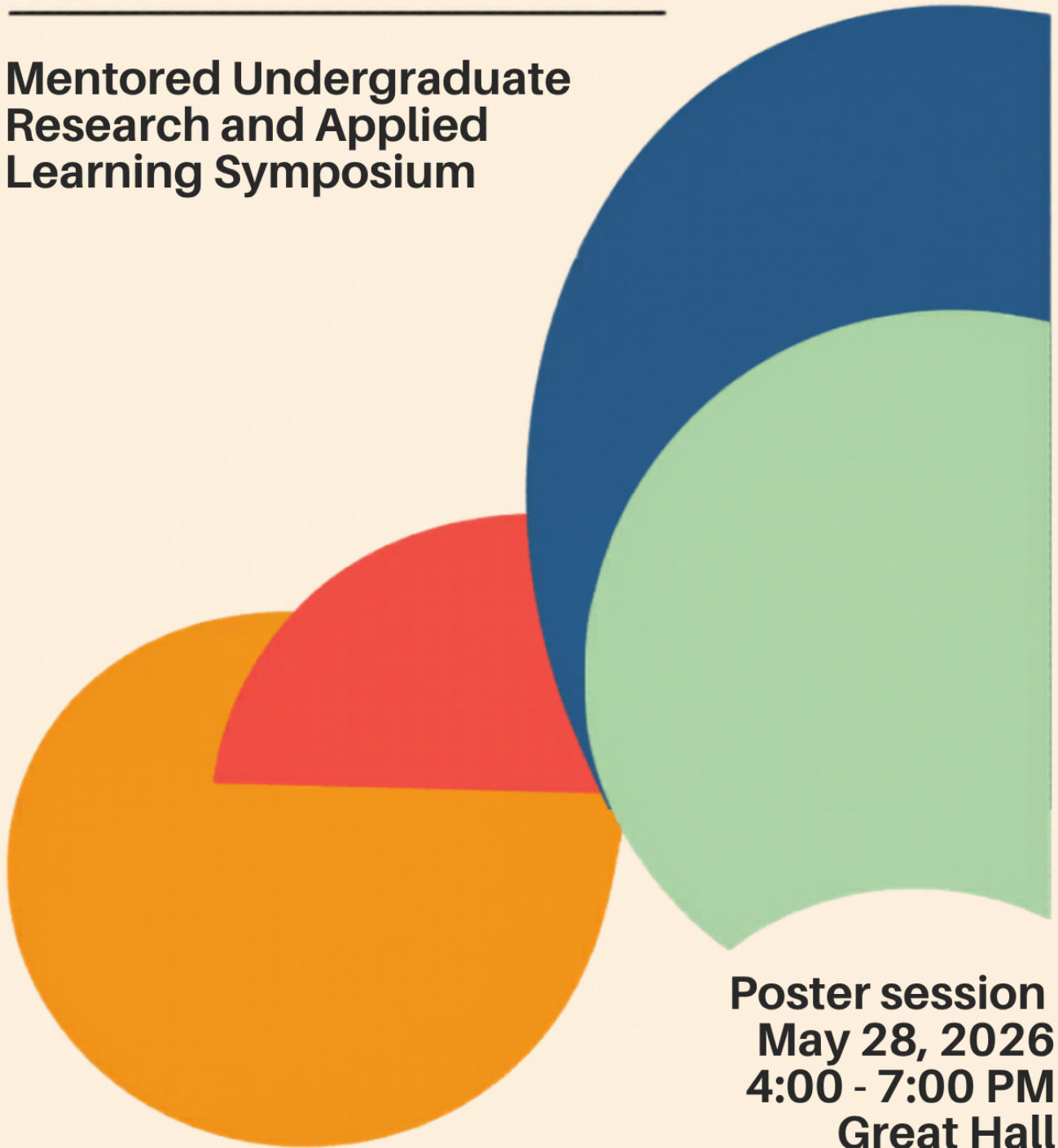


MURALS

**Mentored Undergraduate
Research and Applied
Learning Symposium**



**Poster session
May 28, 2026
4:00 - 7:00 PM
Great Hall**

Table of Contents

CONFERENCE SCHEDULE	3
OUTSTANDING MENTOR SPOTLIGHTS	4
ABSTRACTS	8

Conference Schedule

4:00 - 4:15 PM	Doors Open and Presenter Check-in
4:15 – 4:45 PM	Welcome & Outstanding Mentor Awards
4:50 – 5:45 PM	Session I
5:45 – 6:00 PM	Break
6:00 – 6:55 PM	Session II
6:55 – 7:00 PM	Thank You and Closing Remarks

Outstanding Mentors



Dr. Miranda Koloski

Dr. Miranda Koloski (co-law-ski) holds dual roles as Assistant Professor of Psychiatry at UCSD and Research Scientist at VASDHS. She completed her PhD in Psychology from the University of New Hampshire and went on to complete her postdoctoral training at UCSD supported by a T32 Fellowship in Biopsychiatry and Neuroscience. She

uses animal models of cognitive behavior to examine neural circuit impairments following traumatic brain injury or neuropsychiatric disorders. Her current research is supported by a VA Career Development Award and a BBRF Young Investigator Award. Miranda recognizes that scientific research is extremely collaborative, and she especially enjoys mentoring undergraduate researchers and helping them launch into their own scientific trajectories.



Dr. Lalit Deshmukh

Dr. Lalit Deshmukh is an Associate Professor in the Department of Chemistry & Biochemistry. His research group explores complex biological problems associated with signal transduction and neurodegenerative diseases, including Alzheimer's disease, ALS, and Parkinson's disease. He is especially interested in understanding the interplay between protein dynamics and function. The Deshmukh lab characterizes the structure-function interplay and conformational dynamics of biological macromolecules using a range of cutting-edge biophysical methods. Their primary research interests are solution NMR spectroscopy, protein phase separation and amyloids, and posttranslational modifications (PTMs).



Dr. Lara Maria Rangel

Dr. Lara Maria Rangel received a B.S. in Biological Sciences from Stanford University in 2006 and a Ph.D. in Neurosciences from the University of California, San Diego (UCSD) in 2012. She conducted her postdoctoral work in the Cognitive Rhythms Collaborative, based at Boston University and the Massachusetts Institute of Technology, where she investigated the rhythmic coordination of neural spiking activity in the rodent hippocampus. In 2015, she became a UC Chancellor's Postdoctoral Fellow at UCSD, and began investigating the relationship between local circuit level processes in the brain and extracranially measured brain rhythms. Her research tests whether rhythmic activity is important for coordinating the processing of information in organized networks of neurons. Her goal is to provide new insight into the single cell interactions underlying the occurrence of brain rhythms measured in rodents and humans.

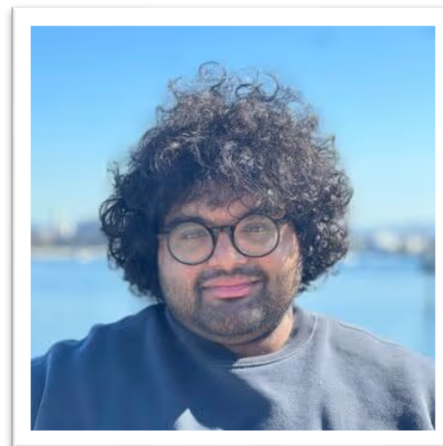


Dr. Neville Bethel

Dr. Bethel studied under Michael Grabe at UCSF as a biophysics PhD student. Using computational techniques such as molecular dynamics, enhanced sampling, and numerical integration, he investigated membrane remodeling transmembrane proteins. As an HHMI Hanna Gray Postdoctoral Fellow and under the mentorship of David Baker at the Institute of Protein Design, he utilized deep learning, Rosetta and electron microscopy to design and validate a new family of highly modular protein oligomers. The Bethel lab builds on many of these approaches to investigate protein conformational change, allostery and to build new molecular switches for cell biology applications.

Luke Sebastian, B.S.

Luke earned his BS in Biochemistry from Boston College in 2021. He then worked in the structural biology core at the Dana-Farber Cancer Institute, where he purified recombinant proteins and characterized them using X-ray crystallography. His research focuses on modifying TALE nucleases to target various forms of DNA, aiming to develop a more robust gene editing system. Outside the lab, Luke studies Japanese, explores different restaurants around San Diego, and enjoys playing video games.



Abstracts

Anika Agarwal

Computer Engineering/ ECE, Warren

Mentored by Amy Ousterhout

Who Gets the Lock? Characterizing Scheduler Behavior During Linux Mutex Handoff

When a mutex is released in a multi-core system, the operating system must answer two fundamental questions: where (which CPU core) the waiting thread should run, and how that thread should be awakened (e.g., whether wakeup involves inter-processor interrupts, or IPIs). In this poster, we examine mutex handoff behavior under the Linux EEVDF scheduler to understand these questions. Using controlled microbenchmarks combined with kernel tracing, we measure if wakeups occur on the same core or across cores, how frequently cross-core wakeups involve IPIs, and how these scheduling decisions affect handoff latency under different workloads. Our study aims to provide an empirical characterization of mutex wakeups under the EEVDF scheduler. This investigation serves as a preliminary step toward our work exploring new mutex wakeup scheduling mechanisms enabled by the new hardware feature in x86, user interrupt.

Geselle Aguirre Luna

Psychology, Eighth

Mentored by Julie Wetherell

Mindfulness, Exercise, and Education classes and their effects on loneliness in Older Adults

Chronic loneliness is a pressing issue that often leads to a significant decline in overall well-being. Many older adults struggle with chronic loneliness, which puts these individuals at a higher risk for mental and physical health problems. Chronic loneliness can even lead to higher mortality rates among older adults. Previous studies have examined how different interventions could mitigate the negative effects of loneliness. From these studies, it has been concluded that combinations of Mindfulness-Based Stress Reduction (MBSR), health education, and exercise classes prove to be helpful when treating loneliness in older adults. However, it is possible that the social contact provided

through these interventions may be responsible for reductions in loneliness. Therefore, we can hypothesize that mindfulness, exercise, and health education interventions will be equally effective in treating loneliness when practiced on their own. In order to observe how effective these different interventions are in alleviating feelings of loneliness, participants were placed in one of three group conditions: exercise only, mindfulness only, and health education classes. Participants also completed surveys using the UCLA loneliness scale to estimate how lonely participants were feeling. We will compare these scores across two different time points: during and post-pandemic. An analysis of covariance (ANOVA) will be used in order to determine the differences between groups across both time points. Using an ANOVA will allow us to observe the significance of our results. These results will allow us to examine the effectiveness of these interventions when treating the negative effects of loneliness in older adults.

