorded.



TITLE: **MLP-1 REGULATES GAMMA-ENAC FUNCTION WITHOUT ALTERING PROTEIN ABUNDANCE**

PRESENTER: **MAKANI MSANGI**

MENTOR: **DR. DOUGLAS EATON**

PROGRAM: **SUPERR- BIOMEDICAL SCIENCES**

Marcks-like protein 1 (MLP-1/MARCKSL1) has been proposed to regulate epithelial sodium channel (ENaC) activity by organizing phosphatidylinositol 4,5-bisphosphate (PIP2) near ENaC at the apical membrane. Because gamma-ENaC maturation involves endoplasmic reticulum/Golgi glycosylation and partial cleavage before membrane delivery, this study tested whether loss of MLP-1 alters gamma-ENaC abundance in membrane or cytosolic fractions and whether electrical function changes despite unchanged protein abundance. Membrane and cytosolic proteins were isolated from murine wild-type (WT) and MLP-1 knockout (KO) tissue and analyzed by Western blot using anti-gamma-ENaC antibody. Gamma-ENaC signals were normalized to total protein staining and compared by genotype and sex using 2-way ANOVA. Transepithelial electrical measurements were collected using an EVOM2 epithelial voltohmmeter from 3 WT, 3 KO, and 3 blank culture wells to track resistance, voltage, and current. Western blot analysis showed no significant genotype effect on normalized gamma-ENaC abundance in either the membrane fraction ($F(1,5)=0.004$, $p=0.952$) or cytosolic fraction ($F(1,5)=0.069$, $p=0.804$). These findings suggest that MLP-1 loss does not substantially alter gamma-ENaC synthesis, glycosylation-dependent maturation, or bulk membrane localization. In contrast, EVOM2 measurements showed lower current in KO wells than WT wells, with an approximately 2-fold reduction in KO current ($t=11.3$, $p<0.001$). Together, these preliminary results support a post-trafficking model in which MLP-1 affects ENaC function rather than total gamma-ENaC abundance. This is consistent with MLP-1 acting as a localized chaperone that presents PIP2 to membrane-associated gamma-ENaC, although ENaC-specific inhibition and direct PIP2 measurements are needed to confirm this mechanism.



TITLE: EFFECTS OF PHAGE COCKTAILS ON CROP GROWTH AND BENEFICIAL PLANT-MICROBE INTERACTIONS

PRESENTER: ALISON MYERS-BECK

MENTOR: DR. NIC VEGA

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Bacterial communities promote plant growth and stress tolerance through the production of phytohormones, ultimately driving plant resilience and production. Phage, in turn, can shape bacterial communities, and yet their effects on commensal communities in commercial agricultural settings remain poorly understood. In response, this project aims to investigate how phage host-range evolution can restructure bacterial communities and the ecological functions they support, to develop a better understanding of how phage treatments can affect the communities in agricultural settings. Using Pisum sativum as a model system, along with Pseudomonas fluorescens sp. STAD384, Pseudomonas fluorescens sp. MVP1-4, and Pseudomonas brassicacearum sp. Q8R1-96 as the mutualistic bacterium – we isolated eight phages that have varying rates of infectivity. During the growth of the pea plants, data is being collected on plant resilience, such as size and reproductive capacity. Soil samples are being collected throughout the experiment to be used later to determine if there was continued presence of bacteria, as well as changes in successful phage infection. The implications of this work are significant to the use of phage-based biocontrol in agricultural settings, as this will provide more insight into how selective the process for phage isolation must be for effective biocontrol without disrupting beneficial plant-microbe interactions.



TITLE: OPTIMIZATION OF CHROMOPHORES FOR THE DEVELOPMENT OF VIBRATIONAL PROBES FOR REDOX SPECIES IN BIOLOGY

PRESENTER: JAKOB NARROW

MENTOR: DR. DANIELA BUCCELLA

PROGRAM: CCC- NATURAL AND PHYSICAL SCIENCES

Understanding redox biology requires molecular probes that can report on intracellular low-abundance redox species with precision. Redox dyshomeostasis drive processes ranging from oxidative stress to cancer progression, making sensitive tools for tracking these species essential to understanding disease. Activity-based probes (ABPs) exploit selective chemical reactivity to generate a detectable signal upon reaction with a specific target and can enable the visualization of these species by microscopy. Recently, stimulated Raman scattering (SRS) microscopy has emerged as a valuable alternative to fluorescence microscopy for imaging biological systems, as SRS is less prone to photobleaching and quenching and enables simultaneous detection of multiple species without spectral overlap due to narrow vibrational peaks. The development of activity-based probes detectable by electronic pre-resonance stimulated Raman scattering (epr-SRS) microscopy requires red-absorbing chromophores incorporating a bioorthogonal bond (e.g., nitriles) whose vibrational frequency can be modulated by changes in the electronic structure of the molecule. In addition, the chromophore must also remain amenable to functionalization with reactive trigger groups that respond selectively to the analyte of interest. In this work, we synthesized and characterized promising chromophores via UV-visible absorption, fluorescence, and Raman spectroscopy. Supported by density functional theory (TD-DFT) calculations, we evaluated the series of donor-π-acceptor chromophores containing distinct electron-acceptor groups. Comparison of experimental with computational results enabled evaluation of the effect of the acceptor on the epr-SRS intensity. Collectively, our findings inform strategies to develop responsive vibrational probes for monitoring redox biology.



TITLE: DOES TRANSCUTANEOUS VAGUS NERVE STIMULATION ENHANCE NEUROVASCULAR MODULATION BY MINDFULNESS-BASED STRESS REDUCTION IN CHRONIC KIDNEY DISEASE?

PRESENTER: ELINA NATU

MENTOR: DR. JEANIE PARK

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Cardiovascular disease risk in chronic kidney disease (CKD) is associated with sympathetic nervous system (SNS) overactivity and reduced parasympathetic activity. Mindfulness-based stress reduction (MBSR) was previously found to reduce SNS reactivity to stress in CKD. Transcutaneous vagus nerve stimulation (tVNS) has been shown to improve parasympathetic activation but the effects in CKD have not been explored. We hypothesized that tVNS enhances reductions in neurovascular activity and reactivity to stress mediated by MBSR in CKD. Twenty-two adults with CKD stages III-IV (mean age 63±8 y, 65% female, 59% black) were enrolled in an 8-week randomized controlled trial. During baseline, muscle sympathetic nerve activity by microneurography, heart rate, and beat-to-beat blood pressure (BP) were continuously measured during resting (5-10 minutes), mental math (3 minutes), static handgrip (3 minutes), and a cold pressor test (1 minute). Participants were randomized to an active or sham stimulation group, both with MBSR, before returning for an end-of-study (EOS) visit. Independent t-tests, Mann Whitney U tests, chi-squared tests, a repeated-measured mixed ANOVA, and Pearson correlation tests were run.

Both groups were matched for baseline characteristics. There were no differences between resting values from baseline to EOS. A decreasing trend was observed in the active group that was positively associated with eGFR (Systolic BP; r=0.673, p=0.0468). During stressors, BP reactivity was higher within the active group but there were no differences between groups.

TVNS does not enhance neurovascular modulation mediated by MBSR during resting and stress. Individuals with worse kidney function may experience greater benefits during resting.



