UNDERGRADUATE RESEARCH SYMPOSIUM

Presented by the Undergraduate Research Support Office

10 April 2025	4– 6 pm	Penn Pavilion Duke University

Duke | UNDERGRADUATE RESEARCH SUPPORT OFFICE

undergraduateresearch.duke.edu/symposium

WELCOME

As the Director of the Undergraduate Research Support (URS) Office, I am delighted to welcome you to the 2025 Duke Undergraduate Research Symposium!

Duke University empowers students to explore their interests and engage in meaningful scholarly endeavors. Whether conducting ethnographic studies to explore cultural influences, creating art or writing to illuminate a research project, experimenting to uncover cellular functions linked to disease, developing animal models to study behavior, or applying AI and machine learning to deepen our understanding of the world, our students are making remarkable contributions. I hope you take note of their exceptional work showcased in their presentations!

The URS Office collaborates with faculty, the community, and campus partners to promote undergraduate research. We provide programming to assist students in discovering research opportunities and maximizing their experiences. Additionally, the office offers funding for fellowships, assistantships, conference participation, and supplies for independent studies.

Each year, in partnership with Duke's Trinity College of Arts & Sciences, URS hosts this symposium to celebrate and showcase undergraduate research across campus. Some students are in the early stages of their projects, while others are nearing the completion of their thesis work. I encourage you to engage with the presenters, explore their research journeys, and ask questions—they are eager to share their work with you!

Thank you for being a part of this event today!

Warm regards,

Jessica R. Harrell, Ph.D.
Director, Undergraduate Research Support Office

Session I List: 4:00 – 4:45 pm

Presenters are organized by discipline and then alphabetically by last name.

Behavioral Sciences / Psychology

- Buduen, Elizabeth – *Understanding motivation control beliefs using AI-driven qualitative interviews*
- Chen, Geo – *LGBTQ+ youth face increased risk for early life unpredictability and adolescent psychopathology*
- Inumarty, Achintya – *Beyond Mental Distress: Examining the Validity of Two Measures of Positive Mental Health*
- Rogers, Jaclyn – *Learning Value Perceptions*

Health / Clinical Research

- Clarke, Chelsea – *The Impact of Analgesic Regimens on Mobility After Lumbar Spine Surgery: A Systematic Review*
- Du, Kunyu (Kimi) – *Single-breath Fractional Ventilation Derived From 129Xe MRI: Repeatability In IPF*
- Maddock, Katie – *Factors Associated with Sexual Avoidance among Breast Cancer Survivors with Type 2 Diabetes*
- Reddy, Katherine – *Evaluating Public Awareness for Improved Diagnosis and Treatment of Rare Breast Cancers*
- Yeam, Jenna – *Challenges to Dying Well and Death Doula Work*

Biological and Biomedical Sciences

- Amirneni, Siddharth – *A Gut Sense for Dietary Protein*
- Balkanli, Efe – *The Effect of Social Experience on Courtship Behavior in Drosophila*
- Booth, Mya – *Engineered Lipid Nanoparticles for Heart Regeneration*
- Carugati, Claudia – *Exploring the genetic framework governing vacuole biogenesis within the zebrafish notochord*
- Chung, Eujin – *Optimizing Delivery of the ApoE-mimetic Peptide, CN-105, to Improve Outcomes after SCI*
- Deutsch, Zachary – *Computational Pipeline for Cell Type Annotation of HuBMAP Spatial-omics Data*
- Ding, Cynthia – *Hyperphosphorylated Tau in the Locus Coeruleus of Young Rhesus Monkeys*
- Field, Rachel – *Molecular and Cellular Impacts of UBE2A Mutations Linked to XLID Type Nascimento*
- Fulton, Amy – *Hyaluronic-Acid Based Engineered VEGF Biomaterial Gel for Osteogenesis of Neurosurgical Craniot*
- Gao, Aretha – *Validation of Novel Regulatory Elements that Influence TOX Expression and T Cell Exhaustion*
- Gurwitch, Ethan – *Elucidating Humidity-Clock Interplay in Arabidopsis*

- Hoteit, Maya - *MicroRNA-K as a potential therapeutic target for preventing cardiac hypertrophy*
- Huynh, Khang - *Identifying Key Genetic Regions for Cell Sheet Morphogenesis on Chromosome 3R*
- Jung, Issac - *DRMTX Regulates Neuroendocrine Progression and Serves as a Therapeutic Target in NEPC*
- Kobayashi, Mao - *Organ and Cell Morphologies Governing Circumnutation in Rice Roots*
- Kornfeld, Walter - *Social Aging in Ring-tailed Lemurs (Lemur catta)*
- Lam, Katie - *Investigating the role of HAR1984 in neurogenesis and development*
- Lee Heberling, Nicole - *Lemur Fecal Parasitology*
- Lessing, Reed - *Neonatal protein malnutrition impairs microglia density and function in the hippocampus*
- Li, Katie - *The Role of Ecdysone, and Aldoketoreductase (AKR) on Manduca Sexta Wing Disk Growth and Develop*
    - Co-Presenter: Grace Wang
- Lowrance, Tom - *Reconciling Biological and Chronological Age During Development*
- Matarangas, Ariana - *Investigating LCP1-mediated oncogenic signaling in Chondrosarcoma metastasis*
- Pratt, Harrison - *Granulovacuolar Degeneration Associated With Lysosomal Permeabilization via LLOMe*
- Reaves, Jordan - *Defining how the m6A-methyltransferase complex targets hepatitis C viral RNA*
- Regan, David - *Investigating the Impact of 5-Hydroxymethyl-2-furfural (HMF) on Pancreatic beta-Cell Lines*
- Robelo, Daniel - *The association of forgiveness with physiological responses to memories of past wrongdoings*
- Ruiz, Ariella - *Effects of Variation in Sex Chromosome Copy Numbers on the Expression of the Cohesin Complex*
- Sala, Angelina - *Investigating the molecular mechanisms of SCD while exploring stakeholder perspectives*
- Sanchez, Sebastian - *A Simple and Sensitive Wearable SERS Sensor Utilizing Plasmonic-Active Gold Nanostars*
- Scheiner, Ainsley - *Investigating the Role of MAP Kinase Pathway in Cell Division During Starvation in C. elegans*
- Seghers, Erik - *Identification of Nedd4 proteoforms induced by proteotoxicity and NAB2 exposure*
- Shen, Sophia - *Identifying New Targets of Salmonella Induced GSK3 Tyrosine Phosphorylation*
- Tandar, Megan - *Investigating Radioresistance-Induced Epigenetic Reorganization in Colorectal Cancer*
- Toshniwal, Muskaan - *Characterization of Mouse Models of Pain following Adoptive Transfer of SLE Serum*
- Wang, Michael - *GRK2-Mediated Regulation of Brain-Derived Neurotrophic Factor in the Ischemic Heart*

- Wardell, Robert – *Elucidating Neurotoxicity Reversal Pathways in Cellular Models of Parkinson's Disease*
- Yang, Allison – *Identification of recombinant antibody pairs for a Lujo virus diagnostic assay*
- Zhang, Sophia – *Quantifying the Potential of Various Delivery Methods for Dual-Epitope Peptide Nanofiber Treatments*
- Zhang, Kat – *Engineering Odorant Receptors to Enhance Expression in Heterologous Cells*

Humanities

- Paz-Martinez, Yadira – *The Undocumented Republican Latino Vote*

Physical Sciences

- Fadul Chavez, Eduardo – *Progress Towards the Synthesis and Characterization of Nedd4 E3 Ubiquitin Ligase Ligands*
- Sbaiti, Bashir – *Machine Learning Deciphers Interchromophore Couplings from Multidimensional Electronic Spectra*
- Valan, Joel – *Synthesis of isotactic poly(propylene succinate) with functional end-group fidelity*

Quantitative Sciences

- Fox, Alexis – *A Unifying Information-theoretic Perspective on Evaluating Generative Models*
- Goel, Shrey – *MeMDLM: De Novo Membrane Protein Design with Property-Guided Discrete Diffusion*

Social Sciences

- Gupta, Rohan – *On the Experience and Emotional Cost of Compassion: Comparing Christians and Buddhists*
- Herndon, Ana – *Major Motivations: Undergraduate Student's College Major Selection, Experiences, and Retention*
    - Co-Presenter: Tiana Clemons
- Krovitz, Sarine – *We Paint to the Sky: Mural Making and Social Action in Post-Dictatorship Chile*
- Li, Abby – *The Benefits and Challenges of Virtual Worship for Flourishing*
- Rivero, Alissa – *High School Group Work Experiences*
- Rivero, Alissa – *The Emergence of Children's Cooperation*

Session II List: 5:15 – 6:00 pm

Presenters are organized by discipline and then alphabetically by last name.

Behavioral Sciences / Psychology

- Blank, Carly - *Children's science self-efficacy and attitudes: Impacts of content area and previous experience*
- Brown, Maria - *Attitudes toward success and failure have implications for self-regulation and well-being*
- Dhingra, Umang - *Social Affiliation and Resistance to Belief Revision in Childhood*
- Evonlah, Milli - *PATERNAL CANNABIS EXPOSURE EFFECT ON ADOLESCENT OFFSPRING GLUTAMATERGIC AND CHOLINERGIC SYSTEMS*
- Tang, Kai - *Understanding motivation control beliefs using AI-driven qualitative interviews*

Health / Clinical Research

- Brown, Austin - *Help Desk: A student-led screening and referral intervention for unmet social needs*
    - Co-Presenters: Ariana Vaida, Anthony Zhao, Amitesh Verma
- Chemmanoor, Susan - *The Role of Patient Education in Improving Health Knowledge in Elective Spine Surgery*
    - Co-Presenter: Avery Bernazard
- Cho, Eugene - *Barriers to Neurosurgical Service Delivery in Sub-Saharan Africa*
    - Co-Presenter: Heather Raslan
- Junaid, Maria - *The Impact of Preoperative Psychological Interventions on Spine Surgery Outcomes*
- Powell, Cody - *Relationships between pain, activities of daily living, and perceptions of overall health*
    - Co-Presenters: Anika Dhuler, Breanna Barrett
- Ray, Astha - *Perspectives of Black and White Family Members on Medical Decision Making for ICU Patients*
- Tarpeh, Johrdyn - *DECLINING ENDURANCE IN CHILDREN: REVIEW OF BRUCE TREADMILL PROTOCOL ENDURANCE TIMES SINCE 1978*

Biological and Biomedical Sciences

- Bleichner, Lukas - *Expression and Purification of Rab1A for Biochemical Analysis of the Rab1A:NAB2 Interaction*
- Bochner, Aliza - *Sex-Specific Regulation of Adiposity by Cardiac GRK2 in Heart Failure*
- Brandler, Katie - *Ecdysteroid Regulation of Developmental Timing in Manduca sexta*
- Carlson, Katherine - *Functional and Genetic Characterization of Single Ventricle Disease*
- Chen, Erin - *Investigating Trends in Aquatic Insect Emergence to Understand Aquatic-Terrestrial Nutrient Cyc*
- Colwell, Christina - *Breaking Cancer's Disguise Through Enhanced Immune Detection*
- Cox, Lydia - *Herbarium Collections Disentangle Climate Effects on Carnivorous Plant Phenology*

- Cox, Sophia – *Is Land Cover Associated with Ground Invertebrate Diversity?*
- Dollard, Erin – *Adapting methods for heritable genetic editing in Junonia coenia*
- Fan, Rebecca – *Biochemical Insights into Ligand-Specific Transducer Recruitment by C-C Chemokine Receptor 7*
- Gorbatov, Sarah – *Developing novel reporters to visualize lipoprotein lipase activity in zebrafish*
- Huang, Angelina – *Genomic Analysis of Gynandromorph Butterfly With Two Genomes*
    - Co- Presenters: Shriya Minocha, Avi Heyman, Daniel Levin
- Kaul, Anavi – *Multi Kidney Disease Modelling using hiPSC-Derived Biomimetic Glomerulus-on-a-Chips*
- Kelleher, Quindlan – *Illuminating unique features of the regulatory genome in human and chimpanzee cells*
- Khabibullina, Elina – *STEAP1 Facilitates Metastasis in mCRPC: A Rationale for Targeted ADC Therapy*
- Li, Renee – *Molecular Evidence for the Role of Olfaction in Antbird Foraging*
- Li, Sophie – *Maternal High-Fat Diet Alters Microglial Crym Expression in Male Offspring*
- Liu, Christina – *MicroRNA-K Driven Regulation of GRK2 Expression in Attenuating Cardiac Hypertrophy*
- Meng, Zimiao – *The Ncd Kinesin-14 Tail: Analysis of AI-Driven Structural Predictions*
- Menke, Kavya – *Hormone Concentration Variation and Social Behavior in Female Dominant vs. Codominant Lemurs*
- Moon, Nicole – *Context-Dependent Role of B-Cells in Tumorigenesis: Influence of the Tumor Microenvironment*
- Oduru, Srijan – *Metabolic regulation of HIF-1a by alpha-ketoglutarate in Acute Myeloid Leukemia*
- Okafor, Chibuike – *Tracing Water Transport Over Time With Deep Sapwood and Heartwood Isotopic Breakthrough Curves*
- Pasumarthy, Sushrit – *PD-L1 Overexpression Mitigates CD8+ T Cell-Mediated Cytotoxicity in Mammary Cancer Cells*
- Rastogi, Pranav – *Differential Effects of BMP13 on Adult and Juvenile Cartilage*
- Rodriguez, Hailey – *GRK2 and Sirtuin 3: Uncovering a Novel Protein-Protein Interaction Mediated by S-nitrosylation*
- Roman, Natalia – *Engineered Multichannel Biomimetic (T-LAB) of the Tumor-Lymphatic Architecture*
- Roya, Nawra – *Screening for Dorsal Closure Genes on the 3R Chromosome of Drosophila melanogaster*
- Sharp, William – *Human Piezo1 and Piezo2 Single Channel Conductance is Modulated by Alternative Splicing*
- Villanueva Govea, Jaqueline – *From Hypothetical to Functional: Characterizing Two Related Mannoproteins in Cryptococcus neoformans.*
- Wang, Huiwen – *Neural Encoding of Vocal Variability in Zebra Finch Song Learning*
- Zhang, Ura – *A Genetic Tool to Investigate the Persistent Activation of CCR7 by CCL21*

Physical Sciences

- Chen, Matthew – *Exploration of the Effect of Noise on Entanglement within Finite-dimensional Qubit-Systems*
- Ding, Mayah – *Synthesis of 15N2-diazirine probes for in vivo HP-MR imaging of human biological pathways*
- Ji, Lang – *Control of Oxygen Vacancy in Manganite Heterostructures by Ionic Liquid Gating*
- Kelleher, Rowan – *Simulation based R&D for a Iron-Scintillator Sandwich Calorimeter*
- Ockert, Gavin – *Measuring the Thermal Sunyaev-Zel'dovich Effect in Galaxy Clusters with ACT*
- Wang, Emily – *Dialing It In: Tradeoff Between High Yield and Low Slippage in Electron Bifurcation*

Quantitative Sciences

- Lee, Hyunjin – *ChatGPT in Network Meta-Analyses: Prompt Engineering Strategies for Automating Data Extraction*
- Rizavi, Kulsoom – *Our AI Overlords: Can LLM-driven agents accurately simulate US senators?*
- Wu, Yutong – *Functional Connectomes of Neural Networks*

Social Sciences

- Decker, Chloe – *Opioid Settlement Spending Across North Carolina: Which families are best served?*
- Drakes, Antonio – *Improving College Student Survey Response Rates: A Case Study at Duke University*
- Law, Lucy – *The Presence of Absence: Palimpsest and Identity in Hong Kong*
- Morrison, Madeline – *Childhood vaccination prevalence and perception in Roatán, Honduras*
    - Co-Presenters: Reena Kagan, Arya Kumar, Grace Muriithi
- Nuzzolo, Matthew – *The Productivity Cost of Hearing Loss: A Systematic Review*
- Orozco, Jose – *Reexamining the interpretation of English definite plurals by L1 Spanish speakers*
- Razon, Reagan – *Uplifting Black Girls and Mothers: Multi-Layered Mentoring and Community Cultural Wealth*

SESSION I PRESENTERS:

4:00 – 4:45 PM

Presenters are organized by discipline and then alphabetically by last name.

BEHAVIORAL SCIENCES / PSYCHOLOGY

Presenters are organized by discipline and then alphabetically by last name.

Understanding motivation control beliefs using AI-driven qualitative interviews

Elizabeth Buduen

Faculty Mentor: James Shah

Authors: Elizabeth Buduen, Kai Tang, Zhuying Guo, Maria Brown, Skyler Wyly, James Shah, PhD

Discipline: Behavioral Sciences / Psychology

Abstract:
Extending research on the significance of individuals' implicit beliefs for goal pursuit and self-regulation, the present study examines how individual's 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 nature and 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. In the current study, participants are recruited to complete an AI-driven qualitative interview through Engage by CloudResearch. The Engage AI Analysis software summarizes interviews, highlights noteworthy responses, and quantifies themes that are related to participants' beliefs about the controllability of motivation and their ability to self-regulate during goal pursuit. The sample size is determined by theoretical saturation, resulting in a sample size of 60 participants. This study is part of a set of ongoing studies exploring the effects of motivation control beliefs on goal progress, persistence, and regulatory strategy use.

LGBTQ+ youth face increased risk for early life unpredictability and adolescent psychopathology

Geo Chen

Faculty Mentor: Kimberly Carpenter

Authors: Geo Chen, Connor Haughey, Sarah Lempres, Adjoa Ewool, Helen Egger, William E. Copeland, Margaret Sheridan, Kimberly Carpenter

Discipline: Behavioral Sciences / Psychology

Abstract:
More than half of all children in the U.S. experience some form of early life adversity, a well-established risk factor for later psychopathology. Recent research highlights childhood unpredictability (e.g., uncertain meal times) as a distinct dimension of adversity with unique consequences for mental health. In addition, LGBTQ+ individuals are disproportionately exposed to childhood adversity and exhibit higher rates of psychopathology, yet little is known about how LGBTQ+ identity influences the longitudinal effects of childhood unpredictability. This study is the first to examine whether LGBTQ+ youth experience higher levels of childhood unpredictability and how it predicts adolescent psychopathology. In a longitudinal sample of adolescents and young adults, we assessed childhood unpredictability and psychopathology. Analyses tested four key questions: (1) Does childhood unpredictability predict psychopathology? (2) Do LGBTQ+ youth report greater childhood unpredictability? (3) Does identifying as LGBTQ+ predict psychopathology? and (4) Do LGBTQ+ youth who experience high unpredictability exhibit the highest psychopathology? Analyses controlled for age, sex assigned at birth, and race. Results indicate that LGBTQ+ youth reported higher levels of both childhood unpredictability and adolescent psychopathology. However, LGBTQ+ identity did not moderate the relationship between unpredictability and psychopathology, suggesting that the adverse effects of unpredictability are consistent across youth. These findings underscore the urgent need for interventions that provide stability and mitigate the impact of early adversity, particularly for LGBTQ+ youth, who remain at elevated risk for both unpredictability and mental health challenges.

Beyond Mental Distress: Examining the Validity of Two Measures of Positive Mental Health

Achintya Inumarty

Faculty Mentor: Rae Proeschold-Bell

Authors: Achintya Inumarty, Jia Yao, Can Cui, Rae Jean Proeschold-Bell

Discipline: Behavioral Sciences / Psychology

Abstract:
Although the field of positive psychology has progressed over the past 20 years, the majority of global mental health studies fail to measure positive mental health alongside measures of mental distress. Yet promoting positive mental health, and not just ameliorating mental distress, has the potential to prevent future cases of depression and anxiety. Further, factors that reduce symptoms of mental distress differ from the factors that promote indicators of positive mental health, underscoring the importance of measuring both. Two widely utilized measures of positive mental health in current literature include: (1) the 14-item Mental Health Continuum-Short Form (MHC-SF), developed by sociologist Corey Keyes to measure positive emotions, psychological functioning, and social functioning, and (2) the 10-item Harvard Flourishing Measure, designed by biostatistician Tyler VanderWeele to assess five core constructs - happiness and life satisfaction, mental and physical health, meaning and purpose, character and virtue, and close social relationships - each measured by two items. We included both measures in a holistic health survey of North Carolina United Methodist Church clergy in 2023 (n = 555) to evaluate and compare these instruments' psychometric properties. For this presentation, we will report on the measures' reliability (Cronbach's alpha: 0.94 for MHC-SF, 0.91 for Harvard Flourishing Measure), variance across demographic subgroups, ceiling/floor effects, convergent validity, and their current utilization in studies globally. While the measures exhibited a strong correlation (r = 0.71), exploratory factor analysis revealed that they each capture distinct dimensions of positive mental health, reinforcing their use as complementary rather than interchangeable tools. By providing these findings alongside a detailed breakdown of each measure's items, we hope to inspire global mental health researchers to measure positive mental health in their studies and make informed decisions on each measure's use.

Learning Value Perceptions

Jaclyn Rogers

Faculty Mentor: James Shah

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

Discipline: Behavioral Sciences / Psychology

Abstract:
The presented studies seek to examine how the value we place in learning may come to shape our attitudes toward success and failure, with significant implications for subsequent self-regulation. Learning value perceptions refer to how individuals view and interpret the experiences of success and failure through the subsequent lessons that can be learned from these experiences. The first study examined how learning value perceptions may mediate the impact of attitudes toward success and failure on goal progress. We ran a preregistered two-session study to examine the effect of attitudes toward success and failure, and learning value perceptions, on learning from and building on successes and failures, goal progress, and overall well-being. We recruited a nationally representative sample of 300 participants on Connect, an online participant platform by CloudResearch, with 262 participants completing both sessions. We followed participants over a two-week interval, measuring attitudes towards success and failure, learning value perceptions, and learning from experiences of success and failure. To examine the downstream effect of these factors, we measured well-being, self-efficacy, optimism, and progress on two of their goals. The second study examines how learning value perception affects feedback across several domains, including feedback-seeking, feedback usage, and feedback orientation. In addition, we measured how learning value perceptions affect fear of failure, goal orientation, and adaptive learning from errors. We recruited a nationally representative sample of 400 participants on CloudResearch Connect in a cross-sectional, observational study. These studies demonstrate the potential impact of learning value perceptions on how people interact with experiences of success and failure and provide insight into how these perceptions influence how people engage with feedback. These studies are part of a set of ongoing studies exploring the effects of learning value perception on goal progress, learning, and feedback adapt

HEALTH / CLINICAL RESEARCH

Presenters are organized by discipline and then alphabetically by last name.

The Impact of Analgesic Regimens on Mobility After Lumbar Spine Surgery: A Systematic Review

Chelsea Clarke

Faculty Mentor: Rory Goodwin

Authors: Chelsea Clarke, Seeley Yoo, Mariana Bouchan, Gabriella Lozano, Dana G. Rowe, Antoinette Charles, Emily Luo, Jacqueline M. Emerson Samantha Kaplan, Melissa M Erickson, C. Rory Goodwin,

Discipline: Health / Clinical Research

Abstract:
Postoperative pain management is essential in lumbar spine surgery to optimize functional recovery and mobility. This study aimed to systematically review the efficacy of various intraoperative and postoperative pain management strategies in improving functional mobility in patients undergoing lumbar spine surgery. A systematic review and meta-analysis were conducted following PRISMA guidelines. The literature search included MEDLINE, Embase, and Web of Science databases up to October 29, 2024. Studies assessing intraoperative and postoperative pain management regimens in adult lumbar spine surgery patients were included. Primary outcomes included measures of ambulation, disability indexes, and daily functional activities. Data extraction, quality assessment, and statistical analyses were performed by three independent reviewers, with one additional author to resolve conflicts. Study quality was assessed using the Methodological Index for Non-Randomized Studies (MINORS) criteria. Descriptive statistics, meta-analysis, and narrative analysis summarized outcomes and evaluated interventions for functional mobility. The review included 44 studies with a total of 4,252 patients. Intraoperative nerve blocks demonstrated significant reductions in time to ambulation and consistent functional mobility improvements. Multimodal medication regimens, such as pregabalin and acetaminophen, significantly lowered disability scores. However, postoperative nerve blocks showed mixed efficacy, with delayed administration limiting functional improvements. Adverse events, such as opioid-induced urinary retention, were more common in opioid-based regimens, whereas non-opioid alternatives showed safer profiles. Intraoperative nerve blocks and multimodal medication regimens effectively improve postoperative mobility, highlighting their importance in patient-centered care. However, variability in outcomes underscores the need for tailored pain management strategies. Future research should focus on standardizing protocols, exploring long-term functional outcomes, and optimizing interventions for diverse patient populations.

Single-breath Fractional Ventilation Derived From 129Xe MRI: Repeatability In IPF

Kunyu (Kimi) Du

Faculty Mentor: David Mummy

Authors: Kunyu Du, Suphachart Leewiwatwong, Yuh-Chin Huang, Bastiaan Driehuys, David Mummy

Discipline: Health / Clinical Research

Abstract:
Current methods for assessing ventilation heterogeneity via hyperpolarized 129Xe MRI generally rely on histogram-based techniques suchas rescaling to arbitrary thresholds or image-based clustering to calculate the ventilation defect percent (VDP). These approaches are based on relativesignal intensities and are not intuitively related to physiology. Here, we present a novel method to calculate fractional ventilation (FV) from single-breath 129Xe MRI and evaluate its repeatability compared to conventional 99th percentile histogram rescaling. 23 participants with idiopathic pulmonary fibrosis (IPF) (8F, age 74.5±5.7) underwent 3D radial ventilation imaging with RF-depolarization bias correction at baseline and after three months. FV was calculated for each participant by dividing the total xenon signal measured within the segmented lung mask by the known volume of the inhaled xenon dose, modified to account for anatomical dead space. The resulting "xenon signal to volume" ratio was then used to estimate voxel-wise FV, defined as the volume of xenon mixture per voxel (as estimated from the xenon signal) divided by the voxel volume. VDP using the FV method (VDP-FV) was computed as the percentage of the histogram ≥2sd below the healthy reference mean derived from a healthy reference cohort. Repeatability between baseline and 3-month follow-up was assessed using Bland-Altman analysis, the intraclass correlation coefficient (ICC), and the coefficient of repeatability (CR) for both the VDP-FV and VDP using the 99th percentile histogram normalization (VDP-99). Mean FV in the healthy reference cohort was 0.32±0.16 vs. 0.24±0.11 in IPF at baseline (p=0.003). Mean FV in IPF at 3-months was0.21±0.092 (p=0.18 vs. baseline). The baseline VDP-FV was 10.5±6.53% vs. 4.02±4.05% for VDP-99. The limits of repeatability (LoR) for VDP-FV were[-6.36%-10.80%], ICC=0.80 and CR=8.79, vs. LoR of [-6.86%-8.84%], ICC=0.53, and CR=8.02 for VDP-99. Our proposed FV method provides physiologically plausible estimates of regional fraction ventilation based on first principles, unlike conventional methods of assessing ventilation heterogeneity based on relative intensity. Despite VDP-FV having a larger average magnitude than VDP-99, both methods had similar LoR. However, the ICC for VDP-FV was strikingly higher than for VDP-99, indicating more consistent measurements over the 3-month time period. Work is ongoing to further improve the robustness and repeatability of this measurement.

Factors Associated with Sexual Avoidance among Breast Cancer Survivors with Type 2 Diabetes

Katie Maddock

Faculty Mentor: Juliann Stalls

Authors: Katie Maddock, Louise Adillon, Navya Kancharla, Ali Wilson, Caroline S. Dorfman, Ph.D., Leonor Corsino, M.D., M.H.S, Gretchen Kimmick, M.D., Cheyenne Corbett, Ph.D., Rebecca A. Shelby, Ph.D., Juliann M. Stalls, Ph.D.