Heba Ahmed

Economics, Eighth

Mentored by Claire Edington

The Rest Cure vs. The West Cure: The Economics Behind the Treatment for Hysteria

Hysteria is a sickness characterized by unexplainable behavioral and physical ailments. Until the nineteenth century, hysteria was a female illness. The term hysteria is derived from the Greek word hystera, meaning “uterus” or “womb.” Greek physicians thought that the main cause of hysteria was the wandering womb, where the womb moves aimlessly throughout the body and disrupts other organs. This philosophy became widely accepted, and physicians focused on the uterus to treat hysteric women for thousands of years.

Starting in the nineteenth century, physicians began to believe that the nerves were responsible for hysteria; hysteria redefined itself as a disturbance of the mind that presents in the body. Thus, the illness wasn’t restricted to female patients anymore. Treating both female and male hysterics became common. One such physician who did this was Silas Weir Mitchell. An American neurologist, Mitchell developed the rest cure, which consisted of total isolation and rest; patients were taken care of by medical staff, were on strict bed rest, and could not do anything considered to be taxing to the brain. However, this cure was only used for female patients. Men were treated with the West cure: male patients headed West and were instructed to stimulate their bodies and minds. This paper argues that this contrast in cures is the result of how women and men were viewed in the labor market. Society’s economic valuation of women differed greatly from

men's perceived economic worth, and this translated itself into the medical field with Mitchell's cures.

Anika Akkinepally

Cell and Molecular Biology/Biology Department, Warren

Mentored by Brian Zid

Ribosome Quality Control in Mitochondrial Protein Import Stress

Abstract redacted due to proprietary information.

Glennalyn Jhen Alaras

Microbiology/Behavioral Evolution and Ecology, ERC

Mentored by Noah Rose

Behavioral Analysis and Phenotyping in Aedes aegypti

Urbanization, global mobility, and rising temperatures have accelerated the spread of *Aedes aegypti*, a mosquito responsible for transmitting dengue, Zika, chikungunya, and yellow fever. Alongside this expansion, an urban-adapted, human-specialist form of *Ae. aegypti* has emerged, raising concerns about increased arbovirus transmission. This project integrates artificial intelligence with multidimensional behavioral phenotyping to compare human-specialist and ancestral generalist *Ae. aegypti* populations, with the goal of identifying behavioral adaptations that facilitate urban specialization. Ecological surveys suggest that larvae from these two forms experience distinct developmental environments. Generalist larvae inhabit predator-rich forest habitats with stable food availability, whereas human-specialist larvae develop in nutrient-limited but relatively predator-free urban containers. Preliminary observations indicate that human-specialist larvae exhibit slower development and reduced predator-avoidance behaviors, while forest generalists show higher activity levels that may enhance survival under predation risk.

To quantify these behavioral differences, larval activity will be recorded in a uni-directional partitioned enclosure under three treatments: exposure to predatory

Toxorhynchites, water previously containing Toxorhynchites, and water previously containing *Ae. aegypti*. Video-based analysis using the deep-learning platform SLEAP will generate full-body movement trajectories, which will be transformed into behavioral features using learning-based tools such as VAME or TREBA. Statistical comparisons (ANOVA) will assess treatment-specific differences in movement patterns, and trajectory data will be segmented into interpretable behaviors such as foraging and hiding. By integrating ecological context, behavioral assays, and AI-driven analytics, this research aims to clarify the evolutionary mechanisms shaping larval behavior and vector competence in *Ae. aegypti*, ultimately improving our understanding of how urban environments drive mosquito adaptation.

Waleed Alghaithi

Computer Science, Warren

Mentored by Taylor Berg-Kirkpatrick

Uncovering the Limits of Spatial Reasoning in Artificial Intelligence

This research investigates how well Vision-Language Models handle spatial reasoning by testing the Qwen3-VL-30B model. Using the LEGOLite benchmark, the model was evaluated on four categories: height, position, rotation, and ordering. Initial tests showed mixed results. The model performed best on position tasks but completely failed at ordering. To understand why this happens, the study tracked the network's internal experts to see exactly how it processes information. The results showed a strict separation between text and images. The model sends visual and textual data to completely different internal areas, sharing no expert nodes among its most active parts. Also, processing images required the model to activate many more experts compared to processing text. These findings show that errors in spatial reasoning arise specifically from the visual components of the model, not from an inability to read the text prompt. Ongoing work focuses on identifying and isolating these specific visual experts to find clear ways to improve spatial reasoning in artificial intelligence.

Kristin Antonio

Education Sciences, Marshall

Mentored by Amanda Solomon Amorao

“We’re More American Than They’ll Ever Be”: Race, Citizenship, and Patriotism Among San Diego Fil-Ams

While notable research has been done into the history of Filipina/o/x American (Fil-Am) communities in Southern California (Espiritu, 2003; Bonus, 1997), many of these analyses fail to take into account the unique construction of San Diego’s Fil-Am community as a result of two primary factors: enlistment into the U.S. Navy as a dominant avenue for Filipino immigration to San Diego and San Diego’s physical proximity to the U.S.-Mexico border during an anti-immigrant political climate. This particular historical and geographic context has positioned enlistment into the U.S. Navy as a “common sense” mode of being Fil-Am in San Diego through the perception of military service as a means of becoming an ideal immigrant-citizen (in stark contrast to the image of an “illegal alien”). Through analyzing the historical conditions of Filipina/o/x American immigrants, veterans, and military-affiliated communities from the beginning of the 20th century to the present day, this paper aims to explore the specific political alignment of the San Diego Fil-Am community to unravel the connections between race, citizenship, and patriotism and imagine alternative configurations of Fil-Am identity grounded in collective liberation. This paper also briefly explores the potential of grassroots, community-based youth mentorship initiatives to push back against the seemingly de facto enlistment of these community members into the military. Such analysis is crucial for challenging White supremacist logic that conflates proximity to Whiteness with “worthiness” of a place in the United States.

Abigail Baez-Granados

Cognitive and Behavioral Neuroscience, Muir

Mentored by Andrea Chiba

Behavior changes in children within a classroom vs testing setting

Abstract redacted due to proprietary information.

Helen Bai

International Studies Political Science/ISP, Revelle

Mentored by Guoer Liu

Silk Roads, Side Deals: How Bilateral Governance Shapes the Belt and Road Initiative

This project examines how the Belt and Road Initiative's reliance on bilateral governance affects transparency, coordination, and development outcomes across participating countries. Since its launch in 2013, the BRI has become one of the world's largest infrastructure and development programs, connecting China with partner states across Asia, Africa, Europe, and Latin America. However, unlike many multilateral development initiatives managed through institutions such as the World Bank or regional development banks, the BRI often operates through bilateral memoranda of understanding, state-to-state negotiations, and project-specific agreements. This structure gives China and partner governments flexibility, but it may also weaken oversight, limit public access to information, and produce uneven outcomes across countries.

Using institutionalist theories of transaction costs, information asymmetry, and collective action, this research asks whether the absence of a centralized multilateral governance mechanism contributes to inconsistent implementation and accountability problems. The project focuses on how bilateral arrangements shape negotiation processes, financing transparency, project monitoring, and local stakeholder participation. It also considers whether these governance patterns create different experiences for government officials, private businesses, and affected communities.

The study will use a qualitative research design based on secondary literature, policy documents, and primary interviews with government officials in BRI partner countries and business representatives who have worked with Chinese firms or BRI-related projects. By comparing how different actors experience BRI governance, this project aims to show that the BRI's institutional structure is not just an administrative detail, but a central factor shaping the initiative's political and developmental effects.

Suravi Bajaj

Neurobiology/Biological Sciences, ERC

Mentored by Weg Ongkeko

Title: Of Rats and Men: Transcriptomic Convergence Between Alzheimer's Disease and Microplastic Exposure

Background: Micro- and nanoplastics (MNPs) have been detected in human blood, fluid and tissue, yet their neurobiological impact is poorly understood. Rodent models show that MNPs can cross the blood-brain barrier and alter AD-relevant neurotransmitter

pathways. However, this study integrates human molecular data to investigate whether MNPs contribute to early Alzheimer's disease (AD) related processes.

Methods: We performed single-cell RNA sequencing of public transcriptomic datasets involving MNP-exposed rats and human AD brain tissue (cortex and hippocampus). Differential expression analysis generated MNP-responsive, while human single-cell data were aggregated into cell-type profiles and ranked by AD association using DESeq2 across major neural, glial, and vascular populations. Rat genes were mapped to their human orthologs, and cross-dataset convergence was assessed using multilevel fast gene set enrichment analysis (fgsea). Leading-edge genes from significant enrichments were then used to identify candidate driver genes.

Results: The transcriptional pathways responsive to microplastics overlapped more significantly with those in microglia and other AD-relevant cell types than in the hippocampus. In microglia, genes that were downregulated following microplastics exposure showed the most significant enrichment in AD-ranked datasets, mainly involved in innate immune signaling, lipid metabolism, synaptic organization, and glial activation, all of which are pathways strongly implicated in AD pathobiology.

Conclusions: This study provides a systems-level framework linking the biology of environmental exposure to neurodegenerative vulnerability and identifies candidate pathways for further mechanistic investigation. Ongoing validation studies will further examine the overlap in gene signatures and guide future analyses.

Gurshaan Bajwa

Molecular and Cell Biology/School of Biological Sciences, Warren

Mentored by Matthew Daugherty

Visualizing Differences in RNA Sensitivity by PARP13 Isoforms using a GFP Reporter Assay

Poly-ADP-ribose Polymerases (PARPs) are a family of cellular enzymes that catalyze ADP ribosylation. Humans encode 17 different PARPs. All members of the PARP family contain an ADP-ribosyl transferase domain with varying layouts. This study focuses on PARP13, an antiviral protein, that exists in two isoforms - PARP13L (elongated) and PARP13S (truncated). It is hypothesized that the antiviral properties of PARP13 are due to its ability to bind RNA. One unique feature about PARP13 is that it is catalytically inactive. This distinguishes a stark difference between the isoforms as PARP13L contains an inactive catalytic domain via a membrane-localized CaaX motif while PARP13S lacks

this domain and is not membrane-localized. This project examines the differences in viral RNA sensitivity to PARP13 isoforms using a transfection-based green fluorescent protein (GFP) reporter assay. This assay tests various sequences of viral RNA fragments attached to the 3' UTR. These fragments are modeled by pathogens that PARP13 isoforms are known to target, such as the Sindbis virus (SINV). PARP13 isoforms are transfected into HEK293T cells containing either GFP with a viral fragment or an empty vector. The cells are then imaged and fluorescence is quantified. Preliminary results show that both PARP13L and PARP13S suppress GFP reporter expression when viral RNA fragments are present, supporting their antiviral activity. However, some differences can be observed in the level of viral fragment inhibition between the two isoforms. More experiments are being conducted to determine whether the extent of inhibition of viral fragments depends on the amount of PARP13 isoform present.

