



ANNUAL UNDERGRADUATE RESEARCH SYMPOSIUM

April 16, 2026 | 2-6 pm | The Edge, Bostock Library

2-3 PM

THE RESEARCH
ADVANTAGE:
LAUNCH YOUR
CAREER
ALUMNI PANEL

3-4 & 5-6 PM

POSTERS &
FLASH
TALKS

4-5 PM

TRINITY
LEADERSHIP
REMARKS &
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SENIOR THESIS
TALKS

2-6 PM

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This event is produced in collaboration with Muser and Duke University Libraries

WELCOME!

As Director of the Trinity College of Arts and Science's Undergraduate Research Support (URS) Office, I am pleased to welcome you to the 2026 Duke Undergraduate Research Symposium.

We are grateful to expand our partnership with Duke Libraries and to host this year's symposium in Bostock Library. Establishing the URS office in this central location has increased our visibility and strengthened the guidance and support we provide to students as they navigate research opportunities. We also appreciate our collaboration with MUSER, which has allowed us to introduce concurrent flash talks to the symposium, expanding opportunities for students to share their work through oral presentations.

This year, we launched the Trinity Student Team for Advancing Research (T-STAR) initiative. Our T-STAR ambassadors represent diverse disciplines and help promote research engagement, share resources with peers, and provide valuable feedback that has helped shape both our programming and this symposium. Inspired by T-STAR input, we are pleased to welcome Duke alumni to participate in our panel session, *The Research Advantage: Launch Your Career*. These alumni will share how research experiences helped shape their professional paths and the skills that continue to influence their careers. Many other alumni are attending today's event as well. I encourage you to take advantage of this opportunity to network and discuss your research interests with them!

We are also proud to introduce the Distinguished Senior Thesis Talks, featuring three seniors representing the Natural & Quantitative Sciences, Social Sciences, and Arts & Humanities. Their work highlights the depth of inquiry, creativity, and dedication that undergraduate research fosters.

Today's presenters represent many stages of the research journey, from early exploration to thesis completion. I encourage you to engage with the presenters, ask questions, and celebrate the curiosity and innovation that define undergraduate research at Duke.

Thank you for being part of this important event.

Warmly,

Jessica R. Harrell, Ph.D.

Director, Undergraduate Research Support Office
Trinity College of Arts and Sciences
Duke University



WHAT IS URS?

OUR MISSION:

The mission of Trinity College of Arts & Science's Undergraduate Research Support Office (URS) is to encourage and support students and faculty engaging in meaningful research via mentor-mentee relationships through training, programming, opportunities, and funding.

LEADERSHIP

- Scott Huettel, PhD, Senior Associate Dean for Research in Trinity College of Arts & Sciences
- Jessica R. Harrell, PhD, Director of Undergraduate Research Support Office
- Sarah Koop, Program Coordinator

STUDENT SUPPORT

- Kavya Nandagiri, Student Assistant
- Erika Rispoli, Student Marketing Assistant

STAY CONNECTED WITH URS!



Effects of Heavy Metal (Lead and Cadmium) Exposures on Neurodevelopment

Faculty Mentor: Susan K Murphy, Ph.D.

Authors: Syeda Aafreen, Guru Ulaganathan, Susan Murphy

Abstract:

Heavy metals such as lead and cadmium have long been considered developmental neurotoxins, and vulnerable populations are often disproportionately affected by exposure. Heavy metals are dangerous due to their ability to cross the blood-brain barrier and produce several neurodevelopmental problems, including problems with cognition, motor skills, and learning ability. However, the mechanisms by which neurotoxins disrupt neurodevelopment and neurodifferentiation are not well understood, and the objective of this project is to better understand how lead and cadmium exposure influence early brain development. The main hypothesis is that lead and cadmium exposure both harm neurodifferentiation. Specifically, heavy metal exposure may lead to different neural cell type proportions during development, which would disrupt the delicate balance required for proper neural functioning. In order to test this hypothesis, we will use Brain Spheres, where human induced pluripotent stem cells (hiPSCs) are differentiated into neural progenitor cells (NPCs) that differentiate further into a 3D model. This organoid model produces different neural cell types, including various neurons, astrocytes, and oligodendrocytes, similar to how these cells develop in the human cortex. Brain Spheres are best suited for this research due to their myelination, self-directed transition during neurodifferentiation, and size-constrained growth that allows for reproducibility. There are limited organoid studies with physiologically relevant doses of lead or cadmium. In this study, neural progenitor cells will be exposed to control (vehicle), low-dose, and high-dose concentrations of either lead or cadmium followed by monitoring for eight weeks. Morphological changes to the cells will be visualized with brightfield microscopy. Molecular cell type proportions and neural gene expression levels will be analyzed with RT-PCR. Results will advance our understanding of the sensitive time periods and cell types that are especially vulnerable to heavy metal exposures during early brain development, providing insights into consequences for neurodifferentiation. Ultimately, these studies will help to better inform policymakers and the public on the neurodevelopmental consequences of lead and cadmium exposures, supporting implementation of necessary changes to promote health equity.

Cross-cultural study on essential moral self

Faculty Mentor: Dorsa Amir

Authors: Shakhrizoda Abdujabborova, Runzi Ma, Julia Smith, Nina Strohminger, Julia Phelps, Dorsa Amir

Abstract:

Many traits make a person who they are, but some traits contribute more to a person's sense of self than others. Previous research has found that morality is more central to the self than other traits, such as memory, perception, personality, and preference. Since previous effects have only been established in the context of the US, our work has extended these findings to 5 more countries with diverse cultural backgrounds. To examine similarities and differences in how people perceive the essential moral self, we surveyed adult participants from the US, Mexico, Colombia, Ghana, India, and the Philippines (with work in China and Kazakhstan in progress). We asked participants to rate the centrality of various traits, and, importantly, allow for cultural variation in moral beliefs by directly measuring perceptions of morality. Despite cultural differences in the concept of the self and beliefs about morality, we found that people around the world consider morality to be central to the self with striking regularity. This suggests that considering morality to be particularly essential to the self may be a universal human tendency.

Use of Neural Conduits and Artificial Grafts for Nerve Repair and Reconstruction

Faculty Mentor: Matthew Becker, Ph.D.

Authors: Sara Abusulb, Yin Mei Chan, Nicola G. Judge, Yang Hu, Rebecca K. Willits, Neill Li, Matthew L. Becker

Abstract:

Peripheral nerve injuries present significant challenges to functional recovery due to limitations in the natural repair processes of the peripheral nervous system and an almost complete absence of regeneration in the central nervous system. The current gold standard for tension-free repair, nerve autografts, is associated with several disadvantages including donor site morbidity, limited tissue availability, and the need for additional surgical procedures. While alternative clinical solutions have been developed, outcomes remain inconsistent, particularly for large nerve transection injuries. This project addresses the limited capacity for full functional recovery following nerve damage by investigating biomaterial-based strategies that exploit innate repair mechanisms and provide directional cues for neurite growth.

This work focuses on the fabrication and evaluation of aligned nanofiber scaffolds functionalized with spatial peptide concentration gradients to induce directional neurite migration. Allyl-functionalized poly(ϵ -caprolactone) (allyl-PCL) nanofibers were fabricated using touch-spinning techniques to produce aligned fibers with controlled diameters. The aligned architecture mimics native nerve tissue and provides topographical guidance for neuronal extension. Scaffolds were subsequently functionalized with laminin-derived YIGSR peptides using thiol-ene click chemistry and UV photomask patterning to generate controlled concentration gradients along the fiber axis. Fluorescence imaging confirmed successful gradient formation and spatial control of peptide presentation across the scaffold.

To evaluate biological response, neurons differentiated from mouse embryonic stem cells and primary Schwann cells were cultured on gradient-functionalized scaffolds. Neurons were seeded at the low-concentration end of the gradient and cultured over multiple time points to assess directional neurite outgrowth. The combination of aligned nanofiber topography and biochemical gradients was designed to provide both contact guidance and haptotactic cues, promoting directional neurite extension. Scaffold morphology and fiber diameter were characterized using scanning electron microscopy, while immunohistochemistry and fluorescence imaging were used to quantify neurite outgrowth and cell migration.

These findings support the use of gradient-functionalized nanofiber scaffolds as a promising strategy for enhancing nerve regeneration. By combining topographical alignment with biochemical signaling, this approach aims to improve directional neurite growth and accelerate functional recovery following peripheral nerve injury. This work highlights the potential of engineered nanofiber substrates with tethered concentration profiles to bridge gaps in current nerve repair strategies and advance biomaterial design for neural tissue regeneration.

Comparing Dedicated Ventilation and Gas Exchange Scans for Lung Ventilation with ^{129}Xe MRI

Faculty Mentor: David Mummy

Authors: Anurag Anugu, Kunyu Du, Bastiaan Driehuys, David Mummy

Abstract:

Hyperpolarized ^{129}Xe MRI allows for the visualization of regional lung ventilation. Traditionally, ventilation has been measured using a dedicated ventilation scan requiring a full xenon dose. More recently, ventilation has also been measured with a gas exchange scan that captures both ventilation and gas exchange with a single dose. This combined method can obtain information that would otherwise require multiple doses, but at the cost of reduced image resolution and potentially lower signal-to-noise ratio (SNR). This study evaluated whether the combined gas exchange scan provides ventilation measurements that are comparable to a dedicated ventilation scan. Ventilation defect percent (VDP), which represents the percentage of the lung that is poorly ventilated, is an important quantitative biomarker in the field of hyperpolarized ^{129}Xe MRI. We compared VDP between the two scan types using two normalization methods: standard 99th percentile rescaling (VDP-99), which normalizes the ventilation distribution between 0 and 1 for each scan, and a fractional ventilation method (VDP-FV) that additionally accounts for the amount of inhaled xenon gas when creating a subject's ventilation distribution. Data from 49 participants with idiopathic pulmonary fibrosis were analyzed. Subjects with incomplete inhalation, significant metal artifacts, or SNR <10 were excluded. VDP was defined as the percentage of the histogram with values \leq (mean - 2 SD) of a young healthy reference population. Agreement between methods was assessed using Bland-Altman analysis. Bland-Altman analysis (Gas Exchange Scan - Dedicated Ventilation Scan) of VDP-99 showed a mean bias of -7.2% (95% limits of agreement: -24.8% to 10.4%). For VDP-FV, the mean bias was 10.9% (95% limits of agreement: -8.2% to 30.0%). Agreement was moderate for VDP-99 and weaker for VDP-FV, with the gas exchange scan showing reduced sensitivity to VDP in VDP-99 and higher VDP values in VDP-FV. These results suggest that while a gas exchange scan is sufficient for general assessment of lung function, a dedicated ventilation scan may still be necessary for detecting subtle ventilation defects.

Striatal Cell Type-Specific mGluR5 Protein Interactions Underlying Levodopa-Induced Dyskinesia

Faculty Mentor: Nicole Calakos, M.D., Ph.D.

Authors: Andrew Bae, Cameron Morris, Zachary Caffall, Nicole Calakos

Abstract:

Parkinson's disease (PD) affects over 10 million people worldwide and is characterized by the progressive loss of dopaminergic neurons in the substantia nigra pars compacta, leading to debilitating motor dysfunction. While levodopa (L-DOPA) remains the gold-standard treatment, approximately 80% of patients develop levodopa-induced dyskinesia (LID) in the advanced stages of the disease, which is characterized by involuntary, purposeless movements that severely diminish quality of life. Emerging evidence implicates metabotropic glutamate receptor 5 (mGluR5) as a key mediator of motor dysfunction in PD, including LID. Recent mechanistic studies suggest LID is accompanied by cell type-specific changes in mGluR5 protein complex in striatal direct and indirect pathway projection neurons (dSPNs and iSPNs, respectively). However, no tool to date has had the capability to exhaustively map mGluR5's cell type-specific proteome in a healthy and pathological environment. Here, we employ a novel mGluR5-BioID proximity labeling mouse model to map mGluR5's proximal proteome specifically within dSPNs and indirect pathway neurons (iSPNs) under conditions that drive LID. Mice underwent unilateral 6-OHDA lesioning of the medial forebrain bundle to replicate dopaminergic denervation, followed by 21 consecutive days of levodopa treatment. Successful PD modeling and LID induction were confirmed biochemically via substantial tyrosine hydroxylase loss in lesioned hemispheres and behaviorally via abnormal involuntary movement (AIMs) scoring and DANNC markerless 3D turning analysis. Neutravidin pulldowns confirmed Cre-dependent enrichment of biotinylated mGluR5-proximal proteins in both dSPN and iSPN cohorts, and samples have been submitted for mass spectrometry-based proteomics. These findings establish a validated experimental pipeline for the first cell type-resolved map of the mGluR5 proximal proteome in a LID model, with proteomic analyses anticipated to generate testable hypotheses for novel therapeutic targets to reduce dyskinesia severity in PD patients.

Social Experience Effects Sleep Behavior Through the Olfactory System

Faculty Mentor: Pelin Volkan, Ph.D.

Authors: Efe Balkanli, Ashley Jia, Pelin Volkan

Abstract:

Social interaction plays a fundamental role in shaping our thoughts, actions, and overall health. To study the effect of social isolation, we use the fruit fly *Drosophila melanogaster* as our model organism because of its conserved molecular and circuit mechanism and genetic accessibility. Previous data in the Volkan Lab and other labs shows that socially isolated fruit flies show a reduction in sleep behavior compared with socially enriched flies. To investigate the molecular and circuit mechanism of this sleep change, this project investigated the role of the olfactory system in regulating sleep behavior during social isolation. Specifically, Orco is an essential component of insect odorant receptor complexes, required for proper olfactory signaling, including pheromone detection. To investigate how loss of olfactory input influences sleep behavior, we analyzed Orco loss-of-function mutants for two independent Orco alleles Orco1 and Orco2. We find that both Orco mutants reduce daytime sleep difference between GH and SH flies observed in wild type. Specifically, SH shows a general increase in daytime sleep to match with the GH. Additionally, nighttime sleep differences observed in control flies are abolished in Orco mutants. Together, these results demonstrate that olfactory signaling, likely through pheromone-mediated social interactions, contributes to the regulation of sleep architecture and activity in *Drosophila*. Loss of Orco function reduces sensory input that normally promotes wakefulness, leading to increased sleep consolidation and decreased behavioral variability in terms of sleep.

Cardiac GRK2 Drives Adipose Remodeling through Dysregulated Lipolysis and Insulin Signaling in Heart Failure

Faculty Mentor: Dr Walter Koch

Authors: Aliza Bochner, Stephanie Kereliuk, Maya Hoteit, Eve Melbouci, Rajika Roy, Walter J. Koch

Abstract:

Heart failure is increasingly recognized as a systemic disease in which cardiomyocytes secrete signaling factors that influence adipose tissue function and systemic metabolic regulation during cardiometabolic stress. G protein-coupled receptor kinase 2 (GRK2), a key regulator of β -adrenergic receptors in the heart, is upregulated during cardiac stress, yet its role in heart-adipose communication remains unclear. Understanding how cardiac GRK2 influences systemic adiposity and insulin signaling may uncover new therapeutic strategies for cardiometabolic disease. We hypothesized that cardiac GRK2 regulates adiposity and insulin signaling during cardiometabolic stress in a sex-specific manner. Using a pressure overload-induced heart failure model, sex-dependent alterations in white adipose tissue (WAT) were observed. Male mice with heart failure exhibited reduced WAT depots, whereas female mice showed no significant changes. WAT from male mice in heart failure displayed adipocyte hyperplasia and impaired lipolytic responses *ex vivo* compared to controls. Under lipolytic and anti-lipolytic conditions, regulation of lipolysis was assessed through phosphorylation of hormone-sensitive lipase (HSL) at three PKA-mediated serine sites, while anti-lipolytic signaling was evaluated through protein kinase B (AKT) and phosphodiesterase 3B (PDE3B). Additional markers of adipocyte regulation, perilipin and adiponectin, were also examined. Cardiac GRK2 overexpression in heart failure dysregulated total HSL, HSL Ser563, and AKT signaling, suggesting that cardiac GRK2 influences lipid substrate mobilization and adipose lipolytic regulation. These findings indicate that cardiac GRK2 contributes to heart-adipose crosstalk during heart failure and modulates adipose function, contributing to dysregulated lipid metabolism during cardiometabolic disease.

Quantifying Contractility in Human Cardiac Organoids

Faculty Mentor: Dr Ravi Karra

Authors: Mya Booth, Anneka Beard, Michael Thomas, Lauren Parker, Ravi Karra

Abstract:

Heart failure is a leading cause of morbidity and mortality worldwide, in large part due to the limited regenerative capacity of the adult mammalian heart. Myocardial infarction is characterized by the loss of cardiomyocytes and replacement with fibrotic scar tissue, which contributes poorly to overall contractile function. In recent years, human induced pluripotent stem cell (iPSC)-derived 3D approximations of human cardiac tissue, such as human cardiac organoids (hCOs), have become popular platforms to model human cardiac pathophysiology. However, methods for quantifying contractile function in hCOs remain limited. To address this gap, we developed an analysis pipeline to quantify hCO contractility using brightfield imaging. Briefly, videos of spontaneously beating hCOs are recorded, and hCO area is segmented to plot hCO area versus time. We performed peak analysis to extract contractile parameters, including area displacement (μm^2), time to peak (s), and contraction velocity ($\mu\text{m}/\text{s}$). While these metrics provide a useful description of contractile dynamics, they do not directly capture contractile force. A limitation in estimating force in hCOs is that they are maintained in suspension culture, where they are not subject to external mechanical load. To overcome this, we propose introducing a tunable mechanical environment by embedding hCOs in alginate-based hydrogels of defined stiffness. We hypothesize that constraining hCO contraction within matrices of increasing stiffness will reduce contractile deformation in a manner that reflects the underlying force-generating capacity of the tissue. To establish feasibility, we generated alginate hydrogels with tunable mechanical properties by varying the concentration of calcium gluconate between 0.3–1% and ratio of alginate between 0:1 and 1:1. Bulk viscoelastic properties were characterized by rheometry, yielding hydrogels spanning a range of viscosities between 10.32–202.44 mPa·s. In ongoing work, hCOs will be embedded within hydrogels of defined stiffness, and contraction-induced area changes will be quantified using our imaging pipeline. By relating matrix stiffness to displacement, we aim to generate a stiffness–deformation relationship that can be used to estimate relative contractile force. Together, this platform establishes a scalable and quantitative framework to study how mechanical environment influences cardiac contractile function in human organoid systems.

Investigating Mitogen-Driven ERK Signaling in Human Cardiac Organoids

Faculty Mentor: Dr Ravi Karra

Authors: Alena Brandt, Lauren Parker, Michael Thomas, Ravi Karra

Abstract:

Heart disease is a leading cause of death in the United States, in part due to the adult human heart's limited regenerative capacity. Although multiple cardiac mitogens are thought to promote heart regeneration in zebrafish and neonatal mammals, none of these factors have been translated into effective therapeutics for the injured human heart. Several putative mitogens, including vascular endothelial growth factor (VEGF), neuregulin-1 (NRG1), and insulin-like growth factors 2 (IGF-2), are thought to act through the ERK signaling pathway to coordinate a downstream cardiac regenerative program. However, it is unclear how different cardiac mitogens differentially modulate ERK signaling and whether these differences contribute to the potency of cardiomyocyte cell-cycle re-entry. To study mechanisms of ERK signaling in human heart tissue, we generated a lentiviral construct ubiquitously expressing a modified ERK-specific kinase translocation (modERK) sensor. When adding epidermal growth factor (EGF) to HEK293T cells transfected with the modERK sensor and imaging for relative fluorescence intensity units (RFU), we found that increasing concentrations of EGF resulted in an increasing nuclear GFP intensity (0.1 μ M EGF: 0.09973 RFU \pm 0.0054, 100 μ M EGF: 0.1141 RFU \pm 0.0042, $p = 0.0233$, mean \pm SD). This suggests that the modERK sensor can be used to monitor nuclear ERK activity. Subsequently, we have now generated monoclonal induced pluripotent stem cell (iPSC) lines expressing the modERK construct and successfully been able to differentiate them into iPSC-derived cardiomyocytes (CMs) and three-dimensional iPSC-derived human cardiac organoids (hCOs). These tools will provide a model to study ERK dynamics with live imaging in human cardiac tissues. By studying differences in ERK signaling with different cardiac mitogens, we will hopefully identify common and divergent downstream signaling biases that can be used to optimize therapeutic cardiomyocyte proliferation.

Antecedents of a tendency to become overinvolved

Faculty Mentor: Dr James Shah, Ph.D.

Authors: Maria Brown, Skyler Wyly, Rick Hoyle, James Shah

Abstract:

Participation in cocurricular activities cultivates college students' satisfaction with the college experience and can promote opportunities for learning and cognitive development. However, overinvolvement in activities is related to increased feelings of stress and burnout due to a perceived effort-reward imbalance. The present study examines how motivational factors, such as a desire for approval and future rewards, influences students' effort and leads to overinvolvement. We propose the internal factors driving overinvolvement are intrinsic motivation for challenge seeking and coping by distraction, while external factors include parental expectations and pressures, and a desire to appear competent to peers. The impact of overinvolvement on stress is also analyzed. Data for the first analysis comes from a 4-year longitudinal study of students' resilience and well-being (N = 1,469), that focuses on undergraduates' propensity for overinvolvement. Students with high levels of academic challenge motivation and parental pressures have a greater tendency to become overinvolved. A greater tendency to become overinvolved and a desire to avoid being negatively perceived by one's peers increase student stress levels. These motivational factors may have significant implications for how student stress can be reduced through changes in students' motivational sources.

Motivation control beliefs and their impact on regulatory strategy use during goal pursuit

Faculty Mentor: Dr James Shah, Ph.D.

Authors: Elizabeth Buduen, Skyler Wyly, Maria Brown, Carlie Scheer, Sunny Zhu, Zhuying Guo, & James Shah

Abstract:

Extending research on the significance of individuals' implicit beliefs for goal pursuit and self-regulation, these studies examine how individuals' beliefs about the nature of motivation and the control they have over it may impact self-regulation and overall well-being. More specifically, we examine how beliefs about the controllability of motivation might relate to the motivational strategies one uses to increase or maintain motivation, as well as the longer-term benefits of controlling motivation for persistence and well-being. Study 1 (N = 405) suggests that motivation control beliefs promote positive self-regulatory behaviors and well-being. In addition, motivation control beliefs (mediated by implementation intentions if-then planning) predict flourishing, grit, and work-life balance. Study 2 (N = 304) suggests that belief in the controllability of motivation increases use of self-regulatory strategies when pursuing goals and this effect was not moderated by individuals' capacity for self-control. Study 3 (N = 274) suggests that belief in the controllability of motivation increases persistence in a behavioral measure of motivation using an anagram task.

Cellular stress alters the localization of exon–junction core proteins, MLN51 and EIF4A3

Faculty Mentor: Christopher Nicchitta, Ph.D.

Authors: Ekaterina Buzina, Celeste Marin, Christopher Nicchitta

Abstract:

Stress granules (SGs) are dynamic cytoplasmic ribonucleoprotein (RNP) assemblies that form in response to cell stress. SGs are composed of mRNPs, translation factors, RNA binding proteins, and a subset of the mRNA transcriptome. Although stress granules are a conserved feature of the cellular stress response, the molecular determinants that specify which mRNAs are recruited to SGs are not well understood. Previous studies revealed that mRNA recruitment to stress granules is disrupted by transcriptional inhibition, raising the possibility that nuclear mRNA processing events influence stress granule targeting. In light of this finding, this work explores whether components of the exon junction complex (EJC), a multiprotein complex which is deposited at mRNA splice sites co-transcriptionally, contributes to the SG mRNA recruitment process. Preliminary data indicate that of the four primary EJC components two, MLN51 and EIF4A3, localize to SGs during cell stress. In contrast to eIF4A3, MLN51 exhibits very pronounced stress- and transcription-dependent SG localization, suggesting that MLN51 may function independently of the EJC to promote or assist mRNA recruitment to stress granules. Future studies will investigate whether MLN51 serves as a SG “licensing factor”, where MLN51-associated mRNAs are selectively recruited into SGs. These studies are expected to provide insight into the mechanisms that shape stress granule composition and reveal how nuclear history can influence the fate of mRNAs during cellular stress.

Contribution of K⁺ Channels to the Regulation of Forces in D. melanogaster Dorsal Closure

Faculty Mentor: Dan Kiehart

Authors: Sophia Byrd, Katrina Focht, Melissa Sican, Janice Crawford, Daniel Kiehart

Abstract:

Cell sheet morphogenesis is the motion and reshaping of cell sheets that occur during tissue and organ development. Dorsal closure (DC) is a stage during *Drosophila melanogaster* embryogenesis that is a model for cell sheet morphogenesis. DC parallels and informs vertebrate development events including wound healing, neural tube formation, heart closure, palate formation, and gastrulation. During DC, two lateral epidermal sheets migrate dorsally and zip together at the canthi, enclosing the amnioserosa cells, a layer of squamous epithelium bordered by an actin-rich purse-string cable. A force imbalance governs the progression of the purse strings toward the dorsal midline of the embryo. Forces exerted on the purse strings by the amnioserosa and tension in the purse strings favor closure, while forces exerted on the purse string by the bulk of the lateral epidermis oppose closure— together they contribute to the net force responsible for closure. Previous experiments by Saias et al. suggest that individual amnioserosa cell volume shrinkage regulated by K⁺ channels generates a force that causes the amnioserosa to shrink (see Saias et al. (2015) in *Developmental Cell* 33(5), 611–621). Tetraethylammonium chloride (TEA) is a cationic K⁺ channel blocker. Dechorionated embryos were stripped of their vitelline envelopes (“peeled”) and TEA was administered in an isotonic buffer using perfusion. Saias et al. used microinjections to deliver TEA, limiting the ability to accurately evaluate dose, assuming even diffusion of TEA from the injection site, and precluding the ability to analyze TEA washout. Here we use live time-lapse confocal microscopy to observe the effects of TEA applied to peeled embryos. A UAS-GAL4 construct expresses free GFPs in the cytosol of amnioserosa cells and marks the cell outlines with RFPs (labeling cadherin). Changes in individual cell volume will be measured with changes in the GFP fluorescence intensity. Data collection is ongoing. Understanding the role of ion channels in force generation and how such changes are coordinated with actomyosin based contractions and stored elasticity during dorsal closure is expected to have applications in wound healing and developmental biology in vertebrates.