TITLE: EARLY HIPPOCAMPAL DAMAGE ALTERS INHIBITORY CIRCUITRY IN THE AUDITORY CORTEX: A PILOT STUDY IN A MONKEY MODEL OF NEURODEVELOPMENTAL DISORDERS

PRESENTER: KAITLIN NGUYEN

MENTOR: DR. HILARY RODMAN

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Early-life brain damage—such as concussions, infections, and severe dehydration—disrupts normal development in both humans and non-human primates. Specifically, early hippocampal (HC) damage in macaque monkeys disrupts inhibitory circuitry, which comprises vast networks of neurons that reduce the electrical output of the neurons they connect to. This disruption extends to connected structures, such as the prefrontal cortex and amygdala. However, whether such impacts on inhibitory circuitry extend to sensory areas like the auditory cortex remains largely unknown. Neurodevelopmental disorders such as schizophrenia and autism are associated with auditory processing deficits (e.g., hypersensitivity, hyposensitivity, and hallucinations) alongside deficits in inhibitory circuitry. To determine whether early HC damage contributes to these auditory abnormalities, we examined postmortem primary auditory cortex (A1) tissue from adult macaques that developed normally (n = 6) and from those that received HC lesions in infancy (n = 6). We quantified parvalbumin-positive (PV+) interneurons—a specific subset of inhibitory neurons—as our key population. As lesions were performed separately in each hemisphere, we compared PV+ cell counts both across groups and by hemisphere using two-tailed t-tests. Although we found no significant difference in PV+ density between groups, the lesion group consistently trended toward higher density, mirroring previous observations in connected brain structures. These preliminary findings highlight the need for more detailed investigation of sensory inhibitory circuitry, particularly to clarify whether A1 is genuinely resilient and whether other sensory areas, such as the visual cortex, exhibit significant alterations.



TITLE: DEVELOPMENT AND VALIDATION OF A NOVEL MULTI-SENSOR SILICONE KIDNEY MODEL FOR INTRARENAL PRESSURE MEASUREMENT DURING URETEROSCOPY

PRESENTER: SAMUEL NIEDER

MENTOR: DR. BRENDAN BROWNE

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Intrarenal pressure (IRP) above 30 mmHg during ureteroscopy can force irrigation fluid and urine into renal tissue, raising urosepsis risk. It remains unclear how reliably pressure at one site reflects pressure throughout the collecting system, or how ureteral access sheath (UAS) suction affects it. We developed and validated a multi-sensor silicone kidney model measuring IRP simultaneously across the collecting system to address both questions.

A kidney collecting system was 3D-printed and cast in silicone with 8 pressure transducers embedded in the renal pelvis and each major calyx, accepting a 10 French UAS, creating a watertight closed system. Irrigation was delivered via pressure bag across 15 conditions: 3 inflow pressures (150, 200, 250 mmHg) crossed with 5 suction states – none, and 100 and 200 mmHg each in passive (UAS slider open) and active (UAS slider closed) modes. The ureteroscope was navigated throughout the kidney during continuous recording (~2 Hz, ~50 s per condition). Analyses used two-sample t-tests and correlation coefficients.

All 8 sensors tracked in near-perfect synchrony ($r=0.996$) within a ~5 mmHg band. Active suction reduced mean IRP 80–100% (to 0–12 mmHg), holding it below 30 mmHg at every setting; passive suction reduced IRP only 18–54%, staying below threshold in 1 of 6 settings (all $p<0.001$).

IRP changes propagated in near-lockstep across all 8 sites, indicating the collecting system in this model behaved as a single connected compartment, supporting single-site IRP monitoring. Furthermore, active suction provided significant reduction at maximal inflow, whereas passive suction was less impactful.

TITLE: GM2A AS A LOCAL REGULATOR OF ANTIGEN PRESENTATION AND ANTIGEN-PRESENTING CELL DIFFERENTIATION IN TRANSPLANT IMMUNITY

PRESENTER: AUSTIN OGBUEFI

MENTOR: DR. AUBREY REED

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Transplantation is the only curative treatment for end-stage renal disease. However, transplant requires systemic immunosuppression that causes a loss in protective immunity, highlighting the need for strategies that promote local graft tolerance without broad systemic immunosuppression. Ongoing work in our lab has sought to investigate the role of tissue intrinsic GM2 activator protein (GM2A) in modulating immunity. We have shown that GM2A-deficient (GM2A-/-) grafts reject more rapidly than wild-type (WT) grafts. However, the immunologic mechanism remains unclear. In my project, we hypothesized that GM2A influences antigen-presenting cell (APC) composition and their ability to activate allogenic CD8+ T-cells.

Splenocytes from WT and GM2A-/- mice were pulsed with increasing concentrations of SIINFEKL peptide, a foreign peptide to mice. Flow cytometry was used to quantify APC subset frequencies and to measure SIINFEKL display on major histocompatibility complex class I (MHC-I), a surface molecule that presents peptide antigens to CD8+ T-cells. Peptide-pulsed splenocytes were then co-cultured with CellTrace Violet-labeled OT-I CD8+ T-cells for 3 days to assess proliferation and activation.

GM2A-/- samples contained higher frequencies of B cells and macrophages compared to WT while dendritic cell (DC) frequencies were unchanged. Interestingly, GM2A-/- DCs showed a higher percentage of SIINFEKL-H-2Kb+ cells at low peptide concentrations as compared to WT DCs. CD8+ T-cell proliferation and activation were not significantly different between WT and GM2A-/- co-cultures.

These preliminary findings suggest that GM2A deficiency alters APC composition and may increase the frequency of peptide-presenting DCs at low peptide concentrations. Understanding this pathway may support strategies to increase GM2A expression in donor organs, potentially through ex vivo organ perfusion, to promote graft tolerance while limiting systemic immunosuppression.

TITLE: INFLUENCE OF MESO- ARYL GROUP VARIATION ON THE OPTICAL PROPERTIES OF DIPYRRINS

PRESENTER: ALEX PAGE

MENTOR: DR. AUSTIN SCHARF

Fluorescent and phosphorescent molecules are widely used as tracer molecules in biological imaging applications. Dipyrrins have been known to exhibit unique optical properties due to their large conjugated systems. Dipyrrins consist of two pyrrole rings connected by a methyne bridge. Dipyrrins are commonly known as half-porphyrins. Porphyrins are macrocyclic molecules containing four interconnected modified pyrroles; for example, a common porphyrin is heme. Variation of the meso- aryl group has not been studied in 1,9-bis(adamantyl) dipyrrins. In response to this, a series of 1,9-bis(adamantyl) dipyrrins with varying meso-aryl groups have been synthesized to investigate the role of free rotation about the C-C bond at the dipyrrin meso position, extension of the π system, and electron-donating or -withdrawing capacity of the meso-aryl group on the optical properties of 1,9-bis(adamantyl) dipyrrins. Their UV-visible and fluorescence spectra have been obtained, and we describe the influence of meso-aryl variation on the optical properties of 1,9-bis(adamantyl) dipyrrins. Our results lead to progress to synthesize a paramagnetic dipyrrin that exhibits near IR phosphorescence emission. Near-IR phosphorescent molecules hold significance as tracer molecules for biological imaging applications.

TITLE: **PROGRESS TOWARDS CONVERGENT SYNTHESIS OF CREMIMYCIN**

PRESENTER: **ALEX PAGE**

MENTOR: **DR. AUSTIN SCHARF**

PROGRAM: **OXFORD- NATURAL AND PHYSICAL SCIENCES**

Fluorescent and phosphorescent molecules have diverse usage in the fields of medicinal chemistry and biology as molecular indicators, and maximizing their optical properties is crucial for their function as tagging molecules. Dippyrin complexes (such as BODIPY) are often used as such fluorescent indicators due to their intense optical properties, and substantial paramagnetism when complexed with metals such as lithium. If one such Dippyrin may be altered to the point of absorbing infrared light, then there are interesting implications for a new methodology of a medicinal dye that requires no invasive procedures nor X-ray exposure. A series of meso-substituted dippyrin complexes differing in rotational freedom, π-conjugation, and electronegative properties have been synthesized and their optical properties have been recorded.