Ai Hue Banh

Pharmacological Chemistry/ Department of Chemistry and Biochemistry, Revelle

Mentored by Conor Caffrey

Anti-trypanosomal activity of plant extracts from the Democratic Republic of Congo

Human African trypanosomiasis, caused by *Trypanosoma brucei*, remains a neglected tropical disease with limited therapeutic options, highlighting the need for new, effective, and

low-toxicity treatments. In this study, plant-derived extracts were screened for inhibitory activity against *Trypanosoma brucei brucei* to identify potential antitrypanosomal compounds. Crude extracts were evaluated using in vitro growth inhibition assays to determine their effect on parasite viability. To assess selectivity, cytotoxicity was measured in

parallel using Human Embryonic Kidney 293 (HEK293) cell lines.

Screening identified four extracts that exhibited strong inhibitory activity against *T. brucei*

brucei while maintaining low toxicity toward mammalian cells. These hits represent promising candidates for further investigation. The observed activity suggests that these extracts may contain bioactive compounds with potential therapeutic relevance.

Joey Barros

Molecular and Cell Biology, Warren

Mentored by Priyadarshini Pantham

Investigating the biological mechanisms of kidney-related complications during preeclampsia

Abstract redacted due to proprietary information.

Matthew Benny

Education Sciences, ERC

Mentored by Alison Wishard Guerra

Borderland Barriers: Navigating Neurodevelopmental Diagnosis in Southern California

I would like to further understand the experiences of these immigrant families when in the process of getting their children diagnosed and treated. In what way do these particular challenges immigrant families within San Diego and Imperial County face when trying to get their children diagnosed and treated for a wide variety of disabilities? Ultimately, to what extent do language barriers, medical & educational bureaucracy & lack of resources come up regularly in the parent interview and survey responses from the larger “Music for Growing Minds: A Music-Based Intervention for Language Development” research study as potential factors influence their willingness to seek diagnoses or psychological services for their children?

Anna Bertlin

Biological Anthropology (BS), ERC

Mentored by Justin Seltzer

Retrospective Analysis of Emergency Department Cardiac Arrest: Analysis of Causes and Interventions

Naloxone is an opioid receptor antagonist used to reverse respiratory depression secondary to opioid overdose. Naloxone use in cases of cardiac arrest is common, especially in cases of possible drug overdose. Pre-clinical research also suggests there may be additional mechanisms favoring its use in undifferentiated cardiac arrest, though retrospective clinical studies have produced mixed results. While some authors argue universal naloxone administration is a low-risk intervention during cardiac arrest, others suggest use may simply delay other, better supported interventions.

We propose a retrospective cohort study of adult patients presenting to the emergency department in cardiac arrest at the University of California, San Diego hospitals from 2015-2025. We hypothesize that administration of naloxone administration for undifferentiated cardiac arrest patients does not increase the rate of return of spontaneous circulation. Using retrospective chart review, we will evaluate patients 18 years and older who received naloxone during cardiopulmonary resuscitation in the emergency department. The primary outcome is the return of spontaneous circulation. Secondary outcomes include survival to hospital discharge and neurologic outcome at discharge.

Laya Binu

Astronomy and Astrophysics, Sixth

Mentored by Floor Broekgaarden

The Structured Uncertainty of Massive Stars: Population-level Differences in Rapid Population Synthesis

To understand the processes through which massive stars evolve and leave behind remnants, rapid population synthesis models are used to simulate large numbers of stars to test how various initial parameters can affect their evolution and the remnants left behind. As the remnants produced by stars can be detected through gravitational waves, these models are a way of determining what kind of stars may have existed based on the compact-object mergers being detected now. However, these models rely on uncertain single and binary massive star evolution physics, and different codes can produce systematically different simulation outcomes even when adopting similar input assumptions, the effects of which are challenging to quantify. Previous work has shown that such differences can lead to seemingly unpredictable outcomes for individual systems; here we show that, when viewed across the full parameter space, these differences are not random but instead exhibit clear, structured patterns across mass and

metallicity. In this work, we quantify differences between two commonly used population synthesis codes, COMPAS and StarTrack, by comparing the mapping between zero-age main sequence (ZAMS) mass and compact-object mass across a wide range of metallicities. We find that differences between the codes are strongly parameter-dependent and become increasingly pronounced at higher initial masses and lower metallicities. Importantly, these differences are not randomly distributed across parameter space, but instead arise from three dominant physical processes: (i) metallicity-dependent stellar winds, (ii) luminosity-driven LBV mass loss, and (iii) remnant-mass prescriptions associated with pair-instability physics.

Melissa Bui

Human Biology (Department of Biological Sciences), Revelle

Mentored by Irina Kufareva

Evaluation of Predicted Peptide Ligands for the Orphan GPR37L1 Using BRET-Based Internalization Assays

Abstract redacted due to proprietary information.

Jacob Butler

Physics, Warren

Mentored by Alex Frano

Using Small Angle Light Scattering to Probe the Molecular Structure of Swelling Hydrogels

Hydrogels are a class of soft matter that are formed by cross-linking chains of polymers into a porous gel that swells when introduced to water. Hydrogels are important materials to engineering and medicine, and have notably been cited as good candidates for complex drug delivery mechanisms, wound dressing, and wastewater treatment.

Studies have been done to investigate their molecular structure, but existing work largely involves taking static images using techniques like electron microscopy. These methods are useful for gaining a base understanding, but the preparation process often involves extreme freezing or near-vacuum conditions for the samples, which has been shown to have a significant effect on their performance by introducing new porosity artifacts. Furthermore, in these preserved states, hydrogels are unable to swell as they normally would. Our goal is to explore the nano-scale properties of hydrogels and their development over time using Small Angle X-ray Scattering (SAXS) and Small Angle Visual Light Scattering (SAVS): techniques that allow them to be studied while in the presence of water.

A series of scattering images, taken over the course of a few hours at different humidity levels and temperatures, shows us the effects of these variables on the form and structure factors of the hydrogel. This data will help us characterize the way the pores of the hydrogel grow, which is essential information as we begin to use these substances in precise engineering and medical contexts.

Bowen Cai

Critical Gender Studies, Seventh

Mentored by Daphne V. Taylor García

Policy Cost-Sharing and Gendered Employer Avoidance: A Text Analysis and Correspondence Audit across the United States and China

Employers may avoid hiring women of childbearing age because they expect these workers to take family leave, creating costs the firm must cover. Whether employers act on this expectation depends on policy design. When public insurance funds cover most of the cost of parental leave, employers have little reason to screen out mothers. When employers pay the cost themselves, they have a strong reason to do so. This study combines three methods to test this logic: a comparative policy analysis of family leave systems, a text analysis of job postings for gendered avoidance language, and a correspondence audit experiment. The audit sends matched fictitious resumes to real job openings. Resumes vary on two dimensions, perceived gender and perceived caregiving status, creating a two-by-two design. Gender is signaled through applicant names. Caregiving status is signaled through volunteer experience and cover letter wording. Applications target both high-skill and low-skill positions in strong-protection and weak-protection regions in each country. In the United States, California provides paid family leave and pregnancy disability insurance, while Mississippi offers only unpaid federal

FMLA coverage. In China, Shanghai and Guangdong maintain well-funded maternity insurance pools, while Gansu and Guizhou rely on underfunded systems where employers bear most costs directly. Preliminary results from initial U.S. applications show that the callback penalty for women with caregiving signals is concentrated in the weak-protection state, and that gendered language in job postings varies by skill level. Data collection in additional regions is ongoing. These early findings support the prediction that policy design shapes employer discrimination.

Felicia Cai

Cognitive and Behavioral Neuroscience, Revelle

Mentored by Binhai Zheng

Role of Stress Granule proteins in axonal regeneration after spinal cord injury

Axon regeneration after spinal cord injury is a critical study as it provides information regarding neuron communication and enables restoration of motor function and recovery. When axons are damaged or experience injury, neurons are unable to regenerate and therefore, communicate with lost targets, disrupting signal transmission and leading to sensory and motor impairments. Without effective regeneration, these deficits can reduce a person's independence and quality of life. Stress granules are nonmembranous cytoplasmic compartments which form in cells under environmental stress conditions, preventing the mRNA trapped inside the granules from being translated. Following spinal cord injury, cells recognize environmental stress, and formation of stress granules is initiated. TIA1 and G3BP1 are proteins essential for the formation of stress granules, which regulate local protein synthesis, controlling storage and translation of axonal mRNAs, impacting neural repair. The primary goals are to understand the effects of TIA1 and G3BP1 in stress granule formation and axonal growth. The methods intended to be used in this study include breeding conditional knockout mice and analyzing slices of their brains, medullas, and spinal cords in order to assess the effect of the deletion of these proteins during axonal regeneration and sprouting. Stimulating axon regeneration is the ultimate goal in improving outcomes for those dealing with spinal cord injury.

Nicole Cao

Biochemistry, Muir

Mentored by Christian Metallo

Changes in the Lipid Profile and Amino Acid Composition of Various Organs Following Oophorectomy in Women

Abstract redacted due to proprietary information.

Diego Cecena

General Biology, Revelle

Mentored by Eric Zorrilla

Effects of Rgs7bp Knockout on Alcohol Drinking in Male and Female Mice

Alcohol use disorder (AUD) is a prevalent, growing public health issue in need of novel therapeutic targets. Regulator of G-protein Signaling (RGS) proteins are intracellular regulators of G-protein-coupled receptor (GPCR) signaling, and RGS7-binding protein modulates signaling of RGS7 subfamily proteins (RGS6, 7, 9, 11) via subcellular localization of their G β 5 partner complexes. The presented study test the hypothesis that RGS7BP influences voluntary alcohol consumption using adult male and female Rgs7bp knockout (KO; MGI: 3373065) and wild-type (WT) mice (KO: n = 12; WT: n = 9). Mice received ad libitum chow and water plus intermittent (3x/week, 24-hr/day) access to ethanol (IAE, 20% v/v ethanol) [EtOH] using a two-bottle choice (vs. water) paradigm. Genotype effects on EtOH intake and preference, body weight, and EtOH clearance were assessed across 10 weeks. After 10 weeks of exposure, genotypes were compared for negative affective behavior during acute withdrawal in the elevated plus-maze, marble burying, bottle brush, and forced swim tests. Across the 24-hour access period, Rgs7bp KO drank more ethanol (g/kg) than wt (Genotype, $p < 0.05$), and females drank more than males (Sex, $p < 0.05$). Females also drank more than males during the initial 2-hour binge period (Sex, $p < 0.05$). Ethanol (EtOH) preference ratios did not differ significantly across groups at the 2 -or 24-hour time points ($p > .05$). The results support the hypothesis that Rgs7bp modulates daily ethanol intake and negative affective behavior (anxiety tendencies) under intermittent access.