The bitter choice: a gut sense for medicine

Faculty Mentor: Diego Bohorquez, Ph.D.

Authors: Kayla Cao, Naama Reicher, Diego Bohórquez

Abstract:

Sickness alters feeding behavior—a phenomenon that many have experienced anecdotally and observed scientifically. Multiple animal species have been observed favoring medicinal compounds to treat illness despite their bitter taste. Food choices are driven by taste sensing in the tongue and chemosensation in the gut, where specialized sensory neuropod cells that connect the gut to the brain in one synapse detect nutrient signals to guide feeding decisions. However, how these sensory systems respond to medicinal compounds in health and sickness remains unexplored. The majority of medicinal compounds activate bitter taste receptors, which are located on both the tongue and in the gut. Although we know what bitter taste receptors signal in the tongue, their role in the gut is unknown. Therefore, I hypothesize that the expression of bitter taste receptors in the gut is altered during sickness, positioning the gut as a critical site for medicinal sensing. In order to explore how sickness affects bitter taste receptor expression, Real-Time quantitative PCR (RT-qPCR) was conducted in tongue taste cells and gut neuropod cells following lipopolysaccharide (LPS)-induced sickness. While no expression changes occurred in tongue taste cells, neuropod cells in the proximal small intestine displayed significant downregulation of bitter taste receptors. To examine how these molecular changes impact behavior, we employed the same sickness model in mice and tracked their voluntary consumption of food, water, and water supplemented with ibuprofen, a nonsteroidal anti-inflammatory drug (NSAID) that reduces inflammation. LPS-injected mice displayed significant decreases in feeding and drinking. However, when ibuprofen was supplemented in the drinking water, LPS-injected mice drank more and consumed food at levels comparable to healthy controls. Taken together, these results demonstrate a gut-specific mechanism in which sickness suppresses bitter taste receptor expression in neuropod cells. This mechanism may be tied to a behavioral shift in which sick mice increase consumption of a medicinal compound, restoring feeding behavior to healthy levels. This project is critical for understanding how sickness alters chemosensation, potentially revealing fundamental mechanisms governing how animals medicate during sickness.

Combining CLUVENA and SDF Nanoparticles for Promoting a Pro-Repair Environment Post-Stroke

Faculty Mentor: Tatiana Segura

Authors: Angela Quintanilla-Capawana, Jeremy Thomas, Tatiana Segura

Abstract:

Ischemic stroke causes a cascade of oxidative stress and cell death that drives irreversible tissue damage and limited endogenous regeneration. Some of the major drivers include insufficient angiogenesis and axonogenesis within the infarct core. Biomaterial-based therapies offer a promising strategy to promote tissue repair by locally delivering pro-regenerative cues. In this work, we investigate a combinatorial biomaterial platform that integrates stromal cell-derived factor (SDF-1 α) and vascular endothelial growth factor (VEGF) within microporous annealed particle (MAP) hydrogels. SDF-1 α , a chemokine that recruits progenitor cells, has been previously shown to result in perfused vessels through the stroke core. It is immobilized on heparin-based nanoparticles to enable sustained presentation. VEGF has also been shown to prompt angiogenesis and is delivered in a clustered format (CLUVENA) to enhance receptor activation and pro-repair signaling. This formulation is designed to modulate immune responses, promote tissue repair, and improve functional recovery post-ischemic stroke.

Defining the Roles of U12 Intron–Containing Genes in Zebrafish Lysosome–Rich Enterocytes

Faculty Mentor: Daniel Levic, Ph.D.

Authors: Claudia Carugati, Andressa Pacheco Czaikovski, Michel Bagnat, Daniel S. Levic

Abstract:

In the developing mammalian gut, dietary proteins are internalized by cells lining the small intestine and are digested intracellularly. This process is mediated by a specialized population of intestinal cells called lysosome–rich enterocytes (LREs), which are essential for growth and survival. LREs are also found in stomachless fish, such as zebrafish. Our previous work showed that LREs internalize dietary proteins via an apical endocytic pathway mediated by a multi–ligand protein complex. However, the regulatory networks that control LRE function are still not well understood. Through a forward genetic screen, our lab identified a zebrafish mutation affecting the *pdcd7* gene, which encodes a subunit of the minor spliceosome. Mutants exhibit widespread U12–type intron retention and reduced protein uptake by LREs. The relationship between U–12–type intron–containing genes and LRE function has not been previously explored. To uncover molecular drivers of these defects, we conducted transcriptomic analysis and identified a subset of U–12–type intron–containing genes that are predicted to regulate LRE endocytosis and trafficking. Among these genes, I have focused on *vps52* (Vacuolar Protein Sorting–Associated Protein 52), which encodes a conserved protein involved in vesicular transport and recycling between the trans–Golgi network, endosomes, and plasma membrane. I found that *Vps52* is necessary for the correct localization of endocytic machinery at the apical membrane of LREs. To test whether this mislocalization phenotype is caused by impaired plasma membrane recycling, I developed a pulse–chase assay to quantitatively examine protein endocytosis and recycling in LREs using apical cell surface biotinylation. I found that apical membrane proteins are recycled within 30 minutes and that the kinetics of recycling and vacuolar trafficking of protein cargos are coordinated. This assay is currently being used to examine the roles of *vps52* and other candidate genes in the internalization and recycling pathways of LREs. Overall, these findings are important for describing mechanisms of dietary protein absorption and utilization during neonatal development to better understand protein malabsorption syndromes.

Interleukin-7 Reshapes Multilineage Hematopoietic Recovery Following Radiation Injury

Faculty Mentor: Benny Chen, M.D.

Authors: Thomas Chang, Yiqun Jiao, Meihong Cai, Yujing Zou, Sadhna O. Piryani, Benny J. Chen

Abstract:

Opportunistic infection remains a major cause of mortality after hematopoietic radiation injury due to depletion of innate and adaptive immune cells. NT-17, a long-acting recombinant human IL-7 is a critical cytokine for T-cell development. Previous work from the Chen Lab demonstrated that NT-17 enhances T-cell recovery after radiation injury. However, its effects on myeloid lineage cells are not clear.

To study the effects of NT-17 on myeloid cell recovery post-irradiation, mice received total body irradiation followed by NT-17 treatment (10 mg/kg) at 24 hours and days 7, 14, and 21. Complete blood counts were then followed over time. The results demonstrated that NT-17 accelerated neutrophil and monocyte recovery while transiently delaying erythroid and platelet regeneration. These effects were consistent across radiation doses, sexes and age groups from juvenile to senior, suggesting a robust, conserved mechanism.

To test whether these responses depend on lymphoid cells, hematopoietic recovery was assessed in lymphoid-deficient strains. In Rag1^{-/-} mice (lacking T and B cells) and Nude mice (T-cell deficient), neutrophil and monocyte counts increased while red blood cells and platelets stagnated, indicating direct effects on progenitors. μ MT⁻ mice (B-cell deficient) exhibited wild type trends while NSG mice (lacking T, B, and NK cells) had no observed effects on platelets and B220 low. These findings confirm that NT-17's hematopoietic effects could be independent of lymphoid influence.

These results reveal that NT-17 promotes hematopoietic recovery through both direct progenitor modulation and indirect immune pathways. NT-17 promotes myelopoiesis stimulating cytokines and does not directly inhibit erythroid or platelet production. Ongoing single-cell RNA sequencing will delineate the transcriptional programs governing IL-7's multilineage effects, advancing its potential as a therapeutic to enhance hematopoietic regeneration after cytotoxic injury or transplantation.

Novel Optical Parallelized Diffuse Correlation Spectroscopy Distinguishes Task-Specific Prefrontal Cortical Activity

Faculty Mentor: Scott Huettel

Authors: Akhilesh Chegu, Lucas Kreiss, Paul McKee, Melissa Wu, Roarke Horstmeyer, Scott Huettel

Abstract:

Non-invasive optical imaging measures physiological markers of brain activity at high temporal resolution, with fewer restrictions, and at a lower cost than traditional neuroimaging techniques. Here we explore the potential of a new technique, Parallelized Diffuse Correlation Spectroscopy (PDCS), which measures the scattering of near-infrared light using a single-photon avalanche diode (SPAD) array. Fluctuations in the resulting speckle patterns create a calculated blood flow index (BFI) that provides insights into capillary perfusion, often underestimated by traditional absorbance-based techniques. Building on prior work distinguishing prefrontal cortex (PFC) blood flow in resting vs. task-activated states, this study evaluates PDCS' ability to differentiate PFC activation across executive functioning tasks. Participants completed a Go-No-Go task (targeting the right inferior frontal cortex [RIFC]) and a Verbal Fluency Task (VFT; targeting the left inferior frontal cortex [LIFC]) while PDCS measured regional cortical blood flow. Results were compared to functional near-infrared spectroscopy (fNIRS), a well-established technique that tracks cortical blood oxygenation via light absorption. PDCS data revealed distinct task-specific activation: Go-No-Go increased RIFC activation relative to LIFC and VFT, while VFT increased LIFC activation relative to RIFC and Go-No-Go. These findings demonstrate PDCS' sensitivity to subtle, region-specific neural activity, supporting its potential as an effective tool for optical blood-flow neuroimaging.

Early-life Sugar Drives Plasticity in Gut-Brain Connections

Faculty Mentor: Diego Bohorquez, Ph.D.

Authors: Inhee Cho, Zachary Lorsch, Diego V. Bohórquez

Abstract:

Early food exposure drives lifelong dietary preferences. Sugar is a food highly palatable to humans, and early exposure to sucrose has been associated with higher rates of metabolic and chronic disease. However, it is unclear if these conditions arise due to the early sucrose itself, or if early-exposure predisposes individuals to consume more sugar as adults. While historically attributed to oral mechanisms, recent evidence shows that the gut may play a role in sugar reinforcement. Neuropod cells are gut sensory cells that rapidly signal from gut to brain via the vagus nerve. These cells are activated by luminal sugar and can lead to sugar preferences in the short-term. However, whether neuropod cells play a role in long-term dietary preference is unknown, and the prevailing dogma about rapid turnover of gut epithelial cells (3-5 days) has limited exploration of neuropod cells in this context. Preliminary data from our lab has identified a population of neuropod cells that survive up to 6 months in mice. Interestingly, these “long-lived” neuropod cells are more likely to be in proximity with vagal nerve fibers. As such, we hypothesize that long-lived neuropod cells are a viable template for long-term sugar preference via gut-brain pathways. Here, I explore whether neuropod cell activation by sugar increases connections with vagal neurons and facilitates survival. To test this, I exposed mice to excess sugar in the post-weaning adolescent period and analyzed the number of long-lived neuropod cells and their synaptic contacts 24 days later. I found a sex-specific effect of this exposure whereby male, but not female mice had more long-lived neuropod cells in proximity to vagal neurons following early-life sucrose exposure. These mirror our behavioral findings that early-life sugar exposure increases sugar preference in male, but not female mice and provides additional evidence that early-life sugar exposure can modify neuropod cells to lead to a durable sugar preference.

Functional Expression and Ligand Screening of the Mosquito Odorant Receptor AgOR48

Faculty Mentor: Hiroaki Matsunami, Ph.D.

Authors: Kate Junehyo Choi, Rhodry Brown, Hiro Matsunami

Abstract:

Insects such as *Anopheles gambiae*, the mosquito that transmits malaria, rely heavily on their sense of smell to locate hosts and respond to environmental cues. These behaviors are mediated by odorant receptors (AgORs), which function as ligand-gated ion channels made up of a tuning receptor and the conserved co-receptor ORco. A major challenge in studying modern insect odorant receptors is that they do not express well in heterologous cell culture systems, which makes it difficult to test many potential ligands efficiently. Although AgOR48 has shown some ligand responses in the empty neuron system, that approach requires generating a new transgenic fly for each receptor or mutant, making broader functional analysis slow and labor-intensive. The primary goal of this project is to establish conditions that allow reliable functional expression of modern insect ORs in cell culture, using AgOR48 as a working model. Once established, this system can be used to better understand the structure and function of these receptors and to more efficiently test candidate ligands. Preliminary experiments indicate that successful expression depends on finding the correct balance between AgOR48 and ORco to ensure proper trafficking, channel formation, and stability. Lower expression levels of AgORco (1/9x, 1/27x, and 1/81x) produced clear activity, whereas higher concentrations did not yield detectable responses, suggesting that overexpression destabilizes the receptor complex. These results emphasize the importance of optimizing the OR:ORco ratio for functional activity in vitro. Using these optimized conditions, I will perform ligand screening assays to identify compounds that activate AgOR48. In parallel, I will generate a three-dimensional structural model of AgOR48 using AlphaFold3 to predict potential ligand-binding sites and help interpret functional results. Establishing a workable cell-based expression system for AgOR48 will make it possible to study ligand interactions more efficiently and will contribute to a broader understanding of modern insect odorant receptor function.

How People Conceptualize Class Privilege: The Haves and The Have Nots

Faculty Mentor: Maureen Alyson Craig

Authors: Taylor Dannis, Ilayda Orhan, Riana M. Brown, Maureen A. Craig

Abstract:

As economic inequality in the United States continues to rise, disparities in access to resources, opportunities, and power increasingly shape individuals' life outcomes. Yet, research examining how people conceptualize different types of class privilege and inequality is scarce. We posit that privileges can be of two types: prescriptive—advantages that everyone should have—and proscriptive—advantages that no one should have. To test whether people think about privileges as prescriptive and proscriptive, in Study 1, participants were asked to list things that everyone should have and things that no one should have. Text analysis of the open-ended responses revealed that participants generated distinct examples of prescriptive and proscriptive class privileges. Common prescriptive privileges included access to healthcare, education, and food, whereas common proscriptive privileges included excessive possessions, evading the law, and political influence. In Study 2, participants were asked to generate examples of economic inequality more broadly. The most common examples for economic inequality were healthcare, education, wage gap, and housing, which more closely align with our conceptualization of prescriptive (rather than proscriptive) privileges. Participants often framed these in terms of what people should have access to (affordable healthcare or high quality education) instead of what they should not have access to. Our results find compelling initial evidence for individuals being able to think about privilege and inequality through a prescriptive–proscriptive framework and that thinking about prescriptions, in particular, may be prevalent.

Developing High Verdet Constant Carbon Nanotubes Materials for Magneto-Optic Function

Faculty Mentor: Michael Therien, Ph.D.

Authors: Sicheng Ding, James A. Alatis, Xin-Yi Ye, Andrew Ploskunak, Riley H. Stephenson, Peng Zheng, David N. Beratan and Michael J. Therien

Abstract:

The Faraday effect, defined as the rotation of linearly polarized light in the presence of an applied magnetic field, is governed by the Verdet constant, a key parameter describing magneto-optical response. Conventional magneto-optical materials often exhibit poor performance in the short-wave infrared (SWIR) region or depend on heavy metals and rare-earth elements, resulting in high cost and limited scalability. Therefore, the development of lightweight, flexible materials with large Verdet constants and strong SWIR activity is of considerable interest for next-generation magneto-optical technologies. Herein, we report the design and synthesis of single-walled carbon nanotube (SWNT)-based hybrid materials with enhanced magneto-optical properties. To identify optimal nanotube backbones, aqueous two-phase extraction (ATPE) was employed to separate semiconducting SWNTs (s-SWNTs) and metallic SWNTs (m-SWNTs). Chemical functionalization strategies were further explored to modulate the electronic structure of SWNTs. Reactions involving diazonium salts and [2+2] cycloaddition disrupt the sp^2 carbon lattice, introducing sp^3 defects that generate mid-gap states. These defect sites provide opportunities for stabilizing organic spin centers and tuning electro-optical and magneto-optical behavior. Building on this approach, we aim to incorporate metal bipyridine complexes onto SWNTs via defect-mediated functionalization. The corresponding metal complex precursors have been successfully synthesized prior to nanotube integration. Following functionalization, Magnetic Circular Dichroism (MCD) measurements will be used to quantify Faraday rotation in these SWNT-based hybrid superstructures across different metal centers. By systematically correlating composition, electronic structure, and magneto-optical response, this work seeks to optimize the Verdet constant and establish scalable, carbon-based alternatives to conventional magneto-optical materials for SWIR applications.

Synthesis of $^{15}\text{N}_2$ -diazirine probes for in vivo HP-MR imaging of amino acid metabolism

Faculty Mentor: Qiu Wang, Ph.D.

Authors: Mayah Ding, Eni Minerali, Qiu Wang

Abstract:

Amino acids play critical roles in tumorigenesis, serving as nutrients for biosynthesis of macromolecules, signaling molecules, and supplementation of the Krebs cycle. Thus, visualizing the metabolism of various amino acids in vivo is crucial to better understanding cancer cell metabolism, cancer screening, and identifying possible targets for treatment. While existing probes for amino acid metabolism have been useful, their practical use has been limited due to the concerns on sensitivity or stability. This work aims to address these shortcomings through developing novel $^{15}\text{N}_2$ -diazirine tagged amino acid probes, with a focus on glutamine and methionine. These ^{15}N -based probes can be hyperpolarized using dissolution dynamic nuclear polarization (d-DNP), providing a highly sensitive, non-invasive approach to visualizing metabolites in vivo. Successful synthesis of these probes will provide promising new strategies for better cancer imaging, expanding the imaging toolbox for clinical research.

Elevated Plasma p-Tau217 in Tuberous Sclerosis Complex Reveals Biological Convergence with Alzheimer's Disease

Faculty Mentor: Andy Liu, M.D.

Authors: Cynthia Ding, Jocelyn Baumel, Michael Lutz, Andy Liu

Abstract:

Tuberous sclerosis complex (TSC) is a rare autosomal dominant neurodevelopmental disorder caused by loss-of-function mutations in TSC1 or TSC2, resulting in chronic hyperactivation of the mechanistic target of rapamycin (mTOR) pathway. In addition to a wide spectrum of cognitive, behavioral, and psychiatric features collectively termed Tuberous Sclerosis Complex–Associated Neuropsychiatric Disorder (TAND), individuals with TSC can develop progressive cognitive decline in adulthood that shares clinical and pathological features with Alzheimer's disease (AD). Neuropathological studies have shown accumulation of AD-type mixed 3R/4R tau isoforms in adults with TSC, but tauopathy in TSC is characterized by distinct post-translational modifications, regional distributions, and an amyloid-independent pathogenesis. To further explore the biological convergence of TSC and AD, this study compared plasma levels of p-tau217, a sensitive and specific marker of early AD pathology, in 140 TSC and 32 AD patients. Findings revealed elevated levels of plasma p-tau217 in individuals with TSC at younger ages, with a parallel age-related trajectory between TSC and AD cohorts. These results indicate a novel link between TSC and AD that substantiates shared downstream neurodegenerative pathways. Furthermore, these results support the potential utility of p-tau217 as a minimally invasive biomarker for TAND severity, neurodegenerative risk, and AD-like prognosis in TSC and as a tool to guide mTOR-targeted therapeutic strategies.

Learning Life from Novel Reading: Quixotism and Education in Eighteenth-Century Women's Writing

Faculty Mentor: Charlotte Sussman, Ph.D.

Authors: Lily Egol

Abstract:

“Mountains of dirt and trash,” “rank treason against the royalty of Virtue,” and “the most pernicious reading in the world”: in late eighteenth-century England, the novel, then a relatively new literary genre, was widely considered the lowest kind of literature, accused of encouraging dangerously romantic sentiment and transgressive behavior. This discourse was overwhelmingly gendered, concerned with controlling the development of women’s minds by regulating what they read. Yet, this discourse was not merely limited to the simple question of whether or not it was acceptable for women to read novels; instead, it expanded over time to consider what novels are appropriate to read and why, and how to guard inexperienced women against naïve or perilous reading practices. My research explores the involvement of eighteenth-century literary women in this ever-evolving debate over women’s novel reading. This includes both a survey of women-authored conduct books that work to reframe the terms of the debate (works by Hester Mulso Chapone, Sarah Pennington, Catherine Macaulay, Sarah Green, and Ann Wingrove), and analysis of two novels whose themes center on the question of reading. These two novels, Charlotte Lennox’s *The Female Quixote* (1752) and Jane Austen’s *Northanger Abbey* (1817), each center on a naïve, or “quixotic,” protagonist who conflates fiction with reality, and whose eventual education helps to teach the novel’s audience improved judgment. These novels, which investigate and expand on many of the questions suggested by the conduct literature, demonstrate the potential of the novel as an instructive, rather than destructive, genre for the formation of young women’s minds. They teach women rational thought and interpretative judgment that will aid them as they enter the world. I understand these two novels, as well as the women-authored conduct literature, as innovations in an emergent female literary tradition, in which women writers mentor their younger audiences by helping them to negotiate enthusiasm for novels within the conditions of propriety that shaped eighteenth-century women’s lives.

Discovering AI Applications for TBI Care: Qualitative Study of Pressing Care Challenges

Faculty Mentor: Bradley Kolls, M.D.

Authors: Akhil E, Colin Belton, Vivienne Wluka, Brian Lerner, Pranav Manjunath, Yesel Trillo-Ordonez, Chisom Ezigbo, Dylan Rosen, Maya Hoteit, Michelle Moon, Millie Evonlah, Ana Despa, Aparnaa Velayudhan, Blake Passe, Daniel Elsharkawy, Lena Wang, Sophia Saxonhous

Abstract:

Traumatic brain injury (TBI), caused by a physical blow to the brain, affects nearly 5 million Americans annually and is a leading cause of death and disability in young adults. Accurate prognosis and treatment remain challenging due to the complexity of patient data and conditions. We present an exploratory investigation of the challenges facing TBI care in the United States, as well as the potential for Artificial Intelligence (AI) applications to streamline and enable TBI care.

An interdisciplinary team of student researchers conducted interviews with clinicians. This team documented the interviews and conducted a rapid content analysis of the major themes that emerged from them.

Results from these interviews and their analysis reflect the potential AI applications possess to transform the clinical workflow for TBI care. Clinicians struggled with inconsistent documentation and variability in patient outcomes, making TBI management difficult, and they believed AI could enhance workflow efficiency, justify insurance coverage, and aid in predicting early prognosis. Clinicians, however, expressed concerns about trust issues surrounding AI, biases in models, and a lack of AI education among providers.

This work represents a significant practical investigation into the responsible use of AI in high-stakes settings, specifically hospitals and TBI care. Our work, in particular, accounts for the perspectives of clinical providers, who form the core of these settings, and responsible AI must take these stakeholder views into account for ethical model development. This work also clarifies the intricacies of the healthcare system and the data it generates, both of which are essential for developing AI tools that work as intended to streamline and improve care.

Examining the Effects of Electronic Cigarette Vapor on Early Pregnancy Initiation

Faculty Mentor: Dr Margeaux Marbrey, Ph.D.

Authors: Elizabeth Fein, Samuel Cripps, Margeaux W. Marbrey

Abstract:

Electronic cigarette use is increasingly prevalent among reproductive-aged women and is often perceived as a safer alternative to traditional cigarettes, but its effects on fertility and early pregnancy remain poorly understood. Given that approximately one in six people globally experience infertility, investigation of potential reproductive risks associated with e-cigarette use is critical. Early pregnancy is a complex molecular process. In the mouse, blastocysts reach the uterus on day 3.5 of pregnancy and implant between days 4 and 5, a tightly regulated period known as the window of implantation. On day 5, implantation sites undergo decidualization, a process involving differentiation and proliferation to support embryo growth. Any disruption to the precise molecular signaling during these early stages can cause implantation failure. Our previous studies concluded that e-cigarettes delay implantation but were unable to determine whether this was due to a delay in embryo transport to the uterus, a lack of appropriately timed uterine receptivity, or reduced pre-implantation embryo number. Thus, we examined how e-cigarette exposure before and during pregnancy influences pre-implantation embryo number and location, uterine signaling pathways regulating implantation, and post-implantation embryo development. We hypothesized that e-cigarettes delay timely embryo transport to the uterus, decrease the number of available embryos that implant, and impair post-implantation development and decidualization. Mice were exposed via inhalation to e-cigarette vapor or room air before and during pregnancy, and the uterus and embryos were assessed at pre- and post-implantation time points. Embryo number and size were assessed via histological analysis while markers of uterine receptivity, oxidative stress, and decidualization were measured via immunostaining and qRT-PCR. We found that e-cigarettes decrease pre-implantation embryo number (n=8), do not affect the number of available embryos that implant (n=6), and, surprisingly, increase post-implantation embryo development and decidualization (n=6). In addition, e-cigarettes may disrupt embryo spacing and increase oxidative stress in the receptive uterus. Overall, this work contributes to a more comprehensive understanding of how e-cigarette vapor affects early pregnancy and implantation, providing valuable insight for future reproductive research and clinical decision-making related to fertility.

Using Tilmanocept as a molecular marker for diagnosing Cardiac Sarcoidosis

Faculty Mentor: Dr Ravi Karra

Authors: Jacob Fernandez, Rachel Weirnick, Charlie J. Pyle, Mohamed Elganainy, David M. Tobin, Ravi Karra

Abstract:

Sarcoidosis is an idiopathic, life-threatening disease characterized by the presence of non-caseating granulomas composed of macrophages and T-lymphocytes. Since Cardiac Sarcoidosis (CS) manifests with vague cardiopulmonary symptoms, diagnosis is particularly challenging. The gold standard for diagnosing CS is an endomyocardial biopsy, yet this method can be unreliable due to the scattered distribution of granulomas in the myocardium. Technetium-99m-labeled Tilmanocept is a receptor-binding radiopharmaceutical containing multiple mannose groups, which bind selectively to the mannose receptors highly expressed on M2 macrophages. We are interested in the use of Tilmanocept as a specific, non-invasive method for diagnosing CS through its ability to label granulomas. To determine if CD206+ areas were more prevalent in CS, heart tissue from patients with CS and other cardiac inflammatory conditions was compared. Heart tissue was immunostained for CD206 and later analyzed by measuring CD206+ area. Additionally, Cy-5 labeled 10kDa Tilmanocept was resuspended and incubated on heart tissue sections from cardiac sarcoidosis patients, after which binding was assessed. Through this analysis, it was determined that: (1) CD206+ cell density is 15 to 95-fold higher in cardiac sarcoidosis compared to other conditions, and (2) Tilmanocept colocalized with CD206+ cells to specifically mark CS granulomas in tissue sections of multiple patients. These results highlight Tilmanocept's ability to distinguish between CS and other cardiac conditions. Furthermore, it demonstrates Tilmanocept's unique potential to be utilized as a diagnostic for CS through tilmanocept-based imaging.