TITLE: **CO-RACIAL VOTING AND TICKET-SPLITTING IN A BATTLEGROUND: EVIDENCE FROM GEORGIA'S 2024 CAST VOTE RECORD**

PRESENTER: **MARIA CLARA PEDROZA SANTOS**

MENTOR: **DR. BERNARD FRAGA**

PROGRAM: **LGS SOAR- SOCIAL SCIENCES**

U.S. presidential campaigns disproportionately target swing states due to the institutional structure of the Electoral College. Party loyalty, however, extends beyond presidential elections and shapes electoral outcomes across both state and federal contests. American politics scholarship presents competing perspectives on the extent of party loyalty in contemporary elections. One strand of research emphasizes the rise of 'blind' or identity-driven partisanship, in which voters rely heavily on party identification across electoral contexts. In contrast, other studies highlight persistent patterns of ballot roll-off, defined as a decline in participation across successive contests on the same ballot, and ticket splitting, suggesting that lower-tier elections are not fully determined by partisan alignment. Georgia offers a particularly compelling case for this analysis: it is one of the nation's most closely contested presidential battlegrounds and home to a racially and demographically diverse electorate, making it an ideal setting to examine how voters navigate the ballot. Yet despite this, the relationship between race, voter turnout, and ballot behavior remains largely absent from existing research on partisan straight-ticket voting versus roll-off, particularly in explaining Georgia's shift from Democratic support in 2020 to Republican gains in 2024. Using precinct-level analysis and cast-vote records data linked to racial composition, we explore how split-ticket voting varies across minority and non-minority communities. We also assess whether increased Black support in 2024 reflects vote choice for President Trump versus longer-term realignment, and we measure the level and spatial pattern of crossover voting in the 2024 election. Preliminary results show systematic ticket-splitting in Georgia's 2024 elections, with voters supporting Kamala Harris in the presidential contest being more likely to split their tickets than those supporting Donald Trump, which varied by race composition. These results have broader implications for understanding party loyalty in battleground states and contribute to research on race and American politics.

TITLE: **IDENTIFICATION OF EXTRAGENIC SUPPRESSORS FOR RNA EXOSOME-LINKED NEURODEGENERATIVE DISEASE USING BUDDING YEAST MODELS**

PRESENTER: **SELENE PERCHER**

MENTOR: **DR. ANITA CORBETT**

A set of neurodegenerative diseases has been linked with missense mutations in genes encoding subunits of the RNA exosome complex, which processes or degrades most cellular RNAs. It is unknown why these mutations cause specifically neurodevelopmental symptoms, nor is there any known treatment. This study investigates one specific mutation in the human EXOSC5 gene, which encodes a structural subunit of the RNA exosome complex, that was identified in patients with a rare neurodevelopmental disorder. For this mutation, we aim to find extragenic suppressors, spontaneously acquired mutations that compensate for the growth phenotype of the diseased cells, to identify genetic interactions between the RNA exosome and other proteins, ultimately providing a lead for potential therapeutic targets for RNA exosome-linked disease treatment. We used Saccharomyces cerevisiae, budding yeast, to model the function of the RNA exosome, as it has been used extensively for this purpose in previous studies. By screening thermosensitive yeast cells for colonies that grow most similarly to non-diseased cells under temperature-induced growth stress, we found a few suppressor candidates. From whole-genome sequencing, we identified two genes with potential to have caused the suppression based on the impact of their amino acid changes and known knockout phenotypes: YER187W and AIM18. My initial findings suggest that a knockout of YER187W and AIM18 does not replicate the phenotype of the suppressor strains.

TITLE: **INVESTIGATING THE ROLE OF PA5471 RNA LIGASE ACTIVITY IN MEXXY EXPRESSION**

PRESENTER: **CHAUNESSY PLATER**

MENTOR: **DR. CHRISTINE DUNHAM**

PROGRAM: **CCC- BIOMEDICAL SCIENCES**



Antibiotic resistance has contributed to 1.27 million deaths and has been associated with an estimated 5 million more, according to the CDC in 2019. Bacteria, including the critical opportunistic pathogen Pseudomonas aeruginosa (PA), have developed a multitude of mechanisms to combat antibiotic treatment, such as through multidr[GU1.1]ug efflux pumps which are a prevalent mode of resistance. The MexXY-OprM pump within PA is part of the Resistance-Nodulation Division (RND) superfamily, which is unique to Gram-negative bacteria, and has non-constitutive expression inducible by the ribosome-targeting antibiotics used to treat critical PA infections. Precedent literature has established PA5471 as a key protein in the genomic regulatory pathway of MexXY, however, further data suggests the involvement of an alternative mechanism. PA5471 has sequence homology with RtcB2 ligase in E. coli and a putative PrfH gene neighbor, leading to the hypothesis that PA5471 has a role as an RtcB ligase in the regulation of MexXY expression. To address this hypothesis, we identified and mutated key catalytic residues within PA5471 that we propose are essential for RNA ligase activity, and previous work in the lab confirms that mutating the active site residue H294 increases antibiotic susceptibility. These variants were later purified and will be used in future experiments including binding and ligation assays to gain further insights into the structure-related function of the putative enzyme. These results aim to inform the conception of antibiotic adjuvants to restore the efficacy of current mandated medicine.

TITLE: COMPUTATIONAL CORRELATES OF SKIN CONDUCTANCE RESPONSES (SCR) DURING FEAR LEARNING

PRESENTER: MAHITA POLINENI

MENTOR: DR. VANESSA BROWN

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Fear conditioning paradigms provide a powerful framework for investigating associative learning and the mechanisms underlying the development of fear. In a differential fear conditioning paradigm, participants learned associations between conditioned stimuli (CS+) paired with an aversive unconditioned stimulus and safe stimuli (CS−) that never paired with unconditioned stimulus. Skin conductance responses (SCRs) served as an index of autonomic fear responding throughout the task. While traditional analyses focus on observable physiological and behavioral responses, they do not directly capture the latent cognitive processes that drive learning over time. The present study applies the Rescorla-Wagner (RW) model, a classical associative learning model, alongside the Hierarchical Gaussian Filter (HGF), a computational Bayesian model of learning, to examine hidden belief-updating processes during fear acquisition.

The RW and HGF will be fit to individual participant physiological data to estimate latent cognitive states. While the RW model will estimate the shock expectancy, the HGF model can provide additional estimates about latent cognitive states, including beliefs about threat probability, uncertainty, environmental volatility, and precision-weighted prediction errors. These inferred variables about latent cognitive states will then be related to SCR trajectories to determine how changes in internal cognitive states are expressed through physiological responses during the fear learning paradigm. Comparing the RW and HGF models will allow us to evaluate whether accounting for higher-order beliefs and uncertainty provides a more comprehensive characterization of fear acquisition than traditional associative learning alone.

By integrating computational modeling with psychophysiological measures, this project aims to move beyond descriptive analyses of SCR amplitude and toward a mechanistic understanding of fear learning. Identifying latent learning processes underlying conditioned fear may provide greater insight into why individuals differ in the acquisition of threat associations. More broadly, this work demonstrates the utility of computational psychiatry approaches for characterizing hidden cognitive mechanisms that contribute to adaptive and maladaptive learning and may ultimately inform future research on anxiety disorders and other conditions characterized by altered threat processing.



TITLE: FOUNDATIONS OF GENOME STABILITY: MAPPING GENOME-WIDE R-LOOP ENRICHMENT

PRESENTER: EVAN POLLEY

MENTOR: DR. JITENDRA THAKUR

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Cell viability is heavily dependent on genomic stability, which prevents processes leading to cellular dysfunction and disease. Chromosomal architectural structures such as centromeric and pericentromeric chromatin have a high impact on genome stability by facilitating kinetochore assembly and cohesion between sister chromatids during cell division. The role of specific non-B-form DNA structures, termed R-loops, which are still not completely understood in these regions. Previously published work has characterized the structure of these non-B-form DNA structures, but mapping the presence across satellite repeat regions such as the centromere, pericentromere, and telomere has been limited by the existing methodologies. This research project addresses these limitations by using the DRIP-seq protocol to map R-loop enrichment in the satellite-dominated regions. We would expect that the findings of this project to support the idea that centromeres exhibit lower R-loop enrichment compared to pericentromeric and telomeric regions. Large genomic fragments, caused by a substandard digestion process, bias results by overexpression. Correspondingly, our project also aims to optimize the fragmentation process in order to solely identify genuine positive R-loop signals. Large genomic fragments, caused by a substandard digestion process, bias the results by overexpression. In optimizing these methods, this research can clarify the structural role of R-loops in satellite-dominated regions and determine their role in the regulation of genomic stability.