Cassandra Chang

Human Biology/School of Biological Sciences, Eighth

Mentored by Sylvia Evans

Cell Cycle Activity in Cardiomyocytes Following Tamoxifen-Induced MerCreMer Activation

The tamoxifen-inducible Myh6-MerCreMer system is used for cardiomyocyte-specific gene recombination in adult mice. Tamoxifen (TAM) is usually administered to activate Cre in this system, allowing precise control of gene expression. Despite its wide application, there have been reports of DNA damage and induction of cardiomyocyte cell cycle activity. Previous studies have reported that Cre activation itself may induce DNA damage, apoptosis, and transient DNA synthesis in the heart. This study aims to determine whether TAM-induced activation of the Myh6-MerCreMer system causes DNA damage and promotes cardiomyocyte cell cycle progression, or instead induces a non-proliferative stress response. However, these effects have not been rigorously distinguished between cardiomyocytes and non-cardiomyocytes. This study therefore aims to determine whether TAM-induced activation of the Myh6-MerCreMer system promotes cardiomyocyte cell cycle activity or instead reflects a non-proliferative stress response. To test this, adult Myh6-MerCreMer mice will receive TAM and 5-ethynyl-2'-deoxyuridine (EdU) injections to label newly synthesized DNA. Then hearts will be collected, followed by cryosectioning and analysis using intronic RNAscope probes. Confocal microscopy and quantitative image analysis will assess whether the cardiomyocytes have undergone DNA synthesis as an indicator of cell-cycle re-entry.

Charlotte Chang

Human Biology, Eighth

Mentored by Omar Akbari

Generation of an Opsin10 Knockout Line in Aedes aegypti

Aedes aegypti mosquitoes are a vector for various diseases including dengue, Zika, and yellow fever and rely on visual cues for host seeking behavior. The opsin10 gene encodes a rhodopsin-like light sensitive protein in receptor cells. Here, we outline the development of the heritable opsin10 gene knockout line using CRISPR-Cas9. Heterozygous and homozygous mutants were confirmed by sequencing and used to

assess effects on visual function and host-seeking. This line enables investigation of photoreception in mosquito behavior and supports new vector control strategies.

Jeremiah Cheav

Biochemistry, ERC

Mentored by Fatemeh Askarian

The expression of LPMO in Enterococcus faecalis (EF)

Lytic Polysaccharide Monooxygenases (LPMOs) are enzymes that rely on the redox chemistry of copper to oxidize polysaccharides. The redox chemistry allows the breakdown of recalcitrant polysaccharides associated with an increased rate of infection. Our project aims to investigate the expression of LPMO in *Enterococcus faecalis* (EF) by evaluating the growth of EF WT V583 and Δ LPMOEF in artificial pooled human urine (aPHU) and artificial urine medium (AUM). We will also examine if LPMOEF deletion is impacted by the differing adaptations of aPHU and AUM.

Christine Chen

Molecular and cell biology, ERC

Mentored by Dmitry Lyumkis and Andres Rivero-Gamez

Identifying Molecular Interactions Driving Retroviral Integration into Chromatinized Targets

To establish permanent infections, retroviruses insert their genetic material into the genome of the host, a process known as integration. This step is mediated by a viral nucleoprotein complex known as intasome, which consists of a multimer of integrase viral proteins assembled around the viral DNA. Although integration has been extensively studied using free DNA, the DNA within the nuclei of eukaryotic cells is wrapped around histone proteins, forming the basic unit of chromatin known as nucleosomes. Much less is known about how retroviruses integrate into this more realistic chromatin environment.

Our lab has been utilizing the mouse mammary tumor virus (MMTV) as a model to study integration onto chromatinized substrates. Recently, we obtained several cryogenic electron microscopy (cryo-EM) maps to determine how intasomes interact with nucleosomes. We solved two different intasome-nucleosome complexes showcasing how MMTV integrates at specific positions along the nucleosome. Additionally, one of these complexes pointed towards the possibility of cross-nucleosome interactions by individual intasomes. This indicates that MMTV may have the ability to target chromatinized DNA directly and may coordinate integration across neighboring nucleosomes. We are currently building atomic models of these complexes to pinpoint the exact residues within the viral integrase that contact the nucleosomes. Once identified, we plan to mutate these residues and test how those changes affect integration activity. These experiments will help us understand which interactions are essential for successful integration and how they might be disrupted. Our findings will provide new insight into how retroviruses interact with chromatin.

Erica Chen

Clinical Psychology, ERC

Mentored by Alison Wishard Guerra

Parental Involvement in Music Interventions to Enhance Language Outcomes for Toddlers with Delays

Post-pandemic speech delay diagnoses among toddlers remain historically high (16–17%), disproportionately affecting underserved bilingual populations and children with Autism Spectrum Disorder (ASD), with therapeutic bottlenecks particularly acute in areas like San Diego. Guided by Bronfenbrenner’s Ecological Systems Theory, this study addresses these gaps by examining how parental engagement directly affects the effectiveness of language intervention. Although traditional approaches often use general content, research supports that personalizing therapy around a child’s “special interests” markedly increases motivation and skill generalization.

Through the Music for Growing Minds lab, this study uses a mixed-method correlational design embedded in a randomized controlled trial of children ages 2–6. The core research question is whether active parental involvement in AI-personalized music interventions enhances language development. Quantitative measures include standardized assessments (EOWPVT-4, GFTA-3) and surveys of home musical engagement, while qualitative interviews capture how parents implement interventions and how these interventions affect family dynamics.

By integrating home environments and clinical interventions through AI-personalized music, this research directly evaluates whether structured parental participation enhances expressive vocabulary and articulation. The objective is to develop an adaptable model that addresses therapeutic delays among neurodivergent and underserved children by identifying parental engagement as a critical leverage point.

Hillary Chen

Clinical Psychology/Cognitive Behavioral Neuroscience, Seventh

Mentored by Giordano de Guglielmo

Polydrug (Oxycodone-Cocaine) Use and Drug-Preference Implications on Future Treatment Options

Abstract redacted due to proprietary information.

Richard Chen

Sociology, Marshall

Mentored by Roy Perez

Beyond Tragedy: Queer Survival and Futurity in Post-2015 East Asian Cinema

This project examines how post-2015 East Asian queer cinema reimagines queer survival and futurity beyond the tragic narratives that defined earlier Sinophone films such as *Happy Together* (1997) and *Lan Yu* (2001), in which queer intimacy is bound to exile, loss, and death. Through close readings of *Suk Suk* (2019), *Your Name Engraved Herein* (2020), and *Marry My Dead Body* (2022), I argue that contemporary East Asian queer films develop alternative narrative strategies that depart from both earlier fatalism and Western frameworks of queer liberation centered on visibility and rupture from the family.

I identify three strategies through which these films imagine queer futurity: kinship integration (embedding queer relationships within existing familial structures rather than against them), endurance across time (locating queer possibility in long temporal horizons of waiting and return), and strategic concealment (reframing silence and the

closet as survival tactics rather than conditions of repression). Drawing on Muñoz's queer futurity and queer of color critique alongside Sinophone scholarship (Petrus Liu, Fran Martin, Howard Chiang), I argue that dominant analytical concepts such as "coming out" and "visibility" can obscure how queer life is negotiated in East Asian cultural contexts shaped by Confucian familial obligation, collective selfhood, and the politics of discretion.

Through formal analysis of narrative structure, temporality, and the use of silence, this project contributes a comparative account of East Asian queer cinematic futurity grounded in the films' own cultural logics rather than imported paradigms.

Riya Chhabra

Human Biology, Warren

Mentored by Weg Ongkeko

Spatial Epithelial-Neuronal-Immune Crosstalk Driving Perineural Invasion in Head and Neck Squamous Cell Carcinoma

Perineural invasion (PNI)—the infiltration of tumor cells within, around, or through nerve fibers—is a hallmark of aggressive tumor biology and an independent predictor of poor prognosis in head and neck squamous cell carcinoma (HNSCC). Despite being reported in up to 90% of cases, the spatial and molecular mechanisms underlying PNI remain poorly defined. Here, we apply spatial transcriptomics to characterize the cellular and microenvironmental features that drive PNI and its associated immune contexture.

Spatial transcriptomic datasets (GSE300147, GSE252265, GSE281978) were processed using standardized pipelines for quality control, normalization, and unsupervised clustering (UMAP). Cell populations were annotated using canonical markers, identifying epithelial, neural, Schwann, immune, and axon guidance-related clusters. Composite module scores quantified PNI activity, neuronal and Schwann identity, axon guidance signaling, and immune infiltration.

UMAP analysis revealed neural-enriched tumor clusters co-localizing with Schwann and axon guidance signatures, consistent with a neural-like invasive niche. PNI strongly correlated with neuronal ($r = 0.89$) and axon guidance ($r = 0.65$) programs, and moderately with Schwann activity ($r = 0.49$). In contrast, PNI was negatively associated with T-cell ($r = -0.26$) and macrophage ($r = -0.12$) scores, suggesting immune exclusion.

GO enrichment analysis supported these findings. PNI-high regions showed activation of chemokine signaling, adhesion, and lipid transport pathways, while PNI-low regions

were enriched for immune functions, including T- and B-cell signaling and cytokine regulation.

Together, these results define a neural-dominant, immune-silent microenvironment driving PNI and highlight nerve–tumor signaling and localized immune evasion as mechanisms of invasion.

Kelli Childs

Biochemistry, Revelle

Mentored by Alexis Komor

High Throughput Base Editor Screen Validation

Base editors (BEs) are a next-generation CRISPR-Cas9-based genome editing method that uses deamination to convert a single nucleotide from a C•G to T•A base pair (cytosine BE, CBE) or an A•T to G•C base pair (adenine BE, ABE). Since the first BE's development in 2016, countless additional variants have followed, catering to different PAM requirements, editing windows, and organism specificity. These BEs are directed to their target site in the genome by a guide RNA (gRNA), which has a 20-base programmable spacer sequence that matches the target site. For any target edit, this spacer sequence must be optimized. Thus, there is a need for an efficient screening platform to identify gRNA:BE combinations that maximize editing efficiency and achieve the desired editing outcome in high throughput. To address this, my graduate student mentor has developed BESTIE: the Base Editor Screen To Interrogate Efficiency, which is a high-throughput system that allows researchers to screen hundreds to thousands of gRNA:BE combinations at once. To validate the BESTIE platform at the ERCC2 locus, top-performing gRNA:BE combinations identified from the screen were individually tested in HEK293T cells. Successful validation in disease-relevant cell types demonstrates that BESTIE can rapidly identify optimal gRNA:BE combinations in high throughput, thereby saving researchers significant time and accelerating the development of base editing approaches for therapeutic correction of pathogenic single-nucleotide

variants. The screen also highlights cell-type-dependent chromatin accessibility barriers that can limit editing efficiency at specific regions within loci.