Discipline: Health / Clinical Research

Abstract:
Women managing breast cancer are at increased risk for sexual difficulties, such as vaginal dryness, pain during intercourse, and psychosocial challenges (e.g., anxiety), which can negatively impact their quality of life. These difficulties may be compounded by comorbid type 2 diabetes; blood glucose fluctuations can also contribute to sexual difficulties (e.g., vaginal dryness). Sexual difficulties may lead to avoidance of sexual activity, which may impact relationships, sexual well-being, and quality of life. We examined associations between sociodemographic, medical, and psychosocial factors and sexual avoidance among breast cancer survivors with type 2 diabetes. Breast cancer survivors (stage I-III disease) aged >21 with type 2 diabetes who had completed primary cancer treatment completed self-report measures of sociodemographic, medical, and psychosocial characteristics as well as sexual functioning and avoidance. Descriptive statistics were utilized to characterize the full sample and self-report measures. Only women who reported being married, partnered, or having a sexual partner were included in a regression analysis to examine the role of sociodemographic, medical, and psychosocial characteristics in explaining variance in sexual avoidance. Women (N=53) were M=64.46 years old and represented a variety of racial backgrounds (47.2% White, 37.7% Black, 11.3% American Indian/Alaskan Native, 3.8% Asian). 13.2% of the sample identified as Hispanic. 75.5% were married/partnered. 39.7% were diagnosed at stage II/III. 60.4% were post-menopausal. In a multiple linear regression analysis, Black race (versus other; β=0.230, p=.047), stressors (β=.463, p=<.001), and physical symptoms (β=.261, p=.039) each uniquely contributed to greater sexual avoidance. Identifying sexual difficulties and providing appropriate sexual health referrals (e.g., sex therapy, pelvic floor physical therapy) is an important component of breast cancer care. Our findings highlight the importance of supporting survivors to address chronic life stressors and physical symptoms that contribute to sexual avoidance and indicate that Black survivors may be more likely to experience sexual avoidance.

Evaluating Public Awareness for Improved Diagnosis and Treatment of Rare Breast Cancers

Katherine Reddy

Faculty Mentor: Gayathri Devi

Authors: Katherine Reddy, Beau Blass, Alexandra Bennion, Hannah Woriax, Terry Arnold, Margie Scott, Anh N. Tran, Gayathri R. Devi

Discipline: Health / Clinical Research

Abstract:
Inflammatory breast cancer (IBC), a rare and NIH-designated cancer health disparity, is an aggressive subtype with a unique presentation that often delays diagnosis and treatment. Reproductive risk factors, higher incidence rates among marginalized populations, and social drivers of health (SDoH) limit healthcare access, making IBC an important focus for mitigating health disparities. Previous research with primary care providers (PCPs) and IBC patients underscored the need to assess IBC awareness among members of the general public, leading to the focus on evaluating the public's knowledge and health-seeking behaviors related to IBC and other rare breast cancers. Surveys for PCPs, patients, and the public were developed with guidance from a Community Advisory Board and refined through cognitive interviews. PCPs and IBC patients were identified from North Carolina medical centers and community practices. Public participants were recruited via email, social media, and direct outreach at urban and rural clinics serving low-income, medically complex patients, as well as diverse community events. Data were analyzed using descriptive statistics and t-tests (p<0.05). Among public participants (n=170; 77% Female, 55% White, 21% Black, 12% Asian, 9% Hispanic, 7% American Indian/Alaskan Native, 4% Pacific Islander, 61% ages 25-44, 43% with household incomes <$99,000, 41% based in North Carolina), 20% had never heard of IBC (p<0.0001). Misconceptions included: 70% incorrectly identifying breast lumps as a symptom (p<0.0001); 40% not recognizing overweight status as a risk factor (p=0.009); 36% not identifying the characteristic "pitted" skin appearance (p=0.0003); and 35% not recognizing changes in breast size/shape as a symptom (p=0.0001). Healthcare-seeking barriers included fear of diagnosis, difficulty discussing symptoms, lack of insurance, transportation, and religious concerns. Encouragingly, 97% of participants were willing to share IBC information, particularly with family and friends (p <0.0001). Most supported integrating visual aids and educational materials into survey administration. Findings highlight the need for public education alongside provider- and patient-focused research to reduce the health disparities associated with rare cancers. Addressing modifiable SDoH in diverse communities is critical to improving early detection and management of IBC and other rare cancers in primary care.

Challenges to Dying Well and Death Doula Work

Jenna Yeam

Faculty Mentor: Dan Ariely

Authors: Jenna Yeam, Dan Ariely, Anne Allison

Discipline: Health/ Clinical Research

Abstract:
With increasing life expectancy, the decline of multi-generational households, and the over-medicalization of death and dying, individuals in their end of life, and their loved ones, experience unnecessary suffering from points of friction that arise in an end-of-life journey. In response, end-of-life professionals called Death Doulas are emerging to fill critical gaps in care. Death Doulas are non-medical caretakers who address the psychological, emotional, existential, and practical needs of the dying and their loved ones. The study aims to identify what is going wrong at the end of life by identifying points of friction and intra-friction relationships. The study draws on Death Doula's experiences to provide a non-medical perspective from a non-medical figure that is not personally related to the dying person nor the circle of care to explain what is going wrong, including frictions' causes, consequences, and character. I completed 67 semi-structured interviews with INELDA-certified US Death Doulas. Following interview transcription and data cleaning, I conducted an inductive codebook thematic analysis. The findings highlight points of friction, using the actions and inactions of the dying person and their circle of care as the entry point. Key themes include the failure to identify dying person's wishes, unquestioned adherence to medical advice, underutilization of palliative care services, lack of awareness and misconceptions about palliative care options, exclusion of loved ones in EOL decision-making, inadequate discussions about EOL preferences, prioritizing family desires over the dying person's wishes, avoidance of open discussions about death, and a lack of communication regarding EOL and post-death care wishes.In the process, the theme of death and dying awareness and education consistently emerged as an underlying cause of frictions, which highlights a need for greater death education, awareness, and death positive activism. Further research is necessary to evaluate the potential role medical and non-medical professionals may play to establish a sense of patient and family control, enhance informed-decision making, and expand the care model to incorporate greater emotional and spiritual support. In addition, community-engaged approaches to death education may be used to improve local EOL experiences.

BIOLOGICAL AND BIOMEDICAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

A Gut Sense for Dietary Protein

Siddharth Amirneni

Faculty Mentor: Diego Bohórquez

Authors: Siddharth Amirneni, Marco Toc, Peter Weng, Diego Bohórquez

Discipline: Biological and Biomedical Sciences

Abstract:
Objectives. Dietary protein is essential for life. When protein content of food is low, individuals overeat to achieve adequate protein intake. In 2015, Dr. Diego Bohórquez identified specialized gut epithelial cells called "neuropods" that form synaptic connections with the vagus nerve to relay sensory signals to the brain. It has been shown that neuropod cells drive sugar consumption, but their role in driving protein-seeking behavior remains unexplored. This study evaluates the role of neuropods in driving protein-seeking behavior. Methods. To evaluate the effect of dietary protein content on cumulative intake, mice were provided either protein-complete or protein-deplete diets. To further investigate whether protein intake is mediated by the gut, taste-blind mice were exposed to protein-complete and protein-deplete diets followed by a two-bottle preference assay to evaluate their preference for an amino acid solution. Using vagal electrophysiology, we evaluated whether an intraduodenal infusion of amino acids elicits gut-to-brain signaling. Results. Mice consumed less of the protein-deplete diet than the complete diet, suggesting a tendency to avoid diets lacking protein. When mice were protein deficient, wild-type mice strongly preferred the amino acid solution over vehicle. This effect persisted in taste-blind mice, implying gut-sensing as a key factor for protein appetite. Vagal electrophysiology further supported this finding by showing an immediate increase in vagal firing rate after mice received an intraduodenal infusion of amino acids. Conclusions. In protein-deficient states, neuropod cells mediate protein-seeking behavior through gut-brain communication via the vagus nerve. This study identified a gut sensory mechanism involved in protein appetite, providing potential targets for developing novel interventions to address protein malnutrition and nutritional imbalances.

The Effect of Social Experience on Courtship Behavior in Drosophila

Efe Balkanli

Faculty Mentor: Pelin Volkan

Authors: Efe Balkanli, Chengcheng Du, Ashley Jia, Pelin Volkan

Discipline: Biological and Biomedical Sciences

Abstract:
Social experiences influence animal behaviors, particularly in the context of courtship. This study investigates the effects of social experience on the courtship behavior in Drosophila melanogaster fruit flies, aiming to elucidate the underlying molecular mechanisms. We hypothesized that social isolation would alter courtship behaviors through changes in gene expression in different neural circuitries. Our results demonstrate that socially isolated males exhibit more vigorous courtship towards virgin females compared to their group-housed counterparts. To explore the molecular basis of these behavioral changes, we performed single-cell RNA sequencing on fruitless and doublesex positive cells to identify differentially expressed genes (DEGs) associated with social experiences. We subsequently conduct RNAi knockdown experiments targeting DEGs in specific neuronal circuits. Our findings revealed several promising candidate genes that might be involved in regulating social experience induced courtship changes. This presentation will provide valuable insight into the molecular mechanisms underlying social isolation-induced changes in the courtship behavior in Drosophila, offering a foundation for further investigation into the complex interplay between social experience, and behavioral outputs in fruit flies and potentially other species.

Engineered Lipid Nanoparticles for Heart Regeneration

Mya Booth

Faculty Mentor: Ravi Karra

Authors: Mya Booth, Aigin Heydari, M.D., Ravi Karra, M.D.

Discipline: Biological and Biomedical Sciences

Abstract:
Treatments for heart failure primarily focus on managing symptoms rather than repairing damaged cardiac tissue. While gene therapy offers a promising approach for heart regeneration, the lack of effective delivery systems remains a major challenge. Adeno-associated viruses (AAVs) are the most commonly used gene delivery vectors, but they are limited by immune responses, restricted payload capacity, and the inability to enable repeating dosing. Lipid nanoparticles (LNPs) present a safer, more flexible, and repeatable alternative. However, none have been specifically optimized for targeted cardiac gene delivery. In this study, a LNP formulation incorporating palmitic acid, a saturated fatty acid known for its role in cardiac imaging, was developed. Palmitic acid's radioactive form, C-11 palmitic acid, is used in positron emission tomography (PET) scans to detect infarcted areas in the heart. A microfluidic mixing method was used to incorporate palmitic acid into LNPs for mRNA delivery. In vivo results show that cardiomyocytes uptake palmitic acid. These findings suggest that palmitic acid-modified LNPs have the potential to serve as a targeted approach for cardiac gene therapy, addressing a critical gap in heart failure treatment.

Exploring the genetic framework governing vacuole biogenesis within the zebrafish notochord

Claudia Carugati

Faculty Mentor: Daniel Levic

Authors: Claudia Carugati, Daniel S. Levic

Discipline: Biological and Biomedical Sciences

Abstract:
Understanding the molecular and biomechanical processes underlying notochord morphogenesis is critical for understanding vertebrate development. To investigate the role of vacuolated cells in zebrafish notochord formation, we developed a series of genetic tools and stable transgenic lines. First, we generated stable knockout lines for the two zebrafish genes of the MiT/TFE family of transcription factors by inducing CRISPR/Cas9-mediated deletions at the start of their coding sequences. These loss-of-function mutants enable functional dissection of transcriptional regulation during notochord development. Second, we engineered a promoter insertion in the cavin1b locus to drive expression of Rab32 fused to TurboID and a P2A-linked fluorescent protein. This construct will biotinylate proximal proteins on the cytosolic side of the vacuole membrane, and following the establishment of a stable line, will be used in proteomics experiments to map the molecular environment surrounding vacuolated cells. Lastly, we inserted a fluorescent reporter construct—GFP tagged to myl12.1, under the control of the cavin1b promoter. This line serves as a dynamic reporter of intracellular tension within vacuolated notochord cells. Collectively, these tools will be useful to investigate the development and morphogenesis of vacuoles within vacuolated cells. This is important as vacuolated cells are highly conserved across species, including zebrafish and pigs, as shown by molecular and proteomic analyses.

Optimizing Delivery of the ApoE-mimetic Peptide, CN-105, to Improve Outcomes after SCI

Eujin Chung

Faculty Mentor: Timothy Faw

Authors: Eujin Chung, Sanoe Rapozo, Paola Abad, Haichen Wang, Ping Fan, Ellora Haukenfrers, Ivan Spasojevic, Simon Gregory, Daniel T. Laskowitz, Timothy D. Faw

Discipline: Biological and Biomedical Sciences

Abstract:
Spinal cord injury (SCI), the second leading cause of paralysis in the U.S., affects more than 27 million people worldwide with far-reaching physical and emotional effects. Despite years of research, there are no FDA-approved therapeutics that alter the trajectory of SCI recovery. As such, there is a critical need for post-SCI therapeutics that reduce damage, improve sensory and motor function, and ultimately improve quality of life. CN-105 is a novel apolipoprotein E-mimetic peptide that reduces neuroinflammation and promotes neuroprotection in preclinical brain injury models. Whether CN-105 could improve outcomes after SCI is unknown. As a first step, we sought to quantify the pharmacokinetics of a single dose of CN-105 after contusive SCI in mice and the delivery parameters that most effectively reduce neuroinflammation after SCI. First, mice received a moderate SCI at T9 followed by an intravenous dose of CN-105 (5 mg/kg) 45-minutes post-injury. Mice were euthanized at 5 min, 15 min, 30 min, 60 min, and 180 min post-injection. We extracted plasma and the injury epicenter for pharmacokinetic analysis. Near exponential elimination (in ng/g per minute) occurred from both plasma and the spinal cord with a half life of 25 and 52 minutes, respectively. In a second experiment, mice were randomized into 16 groups across drug (CN-105 at 0.05 mg/kg, 0.50 mg/kg, or 5.00 mg/kg) or vehicle (0.9% saline), single or repeated dose, SCI or laminectomy, and 4-hour or 7-day survival. We monitored weight daily and assessed locomotor recovery via Basso Mouse Scale. Injury epicenters (1 cm) were extracted for single-nuclei RNA sequencing. Preliminary data includes 1,418 neurons, 2,755 microglia, and 3,231 macrophages across 7-day SCI + Vehicle and SCI + Repeated CN-105 (5.00 mg/kg) mice. Between the two groups, we examined the 10 most differentially expressed genes (up and down) across cell types. Findings for macrophages indicate upregulation of Mgl2, a gene involved in dampening immune responses and suppressing T cell activation, in mice receiving CN-105. Data also showed upregulation of the hemoglobin gene Hbb-bs, which is typically upregulated during damage, in the microglia of CN-105 mice. These findings will guide future research to quantify the long-term effects of CN-105 on functional recovery post-SCI, potentially identifying a new therapeutic approach for individuals with SCI.

Computational Pipeline for Cell Type Annotation of HuBMAP Spatial-omics Data

Zachary Deutsch

Faculty Mentor: John Hickey

Authors: Zachary Deutsch, Yang Miao, John Hickey

Discipline: Biological and Biomedical Sciences

Abstract:
Open data facilitates scientific collaboration by allowing researchers to leverage, share, and combine data. The Human BioMolecular Atlas Program (HuBMAP) is a research consortium focused on collecting single-cell datasets of healthy organs of the human body. However, many HuBMAP datasets lack cell type annotations. Our group is using our background in spatial-omics data analysis to annotate these datasets as a reference and provide a template for other researchers based on best practices we have published. Thus far, we have created an end-to-end Jupyter Notebook that can be used within virtual machines provided by the HuBMAP consortium to annotate the small and large intestine datasets within the HuBMAP Data Portal. In the future, we also aim to annotate other organs on the portal, such as lymph nodes, spleen, and thymus. These will provide valuable annotations that will enable scientists to both study how the body is organized and as a healthy reference to diseased datasets they collect.

Hyperphosphorylated Tau in the Locus Coeruleus of Young Rhesus Monkeys

Cynthia Ding

Faculty Mentor: Anita Disney

Authors: Cynthia Ding, Anita Disney

Discipline: Biological and Biomedical Sciences

Abstract:
Alzheimer's disease (AD) is the sixth leading cause of death in the US, with the number of cases projected to triple by 2060. Current drugs aim to clear beta-amyloid plaques in the brain but are ineffective at stopping disease pathology. Thus, research is pivoting to focus on hyperphosphorylated tau (pTau), another hallmark of AD that may also be amplifying beta-amyloid plaques. pTau is first seen in the locus coeruleus (LC), a small structure in the brainstem, during early adulthood decades before AD symptoms arise. The LC innervates brain regions critical for memory, attention, and higher cognition. These are also where the first cognitive deficits are witnessed in AD. Could the LC be responsible for spreading pTau and initiating AD? To answer this question, we use rhesus monkeys because they spontaneously develop tau pathology, amyloidosis, and cognitive decline consistent with early-stage AD in humans. However, it is not yet known whether rhesus monkeys have pTau in the LC, so we must first address this gap. Brainstem blocks containing the LC of four females and four males, ranging from juvenile to late adulthood, were sectioned. Subsequently, immunohistochemical staining was conducted for phosphorylation sites on tau seen in AD (serine 214, and serine 202). Juvenile monkeys of 2 years old showed minimal staining in LC; but staining in the LC of monkeys as young as 4 years old was indicative of tau pretangles, seeding, and oligomeric plaques in astrocytes. Mature neurofibrillary tangles were seen in the LC of a young adult male of 14 years old. These preliminary results suggest rhesus monkeys are a reliable model for studying AD pathology. Further steps entail analyzing the progression of tau pathology in the LC of rhesus monkeys, and the exploration of whether the LC is responsible for spreading pTau.

Molecular and Cellular Impacts of UBE2A Mutations Linked to XLID Type Nascimento

Rachel Field

Faculty Mentor: Gustavo Silva

Authors: Rachel Field, Gessica Barros, Gustavo Silva

Discipline: Biological and Biomedical Sciences

Abstract:
Mutations in the ubiquitin-conjugating enzyme UBE2A are linked to X-linked intellectual disability type Nascimento, which manifests as moderate to severe intellectual disability, speech impairment, craniofacial dysmorphisms, urogenital abnormalities, and additional symptoms. Although a range of mutations with diverse clinical presentations have been identified, very little is known about how the mutations affect protein functionality and thus lead to disease. Therefore, we developed a yeast model system to systematically compare disease-associated UBE2A variants and examine their effects on gene expression, protein stability, protein function, and impact in cellular physiology. Our findings demonstrate that mutations such as Q128X reduce UBE2A protein levels, whereas the Q93E mutation increases protein abundance when expression is under the same promoter. Analysis of gene expression suggests that different mechanisms are responsible for defining this aberrant abundance of individual UBE2A mutants. We next showed that this altered protein abundance disrupts the UBE2A-mediated pathway, redox control of translation by ubiquitin (RTU). Our group has shown that the yeast homolog of UBE2A, Rad6, mediates global repression of translation under oxidative stress by conjugating K63-linked polyubiquitin to ribosomes. By measuring translation rates and using immunoblotting assays, we determined that UBE2A complements Rad6 translation repression function in yeast, and mutants like Q128X and Q93E disrupt this activity. Surprisingly, while mutants like Q128X exhibit decreased accumulation of K63-linked polyubiquitin, which is aligned with a loss of function phenotype, the Q93E variant shows increased accumulation. Furthermore, consistent with the idea of impaired translation control, UBE2A mutant variants show substantial sensitivity to hydrogen peroxide, similar to null RAD6-deleted strains. Together, our results reveal that selective patient-derived UBE2A mutations might lead to Nascimento Syndrome through distinct molecular and functional mechanisms. Our work further illustrates that dissecting the impact of each mutation on UBE2A expression and function will be critical to develop selective therapies and better understand the varied clinical manifestation observed in patients.

Hyaluronic-Acid Based Engineered VEGF Biomaterial Gel for Osteogenesis of Neurosurgical Craniot

Amy Fulton

Faculty Mentor: Eduardo Chaparro

Authors: Amy Fulton, Eduardo Chaparro, Brian Mace, Anjali Tatini, Govind Gurnani, Yana Al Inaya, Lia Lapidot, Emma Whitehead, Nhi Phan, Tatiana Segura, David Hasan

Discipline: Biological and Biomedical Sciences

Abstract:
Skull healing and repair is a significant area of potential research in neurosurgery. Many brain surgeries require removal of a bone flap from the skull, which even when replaced can take time to heal and have potential associated risks, especially when held in place with a metal plate, as is common practice. Craniotomy burr hole surgeries often do not end in replacement of the skull flap and result in an undesirable scalp depression. In addition, cranioplasty to repair damaged skulls is a useful procedure but associated with significant morbidity. This preliminary study proposes to investigate the use of an angiogenic biomaterial gel, "Cluvena," for use in skull repair. This gel will be implanted in craniotomy sites on mice without replacement of the skull flap. Healing of the surgical site after three weeks will be quantified using imaging technology and compared to control group mice receiving craniotomy but no gel. This procedure will therefore assess the potential utility of this gel in promoting skull regrowth, which has valuable implications in neurosurgery as well as several other fields which would benefit from tools for bone repair, including dentistry, orthopedics, and geriatrics.

Validation of Novel Regulatory Elements that Influence TOX Expression and T Cell Exhaustion

Aretha Gao

Faculty Mentor: Charles Gersbach

Authors: Aretha R. Gao, Christian D. McRoberts Amador, Charles A. Gersbach

Discipline: Biological and Biomedical Sciences

Abstract:
T Cells are critical components of the body's immune system, responsible for recognizing and eliminating virally infected and cancerous cells via antigen recognition. In the context of immunotherapy, T-Cell memory is associated with favorable clinical outcomes while T-Cell exhaustion is associated with negative clinical responses due to a decrease in T-Cell proliferative capacity and cytotoxic potential. T-Cell exhaustion is a dysfunctional cell state that is induced by chronic stimulation of the T-Cell receptor through repeated antigen encounters. TOX, a transcription factor (TF), has been shown to transcriptionally and epigenetically program and drive CD8+ T-Cell exhaustion. Therefore, understanding the biological mechanisms of TOX and regulating its expression could have powerful clinical implications as it could inform therapeutic strategies to reverse or reinvigorate exhausted T Cells. To investigate TOX and its role in exhaustion, we performed matched screens to chronic versus acute T-Cell stimulation using CD8+ T Cells derived from three human donors and a pooled lentiviral library containing coding sequences of all human TFs. Our screen showed that previously identified and novel TF regulators of TOX emerged as hits unique to either the chronic or acute stimulation setting. We hypothesized that transcription factors regulating TOX expression uniquely under chronic stimulation will either repress or drive the CD8+ T Cell exhaustion programming. Phenotypic validation using Fluorescence-Activated Cell Sorting (FACS) revealed that these TFs were modulating expression of key immune checkpoint markers, including PD-1, LAG-3, and TIGIT, as well as memory-associated markers. Based on this data, we identified a subset of TFs that either drive exhaustion by up regulating exhaustion markers or push T Cells away from exhaustion by down regulating exhaustion markers and/or up regulating memory markers. We further characterized this subset using Bulk RNA-seq to profile transcriptomic changes associated with each TF. Additionally, a SHARE-seq screen targeting chronic-unique TFs was performed to capture the transcriptome through scRNA-seq, chromatin accessibility through scATAC-seq, and the TF being over expressed. Future studies will functionally validating candidate TFs using cytokine expression assays and tumor co-culture killing models.

Elucidating Humidity-Clock Interplay in Arabidopsis

Ethan Gurwitch

Faculty Mentor: Xinnian Dong

Authors: Ethan Gurwitch, Dr. Sargis Karapetyan, Dr. Xinnian Dong

Discipline: Biological and Biomedical Sciences

Abstract:
Due to the Earth's rotation around the sun and its axis, we experience a day-night cycle. Consequently, most organisms have evolved an intrinsic oscillator known as the circadian clock. The circadian clock perceives the periodic environmental signals, known as Zeitgebers, such as light and temperature, and uses them to synchronize the internal rhythms of the organism to the environment. For example, downstream from the plant clock, processes like flowering time/pollination, leaf movement, growth, germination, stomatal opening, plant defense, and more are affected. Recently, like light and temperature, relative humidity has also been shown to be a Zeitgeber that reinforces the plant circadian clock under the light/dark (LD) cycle. However, the mechanism by which humidity affects the plant's circadian clock is unknown. Furthermore, the small phase shift of the humidity oscillation compared to the LD cycle was shown to be critical for the clock reinforcement. To study the association between humidity and the plant clock, we used the detailed F2014 circadian clock model developed by Fogelmark and Troein. We incorporated an unknown intermediate sensitive-to-humidity protein (SHIP) into the model, which relays the light and humidity oscillation signals to clock gene transcription. By performing nonlinear optimization of the parameters to fit the objective functions obtained from the experiment, we systematically explored all possible combinations of how light, dark, humidity, and aridity regulate the SHIP. We then used a transgenic line of Arabidopsis plants with a bioluminescence reporter for CCA1 to verify model predictions. Our results indicate that the SHIP accumulates in the early evening, in aridity, and subsequently responds to high humidity before dawn.

MicroRNA-K as a potential therapeutic target for preventing cardiac hypertrophy

Maya Hoteit

Faculty Mentor: Walter Koch

Authors: Maya Hoteit, Stephanie Kereliuk, Walter Koch

Discipline: Biological and Biomedical Sciences

Abstract:
Small non-coding RNAs, including micro-RNAs (miRs), have emerged as potential biomarkers and therapeutic targets for heart failure. MiRs are small non-coding RNAs (approximately 22 nucleotides in length) that regulate gene expression and fine-tune cellular protein levels. Our lab recently identified a novel miR, miR-K, which appears to have unique cardio-protective properties in the heart, but is not well characterized. We hypothesize that miR-K exerts is cardio-protective effects by attenuating cardiac hypertrophy. Neonatal rat ventricular myocytes (NRVMs) were used as an in vitro model system. Hypertrophy was induced with the alpha1-adrenergic agonist phenylephrine (PE; 10uM for 48 hours) and cardiomyocytes were treated with a miR-K mimic or scramble control. Following treatment, cells were stained with wheat germ agglutinin (WGA) conjugated to Alexa Fluor 594 to visualize cardiomyocyte membranes via fluorescent microscopy. Images were captured using an EVOS M7000 Imaging System and cell surface area was quantified in ImageJ. In NRVMs pre-treated with miR-K for 24 hours followed by PE for 48 hours, miR-K completely attenuated cellular hypertrophy by reducing cell surface area by 53.7% when compared to scramble control cells treated with PE. Additionally, in NRVMs with established hypertrophy (stimulated with PE for 48 hours prior to treatment of with miR-K for 24 hours), miR-K reversed cardiomyocyte hypertrophy, as cell surface area returned to baseline levels (NRVMs that did not receive PE stimulation prior to miR-K treatment) and a 6.4% reduction in cell surface area was observed when compared to PE-scramble control cells. These results show that miR-K prevents PE-induced cardiomyocyte hypertrophy and partially reverses established hypertrophy, demonstrating its potential role as a regulator of pathological cardiac hypertrophy. Future studies will assess whether miR-K exerts similar anti-hypertrophy effects in response to other pathological stimuli, such as isoproterenol or angiotensin II, to further evaluate its potential as a cardio-protective therapy.

Identifying Key Genetic Regions for Cell Sheet Morphogenesis on Chromosome 3R

Khang Huynh

Faculty Mentor: Janice Crawford

Authors: Khang Huynh, Melissa Sican, Ainsley Shan, Janice Crawford, Dan Kiehart

Discipline: Biological and Biomedical Sciences

Abstract:
Morphogenesis is an incredibly important process in many organisms as it involves the highly conserved movement of cell sheets to achieve a final form. Morphogenesis holds significant implications for heart and palate formation, wound healing, gastrulation, and neural tube development. The process of dorsal closure (DC) in Drosophila melanogaster embryos mimics the hallmark cell sheet movements observed in morphogenesis and thus serves as an effective model for investigation. During dorsal closure, contractile forces drive lateral epidermis cell sheets to zip up toward the midline of the dorsal opening. This dorsal opening is initially compromised by another cell sheet called amnioserosa. As the lateral epidermis sheets close, these cells ingress and apoptose. The Kiehart lab aims to explore how various genes impact this process through the deficiency screen project. The Kiehart lab utilizes the Bloomington deficiency kit, which is a set of genomic deletions that collectively delete 98.5% of the right arm of the 3rd chromosome. These stocks are crossed with a Drosophila melanogaster line containing a fluorescence gene on the second chromosome and marker genes on the third chromosome. During cross one, virgin females of imaging background; Ly/TM3, Sb, Ser, TwiGFP are crossed with males of Df(3R)n/Balancer. Cross two was established using homozygous progeny consisting of 10 virgin females and 8 males of imaging background/+; Df(3R)n/TM3, Sb, Ser, TwiGFP. The embryos are dechlorinated and manually screened for hallmark "heart-like" openings. From the remaining embryos, the Kiehart lab employs genetic and live-imaging techniques to visualize dorsal closure. Specifically, I screened Df(3R)61, Df(3R)74, Df(3R)79, Df(3R)91, Df(3R)95, Df(3R)100, Df(3R)102, and Df(3R)103. Five of these deficiencies have a phenotype, two had pre-DC phenotypes, and one had no phenotype. Following initial screening for Df(3R)100, Df(3R)102, and Df(3R)103, I used smaller deletions, called subdeficiencies, to narrow down particular regions of interest and identify the key genetic players that cause abnormal phenotypes. These subdeficiencies are Df(3R)Exel6218 and Df(3R)Exel7379. An improved understanding of these genes will provide insight into the incredibly robust process of morphogenesis.