TITLE: PRELIMINARY EVIDENCE FOR AUDITORY INFORMATION-SEEKING IN RHESUS MACAQUES (MACACA MULATTA)

PRESENTER: BLUE PRAXIS

MENTOR: DR. ROBERT HAMPTON

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Research shows that animals can monitor their own uncertainty and adaptively seek additional information before committing to a perceptual decision (Brady & Hampton, 2021). This behavior has been taken as evidence for metacognitive capacity. Most demonstrations of this in nonhuman primates have used visual stimuli, leaving open whether the same self-monitoring extends to other sensory modalities. Brady and Hampton (2021) developed a visual paradigm in which rhesus macaques could increase stimulus brightness to gather more information before responding; here we adapt that paradigm to the auditory domain. Macaques first undergo match-to-sample training to classify four distinct auditory stimuli using corresponding response images, followed by psychometric assessment of classification accuracy across a range of loudness levels. In Experiment 1, after training subjects to use a volume-increase response, we evaluate information-seeking by varying initial stimulus loudness and manipulating the volume change per touch response. In Experiment 2, unclassifiable novel sounds are introduced as probe trials. In Experiment 3, fixed-value probe trials lock stimulus loudness after the first response, allowing comparison of objective accuracy and subjective information-seeking at each level. We test four hypotheses. First, if subjects monitor evidence accumulation to control their decisions, then they should produce more volume-increase responses on trials where volume accumulates slowly. Second, if subjects monitor evidence accumulation, then they should make more volume-increase responses when a trial starts silent than when it starts loud. Third, if monkeys monitor their decision state rather than acoustic properties, then they should make more volume-increase responses on unclassifiable trials than classifiable trials. Fourth, if subjects monitor their uncertainty to guide information-seeking, then the probability of volume-increase responses should be inversely related to classification accuracy.

TITLE: GENERATING AND CHARACTERIZING HPV 16 L1 MUTANTS TO INVESTIGATE THE IMPACT OF ANTIGEN VALENCY ON THE LONGEVITY OF ANTIBODY RESPONSES

PRESENTER: JAHIANNA RAMÍREZ MONTALVO

MENTOR: DR. ERIN SCHERER

PROGRAM: INSPIRE- BIOMEDICAL SCIENCES

Human papillomaviruses (HPV) cause multiple cancers globally, especially HPV type 16 (HPV 16). To prevent both HPV infection and disease, HPV vaccines were developed that consist of virus-like particles (VLPs) that resemble the virus but do not replicate as they lack the viral genome. VLPs are composed of 360 copies (360-mers) of the major capsid protein, L1. Previous studies have shown that antigen valency is important for the durability of the antibody response, but it is unknown whether the complete L1 VLP structure is necessary or if L1 pentamers (5-mers) or L1 monomers (1-mers) are sufficient to generate durable HPV vaccine immunity. To investigate this question, we performed mutagenesis on an L1 (HPV16L1ΔN9/T10G) expressing plasmid in E. coli to generate three mutants that form 5-mers: L1ΔN9/T10G/C175A, L1ΔN9/T10G/C428A, and L1ΔN9/T10G/Δ408-431. C175A and C428A disrupt the disulfide bonds between 5-mers, and Δ408-431 removes helix 4 to prevent the 5-mers from associating into 360-mers. Ongoing work will determine which mutant produces the highest 5-mer yield. Future work will introduce mutations in helix 5 (5-mer + L464A, 5-mer + G465A, 5-mer + R466A) to generate 1-mers. These different valency L1 antigens will be administered in vivo to mice to assess whether 360-mers, 5-mers, and 1-mers generate equivalently strong or durable antibody responses. If lower valency L1 antigens generate antibody responses similar to those of 360-mers, they could offer a more cost-effective vaccine alternative for resource-limited settings. If not, these results will inform the effect of antigen valency in vaccine-induced immunity to guide future vaccine development.



TITLE: THE ROLE OF MUSIC IN EMOTIONAL COPING AMONG BLACK MEN

PRESENTER: JEREMIAH RICHARDSON

MENTOR DR. CARL SUDDLER

PROGRAM: LGS SOAR- SOCIAL SCIENCES

Mental Health challenges in men, specifically Black men, are often not spoken of in the Black community due to Black men having to be perceived as emotionally stoic individuals. It is a sensitive topic that has been approached by Black men reluctantly, causing them to be less likely than other groups to seek professional mental health care. Research has noted that evidence-based music therapy improves mood and reduces emotional distress. This qualitative phenomenological study will explore why Black men rely on music as a coping mechanism rather than seeking professional mental health care. Using this approach will allow me to conduct semi-structured interviews with Black men aged 18 and older, delving into their lived experiences and perceptions of mental health and music. Through this study, using the Emotion Regulation Theory and Help-Seeking Theory, relevant themes of traditional and societal masculine norms, emotional expression, cultural stigma, and the therapeutic role of music will be explored to better understand the lived experiences of Black men and their perceptions of professional mental health care. These findings can provide insight and understanding into relevant cultural approaches to mental health interventions for Black men, why they prefer music, and how music can be introduced through therapeutic approaches in the future.

Keywords: Black men, emotional regulation, music, mental health, coping mechanisms



TITLE: THE ROLE OF NEIGHBORHOOD COLLECTIVE EFFICACY ON PARENTING STRESS AND CHILD EXTERNALIZING BEHAVIOR

PRESENTER: ASHA ROLAND

MENTOR: DR. PATRICIA BRENNAN

PROGRAM: LGS SOAR- SOCIAL SCIENCES

While a substantial body of evidence has demonstrated an association between perceived stress in parents and externalizing behaviors in children (i.e., aggression, inattention, defiance, etc.), external factors that may buffer this relationship are rarely examined. Previous studies indicate that ecological factors such as neighborhoods can influence child development and behavior. Therefore, we examined if higher levels of parent-reported perceived stress will be associated with greater externalizing behavior in their children, and if this relationship is moderated by neighborhood collective efficacy. Data was extracted from the Environmental influences on Child Health Outcomes (ECHO) study cohort Atlanta, Georgia from 2024, and measures perceived stress, neighborhood collective efficacy, and child externalizing behavior in African American mothers and their children. Covariates including age, gender, and maternal education were examined in a multiple linear regression, including an interaction term between neighborhood collective efficacy and parental perceived stress. Greater parental perceived stress was associated with higher levels of child externalizing behavior ($B = 0.220$, 95% CI [0.053, 0.388], $p = .010$), whereas neighborhood collective efficacy did not moderate this association ($B = 0.009$, 95% CI [-0.011, 0.029], $p = .389$). The absence of a moderating effect may reflect unmeasured contextual factors, such as residential instability, which may have limited opportunities for families to establish neighborhood collective efficacy. Additionally, the sample was skewed toward lower neighborhood collective efficacy, potentially reducing the variability needed to detect a moderating effect. Future research should consider other environmental moderators, such as ethnic/racial diversity, and utilize longitudinal designs to better understand contextual factors that may buffer the effects of parental stress on child behavioral outcomes.



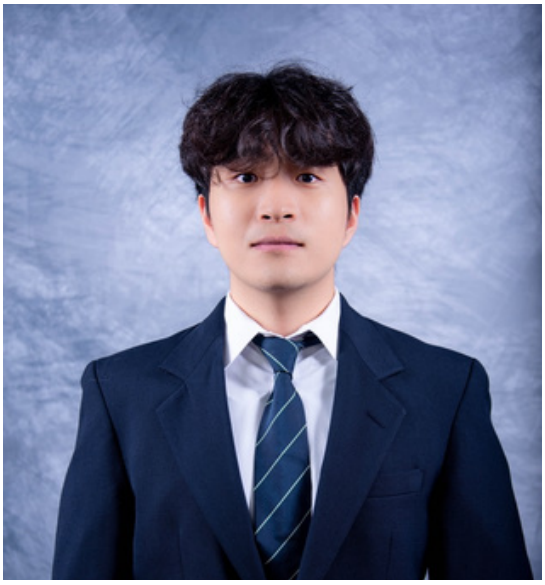
TITLE: THERAPEUTIC TARGETING OF HEAD AND NECK CANCER VIA BDP9066-INDUCED PANOPTOSIS