Felicia Chiu

Human Biology, Sixth

Mentored by Stanley Lo

Asian American undergraduate experience with racism in STEM

Abstract redacted due to proprietary information.

Yuran Choi

Biochemistry/Chemistry and Biochemistry, Revelle

Mentored by Michael Burkart

Solvatochromic probes capture inter-domain interactions in carrier protein-dependent biosynthesis

Carrier protein (CP)-dependent biosynthesis pathways produce a broad range of important metabolites, including many clinically relevant natural products. These pathways rely on a carefully orchestrated series of enzymatic reactions mediated by a central carrier protein and multiple partner proteins. However, the protein-substrate and protein-protein interactions that enable these processes are often subtle, transient, and difficult to monitor in situ. Solvatochromic fluorophores offer a promising strategy to probe these interactions. These fluorescent molecules exhibit shifts in emission wavelength and intensity depending on their local chemical environment, allowing them to report changes in protein interactions. Such probes can be chemically synthesized, selectively attached to carrier proteins, and used to visualize CP-dependent pathways involving partner proteins such as fatty acid synthases (FAS), polyketide synthases (PKS), and nonribosomal peptide synthetases (NRPS). In this work, we demonstrate the application of solvatochromic probes to monitor inter-domain interactions within type I NRPS system. Using mutagenesis at the peptidyl carrier protein-epimerization (PCP-E) domain interface, interactions were detected with the solvatochromic 5-(4''-

dimethylaminophenyl)-2-(4'-phenyl)oxazole (dapoxyl) pantetheinamide probe. These findings highlight the utility of solvatochromic probes for detecting dynamic inter-domain protein interactions and suggest broader applications for studying carrier protein-mediated biosynthetic pathways.

Siwen Cui

Molecular and Cell Biology, Sixth

Mentored by Debanjan Dhar

TREM2-dependent Macrophage Signaling in Chronic Liver Diseases

Abstract redacted due to proprietary information.

Rita Davda

Molecular and Cell Biology, Marshall

Mentored by Amir Zarrinpar

Circadian Regulation of Pro-Angiogenic Gene Expression Influences Timed Anti-VEGFR Therapy in a MC38 Colorectal Cancer Model

Circadian rhythms, the internal biological clock controlled by environmental cues and core clock genes, regulate rhythmic transcription of cancer-driving genes. Pathogenic angiogenesis is a therapeutically targeted hallmark of cancer, though the relationship between circadian timing and angiogenesis remains unexplored. Here, we investigate circadian expression of pro-angiogenic genes in colorectal tumors and whether aligning anti-angiogenic therapy with these rhythms improves treatment efficacy. Building on prior findings that transgenic colorectal tumors exhibit rhythmic pro-angiogenic gene expression, we aim to test timed anti-angiogenic therapy in the MC38 colorectal cancer (CRC) mouse model. To verify circadian gene regulation in this model, we implanted MC38 tumors into mice before tumor collection at six timepoints across a 24-hour period. RT-qPCR of tumor tissue assessed rhythmicity of pro-angiogenic genes *Vegfr1* and *Vegfr2* and established target timepoints for chronotherapy. We will perform timed-

administration therapy with a VEGF receptor family inhibitor to optimize chronotherapy strategies to improve CRC treatment outcomes.

Isaac De Lara

Clinical Psychology B.S, Muir

Mentored by Caren Walker

Moving beyond country-level

what do you think of this?: Cross-cultural variation in cognition is increasingly well-documented, with studies showing differences across a wide range of domains, including reasoning, attention, categorization, and social cognition. However, less research has examined the developmental origins of this variation, particularly in Central and South American contexts. In addition, much of the existing literature treats countries as relatively homogeneous cultural units, often using country-level comparisons as a proxy for culture. This approach may obscure meaningful within-country variation in children's developing cognition. The present study addresses this gap by examining cognitive variation among Mexican preschoolers tested across three sites: Monterrey, Tijuana, and Tampico. Because Monterrey and Tijuana are both border-region cities, we compare children from these sites collectively to children from Central Mexico (Tampico). Preschoolers completed six tasks spanning relational and similarity reasoning, visual attention, and social cognition: causal Relational Match-To-Sample, Taxonomic-Thematic Triads, Picture Free Description, Feature Task, Uniqueness Preference, and Symbolic Self-Inflation. By examining variation across sites within a single national context, this study asks whether cognitive patterns typically studied through cross-national comparisons also vary meaningfully within Mexico. Findings will contribute to a more nuanced understanding of culture and cognitive development by highlighting the importance of regional and local context in early childhood.

Bien Antonio Dela Cruz

Human Biology/School of Biological Sciences, Muir

Mentored by Daniel Hollern

The Role of Tumor Extracellular Vesicles in B Cell Activation

Abstract redacted due to proprietary information.

Christopher Deng

Bioengineering: Bioinformatics, Eighth

Mentored by James Ford

Multimodal Deep Learning Prediction of Sepsis Mortality Using EHR and Chest X-ray Radiomic Data

Sepsis mortality prediction is crucial for prognostication, patient disposition, and therapeutic decision making. Existing sepsis mortality prediction models often utilize structured EHR variables in their predictions. However, no published models integrate chest radiograph images into their framework. Chest radiograph images often capture clinically meaningful information related to pneumonia, pulmonary edema, ARDS, and cardiac enlargement. The goal of this project is to develop and internally validate a multimodal machine learning model that integrates structured EHR variables from MIMIC-IV with chest radiograph DICOM images from MIMIC-CXR to predict sepsis outcomes. The study population will include adults who meet a retrospective Sepsis-3 definition, have at least one chest radiograph in MIMIC-CXR, and have sufficient EHR data during the baseline window. A CNN-based model will be used to extract imaging features from chest radiograph images, which will be fused with EHR features in a multimodal architecture. The performance of the multimodal model will be compared with structured-data-only and imaging-only baselines.

Prisha Desai

Neurobiology / School of Biological Sciences, Seventh

Mentored by Dawn Schiehser

Comparative Analysis of MDS-UPDRS Scores in Parkinson's Disease Veterans With and Without Mild to Moderate TBI

Abstract redacted due to proprietary information.

Architha Dhavala

Biology with a Specialization in Bioinformatics/Biological Sciences, Sixth

Mentored by Hojun Li

A Single-Cell RNA-seq Modeling Framework to Quantify Hematopoietic Reconstitution Following Bone Marrow Transplantation

Bone marrow transplantation (BMT) remains the only curative treatment for hematological disorders such as leukemia, thalassemia, and Diamond-Blackfan anemia. BMT success depends on engraftment of hematopoietic progenitors into the recipient's bone marrow niche, followed by reconstitution of red blood and immune cell populations. In the clinical setting, engraftment is said to occur ~15 days post-transplantation with reconstitution tracked by milestones that coincided with when neutrophils and monocytes were observed to have risen to healthy levels. Despite its extensive use in medicine, only recently has it been shown that hematopoietic reconstitution varies substantially across patients depending on graft type and lineage composition. This indicates that classifying reconstitution stages through chronological time fails to reflect a patient's biological recovery state.

We present a transcriptomics-based Transplant Time Metric (TTM) as a quantitative method, driven by single-cell RNA sequencing data from approximately 78,000 bone marrow cells collected from 12 transplant patients across timepoints, for estimating hematopoietic reconstitution. Gene expression programs associated with recovery were identified using DREAM pathway scores, literature-derived modules, and NMF-derived gene programs. The programs most informative of reconstitution were selected as features for the TTM. The TTM was developed by evaluating regression, random forest, and XGBoost, which returned scores correlated with chronological transplant time and classifications that maximized ROC-AUC. The TTM models were assessed for consistency with known biology, especially for HSCs, MPPs, and LMPPs due to their central role in rebuilding the immune system. This research advances understanding of hematopoietic reconstitution and supports biology-driven monitoring of post-transplant recovery.

Ella Di Liberti

Physics, Revelle

Mentored by Alex Frano

Using Small Angle Light Scattering to Probe the Molecular Structure of Swelling Hydrogels

Hydrogels are a class of soft matter that are formed by cross-linking chains of polymers into a porous gel that swells when introduced to water. Hydrogels are important materials to engineering and medicine, and have notably been cited as good candidates for complex drug delivery mechanisms, wound dressing, and wastewater treatment.

Studies have been done to investigate their molecular structure, but existing work largely involves taking static images using techniques like electron microscopy. These methods are useful for gaining a base understanding, but the preparation process often involves extreme freezing or near-vacuum conditions for the samples, which has been shown to have a significant effect on their performance by introducing new porosity artifacts. Furthermore, in these preserved states, hydrogels are unable to swell as they normally would. Our goal is to explore the nano-scale properties of hydrogels and their development over time using Small Angle X-ray Scattering (SAXS) and Small Angle Visual Light Scattering (SAVS): techniques that allow them to be studied while in the presence of water.

A series of scattering images, taken over the course of a few hours at different humidity levels and temperatures, shows us the effects of these variables on the form and structure factors of the hydrogel. This data will help us characterize the way the pores of the hydrogel grow, which is essential information as we begin to use these substances in precise engineering and medical contexts.

Reena Ding

Bioinformatics, Revelle

Mentored by Weg Ongkeko

Blood-Derived Exosomal RNA as a Diagnostic Tool in a Pan-Cancer Landscape

Exosomal RNA (exoRNA) is a promising noninvasive biomarker for cancer detection, reflecting both tumor-derived signals and systemic physiological changes. In this study, I

developed a machine learning framework using exoRbase expression data to classify multiple cancer types and distinguish cancer from healthy controls. A multi-class supervised model (70/30 train–test split) was trained to differentiate among breast cancer (BRCA), colorectal cancer (CRC), hepatocellular carcinoma (HCC), pancreatic ductal adenocarcinoma (PDAC), and healthy samples. Feature selection analyses identified optimal performance at approximately 200 features.

The multi-class model achieved strong performance, with highest accuracy in BRCA (95.8%) and PDAC (81.7%). Confusion matrix analysis showed overlap between CRC and HCC, suggesting shared exosomal RNA signatures. To further evaluate classification performance, separate binary models were trained for each cancer type against healthy controls. These cancer-specific models demonstrated high robustness, with AUC values of 0.989 (BRCA), 1.000 (CRC), 0.985 (HCC), and 0.974 (PDAC).

Feature importance analysis from the multi-class model identified the top 20 genes contributing to classification across all groups. Several highly ranked features included Y chromosome–associated genes (e.g., RPS4Y1, EIF1AY, DDX3Y), as well as biologically relevant transcripts such as GPX4 and MALAT1, indicating that both biological signal and cohort composition may influence model performance.

Overall, these results demonstrate that exoRNA profiles can effectively support both multi-class cancer classification and cancer-versus-healthy discrimination, highlighting their potential as minimally invasive diagnostic biomarkers.