DRMTX Regulates Neuroendocrine Progression and Serves as a Therapeutic Target in NEPC

Issac Jung

Faculty Mentor: Jungwook Park

Authors: Issac Jung, Yunsol Jo, Jungwook Park

Discipline: Biological and Biomedical Sciences

Abstract:
Neuroendocrine prostate cancer (NEPC) is an aggressive, therapy-resistant subtype of prostate cancer that can develop from prostate adenocarcinoma (PrAd) and castration resistant prostate cancer (CRPC) following treatment. While DNA methyltransferases have been implicated in NEPC progression, the role of DRMTX remains underexplored. Here, we investigate the functional role of in NEPC lineage plasticity and tumor growth and evaluate the therapeutic potential of its selective inhibitor, DRMTX Inhibitor.
Our analysis of publicly available RNA-sequencing datasets (Beltran et al., 2011; 2016) revealed elevated DRMTX expression in NEPC relative to PrAd. To better understand its functional role, we established DRMTX knockout (sg) NEPC cell lines using CRISPR-Cas9. CellTiter-Glo assays performed on these cell lines showed a 40–50% reduction in cell viability following DRMTX loss compared to control group NEPC cells. Flow cytometry with Annexin V/PI staining confirmed increased apoptosis in sgDRMTX lines, indicating that DRMTX plays an essential role in NEPC cell proliferation and survival.
To evaluate DRMTX function in vivo, we engineered doxycycline-inducible DRMTX knockdown xenografts in immunodeficient NSG mice. Tumor volumes in knockout DRMTX xenografts were reduced by ~50% relative to controls. Immunohistochemistry (IHC) and immunoblot analyses showed decreased expression of proliferation markers (e.g., Ki-67) and increased apoptotic markers (e.g., cleaved caspase-3). Further, the loss of DRMTX led to the downregulation of neuroendocrine lineage markers and transcription factors, suggesting that DRMTX plays a critical role in maintaining NEPC lineage identity.
Given DRMTX's role in NEPC viability, we tested the therapeutic potential of DRMTX Inhibitor Boamamine X, a quinone antibiotic that selectively inhibits DRMTX by binding to the enzyme's catalytic site. In vitro studies found that Boamamine X treated NEPC cell lines had significantly decreased viability compared to the control groups treated with DMSO. In vivo, treatment of NEPC xenografts with Boamamine X resulted in significantly reduced tumor growth. IHC and immunoblotting of treated tumors confirmed reduced proliferation, increased apoptosis, and downregulation of neuroendocrine markers, mirroring genetic DRMTX ablation.
Our study identifies DRMTX as a key regulator of NEPC growth, survival, and lineage plasticity, and highlights Boamamine X as a promising therapeutic candidate for NEPC.

Organ and Cell Morphologies Governing Circumnutation in Rice Roots

Mao Kobayashi

Faculty Mentor: Mao Kobayashi

Authors: Mao Kobayashi, Medhavinee Mijar, Mingyuan Zhu

Discipline: Biological and Biomedical Sciences

Abstract:
Circumnutation is a helical movement of organ tips observed uniquely in plants and plays a crucial role in early-stage development. In rice, primary root circumnutation contributes to stable seed positioning and enhanced soil anchorage. Circumnutation also allows rice primary roots to continuously sense and navigate around obstacles. This movement provides a buffer period for roots to detect barriers before direct contact and reduces impact force by increasing the surface area of interaction. Our previous study on rice hk1 mutants, in which Histidine Kinase 1, an enzyme involved in the cytokinin signaling pathway, is disrupted, revealed that auxin gradients regulated by ethylene drive circumnutation (Taylor 2021). Still, the cellular mechanisms governing this process and their influence on organ-level behavior remain unclear. This project aims to identify key cellular parameters that regulate circumnutation patterns, providing insights into cellular coordination and potential molecular mechanisms underlying this movement. We conducted three independent experiments to assess these factors. First, we compared wild-type X. Kitaake rice roots to the hk1-3 mutant, which carries a mutation in the HK1 (histidine kinase) gene and exhibits a strong circumnutation phenotype for effect of genetic perturbation. Second, we analyzed natural cultivars with distinct circumnutation behaviors to investigate the role of other regulatory genes yet to be isolated. Finally, we assessed the impact of external stress by increasing Gelzan concentration from the standard 0.15% and observing root behavior. Using confocal microscopy and automated time-lapse imaging, we identified a strong correlation between root tip amplitude and three cellular parameters: aspect ratio, cell number, and mature cell length, with mature cell length showing the strongest relationship ($r = 0.63$, $p < 0.05$). Computational simulations, developed in collaboration with physicists at the Georgia Institute of Technology, further confirmed that mature cell length predominantly influences movement amplitude. The consistency between the model and empirical data reinforces the simulation's credibility as a model for manipulating circumnutation. The study provides potential parameters that can be manipulated for engineering roots and their behaviors. Future studies will further explore the genetic and molecular mechanisms underlying the changes in cell length through molecular cloning and RNAseq data.

Social Aging in Ring-tailed Lemurs (Lemur catta)

Walter Kornfeld

Faculty Mentor: Leslie Digby

Authors: Walter Kornfeld, Leslie Digby

Discipline: Biological and Biomedical Sciences

Abstract:
Social aging refers to changes to an animal's social behavior as it ages. Aging in primates is often accompanied by decreased social engagement and negatively valenced social interactions (e.g. fewer social interactions but equal aggressive interactions with age). A key question is whether social aging is due to negative impacts of aging such as cognitive decline or if it reflects the positive impacts of having had more time to cultivate social relationships. Ring-tailed lemurs (Lemur catta) are often kept in captive settings where they routinely live into their thirties—a decade longer than the longest lifespans typically seen in the wild—so understanding social aging in this species is paramount for their well-being. As such, further research is needed in this area. We used focal animal sampling to record the behaviors of 18 captive ring-tailed lemurs at the Duke Lemur Center. Lemurs were observed in indoors enclosure, outdoors enclosure, and free-ranging in forested habitats. Using Generalized Linear Models (GLMs) with beta distributions and Poisson distributions , we analyzed how aging, access to forest enclosure, sex, and group size correlate with social behavior. We found that geriatric adults (aged 23-32) spent significantly less time engaged in all social behaviors as well as in affiliative social behaviors compared to prime-age adults (aged 9-13) and middle-aged adults (16-19.5). The GLM supports that sex, group size, and forest access were not significant predictors of percentage of time engaged in social behaviors. We also found no significant correlation between age and rates of initiating aggressive behavior nor rates of initiating affiliative behavior. These findings disagree with previous work on ring-tailed lemurs which found no impact of age on social behavior: the difference in results may be due to how age groups are defined within the respective studies. Our findings suggest that ring-tailed lemurs exhibit the same pattern of social aging shown by most (but not all) primates, characterized by less social engagement overall. We did not find support for the hypothesis that rates of initiating social behaviors decrease with age; rather, our findings suggest that durations of time engaged in social behavior decrease.

Investigating the role of HAR1984 in neurogenesis and development

Katie Lam

Faculty Mentor: Debby Silver

Authors: Katie Lam, Federica Mosti, Elaine Guevara, Debby Silver

Discipline: Biological and Biomedical Sciences

Abstract:
The human brain exhibits a significantly expanded cerebral cortex and increased neural progenitor proliferative capacity compared to chimpanzee brains. This expansion is driven in part by intermediate progenitors (IPs), a specialized population of neural progenitors that contribute to neurogenesis and cortical folding. Despite humans and chimpanzees sharing over 95% genetic similarity, differences in brain morphology may stem from noncoding regulatory sequences rather than protein-coding genes. Human Accelerated Regions (HARs) are stretches of noncoding DNA that are highly conserved across mammals but contain small base pair changes in humans. Many HARs are located near genes involved in neuronal proliferation and differentiation, suggesting they play a role in brain development. Previous work focused on HAR1984, an enhancer region with five base pair changes in humans, predicted to be active in neuronal cells during development. To explore HAR1984's potential role in in human brain development, I conducted several experiments in vivo and in vitro: analyzing mouse models with homozygous and heterozygous HAR1984 deletions and performing 2D differentiations of chimpanzee cells with human HAR1984. HAR1984 deletion induced folding in the mouse cortex and resulted in a decrease in neural progenitor numbers. Subsequently, I replaced chimpanzee HAR1984 with the human orthologous sequence in chimpanzee cells (Pt-HAR1984Hs/Hs). Maintaining 2D differentiations of these chimpanzee cells revealed an increased number of mitotic cells in the humanized cell lines. The expression of HAR1984 target genes TRA2B and ETV5, crucial for neuronal differentiation and cortical development, was also increased in the chimpanzee cell lines with human HAR1984. My results highlight how noncoding regulatory sequences contribute to the unique expansion and complexity of the human brain. These findings suggest that HAR1984 enhances neuronal proliferation and differentiation in humans, playing a crucial role in the evolutionary expansion of the human cerebral cortex.

Lemur Fecal Parasitology

Nicole Lee Heberling

Faculty Mentor: Christine Drea

Authors: Nicole Lee Heberling, Caroline Shearer, Marie Nathalie Rafanomezantsoa, Christine Drea

Discipline: Biological and Biomedical Sciences

Abstract:
Madagascar is a biodiversity hotspot, with the fourth greatest primate diversity globally. Its endemic lemurs – the most endangered mammals on the planet – represent about a third of the world's primate species. Better understanding of the factors impacting their health may help conservation initiatives. Past research has associated the presence of parasitic worms – helminths – with greater testosterone (T) in many species. Despite some helminth identification in lemurs, for many species, there is little to no information available. Our goals were to identify and describe helminth species present, at different ecological sites, in lemur hosts that have varying T concentrations. We compared the helminth parasites infecting the gut of two closely related brown lemur species, the crowned lemur (Eulemur coronatus), with high-testosterone females and Sanford's lemur (E. sanfordi), with purportedly low-testosterone females, for which wild groups occur in the same isolated forests of northern Madagascar. We collected 113 fecal samples from 104 individuals (N = 52 per species in Amber Mountain National Park (MANP), a resource-rich site with greater rainfall, and Ankarana Special Reserve (ASR), a resource-lean site with lower rainfall, throughout the dry seasons of 2023-2024. We scanned samples for adult worms for initial survey and identification, then used standard fecal floatation techniques to count eggs, identify the helminth species, and obtain diagnostic images. We identified adult Lemuricola spp. as well as eggs from Lemuricola spp., Callistoura sp. 1, Callistoura sp. 2, Trichuris spp., Strongylida, and tentatively Trichostrongyloidea and unidentified cestodes. Almost every sample was infected to some degree, and there was a high prevalence of Callistoura spp. We found that infections of Lemuricola and Callistoura spp. were significantly greater at MANP than at ASR for both hosts, consistent with wetter conditions. To date, Trichuris spp. in female lemurs appear to be greater in MANP than ASR, and Sanford's males may have more Trichuris spp. infections than crowned males at both locations; however, both sexes in both species had appreciable androgen concentrations. The overwhelming effects of rainfall seemed to override any finer species and sex differences in helminth prevalence between host species and sex. Ultimately, this research helps us better understand intrinsic and extrinsic factors affecting the gut health of these endangered, sympatric species.

Neonatal protein malnutrition impairs microglia density and function in the hippocampus

Reed Lessing

Faculty Mentor: Cagla Eroglu

Authors: Reed Lessing, Carina Block, Ph.D., Michel Bagnat, Ph.D., Cagla Eroglu, Ph.D.

Discipline: Biological and Biomedical Sciences

Abstract:
Protein malnutrition presents a global health challenge and profoundly impairs brain development and cognitive function. However, because various environmental factors have confounded past studies in human and animal models, how early-life protein malnutrition induces changes in brain development remains largely unknown. Digestion is fundamentally different in early life versus adulthood. In suckling mammals, the stomach has a high pH and low protease activity, causing milk proteins to arrive at the small intestine largely intact. There, specialized intestinal epithelial cells known as lysosome-rich enterocytes (LREs) facilitate intracellular digestion and transcellular transport during this early time window. Importantly, during natural weaning, LREs are replaced by mature enterocytes, which can neither uptake nor digest intact proteins. Here, we model neonatal protein malnutrition in mice by conditionally deleting the adaptor protein Dab2, a critical component of LRE endocytic machinery, from the intestine, preventing protein uptake and inducing stunting in mice without manipulating maternal care. Using this model, the current study utilized immunohistochemistry and confocal microscopy to investigate the effects of neonatal protein malnutrition on hippocampal development by measuring the density of neurons, microglia, astrocytes, and oligodendrocytes in Dab2 conditional wild-type and knockout mice. We show that intestinal deletion of Dab2 impairs microglia density and depletes lysosomal content within microglia at postnatal day six, while neuron, astrocyte, and oligodendrocyte density remain unchanged. These results suggest that neonatal protein malnutrition may disrupt the neuroimmune axis and, at later timepoints, alter neural circuit formation in the hippocampus, a brain structure with known involvement in episodic and spatial memory. Ultimately, understanding how the loss of dietary proteins influences brain development will aid the advancement of novel interventions to combat global protein malnutrition.

The Role of Ecdysone, and Aldoketoreductase (AKR) on Manduca Sexta Wing Disk Growth and Develop

Katie Li and Grace Wang

Faculty Mentor: Fred Nijhout

Authors: Katie Li, Grace Wang, Laura Grunert, Fred Nijhout

Discipline: Biological and Biomedical Sciences

Abstract:
Ecdysone and Aldoketoreductase (AKR) are extrinsic regulators for insect growth and development of imaginal wing disks. The present work characterizes the effect on each of these regulators to better understand their individual roles and influence on wing development in Manduca Sexta.
The experimental group involved ligating larvae (between the thorax and abdomen) followed by timed injections of ecdysone, or AKR. In Manduca sexta, the ecdysone precursor is secreted by the prothoracic glands in the first thoracic segment, which is activated by a factor from the abdomen. Consequently, ligation between the thorax and abdomen isolates the inactive precursor and prohibits its activations. The wing imaginal disks are located in the second and third thoracic segments, requiring active ecdysone for normal growth and development. Therefore, the ligation inhibits their growth. We hypothesized that wing disks in ligated animals would not grow and that injections of ecdysone or the ecdysone activator, AKR, would induce wing disk growth and cell divisions. We, therefore, measured wing disk growth, tracheal development, and mitotic index (as a sign of cell division) in experimental animals and compared these to the state of wing disks in untreated and sham-injected controls. For these studies, imaginal disks were fixed, stained with DAPI, and imaged under a microscope, and their area was measured using the ImageJ software.
The number of mitoses was counted in each of the imaginal wing discs for comparison between experiments and controls. Our results show that ecdysone stimulates tracheal development of the wing veins of the imaginal disks but stimulates little growth during the first two days of the wandering stage. In addition, we found that both injections of ecdysone and injections of the ecdysone activator stimulated a significant amount of cell division during those first two days. We conclude that ecdysone stimulates wing vein development and a small amount of growth during the first two days of the wandering stage. We are currently investigating whether the explosive growth of the wing disks that begin on day 3 is also stimulated by ecdysone.

Reconciling Biological and Chronological Age During Development

Tom Lowrance

Faculty Mentor: Fred Nijhout

Authors: Tom Lowrance, Fred Nijhout

Discipline: Biological and Biomedical Sciences

Abstract:

In many species of animals, age is a perfect predictor of developmental stage. In larvae of the moth, Manduca sexta, for instance, age, body mass, and the developmental stage of the wing imaginal disks are perfectly correlated with each other (r2>0.99). Body growth and growth of the wing imaginal disks both depend on a highly stereotyped level and pattern of secretion of the steroid hormone ecdysone. In larvae of the butterfly, Junonia coenia, by contrast, age, body mass, and developmental stage of the wing imaginal disks are much less closely correlated (r2=0.72), so that neither age nor body mass can be independently used to predict the developmental stage of the wings. The aim of this work was to determine whether it is possible to develop a model that uses a weighted combination of chronological age with other characters to obtain a better prediction of the developmental age of the wings. To construct the model, hemolymph samples are collected from larvae, with unique chronological ages and masses. These hemolymph samples are then run through an ELISA ecdysone assay to measure the concentration of the hormone in the blood. These concentrations can then individually be plotted against organism weight and age to create a predicting model for the ecdysone concentration of Junonia coenia larvae based on their specific age and mass. The results from these assays have thus shown age to be a stronger predictor of ecdysone concentration than mass, however further testing with larger and more diverse sample sizes is needed to yield more definitive results. Creating a strong predicting model for the ecdysone concentration in the larval blood will be crucial in better understanding why these larvae molt and metamorphose at certain ages and weights, and will allow for further exploration of other possible factors that impact their growth.

Investigating LCP1-mediated oncogenic signaling in Chondrosarcoma metastasis

Ariana Matarangas

Faculty Mentor: Julia Visgauss

Authors: Ariana Matarangas, Nicholas Guardino, Caleb Watson, Aron Mebrahtu, Ava Strohmeyer, Jason Somarelli, Benjamin Alman, Julia Visgauss

Discipline: Biological and Biomedical Sciences

Abstract:
Chondrosarcoma (CSA) is a malignancy of bone without effective adjuvant therapies to treat advanced and metastatic disease. RNA-sequencing of our patient-derived cell lines revealed an upregulation in the gene LCP1 (lymphocyte cytosolic protein 1) in primary tumors with metastatic capacity. This was validated in a larger clinical cohort, with increased expression of LCP1 correlating with poor survival. Subsequent in vitro and in vivo analyses confirmed LCP1's ability to promote metastatic behavior in CSA cells, however the exact mechanism is unclear. LCP1 is an actin bundling protein that we hypothesis has a scaffolding role in cell signaling. The present study seeks to investigate if the malignant behavior demonstrated by LCP1 high expressing cells, is dependent on LCP1 mediated activation of the oncogenic JAK/STAT pathway. Our JAK/STAT phosphoprotein microarray and BioID biotinylation assays identified key proteins with altered phosphorylation ratios and proximity-based interactions, including those of the IL6/STAT3 signaling axis. The expression of STAT3 activation was validated through experiments using LCP1 wildtype and siRNA knockdown cell lines when stimulated by interleukin (IL-6) ligands. Understanding these pathway targets for which LCP1 interacts will give insight into identifying therapeutic targets for chondrosarcoma metastasis.

Granulovacuolar Degeneration Associated With Lysosomal Permeabilization via LLOMe

Harrison Pratt

Faculty Mentor: Laurie Sanders

Authors: Harrison W. Pratt, Silas A. Buck, Laurie H. Sanders

Discipline: Biological and Biomedical Sciences

Abstract:
Tau protein aggregates play a significant role in the disruption of neuronal function through formation of neurofibrillary tangles and protein misfolding in neurodegenerative tauopathies like Parkinson's Disease (PD). Granulovacuolar degeneration bodies (GVBs) refer to the accumulation of membrane-bound vacuolar structures that are distinguished by accumulation of cargo in a dense core. GVBs are triggered by tau in in-vivo mouse models and in-vitro primary neuron experiments, and are positive for lysosomal markers and proteolytic activity. A valuable agent for manipulating lysosomal function is L-leucyl-L-leucine methyl ester (LLOMe), a lysosomotropic compound that permeabilizes lysosomal membranes, resulting in lysosomal material releasing into the cell, and we hypothesize this permeabilization contributes to the formation of GVBs. Our ongoing project seeks to analyze the impact of lysosomal membrane degradation using LLOMe on GVB formation in primary neurons, using Immunocytochemistry (ICC). Further, we aim to analyze the role of leucine-rich repeat kinase 2 (LRRK2) expression, which is causative of PD through the G2019S mutation and is associated with tau aggregation, in potentially mediating GVB proliferation. LRRK2 will be analyzed with phospho-Rab12 (pRab12) antibody staining, which both label LRRK2 kinase activity and GVBs.

Thus far, we have studied primary neuron cultures transduced by P301L/S320F tau lentivirus (1:2000) at day in-vitro 3 (DIV3) that induced tau aggregation and GVB formation. We elucidated an ideal exposure concentration of LLOMe as 1mM for 1.5 hours. At DIV17, we induced lysosomal permeabilization with LLOMe. GVBs were labeled using Casein Kinase 1 delta (CK1d), while lysosomal position within neurons was visualized using Cathepsin-D or Lysosomal integral membrane protein type 2 (LIMP-2). Thus far, confocal images reveal that GVB formation can be modulated by changing lysosomal integrity, with LLOMe reducing the number of GVBs observed. Further, we observed a steady trend of lysosomal colocalization with CK1d-labeled GVBs, even when using distinct indicators, confirming that pRab12-positive GVBs are lysosomal structures. In conclusion, we have found that LLOMe can regulate GVD, a novel finding that prompts the further analysis of the lysosomal mechanism by which this regulation occurs, which we posit is via LRRK2.

Defining how the m6A-methyltransferase complex targets hepatitis C viral RNA

Jordan Reaves

Faculty Mentor: Stacy Horner

Authors: Jordan V. Reaves, Katherine M. Bland, Stacy M. Horner

Discipline: Biological and Biomedical Sciences

Abstract:
Addition of N-6methyladenosine (m6A) to viral RNAs is proven to mediate infection of Hepatitis C virus (HCV). m6A is added to cellular mRNAs by a host methyltransferase complex (MTC) consisting of the core enzymatic proteins METTL3 and METTL14 as well as additional accessory factors. We have previously demonstrated that HCV RNA methylation requires the MTC scaffolding protein WTAP to recruit the catalytic heterodimer METTL3 and METTL14 to the viral RNA. VIRMA is a member of the MTC known to have a role in host RNA targeting and stabilization of complex member WTAP during host transcript methylation. We are interested in VIRMAs role in targeting m6A addition to viral RNAs and its interaction with WTAP which has been shown by our lab to be an important mediator of HCV infection and m6A addition. Work in our lab has shown that VIRMA is necessary for methylation of HCV RNA and recruitment of the MTC to viral RNA; however, it is unknown which functional domains of VIRMA are involved in this process. Here, we created VIRMA mutants which disrupt either the protein's RNA binding or WTAP binding domains. We have validated that these mutants abrogate their respective functions via co-immunoprecipitation and RNA immunoprecipitation. We plan to transfect cells with these mutants and observe their impact on HCV genome methylation seen via methylated RNA immunoprecipitation. We hypothesize that disrupting the RNA binding domains of VIRMA will decrease m6A modification of HCV RNA. Better understanding into VIRMA's role in this process will broaden our understanding of how the MTC is differentially targeted during viral infection.

Investigating the Impact of 5-Hydroxymethyl-2-furfural (HMF) on Pancreatic beta-Cell Lines

David Regan

Faculty Mentor: James Bain

Authors: David Regan, Demitrius Hill, Daiwik Munjwani, Ege Özbalkan, David E. Lee, Michael J. Muehlbauer, Hans-Ewald Hohmeier, Mette V. Jensen, James R. Bain

Discipline: Biological and Biomedical Sciences

Abstract:
HMF, a suspected carcinogen, forms when sugars such as glucose and fructose are processed by heat. In a previous experiment in the 832/13 beta-cell line, when cultures were shifted from low-glucose (2.5 mM) to high-glucose media (12 mM), we saw a large increase in intracellular 5-hydroxymethyl-2-furoic acid (Sumiki's acid), a cellular oxidation product of HMF. Given the demonstrated toxicity of HMF, we wondered if human beta cells can concentrate HMF from their environment to harmful levels. Trypsinized confluent cultures of the beta-G 49/206 line were seeded onto fresh plates. After adherence, P100 plates were rinsed with phosphate-buffered saline, then cultured under 10 mL of a low-glucose secretion buffer (2.5 mM) for 60 minutes. Following this, cells were subjected to one of three conditions: 10 mL of low-glucose buffer, 10 mL of high-glucose buffer (12 mM), or 10 mL of high-glucose buffer spiked with HMF (1 mM). Conditioned media and cell lysates were captured at 100 minutes (high-glucose spiked with HMF) and 270 minutes (low-glucose, high-glucose, and high-glucose spiked with HMF). Relative amounts of metabolites were measured by ultrahigh-pressure liquid chromatography/quadrupole, time-of-flight mass spectrometry (UHPLC/QToF MS) on an Agilent 1290/6546 system and by gas chromatography (GC)/MS on an Agilent 8890/5977B system. Glucose concentrations were measured on a Beckman UniCel DxC 600 Synchron instrument. As in our earlier work in the 832/13 insulinoma cell line, the 49/206 beta-cell line was able to take up HMF and oxidize it to Sumiki's acid. In cell lysates in the present study, HMF and Sumiki's acid were only observed in plates dosed with HMF. HMF concentrations rose between 100 and 270 minutes, while levels of Sumiki's acid were relatively stable. Compared to high-glucose cultures that received no HMF, at 270 minutes, HMF-treated cells showed a marked increase in adenine (purine), 6-methyluracil (pyrimidine), spermidine (polyamine), components of fetal bovine serum (urea, norepinephrine), taurine, and several amino acids, perhaps reflecting an acute proteolytic response. Lactate was increased, and a number of Krebs-cycle intermediates were decreased in HMF-dosed cells, suggesting a shift of central fuel metabolism toward glycolysis—but the effect size there was modest. Further work is needed to explore pharmacokinetics and whether HMF is toxic to beta cells at physiologically meaningful doses.

The association of forgiveness with physiological responses to memories of past wrongdoings

Daniel Robelo

Faculty Mentor: Felipe De Brigard

Authors: Daniel Robelo, Gabriela Fernandez-Miranda, Kaylee Miceli, Leonard Faul, Kevin Labar, Felipe De Brigard

Discipline: Biological and Biomedical Sciences

Abstract:
Currently, there is a debate with regards to forgiveness and its relationship with memory. Some support the episodic fading (EpF) account, which states that when forgiving one's episodic (sensory, contextual, temporal, and spatial details) and affective (emotional tone, valence, and intensity at retrieval) characteristics for memories of wrongdoings change. The other party posits the emotional fading (EmF) account, which holds that only the affective characteristics change. Previous data collected from our lab seems to align with the EmF account, which would lead to forgiveness involving lower ratings of intensity and negative valence. This evidence was limited to self-report measures, however, so our current study utilizes physiological measures (electrodermal activity, corrugator supercilii and zygomaticus electromyography, heart rate, and respiration rhythm) using the BIOPAC system (in addition to a 16-item self-report questionnaire) to observe physiological patterns. This allowed us to analyze the phenomenological characteristics of memories of neutral events vs. wrongdoings through objective measures. We found that memories of wrongdoings produce stronger responses for electrodermal activity and corrugator supercilii amplitude than memories of neutral events. Furthermore, memories of wrongdoings high on forgiveness, when compared to those low in forgiveness, displayed lower emotional intensity and less negative valence in self-reported and physiological measures of emotional responses during recall. Our physiological responses matched our self-report measures in corroborating the emotional fading account of forgiveness and hint at the potential use of emotional fading techniques in facilitating forgiveness.

Effects of Variation in Sex Chromosome Copy Numbers on the Expression of the Cohesin Complex

Ariella Ruiz

Faculty Mentor: Adrianna San Roman

Authors: Ariella Ruiz, Adrianna San Roman

Discipline: Biological and Biomedical Sciences

Abstract:
The cohesin complex is a highly conserved protein complex that regulates gene expression through DNA looping, which brings distant enhancers and promoters closer together in three-dimensional space. The gene encoding a core subunit of the cohesin complex, SMC1A, is located on the X chromosome and escapes X chromosome inactivation, meaning that females have higher expression than males. We hypothesize that differing levels of SMC1A in males and females affects the function of the cohesin complex and results in sex differences in genome-wide expression. The goal of this project is to investigate how X chromosome copy number affects the expression level and localization of each protein in the cohesin complex. We utilize indirect immunofluorescence and microscopy to investigate the cohesin proteins in different skin fibroblast cell lines derived from human subjects with varying numbers of X chromosomes. The fluorescent images are quantified using CellProfiler and the data extracted is analyzed in GraphPad Prism. Our preliminary data shows that the nucleic and cytoplasmic concentrations of SMC1A decreased as the number of X chromosomes increased. This result was unexpected, and further research is needed including experiments with more cell lines and optimizing image segmentation using an antibody that labels the cell membrane. Aside from the potential role of the cohesin complex in sex differences, it is also important to study because mutations in the complex result in various disorders, such as Cornelia de Lange Syndrome (CdLS). Studying the expression and localization of the cohesin complex may help us better understand these disorders.