PRESENTER: GYASI RUFFIN

MENTOR: DR. YONG TENG

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Head and neck squamous cell carcinoma (HNSCC) has an overall 5-year survival rate of approximately 40%, and a significant factor contributing to its low survival rate is tumor metastasis. Advanced metastatic forms of HNSCC are commonly treated via immunotherapy; however, a lack of broad response from patients due to the immunosuppressive tumor microenvironment highlights the need for more effective therapeutic strategies. PANoptosis, a pro-inflammatory, immunogenic programmed cell death pathway integrating pyroptosis, apoptosis, and necroptosis, has recently emerged as an effective method to stimulate antitumor immunity through the release of danger-associated molecular patterns and inflammatory cytokines. Currently, effective strategies to therapeutically induce this process are largely unknown. To identify candidate compounds to modulate PANoptosis in HNSCC cells, we performed computational drug sensitivity analyses using the oncoPredict algorithm with GDSC-trained models. This analysis identified BDP9066, a potent and selective serine/threonine kinase inhibitor, as a promising PANoptosis-inducing agent. To determine the ability of BDP9066 to induce PANoptosis in vitro, we used western blotting and flow cytometry to identify PANoptosis-related biomarkers and morphological changes in HN12 cells. Mechanistically, BDP9066 not only enhanced apoptosis, evidenced by an increase in caspase-3 cleavage and reduced membrane integrity, but also induced pyroptosis and necroptosis, evidenced by the cleavage of gasdermin E and phosphorylation of MLKL, respectively. Collectively, these findings suggest that pharmacologic induction PANoptosis by BDP9066 represents a promising therapeutic strategy to enhance antitumor immunity and improve clinical outcomes for HNSCC patients.



TITLE: ASSOCIATION BETWEEN INFLAMMATION AND EXERCISE BLOOD PRESSURE WITH BICARBONATE SUPPLEMENTATION IN CHRONIC KIDNEY DISEASE

PRESENTER: PETER RYU

MENTOR: DR. SOOLIM JEONG

PROGRAM: SUPERR- BIOMEDICAL SCIENCES

Patients with chronic kidney disease (CKD) often have reduced muscle function, chronic inflammation and demonstrate abnormal blood pressure changes during exercise. This preliminary research looked at if there is an association between baseline inflammation and blood pressure response during handgrip exercise after placebo or bicarbonate supplementation.

12 patients with CKD stage III-IV were included in the study (age: 63.0 +/- 11.9 years, BMI: 29.6 +/- 5.5 kg/m2), and systolic blood pressure during 20% rhythmic handgrip and 30% static handgrip exercises were measured using beat-to-beat finger photoplethysmography before and after each supplementation. Inflammatory biomarkers (C-reactive protein [CRP], interleukin-6 [IL-6], tumor necrosis factor-alpha [TNF-alpha]) from blood were measured during the baseline visit to examine associations with blood pressure. Student's t-test, repeated measures ANOVA, and Pearson's r correlation were used to detect significance at p </= 0.05.

No significant difference was found between placebo and bicarbonate groups for change in systolic blood pressure during exercise (p >/= 0.181). Baseline inflammatory biomarkers (CRP [p >/= 0.642], IL-6 [p >/= 0.438], TNF-alpha [p >/= 0.195]) were also not significantly related to blood pressure change.

These preliminary findings demonstrate no significant differences in exercise blood pressure between placebo and bicarbonate groups, and baseline inflammation was not associated with exercise blood pressure.



TITLE: **THE FACE OF LEADERSHIP: CHILDREN'S PERCEPTIONS OF DOMINANCE AND PRESTIGE**

PRESENTER: **SAVVY SCOTT**

MENTOR: **DR. STELLA LOURENCO**

PROGRAM: **XSURE- SOCIAL SCIENCES**

RResearch on leadership has argued for dominance and prestige as two distinct pathways to attaining status. However, recent work suggests these pathways may overlap, as children use facial dominance cues to make judgements such as intelligence, a prestige-related attribute. Here, we investigated whether children also use facial dominance cues to make judgements about different leadership strategies. Twenty-seven children (13 boys, 14 girls; Mage = 8.74 years) completed a baseline condition in which they judged faces on traits including strength, leadership, intelligence, and kindness without contextual information. In a subsequent leadership condition, children heard descriptions of either dominance-type or prestige-type leaders and selected the person they thought best matched each leadership strategy. We hypothesized that if dominance and prestige are distinct, yet overlapping pathways to leadership, then a “sweet spot” would emerge with moderately dominant faces receiving the strongest prestige-type leadership judgements. Consistent with this prediction, children associated highly dominant faces with dominance-type leadership and more neutral faces with prestige-type leadership, suggesting that facial dominance informs judgements of both leadership strategies. These findings support the view that dominance and prestige are distinct but overlapping pathways to leadership and demonstrate that children integrate facial dominance cues with contextual information when forming leadership judgements. Future research should examine whether the overlap between dominance and prestige generalizes across racial groups and cultures.



TITLE: IDENTIFYING SURVIVAL DEPENDENCIES OF TARGETED THERAPY INDUCED PERSISTER CELLS IN ACUTE MYELOID LEUKEMIA (AML)

PRESENTER: NIA SCOTT

MENTOR: DR. SHRUTIBEN BHATT

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Acute myeloid leukemia (AML) is a rare hematological cancer that affects the bone marrow and blood. In AML, immature myeloblasts proliferate rapidly and accumulate within the bone marrow, impairing the production of healthy red blood cells, platelets, and normal white blood cells. Although remission after initial treatment is observed in 75% of the AML patients, patients eventually relapse and become resistant to current therapies. One understudied mechanism of resistance in AML is non-genetic adaptation fueling a reversible state called persister cells. The pathways which persisters rely on their survival and emergence is not well studied in AML. In this study, the survival dependencies of persisters cells in AML was investigated. Previously we have performed single cell RNA-seq on Gilteritinib (GLT) and Venetoclax (VEN) derived persisters in AML cell lines. We validated the hits identified from single cell RNA-seq data by utilizing CRISPR-Cas9 to generate knockouts to identify the gene dependencies of each persister type. We performed dose curves and mCherry chase on parental and KOs treated with GLT and VEN and identified CDKN2B and RIT1 to be important for GLT persisters' survival and RAD23B1, PRC1 and SLC16A6 for VEN persisters. Overall, this study investigated the AML persisters survival dependence and would help to design rational combination treatment to overcome drug resistance in AML.



TITLE: EVALUATING SUPPORTIVE CARE WITH SGLT2 INHIBITORS IN APOL1-MEDIATED KIDNEY DISEASE

PRESENTER: SAACHI SHARMA

MENTOR: DR. JASON COBB

PROGRAM: XSUPERR-

Despite making up 13.5% of the United States population, African Americans account for 35% of patients on dialysis. Much of this disparity is attributable to the apolipoprotein L1 (APOL1) gene. Normally, the gene protects against Trypanosoma brucei (African sleeping sickness), however, two risk alleles, G1 and G2, are common in people of Sub-Saharan African ancestry, and substantially increase the risk of chronic kidney disease. While targeted APOL1 therapies such as opemalirsen are being studied in the APPRECIATE trial, standard-of-care medications including sodium-glucose cotransporter-2 inhibitors (SGLT2i) remain first-line supportive treatment options. In the general chronic kidney disease population, SGLT2i reduce proteinuria and if this effect extends to APOL1 high-risk patients, it could lower urine albumin-creatinine ratios (UACR) below the eligibility thresholds for APOL1-targeted trials and contribute to the high screen fail rates that are currently observed. This retrospective cohort study evaluates whether SGLT2i use is associated with lower proteinuria and slower kidney function decline in the APOL1 positive population. After excluding 3 patients (2 non-adherent, 1 with unavailable records), 29 APOL1 positive patients were analyzed, out of which 10 were SGLT2i users and 19 were non-users. Estimated glomerular filtration rate (eGFR), creatinine, urine protein-creatinine ratio (UPCR), and UACR were recorded at baseline and follow-up, and between-group differences compared using the Mann-Whitney U test. eGFR and creatinine changed by ≥20% in non-SGLT2i users but not in SGLT2i users, whose average changes stayed within the range expected on therapy. Albuminuria and proteinuria findings were inconclusive as UACR rose less in SGLT2i users (+7% vs +45%) while UPCR fell less (−21% vs −56%). These findings suggest SGLT2i may support kidney stability in APOL1 high-risk patients but contrary to the hypothesis that SGLT2i-lowered proteinuria contributes to APPRECIATE screen failures, no significant UACR reduction was detected.