Catherine Dinh

Public Health, Sixth

Mentored by Castillo, Edward

Gone with the Glucose: Trend of Emergency Medicine Encounters among Patients using GLP-1 Medications

Glucagon-like peptide-1 (GLP-1) receptor agonists are medications to treat chronic conditions such as type 2 diabetes and obesity by lowering serum glucose levels and increasing insulin release. Utilizing the electronic medical record consisting of Emergency Department (ED) encounters at the UC San Diego EDs locations (Hillcrest and La Jolla), a retrospective, cross-sectional comparison was conducted to analyze the population of GLP-1 users' demographics and comorbidities change and identify population-level shifts on how they have evolved between 2017 and 2025. Patient characteristics included age, sex, disposition, Charlson Comorbidity Index (CCI) Score,

Body Mass Index (BMI), and Chief Complaint (CC). Using SPSS and Python, the data was qualitatively analyzed with a chi-square test. There was a significant increase in ED encounters among patients with documented GLP-1 and significant differences in age, BMI, CCI score, and chief complaint from 2017 and 2025. By studying this population, the understanding of the relationship between GLP-1 usage and healthcare needs can be enhanced, mitigate unintended harm through informed clinical monitoring, and inform evidence-based treatment guidelines for clinicians to assess patients on the GLP-1 agents.

Dylan Dsouza

Data Science, Revelle

Mentored by Jennifer Smith

Post-Bleaching Resilience Across Coral Restoration Transplantation Strategies: A Decade of Benthic Community Monitoring at Palmyra Atoll

At Palmyra Atoll, an uninhabited reef in the central Pacific, an invasive corallimorph species, *Rhodactis howesii*, had spread across 3 square kilometers of reef following a longliner wreck in 1991. As the metal rusted, this leached iron and other nutrients which likely contributed to the corallimorph outbreak. Corallimorphs are adaptable and fast-growing cnidarians that can outcompete and kill corals and other benthic organisms. The wreck was removed in 2014, creating a unique opportunity to implement experimental restoration strategies.

Active coral restoration is used widely to aid reef recovery, yet how transplantation design shapes long-term community trajectories, recovery, and bleaching resilience remains poorly understood. In 2015, fifteen survey plots were established across five treatments: an untouched control, *R. howesii* removal, and active removal combined with three coral transplantation strategies — by-species plots (donor colonies of *Acropora*, *Montipora*, and *Pocillopora* were aggregated with themselves), cross-species plots (colonies were paired across these three taxa), and randomly mixed plots. Sites were surveyed annually through September 2025, capturing a decade of restoration efforts and the 2023-2025 global bleaching event.

This project examines whether transplantation strategy produces divergent community trajectories, whether species-mixed plots exhibit greater thermal resilience consistent with a portfolio effect hypothesis, and how the surrounding benthic community, particularly algal competitors and crustose coralline algae, impacts coral recovery. Analyses suggest that while coral cover trajectories varied little among transplantation strategies, plots receiving any coral treatment showed significant increases in percent

cover when compared to controls (PERMANOVA, $p < 0.01$), with taxa-specific responses emerging following the bleaching event.

Aria Ehsani

Human Biology, Seventh

Mentored by Christopher Coyne

Predicting Outcomes in Emergency Department Cancer Patients: Evaluating the End-of-Life-Index

Cancer remains a leading cause of morbidity and mortality, with over 2.1 million new cases projected in 2026. Emergency department (ED) utilization among patients with cancer is substantial and reflects gaps in symptom management and care coordination. National data indicate that 51.6% of cancer-related ED visits are potentially preventable, with pain as the most common presenting complaint, and resulting in hospitalization. These patterns suggest a misalignment between care delivery and the needs of patients with advanced disease.

Early palliative care has been shown to improve quality of life, reduce depressive symptoms, and extend survival. Randomized ED trials show early palliative care interventions improve outcomes without negatively affecting survival. Despite this evidence, ED palliative care remains underutilized, underscoring challenges in identifying which patients would benefit most in a time-sensitive setting.

Electronic health record (EHR) tools, such as Epic's End of Life Index (EOLI), identify patients at high risk of 1-year mortality and trigger goal-concordant pathways. However, existing literature emphasizes validation, as vendor-developed models may perform inconsistently in specialized populations, including oncology

This retrospective study evaluates the association between the EOLI and ED utilization, hospitalization, and 90-day morbidity and mortality among patients with cancer at UC San Diego Health. Using EHR data from 2020 to 2025, we assess the tool's utility for predicting outcomes and informing decisions. Data collection and analysis are ongoing.

Improving ED care requires integrating early palliative care interventions and validated prediction tools to better align treatment with patient goals, reduce preventable hospitalizations, and enhance quality of life.

Ian Escuro

Microbiology & Environmental Chemistry / Department of Chemistry & Biochemistry,
Warren

Mentored by Jonathan Slade

Quantitation of Airborne UV Filters in Coastal San Diego

Ultraviolet filters (UVFs) are semivolatile organic compounds added to plastics and personal care products to minimize damage by UV radiation. UVFs are environmental contaminants of emerging concern linked to coral bleaching, DNA damage, and hormone disruption, though they are not broadly regulated or monitored. UVFs have been measured in air in suspended particles (i.e., aerosols) and gases, which can disperse over long distances, causing concern to public health. However, the degree to which atmospheric UVFs partition between aerosols and gases, which can affect their atmospheric lifetime and toxicity endpoints, remains uncertain. To address this ambiguity, air samples were collected from the marine atmosphere off the coast of San Diego on the research vessel Bob & Betty Beyster. Gas phase UVFs were collected on an annular denuder coated with a nonpolar XAD-4 resin. A filter holder with a quartz fiber filter was affixed to the outlet of the denuder to collect aerosols. Gas and aerosol phase concentrations will be determined using Liquid Chromatography Mass Spectrometry (LC-MS) to quantify UVFs. Collection and extraction efficiency tests will be performed on both media to determine the fraction of UVFs that partition between the gas and aerosol phases. Quantitative analysis of UVFs is essential in order to gauge the severity of the risks they may pose to the environment and public health through chronic inhalation.

Ashley Ferland

Human Biology, Biological Sciences, Revelle

Mentored by Lindsey Burnett

Immune Mechanisms Linking Social Support to Pelvic Floor Muscle Regeneration After Birth Injury

This project aims to understand if social support improves pelvic floor muscle recovery after birth injury. Pelvic floor disorders, including urinary incontinence, fecal incontinence, and pelvic organ prolapse, affect approximately 25% of women in the United States and are primarily caused by pelvic floor muscle dysfunction¹. Vaginal childbirth is a significant contributing factor. Clinically, severe obstetric lacerations during childbirth are associated with increased risk of pelvic floor disorders³. This study sought to determine whether social support influences muscle regeneration following a stimulated birth injury, and to identify metabolic factors that may contribute to this recovery process. Pregnant C57/BL6 mice underwent SBIs via vaginal distension. Following delivery, animals recovered for eight weeks under either social isolation or social support conditions. Muscle fiber cross-sectional area was assessed using laminin antibody labeling with automated image analysis. Metabolomics analysis was also performed on collected serum samples. Social support significantly increased muscle fiber CSA compared to social isolation, suggesting enhanced contractile strength and healthier muscle tissue. Metabolomics revealed group-specific clustering patterns, with clear separation between injured and uninjured animals. Key metabolites identified: hippuric acid, 4-hydroxybenzaldehyde, and carnitine; may contribute mechanistically to the observed differences in muscle recovery. Social support promotes greater muscle regeneration following severe birth injury, potentially mediated through distinct metabolomic pathways. These findings highlight the importance of psychosocial factors in postpartum physical recovery.

Mohanna Finnikin

Political Science: Public Law, Marshall

Mentored by Christopher Stout

Slavery's Legal Shadow: The "Punishment for Crime" Exception and the Roots of Racialized Incarceration

The passing of the Thirteenth Amendment is widely celebrated as the United States' constitutional abolition of slavery, marking a formal end to this country's horrific system of racialized bondage that structured American society for centuries. Yet, on the topic of punishment, freedom, and racial inequality, the Thirteenth Amendment holds a paradoxical place in American constitutional history as well. Although its ratification in 1865 was portrayed as a decisive moral victory, the Amendment's inclusion of an explicit "except as a punishment for crime" clause complicates the narrative of its progress. Rather than this amendment representing an unqualified break from the past, like it should have been and fully abolishing the concept of slavery, this exception opened up a

legal backdoor to new forms of coerced labor and racialized punishment under the guise of criminal justice. My research is focusing on the constitutional and historical relationship between the Thirteenth Amendment's "except as a punishment for crime" clause and the development of the prison-industrial complex. Specifically, my project is examining how this constitutional exception has been interpreted in the courts, through different policies passed by Congress and state legislatures, and operationalized through different penal practices from Reconstruction to present day.

Natalie Fong

History/History, ERC

Mentored by Simeon Man

Conditional Citizenship and Chinese American Community: How the Cold War Reshaped Legal and Cultural Belonging

The Cold War provided the US government with an incentive to reshape immigration policies away from explicit racial exclusion, and towards national security concerns, framing immigration through the lens of loosely criminalized "subversion," or opposition to US anti-Communist policies. This was done through the passage of the 1950 McCarran Act, and the 1952 Immigration and Nationality Act, which rendered one deportable and ineligible for entry based on affiliation with a Communist organization. Although the Chinese community obtained the right to naturalization and increasing integration into the wider American society, their right to both legal and cultural citizenship was altered by the 1949 establishment of the PRC, which cast Chinese American organizations, as part of the "Communist front." This paper will explore how the practical enforcement of this conditional citizenship, through the FBI and the Chinese Confession Program, shaped the Chinese American community's identity and politics. While mainstream society advocated for and at times celebrated Chinese American assimilation, the government continued to redefine which classes of immigrations were "acceptable." Ultimately, Chinese Americans' efforts community efforts to gain cultural citizenship were undermined by government security policy and a culture of political repression, which racialized them as "perpetual foreigners."

Lillian Frank

Chemistry, Muir

Mentored by Nathan Romero

Synthesis of Heteroaryl Thianthrenium Salts for Direct Arylation Polymerization

Aryl halides can undergo Direct Arylation Polymerization (DAP) to form conjugated polymers through transition metal cross coupling reactions. Methods such as Suzuki, Stille, and Kumada cross coupling pose difficulties when controlling molecular weight of the polymer, owing in part to the high temperatures typically required for DAP. We hypothesized that altering the aryl halide structure into an aryl thianthrenium salt will allow for DAP reactions to be run at lower temperatures and thereby enabling increased control of the molecular weight. To test this hypothesis, various heteroaryl thianthrenium salts will be synthesized to determine if thianthrenium monomers possess suitable reactivity as pseudo halides. In order to synthesize structurally diverse thianthrenium salts, the focus of this project is to prepare fused ring thiophenes and related heterocyclic building blocks through a series of substitution reactions. Following the synthesis of these fused-ring heterocycles, we will synthesize arylthianthrenium monomers, optimizing for thianthrenation at one or both available sites of the heteroarene. Polymerizing the thianthrenium salts allows for the formation of conjugated polymers that have optoelectronic properties and can be used in a variety of electronic devices.