Investigating the molecular mechanisms of SCD while exploring stakeholder perspectives

Angelina Sala

Faculty Mentor: Andrew Landstrom

Authors: Angelina Sala, Brittany Balint, Robin Perelli, Carla Gonzalez, Kallie Carlson, Gabrielle Monaco, Chris Michaels, Andrew Landstrom

Discipline: Biological and Biomedical Sciences

Abstract:
Pediatric sudden cardiac death (SCD) is often linked to genetic conditions such as arrhythmogenic cardiomyopathy (ACM) and congenital heart disease (CHD). This project takes a multidisciplinary approach to investigate the molecular basis of SCD and the implications of predictive genetic testing in at-risk populations. A biology-focused approach identified a novel genetic mechanism for autosomal recessive ACM associated with loss-of-function variants in TAX1BP3. Using induced pluripotent stem cell-derived cardiomyocytes (iPSC-CMs), pharmacological inhibition of TRPV4 mitigated calcium leak and spark frequency—highlighting a potential therapeutic target for ACM. Additionally, this project investigated several genetic mechanisms of hypoplastic left heart syndrome (HLHS), a severe form of CHD, by evaluating levels of apoptosis and cell proliferation in iPSC-CMs. Preliminary findings suggest increased apoptosis and reduced cell proliferation may lead to the underdeveloped left ventricle seen in patients, however, overall findings warrant further investigation into other mechanisms. On the other hand, a global health approach was incorporated by establishing a Community Advisory Board (CAB) to explore the ethical and clinical challenges of genetic risk prediction in CHD. Thematic analysis from the pilot CAB discussion highlighted concerns around clinical decision-making, resource allocation, and psychosocial impacts—emphasizing the need for standardized guidelines to ensure equitable and responsible use of genetic information. Altogether, this research advances precision medicine in pediatric cardiology by bridging molecular mechanisms with ethical considerations in genetic risk disclosure.

A Simple and Sensitive Wearable SERS Sensor Utilizing Plasmonic-Active Gold Nanostars

Sebastian Sanchez

Faculty Mentor: Tuan Vo-Dinh

Authors: Sebastian Sanchez, Supriya Atta, Yuanhao Zhao, Tuan Vo-Dinh

Discipline: Biological and Biomedical Sciences

Abstract:
Wearable sweat sensors hold great potential for offering detailed health insights by monitoring various biomarkers present in sweat, such as glucose, lactate, uric acid, and urea, in real time. However, most previously reported sensors, primarily based on electrochemical technology, are limited to monitoring only a single analyte at a given time. This study introduces a simple, sensitive, wearable patch based on surface-enhanced Raman spectroscopy (SERS), integrated with highly plasmonically active sharp-branched gold nanostars (GNS) for the simultaneous detection of three sweat biomarkers: lactate, urea, and glucose. We have fabricated the GNS on commercially available adhesive tape, resulting in achieving a low-cost, flexible, and adhesive wearable SERS patch. The limits of detection for lactate, urea, and glucose were achieved at 0.7, 0.6, and 0.7 µM, respectively, which are significantly lower than the clinically relevant concentrations of these biomarkers in sweat. We further evaluated the performance of our wearable SERS patch during outdoor activities, including sitting, walking, and running. To evaluate its overall effectiveness, we simultaneously measured the concentrations of lactate, urea, and glucose during these activities. Overall, our simple, sensitive wearable SERS sensor represents a significant breakthrough by enabling the simultaneous detection of lactate, urea, and glucose present in sweat, marking a major step toward future applications in autonomous and noninvasive personalized healthcare monitoring at home.

Investigating the Role of MAP Kinase Pathway in Cell Division During Starvation in C. elegans

Ainsley Scheiner

Faculty Mentor: Ryan Baugh

Authors: Ainsley Scheiner, Ryan Baugh

Discipline: Biological and Biomedical Sciences

Abstract:
The MAP (mitogen-activated protein) kinase pathway is crucial for cell signaling across all eukaryotic organisms. Using a model organism such as the roundworm C. elegans allows for complex genetic manipulation to produce genetic models explaining the role of MAPK in cellular processes such as metabolism. We hypothesize that PTEN-homolog and insulin signaling protein DAF-18 acts through the MAP kinase proteins MEK-2 and MPK-1 in C. elegans, since the two have similar starvation survival phenotypes. While daf-18 acts independently to repress cell divisions during starvation by inhibiting insulin signaling, it remains unknown if the MAP kinase pathway is required for this developmental arrest. Mpk-1 and mek-2 are homologs of human MAP kinase proteins MAPK and MAPKK, which initiate gene transcription in the starvation resistance pathway. GFP-tagged postembryonic mesoblast (M) cells can be used as reporters for cell division under starved conditions in C. elegans. In this study, M-cell scoring after starvation in mpk-1 and mek-2 mutant worms was employed to answer whether these MAP kinase pathway genes are involved in developmental arrest during starvation. We concluded that there is no M-cell division phenotype for mpk-1 or mek-2. The results of this study indicates that the MAPK pathway is not required to arrest M cell divisions, suggesting that daf-18 represses divisions independently of MAPK.

Identification of Nedd4 proteoforms induced by proteotoxicity and NAB2 exposure

Erik Seghers

Faculty Mentor: Dewey McCafferty

Authors: Erik Seghers, Felix Nwogbo, Dewey McCafferty

Discipline: Biological and Biomedical Sciences

Abstract:
The neuronal precursor cell-expressed developmentally downregulated 4 enzyme (Nedd4) is the founding member of a family of HECT-type E3 ubiquitin ligases that regulate proteostasis in neurodegenerative disorders. In previous studies, our group has determined that Nedd4 is required for the reversal of alpha-synuclein associated toxicity in parkinsonian models when modulated by the N-arylbenzimidazole small molecule, NAB2. We hypothesize that NAB2 changes the substrate specificity of Nedd4 through interacting with a specific proteoform of Nedd4 that may be present upon inducing proteotoxicity. To identify Nedd4 proteoforms that arise in response to expressing the toxic mutant A53T alpha-synuclein protein, we describe the cloning, expression, and generation of transfected cell lines for analysis. Using a Gateway cloning system, we synthesized a plasmid to recombinantly express a tagged, fluorescent-fusion version of Nedd4 in human embryonic kidney (HEK) 293T mammalian cell line. Transfected cells cultured in selectable media and imaged using fluorescence microscopy demonstrate a proof of concept of recombinant expression of tagged Nedd4 fusion protein in a mammalian cell line. Ongoing efforts center on designing lentiviral based expression vectors for alpha-synuclein to be used for co-expression of Nedd4 for proteoform analysis.

Identifying New Targets of Salmonella Induced GSK3 Tyrosine Phosphorylation

Sophia Shen

Faculty Mentor: Dennis Ko

Authors: Sophia Shen, Margaret Gaggioli, Dennis Ko MD., PhD.

Discipline: Biological and Biomedical Sciences

Abstract:
Non-typhoidal Salmonella enterica causes approximately 1 million cases of gastroenteritis annually in the United States, resulting in the highest morbidity rate among all foodborne illnesses. S. enterica depends on secreted protein effectors to hijack host cellular functions and enable further bacterial infection. We previously discovered that the protein effector SarA (Salmonella anti-inflammatory response activator) is required for phosphorylation of the transcription factor STAT3 and leads to increased production of the anti-inflammatory cytokine IL-10 (interleukin-10). SarA facilitates STAT3 phosphorylation through binding of GSK3 (glycogen synthase kinase-3). This interaction alters the amino acid specificity of the serine-threonine kinase GSK3 to phosphorylate a tyrosine in both SarA and STAT3, inducing an anti-inflammatory effect in host cells. We hypothesize that the conversion of GSK3 to a tyrosine-directed kinase will also result in novel protein phosphorylation. We will use mass spectrometry to analyze protein phosphorylation during overexpression of wild type and mutant SarA. Based on these results, we will conduct further analyses through GSK3 knockdown, inhibition, or purification, to determine the direct cause of protein phosphorylation. The conversion of GSK3 to a tyrosine-directed kinase by SarA allows a bacterial protein to reprogram host cell signaling and create a beneficial environment for bacterial infection. Understanding novel GSK3 phosphorylation of other tyrosines will help to uncover SarA's role in S. enterica pathogenicity and its effects on the host cell. Furthermore, studying SarA's manipulation of GSK3 may reveal new pathways and biological processes where GSK3 could play a role and advance knowledge of how kinase-substrate interactions are modified.

Investigating Radioresistance-Induced Epigenetic Reorganization in Colorectal Cancer

Megan Tandar

Faculty Mentor: Christine Eyler

Authors: Megan Tandar, Allison Pittman, Christine E. Eyler.

Discipline: Biological and Biomedical Sciences

Abstract:
Colorectal cancer is the fourth most common cancer in the United States. Rates of diagnoses have doubled in the past decade for adults under the age of 55. Radiation and chemotherapy treatments are often combined to treat rectal cancer. Up to 50% of rectal cancers resist initial therapy with chemotherapy and radiation, necessitating large operations for these patients. Our previous data in lung cancer cell lines implicates radiation-induced activation of enhancers, suggesting that in some tumor types, epigenetic reorganization may determine radioresistance. However, it is unknown if this phenomenon also occurs in colorectal cancer, hindering the development of radiosensitizing strategies for rectal cancers.
To investigate this, we utilized RNA Sequencing (RNA-Seq) and Assay for Transposase-Accessible Chromatin Sequencing (ATAC-Seq) protocols and analyses in cells treated with various doses of radiation to assess whether consistent epigenetic reorganization was present or absent in colorectal cancer cell lines. Four established colorectal cancer cell lines, SW480, HCT116, RKO, and MDST8, were selected for this project. These colorectal cancer cell lines were chosen from a preliminary radiosensitivity assay identifying radiosensitive and radioresistant cell lines. They were given two courses of treatment. The first treatment group was irradiated with a singular 0Gy, 2Gy, and 5Gy treatment and harvested 5 days later. The second group was irradiated with 0Gy or 2Gy daily for 5 days, then harvested 5 days after the final radiation treatment. These radiation doses were chosen to closely match clinically relevant therapies. Each cell line and treatment combination were performed in triplicates, allowing for analyses of 60 samples. RNA-Seq was performed to analyze radiation-induced gene expression changes, while ATAC-Seq analyzed open chromatin regions in the cell line's genome.
Preliminary results suggest that specific enhancers are activated post-radiation treatment in these cell lines, corresponding to specific gene expression changes, indicating potential resistance mechanisms to radiation treatments. The future direction for this research involves designing epigenome-targeting screens to identify radioresistant events. Ultimately, this project contributes to a greater understanding of how radiation-induced epigenetic reorganization may affect cancer progression and outcomes.

Characterization of Mouse Models of Pain following Adoptive Transfer of SLE Serum

Muskaan Toshniwal

Faculty Mentor: Ru-Rong Ji

Authors: Muskaan Toshniwal, Wei He, Ru-Rong Ji

Discipline: Biological and Biomedical Sciences

Abstract:
Abstract
Background
Systemic lupus erythematosus (SLE) is a chronic autoimmune disease in which the immune system targets the body's own tissues. Up to 90% of individuals with SLE report chronic pain—including joint, chest, abdominal pain, and headaches—even during periods of low disease activity. However, the mechanisms driving this persistent pain remain poorly understood. In this study, we aimed to characterize pain behaviors in mice following adoptive transfer of serum from lupus patients and begin investigating the underlying mechanisms.
Methods
Adult healthy mice (n = 6 per group: 3 males and 3 females) received intraplantar injections of 10 µL of either SLE patient serum or healthy control serum in the right hind paw. Pain behaviors were assessed at baseline and after injection. Mechanical sensitivity was measured using von Frey filaments, and cold sensitivity was assessed using the acetone drop test. Data from both groups (control and SLE) were analyzed using GraphPad Prism (v10.2.1).
Findings
Mice injected with SLE serum showed a reduced mechanical threshold within 1 hour of injection compared to controls. In addition, cold sensitivity—as measured by acetone-evoked pain behaviors—was increased in the SLE group. These findings suggest that serum from lupus patients is sufficient to induce both mechanical and cold pain behaviors in mice.
Interpretation
This study supports the idea that circulating factors in SLE serum can drive pain sensitivity in the absence of direct injury. One potential contributor is extracellular DNA (ecDNA), which is known to activate immune pathways in lupus. The next phase will test whether removing ecDNA—via DNase treatment or bead-based capture—reduces pain responses. These experiments may offer new insight into the mechanisms of non-inflammatory pain in SLE and inform future therapeutic solutions.

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

Michael Wang

Faculty Mentor: Walter Koch

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

Discipline: Biological and Biomedical Sciences

Abstract:
Heart failure is the leading cause of death in the US, with limited treatment options available to improve survival for patients with ischemic heart failure. GPCR Kinase 2 (GRK2), a key regulator of b-adrenergic receptors (b-ARs) in the heart, is upregulated after cardiac injury and stress. Previous work shows that cardiomyocyte-specific GRK2 knockout mice (cKO-GRK2) are protected from ischemic injury. Brain-derived neurotrophic factor (BDNF) is a pro-survival factor, with autocrine and paracrine effects in the post-ischemic heart and our lab has recently shown BDNF can be regulated in the heart by b-AR signaling. Reduced BDNF signaling is linked to both neurological and cardiac disorders, yet the role of cardiac GRK2 in BDNF regulation is unknown. We hypothesize that GRK2 negatively modulates myocardial BDNF expression and contributes to ischemic heart injury. To investigate this, we used neonatal rat ventricular myocytes (NRVMs) and cardiac-specific GRK2 overexpressing (cOE-GRK2) and cKO-GRK2 mice subjected to myocardial infarction (MI) via permanent coronary ligation. In NRVMs, inhibition of GRK2 using paroxetine (a GRK2-specific inhibitor) or the bARKct (a peptide inhibitor of GRK2) significantly increased BDNF protein expression. siRNA-mediated GRK2 knockdown, combined with recombinant BDNF stimulation, led to reduced phosphorylated AKT levels (a pro-survival factor) compared to control and GRK2-overexpressing NRVMs. In cOE-GRK2 mice, BDNF protein expression was significantly reduced in both remote and ischemic heart regions four-weeks post-MI compared to controls. Conversely, cKO-GRK2 mice exhibited increased BDNF expression in the infarcted region 24 hours post-MI and higher myocardial BDNF levels at one-week post-MI compared to cOE-GRK2 mice. These findings demonstrate that GRK2 inhibition or knockout increases BDNF expression in NRVMs and the infarcted heart, whereas GRK2 overexpression reduces BDNF levels, particularly in response to ischemic injury. These findings suggest that GRK2 is a key regulator of myocardial BDNF, which may influence cardiac repair and survival signaling post-MI. Future work will explore the underlying mechanisms of GRK2-mediated BDNF regulation in ischemic heart disease.

Elucidating Neurotoxicity Reversal Pathways in Cellular Models of Parkinson's Disease

Robert Wardell

Faculty Mentor: Dewey McCafferty

Authors: Robert Wardell, Hunter DeHaan, Dewey McCafferty

Discipline: Biological and Biomedical Sciences

Abstract:
Parkinson's Disease (PD) is characterized by proteotoxicity from the aggregation of alpha-synuclein and trafficking disruption between the Endoplasmic Reticulum and the Golgi Apparatus. A series of N-aryl benzimidazole (NAB) compounds were recently discovered that had a pronounced effect against synuclein toxicity in mammalian cells, but the development of the NAB library was limited by constraints in the synthetic approach. More recently, Hunter DeHaan from the McCafferty Lab developed a new synthetic approach that has expanded the amount of NAB derivatives, necessitating a comprehensive study of these novel compounds to determine optimal structural features and elucidate the precise molecular mechanisms underlying their ability to reverse synuclein toxicity. NAB2 is known to bind tightly to a potential therapeutic target for PD, the Neuronal Precursor Cell-expressed Developmentally Downregulated 4 Enzyme (NEDD4), an E3 ubiquitin ligase, expanding NEDD4's substrate specificity. This research aims to investigate efficacious derivatization of the NAB scaffold by conducting proteotoxicity reversal assays in Saccharomyces cerevisiae, followed by testing on human-derived neuroblastoma cell lines. Second, this research aims to investigate the interaction between NAB2 and NEDD4, and how this interaction affords NEDD4 a gain-of-function activity to ubiquitinate non-PxY substrates like the TFG protein. The NAB2 induced NEDD4 interactome will be characterized through proximity labeling methods to elucidate NAB2's effects on trafficking mechanisms. If successful, these studies will better illuminate the role NEDD4 plays in proteotoxicity signaling. Additionally, by enhancing our understanding of NAB derivatives' mechanisms and determining their optimal structure, this research aims to identify more potent lead compounds for the development of therapies targeting Parkinson's, potentially opening new avenues for treating various synucleopathies.

Identification of recombinant antibody pairs for a Lujo virus diagnostic assay

Allison Yang

Faculty Mentor: Michael Gunn

Authors: Allison Yang, Alex LaTrenta, Breanna Wimbush, Barbara D Lipes, Michael Dee Gunn

Discipline: Biological and Biomedical Sciences

Abstract:
Lujo virus is a highly contagious arenavirus with an 80% fatality rate that emerged in Africa in 2008. It has been the first highly pathogenic arenavirus discovered in Africa within the past 4 decades. Despite its clear virulence and the potential danger of an outbreak, no point-of-care diagnostics currently exist to detect Lujo Virus. To address this need, we are developing recombinant antibodies to create a rapid, sensitive Lujo Virus diagnostic assay. We chose Lujo Glycoprotein 1 (GP1) antigen as a diagnostic target. Previously, we created a M13 phage display antibody library from mice immunized with Lujo GP1. From this library, several candidate diagnostic antibodies were isolated and characterized for specificity by ELISA. Currently, we've expressed and purified Lujo GP1 with a C-tag, which is being used in sandwich ELISAs to determine the most sensitive pair of antibodies. The antibodies with the lowest limit of detection will be used to assemble a pilot point-of-care assay. As illustrated by the recent coronavirus emergence, existence of a ready-to-go point-of-care assay would be valuable to limit virus transmission. Given the high fatality rate of Lujo virus, it would be critical to have such a diagnostic ready in the event of a Lujo virus outbreak.

Quantifying the Potential of Various Delivery Methods for Dual-Epitope Peptide Nanofiber Treatments

Sophia Zhang

Faculty Mentor: Joel Collier

Authors: Sophia Zhang, Shamitha Shetty, Pablo Cordero Alvarado, Maria Kulapurathazhe, Joel Collier

Discipline: Biological and Biomedical Sciences

Abstract:
Current therapies for pulmonary inflammation are often inconvenient and provide limited immune response, typically targeting a single inflammatory cytokine rather than the complex system. Dual-epitope peptide-based nanofibers offer a promising alternative to these traditional treatments. This study examines the immune response in mice treated with C29 or Q11 self-assembling peptide nanofibers raising neutralizing B cell responses against IL-1B and TNF. Mice were immunized subcutaneously or intranasally with C29 and Q11 peptide nanofibers conjugated with IL-1B epitopes, TNF epitopes, or both. After ten weeks, serum IgG antibodies were purified, and monoclonal TNF and IL-1B antibody concentrations were quantified using neutralization assays with WEHI-164 and HeLa cells, respectively. Results showed that C29 nanofibers generated greater concentrations of antibodies, and that dual-epitope intranasal elicited higher antibody concentrations, with dual-epitope intranasal delivery being the most effective. These findings highlight the potential of dual-epitope nanofibers to treat pulmonary inflammation. Future work will analyze monoclonal antibodies present in bronchoalveolar lavage fluid to better assess the lung-specific immune response.

Engineering Odorant Receptors to Enhance Expression in Heterologous Cells

Kat Zhang

Faculty Mentor: Hiroaki Matsunami

Authors: Katherine Zhang, Mona Marie, Hiroaki Matsunami

Discipline: Biological and Biomedical Sciences

Abstract:
Our sense of smell relies on a vast and chemically diverse array of odor molecules that interact with numerous odorant receptors (ORs), yet many aspects of this process remain poorly understood. A major challenge in studying these G protein-coupled receptors is their poor functional expression on the cell surface in heterologous systems, limiting biochemical analysis and insights into their ligand-binding properties. Here, we investigate structural features that influence OR expression and odorant response. The ligand-binding pocket of ORs is formed by a combination of transmembrane domains (TMs) 2–7 and extracellular loops. We hypothesized that modifying N-terminal regions around transmembrane domain 1, in combination with C-terminal cytoplasmic domain modifications, would enhance surface expression of ORs while maintaining ligand selectivity. To test this, we selected OR5A2, OR7D4, and OR4S1—three receptors known for poor expression. Using FACS and the GloSensor cAMP assay in HEK293T cells transiently expressing native and engineered ORs, we found that C-terminal modifications significantly improved surface expression of ORs. N-terminal modifications further enhanced surface expression of OR5A2 and OR4S1 but had the opposite effect on OR7D4. Despite these modifications, ligand selectivity of the engineered ORs appeared unaltered. Our findings provide key insights into structural constraints affecting OR expression in non-olfactory cells.

HUMANITIES

Presenters are organized by discipline and then alphabetically by last name.

The Undocumented Republican Latino Vote

Yadira Paz-Martinez

Faculty Mentor: Jay Pearson

Authors: Yadira Paz-Martinez, Jay Pearson

Discipline: Humanities

Abstract:
Latino civic engagement in the United States has increased in recent years. This research examines the political preferences of undocumented Latino immigrants in the United States. Specifically, this work focuses on undocumented Latino immigrants' alignment with the Republican Party and Donald Trump despite the party's traditionally anti-immigrant rhetoric. Through 20 interviews conducted with undocumented Latino immigrants in North Carolina and Texas, the study identifies emerging key motivations for supporting the Republican Party. These views reflect their desire for economic security and a prosperous future for their children, which they associated with the Republican Party's policies and conservative values. Participants emphasized favorable economic conditions during the Trump administration, such as lower gas prices, job creation, and agricultural advancements, contrasting these with the perceived economic failures of the Biden administration. Despite the interviewees' undocumented status, they expressed significant concerns about the border crisis and advocated for stricter border enforcement to prevent further undocumented immigration. Additionally, the study highlights widespread frustration with the Democratic Party's lack of progress on immigration reform, prompting many participants to see the Republican Party as a potential ally in achieving a pathway to legal status.

PHYSICAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

Progress Towards the Synthesis and Characterization of Nedd4 E3 Ubiquitin Ligase Ligands

Eduardo Fadul Chavez

Faculty Mentor: Dewey McCafferty

Authors: Eduardo Fadul Chavez, Anastasia Thun-Hohenstein, Dewey McCafferty

Discipline: Physical Sciences

Abstract:
Ubiquitylation is a covalent posttranslational modification that influences a tremendous number of normal and disease-related cellular functions. The neuronal precursor cell-expressed developmentally downregulated 4 enzyme (Nedd4) is the founding member of a family of HECT-type E3 ubiquitin ligases that regulate proteostasis in various conditions including cancers and neurodegenerative disorders. The Nedd4 family is characterized by a multi-domain architecture comprised of a C2 domain for membrane localization, four WW domains for substrate recognition, and a catalytic HECT domain. Members of the Nedd4 family are known to recognize substrates through their multiple WW domains, which recognize PY motifs (PPxY and LPxY sequences) as well as phospho-threonine or phospho-serine residues. Unfortunately, there are no small molecule or protein-protein interaction inhibitors with sufficient selectivity to modulate the activity of Nedd4. To address this unmet need, we describe here progress towards the synthesis and characterization of PPxY-containing polymer/peptide multivalent ligands designed to inhibit Nedd4 ubiquitylation through simultaneous occupancy of its four WW domains.

Machine Learning Deciphers Interchromophore Couplings from Multidimensional Electronic Spectra

Bashir Sbaiti

Faculty Mentor: David Beratan

Authors: Bashir Sbaiti, Jonathan Schultz, Kelsey Parker, David N. Beratan

Discipline: Physical Sciences

Abstract:
Electronic and vibrational (vibronic) couplings between molecular excited states play a significant role in many biophysical processes, such as energy transfer among the pigments of natural light-harvesting antenna complexes. Two-dimensional electronic spectroscopy (2DES) has emerged as a powerful experimental technique that is particularly sensitive to vibronic couplings. However, the chemical information encoded in 2DES data is frequently difficult to access, as different molecular properties influence the spectra in many non-trivial and often overlapping ways. Here, we employ a (2+1)-dimensional convolutional neural network, abbreviated (2+1)D-CNN, to accurately map simulated 2DES spectra of molecular dimers to the strength of their underlying Coulombic couplings (i.e., the principal interaction responsible for photosynthetic energy transfer). In contrast to lower-dimensional network architectures, the (2+1)D-CNN approach accesses both the time- and frequency-dimensions of the 2DES signal, in turn enabling a thorough machine-learning analysis of the time-dependent photophysical dynamics. We find that the (2+1)D-CNN algorithm classifies regimes of dimer electronic couplings with a 10-fold cross-validation accuracy of 96.2%. By examining the optimized filters within the CNN, we find that both the frequency-domain peaks in individual 2DES spectra and their time evolution, (e.g., quantum beating) are critical to the performance of the (2+1)D-CNN. We also generate and analyze class-activation maps (CAMs) to reveal which spectral features are most important to the model classifications. The results of this work provide a holistic machine learning approach to address inverse problems in time-resolved multidimensional spectroscopy. Future studies that incorporate experimental considerations, such as noise and finite laser bandwidths, will aid in bridging applications of the (2+1)D-CNN approach to experimental 2DES data. Our work broadly demonstrates that machine learning protocols afford new ways to extract physically meaningful information from ultrafast spectroscopic measurements of molecular structures.

Synthesis of isotactic poly(propylene succinate) with functional end-group fidelity

Joel Valan

Faculty Mentor: Matthew Becker

Authors: Joel Valan, Matthew E. Bonacci, Matthew L. Becker

Discipline: Physical Sciences

Abstract:
Stereocomplexation (SC) is a type of physical crosslinking between two enantiopure (isotactic) polymer chains of opposite chirality. This interaction is driven by steric interlocking, dipole-dipole interactions, and hydrogen bonding, resulting in the formation of crystalline domains. Isotactic poly(propylene succinate) (i-PPSu) is a bioresorbable polyester that exhibits stereocomplexation; however, incorporation as a physical crosslink in hydrogel networks has been prohibited by a lack of end group fidelity. In this work, i-PPSu was synthesized through an atom economic ring opening copolymerization (ROCOP) using a binary chiral salcyCo(III)/iminium salt catalyst system with 2-hydroxy methacrylate (2-HEMA) as an initiator. By tuning the stoichiometry between the initiator and catalyst, i-PPSu with a methacrylate end group was produced with high regioregularity (>96 %ee). We confirmed the chemical composition with 1D NMR, DOSY NMR, MALDI-TOF-MS, GC-MS, and SEC. Stereocomplex formation of i-PPSu was confirmed through DSC and XRD. The methacrylate end-capped i-PPSu provides functionality for various downstream reactions, such as Michael additions and thiol-ene ‘click’ chemistry. Future work aims to tether i-PPSu onto a hydrophilic scaffold to produce hydrogel precursors. We hypothesize incorporating SC-PPSu crosslinking into a hydrogel network will provide a handle for tunable degradation for applications in 3D tissue surrogate systems.

QUANTITATIVE SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

A Unifying Information-theoretic Perspective on Evaluating Generative Models

Alexis Fox

Faculty Mentor: Samarth Swarup

Authors: Alexis Fox, Abhijin Adiga, Samarth Swarup

Discipline: Quantitative Sciences

Abstract:
Considering the difficulty of interpreting generative model output, there is significant current research focused on determining meaningful evaluation metrics. Several recent approaches utilize "precision" and "recall," borrowed from the classification domain, to individually quantify the output fidelity (realism) and output diversity (representation of the real data variation), respectively. With the increase in metric proposals, there is a need for a unifying perspective, allowing for easier comparison and clearer explanation of their benefits and drawbacks. To this end, we unify a class of kth-nearest-neighbors (kNN)-based metrics under an information-theoretic lens using approaches from kNN density estimation. Additionally, we propose a tri-dimensional metric composed of Precision Cross-Entropy (PCE), Recall Cross-Entropy (RCE), and Recall Entropy (RE), which separately measure fidelity and two distinct aspects of diversity, inter- and intra-class. Our domain-agnostic metric, derived from the information-theoretic concepts of entropy and cross-entropy, can be dissected for both sample- and mode-level analysis. Our detailed experimental results demonstrate the sensitivity of our metric components to their respective qualities and reveal undesirable behaviors of other metrics.