Comparing AI and Human Evaluation of Trustworthiness

Faculty Mentor: Scott Huettel

Authors: Sara Fernandez, Clara Sandu, Scott Huettel

Abstract:

Artificial Intelligence (AI) models are increasingly relied upon for advice when people make social, economic, and moral decisions. We investigated differences in how humans and a trained AI model evaluated trustworthiness, using data collected during a modified one-shot trust game in which Investees wrote “trust statements” signaling trustworthiness to an Investor. Human advisors (n = 204) and a custom GPT model provided investment advice by assigning trust ratings to these statements and ranking 10 semantic and rhetorical features by importance in the evaluation process. We compared how AI and human advisors ranked these features. Human advisors showed weak but significant concordance ($W_t = 0.153$, $p < 0.001$). Although Wilcoxon signed-rank tests revealed significant, weak agreement between human and AI feature rankings, permutation tests indicated that this agreement did not reliably exceed chance levels, yielding mixed evidence for meaningful alignment. Feature-level analyses revealed systematic differences: Consistency, ethical or moral reasoning, evidence of past trustworthy behavior, explicit commitment to reciprocate trust, feasibility of promises, and transparency were ranked significantly differently by AI and human advisors at the $\alpha = 0.05$ level. These discrepancies may point to specific limitations of current AI social reasoning. Ongoing analyses use natural language processing to test whether self-reported feature rankings predict advisors’ trust ratings when accounting for features identified directly from the text. This will clarify whether observed differences in reported feature rankings reflect true differences in decision-making or inconsistencies in how advisors explain their own judgments.

Automated Deep Learning High Throughput Screening Workflow for Improving Gene Transfection

Faculty Mentor: Fan Yuan, Ph.D.

Authors: Paul Fong, Fan Yuan

Abstract:

Electrotransfection is a widely used method for non-viral gene delivery. To improve its efficiency and the viability of cells post-electrotransfection, we will develop automated, deep learning approaches for optimization of electrotransfection conditions. Our proposed novel technique utilizes a custom lab-on-chip (LOC) platform for ultra-high throughput screening. The LOC utilizes laser-induced graphene (LIG) to generate modular electrodes that can create a carefully controlled electric field. Next, the surface can be treated with plasma and fibronectin to optimize the surface for cell adhesion and growth. Thus, gene delivery to adherent cells cultured on the surface of the device can be completed through electric pulsing. Conditions for electrotransfection can be screened using our device when combined with our high throughput image processing methods, allowing us to develop a predictive model to enhance electrotransfection efficiency.

Uncovering VAMP3-Mediated Host-Parasite Interactions in Liver-Stage Malaria

Faculty Mentor: Emily Derbyshire, Ph.D.

Authors: Chelsea Gan, Michael E. Chirgwin, Emily R. Derbyshire

Abstract:

Malaria remains a global health threat, with over 250 million cases and 600,000 deaths annually. Before progressing to the blood stage, the malaria parasite develops asexually and asymptotically in the liver. Although protein trafficking is critical for parasite proliferation in host hepatocytes, the mechanisms governing vesicle fusion during the liver stage of infection remain unclear. This study aims to elucidate how vesicle fusion is regulated during infection and how Plasmodium may exploit host vesicle-fusion machinery. One proposed mechanism involves hijacking host SNARE complexes, which mediate vesicle fusion with the target membrane. Previous research in our lab has shown that when vesicle-associated membrane protein 3 (VAMP3), a key regulator of endosomal recycling and membrane fusion, was knocked down, Plasmodium exhibited significant decreases in its load and size. Furthermore, VAMP3 is recruited to the parasite vacuole throughout liver-stage infection. We hypothesize that Plasmodium encodes its own SNARE proteins that form SNARE complexes with host VAMP3. To identify potential host-parasite SNARE interactions, we used AlphaFold 3 to model the three proteins required to form the SNARE complex. Models predicting strong protein-protein interactions between host and Plasmodium proteins were validated using co-immunoprecipitation assays. Using HA-magnetic beads, we successfully co-immunoprecipitated five overexpressed *P. berghei* SNARE proteins (PBANKA_0307600, PBANKA_1012900, PBANKA_1346800, PBANKA_1316200, and PBANKA_1418800) with endogenously tagged 2xV5-VAMP3. Current efforts focus on validating the localization of the Plasmodium protein to the parasitophorous vacuolar membrane (PVM), the host-parasite interface where nutrient exchange occurs. Together, these findings reveal a previously underexplored host-parasite interaction and suggest that targeting VAMP3 could be a promising approach to combat malaria.

Dynamics and Stability of Coupled Rotating Magnetic Systems

Faculty Mentor: Thomas Witelski

Authors: Nimaye Garodia, Thomas Witelski

Abstract:

This project investigates the dynamics of a coupled nonlinear system consisting of two rotors, each with three radially oriented permanent magnets. A theoretical framework based on the Euler–Lagrange formulation and point–dipole magnetic interactions was developed to derive equations of motion, which were solved numerically. An experimental setup using 3D–printed components, embedded magnets, and computer vision tracking enabled validation of the model. A novel formulation for induced eddy–current damping was derived and experimentally verified. Results reveal that the globally stable steady–state configuration occurs near a highly unstable arrangement, while a symmetric configuration is only weakly stable and susceptible to finite perturbations. These findings provide insight into the complex behavior of magnetically coupled rotors, with applications in energy harvesting and rotating machinery, and motivate future work on chaotic dynamics and multi–rotor scaling.

Minimal-Action Discrete Schrödinger Bridge Matching for Peptide Sequence Design

Faculty Mentor: Dr Pranam Chatterjee, Ph.D.

Authors: Shrey Goel, Pranam Chatterjee

Abstract:

Generative modeling of peptide sequences requires navigating a discrete and highly constrained space in which many intermediate states are chemically implausible or unstable. Existing discrete diffusion and flow-based methods rely on reversing fixed corruption processes or following prescribed probability paths, which can force generation through low-likelihood regions and require countless sampling steps. We introduce Minimal-action discrete Schrödinger Bridge Matching (MadSBM), a rate-based generative framework for peptide design that formulates generation as a controlled continuous-time Markov process on the amino-acid edit graph. To yield probability trajectories that remain near high-likelihood sequence neighborhoods throughout generation, MadSBM 1) defines generation relative to a biologically informed reference process derived from pre-trained protein language model logits and 2) learns a time-dependent control field that biases transition rates to produce low-action transport paths from a masked prior to the data distribution. We finally introduce guidance to the MadSBM sampling procedure towards a specific functional objective, expanding the design space of therapeutic peptides; to our knowledge, this represents the first-ever application of discrete classifier guidance to Schrödinger bridge-based generative models.

Chewing, Context, and Cognition: Exploring Social–Cognitive and Norm–Violation Frameworks of Misophonia

Faculty Mentor: M. Zachary Rosenthal, Ph.D.

Authors: Eliza Goldstein, Zachary Rosenthal.

Abstract:

Misophonia is characterized by negative emotional and physiological reactions to sounds, most often chewing. These reactions, typically anger, disgust, or anxiety, can lead to avoidance, interpersonal strain, and functional impairment (Swedo et al., 2022). Despite research on misophonia’s clinical features, mechanisms underlying sound–related distress remain unclear. Two theoretical perspectives offer explanations. The social–cognition framework (Berger et al., 2022) proposes that reactions are heightened when sounds are produced by close others rather than strangers, while the norm–violation framework (Norena, 2021) suggests that distress arises when sounds breach cultural etiquette norms. Together, these accounts conceptualize misophonia as not solely a disorder of sensory sensitivity, but one in which social meaning, relational context, and evaluative judgments play a central role. The present study tests these models by manipulating the sound source and etiquette adherence in misophonic and control participants recruited through Prolific. The Duke Misophonia Questionnaire, one of several self–report measures assessing sound tolerance and related traits, will classify participants as meeting misophonia criteria or as controls. All participants then complete a vignette task manipulating social meaning (family member vs. stranger) and etiquette adherence (norm–adherent vs. norm–violating chewing) in a 2 × 2 within–subjects design with conditions matched in length, tone, and grammatical structure. Following each vignette, participants rate subjective distress, emotional arousal, perceived accuracy of the vignette to their lives, and perceived intention and appropriateness. Exploratory analyses will examine whether individual differences in social norms, moral standards, anxiety, and perceived stress moderate these effects. We predict both groups will rate norm–violating chewing as more distressing than norm–adherent behavior, and sounds produced by family members as more aversive than those by strangers, with effects amplified among misophonic participants. The greatest distress is expected for norm violations by family and the least for norm–adherent behavior by strangers, while the intermediate conditions are exploratory. Ultimately, this work aims to clarify why misophonic distress varies across contexts and to identify clinically relevant mechanisms related to interpersonal meaning and norm evaluation.

Characterizing how lipoprotein lipase regulates lipid metabolism in zebrafish

Faculty Mentor: John Rawls, Ph.D.

Authors: Sarah Gorbatov, Jia Wen, John Rawls

Abstract:

Abnormal lipid metabolism contributes to cardiovascular disease. Triglycerides, the primary component of dietary fat, are transported as lipoproteins and metabolized by the rate-limiting enzyme lipoprotein lipase (LPL). LPL is secreted by tissues such as liver, adipose, and muscle and transported to the nearby capillary luminal surface, where it hydrolyzes circulating lipoproteins and releases free fatty acids back to those tissues. Interestingly, in addition to these known Lpl-expressing tissues, our preliminary data reveal that the homolog *lpla* is also expressed in the ileal region of the zebrafish intestine. In mutants lacking the *lpla* inhibitor gene, we observed lipid accumulation in the ileum after high-fat feeding, suggesting that ileum-derived *Lpla* can degrade lipoproteins. However, why the gut produces *Lpla* and whether gut-derived *Lpla* contributes to systemic lipid metabolism remain unclear. To investigate, we created an *Lpla* fluorescent reporter via CRISPR-Cas9 knock-in of the mScarlet fluorophore gene at the *lpla* C-terminus. We are using confocal imaging to assess its general localization and expression levels. In parallel, we generated an *lpla* whole-body knockout mutant and are regionally overexpressing *lpla* using tissue-specific promoters. Ectopic expression in the jejunum lowered serum lipid levels and caused lipid accumulation in the jejunum but not ileum. Our findings indicate that *Lpla* is sufficient to alter systemic lipid levels and that the enzyme acts locally, recruiting fatty acids only to the tissue where it is expressed. Ongoing experiments with the *lpl*-mScarlet reporter and regional overexpression constructs aim to fill in the knowledge gaps, hopefully informing therapies for cardiovascular disease.

Direct SERS Detection of mRNA Cancer Biomarkers Using Spikey Nanorattle Biosensors

Faculty Mentor: Tuan Vo-Dinh, Ph.D.

Authors: Elliot A. Grant, Khang D. Hoang, Joy Q. Li, Supriya Atta, Zimeng Li, Jinjia Zhou, Gabriel D. Kantor, Christina E. Akpan, Tyler Vasse, Walter T. Lee, Tuan Vo-Dinh

Abstract:

Head and neck squamous cell carcinoma (HNSCC) remains one of the most common and lethal malignancies worldwide, originating mucosal epithelium of the oral cavity, pharynx, and larynx. Patient survival is strongly dependent on early diagnosis. In many low- and middle-resource settings, access to conventional molecular diagnostics remains limited due to the cost, complexity, and infrastructure requirements of conventional assays, underscoring the need for rapid, sensitive, and portable detection strategies. Here, we present a plasmonics-enhanced biosensing platform based on spikey nanorattles (SpNR) that enables direct, amplification-free surface-enhanced Raman scattering (SERS) detection of cancer-associated mRNA biomarkers. Our assay targets cytokeratin 14 (KRT14), an epithelial-specific mRNA that is overexpressed in HNSCC and has emerged as a promising diagnostic marker of malignant transformation. Detection is achieved using a magnetic bead-based sandwich hybridization scheme coupled with SpNR engineered in a core-gap-shell architecture to maximize electromagnetic field enhancement and Raman signals from target-bound probes. The resulting platform achieves a limit of detection of 90 femtomolar for KRT14 mRNA, demonstrating exceptional sensitivity without sample amplification. In a pilot study involving clinical tissue samples, the biosensor reliably distinguished HNSCC-positive from HNSCC-negative specimens, underscoring its diagnostic specificity and translational relevance. Collectively, these results demonstrate the feasibility of a highly sensitive, plasmonic assay for nucleic acid detection. By combining ultra sensitivity, simplicity, and portability, this approach offers a practical pathway toward point-of-care molecular diagnostics and highlights the broader potential of plasmonic nanostructures and SERS-based technologies for early cancer detection in resource-limited clinical environments.

Effects of APOE Genotype and GLP-1 on Spatial Learning and Memory in the Morris Water Maze

Faculty Mentor: Alexandra Badea, Ph.D.

Authors: Samantha Gregware, Darius Catrina, Aarushi Singh, Aurora Lu, Jacob Chen, Anjali Tatini, Dhanista Anem, Yu Liang, Ines Poves Acle, Robert Anderson, Alexandra Badea

Abstract:

The $\epsilon 4$ allele of Apolipoprotein E (APOE) is a major genetic risk factor for Alzheimer's disease and has been associated with impairments in spatial learning and memory. Increasing evidence linking metabolic dysfunction, including type 2 diabetes, to Alzheimer's disease has motivated investigation into metabolic pathways influencing neurodegeneration. In particular, GLP-1 receptor agonists, used to treat diabetes, have emerged as modulators of body weight and cognitive function.

This study investigated the effects of APOE genotype ($\epsilon 2$, $\epsilon 3$, $\epsilon 4$), body mass change, and treatment phase on spatial learning and memory using the Morris Water Maze (MWM). A cohort of 27 mice expressing humanized APOE genotypes underwent MWM testing following high-fat diet exposure and GLP-1 treatment. Learning performance was assessed across five training days using total swim distance and spatial strategy (ratio of southwest distance to total distance). Memory was evaluated using probe trials on Day 5 and Day 8. Linear mixed-effects models analyzed learning trajectories, accounting for repeated measures, while generalized linear models assessed probe performance. Body mass change (Δ mass) was calculated as percent change between baseline and post-treatment weights and included in regression analyses.

Mice demonstrated robust learning across training days, with total swim distance significantly decreasing over time (mixed model, $p < 0.001$). Spatial strategy (SW/total distance) also improved ($p < 0.01$), indicating more efficient navigation. No significant differences in learning slope or strategy were observed across APOE genotypes. In probe trials, performance declined from Day 5 to Day 8 (significant main effect of day), suggesting reduced memory retention. No significant genotype effects or genotype-by-day interactions were detected. Body mass change showed weak, non-significant associations with learning slope ($\beta \approx 0.006$, $p = 0.299$) and probe performance ($p > 0.4$). Overall, APOE genotype and body mass change did not significantly influence MWM performance under these conditions, despite clear learning effects over time. These findings suggest limited genotype-dependent behavioral differences following GLP-1 treatment in this cohort. Ongoing work integrates MRI-based neuroimaging analyses, including brain volume quantification and brain age prediction, to assess whether structural changes may reveal genotype- or treatment-dependent effects not captured by behavioral measures.

Investigating the copper-dependent antifungal activity between biologically relevant shortened peptides within the histatin family

Faculty Mentor: Katherine Franz, Ph.D.

Authors: Rohan Guddanti, Mackenzie Smith, Kath Franz

Abstract:

While the ability of histatin-5 (Hist-5), a naturally occurring histidine-rich peptide found in human saliva, to induce cell death in pathogenic yeast such as *Candida albicans* in the presence of copper is well established, the same cannot be said for that of phosphorylated or non-phosphorylated histatin-1 (Hist-1). The present research sought to compare the anti-fungal potency of phosphorylated and non-phosphorylated Hist-1 to Hist-5 by using truncated peptides in cellular antifungal assays with added copper. To achieve this, the first twelve amino acids of Hist-5 (Hist-5(1-12)) and non-phosphorylated Hist-1 (npHist-1(1-12)) were synthesized and purified. The first 12 amino acids of phosphorylated Hist-1 (pHist-1(1-12)) have been synthesized but not yet purified. This work agrees and expands on previous literature demonstrating the anti-fungal potency of Hist-5(1-12) in the presence of copper. However, a protecting effect when over 100 μM of Hist-5(1-12) was introduced to *C. albicans* cells was also observed, even in the presence of excess copper. The npHist-1(1-12) checkerboard assays demonstrate that this peptide has anti-fungal ability comparable to Hist-5(1-12) when high concentrations of peptide and copper are present. Additionally, while the anti-fungal ability of npHist-1(1-12) was enhanced by high concentrations of copper, the anti-fungal ability of the peptide did not seem to have a copper dependency. In fact, unlike Hist-5(1-12), npHist-1(1-12) demonstrates moderate anti-fungal ability in the presence of copper. Finally, npHist-1(1-12) also appears to have a copper protecting effect at concentrations 200 μM , even in the presence of excess copper. The current results demonstrate that npHist-1(1-12) has versatility in promoting both wound healing and *C. albicans* cell death, especially in the presence of copper. Given the high lethality of Candidiasis infection, especially among the immunocompromised, continued research into npHist-1(1-12)'s anti-fungal ability remains extremely important.

A Data-Centric Analysis of the Impact of Training Data Quality vs. Quantity on P300 Brain-Computer Interface Performance

Faculty Mentor: Leslie M Collins, Ph.D.

Authors: Arnav Gupta, Albert Liu, Eliza Haines, Riyadh Alghamdi, Aniketh S. Kota, Leslie M. Collins, Boyla O. Mainsah

Abstract:

The current standard for training brain-computer interface (BCI) machine learning models is user-specific. There is a high interest in developing generic models that are trained on data from other users to minimize BCI calibration time; however, this is limited by noisy, non-stationary brain signals and high inter-user variability. We investigate the trade-off between training data quality and quantity on P300 BCI performance in individuals with amyotrophic lateral sclerosis (ALS) with representative traditional machine learning (stepwise linear discriminant analysis, SWLDA) and deep learning (EEGNet) models. Results show that data quality and domain alignment are more critical than dataset size: user-specific models trained on significantly less data outperformed generic models; generic models trained on ALS data outperformed models trained on non-ALS data; block-averaging of features was mostly detrimental to EEGNet but beneficial to SWLDA; and accounting for inter-stimulus interval differences between ALS and non-ALS data had minimal effect. Our findings highlight the importance of individualized model tuning for reliable P300 BCIs.

Association between health literacy and cancer history with medical trust among adults in the United States

Faculty Mentor: Nosayaba (Nosa) Osazuwa–Peters, MPH, PHD

Authors: Huda Haque, Morgan C. Byrd, Ph.D., Joab Odera, Ph.D., Nosayaba Osazuwa–Peters, Ph.D., M.P.H., B.D.S.

Abstract:

Introduction: Health literacy, the ability to understand health information, shapes health-seeking behaviors. Among individuals with a history of cancer, low health literacy is associated with poor outcomes. In an era of disinformation, examining how health literacy and cancer history interact with trust can elucidate how patients make decisions..

Methods: We analyzed data from the Health Information National Trends Survey (HINTS), a nationally representative dataset, for the 2014, 2018, 2020, 2022, and 2024 cycles. Health literacy (Low: never, rarely, sometimes; High: always), personal cancer history (ever vs. never), and age (18–39, 40–64, 65+) were examined in relation to trust in doctors, family, and religious organizations for medical information (Low: not at all, a little, some; High: a lot). Survey-weighted logistic regression used jackknife replicate weights in R; age interactions were tested using Rao–Scott likelihood ratio tests. Latent class analysis (LCA) identified subgroups characterized by demographics, cancer history, and health literacy. **Results:** Higher health literacy was significantly associated with greater doctor trust (aOR 4.50, 95% CI 3.61–5.60), consistent across age groups and cycles. Cancer history was not associated with doctor trust, and trust did not vary by cycle. For family trust, associations differed by age (interaction $p=0.03$), with greater trust among younger adults with higher health literacy (18–39: aOR 2.02, 95% CI 0.91–4.51). Family trust declined in later cycles (2022 vs. 2014: aOR 0.58; 2024 vs. 2014: aOR 0.56), suggesting COVID–19–related shifts. Cancer survivors were less likely to trust religious organizations (aOR 0.61, 95% CI 0.43–0.87), and older adults were more likely. LCA identified five demographic profiles with distinct trust patterns. The younger, more educated class showed the highest physician trust and lowest religious trust, while the class including more Hispanic or Non–Hispanic Black members showed the strongest family trust. Cancer history was associated with physician trust within one class, suggesting context–dependent effects not captured by regression alone.

Conclusion: These findings highlight how health literacy, cancer history, and demographic context jointly shape trust in health information sources. Targeted outreach strategies addressing these distinct trust profiles may promote informed health decision–making, particularly for cancer survivors and older adults.

Guiding AlphaFold2 to Predict Multidomain Protein Conformations

Faculty Mentor: Dr Phil Romero, Ph.D.

Authors: Ashley Hsu, Mohammed AlQuraishi, and Julia R. Rogers

Abstract:

Protein structures provide valuable insights for understanding biological functions, explaining disease mechanisms, and designing drugs. AlphaFold2 (AF2) has achieved near-experimental success in predicting static protein structures but remains limited in modelling large, multidomain proteins and their alternative conformational states. While AF2 can accurately model stable, conserved domain-domain interactions, it struggles to model transient domain-motif interactions that also govern the equilibrium between the different conformational states of a multidomain protein. Our approach leverages a complementary predictor of domain-motif interactions to guide AF2 to sample these different conformations. More specifically, we translate predicted domain-motif contacts into distance restraints that are incorporated into AF2's distogram inputs to bias model predictions towards a specific conformation. To define these restraints, we curated a dataset of 3,229 domain-motif complexes from the Protein Data Bank and derived domain family-specific distance distributions. Additionally, we explore the use of a custom multidomain multiple sequence alignment to balance evolutionary priors with structural guidance to improve AF2's ability to generate diverse conformational states. We then apply our method to SHP2, a multidomain signaling protein with known autoinhibitory domain-motif interactions. An ability to accurately model conformational ensembles of multidomain proteins has the potential to facilitate the design of novel multidomain allosteric signaling systems and yield mechanistic insights into conformation-altering pathophysiologies.

Inconsistent Outcomes of ABO-Mismatched Kidney Transplantation Due to a Potential ABO Blood Grouping Discrepancy in Nonhuman Primate Model

Faculty Mentor: Jean Kwun, D.V.M., Ph.D.

Authors: Ruoshui Hu, Ashley Dravik, Emma Martin, Janghoon Yoon, Annette Jackson, Jean Kwun

Abstract:

Rhesus macaques (RMs) are commonly used in transplantation research and serve as a relevant model for studying MHC or ABO mismatched organ transplantation. While MHC (MAMU) typing provides definitive information on MHC disparities between donors and recipients, genetic analysis of glycosyltransferases does not reliably determine ABO blood type. The lack of native ABH antigen expression on red blood cells also makes conventional hemagglutination testing unsuitable in nonhuman primate models. This study aims to genetically and serologically confirm the ABO typing (particularly AB) of donor RMs showing variable outcomes of ABO-incompatible (ABOi; AB-to-B) kidney transplantation.

All RMs were genotyped for MAMU and ABO using MiSeq-based amplicon sequencing. Three (3) type B RMs received maximally MAMU mismatched kidney transplantation from AB donors. All recipients received conventional triple immunosuppression (Tacrolimus/MMF/Steroid). Sera from three Type B rhesus recipients (n=3) and their Type AB donors were analyzed using the Bio-Rad ID Gel Card Indirect Antiglobulin Test. Agglutination strength was analyzed with the titer defined as the highest dilution exhibiting a positive reaction. Both donor and recipient sera were tested against A1 and B RBCs to define anti-A and anti-B profiles.

Even with ABOi without desensitization, one animal showed long-term allograft survival. All type B recipients showed the expected anti-A antibody hemagglutination pattern, consistent with the recipient ABO typing result. However, in the case of long-term survival, AB donor showed serologic profiles of the type B which is showing positivity observed in type A cards with anti-A antibody with not anti-B antibody hemagglutination suggested serologic type B expression. The discrepancies between genomic and serologic profiles were consistent in the allograft survival.

The results demonstrated that ABO genotyping based on the glycosyltransferase gene does not fully predict the serologic ABO phenotype, likely due to weakened or absent antigen expression, which may influence outcomes in ABO-incompatible kidney transplantation in NHP models. Incorporating serologic testing alongside genetic typing provides a more accurate assessment of ABO status for studies involving ABO-incompatible transplantation in nonhuman primates.

Establishing Energy Thresholds for Targeted Cherenkov Light Photoactivation

Faculty Mentor: Tim Haystead, Ph.D.

Authors: K. Jha, V. Radosova, L. Bolino, O. Canter, P. Hughes, D. Alcorta, S. Emam, M. Oldham, T. Haystead

Abstract:

Purpose: To simulate how Cherenkov light (CL) produced during radiation therapy can activate targeted photodynamic molecules. To experimentally determine dose and concentration thresholds for biological effects in-vitro.