TITLE: EXAMINING THE DEGRADATION RATES AND SATELLITE CELLS RELEASED FROM FIBRIN CLOT SCAFFOLDS IN THE PRESENCE AND ABSENCE OF PLATELET-LIKE PARTICLES (PLPS)

PRESENTER: YOOBIN SONG

MENTOR: DR. ISABEL WALLGREN

Introduction: Peripheral artery disease (PAD) is the number one cause of non-traumatic lower-limb amputation, yet, current treatments focus on comorbidities. Satellite cells (SCs) are skeletal muscle stem cells that repair muscle tissue by fusing into muscle fibers and secreting angiogenic cytokines. We aim to deliver SCs in a fibrin scaffold as a potential therapeutic for PAD. Platelet-like particles (PLPs), synthetic platelets composed of ultralow-crosslinked (ULCs) microgel cores, conjugated with fibrin-binding antibodies, crosslink fibrin, increasing stability. Our objective was to examine whether incorporating PLPs into a fibrin scaffold impacts the in vitro degradation rate or the rate of SCs release from scaffold during in vitro culture. ULCs were used as a nonfunctional control particle. We hypothesized that PLPs would slow clot degradation and cell release, whereas ULCs would have no effect.

Methods: Fibrin clots (2mg/mL fibrinogen, 2U/mL thrombin, ±400k SCs, ±ULCs or PLPs) were cultured for 21 days. Every 3 days, we collected media, weighed clots, and centrifuged media to pellet any cells released. Cells were then stained with Trypan Blue and counted with a hemocytometer to quantify live and dead SCs.

Results: From Day 3, cellular groups degraded significantly faster than the acellular groups, which maintained >96% of initial mass by Day 21, while all cellular groups reached half mass by Day 6. By Day 21, Fibrin+SCs degraded the most and +PLPs+SCs degraded the least.

Conclusion: The preserved mass of acellular clots suggests SCs drive degradation. The significance between the +PLPs+SCs and +ULCs+SCs groups in the total number of SCs released suggests that ULCs may hinder proper clot polymerization and promote degradation. Additional replicates are underway to investigate findings. The significantly lower number of live cells released from the +PLP+SCs group compared to the Fibrin+SCs control may suggest that live SCs are being retained.

TITLE: EFFECTS OF REPETITION AND DELAY ON FAMILIARITY IN RHESUS MACAQUES

PRESENTER: JOHNNY STUMPFF

MENTOR: DR. ROBERT HAMPTON

Familiarity is a memory retrieval process indicating prior experience with a stimulus. Unlike other cognitive processes such as recollection and working memory, familiarity is a passive, general indicator of stimulus recency. Using a novel paradigm, Brady et al. (2021) found that rhesus macaques achieved high accuracy in relatively few sessions on recognition tests that required familiarity. This result raises new questions about the variables that affect the strength of familiarity in rhesus macaques. In Experiment 1, we will replicate the third experiment of Brady et al.'s 2021 study from Journal of Experimental Psychology: Learning, Memory, and Cognition. This experiment begins with a study phase in which rhesus macaques study lists ranging from eight to forty images three times, with image order being rerandomized in each list presentation. Each session concludes with a test phase in which monkeys are rewarded for selecting previously studied images rather than novel distractors. In Experiment 2, we will manipulate the number of image repetitions in the study phase. We hypothesize that if repeated stimulus exposure strengthens familiarity, then increasing exposures will increase accuracy for any given image. Importantly, images in the study phase of Experiment 2 will be presented consecutively, rather than in multiple rerandomized lists. This design feature allows us to study potential serial position effects for familiarity in rhesus macaques. In Experiment 3, we will increase the delay between the study phase and test phase to investigate how the strength of familiarity memory changes over time. We hypothesize that if familiarity declines over time, then accuracy will decrease as delay increases. This work will provide insight into the evolutionary origins of familiarity in humans.

TITLE: QUANTIFICATION OF SKELETAL MUSCLE SYMPATHETIC INNERVATION PROVIDES A FRAMEWORK FOR STUDYING METABOLIC DYSFUNCTION FOLLOWING NEUROTRAUMA OR NEURODEGENERATIVE DISEASES

PRESENTER: KATIE SWAN

MENTOR: DR. NIKKI BOON

Neuromuscular junctions (NMJs) and muscle fibers receive sympathetic input through adrenergic signaling. Sympathetic signaling is essential for maintaining NMJ stability and regulating skeletal muscle growth, size, force production, and metabolism. Because skeletal muscle is a major regulator of systemic metabolism, disruption of sympathetic signaling may have consequences that extend beyond the neuromuscular system to affect whole-body metabolic homeostasis. Our understanding of the baseline neuroanatomy of sympathetic innervation in skeletal muscle remains limited, hindering our efforts to determine how its disruption after neurotrauma alters muscle physiology and whole-body metabolism. We hypothesized that the metabolic phenotype of skeletal muscle is proportional to the level of sympathetic innervation and adrenergic signaling it receives, and disruption of sympathetic signaling impairs whole-body metabolic function and metabolic flexibility. Here, we found that hindlimb sympathetic innervation is anatomically organized and muscle-specific, with L2 serving as the primary source of innervation across muscles. Additionally, both sympathetic axon density and NMJ β2-AR enrichment are consistent and preserved across muscle types but differences in whole muscle β2-AR expression could contribute to metabolic phenotypes. Finally, sympathectomy attenuates the normal circadian oscillation in RER, indicating impaired metabolic flexibility, and sympathectomy decreases CPT1 enzyme activity and CPT1 dependent long chain fatty acid oxidation.

TITLE: **ACTIVITY-CLIFF EXPLANATION-SUPERVISED GRAPH NEURAL NETWORKS FOR SOLUBILITY PREDICTION**

PRESENTER: **IAN TAM**

MENTOR: **DR. BUSHRA ALAM**

PROGRAM: **CCC- NATURAL AND PHYSICAL SCIENCES**

The importance of solubility prediction in pharmaceutical discovery and materials science has motivated the development of machine-learned (ML) solubility models. Graph neural networks (GNNs) are especially useful because they leverage graph-based molecular representations and allow post-hoc explanation methods to provide atom-level attributions that increase interpretability for these otherwise opaque models. Previously, our lab developed an Activity-Cliff-Explanation-Supervised GNN (ACES-GNN) framework that incorporates explanation supervision for activity cliffs (pairs of structurally similar molecules with markedly different bioactivity) into model training. We demonstrate the transferability of this framework to solubility cliff prediction by evaluating it across four solvents and benchmarking it against physicochemical- and graphlet-based models. This work highlights the broader potential of explanation-guided learning for structure-property prediction across chemistry, beyond bioactivity.



TITLE: CHARACTERIZATION OF NKG2A+CD8+ T-CELLS DURING SIV INFECTION IN RHESUS MACAQUES

PRESENTER: DAIRA TAVAREZ

MENTOR: DR. MIRKO PAIARDINI

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Despite the success of antiretroviral therapy (ART) in suppressing HIV replication, the persistence of viral reservoirs remains a major barrier to an HIV cure. To promote the antiviral functions of CD8+ T and NK cells and the immune-mediated clearance of these reservoirs, the Paiardini laboratory evaluated sequential heterodimeric IL-15 (hetIL-15) and IL-21 treatment in ART-suppressed, SIV-infected rhesus macaques (RMs). Single-cell RNA sequencing (scRNA-seq) of lymph node (LN) cells identified a population of putative Natural Killer (NK)-like CD8 T-cells expressing multiple NK-associated genes, including KLRC1 (NKG2A), the levels of which predicted control of viral replication in the absence of ART.