MeMDLM: De Novo Membrane Protein Design with Property-Guided Discrete Diffusion

Shrey Goel

Faculty Mentor: Pranam Chatterjee

Authors: Shrey Goel, Vishrut Thoutam, Edgar Mariano Marroquin, Aaron Gokaslan, Arash Firouzbakht, Sophia Vincoff, Volodymyr Kuleshov, Huong T. Kratochvil, Pranam Chatterjee

Discipline: Quantitative Sciences

Abstract:
Masked Diffusion Language Models (MDLMs) have recently emerged as a strong class of generative models, paralleling state-of-the-art (SOTA) autoregressive (AR) performance across natural language modeling domains. While there have been advances in AR as well as both latent and discrete diffusion-based approaches for protein sequence design, masked diffusion language modeling with protein language models (pLMs) is unexplored. In this work, we introduce MeMDLM, an MDLM tailored for membrane protein design, harnessing the SOTA pLM ESM-2 to de novo generate realistic membrane proteins for downstream experimental applications. Our evaluations demonstrate that MeMDLM-generated proteins exceed AR-based methods by generating sequences with greater transmembrane (TM) character. We further apply our design framework to scaffold soluble and TM motifs in sequences, demonstrating that MeMDLM-reconstructed sequences achieve greater biological similarity to their original counterparts compared to SOTA inpainting methods. Finally, we apply a generalized Bayesian optimization procedure that uniquely uses saliency maps to facilitate the generation of soluble membrane proteins, paving the way for experimental applications. In total, our pipeline motivates future exploration of MDLM-based pLMs for protein design.

SOCIAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

On the Experience and Emotional Cost of Compassion: Comparing Christians and Buddhists

Rohan Gupta

Faculty Mentor: Patty Van Cappellen

Authors: Rohan Gupta, Cheryl S. Tan, Kunalan Manokara Ph.D., & Patty Van Cappellen Ph.D.

Discipline: Social Sciences

Abstract:
Although often classified as a positive emotion, compassion –feeling care for the suffering of others – can also be an emotionally exhausting endeavor. We explored this contradiction in the context of religious identities by examining the role of one's religious background on perceptions of affective valence and emotional cost of compassion. Buddhists (n = 174) and Christians (n = 195) first reported the degree of pleasantness and unpleasantness they typically experience when feeling compassion, then rated how emotionally exhausted they felt after choosing to experience compassion. Results indicate that Buddhists (as compared to Christians) perceived compassion to involve less negative affect – but were also more emotionally exhausted after extending compassion. Affective valence accounted for why Buddhists incurred a greater emotional cost (mediation), reflecting either an expectation–reality mismatch, or a willingness for deep engagement. Our findings suggest that religious identity plays a central role in people's understanding of compassion – both in terms of how it is experienced as well as the emotional burden of extending it.

Major Motivations: Undergraduate Student's College Major Selection, Experiences, and Retention

Ana Herndon and Tiana Clemons

Faculty Mentor: Whitney McCoy

Authors: Ana Herndon, Tiana Clemons, Alexis Cruz-Ayala, Whitney McCoy, Ph.D, Mine Cetinkaya-Rundel Ph.D

Discipline: Social Sciences

Abstract:
Higher education can be a critical conduit for facilitating social and economic change. Major selection may assist with these outcomes by affecting one's future salary, as STEM Majors often have higher incomes. However, minoritized students are not represented at equal rates as their peers within STEM majors. We surveyed 160 students from universities in the southeastern region to understand minoritized students' experiences within Math-Oriented Majors. This research explores ways to increase retention and highlight minoritized students' experiences within the context of math-oriented majors.
We ask the question of how self-efficacy is created or stunted for minoritized students within the context of math-oriented majors.
This study utilized a mixed methods approach through a survey instrument used to analyze institutional, socioeconomic, and social factors that exist as drivers of minoritized students' major selection and retention within STEM+ majors. STEM and math-oriented fields not traditionally defined as STEM, such as economics and finance.
Of the 160 respondents, we had 78 students who completed the survey. We found insights into students' major motivations: (1) Curiosity & Interests comprising 43.9%, (2) Professional Goals and (3) Learning Experiences at 16.7%, (4) Personal Experiences at 12.1%, and (5) Values & Beliefs at 6%.
Our quantitative analysis found that the distribution among those who did not continue with a STEM-related field was higher among minoritized students at 38% compared to 21% among non-minoritized students. However, the sample size of minoritized students identified as students who stayed or left their STEM-related major is significantly smaller (18 students) than that of non-minoritized students (46 students). We will continue with supplemental interview data focusing on students' motivations and experiences. Our goal is to interview 20-30 URM Former/Current STEM students.

We Paint to the Sky: Mural Making and Social Action in Post-Dictatorship Chile

Sarine Krovitz

Faculty Mentor: Adam Rosenblatt

Authors: Sarine Krovitz, Adam Rosenblatt

Discipline: Social Sciences

Abstract:
For over 50 years, the Brigada Ramona Parra, the muralist brigade of the Chilean Communist Youth, has used muralism to spread political ideology, protest the Pinochet dictatorship, and demand justice for dictatorial violence across Chile. The Brigade employs a particular focus on collective and participatory mural-making, bringing communities, schools, strangers, and relatives of the disappeared together to paint. Grounded in intergenerational interviews with current and former brigadistas of the Brigada Ramona Parra, I draw from a body of interdisciplinary theory, including social practice art and social action art therapy, to examine how the Brigade's collaborative mural-making process aims to activate political, social, and organizational impacts in local communities. I further explore how this participatory process works as an act of trans-generational, political memory-making for murals painted in honor of Chile's detenidos desaparecidos, thirty years post-dictatorship. Rather than only analyze the Brigade's murals, this thesis explores the contemporary Brigada Ramona Parra's mural-making process as social action in and of itself.

The Benefits and Challenges of Virtual Worship for Flourishing

Abby Li

Faculty Mentor: Patty Van Cappellen

Authors: Abby Li, Dr. Patty Van Cappellen, Megan Edwards

Discipline: Social Sciences

Abstract:
Background: Propelled by the pandemic, virtual worship services have become common practice for many Evangelical Christian congregations seeking to maintain worship experiences when in-person attendance is inconvenient or impossible. Though some people have returned to in-person services as pandemic-related restrictions have eased, virtual worship has risen globally, and virtual religious services are here to stay. While the benefits of in-person worship have been studied extensively, little research has been done to understand the impact of virtual worship on well-being and flourishing. Methods: To examine the impact of virtual worship on flourishing, participants (N= 40; half virtual attenders and half in person attenders) are being recruited to participate in an interview-based study. Participants are asked why they attend services in their respective modality and asked to describe their emotional, social, and physiological experiences within worship. Results: Qualitative analyses will help determine and understand 1) the major flourishing-related benefits and challenges associated with virtual/in-person worship participation; 2) the emotional, social, and physiological mechanisms through which worship affects flourishing. These findings will shed light on the impact of virtual worship participation on flourishing.

High School Group Work Experiences

Alissa Rivero

Faculty Mentor: Bridgette Hard

Authors: Alissa Rivero, Jeslyn Brouwers, Susan Wynn, Bridgette Hard

Discipline: Social Sciences

Abstract:
Developing collaborative skills, and positive attitudes toward collaboration, is essential to students' future workplace success. As collaboration becomes increasingly valued in the workplace, academic institutions have adopted team-based learning models, where students develop soft skills through group work (Kozlowski & Ilgen, 2006). Instructors frequently incorporate group projects into their courses to replicate real-world workplace scenarios, challenging student groups to navigate complex tasks and meet deadlines autonomously (Ettington & Camp, 2002). Yet, by the time students reach college, many students have negative attitudes toward group work, citing challenges with accountability and conflict resolution (Brouwers et al., in prep.) In a recent intervention within a psychological methods and statistics course, researchers incorporated team-building activities into a semester-long group project to improve students' collaborative experiences (Rivero et al., in prep.). Although students reported more positive experiences during the group project compared to students in the baseline semester, their broader attitudes toward group work remained unchanged—suggesting that beliefs about collaboration may solidify before college and persist even after successful group work.
To investigate the roots of these early attitudes, we are conducting interviews with high school teachers at a local public school. We hope to understand how teachers integrate group work in their classrooms, what aspects of group work are most challenging for their students, and what strategies they've used to improve student group work experiences. By understanding the root causes of frustrations such as unequal contribution, we hope to identify potential pedagogical interventions that prevent early, negative experiences with group work from having downstream effects on students' future collaborative experiences. This study aims to bridge the gap between K-12 and higher education group work practices, fostering a culture of effective collaboration that benefits students across all stages of their learning. These findings will inform a "recommendations and best practices" guide for teachers.

The Emergence of Children's Cooperation

Alissa Rivero

Faculty Mentor: Michael Tomasello

Authors: Alissa Rivero, Jared Vasil, Michael Tomasello

Discipline: Social Sciences

Abstract:
Human cooperation is unique. Humans not only coordinate with others but also generalize this coordination to other domains, allowing us to collaborate in nearly all spheres of daily life. At the same time, we are not born with the ability to cooperate; instead, we learn how to do so across early childhood. While we know that children cooperate at the dual-level by 16 months, there are no studies on children younger than age 5's group-level cooperation. However, at age 3, children undergo a normative turn, where they shift from thinking of joint goals to larger group goals. To determine whether this groupmindedness translates to behavioral group cooperation, we used a 2x2 between-subjects design to examine children's collaborative success in a pure coordination task. We assigned 2- and 3-year-olds to tackle the pure coordination task in same-aged dyads and triads. Children were individually taught to unlock a box for a reward by using the same color key (red or blue) as their collaborator(s). Children participated in one group warm-up trial, three test trials, and one domain generalization trial. In the domain generalization trial, children were given animal keys (pig and cow) instead of color keys (blue and red). While 2-year-old children were successful at collaborating in pairs, they were unsuccessful in groups of three (in the test trials and domain generalization trial). By age 3, children were equally successful at dual-level and group-level coordination (in the test trials and domain generalization trial). Furthermore, 3-year-olds were significantly more likely to coordinate (by looking, showing, pointing, and telling) to open the box than 2-year-olds. Overall, this research contributes to our understanding of the ontogeny of group-level cooperation while supporting broader theories of sociocultural development.

SESSION II PRESENTERS:

5:15 - 6:00 PM

Presenters are organized by discipline and then alphabetically by last name.

BEHAVIORAL SCIENCES / PSYCHOLOGY

Presenters are organized by discipline and then alphabetically by last name.

Children's science self-efficacy and attitudes: Impacts of content area and previous experience

Carly Blank

Faculty Mentor: Sarah Gaither

Authors: Carly Blank, Sydney Revell, Maria Brown, Jessa Stegall, Mercedes Muñoz, Dena Silver, Janvi Kavathia, Charli Cordoves, LaNaiah Frieson, Peregrine Bratschi, Tamar Kushnir, Sarah Gaither

Discipline: Behavioral Sciences / Psychology

Abstract:
Science capital, the measure of an individual's science-related knowledge, attitudes, experiences, and resources, begins to develop in childhood and can have a lasting impact on an individual's decision to pursue higher education and a career in science-related fields. Informal learning settings, such as museums, can have a positive effect on children's attitudes to science, as seeing that "science is everywhere" increases science capital. This project in partnership with the Durham Museum of Life and Science taught children about either 'stereotypical science' or 'non-stereotypical science' museum exhibits through a dialogue-based storybook. Participants were 4 to 9 years old, (n = 121, 60 boys, mean age = 6.637, child race = 44.6% white, 18.2% mixed race, 16.5% African American, 9.1% Hispanic, 6.6% Asian, 5% other/did not report). Children's self-reported beliefs about their science abilities and interest in science were then measured, and responses were analyzed both quantitatively and qualitatively. Children introduced to 'non-stereotypical science' reported higher perceived closeness to an imaginary scientist and identity as a scientist compared to children introduced to 'stereotypical science' (60% of children in the non-stereotypical condition chose 'I am a scientist' over 'I do science' compared to 45% of the stereotypical condition). Qualitative analysis revealed common themes both surrounding positive science attitudes, such as experience doing science at school or similar perceived traits between themselves and a scientist, and negative science attitudes, such as a high perceived workload associated with being a scientist.

Attitudes toward success and failure have implications for self-regulation and well-being

Maria Brown

Faculty Mentor: James Shah

Authors: Maria Brown, Skyler Wyly, Zhuying Guo, James Shah

Discipline: Behavioral Sciences / Psychology

Abstract:
While considerable work in social psychology has documented the impact of success and failure on subsequent behavior, relatively little has explored how such experiences may impact what we generally come to believe about such experiences. Indeed, these implicit attitudes toward success and failure may exert a distinct influence on behavior, as we explore across five studies. We suggest that people's implicit attitudes toward success and failure have implications for learning from and building on these experiences, self-regulatory behaviors, and their general well-being. Study 1 and Study 2 suggest that more positive attitudes toward success and failure each reduce stress and promote well-being, gratitude, resilience, self-improvement, and grit in different ways. Study 3 and Study 4 explore how implicit attitudes toward success and failure influence thinking about successes and failures, fear of failure and success, and the learning and motivation individuals draw from experiences of success and failure. Study 5 finds evidence that attitudes toward success and failure both independently affect the intention to address failures and build on successes.

Social Affiliation and Resistance to Belief Revision in Childhood

Umang Dhingra

Faculty Mentor: Tamar Kushnir

Authors: Umang Dhingra, Zoe Finiasz, Tamar Kushnir

Discipline: Behavioral Sciences / Psychology

Abstract:
Humans affiliate through their shared beliefs. When membership in a social group is based on shared beliefs, we are more resistant to revising them (e.g., Druckman & McGrath, 2019; Enders et al., 2022). Children's sensitivity to group membership can influence from whom they learn (Kinzler et al., 2009, 2010, 2011). We ask, does this tendency to exhibit resistance to revision have its roots in childhood? We tested whether children (N=56, MAge=4.85) who affiliate based on shared beliefs would be resistant to revising them upon observing disconfirming evidence. Children were asked to guess which of two blocks would make a machine light up. Then, they met a puppet who shared this belief. In the belief-based condition, the puppet invited them to join a team whose membership was contingent on the shared belief; in the character-based condition, group membership was based on being "really nice." A control condition was included where no information about groups was mentioned. Following this, children observed blocks being placed on the machine. The unendorsed blocks made the machine light up and the initially endorsed ones were inert. Children were asked which block would make the machine go in the presence and the absence of the puppet.
Logistic regression showed that children in the belief-based condition were significantly less likely to revise their beliefs (34.7%), while those in character (76.1%) and control (91.7%) conditions were significantly more likely to revise. These findings suggest that when group membership depends on shared beliefs, children are more resistant to belief revision.

PATERNAL CANNABIS EXPOSURE EFFECT ON ADOLESCENT OFFSPRING GLUTAMATERGIC AND CHOLINERGIC SYSTEMS

Millie Evonlah

Faculty Mentor: Harry Scott Swartzwelder

Authors: Evonlah M, Huang M, Snyder C, Hawkey A, Levin E, Swartzwedler HS, Healey KL

Discipline: Behavioral Sciences / Psychology

Abstract:
As cannabis legalization expands across the United States, understanding its potential cross-generational impacts becomes imperative. Emerging research suggests that male rats with cannabis exposure alters sperm methylation and father offspring with sex-dependent cognitive and reward deficits. Glutamatergic and cholinergic systems are important mediators of cognition and motivation, particularly in the nucleus accumbens (NAc) and dorsal hippocampal (dHPC). This study investigates how paternal cannabis exposure prior to conception affects offspring NAc and dHPC cholinergic and glutamatergic neurobiology, with two models of exposure, intermittent "weekend" use (2x week) and chronic continuous use (7x week). Male rats were administered cannabis extract (CE) containing delta-9-tetrahydrocannabinol (THC, 4 mg/k) or vehicle (saline+5% Tween80) for 28 days. 48 hours after the last exposure, males were mated with drug-naïve females. Adolescent male and female offspring were analyzed for expression of vesicular acetylcholine transporter (VAChT) and vesicular glutamate transporter (VGluT), markers of cholinergic and glutamatergic signaling, in NAc and dHPC subregions. In the NAc, there were subregion specific sex and CE exposure effects on cholinergic and glutamatergic markers. Female offspring of fathers exposed to intermittent CE showed increased VAChT expression in the NAc core, but not shell. Neither CE or sex affected VGluT expression in the NAc core or shell. In the dHPC, there were subregion specific sex and CE exposure effects of glutamatergic markers. In the CA3 male and female offspring had reduced VGluT expression with intermittently exposed fathers, however in DG only female offspring of intermittently exposed fathers showed reduced VGluT expression. Ongoing analyses are investigating cholinergic markers in the dHPC. Increased cholinergic activity in the NAc core may enhance reward-seeking behavior and impulsivity, potentially increasing susceptibility to addiction and hyperactivity-related disorders. Conversely, decreased glutamatergic signaling in the dHPC may impair cognitive flexibility, and memory function, which could contribute to deficits in learning, motivation, and adaptive behavior. These findings suggest that even intermittent paternal cannabis use may induce sex-specific alterations in brain systems.

Understanding motivation control beliefs using AI-driven qualitative interviews

Kai Tang

Faculty Mentor: James Shah

Authors: Kai Tang, Elizabeth Buduen, Zhuying Guo, Maria Brown, Skyler Wyly, James Shah, PhD

Discipline: Behavioral Sciences / Psychology

Abstract:
Extending research on the significance of individuals' implicit beliefs for goal pursuit and self-regulation, the present study examines how individual's 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 nature and 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. In the current study, participants are recruited to complete an AI-driven qualitative interview through Engage by CloudResearch. The Engage AI Analysis software summarizes interviews, highlights noteworthy responses, and quantifies themes that are related to participants' beliefs about the controllability of motivation and their ability to self-regulate during goal pursuit. The sample size is determined by theoretical saturation, resulting in a sample size of 60 participants. This study is part of a set of ongoing studies exploring the effects of motivation control beliefs on goal progress, persistence, and regulatory strategy use.

HEALTH / CLINICAL RESEARCH

Presenters are organized by discipline and then alphabetically by last name.

Help Desk: A student-led screening and referral intervention for unmet social needs

Austin Brown, Ariana Vaida, Anthony Zhao, Amitesh Verma

Faculty Mentor: Susan Spratt

Authors: Austin Brown, Ariana Vaida, Amitesh Verma, Eugene Cho, Achintya Inumarty, Ayush Khanna, Anthony Zhao, Susan Spratt

Discipline: Health / Clinical Research

Abstract:
While unmet social needs are major drivers of health outcomes, most health systems are not fully equipped with the social services to adequately address them. We implemented an intervention that enables undergraduate volunteers to screen patients for unmet social needs and subsequently refer them to community resources. Planning included observation of exemplary programs, development of a community-based organization directory, and evaluation of the center's patient population, clinical workflows, and data infrastructure. A peer-to-peer training model for students was designed by integrating a social determinants of health curriculum. The program works across three different sites in Durham, North Carolina, and has screened 2948 patients and provided 1445 initial referrals from 1/1/2022 to 10/16/2024. The adaptable workflow makes this program a widely-applicable tool for identifying social needs within a healthcare setting and advancing SDOH education for pre-health students.

The Role of Patient Education in Improving Health Knowledge in Elective Spine Surgery

Susan Chemmanoor and Avery Bernazard

Faculty Mentor: Rory Goodwin

Authors: Susan Chemmanoor, Alyssa Bartlett, Sophia Cai, Avery Bernazard, Antoinette Charles, Dana Rowe, Jacqueline Emerson, Emily Luo, Melissa M. Erickson, Rory Goodwin

Discipline: Health / Clinical Research

Abstract:
Health literacy, the ability to effectively utilize information to make health-related decisions, plays a critical role in health outcomes and patient well-being. Poor health literacy rates are associated with worse spine surgery outcomes, especially for low-income, non-white, and older patients. These patients typically experience worsened pain, heightened anxiety, decreased satisfaction, longer lengths of stay, and higher readmission rates. Improving health literacy and patient education prior to elective spine surgery is of critical importance. Investigating the efficacy of informational intervention in improving spine surgery health literacy has broad clinical applications. The purpose of this systematic review is to understand what interventions effectively improve disease knowledge and health literacy in elective spine surgery patients. PubMed, Scopus, and Web of Science were systematically searched for eligible studies published prior to August 2024. Studies were eligible if participants underwent elective spine surgery and were 18 years or older at enrollment. Studies utilizing mobile health strategies, informational videos, pamphlets, and in-depth health-provider briefings were all eligible. Two reviewers assessed each study's risk of bias using the methodological index for non-randomized studies (MINORS). Qualitative analysis was used to assess the relationship between educational intervention and spine surgery patient outcomes. Due to the heterogeneity of the data, statistical analysis was not performed. Extracted data from 11 studies, with a combined cohort of 1662 patients, showed that both discussion-based and virtual interventions that delivered information about the respective surgical procedure and recovery process saw significant improvement in patient information and postoperative anxiety. All studies reported significantly high patient satisfaction scores. However, three studies reporting length of stay, readmission rates, and postoperative pain saw nonsignificant changes in these metrics. Patient education has a clear relationship with improved patient information, satisfaction, and anxiety. Discussion-based and virtual educational interventions effectively improve health literacy, supporting their clinical utility in the perioperative phase to support elective spine surgery patients. Implementing such intervention may reduce health disparities and improve recovery for spine surgery patients.

Barriers to Neurosurgical Service Delivery in Sub-Saharan Africa

Eugene Cho and Heather Raslan

Faculty Mentor: Alvan Ukachukwu

Authors: Eugene J. Cho, Arsene Daniel Nyalundja, Allan Bakesiga, Olaoluwa Ezekiel Dada, Zoey Petitt, Heather Raslan, Isha O. Shah, Glory Agun, Katherine Reddy, Samuel Olawale, Lordstrong Akano, Taye Owoputi, Joseph Mary Ssembatya, Alice Kateregga, Paula Njeru, Yes

Discipline: Health / Clinical Research

Abstract:

Service delivery is a major indicator of neurosurgical care globally, and improvement in care has been limited due to unreliable data on service delivery indicators. By exploring the barriers to neurosurgical service delivery in Sub-Saharan Africa (SSA), interventions can be developed to address deficits and build neurosurgical capacity. Our objective was to identify specific barriers to neurosurgical service delivery in SSA and to propose interventions to address them using a mixed-methods approach. Our approach involved surveys of neurosurgical care providers, surveys of patients/caregivers in 4 select countries (DRC, Nigeria, Uganda, and Zimbabwe), and interviews with neurosurgery providers in the 4 countries. 102 providers completed the surveys. 64.8% indicated that the unavailability of hospital infrastructure was a major barrier. 55.4% expressed dissatisfaction with their monthly pay and 47.1% reported inadequacies in staff availability. Increasing global partnerships was cited as the most important intervention to improve capacity (25%). 150 survey responses from patients/caregivers indicate delays in seeking, reaching, and receiving care. Most patients reported experiencing financial barriers to accessing care as an important barrier, as 87% did not have health insurance. Most patients recommended subsidized treatment (21%) and increasing availability of medical supplies (17%) as interventions. Lastly, 40 interviews of neurosurgical providers and administrators indicate barriers on the individual, hospital, and system levels. Barriers most frequently discussed were patients' socioeconomic status (87.5%), patients' overall understanding of when to seek care (50%), and the financial burden of neurosurgical care (45%). Further, providers proposed solutions regarding increasing equipment (50%), government support (47.5%), and training staff (37.5%). This study represents one of the first comprehensive examinations of barriers to neurosurgical service delivery across individual, hospital, and system levels in diverse SSA countries. By analyzing survey and interview responses, insights gathered can provide a foundation for informing policy and advocating for governments to prioritize neurosurgical capacity-building efforts. Building neurosurgical capacity in low- and middle-income countries requires a multifaceted approach, and this study lays the groundwork for achieving that goal.

The Impact of Preoperative Psychological Interventions on Spine Surgery Outcomes

Maria Junaid

Faculty Mentor: C. Rory Goodwin

Authors: Maria Junaid, Ellen O'Callaghan, Chinelo Agwugebo, Dana Rowe, Seeley Yoo, Alyssa Barlett, Antoinette Charles, Emily Luo, Jaqueline M. Emerson, Samantha J Kaplan, Melissa M. Erickson, C. Rory Goodwin

Discipline: Health / Clinical Research

Abstract:

Introduction: Mental health disorders, primarily anxiety and depression, are prevalent among individuals undergoing spinal surgery. Patients with preexisting mental disorders are at higher risk for adverse postoperative outcomes. Despite the established link between mental health disorders and postoperative outcomes, preoperative psychological interventions are not well utilized in perioperative care. This study aims to evaluate the impact of preoperative psychological interventions across spine surgery postoperative outcomes.

Methods: A systematic review was conducted following PRISMA guidelines to assess postoperative outcomes after the implementation of preoperative psychological interventions in spine surgery. The PubMed, EMBASE, Web of Science, and APA PsycINFO databases were searched from inception until August 06, 2024. Included studies analyzed preoperative psychological interventions and measured postoperative outcomes in adult spine surgery patients. Bias was assessed utilizing the Methodological Index for Non-Randomized Studies (MINORS) and the quality of studies was assessed with the Oxford Centre for Evidence-Based Medicine Levels of Evidence tool.

Results: Relevant data was extracted from 13 studies involving 9316 adults. When pharmacotherapy or stress relief methods were implemented preoperatively, the majority of these studies showed a positive significant association with pain reduction. However, no studies analyzing CBT were associated with pain reduction. All studies analyzing CBT and disability showed positive significant associations with disability reduction, however when pharmacotherapy was assessed, there were no associations with improved postoperative disability. In studies that measured mental well-being, all of the CBT studies and half of those analyzing stress relief methods were associated with increased patient mental well-being. Of note, studies analyzing pharmacotherapy were not associated with improved mental well-being.

Conclusion: This systematic review highlights that a range of preoperative psychological interventions are associated with improved postoperative patient outcomes and describes the current state of literature in an understudied field. Further research is needed to identify optimal intervention timing and evaluate clinical applicability for implementation.

Relationships between pain, activities of daily living, and perceptions of overall health

Cody Powell, Anika Dhuler, and Breanna Barrett

Faculty Mentor: Nicole Arrato

Authors: Cody Powell, Breanna Barrett, Anika Dhuler, Gretchen G. Kimmick, Heidi White, Harvey J. Cohen, Rebecca A. Shelby, Nicole A. Arrato

Discipline: Health / Clinical Research

Abstract:
Objective: Geriatric assessment has been identified as an essential component to caring for patients with cancer who are over 65 years old. Prior research suggests that physical pain and illness perceptions each impact important health behaviors. This retrospective study utilized a brief geriatric screen to examine the relationships between pain levels, activities of daily living (ADLs), and perceptions of overall health for older adults with breast cancer. Implications for methods to improve the patient experience for this population are considered.
Methods: The Senior Adult Oncology Program (SAOP) screening tool was administered to 429 patients age 65 or older at a breast oncology clinic. A total ADL score was computed by summing patient-reported responses to 13 ADL items, such as ability to dress oneself, feed oneself, and remember to take medications. A higher ADL score indicates greater difficulty with these responsibilities. Pain was assessed using a 10-point scale; scores were dichotomized to form a low-pain group (scores 0-4) and high-pain group (scores 5-10). Overall Health was assessed on a 1-10 scale, with higher scores indicating perceptions of greater health. Demographic and medical information was abstracted from patients' electronic health records. Independent samples t-tests examined differences between the high-pain and low-pain groups in total ADL score and self-assessed Overall Health.
Results: The average age of the sample was 76 years old (range = 65-89 years). Approximately half of the sample identified as White (48%); 20% identified as Black. In comparing the high-pain and low-pain groups, the high-pain group reported significantly greater difficulty with ADLs (M score = 3.25, 1.41, respectively; p=.026). Additionally, patients endorsing high pain levels reported significantly worse Overall Health as compared to patients endorsing low levels of pain (M= 7.50, 6.11, respectively; p=.001).
Discussion: Older adults with breast cancer experiencing high levels of pain demonstrated greater difficulty with ADLs and worse perceptions of overall health. It is critical that pain is assessed early and often for older adults with breast cancer. Early identification of high pain levels in this population could allow those in need to receive pharmacological and/or behavioral treatments for pain, which may maintain stability or promote improvement in ADLs and perceptions of one's health. Incorporating brief pain assessments into future screenings.