Methods: HS583, a novel verteporfin-tethered heat shock protein 90 (HSP90) inhibitor, was synthesized in house. Solutions of HS583 in optical cuvettes (1cmx4cm) were exposed to controlled amounts of laser light or external beam radiation (0-8Gy) from a clinical Linac (18MV). Reactive Oxygen Species (ROS) generation was quantified by measuring the oxidation of methionine by ROS and analyzed with HPLC. Cell culture experiments were performed using MDA-MB-231, a triple negative breast cancer, and MCF10A, an immortalized non-transformed breast epithelial line. Cells were cultured and treated with HS583 for 90 minutes before being washed and exposed to various doses of laser light and assayed by WST cell proliferation assay. Experimental results were compared to theoretical Monte Carlo simulations performed using Tool for Particle Simulation software (TOPAS), exploring the relation between CL and ROS generation.

Results: Chemical assays demonstrated that HS583 was capable of converting laser light energy into ROS. Similarly, increasing amounts of ROS were generated with higher doses from external beam suggesting conversion of cherenkov light to ROS by the photodynamic molecule verteporfin. Simulations suggest that with 1 J/cm² 620 nm laser light incident upon it, a 1 μM solution of HS583 absorbs 1.4E12±0.1E12 eV. WST assays showed increased cytotoxicity in MDA-MB-231 when treated with HS583 with an LD50 of 0.24 uM at 2 J/cm², 0.35 uM at 1 J/cm², and 4.45 uM at 0.1 J/cm².

Conclusion: Verteporfin-based photodynamic molecules can enhance tumor control during radiation therapy by CL activation. Tethering verteporfin to an HSP90 inhibitor enables targeted ROS production only in tumor cells, sparing normal tissue toxicity and further increasing the therapeutic ratio.

Temperature-Driven Variation in Arousal Frequency Predicts Fat Depletion in Hibernating Dwarf Lemurs

Faculty Mentor: Ana Breit, Ph.D.

Authors: Huixin Jin, Ana Breit

Abstract:

Hibernation is an inherently dynamic process characterized by repeated torpor–arousal cycles, yet the usual simplified description as reduced metabolic rates overlooks the importance of the structure and frequency of these torpor cycles. In tropical hibernators, where environmental temperatures are warmer and more variable, these cycles may be further modified for better energetic strategies over time. The fat-tailed dwarf lemur (*Cheirogaleus medius*) relies on stored fat reserves in its tail during months-long hibernation, but how energy use changes across the season and under different temperature conditions remains unclear. In this study, we ask whether temperature environments shape interbout arousal frequency, which in turn explains the difference in the rate of fat depletion during hibernation. Additionally, we examine whether individual factors such as age and sex contribute to variation in fat loss among individuals experiencing the same environmental conditions.

16 captive dwarf lemurs were housed in either a fluctuating warm room or a stable cold room to stimulate hibernation. Individuals were matched across rooms by age and sex (5 males and 3 females per room). We tracked body mass as a proxy for energy reserves and quantified interbout arousal frequency at four time points: pre-hibernation (October), mid-hibernation (January and February), and post-hibernation (April). Concurrent biological sampling at those four time points included blood, skin, and urine to support future physiological analyses. The 2025–2026 hibernation season ended in early March 2026, and we saw a progressive decrease in mass across the hibernation period. Interbout arousal frequency varied both across time and between temperature conditions. Individuals in the fluctuating warm room exhibited more frequent interbout arousals, which were associated with faster rates of mass loss. These results suggest that hibernation is shaped by both seasonal progression and temperature context, and the role of torpor–arousal cycling is a key mechanism linking thermal environment to energy depletion. Future work will investigate whether these organismal patterns are reflected at the cellular level by characterizing mitochondrial function in fibroblasts using Seahorse respirometry and measuring oxidative stress with urine-based biomarkers.

Nutrient Context Shapes Decision-Making in Drosophila Oviposition

Faculty Mentor: Rebecca Yang, Ph.D.

Authors: Sungmin Jung, Emmanuel Medrano, Rebecca Yang

Abstract:

Animals constantly make decisions that impact their survival and reproduction. However, those decisions vary depending on context. For example, when food is scarce, an animal may choose a riskier hunting spot, exchanging the added risk for a higher likelihood of finding food, though when food is abundant, they might not take that same risk. While animals must integrate all sensory input and process it in their brain for decision making, the mechanisms that mediate this are not fully understood.

To examine how the brain integrates context to shape decisions, we looked at egg laying of drosophila. Flies constantly choose between substrates, with their decision often flipping depending on context. Furthermore, we have identified the neural circuit that allows flies to make decisions. As such, this system is well positioned to allow us to determine the neural mechanisms of underlying contextual modification of decision.

I explored whether nutritional state, which shapes behavior, modulates decision-making and alters egg-laying in Drosophila. To alter nutritional state, I asked whether flies showed different preferences when asked to make a decision between sugars with differing nutritional values. We first tested a nutritious sugar, sucrose, and saw that the flies strongly rejected this substrate when paired against a plain substrate. Surprisingly, when we then tested a non-nutritious sugar, arabinose, they showed no preference. This suggests that although both sugars are sweet, nutrition is essential for shaping a flies' decision to reject a sweet substrate for egg-laying.

Therefore, the next experiments added nutritious sugar in the middle and saw an increase in rejection suggesting that nutrition is sufficient to promote rejection. To confirm that nutrition is important, we experimented with another nutrient in the form of yeast to see if it was sugar specific, and saw that this nutrient similarly enhanced rejection of a sweet substrate.

Since nutrient-related context clearly influences decision-making, the next step is to uncover the underlying neural mechanisms that allow an organism to detect and respond to these internal states. In the fruit fly, this process is mediated in part by specialized neurons such as Gr43a neurons, which are capable of directly sensing fructose levels within the body. Next, I am interested in understanding if these Gr43a neurons are involved in sensing internal nutrients to then regulate egg-laying decisions.

Hatching and Emergence Success of Leatherback Turtle (*Dermochelys coriacea*) Nests on the West Coast of Puerto Rico

Faculty Mentor: Matthew Godfrey, Ph.D.

Authors: Victoria I. Justiniano Rodriguez, Olga Mariela Muñoz Vega, Dr. Matthew H. Godfrey

Abstract:

The archipelago of Puerto Rico is considered important nesting habitat for leatherback turtles (*Dermochelys coriacea*) in the Caribbean with a reported 500–1,000 crawls per year. (Eckert & Eckert, 2019). Despite long-term nest monitoring and protection on Puerto Rican beaches, there are few recent accounts of hatching and emergence success of leatherback nests in Puerto Rico. This study focuses on the hatching and emergence success of in-situ leatherback nests laid on the west coast of Puerto Rico between 2015–2024, based on data from 1,416 nest excavations conducted by Tortugueros del Oeste, a volunteer-run organization in western Puerto Rico. Volunteers consistently monitor 20 beaches across 9 towns (~80km) during nesting and hatching seasons (February– September) and monitor all nests found throughout the incubation period. After the hatchlings have emerged, the volunteers excavate and record the egg chamber contents for all nests that produce hatchlings; they also excavate nest chambers with no signs of emergence 5 days after the expected hatch date. The data from all 10 years of monitoring indicate an overall average hatching success of 69.3% \pm SEM and an average emergence success of 61.0% \pm SEM. These results are higher than the commonly reported average success of \leq 50% from nesting sites elsewhere in the world, indicating that the west coast of Puerto Rico is highly productive nesting habitat for leatherback sea turtles. The data also showed no significant seasonal or yearly variation in success metrics during the peak hatching months (March– June). These findings provide updated, location-specific data for Puerto Rico, and establish a more accurate baseline for future conservation assessments and regional management strategies.

ML-Aided Portable Spiky Nanorattle SERS Platform for Amplification-Free Cancer mRNA Detection

Faculty Mentor: Tuan Vo-Dinh, Ph.D.

Authors: Gabriel D Kantor, Khang D Hoang, Supriya Atta, Elliot A Grant, Jinjia Zhou, Zimeng Li, Joy Q Li, Yuanhao Zhao, Gloria Dalton, Christina E Akpan, Walter Lee, Tuan Vo-Dinh

Abstract:

Cancer remains a major global health burden, with roughly two million new cases diagnosed annually. Although early detection through screening has improved outcomes in high-resource settings, limited access to diagnostic infrastructure in low-resource regions continues to result in delayed diagnosis and increased mortality. To address this disparity, we present a portable, amplification-free plasmonic biosensing platform for direct detection of mRNA biomarkers in tissue biopsies from patients with head and neck squamous cell carcinoma (HNSCC). This assay leverages surface-enhanced Raman scattering (SERS)-active spiky nanorattles (SpNRs) functionalized with DNA reporter probes, in conjunction with magnetic beads (MBs) functionalized with complementary capture probes. Target mRNA hybridizes to both probe types, forming a sandwich complex that can be magnetically concentrated within a laser interrogation region. The resulting core-gap-shell plasmonic architecture generates highly amplified and spectrally distinct Raman signals proportional to target concentration without the use of target amplification methods such as polymerase chain reaction (PCR). Target recognition was optimized by tuning adenine spacer lengths on both SpNRs and MBs, enhancing hybridization efficiency and signal intensity. The platform achieves a picomolar limit of detection without enzymatic amplification. Integration of machine learning classifiers enabled robust discrimination between HNSCC and healthy cell lines with high sensitivity and specificity. Preliminary validation using patient-derived tissue biopsies demonstrated consistent classification performance. All measurements were conducted using a portable Raman spectrometer, underscoring the system's suitability for point-of-care deployment. This approach provides a rapid, low-complexity alternative to conventional molecular diagnostics, with strong potential for improving cancer detection in resource-limited settings.

Molecular Profiling of hiPSC-Derived Biomimetic Glomerulus-on-a-Chips in Glomerular Disease Modeling and Therapeutic Development

Faculty Mentor: Samira Musah, Ph.D.

Authors: Anavi Kaul, Yize (Eon) Zhang, Amanda Barreto, Monona Zhou, Samira Musah

Abstract:

More than 1 in 7 adults in the US have Chronic Kidney Disease (CKD), a condition marked by progressive kidney function loss. An organ-on-a-chip is a microfluidic device that mimics the structure and function of human organs – our lab's glomerulus-on-a-chip allows us to study CKD and related glomerular injuries in a controlled, physiologically relevant environment. We are investigating three injury models—adriamycin (ADR), diabetic nephropathy (DN), and pamidronate (PAM)—to identify common molecular mechanisms and early podocyte injury biomarkers using a multiomics approach. The ultimate goal is to design gene circuits that respond to key biomarkers and protect podocytes under injury conditions. The chip is developed through a multi-week process, involving PDMS casting, electrospinning silk fibroin membranes, and seeding with endothelial and intermediate mesoderm cells, which differentiate into podocytes. Over the course of our study, we have established functional injury timelines through fluorescent spectrometry of albumin-inulin functional assays. Next we will morphologically characterize the different injury models on the chip using Transmission Electron Microscopy (TEM). We are currently in the process of validating a compiled list of potential biomarkers from previous studies involving RNAseq by mentoring the temporal dynamics of individual expression levels and fold changes; we are also conducting a proteomic analysis of clinical samples. Once validated, we will incorporate these target genes into the designed gene modulation system. Using a Tet-on YAP overexpression system validated in 2D culture and implemented in the glomerulus-on-a-chip model, we found that ADR treatment increased albumin clearance, indicating injury. However, post-injury induction of YAP overexpression via DOX significantly reduced albumin clearance. These findings suggest that YAP overexpression functions as a compensatory mechanism in podocytes following ADR-induced glomerular injury, helping halt further progression of damage in albumin selective filtration function. This presents targeted gene modulation of podocyte injury regulators such as YAP as a promising therapeutic strategy for fighting glomerular disease.

How Differences in Social Structure and Resource Availability Relate to Androgen Concentrations, Pregnancy and Parasite Burdens in Female Dominant (*Eulemur coronatus*) vs. Codominant (*E. sanfordi*) Lemurs

Faculty Mentor: Christine Drea, Ph.D.

Authors: Madiha Khan, Caroline Shearer, Christine Drea

Abstract:

In most male mammals, testosterone promotes reproductive and competitive behavior which can impose costs, including increased susceptibility to parasites. To meet energetic demands, males often face trade-offs between investing in reproduction versus investing in health. Because females typically have low androgen concentrations, we lack understanding about whether they face similar trade-offs. Lemurs offer a unique opportunity to address this gap because various species show androgen-mediated female dominance. We ask if female lemurs incur measurable physiological costs associated with testosterone production by comparing endocrine variables and parasitism in two species that differ in social structure – *Eulemur coronatus* (a female-dominant or FD species) and *E. sanfordi* (co-dominant or CD species) – and co-occur in two ecologically distinct habitats – Montagne d'Ambre National Park (rich site) and Ankarana Special Reserve (lean site) in northern Madagascar. We also examined how reproductive state, particularly late-stage pregnancy, shapes androgen metabolite concentration variation in females. We quantified concentrations of fecal androgen (fAM) metabolites via enzyme immunoassay and assessed relative parasite burden via fecal egg counts. As predicted, preliminary results show greater fAM concentrations across sites in FD females than in CD females; however, both species and sexes show greater fAM concentrations at the lean site than at the rich site, indicating that resource scarcity may drive androgen-mediated competition. Pregnancy also emerged as a major source of variation: late stage-pregnant females showed significantly increased androgen metabolite concentrations compared to early stage-pregnant females, indicating that reproductive state strongly modulates female androgen metabolite concentrations. Contrary to prediction, CD females tend to have higher parasite egg counts than FD females, suggesting an unexpected benefit of female dominance or cost of co-dominance. Consistent with weather-associated patterns, parasitism was greater at the wetter, rich site than at the drier, lean site. Together, these findings indicate that androgen-mediated trade-offs in female lemurs are shaped by a complex variation in interaction across sexes, social systems, reproductive physiology, and habitats.

When GLP-1 analogs fail: harnessing a gut-brain sensory pathway to reduce sugar preference

Faculty Mentor: Diego Bohorquez, Ph.D.

Authors: Laila Khan-Farooqi, Emily Alway, Diego V. Bohórquez

Abstract:

Sugar is a ubiquitous nutrient in the modern foodscape that simultaneously fuels our bodies and harms them. The overconsumption of sugar has been linked to metabolic disorders like obesity and diabetes, one treatment for which are glucagon-like peptide 1 receptor agonists (GLP-1RAs), drugs that imitate hormones released by a subset of gut endocrine cells in response to a meal. These drugs act through slow endocrine signaling to decrease food consumption, but it is unclear if they alter appetite for specific nutrients, like sugar.

Another subset of gut endocrine cells called neuropod cells have primary sensory capabilities, synapsing with vagal afferents within the gut to rapidly communicate information about intraluminal stimuli. Specifically, luminal sugar is sensed through sodium-glucose cotransporter 1 (SGLT1) proteins on the apical surface of neuropod cells. In mice, blocking neuropod cell activity results in the inability to discriminate between caloric sugars and noncaloric sweeteners. Thus, SGLT1-mediated sugar sensing in neuropod cells represents a fast, nutrient-specific pathway that may modulate sugar preference independently of slow hormonal signals like GLP-1.

Here, I examined if semaglutide, a GLP-1RA, reduces sugar preference in mice. I found that semaglutide reduces chow consumption in mice, but does not alter sugar consumption, failing to change a fundamental behavior implicated in metabolic disorders. Then, I generated two new knockout mouse lines lacking SGLT1 in different areas of the gut and recorded sugar preference changes. A total intestinal epithelial knockout of SGLT1 was lethal, while a neuropod cell-specific deletion yielded a slower development of sucrose preference. Thus, SGLT1 in the gut is essential not only for sugar absorption, but also for behavioral patterning of sucrose consumption, a process that is intimately tied to obesogenic eating. By illustrating that GLP-1RAs fail to reduce sugar preference and underscoring the crucial role of SGLT1 on neuropod cells in the gut-to-brain sugar sensing pathway, this work unveils a highly targeted peripheral avenue that could be harnessed to treat a host of metabolic disorders.

E-Cigarette Exposure Disrupts FOXO Pathway Gene Expression in Human Trophoblast Cells

Faculty Mentor: Dr Margeaux Marbrey, Ph.D.

Authors: Meera Khare, Rennica Huang, Margeaux W. Marbrey

Abstract:

The rising popularity of electronic cigarettes (e-cigarettes) as a safer alternative to cigarettes has raised concern regarding their use during pregnancy. E-cigarettes heat liquid containing solvents, nicotine, and flavorings to produce an inhalable aerosol. While traditional cigarette smoking adversely affects pregnancy and fetal health, little is known about how e-cigarettes impact the placenta, the organ responsible for nutrient and oxygen exchange between mother and fetus. Central to placental development are trophoblasts, which invade the uterine wall and remodel maternal spiral arteries to establish low-resistance blood flow. Placental development is partly regulated by the FOXO signaling pathway, which controls trophoblast invasion, cellular stress responses, and vascular remodeling. Its transcription factors are regulated by phosphorylation inhibition through serum glucocorticoid-regulated kinases (SGKs). Disruption of this pathway by environmental exposures can impair placental function. We asked whether exposure to e-cigarette condensates can alter FOXO pathway gene expression in human trophoblast cells. HTR8/SVneo cells were exposed for 6 hours to 1.5% condensates generated from strawberry-flavored e-cigarette liquids (70% vegetable glycerin/30% propylene glycol; 0.6% nicotine). Experimental groups consisted of base liquid alone, base liquid with nicotine, base liquid with flavoring, and base liquid with both flavoring and nicotine. RNA was isolated and analyzed by qRT-PCR and RNA-seq. RNA-seq data were analyzed in Partek Flow using STAR alignment to identify differentially expressed genes, DAVID to explore altered pathways, and DESeq2 to determine differential expression. RNA-seq results confirmed that FOXO-associated stress response and invasion-related genes were altered, and pathway analysis showed significant changes in SGK1-3 ($p < 0.05$). Flavored exposure upregulated SGK1 and SGK3 and downregulated SGK2 relative to base liquid and nicotine-only conditions. qRT-PCR demonstrated downregulation of FOXO1 and upregulation of FOXO1 target prostaglandin-endoperoxide synthase 2 (PTGS2) following exposure to flavored condensates with and without nicotine ($p < 0.05$). Collectively, these results show flavored exposure is associated with dysregulation of FOXO regulators and processes essential for trophoblast invasion and vascular remodeling, highlighting the need to evaluate vaping risks during pregnancy to inform maternal and fetal health policies.

Habitat and Seasonal Drivers of Mast-Eating Bird Distributions in North Carolina

Faculty Mentor: James Clark, Ph.D.

Authors: Jungwon Kim, James Clark

Abstract:

Mast refers to the nuts and fruits produced by woody plants and serves as a critical food source for wildlife, particularly birds and small mammals. In North Carolina (NC), high environmental diversity—including the Appalachian Mountains—creates substantial spatial variation in mast availability, making tree fecundity a key driver of ecological patterns for mast-dependent species. Oak species dominate many NC forests, contributing to a largely hard-mast-based ecosystem with widespread access to acorns. However, mast production is influenced by environmental factors such as terrain and climate, which shape vegetation structure and productivity. Because migratory species ...[JC1] [#_msocom_1], we hypothesize that bird responses to mast availability depend on environmental variability, particularly drought, with winter migratory birds being more sensitive than resident species. Alternatively, because they derive a larger fraction of the diet from plants, including fruits, seeds and nuts, winter residents might be most sensitive to mast supply. From estimates of bird density I we can determine the caloric demand they place on food resources. Mass fluxes of seed production per forest area offer estimates of caloric supply. By combining a vast compilation of citizen science observations called eBird with a nation-wide synthesis of mast data, I will determine the spatio-temporal association between mast supply and bird consumption rates. Specifically, I will isolate mast-consuming bird species, standardizes observation counts by survey duration, and aggregates data across 5 km grid cells in North Carolina alongside spatial estimates of mast availability. Preliminary results show mast-consuming bird abundance has been spatially heterogeneous across North Carolina, with hotspots in Abundances have been substantially higher and more variable in winter compared to summer, suggesting a stronger resource dependence during this season. Preliminary comparison with deciduous and mixed forest cover show a mismatch between coastal abundance hotspots and mast-associated forest distribution. This mismatch suggests that the current assemblage of mast-eating species includes multiple ecological groups, including forest-associated and coastal/wetland-associated species, which respond to different environmental variation in different ways. By quantifying how environmental variation influences the capacity of forests to support consumers this study will aid management efforts in the many regions where changing climate is altering food supply.

Unspoken Legacies: Koryo Saram Women, Education, and Identity in Uzbekistan

Faculty Mentor: Kristen Stephens, Ph.D.

Authors: Jiae Kim, Kristen Stephens

Abstract:

This study aims to understand how Koryo Saram women across generations construct, maintain, and negotiate their cultural identity within diasporic contexts in Uzbekistan. While existing research on Koryo Saram communities has explored historical displacement and collective identity, there is limited focus on gendered, intergenerational perspectives—particularly the lived experiences of women and how cultural knowledge is transmitted or transformed over time. Additionally, there is a lack of qualitative research centering contemporary voices of Koryo Saram individuals across age groups, which limits a nuanced understanding of identity, language, and tradition in post-Soviet contexts. Utilizing a qualitative, oral history approach, this study draws on 22 semi-structured interviews conducted with Koryo Saram women ages 18 to 63, representing second to fifth-generation individuals. This analysis examines generational differences in cultural preservation, including knowledge of Korean and Koryo-mal, engagement with traditions, and perspectives on whether Koryo culture should be actively maintained. Findings suggest that older generations tend to express stronger attachments to cultural preservation and linguistic heritage, while younger generations demonstrate more fluid and individualized understandings of identity, often shaped by globalization and local social contexts. This research provides critical insights into the evolving nature of diasporic identity among Koryo Saram women, emphasizing the role of generational shifts, language loss, and personal agency in cultural continuity. It contributes to broader discussions on migration, identity formation, and the preservation of minoritized cultures, while stressing the importance of centering women's voices in diasporic and post-migration research.

Identifying Modifiable Factors across Adolescent Emotional Development and Mental Health

Faculty Mentor: Bridgette Hard, Ph.D.

Authors: Anushka Kumar, Karmel Choi, Marina Wilson, Teresa Vargas, Randi Schuster, Bridgette Hard

Abstract:

Adolescence is marked by increased vulnerability to depression and anxiety, highlighting the importance of identifying modifiable risk and protective factors. Emotion reactivity represents a key risk factor for adolescent psychopathology, yet developmental mechanisms and preventive strategies remain understudied. We investigated whether perceived social support mediates the prospective association between emotion reactivity and mental health symptoms and whether school-based mental health services moderate the potential impact of emotion reactivity on mental health symptoms. We constructed a multimodal dataset by integrating longitudinal data from an annual school-based mental health questionnaire administered in Massachusetts public schools with school-level data from the Massachusetts Department of Education on the availability of school-based mental health clinicians (N = 5217). Multilevel linear regression models tested the association between emotion reactivity and depression and anxiety symptoms one year later. Bayesian mediation models examined perceived social support as a potential pathway linking emotion reactivity and follow-up mental health, and school-based mental health clinician variables were tested as moderators using multilevel regression. All models clustered at the school level and adjusted for demographic covariates, and sensitivity analyses controlled for baseline mental health symptoms. Emotion reactivity was associated with increased mental health symptoms one year later ($\beta=0.42$, 95% CI=0.39, 0.44, $p<0.001$). Perceived social support significantly accounted for a small proportion of the total association (4.75%, 95% credible interval=3.44%–6.11%, $pd=1$). A modest interaction emerged between emotion reactivity and the total availability of clinicians on mental health symptoms, only after adjusting for baseline symptoms ($\beta=-0.03$, 95% CI=-0.05, 0.00, $p=0.018$), but the relative clinician-to-student ratio was associated with a stronger relationship between emotion reactivity and follow-up symptoms ($\beta=0.03$, 95% CI=0.01, 0.06, $p=0.008$). Our findings support adolescent emotion reactivity as an indicator for early mental health intervention, and we suggest the potential for preventive programs that target social mechanisms. Further research is needed to clarify the role of school-based mental health resources in serving students with emotional vulnerability to inform community-level preventive approaches.

LLM Benchmarking for 2-Dimensional Materials Using Raman Spectra

Faculty Mentor: Haozhe "Harry" Wang, Ph.D.

Authors: Sutharsika Kumar, Jingyun Yang, Dongwoo Suh, Haozhe Wang

Abstract:

Raman spectroscopy is the primary non-destructive characterization tool for two-dimensional (2D) materials, yet spectral interpretation remains largely manual and does not scale to the demands of modern synthesis workflows. We present a fully automated pipeline for large language model (LLM)-guided denoising, classification, and benchmarking of Raman spectra across four 2D materials: graphene, hexagonal boron nitride (h-BN), molybdenum disulfide (MoS₂), and tungsten diselenide (WSe₂). The pipeline operates end-to-end from raw spectral ingestion through signal diagnostics, adaptive denoising, peak-table encoding, and LLM-based material classification, with no manual intervention at any stage. To evaluate and compare model performance, we introduce an Elo-based pairwise ranking framework aided by an LLM judge operating under explicit, material-specific physical grounding criteria, including characteristic vibrational mode positions, diagnostic peak separations, and full-width at half-maximum (FWHM) constraints, moving beyond scalar accuracy metrics to capture reasoning quality and physical consistency. Nine state-of-the-art foundation models spanning three providers (Anthropic Claude, Google Gemini, and OpenAI GPT) are evaluated under a unified prompting protocol across 144 head-to-head games. Claude Sonnet 4.6 and Gemini 3.1 Pro emerge as the strongest performers, with GPT-4o identified as a pronounced outlier exhibiting systematic failures in peak assignment. We explicitly address the scope and limitations of spectral reduction to a peak-table representation, discuss the conditions under which this simplification remains physically valid, and identify large-scale dataset expansion and full spectral encoding as the primary directions for future work. All pipeline outputs, game records, and prompt specifications are released to support reproducibility and extension to additional materials and spectral modalities.

Isolation of Nanobodies to stabilize Carvedilol bound conformation of the β 2-Adrenergic Receptor

Faculty Mentor: Robert Lefkowitz, M.D.