Building on these findings, we aimed to characterize the phenotype and longitudinal dynamics of LN NKG2A+CD8+ T-cells using flow cytometry data from SIV-infected RMs that initiated ART 42 days post-infection (p.i.). LN cells collected pre-infection, 42 days p.i. (pre-ART), 550 and 648 days p.i. during ART were analyzed to determine the frequency and phenotype of NKG2A+CD8+ T-cells longitudinally. Pre-infection, LN NKG2A+CD8+ T-cells displayed a predominantly effector memory (EM; CD95+CD28-CCR7-) phenotype. Compared with memory NKG2A-CD8+ T-cells, NKG2A+CD8+ T-cells exhibited significantly higher expression of the cytotoxic molecule granzyme B and lower expression of PD-1. EM NKG2A+CD8+ T-cell frequencies decreased following SIV infection and were restored to baseline levels with ART. These cells displayed increased cytotoxicity (granzyme B), activation (HLA-DR and PD-1), and proliferation (Ki-67) during untreated infection, with expression of these markers returning to baseline during ART.

These findings provide an initial characterization of LN NKG2A+CD8+ T-cells during SIV infection and ART. Ongoing studies aim to optimize a high-dimensional flow cytometry panel to comprehensively define NK-like CD8+ T-cells identified by scRNA-seq. These studies will provide a foundation for defining the role of NK-like CD8+ T-cells in immune control of SIV infection and evaluating their relevance to HIV cure strategies.



TITLE: COMBINING TWO NATURAL PRODUCTS TO CREATE RECYCLABLE POLYMERS WITH ENHANCED PHYSICAL PROPERTIES

PRESENTER: LIAM TAYLOR

MENTOR: DR. PENGFEI WU

PROGRAM: CCC- NATURAL AND PHYSICAL SCIENCES

Polylipoates and polymuconates are both polymers derived from biological products capable of closed loop recycling. Polylipoates in particular have seen applications in laser 3D printing, medical adhesives, and drug delivery systems. However, they are commonly limited by two factors: low heat tolerance and unstable terminal radicals, both of which can lead to shorter polymer chains and structural integrity issues. Polymuconates exhibit both a high heat tolerance and stable terminal radicals, so we believe incorporating them into polylipoates will lead to valuable new materials with fewer weaknesses. This project aims to create these materials in two ways: copolymerization and crosslinking. Copolymerization has been achieved under green conditions without catalysts, reagents, or solvents using UV photopolymerization to create several resins with different lipoate:muconate ratios. Additionally, lipoate and muconate units have also been grafted together before polymerization to synthesize a multi-headed monomer capable of creating highly branched structures.



TITLE: DEVELOPMENT OF MOTOR-FREE EEG AND EYE-TRACKING PARADIGMS FOR ASSESSING COGNITION IN YOUNG CHILDREN WITH MOTOR IMPAIRMENT

PRESENTER: MARIANA VEGA ARANDA

MENTOR: DR. CAITLIN KJELDSEN

PROGRAM: LGS SOAR- BIOMEDICAL SCIENCES

Early cognitive assessments often rely on motor responses (e.g., pointing, reaching, grasping, object manipulation), making it difficult to separate cognitive ability from motor limitations in children with cerebral palsy or other motor impairments. To isolate cognitive ability from motor skill, we sought to develop a motor-free, neurophysiological approach, specifically, an EEG-compatible video paradigm using short, realistic cause-and-effect events to evaluate early cognition.

Initial stimuli depicting familiar physical events for young children (e.g., a ball bouncing with sound, toy car knocking over a tower of blocks) were generated with Grok AI tools. Each event was created with paired congruent (expected outcome) and incongruent (unexpected or missing outcome) videos. To ensure time-locking utility for EEG, each pair was engineered around a precise critical timepoint when the expected effect occurs. Two child development experts reviewed the initial stimulus pool, selecting the final set via consensus based on visual complexity, realism, ecological validity, and capacity to test early cognitive concepts related to attention, exploration, object permanence, and cause-and-consequence learning.

The development process initially generated 30 videos from real-world prompts, which were then edited using iMovie to ensure precise timing of visual and auditory cues. Following expert review, a finalized stimulus set of 14 videos were selected. This finalized set provides a standardized, motor-free tool to compare neural responses to expected physical relationships versus violations of expectation without requiring any manual manipulation, speaking or pointing.

To validate this newly developed paradigm, we are conducting a pilot study of 60 infants and toddlers aged 9- to 27-months. This trial matches children with motor impairments 1:1 with typically developing peers across 3 distinct age strata spanning the full age range. Each video is presented in random order 5 times during the pilot protocol to allow expansion beyond cause-and-effect to evaluate neural signatures of predictive anticipation. The paradigm is used alongside other motor-minimized measures, including eye-tracking, and the Cognitive domain of the Bayley Scales of Infant Development (4th edition), the current gold standard in neurodevelopmental follow-up. This pilot will provide a foundation for more accessible, objective measures of early cognition, particularly for children with motor impairments.



TITLE: ROLE-STAGE ALLOCATION OF FINITE POLYNOMIAL POLAR APPROXIMATION FOR MUON-TYPE OPTIMIZATION

PRESENTER: SAM WANG

MENTOR: DR. YUANZHE XI

PROGRAM: SURE- TECHNOLOGY, ENGINEERING, MATHEMATICS

Muon-type optimizers make use of gradient and momentum matrix to generate effective update directions. However, due to the fact that this technique employs orthogonalization repeatedly, finding the right update direction becomes quite costly since it incurs costs at each iteration. Existing work has focused mainly on creating various spectral maps while not paying enough attention to whether the budget for orthogonalization is equal for different stages of training and roles of parameter. In this study, we propose role-stage schedule that reserves full five-step Muon for the parts of training where it appears most valuable and uses a cheaper four-step map elsewhere. By conducting experiments with GPT-2 on the FineWeb dataset, we apply the concept of effective rank, spectral spread, gradient alignment, update norm, and runtime diagnostics. The resulting method uses Muon5 during the first 1% and last 5% of training, keeps Muon5 for MLP projection matrices, and applies a scaled four-step Muon map during the middle phase. On GPT-2 small, it reduces the polynomials cost by about 14% and optimizer time by roughly 12% while matching or in some cases even slightly improving the validation loss of the default Muon5. These results demonstrate that MUON-style orthogonalization does not require uniform application and lead the way to matrix-aware optimizers which can adapt their computational effort based on the parameter, the stage of training process and actual runtime cost.



TITLE: INVESTIGATING INVOLVEMENT OF THE MONARCH GUT MICROBIOME IN PARASITE RESISTANCE USING ANTIBIOTICS

PRESENTER: SUSANNA WANG

MENTOR: DR. JAAP DE ROODE

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Parasites are organisms that exploit the resources of their host, reducing the host's lifespan and quality, but what the host eats can reduce the severity of parasitic infection through the gut microbiome. The complexity of the gut microbiome in monarch butterflies has been explored, but the specific mechanism within the gut microbiome that confers the butterflies' parasite resistance is still not known. By looking at the effects of different antibiotics that target different mechanisms, such as biofilms, bacterial ribosomes, or bacterial cell walls, in the caterpillar's gut microbiome, we hypothesize that the specific systems implicated in parasite resistance can be deduced. We sprayed three experimental groups and one control group of monarchs with their respective treatments from egg to second instar, or molting stage. The treatments included rifamycin, tetracycline, vancomycin, and DI water as a control. Because each antibiotic we tested targets a different mechanism in the gut microbiome, the importance of certain gut microbiome structures can be concluded. Monarchs were then reared to adulthood until death based on standard lab procedures, and we collected data at all stages on infection score, lifespan, and pupation time. Infection scores are visually determined based on parasite surface area on the monarch pupae. The results of this experiment can lead to future research on what specific systems are most important for parasite resistance in monarch butterflies, which is a leading natural factor in their declining population, allowing for better conservation of the species.