Perspectives of Black and White Family Members on Medical Decision Making for ICU Patients

Astha Ray

Faculty Mentor: Deepshikha Ashana

Authors: Astha Ray, Kayla N. Thompson, Kimberly S. Johnson, Christopher E. Cox, Martha Lee, Katelyn Dempsey, Deepshikha C. Ashana

Discipline: Health / Clinical Research

Abstract:
Shared decision making (SDM) is a collaborative process among clinicians, patients, and their families to make medical decisions that align with patients' preferences. SDM in intensive care units (ICUs) is challenging because patients are often seriously ill and lack decisional capacity; thus, urgent, cognitively complex, and highly emotional decisions regarding the use of life-prolonging therapies must be made by their families who lack established relationships with ICU clinicians. Furthermore, recent evidence suggests that ICU clinicians may be less likely to engage in SDM with Black as compared to White patients and families. Our goal was to compare the perspectives of Black and White families on their experiences of SDM. Eligible family members self-identified as Black or White and were involved in surrogate decision making for patients mechanically ventilated for ≥ 48 hours at one US health system. We conducted semi-structured interviews with families virtually. Interviews used narrative prompts about experiences of decision making and semi-structured prompts about trust, communication, and emotional support as related to decision making. Two coders blinded to family race conducted concurrent open coding of all transcripts of audio-recorded interviews in NVivo and met weekly to resolve discrepancies via consensus. To identify racial differences in SDM experiences, both coders and the senior author were unblinded to race and then used code frequencies and matrix coding to independently identify themes that were accepted only with consensus after group discussion. Among 43 interviewed family members, 25 (58%) identified as Black and 18 (42%) as White. Thirty-five (81%) were female, 22 (51%) were the spouse of the patient, and 14 (33%) were the child of the patient. Fifteen (35%) patients died during their hospital stay. We identified 4 SDM-relevant themes that were disproportionately prevalent in interviews with Black family members: they experienced pressure to make decisions that aligned with the ICU team's recommendations and timeline, they needed to code-switch to ensure their advocacy was welcomed rather than perceived as intrusive, they were disregarded by the ICU team, and they perceived inconsistencies between multiple dimensions of trust. These results may identify targets for future clinician-focused interventions to improve equity in ICU SDM.

DECLINING ENDURANCE IN CHILDREN: REVIEW OF BRUCE TREADMILL PROTOCOL ENDURANCE TIMES SINCE 1978

Johrdyn Tarpeh

Faculty Mentor: Katherine Hansen

Authors: Johrdyn Tarpeh, Jordan Ezekian, Hoang Nguyen, Katherine Hansen

Discipline: Health / Clinical Research

Abstract:

Purpose: The Bruce treadmill protocol is a commonly used protocol for treadmill-based exercise testing in children. However, normative data for endurance time dating from 1978 remains the clinical reference, despite shifting population anthropometrics and fitness level. This review evaluates trends in endurance times of healthy children since 1978.

Methods: Studies were included that met the following criteria: (1) subjects aged 4-18 years old with no identified cardiac or pulmonary pathology, (2) non-metabolic maximal effort treadmill-based exercise tests (achieved ≥85% predicted peak heart rate), (3) utilization of the standard Bruce protocol, and (4) written in English. Endurance times were grouped into three age categories (4-9 years, 10-15 years, 16-18 years). Bootstrap resampling was performed to estimate the mean and standard deviation for each age group, gender, and time period by repeatedly resampling endurance times with replacement (10,000 iterations). The bootstrapped mean was calculated as the average of these resampled means, while the bootstrapped standard deviation was derived from their standard deviation.

Results: A total of 7 studies (n=1868 children) were analyzed. Endurance times declined over time across all age groups in North America (1970s to 2000s) and Europe (1990s to 2010s). In North America, for the 4-9 age group, endurance times in males and females had a combined mean reduction of 1.45 minutes. In the 10-15 age group, endurance had a combined mean reduction of 1.8 minutes. In the 16-18 age group, endurance had a combined reduction of 1 minutes. In Europe, similar declines were observed in the 4-9 and 10-15 age groups. The 16-18 age group was assessed only at one time period. The 4-9 age group saw a combined decrease of 1.4 minutes. The 10-15 age group experienced a combined reduction of 2.72 minutes.

Summary/Conclusion: Prior studies point to a decline in fitness in pediatric patients over time. This review of the literature affirms this finding and also highlights regional differences in anthropometrics and fitness trends. Given that current reference values are based on outdated data, there is a need to re-evaluate endurance time standards for modern pediatric populations. This data also points to a critical need to address declines in fitness in children in the current era.

BIOLOGICAL AND BIOMEDICAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

Expression and Purification of Rab1A for Biochemical Analysis of the Rab1A:NAB2 Interaction

Lukas Bleichner

Faculty Mentor: Dewey McCafferty

Authors: Lukas Bleichner, Dewey McCafferty

Discipline: Biological and Biomedical Sciences

Abstract:
Rab GTPases are a family of approximately 60 small GTPases that regulate intracellular vesicle trafficking and endomembrane system dynamics. Dysregulation of Rab GTPase function is closely linked to trafficking defects and cellular toxicity, hallmark features of neurodegenerative diseases such as Parkinson's disease (PD). The McCafferty lab has been investigating the mechanism of action of NAB2, a small molecule N-arylbenzimidazole, which appears to reverse vesicular trafficking defects and alpha-synuclein-associated toxicity in cellular and animal models of PD. Chemoproteomic analyses identified Rab1A as a putative target of NAB2, suggesting a direct interaction that may modulate the GTPase activity of Rab1A. To facilitate biochemical and biophysical characterization of the Rab1A:NAB2 interaction, we report the cloning, plasmid construction, recombinant expression in E. coli BL21(DE3) Codon+ RIL cells, and purification of GST-TEV-Rab1A at yields exceeding 10 mg/L. These results establish a foundation for mechanistic studies to elucidate the role of Rab1A in NAB2-mediated neuroprotection.

Sex-Specific Regulation of Adiposity by Cardiac GRK2 in Heart Failure

Aliza Bochner

Faculty Mentor: Walter Koch

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

Discipline: Biological and Biomedical Sciences

Abstract:
Obesity is a major risk factor for heart disease and cardiomyocytes secrete metabolic signaling factors that influence systemic organ function, particularly in response to cardiometabolic stress. G protein-coupled receptor kinase 2 (GRK2), a key regulator of beta-adrenergic receptors in the heart, is upregulated in response to stress, yet its role in heart to fat communication remains unclear. Understanding how GRK2 influences systemic adiposity in a sex-dependent manner may uncover new therapeutic strategies for cardiometabolic disease. We hypothesize that cardiac GRK2 regulates adiposity during cardiometabolic stress in a sex-specific manner. Using a pressure overload-induced heart failure model, we observed sex-dependent alterations in white adipose tissue (WAT). Male mice with heart failure exhibited reduced WAT depots, while female mice showed no significant changes. Cardiac GRK2 overexpression further exacerbated WAT loss in male mice with heart failure. Additionally, WAT from male mice in heart failure displayed adipocyte hyperplasia and impaired lipolytic responses to isoproterenol ex vivo compared to WAT from control mice. Notably, male mice with heart failure exhibited a significant decrease in cardiac fatty acid transporter CD36 expression, while females showed no alterations. These findings suggest that cardiac GRK2 plays a sex-specific role in regulating heart-fat crosstalk during heart failure. Future studies will investigate the cardiac signaling factors driving these sex-specific cardiometabolic differences.

Ecdysteroid Regulation of Developmental Timing in Manduca sexta

Katie Brandler

Faculty Mentor: Frederik Nijhout

Authors: Katie Brandler, Frederik Nijhout

Discipline: Biological and Biomedical Sciences

Abstract:
Animals use hormone-signaling mechanisms to start and stop growth. The specific mechanisms regulating growth transitions in insects remain poorly understood. In the tobacco hornworm Manduca sexta, the timing of growth stages is highly synchronized between individual animals. During its fifth larval instar, Manduca sexta transitions from the feeding stage, where it eats and grows (to about 12 grams), into the wandering stage, where it purges its gut contents to prepare for pupation. The synchronous growth of Manduca and other insects is controlled by ecdysone, a steroid hormone that controls molting and metamorphosis. A small peak of ecdysone secretion is responsible for the transition into the wandering stage, between the fourth and fifth day of the fifth larval instar. My project focused on artificially manipulating this small ecdysone peak so seek insight on Manduca sexta's underlying hormonal mechanisms. I attempted to stimulate this ecdysone peak and the simultaneous entry into the wandering stage earlier than these animals typically experience. I hypothesized that experimental Manduca sexta would enter into the wandering stage in significantly less time than controls. Manduca sexta that were injected with 1µg ecdysone entered into the wandering stage 21.3 hours earlier than controls injected with laboratory saline, suggesting that their growth timeline can in fact be manipulated by artificial hormones. However, Manduca sexta injected with 10µL of ecdysone did not show this significant accelerated entry into the wandering stage. This suggests an "overdose effect"; animals may delay their development as a defense mechanism to excessive hormone levels, since insects require a delicate ecdysteroid balance. Additionally, injection of Prothoracicostatic Peptide (PTSP), a known ecdysone biosynthesis inhibitor, did not delay wandering stage entry. This suggests that the small ecdysone peak is not sensitive to PTSP, unlike other ecdysone peaks in Manduca development, possibly because it cannot overcome an additional negative regulation by juvenile hormone (JH). These findings suggest that ecdysone levels play a crucial role in regulating developmental timing in Manduca sexta, highlighting the potential for manipulating growth trajectories in insects. This insight not only advances our understanding of hormone-driven metamorphosis but may also have other applications in developmental biology.

Functional and Genetic Characterization of Single Ventricle Disease

Katherine Carlson

Faculty Mentor: Brittany Balint

Authors: Katherine Carlson, Brittany Balint, PhD, Carla Gonzalez, Andrew Landstrom MD, PhD

Discipline: Biological and Biomedical Sciences

Abstract:
Hypoplastic Left Heart Syndrome (HLHS), a form of Single Ventricle Disease (SVD), is a critical congenital heart defect in which the left side of the heart fails to develop properly, occurring in about 1 in 5,000 live births. To date, the developmental pathways that underlie HLHS are poorly understood, resulting in a lack of preventative therapies and genetic screenings for HLHS.
This study aims to determine whether cardiomyocyte differences, functionally and molecularly, underlie HLHS. Using blood samples from four HLHS probands and four matched controls (eight total cell lines), we will differentiate induced pluripotent stem cells (iPSCs) into cardiomyocytes (iPSC-CMs). Immunofluorescence and short tandem repeat (STR) analysis will be used to validate iPSC identity.
The goal of this study is to analyze the functional differences between iPSC-CMs derived from patients with HLHS and those from control groups; specifically, how do HLHS iPSC-CMs differ from control groups regarding viability? We will assess apoptosis, proliferation, and differentiation capacity in HLHS and control iPSC-CMs to elucidate the mechanisms driving HLHS cardiomyocyte dysfunction. First, we hypothesize that HLHS-derived cell lines have a reduced ability to differentiate into cardiomyocytes compared to controls, which we will analyze through immunofluorescent staining with a cardiac muscle marker (TNNT2). We hypothesize that HLHS cardiomyocytes are more prone to apoptosis and reduced proliferation compared to controls, which we will test using TUNEL (TdT dUTP nick-end labeling) assays for apoptosis and EdU (5-Ethynyl-2'-deoxyuridine) staining for proliferation.
To further investigate genetic factors of SVD, we performed single-cell RNA sequencing on HLHS lines to identify differentially expressed genes and pathways involved in cardiomyocyte differentiation. Genomic sequencing was conducted on SVD patient samples to identify genetic variants linked to early mortality, and the identified variants were confirmed through Sanger sequencing of DNA extracted from patient blood samples. By identifying these fundamental molecular differences in HLHS cardiomyocytes and genetic variations in SVD patients, we can understand the molecular drivers of SVD in development, eventually looking toward improved genetic screening for SVD and cellular-based therapies for SVD rather than relying on numerous surgeries.

Investigating Trends in Aquatic Insect Emergence to Understand Aquatic-Terrestrial Nutrient Cyc

Erin Chen

Faculty Mentor: Emily Bernhardt

Authors: Erin Chen, Heili Lowman, Tamera Wooster, Tyler Edwards, Chris Solomon, Emily Bernhardt

Discipline: Biological and Biomedical Sciences

Abstract:
The emergence of aquatic insects play an important role in the transfer of nutrients from the aquatic environment to the terrestrial environment. Shifts in water temperatures, chemistry, and flow can all impact the size, quantity, and time frame in which insects emerge, which may in turn result in a phenological mismatch between the emergence of aquatic insects and their terrestrial predators. To examine how the time frame of peak insect emergence and counts of insects change, sticky traps were set up to capture emerging insects at 8 stream-adjacent sites in the Hubbard Brook Experimental Forest (HBEF), where researchers have carried out numerous environment-altering treatments to study the impacts on the watershed ecosystem using continuous water chemistry data. We developed an online interactive dashboard that allows users to explore peak emergence dates by year and counts of insects at emergence by date range, taxa, and site. Since weekly record-keeping began in 2018, over 260,000 aquatic insects have been identified across the HBEF streams, with clear peaks in dipteran emergence during both spring and fall seasons. Monitoring insect emergence time and count, coupled with existing water chemistry and flow monitoring, is critical for developing a further understanding of how changes in the aquatic ecosystems impacts nutrient cycling between the aquatic and terrestrial ecosystems.

Breaking Cancer's Disguise Through Enhanced Immune Detection

Christina Colwell

Faculty Mentor: Donald McDonnell

Authors: Christina Colwell, Patrick Juras, Debarati Mukherjee, Ching-yi Chang, Donald McDonnell

Discipline: Biological and Biomedical Sciences

Abstract:
One of the challenges in cancer treatment is the ability of cancer cells to rapidly evolve and develop mechanisms to evade the immune system, allowing them to proliferate unopposed in the human body. One possible strategy to increase immune surveillance is to increase surface expression of the Major Histocompatibility Complex Class I (MHC-I) on cancer cells. Presentation of tumor antigens by the MHC-I complex is the way by which CD8+ T cells recognize and destroy cancer cells. The data from this research shows statistically significant increases in MHC-I when the Calcium/calmodulin-dependent protein kinase kinase 2 (CaMKK2) is degraded or when phosphodiesterase 1 (PDE1) is inhibited in breast cancer cells as measured by Flow Cytometry. These findings suggest CaMKK2 and PDE1 are involved in the regulation of MHC-I and that inhibition of these proteins may enhance immune surveillance and increase the efficacy of immune check point inhibitors, drugs that modulate immune cell activity.

Herbarium Collections Disentangle Climate Effects on Carnivorous Plant Phenology

Lydia Cox

Faculty Mentor: Lydia Cox

Authors: Lydia Cox, Dr. Natalie Z. Kerr, Dr. William F. Morris

Discipline: Biological and Biomedical Sciences

Abstract:
Climate change poses significant threats to many species — particularly habitat specialists such as carnivorous plants — yet it remains unclear if ecologically similar species respond similarly to climate change. To assess climate impacts, I used herbarium specimens spanning over 130 years to investigate flowering phenology and morphology change in six carnivorous plant species native to North Carolina: Dionaea muscipula and 5 species in the genus Sarracenia. I found that these species are experiencing significantly differing shifts in flowering time and morphology, indicating that ecologically similar species do not respond uniformly to climate change, even if inhabiting the same region. My findings reveal significant advances in flowering period in D.
muscipula and S. rubra, and marginal significance for S. purpurea, while D. muscipula and S. jonesii exhibited significant increases in flower stalk height. Flower width shows a significant decreasing tend in D. muscipula, and number of flowers shows significant increases in D. muscipula and S. minor. These flowering trends could impact plant-pollinator relationships, for some carnivorous plant species more than others. This study underscores the utility of herbarium collections in ecology and climate research.

Is Land Cover Associated with Ground Invertebrate Diversity?

Sophia Cox

Faculty Mentor: Stephen Nowicki

Authors: Sophia Cox, Danae Diaz, Stephen Nowicki

Discipline: Biological and Biomedical Sciences

Abstract:
Insects and other invertebrates perform essential ecosystem functions and have undergone significant decline, raising conservation concerns for both invertebrates and the insectivores, such as birds, that eat them. Worldwide insect decline is driven by factors including habitat loss, urbanization, pollution, and invasive species. Additionally, invertebrate abundance and diversity are often higher in habitats with more vegetation, especially with native plants. I investigated the effects of percent natural land cover on ground invertebrate diversity and abundance across four established eastern bluebird nesting sites in the North Carolina Piedmont. Eastern bluebirds rely on invertebrates for food, especially when feeding young, and trends in invertebrate diversity could have effects on eastern bluebird reproductive success. I sampled invertebrates over two four-day periods (late April and early July) using pitfall traps, placing 15 pitfall traps under nest boxes at each of four bluebird nesting sites around Durham, North Carolina. I identified invertebrates to taxonomic order level after collection. In total, I collected over 3500 invertebrates spanning 18 taxa. The most commonly collected taxa were Hymenoptera, Araneae, Coleoptera, Diptera, and Hemiptera. I then calculated Shannon diversity and analyzed the relationship between invertebrate diversity and percent natural land cover across sites. Diversity across sites shows high evenness, with no significant differences between any pair of sites. However, by using percent natural land cover as a proxy for urbanization and assessing the relationship between land cover and diversity, I found a significant, positive correlation: sites with higher natural land cover had higher diversity in April, although not in July, when diversity across sites was significantly lower overall. This study adds further evidence for the robust link between plant cover and invertebrate diversity, while also finding that time of year may have a significant impact on ground invertebrate communities. Future studies could incorporate additional sampling methods such as malaise traps or sweep netting and could evaluate differences between and within sites in more depth, such as proportion of native plant species and use of fertilizers and pesticides. Another next step will be to link invertebrate diversity to eastern bluebird nesting success.

Adapting methods for heritable genetic editing in Junonia coenia

Erin Dollard

Faculty Mentor: Greg Wray

Authors: Erin Dollard, Greg Wray

Discipline: Biological and Biomedical Sciences

Abstract:
Genome editing technologies such as CRISPR/Cas9 and the piggyBac transposon system have revolutionized genetic research but their full potential remains largely untapped in emerging model organisms like Junonia coenia. This study aims to adapt these tools for heritable germline editing in J. coenia, focusing on targeted disruption of the spalt gene, a key regulator of wing patterning.
For CRISPR experiments, pupae were injected with plasmids encoding Cas9 and two guide RNAs targeting spalt, followed by electroporation and heat shock induction. Despite extensive optimization, phenotypic analysis revealed no observable alterations in eyespot morphology, and genomic PCR failed to detect Cas9 or gRNA plasmids, suggesting unsuccessful genome editing. Possible explanations include inefficient plasmid delivery, rapid plasmid degradation, or low Cas9 expression.
For piggyBac transposon experiments, co-injection of a non-autonomous piggyBac vector with transposase mRNA was performed to achieve stable genomic insertions. Preliminary observations indicate successful egg production in control groups lacking transposase, but transgenic individuals failed to lay eggs that could be screened for fluorescent marker expression. This hints at a toxicity issue for the piggyBac vector in pupal gondal tissue, but the experimental number of mating pairs is not high enough to claim statistical significance.
These results highlight the challenges of adapting molecular genetic tools to non-traditional model organisms. While this study identified optimal injection volumes and delivery methods, additional refinements are necessary such as optimizing developmental timing and verifying in vivo Cas9 activity. Further refinement of this work to produce a reliable and functional methodology would reaffirm J. coenia as a valuable system for studying the genetic basis of morphological evolution and pattern formation.

Biochemical Insights into Ligand-Specific Transducer Recruitment by C-C Chemokine Receptor 7

Rebecca Fan

Faculty Mentor: Laura Wingler

Authors: Rebecca Fan, Matt Collins, Laura Wingler

Discipline: Biological and Biomedical Sciences

Abstract:
C-C chemokine receptor 7 (CCR7) and its two endogenous ligands, CCL19 and CCL21, are key in the homing of lymphocytes and dendritic cells to the lymph nodes. The overexpression of CCR7 has been correlated with increased lymph node metastasis and poorer prognosis in various cancers. Targeting chemokines and their receptors in cancer therapy has been challenging due to the complexity of balancing immune activation with immune tolerance. Specifically, the selective signaling of CCL19 binding to CCR7 activates both G protein and beta-arrestin, while CCL21-bound CCR7 preferentially signals through G protein. These differential signaling profiles complicate the pharmacological targeting of CCR7 in cancer and other pathophysiologies. The goal of this project is to identify the critical ligand-receptor interactions required for selective transducer recruitment and signal initiation by CCR7. By combining computational modeling and systematic mutagenesis, we aim to identify and validate the key residues and regions responsible for directing transducer selectivity and signaling bias. Recent work has provided experimental validation of in silico models through reciprocal charge swaps, demonstrating rescued signaling between receptor and chemokine via direct charge-charge interactions. We have identified at least one critical residue involved in these interactions. Further investigation will involve expanding the mutational landscape to assess the effects of these mutations on signaling through a combination of functional assays, including Bioluminescence Resonance Energy Transfer (BRET) assays to measure G-protein activation and Nano-Luciferase-based assays to measure beta-arrestin recruitment. The successful findings of this study will offer deeper biochemical insights into the ligand-selective transducer recruitment by CCR7 and provide the development of more targeted and effective future therapeutic interventions.

Developing novel reporters to visualize lipoprotein lipase activity in zebrafish

Sarah Gorbatov

Faculty Mentor: John Rawls

Authors: Sarah Gorbatov, Jia Wen, John Rawls

Discipline: Biological and Biomedical Sciences

Abstract:
Abnormal lipid metabolism is associated with obesity and cardiovascular disease, amongst other health complications. During lipid metabolism, lipids, mainly present in the form of lipoproteins, are secreted by the liver and intestine into circulation. The lipoproteins are hydrolyzed by lipoprotein lipase (lpla) to liberate free fatty acids for peripheral tissues to absorb. Mammalian literature shows that lpla is produced in adipose tissue, muscle, and other tissues and transported by the chaperone protein GPIHBP1 to the endothelial cell surface to interact with lipoproteins. Our preliminary data suggests that in zebrafish, lpla is expressed by ileal enterocytes. However, zebrafish lack GPIHBP1, so how the gut secretes lpla and where lpla is delivered remain unclear. If we generate an lpla reporter, we can visualize where zebrafish lpla-lipoprotein interactions occur. To achieve this, we chose to use CRISPR-Cas 9 genome editing to knock in the mScarlet fluorophore encoding gene into the C terminus of the lpla gene. Specifically, we first located a CRISPR target site, then amplified the lpla fragment and linearized a plasmid containing mScarlet, and finally combined the two and transformed the resulting construct. Colony PCR sequencing showed a successful clone, but there were nonsynonymous mutations in the lpla fragment, so it is necessary to reamplify and purify it. After that, we will perform site-directed mutagenesis to ensure only the true lpla gene, not the PCR donor, is cut, then do injections with gRNA and imaging. We expect the lpla-mScarlet reporter to help determine if lpla acts in the endothelial cells or extracellular space. Understanding this mechanism can lead to therapeutic developments for abnormal lipid metabolism.

Genomic Analysis of Gynandromorph Butterfly With Two Genomes

Angelina Huang, Shriya Minocha, Avi Heyman, and Daniel Levin

Faculty Mentor: Gregory Wray

Authors: Angelina Huang, Avi Heyman, Daniel Levin, Shriya Minocha, Krista Pipho, Gregory Wray

Discipline: Biological and Biomedical Sciences

Abstract:
Bilateral gynandromorphism is a phenomenon where an organism has cells of both sexes, divided symmetrically along an axis of the body. This study focused on a Heliconius melpomene butterfly, initially identified due to distinct patternings on each wing that are regulated by autosomal genes. This suggested two genomes present within the butterfly. DNA from the leg was analyzed for global SNP sharing, wing pattern loci polymorphisms, and sex chromosome coverage, and used to evaluate the two genomes hypothesis. The DNA from the legs was used to identify which samples shared the highest number of polymorphisms. Global SNP sharing plots verified that the butterfly had two distinct genotypes on either side. Genome-wide SNP Manhattan plots affirmed that these SNP sharing patterns extended beyond just the sex chromosomes to autosomes as well, indicating significant, full-genome differentiation between the two sides. Examples of genomic asymmetry were found in known autosomal wing patterning loci. An Optix-regulated red band on the forewing and a Cortex-regulated yellow bar on the hindwing differ on either side of the butterfly. Side-specific genetic variation in known cis-regulatory elements of these loci was observed by a comparison of sequencing coverage and SNP density, indicating divergent gene regulation between each half of the butterfly. To investigate the difference in sex chromosome coverage, the previously unknown W chromosome was found by aligning the gynandromorph to a de novo H. melpomene rosina assembly and analyzing genome coverage. Distinct coverage differences between the Z and putative W chromosomes mirrored the expected ZW and ZZ genotypes across the butterfly's bilateral halves, confirming the sex-specific split. Through comparative genomics, we also confirm the discovery of this species' W chromosome. Overall, these findings support the existence of two different genomes in the two halves of this specimen and adds to our picture of ways gynandromorphs can develop.

Multi Kidney Disease Modelling using hiPSC-Derived Biomimetic Glomerulus-on-a-Chips

Anavi Kaul

Faculty Mentor: Samira Musah

Authors: Anavi Kaul, Yize Zhang, Amanda Barreto, Bowen Jiang, Samira Musah

Discipline: Biological and Biomedical Sciences

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 injuries in a controlled, physiologically relevant environment. We are investigating four injury models—adriamycin (ADR), liposaccharide (LPS), diabetic nephropathy, 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. Functional assays track plasma protein filtration (albumin and inulin)—from the bottom to top channel of our chip to represent the transition from blood to urine—using fluorescent spectrometry at key time points to monitor injury progression. Key findings show significant podocyte injury occurs only when inflammation is present alongside high glucose, emphasizing the role of cytokines like TNF-α. PAM and ADR both increase filtration, with PAM acting within 2 days and ADR after 5 days, while LPS has minimal impact. HG alone does not significantly alter filtration, suggesting inflammation is necessary for damage. Next steps include refining filtration timepoints (HGIT at 12h–72h, PAM at 12h–120h, ADR at 48h–120h) and performing molecular assays targeting inflammatory (NF-κB) and structural (Rho/Rac/CDC41) pathways to clarify podocyte injury mechanisms.

Illuminating unique features of the regulatory genome in human and chimpanzee cells

Quindlan Kelleher

Faculty Mentor: Greg Wray

Authors: Quindlan Kelleher, Tania Guerrero, Greg Wray

Discipline: Biological and Biomedical Sciences

Abstract:
Throughout evolutionary time our genomes have helped shape our appearances, habits, strengths, weaknesses, and even predispositions to diseases. But what do we truly know about the mechanisms behind these expressions? In truth, very little. In decades prior, phenotypic and genotypic expressions of our genomes have been thought to be mainly controlled by protein-coding genes. Protein-coding genes are sequences of our genome that are transcribed and translated into proteins, leading to different expressions and functions. While protein-coding genes are essential for gene expression and evolutionary processes that lead to genetic variation, non-protein coding sequences are equally relevant. Functional non-protein coding sequences help regulate the genome. Known as the regulatory genome, its elements can turn off certain genes, turn others on, or control the level of expression of a gene. To help bridge this gap of knowledge, my research is focused on identifying active regulatory elements, and analysing their activity across different genetic scales to better understand the regulatory genome. We work with a highly unique collection of induced pluripotent stem cells (iPSC) collected from adult women in four different geographical regions: Africa, Europe, North and South America, and Southeast Asia. Using molecular biology and functional genomics, including cell culture, DNA extraction, cloning, and transfection, we are building a library of genomic DNA. These libraries are used in massively parallel reporter assays to assess activity in the regulatory genome. This research aims to comparatively analyze the regulatory activity of our rich iPSC collection to better understand how our genomes have evolved. In addition, we will develop genetic input libraries and conduct the same assays with a variety of chimpanzee cell lines, to further compare human regulatory activity to our closest living relatives. By deepening our knowledge of how gene expression functions, we can add missing pieces of our past and more recent evolutionary history to augment the resolution of our current picture. We hope to elucidate the regulatory genome and broaden our understanding of the mechanisms behind what makes species and individuals unique.