Authors: Raphael Lee, Xiang Zhang, Natalia Pakharukova, Darwin Cai, Biswaranjan Pani, Robert J. Lefkowitz

Abstract:

G-protein-coupled receptors (GPCRs) constitute the largest class of transmembrane signaling proteins which mediate diverse physiological processes. The β 2-adrenergic receptor (β 2AR) is a GPCR involved in cardiovascular and pulmonary regulation and is a key therapeutic target for heart failure. β -blockers (β -AR antagonists) are orthosteric drugs that bind to β -ARs and inhibit receptor activation and downstream signaling. Carvedilol, an FDA-approved β -blocker, exhibits unique pharmacological properties as a weakly biased agonist favoring β -arrestin-mediated signaling. This unique property of carvedilol is hypothesized to drive its cardioprotective effects and display an enhanced clinical efficacy over other β -blockers. For structural determination of carvedilol specific conformation, we aimed to identify a nanobody (Nb) to selectively stabilize the carvedilol bound state of the β 2AR. A Nb phage display library was screened against purified β 2AR bound to carvedilol over multiple rounds to enrich target-specific binders. Candidate Nbs were expressed and characterized using biochemical and pharmacological assays to evaluate binding specificity and conformational selectivity. Phage display screening yielded multiple β 2AR binding Nbs. Candidate Nbs - Nb2D1 and 3C11 displayed the desired selectivity for carvedilol-bound β 2AR. Sequence analysis and comparisons with previously known β 2AR Nbs revealed a unique CDR3 motif of 2D1. Pharmacological assays show Nb2D1 to be a high affinity β 2AR binder. 2D1 forms stable complexes with the β 2AR suitable for structural studies using cryoEM. Our findings identify Nb2D1 as a high-affinity, conformation specific nanobody stabilizing carvedilol bound state of the β 2AR. Nb2D1's unique CDR3 and pharmacological properties suggest the Nb to engage a distinct conformational epitope in the β 2AR, potentially stabilizing a unique signaling state of the receptor. 2D1 represents a valuable biochemical tool to structurally elucidate the molecular basis of carvedilol's distinct pharmacology and signaling bias at the β 2AR.

Oncogenic Ppm1d truncation promotes R-loop-associated replication stress and PI3K-Akt/MYC-linked transcriptional reprogramming in mouse embryonic fibroblasts

Faculty Mentor: Zach Reitman, M.D., Ph.D.

Authors: Kate J. Lee, Vennesa Valentine, Abigail Groth, Yingying Meng, Joshua Tolliver, Nerissa T. Williams, Lixia Luo, Lee Zou, Zachary J. Reitman

Abstract:

Diffuse midline glioma (DMG) is an aggressive pediatric brain tumor for which radiation therapy remains the standard of care but only transiently delays progression. Up to 25% of DMGs harbor truncating mutations in the protein phosphatase Mg²⁺/Mn²⁺-dependent 1D (PPM1D) gene, whose activating truncations suppress p53 signaling and DNA damage response, promoting tumor growth and radioresistance. Because abnormal R-loop accumulation drives transcription-replication conflict and the p53-SAM axis regulates R-loop homeostasis, we hypothesized that truncating PPM1D mutations induce R-loop-linked replication and transcription stress, creating a therapeutic vulnerability. To test this, we generated a conditional Ppm1d “flex-6” mouse allele (Ppm1d-loxP-exon6-loxP-exon6-E518X-tag) enabling Cre-dependent expression of DMG-derived truncated PPM1D from the endogenous locus. Mouse embryonic fibroblasts (MEFs) isolated from embryos heterozygous for the Ppm1d flex-6 allele were immortalized with SV40 Large T-antigen and treated with AdCre to induce Cre-mediated recombination. Total RNA was sequenced from isogenic MEF lines (n=3/group), and replication stress was assessed by S9.6-RPA proximity ligation assay (PLA). Differential expression analysis identified PI3K-Akt pathway genes (Fgf23, Tmem200a, Pde3a), the transcription factor Alx1, and Snora78, an independent indicator of MYC hyperactivity, among the top 10 upregulated targets, while a hypothesis-driven heatmap showed genotype-linked shifts in metabolic/chromatin regulators (Gamt, Shmt2, Trp53, Suv39h1). Gene set enrichment analysis of MEF RNA-seq (log₂FC [+AdCre vs. -AdCre]) showed significant enrichment for TNF α /NF- κ B signaling (NES 1.54, FDR 0.044) and MYC targets (Hallmark v1 NES 1.83, FDR 0.0035; v2 NES 1.66, FDR 0.0089) in the Ppm1d-truncated state, with leading-edge overlap (Rrp9, Gnl3, Hspd1, Srm) indicating increase in ribosome biogenesis, mitochondrial protein folding, and polyamine production. Consistent with these transcriptional changes, S9.6-RPA PLA foci per nucleus were significantly increased in Ppm1d-truncated MEFs relative to isogenic wildtype controls. Collectively, these findings indicate that Ppm1d truncation drives a MYC/NF- κ B-high, stress-responsive state in MEFs with metabolic/chromatin regulatory shifts. Upregulation of PI3K-Akt pathway genes, Alx1, and Snora78 supports a growth-promoting, MYC-linked program, while increased S9.6-RPA PLA foci indicate elevated R-loop-associated replication stress.

Rpl13a snoRNAs support cytokine production but are dispensable for bacterial clearance

Faculty Mentor: Christopher Holley

Authors: Daniel S. Levin, Joshua B. Parsons, Timothy C. Davenport, Xinhe Yin, Neil J. Freedman, Christopher L. Holley

Abstract:

Reactive oxygen species (ROS) play a critical role in immune defense against pathogens because phagocytes use them to kill captured bacteria. ROS are predominantly produced by NADPH oxidase during oxidative bursts or generated as a byproduct of both normal and impaired mitochondrial respiration. Small nucleolar RNAs (snoRNAs) encoded within the Rpl13a locus support the production of mitochondrial ROS, yet the role of snoRNA-derived ROS in response to infection is not well understood. To better understand their importance, we injected wild-type (WT) and Rpl13a snoRNA-knockout (snoKO) mice with *Listeria monocytogenes*, *Escherichia coli*, or *Staphylococcus aureus* and harvested liver, spleen, and serum 24 hours post-infection for *E. coli* or 72 hours post-infection for *L. monocytogenes* and *S. aureus*. Similar counts of bacteria were measured in both genotypes across the three infection models. Levels of a lipid marker of oxidative stress were approximately two-fold lower in snoKO mice injected with a PBS control, but roughly identical between genotypes during *L. monocytogenes* infection, suggesting that baseline differences in ROS may equalize during infection. Despite the similarities in bacterial burden and oxidative response, snoKO mice had lower levels of circulating pro-inflammatory cytokines IL-1 β , IL-6, and TNF- α during *L. monocytogenes* infection, and reduced IFN- γ , IL-12, and GM-CSF during *S. aureus* infection. These results indicate that while the Rpl13a snoRNAs support an innate inflammatory response, they are not required for bacterial elimination. These findings help provide a description of the ways in which snoRNAs modulate immunity, expanding our understanding of their physiological importance.

Immunoglobulin Endopeptidase Mediated Cytoprotection in Xenotransplantation

Faculty Mentor: Jean Kwun, D.V.M., Ph.D.

Authors: Zishen Li, Janghoon Yoon, Zheng Chen, Davide Schiliró, Rafaela Belloni, Shengli Song, Stuart J. Knechtle, Jean Kwun

Abstract:

Antibody-mediated rejection (AMR) driven by xenoreactive IgG and IgM remains a significant issue for kidney xenotransplantation. IgM endopeptidase unexpectedly demonstrated in vivo efficacy for preventing early xenograft rejection despite presence of IgG (manuscript in preparation). This study investigates the mechanism of endopeptidases' protection effect in vitro to further understand their therapeutic potential to mitigate AMR. Transgenic (GGTA1/hCD55) donor porcine cells were co-cultured with nonhuman primate recipients' plasma samples treated with IceM (IgM cleaving) or IceMG (IgM and IgG cleaving). HLA A2 expressing K530-derived reporter cells were cultured with Ides-treated BB7.2-hIgG1K antibodies (for all endopeptidases: 0, 20, 100, or 200 µg/ml). Cells were then rechallenged with untreated plasma or antibodies. IgM and IgG antibody levels after one or both challenges were measured via flow cytometry. IceM and IceMG selectively reduced the bound antibodies levels for the antibodies they were designed for ($p < 0.05$). Ides effectively reduced the bound Fc levels ($p < 0.0001$ for 100 µg/ml Ides) while Fab levels remained at saturation. The reduction observed for all three endopeptidases remained after the rechallenge, though with slight dosage dependent effects for IceMG and Ides. These findings confirm the endopeptidase-mediated cytoprotection effect, and suggest that the mechanism involves cleaved but bound antibody fragments preventing intact antibodies from binding. Additional studies are required to confirm the respective contributions and interplay between IgM and IgG, and to elucidate how this mechanism can be translated to therapeutic applications.

Modulating paratensile signaling between fibroblast and myofibroblast cells using MAP scaffold

Faculty Mentor: Alejandra Suarez Arnedo

Authors: Fayanne Lin, Koravit Poysungnoen, Alejandra Suarez-Arnedo, Tatiana Segura

Abstract:

Skin wound healing is an intricate process involving multiple interconnected stages with variable outcomes, from near-perfect regeneration to debilitating scarring. There are numerous cellular mechanisms and immune processes associated with wound healing. One of the key processes is the activation of fibroblasts into myofibroblasts, called the fibroblast-myofibroblast transition (FMT), leading to contractile forces and collagen deposition. While myofibroblasts are necessary for skin remodeling and wound closure, their presence can lead to a feedback loop, caused by tensile forces that further activate fibroblasts at the site of the wound. This feedback loop produces pathological scar tissue.

Biomaterials, especially hydrogels, have been used to improve wound healing by influencing cell behavior and interactions. One type of biomaterial that shows potential for improving skin regeneration is microporous annealed particle scaffolds (MAP). MAP scaffolds have led to superior wound healing when compared against chemically identical, non-granular hydrogels, thereby suggesting that the granular nature of MAP contributes to regeneration.

Considering the role of FMT in determining wound healing outcomes, we hypothesize that the granular nature of MAP contributes to wound resolution by offloading tensile forces and modulating fibroblast behavior. This project will elucidate how MAP scaffolds modulate the FMT. Paratensile signaling involves tensile forces generated by myofibroblasts that propagate throughout the ECM, and it is a key factor in promoting fibroblasts towards fibrotic phenotypes.

We hypothesize that the addition of MAP hydrogels in the wound bed will disrupt paratensile signaling, thereby blocking fibroblast activation. We will investigate the extent to which packing and annealing ratios of MAP scaffolds block paratensile signaling using a standardized in vitro fibrosis model. We will use immunofluorescence imaging and flow cytometry to determine the level of blocking, as well as labeling of the collagen scaffold, to measure general contractility as the main quantitative outcome of the disruption of cell mechanical forces. This research will allow us to elucidate why granular materials improve skin wound healing.

MicroRNA-K Driven Regulation of GRK2 Expression in Attenuating Cardiac Hypertrophy

Faculty Mentor: Dr Walter Koch

Authors: Christina Liu, Stephanie Kereliuk, Heidi Cho, Walter J. Koch

Abstract:

Heart failure is the leading cause of death worldwide, affecting over 64 million people. While current therapies delay disease progression, the underlying cellular mechanisms of heart failure go largely untreated. GPCR kinase 2 (GRK2) regulates beta-adrenergic receptor (bAR) signaling under physiological conditions and is upregulated in heart failure, contributing to cardiac dysfunction. Micro-RNAs (miRs) are small non-coding RNAs that modulate gene expression by binding to the 3'-untranslated regions of mature RNA, causing degradation or translational repression. Our lab has identified a novel microRNA, miR-K, as a potential regulator of GRK2 expression. We have found miR-K to be downregulated in human heart failure and elevated in bARKct-overexpressing cardiomyocytes, suggesting a protective role. We hypothesize that miR-K fine-tunes GRK2 expression to attenuate cardiac hypertrophy. Using neonatal rat ventricular myocytes (NRVMs), hypertrophy was induced with phenylephrine (PE) under two conditions: preventive (miR-K mimic before PE) or therapeutic (miR-K mimic after PE). GRK2 and hypertrophy markers (ANP, BNP, Myh7) were quantified using RT-qPCR. In the preventive model, miR-K significantly downregulated GRK2 and reduced hypertrophy marker expression. Anti-miR-K enhanced both, confirming miR-K's protective role. In the therapeutic model, miR-K continued to reduce GRK2 levels and hypertrophy. These findings suggest that miR-K induces cardioprotection by limiting GRK2 upregulation and hypertrophic gene activation under stress. Future work will investigate the therapeutic effect of miR-K in vivo and on cardiac energetics under stress. These findings will be used to elucidate the role of miR-K as a novel therapy for heart failure.

Goal commitment beliefs: Distinct predictors of self-regulation in goal pursuit

Faculty Mentor: Dr James Shah, Ph.D.

Authors: Ella Lodewyk, Skyler Wyly, Elizabeth Buduen, Kai Tang, James Shah

Abstract:

Goal commitment beliefs influence traits that support effective self-regulation and goal pursuit. This leads to behaviors that are consistent with said belief, whether it's persisting, building momentum, or being resilient. Study 1 (N=291) uses a correlational design to examine the relationship between goal commitment beliefs associated with self-improvement, grit, and resilience. Results showed that goal commitment persistence is correlated with grit, and goal commitment growth is correlated with self-improvement. Study 2 (N=300) uses the same design to examine the relationship between goal commitment beliefs and goal-related growth, persistence, and resilience behaviors. Results showed resilience and growth beliefs predicted goal growth behaviors, resilience and growth beliefs predicted goal resilience behaviors, and resilience, persistence, and growth beliefs predicted goal persistence behaviors. Study 3 experimentally manipulates participants' beliefs about goal commitment and measures responses to a goal scenario about goal commitment, expectancy, and future behavior. Learning how we think about our goals can provide insight into how goal commitment affects self-regulation.

Sp8-Defined Gradients and Their Effect on Cortical Pyramidal Neuron Development

Faculty Mentor: Mariana Holguin Lopez

Authors: Isabella Lopez, Mariana Holguin Lopez

Abstract:

The main projection neuron type of the cerebral cortex is the pyramidal neuron (PN), which coordinates excitatory output and is responsible for the processing and integration of essential information. During cortical development, radial glial progenitor cells (RGPs) undergo the process of neurogenesis, which gives rise to all PNs. While previous research has aimed to understand how RGPs are capable of generating the enormous diversity of PNs, the true nature of RGPs is still unclear. Currently there are two models aiming to explain this phenomenon: the first proposes that RGPs are multipotent and have the potential to produce different, if not all, PN subtypes; while some other research suggests that particular RGPs are fate-restricted to generate a specific type of PN from the beginning.

In the Huang Lab, we have developed genetic tools to effectively study the developmental trajectories of PNs. One of these tools was a knock-in mice line of Sp8, a transcription factor (TF) crucial for rostral cortical development. We leveraged this model and studied Sp8's contribution to neuronal development by looking at embryonic and postnatal timepoints. Our line displayed an anteromedial to posterolateral gradient, matching the endogenous expression of Sp8, which gave us the confidence of its use as a lineage tracing tool. Furthermore, we observed that at postnatal stages, there were differences in the cortical distribution of PNs derived from Sp8-positive RGPs, as well as interesting projection patterns of these neuronal subpopulations.

Our preliminary observations are suggestive of fate restriction. However, this project is only one piece to answer the large question of how orthogonal transcription factor gradients influence RGP output. In future directions, we will assess variance in the contribution of TFs with distinct gradients of expression in the anterior-posterior and lateral-medial axes. Our work will provide a more comprehensive understanding of how TFs contribute to organization and development in the postnatal cortex.

Designing “Otherwise”: Community-Engaged Methods for Creating Spatial Justice in the US

Faculty Mentor: Paul B Jaskot

Authors: Kyle MacLellan, Alexandra Zagbayou, Paul Jaskot

Abstract:

This paper examines how architecture and urban planning in the United States have historically functioned as instruments of social ordering, while exploring how community-engaged design can advance spatial justice. It begins from the premise that social structures embed themselves in policy and legislation, shaping what is built, where, and for whom; the resulting landscapes then reinforce the inequalities that produced them, particularly along racial lines. Focusing on Durham, North Carolina, this analysis traces how local development reflects broader planning ideologies, from early 20th-century movements to postwar urban renewal and contemporary gentrification.

Building on this history, the paper examines contemporary community-engaged design practices through practitioner examples in both U.S. and international contexts. These cases demonstrate how participatory methods can reshape design processes and outcomes, but also reveal their inconsistency and reliance on individual initiative rather than institutional standards.

The final section applies these insights to a case study of the adaptive reuse of the Zafa Temple in Durham, where community engagement informs both process and design decisions. This example illustrates how small-scale interventions can model more inclusive approaches to general urban development. Ultimately, this writing argues that achieving spatial justice requires moving beyond isolated efforts toward systemic change—embedding community engagement as a standard practice in planning and design.

Defining the Role of ALDH1A3 in Embryonic Brain Development Under Maternal High-Fat Diet

Faculty Mentor: Staci Bilbo, Ph.D.

Authors: Aman Maredia, Sophie Li, Sushanth Kumar, Staci Bilbo

Abstract:

Maternal high-fat diet (mHFD) is associated with increased risk of neurodevelopmental and psychiatric disorders in offspring. In a mouse model of mHFD, we found that male offspring show reduced brain serotonin and increased microglial engulfment of serotonin neurons during embryonic development. To better understand the mechanistic drivers behind this sex-specific vulnerability, we performed bulk RNA sequencing on embryonic microglia from diet offspring. We found that *Aldh1a3* was one of the highest upregulated genes when comparing mHFD male vs mHFD female offspring microglia. *Aldh1a3* encodes for an aldehyde dehydrogenase and plays a critical role in metabolism. However, the role of ALDH1A3 in microglia and early neurodevelopment remains unknown. We characterized the general role of ALDH1A3 in the regulation of microglial inflammatory cytokine secretion and mitochondrial respiration using the specific ALDH1A3 inhibitor KOTX1. ALDH1A3 inhibition did not alter LPS-induced TNF- α release or basal oxygen consumption in embryonic microglia, suggesting a limited role for ALDH1A3 in regulating inflammatory or metabolic function under baseline conditions. Given that RNA-sequencing of isolated microglia can capture engulfed transcripts rather than true endogenous upregulation, we conducted RNA in-situ hybridization to identify the specific cell types and brain regions exhibiting *Aldh1a3* upregulation in male offspring following mHFD. RNA-FISH revealed limited *Aldh1a3* expression in embryonic microglia and instead identified enrichment in Sox2+ ventricular neural stem cells in the embryonic hindbrain. Future studies will investigate whether the identified *Aldh1a3*-high cells are potential targets of microglial engulfment in mHFD male offspring.

Investigating Correlates of Resting State EEG Features with Joint Engagement in Children with Autism Spectrum Disorder

Faculty Mentor: Alexandra Bey

Authors: Rithvik Marri, David Akinsooto, Elias Peters, Samantha Majors, Dr. Alexandra Bey

Abstract:

Joint engagement, a developmental milestone where a child and caregiver share focus on an object or activity, is foundational for language and social growth. In children with autism spectrum disorder (ASD), disruptions in this process significantly impede developmental trajectories. While social communication deficits define ASD, the underlying neural activity facilitating or impeding shared attention is still poorly understood. Electroencephalography (EEG) offers a cost-effective window into these neural differences. Current research shows potential links between theta power and social attention along with alpha power to cortical excitability. Despite these associations, a direct link between resting-state neural values and joint engagement has not been established. This study begins to look at how resting-state EEG power spectra, specifically theta and alpha oscillations, correlate with a child's ability to have joint engagement. Joint engagement is measured during the free-play portion of the predetermined caregiver-child interaction (CCI) with expert coding of videos to identify periods of engagement. EEG power spectra are extracted from recordings taken while children view neutral stimuli. The exploratory analysis revealed stronger relationships in the ASD compared to the non-ASD cohort between theta/alpha power and JERI variables, along with a strong basis for regression modeling. It also showed connections between other variables that are worth exploring in future work. Identifying predictive biomarkers can enhance the timing of ASD therapies. If EEG can predict receptivity to social behavior, clinicians can identify when to implement behavioral interventions. This moves the field toward personalized medicine that addresses the heterogeneity of ASD.

Ubp8 plays a crucial role in connecting histone modifications and metabolic adaptation

Faculty Mentor: Gustavo M. Silva, Ph.D.

Authors: Jorge Mato Frontela, Clara de Melo, Dr. Gustavo Silva

Abstract:

Transcription initiation through histone 3 lysine 4 di- and tri-methylation (H3K4Me₂ and H3K4Me₃) enables rapid gene expression regulation during metabolic rewiring. H3K4 methylation depends on Histone 2B (H2B) monoubiquitination (H2Bub), where ubiquitin is added by Rad6 and removed by Ubp8, which localizes to mitochondria in respiratory conditions. The human ortholog of Ubp8 (USP22) is widely expressed and has been reported as a critical driver of lethal tumor phenotypes. Resolving the role of Ubp8 in coordinating H2B ubiquitination and respiratory metabolism would open new avenues of thought with immediate impacts in cancer research. I hypothesize that Ubp8 localizing to mitochondria during metabolic rewiring leads to the accumulation of H2Bub, with downstream effects in transcription regulation. Here, I report H2Bub levels increase in wild-type (WT) cells grown in respiratory media compared to glucose. To test Ubp8's role, I deleted UBP8, which raised H2Bub in glucose but eliminated H2Bub in respiratory media. I hypothesized that *ubp8*Δ cells could not respire. Porin 1 measurements showed that *ubp8*Δ cells have reduced mitochondria, indicating that deletion of UBP8 decreased the number of mitochondria. Growth assays showed that these cells failed to grow in respiratory conditions. Because Porin1 levels were not completely depleted, I hypothesized that other factors likely impaired growth, so I asked if the lack of H2Bub impaired transcription initiation through H3K4 methylation. Unexpectedly, H3K4Me₂ and H3K4Me₃ marks persisted despite the absence of H2Bub, implying that Ubp8 regulation in metabolic rewiring simultaneously impacts H2B ubiquitination and H3K4 methylation. Collectively, these findings have important implications for understanding a novel link between mitochondrial function and chromatin regulation, where Ubp8 plays crucial roles connecting both during metabolic rewiring. They also challenge the notion that H3K4Me₂ and H3K4Me₃ require H2Bub to persist, opening avenues to reconsider how these histone marks interact.

Genomic Plasticity Drives Adaptation to Tunicamycin Stress in *Cryptococcus neoformans*

Faculty Mentor: Paul Magwene, Ph.D.

Authors: Anna McPherson, Debra Murray, Claudia Ziri3n-Mart3nez, Paul Magwene

Abstract:

Cryptococcus neoformans is an opportunistic fungal pathogen and the causative agent of cryptococcal meningoencephalitis, a life-threatening infection that primarily affects immunocompromised individuals. *C. neoformans* encounters diverse stresses in the environment, including competition with other microbes that secrete inhibitory compounds. One mechanism by which fungi rapidly adapt to such stresses is aneuploidy, a change in chromosome copy number that can alter gene dosage and promote stress tolerance. In this study, we investigated genomic and phenotypic responses of *C. neoformans* to tunicamycin, a microbial toxin and inhibitor of N-linked glycosylation that induces endoplasmic reticulum stress. We discovered that tunicamycin induces distinct morphological changes in *C. neoformans* colonies compared to untreated controls. To investigate the genetic basis of this phenotype, we used two complementary approaches. First, we performed quantitative trait locus (QTL) analysis on tunicamycin-associated morphological variation in progeny derived from a cross between a clinical strain (Bt22) and an environmental strain (Ftc555-1). This analysis revealed a significant peak on chromosome 10. Since tunicamycin exposure is known to induce aneuploidy in *Cryptococcus*, we also performed whole-genome sequencing of morphologically distinct colonies to examine changes in genetic architecture associated with the phenotype. These analyses identified duplication of several chromosomes, although not chromosome 10, suggesting that multiple genomic mechanisms may contribute to adaptation under tunicamycin stress. To further investigate the role and stability of these chromosomal changes, we examined the effects of pre-adaptation and relaxed selection on colony morphology to evaluate whether stress-associated aneuploidy may be transient. Together, these results suggest that adaptation to tunicamycin stress arises through multiple layers of genomic change, including both locus-specific variation and dynamic aneuploidy, underscoring the role of genomic plasticity in fungal stress adaptation.

Investigating Ventral Striatal Activation During Reward Anticipation in Smokers Attempting to Quit

Faculty Mentor: Dr Maggie Sweitzer, Ph.D.

Authors: Nicol Milev, Maggie Sweitzer

Abstract:

Addiction neuroscience has introduced various theories on how dysregulation of the brain's reward circuit drives disordered substance use. The incentive-sensitization theory posits that chronic drug use develops hypersensitivity to the drug and related cues beyond the drug's initial pleasurable effects. This project aims to analyze data from a completed fMRI study using a rewarded guessing task to assess anticipation of smoking and monetary rewards in chronic smokers actively seeking to quit.

This analysis examined the relationship between smoking behaviors and reward-related activation to monetary and smoking rewards in the striatum, a key structure in the brain's reward circuit. Primary analyses focused on the ventral striatum (VS) during the baseline scan. Our primary objective was to use Cox proportional-hazards models in a survival analysis, with striatal activation as a predictor of time to relapse.

Participants (n = 29) were screened and trained prior to a baseline fMRI session. Following imaging, they completed a 4-week pre-cessation phase where they were instructed to use study VLNC (very low nicotine content) cigarettes and cigarette patches; they were also randomized into two possible behavioral treatment conditions. Following this, they completed a second fMRI scan before a 10-week quit attempt.

Imaging data was preprocessed using fMRIPrep; first- and second-level modeling were conducted using SPM-12. Analyses were ROI-based (masked for striatum) and focused on anticipation during trials where a reward could be won (Money/Puff) compared to trials with no reward (Neutral). Cox regression analyses were conducted in R by extracting eigenvariate estimates from ROIs within the striatum and including them in survival models.