Bianca Frias

Cognitive and Behavioral Neuroscience, Muir

Mentored by Eiman Azim

The lateral reticular nucleus is required for the rapid and precise execution of goal-directed forelimb movements

Dexterous forelimb movements require the coordination of joints and muscles. Their speed and precision are achieved partly through rapid online corrections of motor output. While sensory feedback is required to assess movement outcomes, delays in sensorimotor pathways necessitate the use of faster predictive control to generate online corrections for fast and precise movements. The cerebellum is thought to support these corrections by using internal copies of motor commands to predict the sensory consequences of ongoing movement. The lateral reticular nucleus (LRN) is a brainstem structure that receives

internal copy signals predominantly from the cervical spinal cord and conveys them to the cerebellum. Little is known about how it contributes to the execution and coordination of rapid goal-directed forelimb movements. To address this, we: (1) recorded neural activity during reaching and evaluated the encoding of forelimb kinematics by LRN neurons in mice; and (2) perturbed LRN circuits on multiple timescales and evaluated the impacts on dexterous reaching movements. In vivo single-unit recordings showed that most LRN neurons encode forelimb joint kinematics. The responses of more than half of these neurons preceded changes in ongoing kinematics, consistent in nature with internal motor copies. While chronic ablation of LRN neurons had minimal effect on goal-directed reaching performance, acute optogenetic inhibition caused a reduction in movement speed, consistent with deficits observed in cerebellar patients. Overall, our findings reveal that the LRN conveys kinematic features of impending limb movement and posture to the cerebellum that can be used for online predictive control of forelimb movement.

Monica Galindo

Public Health - Medicine Sciences concentration (Herbert Wertheim School of Public Health and Human Longevity Science); Molecular & Cell Biology (School of Biological Sciences), Marshall

Mentored by Rahul Nene

Emergency Department Presentation for Acute Ischemic Stroke in Imperial County, California

Study Objectives: Imperial County is a rural border county in southeastern California where approximately 85% of the population is Hispanic, with high rates of poverty and limited healthcare infrastructure. The county has only two hospitals with emergency capacity: El Centro Regional Medical Center and Pioneers Memorial Hospital. Neither hospital is a certified stroke center or has in-person neurology services. Intravenous thrombolysis must be given within 4.5 hours of stroke onset and mechanical thrombectomy within 24 hours. Prior research shows that Hispanic patients, rural communities, and populations with low health literacy are less likely to present within these windows. This study evaluates how Imperial County patients access emergency care for acute ischemic stroke, including ED presentation rates, treatment, and transfer patterns.

Methods: This retrospective observational study uses the California Health Care Access and Information (HCAI) database, queried from 01/01/2018 to the most recent available

data. Included patients presented to an Imperial County ED with a primary or secondary diagnosis of acute ischemic stroke (ICD-10 I63.x) or TIA (G45.0-G45.8). Variables include demographics, stroke severity (NIHSS), comorbidities (Charlson Comorbidity Index), thrombolysis and endovascular therapy receipt, ED disposition, and transfer details. A secondary analysis evaluates Imperial County residents presenting to EDs outside the county.

Results: Pending data from HCAI.

Conclusion: Imperial County's relatively closed healthcare system offers a unique opportunity to evaluate stroke care access. Identifying gaps in presentation and treatment patterns will inform future interventions to address disparities in this high-risk population.

Tamanna Gandhi

Human Biology/Department of Biological Sciences, Marshall

Mentored by Cheryl Anderson

Assessment of Healthy Dietary Patterns for Cardiovascular Health in South Asians

Issues: Cardiovascular disease risk is modifiable by dietary practices. Although healthy dietary patterns are strongly associated with lower cardiovascular risk, most indices to measure diet were developed in predominantly non-Asian populations, although it is unclear if appropriate for South Asian populations living in the U.S.

Description: We conducted a literature review to evaluate how healthy dietary patterns that promote cardiovascular health (CVH) are assessed in South Asian populations living in the US. The dietary patterns reviewed include: Healthy Eating Index, Alternative Healthy Eating Index, Healthful Plant-Based Diet Index (hPDI), Planetary Health Diet (PHD), DASH-style diet, and Mediterranean-style diet.

Lessons learned: The hPDI appears the most suitable assessment tool for capturing the diets of South Asian populations living in the US while other indices omit culturally relevant foods. All of the healthy dietary patterns are plant-forward and thus relevant to a large percentage of vegetarians. However, limitations across the indices include difficulty disaggregating mixed dishes, the use of nutrient databases that may not capture traditional South Asian dishes, potential for artificially inflated scores due to wording used about red meat intake, lack of inclusion of herbs and spices, failing to account for culturally specific fats and oils, narrow definitions for added sugars, and exclusion of questions about certain foods such as potatoes, poultry, or dairy products.

Recommendations: Current dietary assessments should be adapted to include questions that capture the dietary behaviors of the South Asian populations living in the US for greater CVH promotion in the US.

Sophia Gao

Math-CS, Math Department, Muir

Mentored by Aaron Schulman

Attention Mech

Memory Mechanisms in Sequence Models: Comparison of Attention and State Space Models on Long-Context Recall

Lan Gao

Molecular and Cell Biology, Revelle

Mentored by Weg Ongkeko

Evaluation of Radiation Therapy's Effect on the Senescence Status of Tumor Microenvironment of HNSCC

Cellular senescence is a stress-induced, irreversible arrest of cell proliferation accompanied by a senescence-associated secretory phenotype (SASP), which may impair the immune system's ability to detect and eliminate cancer cells. Radiation therapy (RT) are standard treatments for head and neck squamous cell carcinoma (HNSCC) by inducing DNA damage. Despite their therapeutic utility, studies have shown that RT-induced DNA damage may also cause immune cell senescence in other cancers. The effect of these therapies on the senescence state of the tumor microenvironment (TME) in HNSCC has not been elucidated. We hypothesized that radiation treatment induces a senescent phenotype in the TME of HNSCC. In this study, we analyzed how radiation therapy influence the senescence-associated gene programs in the TME of HNSCC.

We found that radiation therapy induces functional remodeling and cell-type specific senescence status change in the HNSCC tumor microenvironment. CD8⁺ T cells subclusters enriched in cyclin D3 and CTLA4 show the clearest visual reduction. Cancer associated fibroblasts (CAFs) show increased subcluster diversity, with enrichment of

clusters that are expressing proliferative and inflammatory factors. CD8+ T cells exhibits subcluster-specific decrease in cell killing gene expression post treatment. This suggests radiation therapy could suppresses immune response within the tumor microenvironment. Finally, there is increased contribution of IL1 and SPP1 chronic inflammation signaling pathways to intercellular communication post treatment, with a subset of cancer stem cells exhibiting elevated involvement in these inflammatory pathways.

Alex Garcia

Department of Emergency Medicine, Warren

Mentored by Edward Castillo

Point-of-Care Innovation at the Frontline: Enhancing Concussion Diagnostics in the Emergency Department

Background: Concussions account for approximately 75% of the 2.8 million TBI-related emergency department (ED) visits annually. Current diagnostic workflows are often inefficient, with standard vestibular-ocular screenings (VOMS) facing significant implementation barriers in high-sensory, crowded ED environments. This results in inconsistent diagnostic accuracy and prolonged lengths of stay, contributing to ED overcrowding.

Methods: This is a prospective clinical trial to evaluate a novel virtual reality (VR) headset to assess concussions in the ED. This device captures objective ocular-motor measurements (e.g., saccades, smooth pursuit) to differentiate concussed from non-concussed patients. As of April 28, 2026 the project is currently awaiting Institutional Review Board (IRB) approval, with enrollment slated to begin upon authorization.

Challenges: Potential challenges include the feasibility of headset deployment during peak ED crowding and the exclusion of patients with pre-existing ocular or neurologic pathologies that may confound biometric data.

Significance: The integration of objective, portable VR diagnostics aims to alleviate the burden on acute care systems by providing rapid, standardized assessments. Beyond the ED, the portability of this technology allows for deployment in sports settings, enabling immediate sideline diagnosis and management. Future goals include evaluating the technical and operational feasibility of integrating this device in acute care workflows, in addition to demonstrating the VR headset's predictive value against long-term recovery trajectories to validate earlier intervention and improved outcomes across both clinical and athletic environments.

Miguel Gonzalez

Marine Biology, Revelle

Mentored by Vanessa ZoBell

Occurrence of Ultrasonic Antifouling Devices in the Santa Barbara Channel Islands; Implications for Marine Species and Acoustic Communication

Sound plays a critical role in marine ecosystems, many organisms rely on sound in their daily lives for communication, navigation, and survival. Meanwhile, shipping is also an important source of transporting goods across the globe. Ships generate noise pollution primarily from propeller cavitation, disrupting the environment of marine species. Because the hull of ships provides a ground for settlement, organisms like algae, barnacles, and mussels will settle underneath the ships. Shipping companies use ultrasonic antifouling devices which emit high frequency (20 - 80 kHz) sound waves to prevent organisms from settling on the bottom of ships to keep the hull clean and improve hydrodynamic abilities. There is limited research done on these devices to evaluate whether they are acoustically harmful to marine species. The goal of this project is to assess the occurrence and frequency range of sound emitted from these devices in the Santa Barbara Channel. This project will allow for a better understanding of how wide spread this new technology is used and the potential impacts to marine species.

Simret Gudat

Molecular and Cellular Biology, Muir

Mentored by Scott Biering

Elucidating the Molecular Determinants of DENV Mediated Endothelial Dysfunction and Vascular Leak

Dengue virus (DENV), a mosquito-borne pathogen, causes a range of disease manifestations, from mild fever to severe, potentially fatal conditions associated with vascular leak. The mechanisms behind DENV-triggered vascular leak were initially thought to result from a cytokine storm caused by uncontrolled viral infection. However, recent studies have shown that DENV's nonstructural protein 1 (NS1), secreted by infected cells into the bloodstream, directly triggers vascular leak by interacting with

endothelial cells. Endothelial cells maintain vascular homeostasis by forming a barrier that contains solvents and solutes within the circulatory system. NS1 disrupts this barrier, triggering endothelial dysfunction and leading to the depletion of key structures necessary for barrier function. Although the consequences of NS1 interaction with endothelial cells are known, the molecular determinants critical for this interaction remain largely unknown. DENV NS1 consists of three domains: β roll, wing, and β ladder. The β ladder domain contains both a hydrophobic membrane-embedded region and a hydrophilic surface-exposed region with charged amino acids believed to play a crucial role in interactions with host cells. My lab has created mutant NS1 proteins neutralizing key charged residues in the hydrophilic domain. We hypothesize that these mutations will impair NS1's ability to interact with endothelial cells and trigger endothelial dysfunction. By identifying the critical amino acids involved, we aim to uncover potential targets for therapeutic interventions to address severe dengue.