TITLE: **ASSESSING OFF-TARGET EFFECTS OF GUT INSULIN⁺ CELL THERAPY FOR TYPE 1 DIABETES**

PRESENTER: **RAYNA XIAO**

MENTOR: **DR. WENDY MCKIMPSON**

PROGRAM: **PRIDE PROGRAM**

Type 1 diabetes (T1D) predominantly develops during childhood. It is characterized by immune-mediated destruction of insulin-secreting pancreatic β-cells. Restoring insulin production is therefore a major therapeutic goal. We champion reprogramming gut enteroendocrine cells to produce insulin as a T1D treatment. Previously, we found that FOXO1 ablation in gut neurogenin 3-positive (Neurog3+) endocrine progenitor cells induced the generation of insulin-producing cells in the stomach and intestine. Many of these cells coexpressed MafA, a marker of mature β-cells. To further evaluate the specificity of this approach, here we investigate the impact of FOXO1 ablation on other gut endocrine cell populations throughout the gastrointestinal (GI) tract. We first performed immunofluorescence staining on stomach, small intestine, and colon from 7-month to 1-year old female NOD mice, a T1D mouse model. Comparative analysis between tissue from control mice (NOD) and mice lacking FOXO1 in Neurog3+ cells (NKO) revealed no significant differences in the abundance of cells expressing the hormones serotonin, GIP, and GLP-1. We also isolated and cultured primary cells from the above-mentioned mice. To stimulate insulin+ cell-conversion ex vivo, primary gut cells were treated with FOXO1 and Notch signaling pathway inhibitors. Blocking these pathways triggered significant changes in the expression of Tph1, GLP-1, FOXO1, and Hes1 across different gut regions. Together, this data suggests that FOXO1 ablation in Nerurog3+ cells does not alter the composition of major endocrine cell populations, supporting the therapeutic potential of this strategy for T1D although some optimization may be required when targeting this reprogramming pathway using molecular compounds.



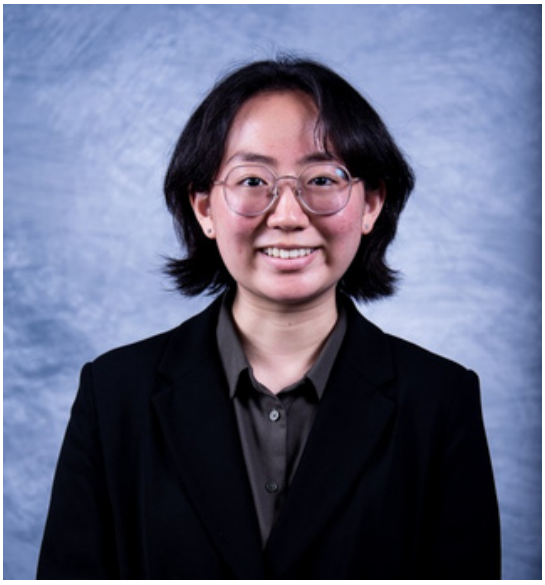
TITLE: **OPTIMIZING COMPUTATIONAL DEEP BRAIN STIMULATION MODELS USING MOTOR-EVOKED POTENTIALS**

PRESENTER: **LUCAS XUE**

MENTOR: **DR. SVJETLANA MIOCINOVIC**

PROGRAM: **SURE- BIOMEDICAL SCIENCES**

Deep brain stimulation (DBS) can effectively improve movement disorder symptoms, but it requires clinicians to spend lots of time modifying settings after surgery to maximize benefits and reduce side effects. Computational DBS models address this problem by allowing different DBS settings to be simulated before they are tested in patients. However, they still lack neurophysiological validation, which limits their predictive accuracy. Our objective in this study was to validate the accuracy of DBS models in predicting DBS side effects using clinically recorded motor-evoked potentials (MEPs). MEPs have been shown to be associated with DBS side effects. Specifically, we aimed to find the most optimal axon diameter to be used in DBS computational models, as axon diameters are biophysically associated with pathway excitability. In three patients with Parkinson's Disease, we estimated activation of the corticospinal bulbar tract (CSBT) using DBS modeling and measured MEPs experimentally in response to the same DBS settings (on average, 30 settings). Using the model, we simulated activations in 10 divisions of the CSBT for 4 different axon diameters (3 to 6 μm) and compared their activation estimates to the clinical MEP data. We found that the optimal diameter varies across different subjects, and in the future, we plan to analyze other DBS model parameters, including different volume conductance models. Finding these ideal parameters to predict DBS side effects can improve the overall predictive ability of DBS models and could lead to more effective DBS treatments.



TITLE: ABERRANT REGULATION OF TRAINED IMMUNITY IN NOONAN SYNDROME

PRESENTER: ERIN YOO

MENTOR: DR. CHENG-KUI QU

PROGRAM: SURE- NATURAL AND PHYSICAL SCIENCES

Noonan Syndrome (NS) is a pediatric genetic developmental disorder frequently caused by gain-of-function mutations in Ptpn11 (SHP-2), a key regulator of the Ras signaling pathway. NS is also associated with an increased risk of developing aggressive myeloid disorders, such as juvenile myelomonocytic leukemia (JMML). Emerging evidence has linked NS to several autoimmune diseases, suggesting chronic pro-inflammatory immune dysregulation in NS patients. However, whether NS alters innate immune memory remains unknown. Trained immunity, the metabolic/epigenetic reprogramming of innate immune cells, enhances responsiveness to secondary restimulation. In this study, we explored whether Ptpn11 gain-of-function mutations are linked to dysregulated trained immunity in NS. Utilizing a unique mouse model of Ptpn11+/+/Mx1-Cre+ (wild-type) and Ptpn11E76K/+/Mx1-Cre+ (mutant) mice, isolated monocytes from each mouse line were differentiated into bone marrow-derived macrophages and subjected to an in vitro trained immunity assay, using β-glucan as the training stimulus, followed by lipopolysaccharide (LPS) restimulation. Cytokine quantification, macrophage-T cell co-culture proliferation assays, and metabolic stress assays were performed after trained immunity was established to evaluate changes in immune responses. Following restimulation, trained mutant macrophages exhibited 3.2-fold and 8.8-fold increases in TNF-α and IL-6 pro-inflammatory cytokine production, respectively, relative to trained wild-type controls. Trained mutant macrophages suppressed T cell proliferation by 57%, exhibited a 31% reduction in glycolytic capacity, and displayed a 45% reduction in maximal respiration, all following restimulation. Together, these findings suggest an aberrant trained immunity response, and support the presence of a chronic pro-inflammatory environment in NS. Although mutant macrophages exhibited exaggerated pro-inflammatory cytokine production, their impaired metabolic function suggests that this heightened inflammatory response may occur alongside dysregulated maintenance of trained immunity. Future studies may further clarify the molecular mechanisms underlying trained immunity regulation associated with Ptpn11 gain-of-function mutations. This pro-inflammatory environment may help explain and clarify the recent emergence of autoimmune diseases in NS patients.

TITLE: **TESTING THE TRUTH: HOW RETRIEVAL PRACTICE MODULATES STATEMENT BELIEVABILITY AND RECOGNITION MEMORY**

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Testing oneself on material, compared with simply studying it again, yields better memory performance over time, a phenomenon known as the retrieval practice effect. However, less is known about the impact of retrieval practice in areas beyond memory. One such area is the judgment of whether information is true. Previous research has found that repeated information is often judged as truer than unseen information, a robust phenomenon called the illusory truth effect. Due to the superiority of testing over repetition for memory, the current hypothesis is that recalling a statement (read → cued recall → accuracy judgment) will produce a larger illusory truth effect than rereading the statement (read → reread → accuracy judgment) after a long delay (≥ 1 day). In the pilot experiment (n = 23), participants read trivia-style facts and practiced each statement either by restudying it (the statement was shown again) or by testing themselves on it (a fill-in-the-blank question) on the first day. On the second day, they made accuracy ratings for these statements and for new, unseen statements on an eight-point scale. We found that both restudied and retrieval-practiced statements were rated much higher than new statements, but no difference was found between the mean ratings of retrieval-practiced and restudied statements. In Experiment 1, we extended the delay between initial exposure and the truth rating to one week and added a six-point recognition task immediately after each truth-rating trial. Preliminary results (n = 27) suggest that the illusory truth effect was larger and that participants recognized more statements with high confidence in the retrieval-practice condition than in the restudy condition. These experiments help us understand not only the effect of repeated misinformation but also the effect of recalling misinformation on its perceived truthfulness.