We hypothesize that striatal activation will be blunted for monetary rewards and hyperactive for smoking rewards, respectively. These patterns of activation will be associated with same-day smoking behaviors and quit outcomes.

Ultimately, our findings will contribute to the growing literature investigating the striatum's role in reward circuit dysfunction, including how the brain differentially responds to smoking versus non-smoking rewards, following chronic substance use. Furthermore, this work will contribute to our understanding of the neural correlates that predict abstinence or relapse during a quit attempt.

Compressions of Care: Layperson CPR as a Social Performance and Cultural Practice

Faculty Mentor: Anne Allison, Ph.D.

Authors: Madeline C. Morrison

Abstract:

Sudden cardiac arrest (SCA) claims an estimated 350,000 to 430,000 lives annually in the United States. Fewer than half of victims receive layperson CPR, although immediate intervention can double or triple survival rates. This cultural anthropology thesis argues that persistent disparities in who receives care cannot be resolved through technical solutions alone because layperson CPR is a culturally mediated social performance. Drawing on ethnographic fieldwork, participant observation at CPR training events across North Carolina and Maine, semi-structured interviews, material culture analysis, and a Qualtrics survey of Duke undergraduates (analytic sample drawn from 175 total respondents, with item-level samples varying by question completion), this project examines the cultural forces shaping whether and for whom lay people intervene. CPR demands a moral inversion of touch, reframing intimate, forceful bodily contact as sanctioned care. This produces hesitation rooted in gendered anxieties around consent and bodily exposure. Standardized training models influence preparedness to perform CPR across different body types. Findings suggest that training manikins encode a narrow "default patient" that is white, lean, and androgynous. Survey results reveal a statistically significant 10-percentage-point gap in students' reported preparedness to perform CPR on bodies that diverge from this norm. Certification systems, Good Samaritan laws, and heroism narratives meant to scale this behavior portray intervention through logics of individualism, positioning CPR as an extraordinary act rather than a collective responsibility. This research calls for a cultural reorientation of CPR training that confronts the embodied hierarchies determining, long before hands compress a chest, whose body is legible as worth saving.

Beyond Pigmentation: Structural Contributions to Transparency in *Danionella cerebrum*

Faculty Mentor: Miranda Sinnott-Armstrong, Ph.D.

Authors: Hayley Navarro, Miranda Sinnott-Armstrong, Sönke Johnsen

Abstract:

Transparency is rare among vertebrates and remains poorly understood in fishes. *Danionella cerebrum*, a close relative of the zebrafish (*Danio rerio*), lacks skin pigmentation and also exhibits an unusual degree of optical transparency despite retaining hemoglobin, suggesting non-pigmentary structural adaptations producing that transparency. Here, we investigated the anatomical basis of transparency in *D. cerebrum* and several other transparent fish species using histological analysis. Comparative observations reveal that transparent fish have modified their muscle collagen, vasculature, and scale morphology. These features may reduce light scattering and improve tissue transparency, suggesting a structural explanation for whole-organism transparency in addition to pigmentation loss. Our findings demonstrate that transparency in *D. cerebrum* may arise from coordinated changes across multiple tissue types, highlighting the importance of internal architecture in vertebrate optical properties. This work establishes a morphological framework for future functional studies and further supports *D. cerebrum* as a tractable model for investigating biological transparency.

Zone-Dependent Attenuation of Renal Allograft Apoptosis by Localized PD-L1 Delivery

Faculty Mentor: Tatiana Segura

Authors: Jackie No, Sydney Jeffs, Tatiana Segura

Abstract:

Solid organ transplantation remains a life-saving intervention limited by the systemic toxicity of conventional immunosuppressive regimens, which broadly impair host immunity and carry significant off-target morbidity. A targeted approach—one that confines immunosuppression to the graft microenvironment—could preserve systemic immune competence while promoting donor-specific tolerance. Here we investigate the use of PD-L1 as a locally delivered immunomodulatory signal to suppress allograft-infiltrating T cells at the point of antigen encounter. PD-L1 engages PD-1 on T cells to deliver inhibitory signals that attenuate T cell receptor signaling and downstream activation cascades, thereby functionally dampening effector responses without systemic immunodepletion. Renal allografts were treated with PD-L1 at two doses (5 μ g and 25 μ g) prior to transplantation into allogeneic recipients. Standard histological assessment by Hematoxylin and Eosin and Periodic Acid-Schiff staining failed to distinguish treated allografts from untreated controls at the whole-tissue level, suggesting that any therapeutic effect operates at a spatial or cellular resolution below the sensitivity of conventional histomorphology. To interrogate graft viability at the cellular level, TUNEL staining was employed to quantify apoptotic cell death via DNA fragmentation. Untreated allografts exhibited markedly elevated apoptosis relative to native and isograft controls, consistent with immune-mediated rejection. PD-L1 treatment, particularly at the 25 μ g dose, significantly reduced apoptosis across the whole graft ($p < 0.0001$). Critically, zone-stratified analysis revealed that this protective effect was non-uniform across renal compartments: the papilla, inner medulla, outer medulla, and cortex each displayed distinct apoptotic profiles, with certain zones exhibiting more robust protection than others. These findings indicate that graft-localized PD-L1 is alloprotective and highlights immune cell infiltration as an overly simplistic measure of rejection, with evidence of robust and regionally specific shifts in viability in PD-L1 treated organs despite robust immune cell infiltration identified on H&E. Elucidating the cellular and immune landscape underlying this zone-dependent protection will require high-dimensional approaches such as flow cytometry and multiplexed tissue imaging (CODEX) to resolve immune infiltrate composition and spatial distribution with precision.

Insulin-like growth factor 2 (IGF2) Promotes Growth in Human Cardiac Organoids

Faculty Mentor: Dr Ravi Karra

Authors: Alícia Ogliari, Lauren Parker, Ravi Karra

Abstract:

Heart failure is a leading cause of death worldwide, affecting over 8 million people in the United States alone. A major barrier for curative therapies is the limited regenerative capacity of the adult mammalian heart. Prior work in our lab identified spatiotemporal coupling between cycling endothelial cells (ECs) and cycling cardiomyocytes (CMs) during physiologic growth in neonatal mouse hearts. Applying ligand-receptor analyses to scRNA-seq datasets from neonatal mouse hearts, we nominated IGF2 from cycling ECs to promote CM cycling via IGF1r. IGF2 is known to be required for CM proliferation during murine heart development and during heart regeneration in zebrafish and neonatal mice. Thus, we hypothesized that IGF2 could stimulate human CM proliferation. We generated human cardiac organoids (hCOs) from induced pluripotent stem cells and supplemented with 50 ng/mL recombinant IGF2 or vehicle. At differentiation day 15 (D15), IGF2-treated hCOs were significantly larger than controls (1.313 ± 0.016 , 1.000 ± 0.081 , $p < 0.0001$). Surprisingly, no difference was observed in the percentage of Ki67⁺ CMs between IGF2-treated and control hCOs ($0.874 \pm 0.0302\%$ vs $0.901 \pm 0.0381\%$, $p = 0.58$). Taken together with prior work in mice and zebrafish, these data suggest that IGF2 is necessary but not sufficient for CM proliferation. Ongoing studies with multiple doses of IGF2 aim to determine whether the increased size of IGF2-treated hCOs is attributable to changes in hCO morphology, CM size, or the expansion of non-myocyte cell populations. By leveraging a human-relevant model, this work provides mechanistic insight into pathways that modify CM cycling capacity.

Easy as it goes: Considering the nature of goal pursuit momentum

Faculty Mentor: Skyler Wyly

Authors: Danny Ortez Lagos, Lillian Curtis, Ella Lodewyk, Layla Axam, James Shah, Skyler Wyly

Abstract:

People pursuing goals experience momentum—a feeling that things are going their way—which boosts confidence and persistence. This research investigates what creates momentum during goal pursuit, focusing on perceptions of the rate and ease of progress, and the strategies people use to build momentum. Fundamental to the perception of momentum during goal pursuit are two factors: ease of progress (i.e., progress toward one's goals requiring less effort), and rate of progress (i.e., progress occurring more quickly). In two experimental vignette studies, using between-subjects (N = 122) and within-subjects (N = 274) designs, we systematically vary ease and rate of progress to examine momentum in work and health-related goals. Both ease and rate of progress were related to momentum, with momentum emerging more strongly when progress is both fast and effortless. In cross-sectional (N = 239) and longitudinal (N = 450) studies examining how the rate and ease of progress affect perceptions of momentum in real-world work and health-related goals, we similarly find that perceptions of the rate and ease of progress, and their combined synergistic effect, are related to the experience of momentum. Strategies focused on habituation and learning can increase an individual's momentum towards achieving goals and affect beliefs about goal momentum. In two studies, we focus on experiences of goal momentum and the specific strategies that lead to momentum. In Study 5 (N = 393), we examine how individuals' momentum-building strategies for habituation and learning in goal pursuit relate to perceptions of momentum on work and health goals. Both habituation and learning momentum strategies and their interactive effects were related to perceptions of momentum. Study 6 (N = 597) examines the relationship between individuals' momentum-building strategies, perceptions of rate of progress and ease of progress (i.e., momentum determinants), and their subsequent experience of momentum in health and work goals. For both health and work goals, momentum-building strategies and determinants of momentum were related to the experience of momentum in goal pursuit, and momentum determinants mediated this process. Taken together, these studies suggest that perceptions of ease and rate of progress lead to the experience of momentum, and that individuals can strategically build momentum on their goals.

Curtis, L.*, Ortez Lagos, D.*, Axam, L., Lodewyk, E., Wyly, S., & Shah, J. Y. (2026, April 16). Easy as it goes: Considering the nature of goal pursuit momentum [Poster session]. Duke University Undergraduate Research Symposium, Durham, NC, United States.

Building recombination maps for the gray mouse lemur using population data

Faculty Mentor: Anne Yoder, Ph.D.

Authors: Sajni Patel, Blair Blakeney, Carolina Segami, Anne Yoder

Abstract:

Recombination — the shuffling of genetic material during meiosis — is a key aspect of genetic diversity and genomic evolution, however meiotic recombination rates remain uncharacterized in many non-model systems, including mouse lemurs (genus *Microcebus*). Here, we estimate recombination rates for wild *M. murinus* (27 individuals) and *M. griseorufus* (20 individuals) using the population-based deep learning software ReLERNN. All individuals were sequenced with Illumina short-reads at mean 10X coverage. We compared the results of ReLERNN using 3 different filtering of called variants and testing different parameters. When we used autosomal biallelic variants that passed GATK hard filtering and assumed an upper ρ/θ ratio of 1.5 or no upper ρ/θ ratio at all, we obtained recombination estimates producing patterns most comparable to other primates. Without specifying an upper ρ/θ ratio parameter, we found the genome-wide recombination rate for *M. murinus* to be 2.76×10^{-9} and for *M. griseorufus* to be 2.71×10^{-9} . When using an upper ρ/θ ratio of 1.5, the estimated genome-wide recombination rate 3.48×10^{-9} for *M. murinus* and 3.09×10^{-9} for *M. griseorufus*, compared to estimates generated without an upper ρ/θ limit. We observed that as chromosome size decreased, recombination rate increased, but the relative recombination rate between both species depended on the chromosome. While we are confident in the relative recombination rate patterns observed between species and across chromosomes, low sequencing depth and uncertainty in parameter assumptions limits confidence in the absolute recombination rate estimates. Although lower coverage, low variant density, and the tendency of ReLERNN to average recombination rates across windows longer than typical hotspot lengths limited hotspot detection, the results provide progress toward the first population-based recombination estimates for these species.

Investigating FOXM1 and FOXO1 as antagonistic mediators of VEGF-induced cardiomyocyte cycling

Faculty Mentor: Dr Ravi Karra

Authors: Katelyn Peña, Anneka Beard, Michael Thomas, Ashley Williams, Lauren Parker, Ravi Karra

Abstract:

A key barrier to developing curative therapies for heart failure is that the adult mammalian heart, unlike that of neonatal mammals, cannot regenerate after injury. Identifying molecular targets that can reawaken regenerative capacity in the adult human heart is a promising therapeutic strategy. Previous work in the lab performed single-cell Hi-C on accessible regions (sciHiCAR) on human cardiac organoids (hCOs) stimulated with VEGF, a mitogen known to induce cardiomyocyte (CM) cycling, to identify differences in gene expression and chromatin accessibility between cycling and non-cycling CMs. From this data set, FOXM1 and FOXO1 emerged as antagonistic mediators of CM cycling, wherein FOXM1 expression is high, and FOXO1 activity is low in cycling CMs. To functionally confirm these associations, we first tested small molecule inhibitors of FOXM1 and FOXO1 in hCOs and neonatal rat ventricular myocytes (NRVMs). The FOXM1 inhibitor RCM1 blunted VEGF-induced CM cycling hCOs ($p=0.0067$) and significantly decreased cycling rate in NRVMs ($p=0.0191$). Conversely, treatment of NRVMs with the FOXO1 inhibitor AS1842856 significantly increased rates of CM cycling ($p<0.0001$). To more specifically evaluate FOXM1, I generated a lentivirus to overexpress FOXM1 in CMs (MHCK::GFP-FOXM1) along with a control lentivirus (MHCK::GFP). Compared to the control lentivirus, overexpression (OE) of FOXM1 significantly increased rates of CM cycling ($p=0.0001$). We then hypothesized that dual FOXM1 overexpression/FOXO1 inhibition would potentiate the pro-cycling effects of either modulation alone. To facilitate dual FOXM1 OE and shRNA-mediated FOXO1 inhibition, we embedded two candidate FOXO1 shRNAs and one non-targeting control (NTC) shRNA within a mir30E scaffold in the 3' untranslated region (UTR) of lentiviral constructs expressing GFP or GFP-FOXM1 downstream of the EF1a promoter. Using HEK293T cells, we have now confirmed that these can achieve a roughly 50% knockdown of FOXO1 expression relative to the non-targeting control (NTC), along with FOXM1 overexpression. Future experiments will test whether dual FOXO1 inhibition and FOXM1 overexpression can more potently stimulate CM cycling compared to each strategy alone.

Investigating a Type III Secretion System Effector cteB in Chromobacterium violaceum.

Faculty Mentor: Edward Miao

Authors: James Peng, Zoe Liu, Fiona Zhang, Ying Wang, Edward A. Miao

Abstract:

Chromobacterium violaceum is an environmental bacterium that typically does not infect immunocompetent individuals. However, infections can be lethal in those who are immunocompromised. *C. violaceum* serves as a valuable model for studying innate immune responses in vivo, as mice lacking T and B lymphocytes (Rag^{-/-}) can effectively clear high-dose infections through mechanisms including pyroptosis, a pro-inflammatory form of programmed cell death. Additionally, the *C. violaceum* infection model provides insight into the coordination of immune cell recruitment to infected hepatocytes, where they form organized structures known as granulomas, characterized by macrophages lining the outer layer of the lesion.

C. violaceum virulence depends on its Type III Secretion System (T3SS), a needle-like apparatus that injects effector proteins into host cells. Previous studies have shown that the *C. violaceum* effector CopE functions as an Rho-GEF that promotes bacterial entry into host cells, whereas CopC suppresses host defense by inhibiting apoptosis. In this study, we investigate another *C. violaceum* effector, CteB, whose purified form induced rapid cell death in HeLa cells. We generated a clean genomic deletion of CteB via allelic exchange and subsequently performed infection studies in mice.

Phenotypic Characterization of Emerging Naganishia Species Compared to Cryptococcus neoformans

Faculty Mentor: John Perfect, M.D.

Authors: Nikolai Piskulich, Jennifer L. Tenor, John R. Perfect

Abstract:

Cryptococcosis is a fungal meningitis caused by the *Cryptococcus neoformans/gattii* species complex; however, other rare *Cryptococcus* species, recently classified into the genus *Naganishia*, have clinical manifestations across both immunocompromised and immunocompetent patient types. These species may differ in stress tolerance, antifungal susceptibility, and virulence factors, which can affect treatment. The goal of this research is to phenotypically characterize *Naganishia liquefaciens*, *N. albida*, and *N. adeliensis* in comparison to *C. neoformans* strain H99 to evaluate dissimilarities. Growth of *C. neoformans* H99 and *Naganishia* was assessed by a spot dilution assay. Strains were inoculated/grown overnight, washed with PBS, and adjusted to 1×10^7 CFU/mL. Ten-fold serial dilutions (10^7 – 10^3 CFU/mL) were spotted (four microliters) onto YPD agar with different stress agents and incubated at varying temperatures for three days. Growth was imaged on days two and three. *N. liquefaciens* exhibited the broadest tolerance and maintained robust growth under most stress conditions. *N. albida* demonstrated high antifungal resistance but had reduced growth under osmotic and oxidative stress. *N. adeliensis* was the most sensitive overall, especially to oxidative and ER stress. *C. neoformans* H99 showed variable tolerance to stress conditions, with high sensitivity to the antifungal assay. These findings showcase species-specific stress tolerance, which may help predict the ecological niches where these species persist and guide antifungal therapies.

Parvalbumin Interneuron Immunohistochemistry in a Hippocampal Optokindling Mouse Model of Epilepsy

Faculty Mentor: Dr James McNamara Sr, M.D.

Authors: Emma Pophal, Yuhong Sun, Joshua Marek, James McNamara

Abstract:

Epilepsy is one of the most common neurological disorders, affecting ~70 million people worldwide, many of whom are children. Despite available anti-seizure medications, 20–30% of patients remain drug resistant, underscoring the need for mechanistic insights to guide disease-modifying therapies. Although inhibitory dysfunction has been studied in seizure models, parvalbumin (PV) interneuron density within the mossy fiber (mf)-CA3 microcircuit has not been examined following repetitive optical seizure induction. We investigated PV interneuron changes during progressive stimulus-evoked seizures using optokindling of the hippocampal mf-CA3 pathway. Mice expressing CheRiff channelrhodopsin in mossy fibers underwent repeated optical stimulation of the dorsal dentate gyrus over ~8 days, resulting in progressively severe seizures. Kindling was defined as at least one Class IV or higher seizure on 3 consecutive days. 24 hours after kindling, immunohistochemistry revealed a significant reduction in PV+ interneuron density in the ipsilateral dorsal CA1, CA2/3 and dentate gyrus of optokindled mice compared to their contralateral hippocampus. However, only in the CA2/3 region did optokindled animals show a significant reduction in PV+ cell density compared to controls, suggesting impaired GABAergic inhibition in the mf-CA3 microcircuit. These findings implicate PV interneuron loss in early epileptogenesis and highlight circuit-specific inhibitory vulnerability as a potential therapeutic target.

Hide-And-Seek: The Development of Randomization and Strategic Behavior Across Age

Faculty Mentor: Dorsa Amir

Authors: Angelie Quimbo, Julia Bainbridge, Gita Paladugu, Norah Rosanbalm, Beatriz Lopes, Dr. Dorsa

Abstract:

Researchers have long contended that humans lack the ability to randomize, but recent work suggests that randomization ability is highly sensitive to context. This raises an important question: are humans truly bad at randomizing, or do we lose the ability to randomize over development? Do we require particular strategic contexts to succeed in randomization tasks? This study examines the developmental determinants of strategic randomness, assessing whether younger children (aged 3-4) are better or worse at randomizing in a strategic interaction than older children (aged 7-8) and adults. Participants (n = 100) complete 15 repeated rounds of a simplified hide-and-seek game in which pairs alternate between hiding and seeking roles to engage in probabilistic reasoning and anti-coordination. Successful performance requires hidere to randomize their choices to avoid predictability, while seekers benefit from identifying patterns in their partner's behavior by detecting and exploiting regularities. Participants also complete age-appropriate behavioral games measuring pattern recognition, mentalization, false belief, and cognitive flexibility. Data collection is ongoing with adults, and planned analyses will examine the effects of age on randomization behavior using linear probability models. This research could further our understanding of whether being able to randomize one's actions is an ability that is lost over the course of development or whether it never appears strongly in humans at all. By situating randomization within a developmental framework, this project aims to advance understanding of which contexts drive human randomization and impact performance.

Learning from failures and successes driven by value perceptions

Faculty Mentor: Dr James Shah, Ph.D.

Authors: Skyler Wyly, Jaclyn Rogers, Zhuying Guo, James Shah

Abstract:

With nearly every experience designated as successes or failures, people may iteratively develop attitudes toward these experiences, which may shape perceptions of their value for learning. Learning value perceptions (LVP) are how individuals view successes and failures through the subsequent lessons that can be learned from these experiences. Four preregistered studies examine how learning value perceptions may impact well-being, goal progress, and feedback behaviors. A study (N = 262) measuring progress on two goals over a two-week interval suggests that LVP fully mediates the effect of attitudes toward success and failure on feedback and goal progress and that more positive attitudes toward success and failure are associated with overall well-being. Two studies (N = 323; N = 322) link LVP to a range of feedback behaviors, such as feedback-seeking, and failure-centric self-regulation, like dealing with errors adaptively. Lastly, a pattern-recognition experiment (N = 328) examines how LVP affects learning from feedback and expectancies. These studies demonstrate the potential impact of learning value perceptions on how people interact with experiences and engage with feedback.

To Trust or Not to Trust: Assessing the Role of Race/Ethnicity and Accent in Trust Decisions Toward Human and AI Counterparts

Faculty Mentor: Angela Vieth

Authors: Annarose Romanelli, Angela Vieth

Abstract:

Previous research has shown that incongruence between a person's race and accent (e.g., a White person speaking in strong Spanish-accented English) leads to expectancy violations which can cause intensified perceptions of the speaker. While previous work has documented effects on perceptions of speakers' warmth and competence, little work has focused on the resulting changes in social behavior toward the speaker, including behaviors that indicate trust. Furthermore, data is limited on whether expectancy violation effects also may occur in interactions with artificial intelligence (AI) assistants. By employing an investment game, this study will investigate: (1) Do variations in race/ethnicity-accent pairings of White and Hispanic human counterparts affect our willingness to trust them? (2) Are the effects similar if the counterparts are recognized as artificial intelligence (AI)? An undergraduate sample (N = 80) of White, native English speakers will be used to explore whether speaking with an accent (Spanish or standard American English) unexpected given a person's ethnicity (Hispanic or White) affects subjects' trust in that person. Trust will be quantified by the amount of money the subject invests in their partner in the investment game. It is predicted that partners who positively violate expectations (e.g., Hispanic target with a standard American English accent) will elicit the highest levels of trust, while the opposite (e.g., White target speaking in a Spanish accent) will elicit the least, and that fully ingroup pairings will be trusted more than those that are categorized as completely out-group. Finally, AI-labeled partners are expected to be trusted less overall, though similar patterns across race/ethnicity-accent conditions are anticipated. These findings would suggest that our trust is biased through variations in face and accent cues, and how well they align with our expectations. This has significant implications, particularly for second-generation Americans, with respect to day-to-day interactions, legal rulings, and employability. The conclusions also may help companies personalize AI assistants in a way that enhances customers' perceptions of their trustworthiness.

Social Experience Dependent Modulation of Immune Gene Expression in the Drosophila Brain

Faculty Mentor: Pelin Volkan, Ph.D.

Authors: Sydney Ross, Shayna Scott, John Ianotta, Chengcheng Du, Apollo Josephson, Pranita Sutrave, Claire Li, Qiwen Wu, Pelin Volkan

Abstract:

Social isolation increases the likelihood of neuropsychiatric and neurodegenerative diseases, with emerging evidence suggesting that impaired neuroinflammation may underlie many of these conditions. Recent research has linked immune dysfunction to various neuropsychiatric and neurodegenerative disorders, emphasizing the immune system's crucial role in maintaining brain health and influencing behavior. Peptides associated with cytotoxicity in Alzheimer's Disease have been identified as antimicrobial peptides (AMPs), supporting the idea that immune dysfunction is a key factor in neurodegenerative disorders. Changes in immune gene expression within the central nervous system, influenced by social experiences, can impact brain function and behavior. However, the mechanisms by which social experiences affect immune gene expression patterns and their influence on the brain remain unclear. In *Drosophila melanogaster*, as in many vertebrates, social isolation elevates certain behaviors while disrupting sleep, learning, and memory. Our bulk RNA profiling experiments on grouped and isolated adult male *Drosophila melanogaster* brains show that group housing significantly increases the expression of immune genes, particularly AMPs. In the *Drosophila* nervous system, AMPs have been found in neurons and fat body cells surrounding the brain, where they play important roles in modulating learning, memory, and behaviors such as sleep. Olfactory pheromone circuits mediated by the Or47b and Or67d pheromone receptors have opposing effects on changes in AMP expression induced by group housing. The transcription factors Fruitless^M and Doublesex^M, which are expressed in the central circuits for socially driven behaviors and process social information, also have antagonistic effects on the social modulation of gene expression. Our observations show that AMPs exhibit distinct neuronal cell body expression patterns in the adult *Drosophila* brain and ventral nerve cord, especially in circadian neurons. Likewise, our work indicates that AMPs exhibit distinct neuronal processes expression patterns in the adult *Drosophila* brain, particularly in sensory and serotonergic neurons. Our findings imply that AMPs may have important, cell-type-specific roles in the nervous system, which could be affected by social stimuli to influence behaviors or maintain neuronal homeostasis.

Impact of oral contraceptives on resting metabolic rate

Faculty Mentor: Herman Pontzer, Ph.D.

Authors: Seneca Russell, Mary Joy, Herman Pontzer

Abstract:

Background: Resting metabolic rate (RMR) accounts for the largest share of daily energy expenditure, and even small disruptions can affect weight regulation, energy balance, and overall metabolic health. Existing research on if/how oral contraceptives (OCs) impact RMR is inconsistent. Clarifying whether OCs influence RMR is important given their widespread use among reproductive-age women.

Objectives: This study examines whether oral contraceptive use is associated with differences in RMR in women 18–30 and whether RMR varies across the follicular and luteal phases of the menstrual cycle.

Methods: RMR was measured via indirect-calorimetry during two laboratory visits per participant (n=21). Participants were classified as either OC users (n=9) or naturally-cycling controls (n=12). Linear models assessed associations between OC status and RMR while controlling for age, fat-free mass, menstrual phase, and visit. Phase-specific t-tests compared within-individual follicular–luteal differences and between-group differences.