STEAP1 Facilitates Metastasis in mCRPC: A Rationale for Targeted ADC Therapy

Elina Khabibullina

Faculty Mentor: Zachary Hartman

Authors: Elina Khabibullina, John Wang, Sirajbir Sodhi, Li-Chung Tsao, Timothy Trotter, Andrew Armstrong, Zachary Hartman

Discipline: Biological and Biomedical Sciences

Abstract:
Prostate cancer (PCa) is the most diagnosed malignancy in men worldwide. Approximately 20% of patients progress to metastatic castration-resistant prostate cancer (mCRPC), a lethal stage of the disease with a median overall survival of only two years. Current treatment options for mCRPC are limited. Six Transmembrane Epithelial Antigen of the Prostate 1 (STEAP1) has emerged as a promising target due to its high expression in prostate tumors and minimal expression in normal tissues. Given its localization and tumor-specific overexpression, STEAP1 represents an attractive candidate for targeted therapies in mCRPC. STEAP1 has been implicated in multiple aspects of tumorigenesis and metastasis—including oxidoreductase activity, modulation of cell-to-cell communication, and promotion of proliferative signaling—but few studies have directly investigated its direct in vivo roles. In our study, we evaluated STEAP1's ability to drive tumor growth by deriving both STEAP1 knock-out and STEAP1 knock-in lines and studying their growth in CB/SCID mice. We additionally established a metastasis model through tail vein injection of transduced CDH-eGFP-Luc PCa lines. After confirming its involvement in metastasis, we shifted our focus to designing an antibody targeting STEAP1. Our findings indicate that while STEAP1 is not directly responsible for driving oncogenic signaling or increasing invasiveness, it remains a conserved marker throughout the metastatic process. This suggests that a STEAP1-targeting antibody may function primarily through immune effector mechanisms rather than by blocking oncogenic signaling. To this end, we used phage display to isolate scFv clones with high binding affinity and minimal off-target reactivity and then engineered a full-length STEAP1 IgG1 antibody. We validated its functionality by confirming activation of Fc receptors FcγRIIaand FcγRIIIa using JURKAT reporter cell lines. Recognizing that effective ADCs depend on proteolytic cleavage of the linker to release their cytotoxic payload, we assessed the antibody's internalization by conjugating it with a pH-sensitive dye. We found that STEAP1 is minimally internalized in native cell lines, which will drive further study on designing protease-cleavable linkers from extracellular proteases overrepresented in the tumor microenvironment.

Molecular Evidence for the Role of Olfaction in Antbird Foraging

Renee Li

Faculty Mentor: Hiroaki Matsunami

Authors: Renee Li, Connor Pawliczak, Gregory Thom, Robert Driver, and Hiroaki Matsunami

Discipline: Biological and Biomedical Sciences

Abstract:
Olfaction is a sense critical to the survival and reproduction of organisms. In vertebrate species, olfaction is predominantly mediated by a large family of odorant receptors (ORs), a class of transmembrane G-protein coupled receptors expressed in olfactory sensory neurons. Most studies on vertebrate olfaction have focused on mammals, with little attention given to birds, who were thought to rely more on senses like vision. However, behavioral studies suggest that several birds use olfaction in behaviors like foraging and kin recognition. One example is the antbirds (Aves: Thamnophilidae), a family of more than 230 species found in tropical Central and South America. Several species of antbirds follow army ant Eciton burchellii raids to prey on small fleeing invertebrates at the front of the raid. E. burchellii colonies move daily and are found on the forest floor, making them difficult to detect by sight. Preliminary behavioral studies suggest antbirds can locate ant raids via detection of ant-related odors, but there are no molecular-level studies investigating antbird ORs. To efficiently screen odorants that may activate antbird ORs, we created antbird consensus ORs, engineered ORs based on consensus amino acid residues of the native ORs, to avoid testing each of the hundreds of native ORs. We performed a literature search to identify compounds found in ant secretions and exposed the antbird consensus ORs to these odors. We found some consensus ORs responded to E. burchellii secretions such as geranylacetone and S-2-heptanol, which is consistent with the hypothesis that antbirds can smell E. burchellii. Our research provides insight into the ecology of antbirds alongside E. burchellii, an important keystone species. To conclude, our results advance bird olfaction research, a historically neglected field, and open up new possibilities for behavioral studies with antbirds and similar experiments on other birds who forage for sparsely located resources.

Maternal High-Fat Diet Alters Microglial Crym Expression in Male Offspring

Sophie Li

Faculty Mentor: Staci Bilbo

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

Discipline: Biological and Biomedical Sciences

Abstract:
Over half of women in the United States are overweight or obese when they become pregnant. High maternal weight correlates with an increased likelihood of neuropsychiatric disorders such as depression and social and communication disorders in offspring. However, the mechanisms by which dietary intake imparts long-term neural dysfunction in offspring are unclear. Using a maternal high-fat diet model, our lab has found increased microglial phagocytosis of serotonin neurons in the developing dorsal raphe nucleus (DRN) of male offspring. To better understand these sex-specific effects from diet, we performed bulk RNA sequencing on embryonic microglia isolated from the hindbrains of offspring of low-fat diet (LFD) and high-fat diet (HFD) dams. Interestingly, our data showed significant upregulation of Crym, a thyroid-hormone binding protein in HFD male offspring when compared to HFD female offspring. The role of CRYM in microglia is largely unknown. Due to the relationship of CRYM with thyroid signaling, we measured levels of thyroid hormones in both the mothers and offspring from LFD and HFD conditions by ELISA. Our results showed that serum TSH levels were slightly elevated in HFD dams while serum T4 levels were slightly decreased in HFD dams. However, T3 levels in offspring hindbrains were unchanged across diet or sex. Although we saw no differences in T3 between LFD and HFD offspring, we suspect there to be sex and diet-specific microglial responses to thyroid hormone because of the shown difference in Crym transcript. Our preliminary studies pinpoint CRYM as a potential novel regulator of sex-specific effects of maternal diet. Future experiments will further explore how thyroid hormone modulates embryonic microglial functions in LFD and HFD offspring.

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

Christina Liu

Faculty Mentor: Walter Koch

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

Discipline: Biological and Biomedical Sciences

Abstract:
Heart failure is the leading cause of death worldwide, affecting 64 million people globally. While there are some therapeutic options used in the clinic to delay disease progression, the underlying cellular mechanisms of heart failure go largely untreated. Mirco-RNAs (miRs) are small non-coding RNAs that regulate gene expression by binding to the 3'-untranslated regions of mature RNA, causing degradation or translational repression. Their ability to fine-tune gene expression has made miRs a promising target for treating heart disease. Specifically, our lab has identified a novel microRNA, miR-K, as a potential cardio-protective factor that attenuates hypertrophy, however the cellular mechanism by which it induces protective effects remains unclear. GPCR kinase 2 (GRK2) which regulates beta-adrenergic receptor (bAR) signaling under physiological conditions, is upregulated in heart failure, leading to chronic bAR desensitization and cardiac dysfunction. We hypothesize that miR-K regulates GRK2 expression, preventing cardiac hypertrophy. Using neonatal rat ventricular myocytes (NRVMs) as our in vitro model system, hypertrophy was induced using phenylephrine (PE), isoproterenol (Iso), or angiotensin II (AngII), and the cells were either pre-treated with or followed by treatment with a miR-K mimic, antagomiR-K, or scramble controls. GRK2 gene expression levels were quantified using RT-qPCR. In cells pre-treated with miR-K followed by hypertrophic stimuli, GRK2 expression was significantly increased compared to controls. Interestingly, increased GRK2 expression was also observed when miR-K was delivered after PE treatment. In contrast, cells treated with antagomiR-K demonstrated reduced GRK2 expression. These findings suggest that miR-K is necessary to induce GRK2 expression under stress conditions and primes the cardiac myocyte to adopt protective mechanisms via enhanced GRK2 expression, preventing hypertrophy. Future work will investigate the molecular pathways involved in hypertrophy, such as ERK1/2, SMAD 2/3, and JAK2-STAT1/3 signaling. These findings will be used to elucidate the role of miR-K as a novel therapy for heart failure.

The Ncd Kinesin-14 Tail: Analysis of AI-Driven Structural Predictions

Zimiao Meng

Faculty Mentor: Sharyn Endow

Authors: Zimiao Meng, Sharyn A. Endow

Discipline: Biological and Biomedical Sciences

Abstract:
Nonclaret disjunctional (Ncd) kinesin-14 is a type of motor protein that binds to microtubules and assembles spindles. It is vital for the separation of chromosomes in Drosophila. Currently, it is difficult to purify and crystallize the whole Ncd protein to determine its structure. Researchers could only obtain the protein structure of the heads/motor domains, but not the tail, of kinesin-14 from its crystallized form. However, the tail's conformation and its interaction with alpha and beta-tubulin are crucial in understanding the functioning of kinesin-14. Newly developed platforms such as AlphaFold 3 leverage machine learning to predict protein structures and interactions, which could be the key to solving the mystery of the Ncd tail structure. These programs do have the limitation of being less accurate when it comes to protein structures not recorded in the protein database. Nevertheless, AI prediction of the kinesin-14 Ncd tail structure could result in knowledge that will help researchers understand how these motor proteins operate and make advancements in the pharmaceutical and medical fields. Using structural prediction programs as well as large language models, we were able to generate possible structures of the Ncd tail in its binding state and compare of the models' accuracy.

Hormone Concentration Variation and Social Behavior in Female Dominant vs. Codominant Lemurs

Kavya Menke

Faculty Mentor: Christine Drea

Authors: Kavya Menke, Caroline Shearer, Christine Drea

Discipline: Biological and Biomedical Sciences

Abstract:
Androgens (e.g. testosterone) mediate male aggression and social dominance, such that concentrations are typically higher in males than females. Generally, raised androgen concentrations have negative health and reproductive consequences in female mammals (e.g. polycystic ovary syndrome). In lemurs, however, it is common for females to exhibit androgen-mediated social dominance over males, of which the consequences for social relationships are not fully understood. By comparing female-dominant (Eulemur coronatus) and codominant (E. sanfordi) species living in sympatry in Madagascar, we aim to understand if and how hormonal variation relates to differences in social relationships. Additionally, to examine potential ecological differences, endocrine and behavioral data were collected from two field sites: a nutrient-rich forest (rich site), and a more desolate, arid environment (lean site). We quantified androgen metabolite (fAM) concentrations in fecal samples for comparisons by sex, species, and site. We also examined social partnerships by recording nearest neighbors (i.e., proximity) during focal observations. Assay results show that female E. coronatus have greater fAM concentrations than do female E. sanfordi, that female E. coronatus and E. sanfordi females have comparable fAM concentrations to conspecific males, and that fAM concentrations are higher in both species and sexes in the lean environment compared to the rich one. Social networks based on nearest-neighbor data show that, in both species, social bonds are strongest between mixed-sex pairs and weakest between males, suggesting that male lemurs tend to be more socially peripheral than females. These comparisons indicate that differences in dominance structure are likely mediated by androgens in both sexes and that the environment, by impacting intraspecific competition, can modulate these behavioral endocrine relationships.

Context-Dependent Role of B-Cells in Tumorigenesis: Influence of the Tumor Microenvironment

Nicole Moon

Faculty Mentor: Zachary Hartman

Authors: Nicole Moon, Sirajbir Sodhi, John Wang, Li-Chung Tsao, Cong Xiao Liu, Zachary Hartman

Discipline: Biological and Biomedical Sciences

Abstract:
B-cells, best known for their role in antibody production, can also modulate tumorigenesis through antigen presentation, cytokine release, and interactions with T-cells. Evidence suggests that whether B-cells promote or inhibit tumor growth may depend on the degree and nature of immune infiltration within the tumor microenvironment (TME). We selected murine tumor models, some characterized as "immune cold" (low immune infiltration) and others as "immune hot" (high immune infiltration), to test the hypothesis that B-cell effects on tumor progression vary based on the immunogenic and stromal architecture of the TME. We employed two mouse models with altered B-cell function: (1) IgHEL mice exhibiting a skewed B-cell repertoire with B-cell receptors (BCRs) specific to hen egg lysozyme (HEL) and (2) CD19-Cre mice lacking functional B-cells. B-cell deficiency was validated through total IgG ELISAs and vaccination response assays. The mice were then inoculated with tumor cell lines differing in immune infiltration: (1) E0771 and MM3MG HER2, "immune cold" mammary tumors with minimal stromal expansion, and (2) CT26, "immune hot" colorectal tumors with extensive stromal areas. Immunohistochemical analyses revealed that E0771 and MM3MG tumors were predominantly epithelial with sparse immune cell infiltration, whereas CT26 tumors displayed rich stromal networks with higher levels of CD19+ B-cells, CD4+ T-cells, CD8+ T-cells, and FoxP3+ regulatory T-cells. Functionally, B-cell knockout in CT26-bearing mice led to significantly increased tumor growth, suggesting that B-cells have an anti-tumor role in this model. In contrast, E0771 and MM3MG tumors grew slower in the absence of B-cells, indicating a tumor-promoting function in these models. These findings support a context-dependent role for B-cells: B-cells may either promote or inhibit tumor progression depending on the TME's immunogenicity and stromal structure. Future work includes flow cytometric analyses to define B-cell phenotypes in each model, investigation of additional "immune hot" tumor lines such as MC38, and experiments to alter CT26 immunogenicity (e.g., introducing various OVA constructs) to assess how antigen localization changes B-cell–mediated responses. Collectively, these studies aim to elucidate the mechanisms underlying B-cell plasticity in cancer and pave the way for more nuanced immunotherapeutic strategies targeting B-cells.

Metabolic regulation of HIF-1a by alpha-ketoglutarate in Acute Myeloid Leukemia

Srijan Oduru

Faculty Mentor: Matthew Hirschey

Authors: Srijan Oduru, Derek Zachman, Matthew Hirschey

Discipline: Biological and Biomedical Sciences

Abstract:
Hypoxia-inducible factor 1-alpha (HIF-1a) transcriptionally drives cancer progression by adapting tumor cells to hypoxic environments. In acute myeloid leukemia (AML), HIF-1a dysregulation promotes angiogenesis, tumor development, and therapeutic resistance. Alpha-ketoglutarate (aKG), a central metabolite of the TCA cycle, influences HIF-1a stability through prolyl hydroxylase domain (PHD) enzymes, which mark HIF-1a for degradation. Given the importance of HIF-1a in AML progression, we aim to delineate how the aKG-HIF-1a axis regulates AML biology. We investigated this by treating AML cells with aKG analogs and assessing HIF-1a protein stabilization and cell viability. We confirmed HIF-1a activity via qPCR of response genes. We then performed regression analyses on AML metabolite and gene marker data from the Cancer Cell Line Encyclopedia to identify potential molecular mediators. Our preliminary data show that the aKG analog dimethyl ketoglutarate (DMKG) exerts markedly distinct effects on HIF-1a stabilization and cell viability across AML models. Some AML cell lines are highly sensitive to HIF-1a targeting, while others show resistance. PDK1, a key HIF-1a target, was induced only in DMKG-sensitive AML cell lines. Regression analyses revealed distinct gene and metabolite signatures between sensitive and resistant cells, highlighting transcription factors like HAND2, a known regulator of angiogenesis, and others involved in cell cycle regulation. Our findings suggest that molecular heterogeneity shapes aKG-HIF-1a axis regulation in AML. We will further probe this mechanism by integrating biochemical assays and metabolomics to map metabolic dependencies that distinguish DMKG-sensitive from resistant AML subtypes. We are also performing thermal proteome profiling of aKG-binding partners to understand the protein-level interactions mediating DMKG's effects. Our research aims to characterize the metabolic landscape and molecular drivers underlying HIF-1a regulation. These findings could provide insights into AML's metabolic heterogeneity and offer new approaches for targeting HIF-1a-driven tumor progression in AML and cancers broadly.

Tracing Water Transport Over Time With Deep Sapwood and Heartwood Isotopic Breakthrough Curves

Chibuike Okafor

Faculty Mentor: Ryan Emanuel

Authors: Chibuike Okafor, Ryan Emanuel, Kevan Minick, Jennie Bahramian, Natalie Locklear

Discipline: Biological and Biomedical Sciences

Abstract:
Analysis of vertical and horizontal water transport in plants has been widely explored to comprehend the mechanisms of water movements within trees. Within forest ecosystems, water storage and movement are vital biomechanical and hydrological processes in soil and plants, especially for plant water uptake. Despite the importance of these water regulation mechanisms within forests and their ecosystems, an understanding of the distribution and transport of water storage in trees over time has not yet been thoroughly examined. To investigate the movement of water within a tree over time, deuterated (2H or deuterium) water was injected as an isotopic tracer into the base (0.5 m from the soil height) of a mature loblolly pine tree at the Duke Forest. Wood cores from borehole heights of 2 m, 7.55 m, and 13.1 m were collected over a 23-day period. We processed concentrations of the 2H deuterium tracer with the Picarro 2120-I laser water isotope analyzer, which tracked the concentrations prior to and after the injections at the three varying borehole heights between the deep sapwood and heartwood layers within the tree. In the loblolly pine tree, within one to four days after the deuterium injection, we observed 2H deuterium enrichment levels above pre-injection measures across the lower, middle, and upper borehole levels of the tree in the deep sapwood and heartwood layers. We observed peak 2H concentrations in the deep sapwood in the middle and upper borehole levels and, primarily, in the middle borehole level in the heartwood layer of the core. This work can inform forest hydrologists and researchers on valuable water movement dynamics and processes.

PD-L1 Overexpression Mitigates CD8+ T Cell-Mediated Cytotoxicity in Mammary Cancer Cells

Sushrit Pasumarthy

Faculty Mentor: Zachary Hartman

Authors: Sushrit Pasumarthy, Jason McBane (BS), Krish Dewan (MD), Dawn Bowles (PhD), and Zachary Hartman (PhD)

Discipline: Biological and Biomedical Sciences

Abstract:
Solid organ transplant recipients are required to take systemic immunosuppressive medication for the rest of their life; this leaves them with significant morbidity associated with a chronically immunocompromised state including infections, kidney toxicity, and cancer. Local overexpression of programmed death-ligand 1 (PD-L1) on allografts offers a promising solution to this problem by leveraging its natural immunosuppressive role in the PD-L1/PD-1 CD8+ cytotoxic T cell pathway. This study models the PD-L1/PD-1 CD8+ cytotoxic T cell pathway using an immunogenic mammary cancer model in order to evaluate the utility of PD-L1 overexpression in preventing immune rejection after transplantation. To assess immune tolerance conferred by PD-L1 overexpression, we conducted a CD8+ cytotoxic T cell killing assay using immunogenic E0771 mammary cancer cell lines. Each line was engineered to express luciferase as a reporter alongside ovalbumin (mOVA) to serve as a model antigen. The experimental groups included E0771 cells overexpressing three distinct PD-L1 constructs: (1) full-length PD-L1 (PD-L1 FL); (2) transmembrane-only PD-L1 (PD-L1 TM); and (3) serum-soluble PD-L1 (PD-L1 SS). E0771 cells without mOVA and SIINFEKL-expressing cells served as negative and positive controls for killing, respectively. OT1 splenocytes were co-cultured with target cells at varying effector-to-target (T cell: cancer cell) ratios, and cell viability was measured via luminescence. Overall, PD-L1 overexpression significantly reduced OT1-mediated cytotoxicity. As effector-to-target ratio decreases from 40:1 to 0, the viability of all PD-L1 over-expressing cells consistently recovered to baseline compared to positive controls without PD-L1. PD-L1 TM regained baseline viability at the highest effector-to-target ratio, followed by PD-L1 SS and PD-L1 FL. At a 20:1 effector-to-target ratio, PD-L1 TM regained baseline viability and proved much more viable than the positive control (p < 0.0001). These findings highlight the immunosuppressive potential of PD-L1 overexpression as an immunotherapeutic for transplanted organs.

Differential Effects of BMP13 on Adult and Juvenile Cartilage

Pranav Rastogi

Faculty Mentor: Amy McNulty

Authors: Pranav Rastogi, Vianna Martinez, Amy L. McNulty

Discipline: Biological and Biomedical Sciences

Abstract:
Introduction: Articular cartilage plays a critical role in joint function, yet its repair capacity declines with age, contributing to osteoarthritis. Growth factors can drive extracellular matrix (ECM) repair following injury; however, Bone Morphogenetic Proteins (BMPs) show both beneficial and harmful effects on cartilage homeostasis. Our lab identified BMP13 as a potential modulator of ECM production and tissue repair with age-dependent effects. However, BMP13 is a relatively understudied growth factor in cartilage, thus we aim to determine the age-dependent role of BMP13 in cartilage health. We hypothesize that BMP13 promotes catabolism in adult tissue and a reparative environment in juvenile tissue. Methods: RNA sequencing: 5mm explants were cultured in 0 or 800 ng/mL BMP13 for 3 days before RNA isolation and RNA-seq analysis. Histology and cell viability: 5mm explants were taken from adult and juvenile pig femoral cartilage and a 3mm center core was removed and re-inserted in the correct orientation to form a cartilage repair model. Explants were cultured in 0 or 800 ng/mL BMP13 for 28 days. At days 14 and 28, explants were either Live/Dead-stained for cell viability or fixed in 10% formalin, paraffin-embedded, and stained for ECM (Safranin-O for proteoglycans, Fast-green for collagen, and Hematoxylin for nuclei) for histological analysis. Biochem: Cartilage repair model explants were papain-digested on day 28 for DNA content analysis. Results and Discussion: RNA-seq results indicated that BMP13 induces proinflammatory effects in both juvenile and adult cartilage. Both groups showed increased expression of ECM-degrading matrix metalloproteinases (MMPs) and the inflammatory mediator nitric oxide synthase 2 (NOS2). Inflammation and MMPs play essential roles in normal healing and tissue remodeling; however, if dysregulated may promote tissue catabolism. Differential effects of BMP13 on cartilage repair were revealed through histological staining of cartilage ECM where adult tissue showed reduced proteoglycan content, while juvenile cartilage retained a robust ECM. Additionally, live-dead staining and tissue DNA indicated that cell viability was reduced in adult but not juvenile cartilage after 28 days of BMP13 exposure. Overall, although BMP13 increases inflammatory effects in both age groups, histological analysis suggests BMP13 degrades cartilage ECM in adult cartilage while juvenile cartilage resists these effects.

GRK2 and Sirtuin 3: Uncovering a Novel Protein-Protein Interaction Mediated by S-nitrosylation

Hailey Rodriguez

Faculty Mentor: Walter Koch

Authors: Hailey Rodriguez, Thiele Osvaldt Rosales, Samuel Slone, Stephanie Kereliuk, Rajika Roy, Walter J Koch

Discipline: Biological and Biomedical Sciences

Abstract:
Heart disease remains one of the leading causes of death globally, claiming millions of lives and incurring billions in costs annually. G protein-coupled receptor kinase 2 (GRK2), a key regulator of cardiac signaling, plays a crucial role in heart failure, with its increased expression and activity linked to impaired cardiac contractility. Although GRK2's primary function is to phosphorylate activated GPCRs, marking them for downregulation, it also interacts with several non-GPCR targets. Furthermore, GRK2 is subject to S-nitrosylation—a nitric oxide (NO)-mediated modification at cysteine residues—that can influence protein function, interactions, trafficking, and degradation. While S-nitrosylation at the Cys340 site inhibits GRK2's kinase activity, its impact on the non-canonical functions of GRK2 remains largely unexplored. This study investigates how GRK2's interactome may change following S-nitrosylation. To identify GRK2-interacting proteins, we employed Biotin Proximity Labeling and Mass Spectrometry assays in human cardiomyocyte cells (AC16) and neonatal rat ventricular myocytes (NRVMs) under NO treatment. Preliminary findings revealed basal interactions between GRK2 and several mitochondrial proteins, including sirtuin 3 (SIRT3), a cardioprotective mitochondrial lysine deacetylase. Notably, the GRK2-SIRT3 interaction was significantly reduced following NO donor treatment in AC16s. Further validation using immunoprecipitation assays confirmed this interaction in AC16s, NRVMs, and the mitochondrial fraction of mouse cardiac lysates. Additionally, a Split Luciferase assay monitored real-time GRK2-SIRT3 interactions post-NO donor treatment. Elucidating these interactions may provide new insights for developing cardioprotective therapies.

Engineered Multichannel Biomimetic (T-LAB) of the Tumor-Lymphatic Architecture

Natalia Roman

Faculty Mentor: Gayathri Devi

Authors: Natalia Roman, Caroline Way, Ralph Erdmann, Pritha Pai, Gayathri Devi

Discipline: Biological and Biomedical Sciences

Abstract:
Background: Emerging evidence in diverse tumor types establishes a link between lymphatic dissemination and collective tumor cell invasion. However, interactions between malignant, oncogenic cells and the lymphatic system remain poorly defined due to the complexity of molecular alterations and the various components of the tumor microenvironment. To simulate the biomechanical features of the tumor-lymphatic microenvironment, we developed a 3D tumor-lymphatic architecture biomimetic (T-LAB) platform, with iterations capable of supporting either a single cell culture or multiple in parallel. Methods: Mathematical and computational fluid dynamics modeling were used to determine the fluid flow, oscillatory flow-induced sheer stress, and system pressure in the 3D-printed macrofluidics platform. The multichannel, high throughput iteration of the T-LAB was supported by an in-house, custom built peristaltic pump with design of hardware, software, and casing. Hardware electronically connected the pump motor to a microcontroller, where various rates of flow were programmed via an original C++ script. Pump casing and circuitry housing were developed and refined using computer aided design (CAD) and 3D printed. Various human breast cancer cell lines and human dermal lymphatic endothelial cells (HDLEC) were seeded on a matrix in the T-LAB and imaged for up to 96h to assess cell morphology, viability, migration, and invasion. Results: Co-culture of inflammatory breast cancer cells with HDLEC in the T-LAB, determined to simulate the fluidic properties of the tumor lymphatic microenvironment, demonstrated tumor cell clusters/emboli formation and collective invasion similar to the clinicopathological features observed in patients. Conclusions: The 3D T-LAB model developed here can be used to culture any type of tumor cell to study topographical features that impact tumor-lymphatic interface, collective invasion, and lymphatic dissemination. The high throughput platform expands on the quality and efficiency of the study by decreasing discrepancy between cultures and optimizing time and space.

Screening for Dorsal Closure Genes on the 3R Chromosome of Drosophila melanogaster

Nawra Roya

Faculty Mentor: Daniel Kiehart

Authors: Nawra Roya, Ainsley Shan, Melissa Sican, Daniel Kiehart

Discipline: Biological and Biomedical Sciences

Abstract:
Dorsal closure is a crucial stage in cell sheet morphogenesis in Drosophila melanogaster that involves the coordinated movement of lateral epidermal cells to close a gap filled by squamous amnioserosa cells on the dorsal side of the embryo. This process serves as a model for studying tissue movement in vertebrates, including gastrulation, neural tube formation, and wound healing. The Kiehart lab has been screening genes on the right arm of D. melanogaster's third chromosome using genetic and live imaging techniques to analyze potential impacts of deficiencies, deleted chromosomal regions that encode for genes. This approach aims to identify genes involved in dorsal closure. My research has focused on the genetic regions deleted encompassed by adjacent deficiencies Df(3R)09,10, 80, 82, and 86 from the Bloomington Deficiency Kit. Stocks from these deficiencies are crossed multiple times with an imaging line, containing fluorescent markers and a balancer chromosome, to obtain the desired genotype for imaging. Imaging of Df(3R)09/Df(3R)10 transheterozygotes, carrying both alleles for each respective deficiency, revealed similar phenotypes to their homozygous counterparts, including abnormal dorsal openings and amnioserosa tearing, often leading to closure failure. Notable genes removed by these deficiencies include CG2082, CG2104, CG10979, degringolade, pollux, Rab23, and Sec8, which are implicated in cadherin binding, cytoskeleton dynamics, cell adhesion, and epithelial morphogenesis. Df(3R)86 exhibited mild dorsal closure defects, such as delayed posterior canthus formation and a cigar-shaped dorsal opening. A notable gene in this region is GP93, which is highly expressed during dorsal closure. Df(3R)80 displayed a jagged purse-string phenotype and delayed posterior canthus formation, resulting in tearing at the lateral epidermis-amnioserosa interface. Potential genes of interest here include Jigr1, Npl4, and Ssadh. While Df(3R)80 and Df(3R)86 phenotypes were not detrimental to dorsal closure. Df(3R)82 resulted in severe tearing of the amnioserosa causing dorsal closure failure, suggesting a potential pre-dorsal closure defect. I propose screening sub-deficiencies in each region to refine genetic regions of interest. Further investigation of Df(3R)09, 10, 80, 82, and 86 aims to identify and elucidate the roles of key dorsal closure genes on chromosome 3R in D. melanogaster.