Results: OC use was a significant predictor of RMR ($\beta = 193$, $p < 0.01$, $t = 2.91$) for the entire sample. By phase, this significance remained in the follicular phase ($\beta = 213$, $p = 0.03$, $t = 2.42$), but not for luteal phase ($\beta = -20.6$, $p = 0.85$, $t = -0.20$). Welch t-tests yielded significant differences across OC status for both phases (F: $t = -4.02$, $df = 14.6$, $p < 0.01$; L: $t = -2.22$, $df = 13.5$, $p = 0.04$).

Conclusions: Findings provide evidence that OC use meaningfully alters RMR in young adult women, and this impact is stronger in follicular phase than luteal. More work should be done on the physiological mechanism driving these results to better understand evolutionary energetics and how modern reproductive interventions shape energy expenditure patterns and physiological variation in contemporary human populations.

Stability-Based Proteomic Methods Add Value to Activity-Based Protein Profiling Studies

Faculty Mentor: Michael Fitzgerald, PH.D.

Authors: Diego J. Sanson, You Zou, Jianli Wu, Gibeom Nam, Ssu-Yu Chen, Jiyong Hong, Jen-Tsan Ashley Chi, Michael C. Fitzgerald

Abstract:

Covalent inhibitors offer powerful therapeutic advantages over non-covalent inhibitors, but like non-covalent inhibitors they require comprehensive profiling to define their on- and off-target activities. Here, we report on the use of two stability-based proteomic methods, Stability of Proteins from Rates of Oxidation (SPROX) and Thermal Protein Profiling (TPP) to identify protein targets of covalent inhibitors using the KRASG12C inhibitor, ARS-1620, and the proteins in H358 cell lysates as a model system. Both methods identified ligand-induced protein folding stability shifts, collectively recovering the known on-target KRAS as well as multiple off-targets. Comparative analyses of the SPROX and TPP results with previously published pull-down datasets highlighted aldehyde dehydrogenase 1A3 (ALDH1A3) as a reproducible off-target that was missed in prior work using activity-based profiling methods. MS-based covalent site mapping identified C314 as the major ARS-1620 modification site on ALDH1A3, and enzymatic assays confirmed dose-dependent inhibition. Covalent docking supported a favorable binding pose within the retinal-binding pocket. Functionally, ALDH1A3 knockdown reduced ARS-1620-mediated cell killing, supporting the role of ALDH1A3 in ARS-1620's mode-of-action. Together, these findings not only demonstrate that stability-based proteomics provides a valuable and effective strategy for covalent drug target identification, but also expand our knowledge of ARS-1620's biological activity.

The Duration of Temporary Markings on Bottlenose Dolphin Dorsal Fins; Insights to Improve Photo-Identification

Faculty Mentor: Andrew Read, Ph.D.

Authors: Naomi Scott, Andrew Read, Kim Urian, and Austin Allen

Abstract:

To better understand the dynamics of secondary markings used for photo-identification, we estimated the accumulation rate and healing time of tooth rakes and other temporary markings on the dorsal fins of nine bottlenose dolphins (*Tursiops truncatus*) maintained at Dolphin Quest Bermuda. This controlled setting allowed us to monitor the evolution and duration of different mark types over a period of six years to identify the most reliable features for photo-identification. For each mark, we calculated duration from appearance to disappearance and assigned them to one of three categories: Tooth Rakes, Scratches, and marks of an origin that Could Not Be Determined (CNBD). Each mark was categorized as Dark, Light, or Faded. Marks generally initially appeared dark, then quickly lightened as part of the healing process. In total, we documented 318 tooth rakes, 92 scratches, 2 nicks, and 85 CNBD. Of these, we used 233 tooth rakes, 64 scratches, and 50 CNBD with a dark phase to calculate the average “Dark to Faded” duration. We also documented the acquisition of two permanent dorsal fin nicks, which were retained throughout the recording period. Tooth rakes lasted an average of 6.19 months; scratches lasted an average of 4.79 months, and CNBD marks had a similar average duration of 4.61 months. The tooth rakes had a much shorter duration than in studies of wild populations that experience cooler water temperatures; the relatively warm water at Dolphin Quest Bermuda likely accelerated epidermal healing. We conclude that tooth rakes can be useful for markings for short-term photo-identification, especially in conjunction with permanent marks such as nicks. Future studies should be conducted in other locations to track the duration of secondary markings on dolphins to provide region-specific recommendations for photo-identification.

Ring-Opening Polymerization of Ambrettolide: A Path to Nanofiber Based Scaffolds for Tendon Repair

Faculty Mentor: Matthew Becker, Ph.D.

Authors: Robert O. Silzer, Nicola G. Judge, Matthew L. Becker

Abstract:

Due to low cellularity and poor vascularization, tendons have limited regenerative capacity following traumatic injury. Current clinical treatments typically achieve partial functional recovery and form tissue that is prone to re-injury. The newly formed tissue consists of disorganized collagen and tenocytes with inadequate morphology, resulting in tendons that are less elastic and mechanically weaker. Aligned nanofiber scaffolds have shown promise as therapeutic platforms for tendon injuries as they mimic tendon fibrous microarchitecture and promote organized tissue regeneration. We aimed to fabricate a novel aligned nanofiber scaffold derived from the synthetic material poly(ambrettolide) (poly(Amb)). Like other polyesters, Poly(Amb) is semi-crystalline, biologically inert, and resists hydrolytic degradation for up to one year. Uniquely, it contains an alkene handle that enables for photo-functionalization of fiber scaffolds without additional synthetic steps beyond the ring-opening polymerization of ambrettolide. In this work, we report the synthesis of poly(Amb) using $\text{Mg}(\text{BHT})_2(\text{THF})_2$ as the catalyst for the first time. Synthetic optimization yielded end-group fidelity and high targetable molecular weights. Thermal and mechanical analysis of the bulk polymer showed semi-crystalline properties and extensibility with regions of elastic deformation. Aligned poly(Amb) nanofiber scaffolds were fabricated by electrospinning and demonstrated mechanical properties that were comparable to triceps, tibialis, and supraspinatus tendons. Thiol-ene "click" surface functionalization of aligned nanofibers demonstrated a viable strategy for peptide functionalization, which can enhance cell adhesion and proliferation during future in vitro studies. Overall, poly(Amb) aligned nanofiber scaffolds demonstrated potential as a therapeutic platform for improving tendon functional recovery and warrant further investigation in physiologically relevant models.

Quantitative TRUPATH Analysis of GLP-1R–Mediated G-Protein Signaling by Endogenous and Therapeutic Agonists

Faculty Mentor: Sudha Shenoy, Ph.D.

Authors: Neel Singh, Sudha Shenoy

Abstract:

Glucagon-like peptide1 (GLP-1) receptors (GLP-1Rs) play a key role in regulating central nervous system functions, particularly within hypothalamic and brainstem circuits that control appetite, nausea, and reward processing. Although therapeutic GLP-1R agonists such as semaglutide, tirzepatide, and retatrutide are widely used to treat metabolic disorders, it remains unclear how these drugs differentially activate intracellular signaling pathways compared to the endogenous hormone GLP-1. This project uses TRUPATH bioluminescence resonance energy transfer (BRET) technology to quantitatively examine GLP-1R–mediated Gs/cAMP signaling as a model for how neuromodulatory signals give rise to intracellular responses in neurons. HEK-293 cells expressing GLP-1Rs and TRUPATH biosensor components will be stimulated with GLP-1, semaglutide, tirzepatide, and retatrutide at controlled concentrations. BRET and bioluminescence signals will be measured to evaluate agonist-dependent activation of the Gs/cAMP pathway. Signal magnitude and efficacy will be compared across all agonists to determine whether therapeutic compounds produce distinct signaling profiles relative to the endogenous ligand. Experimental observations will be integrated with existing neuroscience literature on GLP-1–mediated control of appetite, reward behavior, and nausea. By directly measuring proximal GLP-1R signaling events, this study aims to identify whether clinically used GLP-1R agonists differentially engage intracellular pathways that may contribute to their behavioral and neurological effects.

Disrupted Serotonin (5-HT) from Maternal High Fat Diet Effects on Glutamate and Gamma Amino Butyric Acid (GABA)

Faculty Mentor: Staci Bilbo, Ph.D.

Authors: Stanley, L., Patton, M., Sun, W., & Bilbo, S.

Abstract:

A maternal high-fat diet (mHFD) is connected to a higher likelihood of children developing neuropsychiatric disorders such as autism spectrum disorder (ASD), attention deficit hyperactivity disorder (ADHD), depression, and schizophrenia. The onset of these neuropsychiatric disorders is linked to deviation from normal serotonin (5-HT) levels throughout the brain and body. More specifically, hyperserotonemia, high levels of 5-HT in the blood, accompanied by lower 5-HT in the brain, is associated with ASD, while hyposerotonemia and low levels of 5-HT in the brain are linked to ADHD. Moreover, hypofunction of 5-HT neurons is implicated in depression, whereas hyperfunction is connected to schizophrenia. Also, our lab previously observed increased microglial phagocytosis of 5-HT in the dorsal raphe nucleus (DRN) due to a mHFD. Here, we investigated the cascading effect of these gestational changes in 5-HT attributed to a mHFD to defects later in adulthood in Glutamate, an excitatory neurotransmitter, and Gamma Amino Butyric Acid (GABA), an inhibitory neurotransmitter. We chose to look into these synapses because 5-HT is known to influence synapse formation, connectivity, and network construction during development. To this end, we collected adult male DRN samples treated with a mHFD and used immunohistochemistry to image postsynaptic density protein (PSD95) found in glutamatergic systems, GABA postsynaptic scaffolding protein Gephyrin, and synaptic vesicle protein synaptophysin. Then, we used SYNBOT to analyze the colocalized puncta count consisting of PSD95 and Gephyrin overlaid with synaptophysin to observe any deviation in glutamate and GABA in the mHFD mice versus the control group. We found no change in the number of glutamatergic synapses, and no change in the number of GABAergic synapses. These findings suggest that damage to 5-HT from a mHFD does not further disrupt the function of glutamatergic synapses in adulthood.

LCP1 as a Prognostic Biomarker and Therapeutic Target: A New Hope for Patients with Metastatic Chondrosarcoma

Faculty Mentor: Dr Julia Visgauss

Authors: Ava J. Strohmeyer, Nicholas Guardino, Caleb Watson, Makoto Nakagawa, John Martin, Trudy Zou, Puvindran Nadesan, Aron Mebrathu, Ariana I. Matarangas, Kevin Betsch, Vijitha Puvindinsan, Jason A. Somarelli, Benjamin Alman, Julia Visgauss

Abstract:

Chondrosarcoma (CSA), the second most common primary malignancy of bone, exhibits aggressive behavior and intrinsic resistance to chemotherapy and radiotherapy, resulting in extremely high mortality rates in patients with advanced disease. Wide en bloc resection is the standard treatment, but is often only effective in early-stage disease, and no adjuvant therapies exist for late-stage and/or metastatic CSA. Furthermore, current grading systems are poorly predictive of metastatic potential, and few prognostic biomarkers have been identified. As such, there is an urgent unmet need to identify the molecular mechanisms driving metastatic disease progression, both to improve prognostication and to develop novel therapies for patients facing dismal prognoses. In this study, we compared gene expression profiles between metastasizing and non-metastasizing patient-derived cell lines, identifying lymphocyte cytosolic protein 1 (LCP1) as the most significantly upregulated gene in metastasizing CSA cells. Immunohistochemical analysis of patient tumor samples demonstrated that LCP1 expression increases with tumor grade, and analysis of a large independent clinical cohort confirmed elevated LCP1 expression correlates with poor survival, establishing LCP1 as a clinically relevant biomarker of aggressive disease. Genetic knockout of LCP1 with CRISPR-Cas9 significantly reduced cellular motility, invasive capability, and extracellular matrix adhesion. Lentiviral overexpression, conversely, enhanced these pro-metastatic behaviors. Together, these bidirectional findings confirm that LCP1 causally drives pro-metastatic behavior in chondrosarcoma cells. In a murine model of pulmonary metastasis, LCP1 knockout markedly reduced lung tumor burden, establishing its functional role in metastatic colonization in vivo and establishing LCP1 as a causal driver of metastatic progression. Treatment with Oroxylin A, a direct inhibitor of LCP1, recapitulated the phenotypic effects of LCP1 knockout in vitro, significantly reducing the migratory and invasive capabilities of CSA cells. Critically, these anti-metastatic effects were achieved without affecting cell viability, identifying Oroxylin A as a novel and promising therapeutic candidate for metastatic chondrosarcoma. Collectively, these findings establish LCP1 as a clinically relevant driver of metastatic progression in CSA, a prognostic biomarker and a promising pharmacological target for patients who lack effective treatment options.

Maternal High-Fat Diet Impacts Negative Affect Behaviors in a Sex-Specific Manner

Faculty Mentor: Staci Bilbo, Ph.D.

Authors: Will Sun, Ben Horvath, Michael Patton, Staci Bilbo

Abstract:

A maternal high-fat diet (mHFD) is correlated with higher diagnostic rates of neurological disorders in offspring, including autism, depression, and substance use disorders. Prior work from our lab found that mHFD impacted reward processing and positive valence behaviors in male offspring through microglial-dependent modulation of serotonin projections to the nucleus accumbens. Since the nucleus accumbens encodes both positive and negative valence, we next explored the effects of mHFD on negative affect behaviors. Prior studies have found that mHFD affects anxiety, fear, and aversive behaviors in adult mice; however, such findings are inconsistent and vary among high-fat models. Here, we assessed aversive, anxiety-like, and depressive-like behaviors in adult male and female offspring (P60-90) using a 5-day behavior battery.

We observed behavioral differences that were sex-specific and selective across different domains. In males, mHFD offspring exhibited significantly increased anxiety-like behavior compared to maternal low-fat diet (mLFD) offspring, spending less time in the open arms of an elevated plus maze. However, we only observed nonsignificant trending effects of mHFD on male offspring in the open field test and conditioned place aversion test. We also observed no difference in depressive-like behaviors, measured through a nest building assay and sucrose spray test, between mHFD and mLFD male offspring.

Conversely, mHFD females exhibited increased sensitivity to aversive stimuli, spending significantly less time in the conditioned chamber. Yet, we saw no difference in anxiety-like behaviors between mHFD and mLFD females. We are further interested in how chronic stress may interact with mHFD to precipitate negative affective behaviors in adult offspring. Future work will then investigate the macro-circuits underlying sex-specific effects of mHFD on negative affective behaviors through immunohistochemical staining and c-Fos screenings.

Potential Therapeutic Effects of Omega-5 Fatty Acids in Endometriosis

Faculty Mentor: Zhiqing Huang

Authors: Lila Teitle, Zhiqing Huang

Abstract:

Endometriosis is a chronic condition which causes ectopic growth of endometrial lining outside the uterus. This condition affects 10–15% of women aged 15–49 in the United States with up to 50% of women diagnosed experiencing infertility, making it a significant concern for women of reproductive age. Recent studies have identified a role of ferroptosis, a type of cell death linked to the presence of excessive iron and lipid metabolism, in curbing proliferation of ectopic endometrial cells. This study seeks to investigate various ferroptosis inducers in vitro for their potential therapeutic value in treatment of endometriosis. As a major component of the endometriosis environment, peritoneal fluid was also studied for its effects on the ferroptosis of endometriosis cells. The Omega-5 fatty acids α -ESA and PunA were found to be capable of ferroptosis induction with α -ESA producing stronger effects as a ferroptosis inducer. I also demonstrated that ascites, a fluid which is similar to the peritoneal fluids surrounding endometrial lesions, is effective to inhibit ferroptotic cell death caused by α -ESA and erastin. This suggests that the inhibitory influence of peritoneal fluids on ferroptosis must be considered in treatment of the disease. These results provide evidence that Omega-5 fatty acids may be a viable treatment option for endometriosis patients and provide a basis for future exploration into the inhibitory role of peritoneal fluids in ferroptotic cell death.

Exploring Osmotic Stress-Induced Effects on Calcium Signaling and ECM Homeostasis in the Meniscus

Faculty Mentor: Amy McNulty

Authors: Nikol Trajkovski, A'anna Kelly, George Truskey, Amy L. McNulty

Abstract:

The menisci are fibrocartilaginous tissues essential for proper knee function, which contain inner and outer zones that are distinguished by their extracellular matrix (ECM) composition, vascularity, and differential healing abilities. During joint loading, cyclical fluid flux alters tissue osmolarity, regulating cell signaling and ECM homeostasis. In cartilage, osmotic stress is transduced by calcium-permeable channel Transient Receptor Potential Vanilloid 4 (TRPV4); however, the role of TRPV4 in mediating osmotic stress in the meniscus is unknown. We hypothesized that TRPV4 mediates osmotic stress-induced calcium signaling and ECM homeostasis more prominently in the cartilage-like inner zone than the outer zone. Porcine inner and outer meniscal explants and isolated cells were exposed to hypo- (210 mOsm) or hyper-osmotic (410 mOsm) conditions with or without broad calcium channel inhibition (Ruthenium Red, RR) or TRPV4 inhibition (GSK205). ECM composition and intracellular calcium dynamics were measured. Osmotic stress alone had no detectable effect on ECM composition in either region. However, inhibition of calcium channels revealed region-specific effects on matrix composition. In inner explants, both RR and TRPV4 inhibition decreased sulfated glycosaminoglycan (sGAG) content, and RR reduced tissue water content. In cells, RR reduced average intracellular calcium during hypo-osmotic stimulation in inner cells and during hyper-osmotic stimulation in outer cells. TRPV4 inhibition increased average intracellular calcium under hypo-osmotic conditions in inner cells, while outer cells exhibited no detectable responses. Tissue ECM changes and cellular responses under hypo-osmotic stress to TRPV4 inhibition suggest TRPV4-mediated calcium influx contributes to matrix regulation in the inner meniscus. In contrast, the lack of detectable ECM changes and TRPV4-dependent calcium responses in the outer meniscus, combined with a calcium response to RR, indicates that other calcium channels (e.g., other TRPV, Piezo, and ryanodine receptors) likely mediate hyper-osmotic signaling. Despite measurable calcium signaling responses, osmotic stress alone did not significantly alter ECM composition, suggesting that osmotic stimulation may be a modest regulator of meniscal homeostasis. Collectively, these findings identify TRPV4 as a transducer of osmotic stress and modulator of ECM maintenance in the inner meniscus, highlighting its role in regional matrix homeostasis.

Insights into the lung–brain axis in immunity: How microglia and pulmonary neuroendocrine cells respond to influenza A and air pollution

Faculty Mentor: Staci Bilbo, Ph.D.

Authors: Ariana Vaida, Sarah Monroe, Trisha Vaidyanathan, Dang Nguyen, Staci Bilbo

Abstract:

The lung–brain axis has drawn increased attention for the communication between these two organs during disease states. Studies have shown there are peripheral signals that impact the brain during respiratory challenges, such as infection or exposure to air particulate matter (PM). Diesel exhaust particles (DEP) are used to model PM because the particles are common byproducts of diesel fuel combustion. Upon peripheral signaling, microglia mediate the neuroinflammatory effects; however, the mechanisms of lung–brain communication are not fully understood. This thesis investigates these mechanisms, particularly via pulmonary neuroendocrine cells (PNECs) which uniquely detect and respond to environmental stressors. I hypothesized that neurotransmitters secreted by PNECs, like CGRP and GABA, are used to signal to the central nervous system (CNS) and may impact microglial activation. Sustained microglial changes were identified in the hippocampus and insular cortex after 4–week recovery from repeated exposure to DEP. To understand whether short–term exposure alters the CNS or peripheral response to DEP, I assessed changes in microglia morphology and CGRP expression at three different timepoints: 1, 3, and 14 days post–exposure (dpe). CGRP was upregulated in the lungs 1 dpe; however, I did not observe a significant increase in ramification of microglia in the hippocampus until 3 dpe. Therefore, PNECs in the lungs respond rapidly, whereas the brain response is on a different time scale. My findings align with similar brain region–specific outcomes activated after non–neurotrophic influenza A virus (PR8 infection), suggesting that these brain regions do in fact respond to multiple respiratory challenges. In parallel, I investigated pulmonary immune activation following recovery of acute influenza infection in TRAP2 mice. Expression of pro–inflammatory cytokines and recruitment of macrophages in the lungs was increased among sick mice with reactivated neurons. When CGRP was blocked by the drug rimegepant (Nurtec), there was no change in the immune engram response, challenging my hypothesis that CGRP signaling is influential in the formation of the immune engram. Further investigation of neuronal activation and CGRP reception is needed to better inform the role of PNECs in modulating microglial activation and neuroinflammatory responses during respiratory challenges.

Comparison of microglial transcriptomic gene panel for prediction of Alzheimer's Disease with GWAS genes

Faculty Mentor: Ornit Chiba-Falek, Ph.D.

Authors: Srilakshmi Venkatesan, Michael Lutz, Keats Shwab, Zhaohui Man, Rosella Zheng, Ornit Chiba-Falek

Abstract:

Introduction: Diagnosis of Alzheimer's Disease (AD) currently relies heavily on clinical presentation and the biomarkers pTau217 and A β 42. However, neuropathological pathogenesis can be initiated prior to clinical presentation which complicates the use of these biomarkers for personalized diagnosis and treatment. Through leveraging transcriptomic microglial signatures in the brain and transferring these signatures to blood, we sought to develop a transcriptomic plasma biomarker panel for early-stage diagnosis of AD based on microglial gene expression. In developing the gene panel, we used a variety of statistical methods to select the DEGs reflected in microglia and made a label transfer of diagnoses to transcriptomic data in blood.

Methods: To identify whether the DEGs expressed in the selected microglial gene panels were represented in most recent GWAS studies, we conducted an analysis to determine if there was any overlap between the Bellenguez 2022 Alzheimer's Disease GWAS. We also conducted pathway analysis on the overlapping genes.

Results: Using a panel of 300 genes, AUC for blood samples was 0.7 with strong accuracy to predict the AD class (75%) however accuracy to predict cognitively normal individuals was 53%. The accuracy and specificity of the 50 and 30 panels demonstrated better balance between prediction of the AD and normal classes (65–71%) with similar AUC (0.7) to the 300 gene panel. The 30 gene panel contained two GWAS genes: ELDR and PTDGR. The 50 gene panel included one gene: SERPINE1. The 300 gene panel contained 13 genes: CELF2, PICALM, ELMO1, ATP8B4, SORL1, TRIO, UBE2K, LUC7L3, RBM47, RASA1, JAZF1, HERC1 and CMIP. This set of genes is involved in multiple signaling pathways, including RHO GTPases, RAS GTPases, and MAP kinases, which are critical for cytoskeletal remodeling and cellular signaling. These genes are also involved in endocytosis, RNA splicing and neuron projection development.

Conclusions: With the most substantial GWAS enrichment in the 300 gene panel, there is strong functional significance of genes associated with AD pathobiology. The findings demonstrate that the gene panels capture the genetic signals established in GWAS, supporting the robustness of our microglial gene panel for the blood-based transcriptomic biomarker.

The Role of Cellular Adhesion in Non-stem Cell Tissue Repair in the Drosophila Hindgut

Faculty Mentor: Jessica Sawyer, Ph.D.

Authors: Kenneth Vergel de Dios, Jessica Sawyer, Donald T. Fox

Abstract:

Tissues are maintained by the activity of somatic cells in order to preserve homeostasis. If cells are lost via injury, tissues have various repair mechanisms to compensate for the damage. Broadly, tissues respond to cell loss via stem cell or stem cell-independent responses. While stem cells differentiate to replace lost cells, tissues without stem cells rely on alternative mechanisms. While stem cell-mediated repair has been extensively studied, stem cell-independent mechanisms remain less well understood. The *Drosophila* hindgut serves as a model to study these responses, as it is not maintained by active stem cells.

Two key stem cell-independent mechanisms are observed in the hindgut: compensatory hypertrophy in the pylorus and a cell longevity response in the ileum. In the pylorus, cells enlarge through endoreplication to restore lost tissue content. This response is tightly regulated, suggesting feedback mechanisms that prevent excessive growth and preserve epithelial integrity. In contrast, the ileum exhibits a cell longevity response, where mature cells resist apoptosis and fail to regenerate following damage.

Importantly, these responses are age-dependent. Young hindgut cells are more sensitive to caspase-mediated apoptosis, with compensatory hypertrophy failing to fully restore lost tissue and the ileal cell longevity response breaking down under injury. This highlights a developmental difference in how tissues respond to damage and suggests that regulatory mechanisms shift with age.

Cell adhesion has emerged as a potential regulator of these processes. My project investigates the role of E-cadherin, a transmembrane protein involved in cell-to-cell adhesion, in both compensatory hypertrophy and cell longevity. E-cadherin is upregulated in young animals, further highlighting the importance of age-dependent investigation. Using genetically induced injury models, I examined how altering E-cadherin expression affects these responses in both mature and young hindgut tissues.

Our findings show that modifying E-cadherin expression does not significantly affect compensatory hypertrophy in the adult pylorus or the cell longevity response in the adult ileum. However, in young animals, reducing E-cadherin preserves both compensatory hypertrophy in the pylorus and the cell longevity response in the ileum. Our results introduce cell adhesion proteins as a means to study the mechanisms underlying compensatory hypertrophy and cell longevity in hindgut tissue maintenance.

Divergence of Assisted Entanglement in the Continuum Limit of Scalar Fields

Faculty Mentor: Natalie Klco, Ph.D.

Authors: Siddharth Vijaymurugan, Boyu Gao, Natalie Klco

Abstract:

Quantum field theory is a framework for understanding fundamental interactions where quantum information is inherently present. Exploring entanglement enhances our understanding of quantum information structure of quantum fields, ultimately informing future efforts to utilize this physical resource in quantum information processing applications. Recently, it has been shown that in a partition of a scalar field into disjoint regions A, B, and an external environment C, local measurements performed on C assisted by classical communication can exponentially enhance the entanglement between A and B [1].

Previous results [1] suggest that this assisted entanglement might remain finite at large separations between A and B in the continuum limit. If confirmed, this assisted entanglement would be a fundamental, distance-independent quantity that captures the field's intrinsic quantum informational structure.

We extend these results by numerically investigating the behavior of this assisted entanglement in the continuum limit. We model a discretized lattice scalar field and increase its pixelation while preserving the dimensions of the system. We explore the parameter space defined by the dimensionless quantities mr , md where m is the mass of the field, d is the size of each A and B, and r is their separation distance. By systematically sampling across the mr - md plane, we observe the scaling behavior of the entanglement as lattice spacing goes to zero. This analysis reveals that the entanglement diverges in the continuum limit.

This divergence is analogous to the standard divergence of entanglement entropy in scalar fields, resulting as a consequence of UV divergence. As lattice spacing approaches zero, the measurements performed on the external volume (C) resolve the increasingly higher-energy content of the field. Since these measurements inform the joint state of A and B, the UV divergence is inherited by the assisted entanglement. This parallels prior work [2], where a finite topological entanglement entropy was isolated from the divergent entropy. Our work suggests that a similar technique might be applicable to identify another topologically invariant quantity derived from the assisted entanglement.

[1] B. Gao and N. Klco, "Finite Gaussian assistance protocols and a conic metric for extremizing spacelike vacuum entanglement," *Phys. Rev. A* 113, 012430 (2026).

[2] A. Kitaev and J. Preskill, "Topological entanglement entropy," *Phys. Rev. Lett.* 96, 110404 (2006).

An Unusually Low-Energy Cofactor Facilitates Efficient Energy Transduction in the Nfn-1 Redox Enzyme

Faculty Mentor: David Beratan

Authors: Emily Y. Wang, Andrew J. Smith, David N. Beratan

Abstract:

Electron bifurcation (EB) is an elegant mechanism that underpins biological energy transduction and catalysis. EB proteins separate electron pairs from a common source, delivering them to high- and low-potential acceptor pools, typically at low thermodynamic cost. The EB enzyme NADH-dependent ferredoxin-NADP⁺ oxidoreductase I contains a conspicuously high-potential iron-sulfur cluster cofactor (H1) proximal to the bifurcating flavin. We explore how this bump in the redox landscape influences energy transduction in the enzyme by modeling the correlated multi-electron flux in the enzyme using a fully correlated, three-reservoir master equation approach. We find that the reduction potential bump at the H1 cofactor enhances EB efficiency by suppressing energy-dissipating electron short-circuiting (by enhancing the occupancy effect that is known to suppress short circuiting). While the reduction potential bump at H1 increases EB efficiency, it also decreases EB flux.

Evaluating Telehealth in Rural North Carolina for Sustainable Primary Care Delivery

Faculty Mentor: Sumi Ariely, Ph.D.

Authors: Grace Wang, Jackie No, Dr. Sumedha Ariely, Dr. Diana Silimperi, Ms. Lynn Hardison

Abstract:

Telehealth is increasingly viewed as a strategy for expanding healthcare access in rural regions where barriers such as transportation, provider shortages, and geographic isolation persist. In collaboration with the Pamlico County Health Department (PCHD), this study employed a mixed-methods approach to evaluate both Telehealth and In-person primary care modalities to understand challenges and opportunities for expanding healthcare access in rural communities.

Survey and interview questions were adapted from health science literature and pre-piloted with community members and research advisors. Patients were approached by survey administrators after their appointments and asked to complete the surveys on paper before they left the clinic. The survey took 5-8 minutes to complete and was entered into Qualtrics

Among in-person patients, 24/~100 completed surveys, and three participated in follow-up interviews. Among telehealth patients, 40/~200 completed surveys. All providers—three from telehealth and five from in-person care—completed surveys and interviews. Preliminary responses indicate that satisfaction with care is comparable: 75% of in-person and 71% of telehealth responses reported high satisfaction. While most telehealth patients expressed enthusiasm for continued use, in-person patients showed mixed perceptions about adopting telehealth; not surprisingly, some patients are hesitant to adopt new practices. All providers demonstrated openness to utilizing telehealth, but emphasized the need for adequate training. These findings highlight the feasibility of Telehealth as a modality of care in rural populations. Continued engagement with patients through surveys and interviews will be critical to adapting the program to meet evolving needs and considerations of the expansion of Telehealth towards speciality care.

Investigating GRK2-Mediated Regulation of Brain-Derived Neurotrophic Factor in the Ischemic Heart

Faculty Mentor: Dr Walter Koch

Authors: Michael Wang, Stephanie M. Kereliuk, Heidi Cho, Eve Melbouci, Rajika Roy, Walter J. Koch

Abstract:

Brain-derived neurotrophic factor (BDNF) is a cardioprotective, pro-survival factor with established auto- and paracrine actions in the post-ischemic heart, and reduced BDNF signaling contributes to both neurological and cardiac dysfunction. Our group recently demonstrated that cardiomyocytes generate BDNF following ischemia through TrkB and β_3 -adrenergic receptor activation, a response diminished in heart failure. Because G protein-coupled receptor kinase 2 (GRK2) is upregulated during cardiac stress and promotes ischemic injury, we sought to determine whether GRK2 regulates myocardial BDNF expression. Preliminary findings show that BDNF increases after one week of myocardial ischemia and is further elevated in cardiomyocyte-specific GRK2 knockout (cKO-GRK2) mice, while GRK2 overexpression suppresses BDNF. To define the role of GRK2 in this process, we conducted in vitro studies in neonatal rat ventricular myocytes (NRVMs), modulating GRK2 through adenoviral overexpression, β ARKct-mediated inhibition, siRNA knockdown, and the GRK2 inhibitor paroxetine, and performed in vivo studies in GRK2-overexpressing (TgGRK2) and cKO-GRK2 mice subjected to permanent coronary ligation. BDNF and associated signaling proteins were quantified by protein immunoblotting. GRK2 inhibition or knockdown increased BDNF expression in NRVMs, whereas GRK2 overexpression reduced BDNF, and following myocardial infarction, cKO-GRK2 mice exhibited elevated myocardial BDNF while TgGRK2 mice showed suppressed levels. These findings identify GRK2 as a negative regulator of BDNF in cardiomyocytes and in the ischemic heart, suggesting that GRK2-dependent modulation of BDNF contributes to myocardial injury. Targeting GRK2 may therefore strengthen endogenous BDNF-mediated survival signaling and represent a promising strategy to mitigate ischemic cardiac damage.

Fibro-adipogenic progenitor cell-produced Myostatin and massive rotator cuff tear pathologies

Faculty Mentor: Matthew Hilton, Ph.D.

Authors: Madeleine Weiler, Helen Rueckert, Anthony J. Mirando, Matthew J. Hilton

Abstract:

Rotator cuff tears (RCTs) are one of the most common musculoskeletal injuries that affect the tendon(s) of four critical shoulder muscles that control arm movement and shoulder stability. Following these injuries, patients can develop intramuscular fat, muscle fibrosis, and muscle atrophy, with intramuscular fat in particular being correlated to high retear rates. Previously, our group demonstrated that a non-myogenic mesenchymal cell type localized between myofibers of skeletal muscle, also known as fibro-adipogenic progenitors (FAPs), are directly involved in the RCT pathologies. Additional data from our lab indicate that FAP-specific Myostatin (Mstn), a negative regulator of muscle growth and inducer of muscle atrophy, is upregulated in RCTs and may be responsible for some of the RCT pathologies. First, we established a FAP-specific Mstn knockout mouse line (Pdgfra-Cre;Mstn(fx/fx)) and validated that these mutant mice do not exhibit any muscle changes or defects during development. Next, using an established surgical mouse model of RCTs, we performed injuries on normal control and Pdgfra-Cre;Mstn(fx/fx) mutant mice to examine the impact of the FAP-specific genetic deletion of Mstn on post-injury pathologies. Histologic techniques were then used to assess changes in fat, fibrosis, and atrophy of mutant and control skeletal muscle following RCTs. As compared to normal control mice, Pdgfra-Cre;Mstn(fx/fx) mutant mice exhibit decreases in the RCT pathologies. Collectively these data indicate FAP-specific Mstn involvement in RCT pathologies and identify MSTN/Mstn inhibition as a promising area for future research in humans to minimize retear prevalence.

Pheromone Receptor Modulation of Social Experience-Dependent Sleep Behaviour

Faculty Mentor: Pelin Volkan, Ph.D.

Authors: Emily Wu, Ashley Jia, Sumie Okuwa, Pelin Volkan

Abstract:

Social interaction plays a fundamental role in shaping our thoughts, actions, and overall health. To study the effect of social isolation, we use the fruit fly *Drosophila melanogaster* as our model organism because of its conserved molecular and circuit mechanism and genetic accessibility. Previous findings from the Volkan Lab and others have shown that socially isolated (SH) fruit flies show a reduced sleep and increased locomotor activity compared to socially enriched (GH) flies. To investigate the molecular and circuit mechanism of these behavior changes, this project examines the role of the gustatory pheromone sensory system in mediating sleep and locomotion changes in response to social isolation. Specifically, we focused on gustatory pheromone receptors pickpocket 23 (ppk23) and pickpocket 25 (ppk25), members of non-voltage-gated gustatory cation channels part of the Degenerin/Epithelial sodium channel (DEG/ENaC) family. To determine the function of ppk23, we analyzed ppk23 knockout mutants. Behavioral analysis revealed that loss of ppk23 does not alter the sleep difference between socially enriched and isolated flies; however, it eliminates the difference in both daytime and nighttime locomotion. Specifically, ppk23 mutants show increased nighttime locomotion in GH flies and decreased daytime locomotion in SH flies. To investigate the function of ppk25, we silence ppk25 using Kir2.1. The behavior results showed that ppk25 silencing reduces the difference in daytime sleep by increasing sleep duration in socially isolated flies, while locomotor activity remains unaffected. Together, these results suggest that ppk23 mediates locomotor responses to both grouping and isolation, whereas ppk25 specifically mediates sleep responses to social isolation. To further validate these findings, we are currently using UAS-shibire to acutely inhibit synaptic transmission in ppk23- and ppk25-expressing neurons using ppk23-Gal4 and ppk25-Gal4 drivers. Together, these studies aim to clarify the contribution of gustatory pheromone circuits to sleep regulation under social isolation and to identify sensory pathways linking social experience to behavioral state.

Optimization of a fluorometric assay for detection of cell-bound antibodies

Faculty Mentor: Gow Arepally, M.D.

Authors: Sandy Wu, Sanjay Khandelwal, Gow Arepally

Abstract:

The binding of antibodies to cells is typically done with flow cytometry, a labor-intensive and time-consuming technique that requires specialized instrumentation (flow cytometer). To overcome these challenges, we have developed a high-throughput fluorometric assay to examine the binding of fluorescently labeled antibodies to the cell surface. K562 (erythroleukemic) and Jurkat (T lymphocyte) cell lines were incubated with Alexa Fluor (AF)-labeled antibodies (KKO-AF647 and TRA-AF647), as well as their corresponding antigens, platelet factor 4 (PF4) and heparin (H), in serum free media (SFM) for 45 minutes. After incubation, cells were washed twice in Hank's Balanced Salt Solution (HBSS) buffer, followed by resuspension in HBSS buffer. Binding of antibodies to cells was detected by fluorometry at 670 nm emission/640 nm excitation using SpectraMax M2 (Molecular Devices, San Jose). Once washing conditions were refined to minimize nonspecific signals, we examined background signals using buffer, antibody alone (KKO-AF647) or antigen/antibody (KKO-AF647 containing ICs or KKO ICs). Studies showed minimal signal with KKO alone, isotype with antigen, but markedly enhanced binding with KKO ICs (30–50 fold increased signal relative to other conditions). Signals were dependent on the amount of cells used, as there was a linear increase in fluorescent signal with increasing concentrations of cells: $0.5\text{--}2.5 \times 10^6$ cells/ml. Comparative analysis between K562 and Jurkat cells show that Jurkat cells (191.9 AU + SD: 9.7) have stronger and more consistent fluorescence signals compared to K562 (131.2 AU + SD: 40.5). Additionally, experiments comparing K562 KKO immune complex binding in media versus plasma demonstrated that plasma interferes with the binding of antibodies (SFM: 51.4 AU + SD: 25.6 vs. plasma: 11.1 AU + SD: 2.1). Instrumentation effects were also assessed, as different plate readers displayed variability in signal detection sensitivity, particularly between instruments with and without photomultiplier tubes, underscoring the need for appropriate detection settings. Overall, this simplified, scalable, and efficient fluorometric method can serve as an alternative for cell-associated antibody detection while taking into account the experimental influences of factors including cell concentration, washing conditions, antibody selection, and instrumentation.

Investigating the role of the hillock-like state in squamous lung cancer chemoresistance

Faculty Mentor: Trudy G Oliver, Ph.D.

Authors: Steven Yang; Luke Izzo, PhD; Trudy Oliver, PhD

Abstract:

Squamous lung carcinoma is a subtype of non-small cell lung cancer that is characterized by poor survival. Recent work has identified Krt13+ hillock cells as a novel epithelial population in the normal lung with roles in squamous differentiation, cellular adhesion, immunomodulation, and injury resistance. Expanding on these insights, we investigated whether a hillock-like state exists within squamous tumors and whether it contributes to chemoresistance. Using the *Lox-stop-lox-Sox2;Nkx2-1 flox/flox;Lkb1 flox/flox* (SNL) genetically engineered mouse model, we identified a population of Krt13+ cells uniquely enriched in squamous tumors. Transcriptomic analysis indicated that these cells closely resemble luminal hillock cells of the normal lung and exhibit reduced proliferation compared to Krt5+ basal-like populations. Mechanistically, the transcription factor KLF4 marks a suprabasal population and is necessary for initiating the Krt13+ state. Additionally, we have shown that the basal-like state gives rise to the hillock-like state and that hillock-like cells have the capacity to revert back to a more basal-like population, demonstrating plasticity between these two cell states. Normal lung hillock cells have shown resistance to multiple forms of cellular stress. We therefore hypothesized that hillock-like tumor cells would also exhibit resistance to therapeutic stress. Knockdown of *Klf4* enhances cisplatin sensitivity in SNL-derived organoids and a normal human basal cell line, suggesting a link between hillock differentiation and chemotherapy resistance. Ongoing and future work includes extending these findings to human LUSC cell lines (H520, H226, and H1703) and characterizing the mechanisms of resistance in the hillock-like state. Preliminary data suggest that antioxidant pathways may support resistance to cisplatin in hillock-like cells, and targeting these pathways may improve response to standard-of-care chemotherapy. Collectively, these results define a regulatory relationship between *Klf4* and the hillock-like state in squamous tumors. This state relates epithelial differentiation and injury resistance, with the plasticity between basal- and hillock-like states offering an explanation for the limited impacts of therapy in LUSC and opening new therapeutic avenues.

Identifying Transcriptional Drivers of Nuclear Heterogeneity in the Placenta

Faculty Mentor: Amy Gladfelter, Ph.D.

Authors: Allison Yang, Madeline Keenen, Huan Liang, Rohit Singh, Amy Gladfelter

Abstract:

During pregnancy, the outer layer of the placenta develops into a unique multinucleated structure called the syncytiotrophoblast (STB), which serves as the primary interface between mother and fetus. Cytotrophoblasts (CTBs), the progenitor cells of the placenta, are central to this process, as they proliferate, differentiate, and ultimately fuse into the STB to form the syncytia. The STB covers 12–14 m² of surface area and houses billions of nuclei within a shared cytoplasm. The STB orchestrates critical pregnancy functions such as molecular transport, hormone production, metabolism, and waste exchange. Yet, the mechanisms governing these functions within this multinucleated cell remain poorly understood. Therefore, this begs the question: how can billions of nuclei, coexisting in the same cytoplasmic space, coordinate to perform such a diverse range of functions? I hypothesize that different transcriptional factors drive the formation of distinct nuclear subtypes. To understand these nuclear subtypes, RNA velocity was applied to a snRNA dataset from term placental tissue. This allowed me to track how gene expression changes dynamically over pseudo time by comparing spliced and unspliced mRNA counts. The 2,000 most highly variable genes were selected, and principal component analysis (PCA) was used to conduct RNA velocity estimation. After performing RNA velocity, I performed gene network analysis using Velorama to pinpoint transcription factors that may regulate this differentiation. On a higher level, I hypothesize that these transcriptional factors are locally distributed, influenced by factors such as proximity to vasculature or cytoplasmic density. To evaluate such factors, I'm using quantitative image analysis of placental tissue slices in combination with machine learning based image segmentation to evaluate how nuclear subtypes interact with one another and their surroundings. When these signals become dysregulated, the resulting imbalance can lead to aberrations in STB formation, causing placental dysfunction syndromes, including pre-eclampsia (PE), fetal growth restriction (FGR), and stillbirth. PE alone is a leading cause of maternal and fetal mortality, and yet, there are currently no targeted therapies. Therefore, this research may open the door to targeted therapeutic strategies for conditions like PE, addressing a major unmet need in maternal health.

Predicting Emotional Regulation Using Baseline Medial Prefrontal Cortex–Insula Functional Connectivity in Adults with Clinical Anxiety Disorders

Faculty Mentor: Andrada Neacsiu, Ph.D.

Authors: Yosan Zerai, Nimesha Gerlus, John L. Graner, Andrada D. Neacsiu

Abstract:

The insula, with a core responsibility for supporting interoception and subjective feeling states, is known to play a pivotal role in the pathophysiology of anxiety disorders. Functional connectivity between the insula and medial prefrontal cortex (mPFC) is believed to induce parasympathetic activation during emotional distress by creating a circuitry of subjective evaluation and downregulation of emotional signals, a process found to be dysfunctional in anxiety disorders. Heart rate variability (HRV), an index of the fluctuation in time interval between consecutive heartbeats, is a correlate of parasympathetic activity and emotional wellbeing. Adults with anxiety exhibit lower HRV and ultimately, poorer emotional regulation. Despite evidence illustrating the role of the insula–PFC axis in emotional dysregulation and the role of the insula in physiological modulation, the potential of insula–mPFC functional connectivity to predict parasympathetic physiological symptoms, like HRV, has yet to be explored in anxiety. A better understanding of this neurophysiological process may provide insight into how emotional distress manifests and can be targeted in adults with anxiety disorders. Thus, the aim of this project is to determine if mPFC–insula connectivity can predict a parasympathetic index of emotional regulation following a stress–inducing task in adults who meet clinical criteria for any anxiety disorder. The parasympathetic index examined is HRV. Twenty–one participants who met criteria for a clinical anxiety disorder completed a baseline MRI to determine strength of functional connectivity between the insula and mPFC, followed by a regulation task at which HRV was recorded. A mixed model analysis was used to determine the capacity of the insula–mPFC functional connectivity to predict HRV during regulation. Ultimately, stronger baseline vmPFC–insula connectivity during an emotion regulation task predicted higher HRV, indicative of greater parasympathetic activity, during regulation in adults with clinical anxiety disorders. This specific neural connectivity may be linked to enhanced bottom–up integration of interoceptive signaling, and could serve as a treatment target to help adults with anxiety effectively emotionally regulate.

Enhancing Functional Expression of Odorant Receptors Through Ortholog-Based Protein Engineering

Faculty Mentor: Hiroaki Matsunami, Ph.D.

Authors: Katherine Zhang, Dan Takase, Hiroaki Matsunami

Abstract:

The human sense of smell relies on a vast and chemically diverse array of odor molecules that interact with numerous odorant receptor (ORs) proteins. Despite this complexity, many aspects of olfaction still remain poorly understood. A major challenge in studying these G protein-coupled receptors is their poor functional expression on the cell surface in heterologous or non-olfactory systems, which limits biochemical analysis and insight into their ligand-binding properties. Our goal is to engineer OR constructs with improved surface expression and activation while preserving their native ligand specificity. Here, we build upon previous work which identified N-terminal, transmembrane protein 1 (TM1), and C-terminal modifications that promoted expression but did not contribute to ligand selectivity.

We hypothesized that combining these modifications with orthologous OR sequences that respond to the same odorant would further increase receptor expression by enabling substitutions at non-conserved residues between TM2-TM7. We focused on OR5A2, a receptor known for its difficulty to express on the cell surface, and its response to musk, an important fragrance compound. To evaluate our engineered receptors, we used fluorescence activated cell-sorting (FACS) to assess cell surface expression and the GloSensor cAMP assay to assess receptor activation in HEK293T cells transiently expressing native and engineered OR constructs.

Our results show that orthologous substitutions to the OR5A2 construct increased cell surface expression, particularly when combined with previously described N- and C-terminal modifications. GloSensor cAMP assays further demonstrated that the engineered receptor responded to the musk odorant in the same manner as the native receptor, suggesting that these modifications improve trafficking and expression without disrupting ligand recognition and downstream signaling. Overall, these findings demonstrate that ortholog-based receptor engineering can enhance odorant receptor expression while preserving native function, providing key insight into structural constraints affecting OR expression in non-olfactory cells.x

Epigenetic regulation of placenta cell type differentiation

Faculty Mentor: Amy Gladfelter, Ph.D.

Authors: Emily Zheng, Madeline Keenen, Amy Gladfelter

Abstract:

The placenta is the maternal–fetal interface during pregnancy and facilitates essential processes like nutrient exchange, hormone production, and metabolism.

Cytotrophoblasts (CTBs) are a major placenta cell type and form a layer of progenitor cells that differentiate to replenish the syncytiotrophoblast (STB) layer during pregnancy. The STB is a single, tissue–sized, multinucleated cell that functions as the placenta’s primary exchange barrier. While dysfunctional STB are linked to pregnancy diseases like preeclampsia, the mechanisms regulating STB differentiation remain incompletely understood.

Epigenetic regulation is a key driver of developmental cell fate decisions. Such post–translational modifications are directed by chromatin remodelers and include histone acetylation, methylation, and ubiquitylation to mark genes for active or repressed transcription.

We hypothesize epigenetic regulation may play a key role in CTB to STB differentiation. To test this, we visualized canonically activating and inactivating histone marks including H3K4me3, H3K27me3, H3K9me3, and H4K20me3 in normal and preeclamptic placenta tissue as well as in wild–type and RYBP knockout trophoblast organoids. Using immunofluorescence and confocal microscopy, we qualitatively identified mark expression in individual nuclei.

Our findings suggest non–canonical epigenetic regulation of STB differentiation. Interestingly, STB nuclei demonstrate lower levels of repressive H2A119Ub, H3K27me3, H3K9me3, and H4K20me3 marks than CTBs in tissue and trophoblast organoids. This is notable because differentiated STB are post–mitotic, a state typically associated with repressed chromatin states. STB nuclei also expressed lower levels of H3K4me3, an activating mark, than surrounding CTBs.

This lower expression of repressive marks in STB prompted investigation into the expression of chromatin remodelers that promote repressive marks. Specifically, we stained for RYBP which promotes the repressive H2A119Ub mark and exhibits STB specific expression. Unexpectedly, despite STB having lower expression of H2A119Ub than CTB, we qualitatively observed that STB had higher expression of RYBP than CTB in tissue.

Together, these results suggest STB differentiation may involve non–canonical epigenetic mechanisms. Future quantitative analyses of histone mark expression and investigation of additional regulatory factors, including DNA methylation, can further elucidate trophoblast differentiation mechanisms.

Generosity in context: Comparing sharing of monetary and experiential rewards in the dictator game

Faculty Mentor: Scott Huettel

Authors: Katherine Zhong, Nitisha Desai, Scott Huettel

Abstract:

It is important to understand how people share resources. The most widely used paradigm to study sharing behavior is the dictator game, where the participant unilaterally decides how much of a reward to give another player. While dictator game studies have primarily examined allocations of money, research shows people evaluate the perceived social and emotional significance of experiences differently from money, which may affect situational generosity. Thus, we aim to study whether dictator games with experiences will elicit different levels of sharing. To test this, we adapted the dictator game to a raffle ticket allocation task. In the raffle dictator game task, the participant has 100 raffle tickets that may be shared with another player. Each ticket equals a 1% chance to win the reward for that raffle draw. This reward is either an enjoyable local experience or a matched amount of money. The money values correspond to the value in USD that participants indicated (prior to the raffle dictator game task) they were willing to pay for each experience. Subjects also rated the experiences on six traits that can contribute to subjective valuation: rare, social, memorable, temporal distance (how distant in time they perceive the experiences to be), intent of purchase (how likely they would pursue the experience using their own money and resources), and effort. We predict people will give more tickets when the reward is an experience. Overall, we found that participants (N = 159) are more generous when allocating experiential rewards compared to money. Further, generosity is correlated with participants' subjective ratings of the experiences in three dimensions. Generosity for experiences is higher when the temporal distances are larger. Meanwhile, generosity for experience is lower when the intent of purchase is higher and when the experience is more memorable. These findings illustrate differences in sharing experiential rewards versus money, and provide evidence of factors influencing how people decide to give experiences.

Expectation misalignment in the workplace affects burnout, stress, job satisfaction, and well-being

Faculty Mentor: Dr James Shah, Ph.D.

Authors: Sunny Zhu, Skyler Wyly, Shenwei Zhang, Elena Hayoung Lee, James Shah

Abstract:

Expectations shape many aspects of everyday life, influencing stress levels, the effort we are willing to put in, and our emotional response to outcomes. While we set expectations for ourselves, others also have their expectations for us. Expectation misalignment arises when there are gaps and differences between self-expectations and others' expectations. Existing research highlights the substantial influence of expectations in shaping individual perceptions and performance, particularly those given by people with a higher hierarchy or special importance to us. However, the effects of misaligned expectations are still underexplored. Here, we focus on workplace environments, where hierarchical relationships between employees, co-workers, and supervisors exist. In two studies, these factors and measures of individuals' expectations are assessed in self-report surveys with samples across both the United States and China. Using vignette methods, we then stimulate various misalignment situations to detect participants' responses and performance under each setting. Our findings indicate that expectation misalignments in the workplace negatively affect well-being and work performance, including increased burnout and decreased job satisfaction. Extending this, future research focused on developing interventions targeting realigning expectations may improve employees' well-being and foster more sustainable workplace practices, with potential downstream effects for employee productivity, workforce retention, and organizational efficiency.

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