Human Piezo1 and Piezo2 Single Channel Conductance is Modulated by Alternative Splicing

William Sharp

Faculty Mentor: Jorg Grandl

Authors: William Sharp, Michael Sindoni, Jorg Grandl

Discipline: Biological and Biomedical Sciences

Abstract:
Piezo2 is a mechanosensitive ion channel responsible for many sensational experiences including proprioception and light touch sensitivity. Human Piezo2 has 6 alternatively spliced exons, producing various isoforms with tissue-specific expression differences. However, the effect of alternative splicing in human Piezo2 on intrinsic channel properties remains undiscovered.
To address this, I first analyzed electrophysiological data collected in my lab measuring the sensitivity of human Piezo2 isoforms to membrane tension, the physical stimulus these ion channels sense. My analysis showed human Piezo1, human Piezo2, and isoforms of human Piezo2 differ in their sensitivity to membrane tension, suggesting that alternative splicing may control mechanosensing by human Piezo2.
Second, I focused on the single channel conductance of human Piezo2 isoforms. Piezo2 has a high level of structural homology compared to Piezo1. The only splice variant of mouse Piezo1, mouse Piezo1.1, lacks amino acids known to form a structure that plugs the pore, thereby modifying its single channel conductance. Since an alternatively spliced exon in Piezo2, exon 33, corresponds to the same amino acids absent in mouse Piezo1.1, I asked if exon 33 in human Piezo2 affects single channel conductance. Through cell-attached patch-clamp electrophysiology, I recorded single channel opening events. I found that a construct lacking all exons (Piezo2Min) has a significantly greater single channel conductance (g = 32.1 ± 3.6 pS) than a construct containing all exons (Piezo2Max) (g = 20.4 ± 2.2 pS). These results indicate that alternative splicing in human Piezo2 modifies single channel conductance in addition to tension sensitivity. My current focus is on investigating the necessity and sufficiency of exon 33 in determining single channel conductance of human Piezo2.
These findings indicate that alternative splicing in human Piezo2 is a mechanism of modulation for intrinsic channel properties and is utilized physiologically to meet tissue-specific mechanosensing and channel conductance needs.

From Hypothetical to Functional: Characterizing Two Related Mannoproteins in Cryptococcus neoformans.

Jaqueline Villanueva Govea

Faculty Mentor: Jennifer Tenor

Authors: Jaqueline Villanueva Govea, Jennifer L. Tenor, Dena L. Toffaletti, and John R. Perfect

Discipline: Biological and Biomedical Sciences

Abstract:
Cryptococcus neoformans is the causative agent of cryptococcal meningoencephalitis, an infection that leads to brain inflammation and meninges. A defining feature of C. neoformans is its extracellular capsule, consisting of polysaccharides, proteins, and other molecules that protect the yeast from environmental stresses and bodily immune defenses. Mannoproteins are examples of glycoproteins also found in the capsule. Mannoproteins in C. neoformans can be immunogenic and stimulate the host's immune protection. Little is known about how mannoproteins contribute to the virulence and survival of C. neoformans in vivo. Our previous transcriptomic work on Cryptococcus gene expression in human cerebral spinal fluid (CSF) has identified several genes encoding mannoproteins with a high abundance of transcripts. This study focuses on two predicted glycosylphosphatidylinositol (GPI)-anchored mannoproteins, CNAG_05424 and CNAG_01272, which are likely paralogs. Strains carrying a single or double gene deletion were constructed to aid in the characterization of these genes in C. neoformans. First, plasmids were constructed to facilitate the deletion of the genes at their native site. Next, sgRNA was designed to allow us to use the CRISPR-CAS9 strategy to construct the deletion strain. We successfully deleted single and double deletion strains lacking CNAG_01272 and CNAG_05424. A CNAG_05424 deletion strains was tested in a mouse inhalation cryptococcosis model to assess its role in virulence. The fungal burden was reduced in mice infected lacking CNAG_05424 compared to the wild type strain (H99). Phenotypic characterization of these strains revealed changes in stress resistance, as observed by reduced colony growth size under stress conditions. These results provide strong evidence that supports the conclusion that CNAG_05424 contributes to fungal survival and host-pathogen interaction. We demonstrate that these previously uncharacterized mannoproteins significantly affect Cryptococcus virulence, further advancing our understanding of genes that contribute to the pathogenesis of Cryptococcus.

Neural Encoding of Vocal Variability in Zebra Finch Song Learning

Huiwen Wang

Faculty Mentor: John Pearson

Authors: Huiwen Wang, Miles Martinez, Jiaxuan Qi, Richard Mooney, John Pearson

Discipline: Biological and Biomedical Sciences

Abstract:
Humans learn many motor skills, including vocal learning, through reinforcement learning (RL), a trial-and-error process of gradual adjustment that seeks to maximize reward. While RL typically relies on external rewards, some key behaviors, such as speech, music, or sports, are acquired in the absence of this feedback. Like humans, juvenile male zebra finches learn their vocalizations from an adult male tutor, then refine their song based on practice and feedback. In particular, medium spiny neurons in a song-specialized region of the basal ganglia (sBG) are hypothesized to play a crucial role in this process, shaping the variability introduced into song. However, it is unknown how spiny neuron activity contributes to song variability during song learning . To determine the relationship between spiny neuron activity and juvenile song development, we analyzed data from one-photon calcium fluorescence imaging of sBG neurons obtained while juvenile zebra finches practiced their songs. We find a significant relationship between neural activity in these neurons and acoustic features of the song such as amplitude, pitch, and entropy, even when controlling for the effects of other acoustic features using partial cross-correlations. In a separate analysis, LASSO regression models trained to predict song features from deconvolved calcium fluorescence reveal moderate predictive power of neural activity in predicting several song features. Our recorded population of neurons accounts for a similar proportion of the variance in acoustic features across days, indicating that, on a population level, neural activity in sBG is reflective of song variability. These data are thus consistent with the hypothesis that sBG, in conjunction with other regions in the learning circuit, encodes vocal variability over the course of juvenile learning.

A Genetic Tool to Investigate the Persistent Activation of CCR7 by CCL21

Ura Zhang

Faculty Mentor: Laura Wingler

Authors: Ura Zhang, Pooja Sridhar, Laura Wingler

Discipline: Biological and Biomedical Sciences

Abstract:
CC-chemokine receptor 7 (CCR7) is a class A G-Protein Coupled Receptor (GPCR). It is essential for the homing of naive T cells and dendritic cells (DCs) from peripheral tissues to lymphoid tissues. Chemokine (C–C motif) ligands 19 (CCL19) and 21 (CCL21) are the two endogenous CCR7 ligands and have distinct signaling profiles through this receptor in multiple cell types. Upregulation of CCR7 and CCL21 can contribute to the pathogenesis of both autoimmune disease and cancer. Prolonged stimulation of GPCRs by ligands can lead to overactivation of downstream signaling or, alternatively, to receptor desensitization and downregulation. This study will investigate the impact of persistent activation of CCR7 by CCL21. To accomplish this, we will genetically fuse the CCL21 ligand onto CCR7. Using PCR-based methods, we fused the CCL21 gene to the N terminus of CCR7 and tagged the C terminus of the receptor with a strepII tag for detection. We then generated a stable HEK293 suspension cell line expressing the CCL21-CCR7 fusion protein and used flow cytometry to compare its expression level with that of wild-type CCR7. G protein activation and beta-arrestin recruitment by the wild-type CCR7 without CCL21, wild-type CCR7 with CCL21, and CCL21-CCR7 fusion protein will be assessed using bioluminescence resonance energy transfer (BRET) and split luciferase complementation assay (SLC), respectively, to quantify the impact of fusing CCL21 to CCR7 on its signaling profiles. Given the stability and consistent receptor-ligand stoichiometry afforded by the fusion protein, the characterization of the CCL21-CCR7 fusion protein can potentially provide insights into CCR7 pharmacology and its therapeutic value in diseas

PHYSICAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

Exploration of the Effect of Noise on Entanglement within Finite-dimensional Qubit-Systems

Matthew Chen

Faculty Mentor: Natalie Klco

Authors: Matthew Chen, Natalie Klco

Discipline: Physical Sciences

Abstract:
The field of quantum information and quantum computing has recently experienced a surge in interest due to experimental progress towards the anticipated usefulness of quantum computers to accomplish tasks that classical computers are unable to solve in reasonable time. The current era of quantum computing has been described as the Noisy-Intermediate Scale Quantum Era (NISQ). In other words, quantum devices are currently extremely susceptible to "noise" or error processes that destroy quantum information and reduce advantages of quantum computation over classical computation. Such advantages rely upon an important quantum resource known as entanglement. In general, noise decreases the amount of entanglement in a qubit system. Therefore, this study will examine the effect of noise on entanglement properties in various dimensional qubit systems, using a specific measure known as Negativity and its spectrum. In this study, we will combine numerical and analytic methods to derive expressions characterizing the amount of entanglement left in a qubit system under the effects of a variety of noise channels. For entanglement in many-body contexts, we will focus on even-number qubit systems with bipartite divisions.

Synthesis of 15N2-diazirine probes for in vivo HP-MR imaging of human biological pathways

Mayah Ding

Faculty Mentor: Qiu Wang

Authors: Mayah Ding, Eni Minerali, Qiu Wang

Discipline: Physical Sciences

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. Existing probes for amino acid metabolism rely on different imaging techniques including PET, SPECT, fluorescence, MSI, and MRS, which lack sensitivity or stability for practical use. This work addresses these shortcomings through synthesizing novel 15N2-diazirine tagged amino acid probes, with a focus on glutamine and methionine. These probes can be hyperpolarized using dissolution dynamic nuclear polarization (d-DNP), providing a highly sensitive, non-invasive approach to visualizing metabolites in vivo over longer periods of time. Successful synthesis of these probes will provide promising new strategies for better cancer imaging, expanding the imaging toolbox for clinical research.

Control of Oxygen Vacancy in Manganite Heterostructures by Ionic Liquid Gating

Lang Ji

Faculty Mentor: Divine Kumah

Authors: Lang Ji, Divine Kumah

Discipline: Physical Sciences

Abstract:
We study the impact of ionic liquid gating (ILG) on the structural and transport properties of ultrathin $LaSrMnO_3$(LSMO) films grown on $LaAlO_3$ via molecular beam epitaxy. X-ray diffraction (XRD) and temperature-dependent transport measurements reveal that positive gate bias increases resistivity and induces oxygen vacancies in compressively strained films. Additionally, ILG enables reversible modulation of transport and magnetic properties, linked to oxygen vacancies and carrier concentration changes.

Simulation based R&D for a Iron-Scintillator Sandwich Calorimeter

Rowan Kelleher

Faculty Mentor: Anselm Vossen

Authors: Rowan Kelleher, Anselm Vossen

Discipline: Physical Sciences

Abstract:
An iron-scintillator sandwich calorimeter is being developed for inclusion as part of a second detector at the upcoming Electron-Ion Collider. The detector would provide excellent muon and neutral particle identification through the use of time of flight information collected by the calorimeter. The timing information would also enable energy reconstruction and longitudinal segmentation.
The present study focuses on the optimization of these aspects of the detector. Detector simulations are accomplished with the DD4HEP framework, utilizing GEANT4. Generative AI is used to implement a fast timing parameterization to allow for simulating particle detection without the simulation of tens of thousands optical photons. Machine learning techniques are utilized to identify particles and predict energy. Multi-Objective Bayesian Optimization is performed to identify the detector parameters that maximize energy resolution and particle identification accuracy.

Measuring the Thermal Sunyaev-Zel'dovich Effect in Galaxy Clusters with ACT

Gavin Ockert

Faculty Mentor: Eve Vavagiakis

Authors: Gavin Ockert, Jenna Moore, Eve Vavagiakis

Discipline: Physical Sciences

Abstract:
This study analyzed temperature data from the Atacama Cosmology Telescope (ACT) to measure the thermal Sunyaev-Zel'dovich (tSZ) effect, which is an influence on the cosmic microwave background (CMB) due to interactions between CMB photons and energetic electrons, like those in galaxies and galaxy clusters. Using Python, we adapted existing submap processing tools to take tSZ aperture photometry measurements of known galaxy clusters, which involves a subtraction of background image noise to better approximate the tSZ signal of a large celestial object. We then performed a stacking analysis across many different galaxies. Our model considered and accounted for potentially confounding variables, including dust.

Accurate aperture photometry readings can provide important information about galaxies' physical properties. The resulting tSZ analysis pipeline will lay the groundwork for future analysis of data from projects prioritizing cosmology research, such as the Simons Observatory and Cerro Chajnantor Atacama Telescope (CCAT) Observatory.

Dialing It In: Tradeoff Between High Yield and Low Slippage in Electron Bifurcation

Emily Wang

Faculty Mentor: David Beratan

Authors: Emily Y. Wang, Kelsey A. Parker, Kiriko Terai, Andrew J. Smith, David N. Beratan

Discipline: Physical Sciences

Abstract:
Nature has evolved precise molecular mechanisms to accomplish energy transduction at very low thermodynamic cost by driving an energetically unfavorable reaction at the expense of an energetically favorable reaction. One of these mechanisms is electron bifurcation (EB), a process where an enzyme receives two electrons from a redox donor substrate and sends one electron to a high-potential acceptor substrate and the other to a low-potential acceptor substrate. Design principles of EB are of interest for motivating the development of bio-inspired technologies that accomplish energetically unfavorable reactions with high thermodynamic efficiency. The ideal EB scheme produces high bifurcation yield with low electron slippage. An EB network's redox energy landscape is a key determinant of electron transport kinetics and a bifurcator's steady state behavior. In this study, we use master equation kinetics to simulate EB in a simple physical model. We investigate how an EB network's redox energy landscape can be tuned for the essential EB features of low slippage and high bifurcation yield. Our theoretical study reveals a tradeoff between the low slippage and high yield bifurcation regimes. Moreover, we find that the terminal cofactor on the high potential bifurcation branch controls the relative amount of high yield versus low slippage in an EB design. These findings could inform the design of artificial bifurcators and future studies of EB mechanisms present in nature.

QUANTITATIVE SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

ChatGPT in Network Meta-Analyses: Prompt Engineering Strategies for Automating Data Extraction

Hyunjin Lee

Faculty Mentor: Hwanhee Hong

Authors: Hyunjin Lee, Hwanhee Hong

Discipline: Quantitative Sciences

Abstract:
Network meta-analyses (NMAs) are crucial for synthesizing evidence from multiple studies but remain time- and labor-intensive due to the manual extraction of outcome data. Large language models (LLMs) offer an opportunity to streamline this process, though verifying response accuracy remains a barrier to reliable integration. In this study, we tested prompt engineering strategies using ChatGPT-4o to automate data extraction from randomized controlled trials (RCTs), providing concrete examples and error analyses. As a case study, we replicated the NMA by Hong et al. (2023) on hydroxychloroquine (HCQ) as pre-exposure prophylaxis for COVID-19. The 10 RCTs selected featured standardized outcome reporting and relevance to recent COVID-19-related NMAs, offering a consistent test case. For each trial, we extracted the sample size (N), confirmed COVID-19 cases, and adverse events for HCQ and placebo groups. We tested zero-shot and few-shot prompting across multiple versions with fine-tuning. Few-shot prompting included providing an example RCT and outcome table; zero-shot included none. Fine-tuning involved feedback loops in which ChatGPT was prompted to justify and revise incorrect outputs. Additional strategies included assigning roles to guide the tone, adjusting temperature to control randomness, and using ChatGPT to edit prompts for improved comprehension. For complex cases, we explored whether asking ChatGPT to recreate figures (e.g., CONSORT diagrams) improved accuracy. Descriptive analysis showed inaccuracies generally decreased when transitioning from zero-shot to few-shot and from manual to ChatGPT-assisted fine-tuning. The most accurate version successfully extracted 80% of data points. Common errors included reporting initial instead of final sample sizes and failing to extract data from tables or figures. Our results suggest ChatGPT can extract most requested data with moderate accuracy when combined with structured prompting and validation. While not fully autonomous, it may accelerate early NMA stages and reduce manual burden. Future work includes applying this framework to larger NMAs across diverse clinical topics and exploring OpenAI's application programming interface (API), which allows software to interact directly with ChatGPT, to further automate the process. To assess whether 80% accuracy is sufficient, we are re-running the case study NMA using extracted data to evaluate whether our workflow can replicate results from traditional methods.

Our AI Overlords: Can LLM-driven agents accurately simulate US senators?

Kulsoom Rizavi

Faculty Mentor: David Siegel

Authors: Kulsoom Rizavi

Discipline: Quantitative Sciences

Abstract:
Political scientists have long employed quantitative methods to model legislative decision-making, but recent advancements in Large Language Models (LLMs) have opened new possibilities for simulating complex political behavior. This study examines the potential of LLMs to replicate human decision-making in the context of the US Senate, utilizing a multi-agent framework to simulate the behavior of 100 LLM agents representing the 118th US Senate. The agents vote on real-world bills after engaging in two rounds of discussion, with simulated outcomes compared to actual legislative results to assess accuracy. By expanding upon the foundational work of Baker and Azher (2024), who first demonstrated the potential of LLMs for simulating believable government action, this research introduces a more complex silicon simulation with a larger number of agents and focuses on vote outcomes rather than just text-based debate. The findings hold potential implications for the usage of autonomous agents in decision-making and the development of AI-driven simulations in social sciences.

Functional Connectomes of Neural Networks

Yutong Wu

Faculty Mentor: Tananun Songdechakraiwut

Authors: Yutong Wu, Tananun Songdechakraiwut

Discipline: Quantitative Sciences

Abstract:
The human brain is a complex system, and understanding its mechanisms has been a long-standing challenge in neuroscience. The study of the functional connectome, which maps the functional connections between different brain regions, has provided valuable insights through various advanced analysis techniques developed over the years. Similarly, neural networks, inspired by the brain's architecture, have achieved notable success in diverse applications but are often noted for their lack of interpretability. In this paper, we propose a novel approach that bridges neural networks and human brain functions by leveraging brain-inspired techniques. Our approach, grounded in the insights from the functional connectome, offers scalable ways to characterize topology of large neural networks using stable statistical and machine learning techniques. Our empirical analysis demonstrates its capability to enhance the interpretability of neural networks, providing a deeper understanding of their underlying mechanisms.

SOCIAL SCIENCES

Presenters are organized by discipline and then alphabetically by last name.

Opioid Settlement Spending Across North Carolina: Which families are best served?

Chloe Decker

Faculty Mentor: Beth Gifford

Authors: Chloe Decker, Beth Gifford

Discipline: Social Sciences

Abstract:
Background & Hypothesis: North Carolina received $1.5 billion from the national opioid settlements, with 85
percent of this funding being distributed among the state's 100 counties. Each county must create its own
spending plan, choosing between Option A or Option B funding strategies. Option B allows for counties to allocate funds for child- and family-focused preventative interventions. However, Option B requires counties to engage in a comprehensive strategic engagement process before receiving funds. Of the 81 spending plans submitted so far, only four counties have allocated Option B funds to preventative interventions that support children and mothers. The low uptake of Option B funding strategies is alarming considering the disproportionate negative impacts of the opioid epidemic on North Carolina families. I hypothesize that the burden of meeting the requirements of Option B's strategic engagement process prevented many county governments from pursuing it as a viable option. As a result, counties failed to fund child- and family-focused preventative interventions. Objective: I aim to identify facilitators and barriers that have impacted county usage of Option B funding strategies, particularly for child- and family-focused interventions. Methods: I conducted qualitative semi-structured interviews with stakeholders in six counties across North Carolina. Through these interviews, I identified similarities, differences, and recommendations. Results: My research is still in progress, and I will have reportable results soon. I expect them to align with my original hypothesis, highlighting how Option B's required "strategic engagement process" has prevented counties from funding child- and family-focused interventions. Conclusions: I anticipate that my research will reveal stakeholder perspectives on the local decision-making process, early impacts, and tiered funding structure of North Carolina's opioid settlements.

Improving College Student Survey Response Rates: A Case Study at Duke University

Antonio Drakes

Faculty Mentor: Peter Arcidiacono

Authors: Antonio Drakes, Julie Bennett, Peter Arcidiacono

Discipline: Social Sciences

Abstract:
Over the past twenty-five years, survey response rates among U.S. college students have declined. This poses significant issues for higher education research. In this paper, we describe a study that utilizes a peer-to-peer in-person intercept survey methodology that yields a 96% response rate and a 95% completion rate. The study collects data on first year students at Duke University and their peer groups as defined by who they sit with in the first year dining hall. The survey contains questions related to the respondent's race, sex, socioeconomic status(SES), political beliefs, religious beliefs, and first-generation student status. We advocate that this method can be. The high-quality data collected in this study can be used to evaluate undergraduate peer group diversity along a variety of characteristics. We find that while undergraduate peer groups are relatively homophilous along readily observable characteristics such as gender and race, there exists meaningful heterogeneity among groups along social identity characteristics such as religion, politics and SES.

The Presence of Absence: Palimpsest and Identity in Hong Kong

Lucy Law

Faculty Mentor: Eileen Chow

Authors: Lucy Law, Eileen Chow

Discipline: Social Sciences

Abstract:
In this thesis, I approach Hong Kong through its palimpsestic layers, foregrounding the idea that physical markers of history and identity are constantly being re-formed, erased, and reborn in new forms. I argue that we might think of how Hong Kong's new identity is being silenced and erased through a new framework: that of transitional injustice, which I define as further injustice committed through a transition in sovereignty. According to the Sino-British Joint Declaration, Hong Kong's way of life was supposed to remain unchanged for fifty years following the 1997 Handover, but less than thirty years later, China has violated the treaty's terms. Because Hong Kong never underwent a process of transitional justice or decolonization, Hongkongers never had a discursive space to discuss and form their identity. I present a potential solution to these injustices: Hong Kong as method – the idea that Hong Kong should be allowed to define itself discursively, free from British colonial influence or mainland Chinese national influence. By examining manifestations of Hong Kong as method, such as the Tiananmen Incident vigils, 2019 Anti-Extradition movement, and a subversive bookstore, I trace Hongkongers' identity formation and mainland Chinese suppression in the contemporary era. Hong Kong identity is ephemeral, dynamic, and not only cultural but also historical and material. Many markers of Hong Kong identity have been erased recently; thus, it is vital to read evidence of their absence for meaning.

Childhood vaccination prevalence and perception in Roatán, Honduras

Madeline Morrison, Reena Kagan, Arya Kumar, and Grace Muriithi

Faculty Mentor: Dennis Clements

Authors: Madeline Morrison, Reena Kagan, Arya Kumar, Grace Muriithi, Dennis Clements

Discipline: Social Sciences

Abstract:
Childhood vaccination is a critical component of public health, yet adherence rates vary widely, especially in communities with limited access to healthcare. This program evaluation, conducted at the request of the non-profit Clinica Esperanza, focuses on the island of Roatán, Honduras. Vaccination coverage and beliefs were assessed among caretakers of children aged 11 years or younger. Door-to-door surveys and interviews were conducted with 436 participants across multiple communities to evaluate the prevalence of childhood vaccination, the utilization of vaccination resources, and the knowledge and beliefs of caretakers regarding vaccines. Additional data was gathered from patients in waiting areas of Clínica Esperanza. The surveys collected information on the children's vaccination status, the caretakers' perceptions of vaccines, and demographic factors, allowing for a comprehensive analysis of vaccination adherence and its determinants. Preliminary analysis revealed that overall vaccination rates were extremely high, with 14 out of the scheduled 21 (or 22 for females) vaccine doses having an uptake rate greater than 90%. However, significant disparities were noted for specific vaccines, such as Hepatitis A and the fourth Polio vaccine. Comparisons between La Colonia—a low-income, migrant community that had previously been recorded as having a disparity in vaccination rates—and non-Colonia communities showed comparable mean vaccination scores.

The Productivity Cost of Hearing Loss: A Systematic Review

Matthew Nuzzolo

Faculty Mentor: Matthew Nuzzolo

Authors: Matthew Nuzzolo; Coralei Neighbors, MSc; Ethan D. Borre, PhD; Connor Pratson; Anna Jilla; Kamaria Kaalund; Danah Younis; Gloria Zhang; Osondu Ogbuoji, MBBS, MPH, ScD; Gillian D. Sanders Schmidler, PhD

Discipline: Social Sciences

Abstract:
Hearing loss significantly impacts quality of life and overall health, but its effects on productivity costs, including economic productivity and workforce or educational participation, are substantial and quantifiable. This study aimed to systematically review and synthesize evidence on productivity costs associated with hearing loss across the lifespan in high-, middle-, and low-income countries. Comprehensive database searches were conducted in October 2020 and October 2023. Literature management and review were performed using DistillerSR. Abstracts and full-text articles were screened independently by at least two investigators, with a third reviewer adjudicating any discrepancies. Inclusion criteria required studies to be original quantitative investigations, report indirect economic outcomes, and address language or cognitive outcomes directly tied to educational attainment. Only English-language studies meeting these criteria were included. Data were systematically extracted, and quality indicators were assigned to included studies to ensure methodological rigor. Hearing loss was found to be associated with economic productivity loss as well as inhibition on education attainment and workforce participation. The evidence demonstrates that hearing loss imposes substantial indirect productivity costs across the lifespan, with the burden disproportionately affecting low- and middle-income countries. Early detection, access to assistive technologies, and inclusive educational and workplace policies may significantly mitigate these costs. Policymakers should prioritize interventions targeting hearing loss to reduce its economic impact and enhance workforce and educational outcomes globally. Future research should address gaps in longitudinal data and evaluate the cost-effectiveness of scalable interventions in diverse socioeconomic settings.

Reexamining the interpretation of English definite plurals by L1 Spanish speakers

Jose Orozco

Faculty Mentor: Yunchuan Chen

Authors: Jose Guadalupe Chavez Orozco Jr., Yunchuan Chen

Discipline: Social Sciences

Abstract:
In English, definite plurals like 'the tigers' can only have a definite interpretation, referring to a specific group, and not a generic one. For instance, in 'the tigers like eating meat at night,' 'the tigers' refers to a particular group of tigers, and cannot refer to tigers as a species. However, in Spanish, definite plurals such as los tigres can be either generic or definite. This study conducted a sentence-picture matching truth value judgment task to investigate whether L1 Spanish L2 English learners can acquire the knowledge that English prohibits generic interpretations for definite plurals. Twenty-two L1 Spanish L2 English learners were tested, with the LexTale English proficiency scores ranging from 56.25 to 98.75. Each participant was exposed to both English and Spanish lists. The results indicate that none of the participants knew this constraint in English, contradicting Ionin and Montrul's (2010) findings.

Uplifting Black Girls and Mothers: Multi-Layered Mentoring and Community Cultural Wealth

Reagan Razon

Faculty Mentor: Whitney McCoy

Authors: Reagan Razon, Whitney McCoy

Discipline: Social Sciences

Abstract:
Historically, Black girls in STEM education have faced structural barriers that hinder access to opportunities, affecting their participation in STEM curricula and career fields. Previous research has focused on factors contributing to the underrepresentation of Black girls and women in STEM disciplines. Our study explores the developing STEM identities of Black mothers and their influence on their daughters' socialization in informal settings. Developing STEM counterspaces fosters positive and culturally relevant STEM learning experiences for Black girls. InventHers Institute, developed by Dr. Whitney McCoy, uses a multi-layered mentoring model, providing mother-daughter dyads with hands-on engineering activities guided by equity ethic, building Black student STEM identity to support community empowerment. We conducted focus groups as counterspaces, empowering sites of community building and collective healing, with the young girls and their mothers, asking about STEM identity, perceptions of STEM, and the impact of specific programmatic elements. Our analytical approach was grounded in Community Cultural Wealth. This study presents preliminary findings from the semester-long program, seeking to understand, what are the impacts of a multi-layered STEM counterspace on participants' perceptions of STEM identity? By examining mother-daughter dynamics, our research focuses on the transformative potential of such environments in educational settings and broader societal contexts.

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