Stella Hale

Cognitive Science with specialization in Neuroscience, Marshall

Mentored by Weg Ongkeko

Of Rats and Men: Transcriptomic Convergence Between Alzheimer's Disease and Microplastic Exposure

Background: Micro- and nanoplastics (MNPs) have been detected in human blood, fluid and tissue, yet their neurobiological impact is poorly understood. Rodent models show that MNPs can cross the blood-brain barrier and alter AD-relevant neurotransmitter pathways. However, this study integrates human molecular data to investigate whether MNPs contribute to early Alzheimer's disease (AD) related processes.

Methods: We performed single-cell RNA sequencing of public transcriptomic datasets involving MNP-exposed rats and human AD brain tissue (cortex and hippocampus). Differential expression analysis generated MNP-responsive, while human single-cell data were aggregated into cell-type profiles and ranked by AD association using DESeq2 across major neural, glial, and vascular populations. Rat genes were mapped to their human orthologs, and cross-dataset convergence was assessed using multilevel fast gene set enrichment analysis (fgsea). Leading-edge genes from significant enrichments were then used to identify candidate driver genes.

Results: The transcriptional pathways responsive to microplastics overlapped more significantly with those in microglia and other AD-relevant cell types than in the hippocampus. In microglia, genes that were downregulated following microplastics

exposure showed the most significant enrichment in AD-ranked datasets, mainly involved in innate immune signaling, lipid metabolism, synaptic organization, and glial activation, all of which are pathways strongly implicated in AD pathobiology.

Conclusions: This study provides a systems-level framework linking the biology of environmental exposure to neurodegenerative vulnerability and identifies candidate pathways for further mechanistic investigation. Ongoing validation studies will further examine the overlap in gene signatures and guide future analyses.

Rebecca He

Sociology, Sixth

Mentored by John Skrentny

The Tightrope of the LinkedIn Lens: Gendered Impression Management in Professional Profile Photography

This study examines gender differences in impression management (IM) as expressed through LinkedIn profile photographs among undergraduate members of two career-oriented clubs at a research university: a non-STEM business consulting club and a STEM computer science and engineering club. Drawing on Goffman's (1959) dramaturgical framework and West and Zimmerman's (1987) concept of "doing gender," the study analyzes profile photos of 40 students (10 males and 10 females per club) using IM codebook for rating the professional quality of the professional profile pictures. The coding utilizes a 50-point instrument measuring three dimensions: clothing and attire, facial appearance and gesture, and photographic/compositional quality. A chi-square test of independence ($\chi^2(6) = 14.35, p = .026$) and Mann-Whitney U tests reveal a statistically significant gender gap within the STEM club ($U = 23.0, p = .041, r = .456$), with female CSEC members scoring substantially higher than male members. Female members of both clubs score comparably ($p = .762$), suggesting that elevated impression management effort among women reflects a broad gender-based norm rather than one uniquely triggered by field-specific underrepresentation. Theoretical implications for gendered compensatory labor and digital professional identity are discussed.

Santos Hernandez

Aerospace Engineering / MAE, Revelle

Mentored by Farhat, Beg

Data-Driven Closure Modeling and Stability in Compressible Reduced-Order Models

Reduced-order models (ROMs) provide a computationally efficient framework for approximating complex fluid dynamics in applications such as high-speed aerodynamics and propulsion systems. However, when applied to compressible flows, classical Proper Orthogonal Decomposition (POD)–Galerkin models often exhibit long-time instability and divergence, limiting their reliability for prediction, control, and design.

This research investigates the stability of reduced-order models in compressible shear flows by examining the effects of modal truncation and unresolved nonlinear interactions. The study compares classical stabilization techniques, such as modal damping and eddy-viscosity closures, with data-driven approaches including Sparse Identification of Nonlinear Dynamics (SINDy) and neural network-based closure models.

Using high-fidelity simulation data, reduced-order models will be constructed and evaluated across subsonic and transonic regimes. Model performance will be assessed using metrics such as time-to-divergence, reconstruction accuracy, and modal energy evolution.

By systematically comparing physics-based and data-driven closure strategies, this work aims to identify stability limits and establish best practices for constructing reliable reduced-order models in compressible flow applications.

Sophia Hornbeek

Psychology, ERC

Mentored by Karen Dobkins

The Effect of Perceived Similarity in Self-Esteem on Romantic Relationship Satisfaction

Self-esteem, defined as an individual's overall evaluation of self-worth, is linked to relational security, positive partner perceptions, and greater relationship satisfaction. However, less is known about how perceived similarity in self-esteem influences relationship outcomes. Drawing on research on egocentric projection and positive

illusions, the present study proposes that individuals' perceptions of similarity with their partners, rather than objective similarity, may play a key role in relationship functioning. Specifically, this study examines whether perceived similarity in both global and appearance-related self-esteem predicts romantic relationship satisfaction. It is hypothesized that individuals who perceive their partners as having similar levels of self-esteem will report higher satisfaction, as these perceptions may signal compatibility, mutual understanding, and balanced relational value. Additionally, using an existing dataset, this study will explore whether perceived similarity in global or appearance-related self-esteem is more strongly associated with satisfaction than perceived similarity in personality traits, allowing for a cross-domain comparison. Participants ($N \approx 100$) will be undergraduate students currently involved in monogamous relationships. UCSD participants will report their own and their perceived partner's self-esteem, enabling the calculation of perceived similarity scores, as well as relationship satisfaction, attachment style, relationship duration, and age. This research is important because it clarifies the role of perceived similarity in self-esteem, extending prior work that has primarily focused on actual self-esteem. Understanding this mechanism may provide insight into how perceptions shape relationship outcomes and inform interventions aimed at improving relational satisfaction.

Jack Howard

Political Science/Data Analytics, Muir

Mentored by Chris Stout

The Electoral Geography of Higher Education: How Campus Proximity and Remote Learning Shape Partisan Voting in California

This project examines whether proximity to colleges and universities helps explain precinct-level Democratic vote share in California's 2020 general election. Drawing on a geospatial dataset of more than 7,000 precincts, I combine statewide election returns with institutional location and enrollment data from NCES and IPEDS, along with American Community Survey demographic controls. I construct distance-based and inverse-distance-weighted measures of exposure to nearby colleges, including total student enrollment and the share of students learning remotely, partially remotely, or in person. I then evaluate these measures using multiple modeling approaches, including OLS, LASSO, and Random Forests. The results show that precincts with greater exposure to higher education institutions, especially those near larger and more physically present

student populations, tend to report higher Democratic vote share even after accounting for race, income, education, and population density. Including college exposure variables also improves predictive model performance relative to demographic-only baselines. More broadly, the project argues that colleges function not only as educational institutions, but also as place-based civic and political anchors whose influence extends into surrounding communities. By integrating spatial institutional data into models of political behavior, this research contributes to work on political geography, neighborhood effects, and the contextual foundations of voting behavior.

Dimple Htake Htar

Political Science: Public Law, Sixth

Mentored by Todd Gilmer

Life After Shelf

In the United States, approximately 1.6 billion unopened and unexpired prescriptions are discarded annually, while in conflict-affected regions of Myanmar, essential medicines remain intermittently unavailable despite persistent clinical demand. Drug classes most frequently discarded within the US account for over 80% of essential medicines with the highest unmet demand, indicating that recovery of even 0.5–1% of this surplus could generate 8–16 million viable treatment courses per year. Medicine distribution logistics remain predominantly reactive due to structural non-interoperability between clinical reporting systems (DHIS2) and logistics management platforms (eLMIS), producing asynchronous datasets that prevent joint modeling of patient demand and inventory depletion. This architectural fragmentation eliminates predictive visibility at the facility level, contributing to rising essential medicine stockouts from 29% to 49%. This model addresses this gap through three stages. First, surplus pharmaceuticals were tracked using geocoded facility- and warehouse-level inventory data integrated into a space–time–attribute GIS framework, enabling continuous monitoring of stock accumulation, consumption patterns, and remaining stability windows. Second, stockout risk was predicted by computing hazard functions from Cox and parametric survival models parameterized by time-indexed stock states and spatial covariates, yielding facility–commodity-specific risk estimates over 7-, 14-, and 28-day horizons. Finally, outputs from surplus tracking and stockout prediction were integrated within a matching engine pairing surplus drug lots to at-risk clinics. Modeling suggests that advance stockout forecasting could reduce treatment interruptions by 30–45% and stabilize medication access for 150,000–400,000 patients per year.

Xueqian Huang

Business Economics, Seventh

Mentored by On Amir

Price-Based vs. Quantity-Based Promotions: Effects Across Product Categories with Different Demand Elasticities

Firms in the market often compete intensely. To attract consumers and enhance their competitive edge, firms often carry out promotions. Promotions in the market are mainly divided into price-based and quantity-based types. Price-based promotions usually refer to direct price cuts that allow consumers to purchase the same quantity of products at a lower price. Quantity-based promotions usually refer to increasing the quantity without raising the price, such as “buy one get one free”, allowing consumers to get more products with the same amount of money. When firms adopt different types of promotions, they will have different impacts on sales. Therefore, I want to investigate the performance of price-based and quantity-based promotions. Moreover, people have different demands for different products, so promotions for different products have different effects on consumers’ behavior. We use demand elasticity to define the sensitivity of the quantity demanded for a product to price changes. Products can be classified as normal goods, inferior goods, or luxury goods based on their demand elasticity. When firms run promotions, people’s willingness to purchase products is influenced by the demand elasticity. This study aims to explore the impact of price-based and quantity-based promotions on products with different demand elasticities to determine the optimal promotional model. This is significant because it can provide firms with references for promotional strategies, enabling them to increase sales more effectively and enhance their profitability.

Shaun Israni

Data science/HDSI, Eighth

Mentored by Peter Chi

Phylogenetic Inference for Non-Gaussian Models

On the topic of phylogenetic inference for continuous and discretized traits, a recurring issue is that many widely used methods are either optimized for Gaussian models (e.g., Brownian/OU) or become computationally expensive when we move to more realistic, non-Gaussian trait evolution and observation processes. Recent work suggests that we can expand the class of tractable models by combining classic phylogenetic dynamic programming (Felsenstein-style pruning) with numerical integration, avoiding Monte Carlo while retaining flexibility. The following question/issue arises: how can we design scalable, data-science-oriented inference methods that (i) remain fast on large trees, (ii) handle non-Gaussian trait models and messy observations, and (iii) connect cleanly to optimization viewpoints such as least-squares fitting? My answer to the question is as follows: a modern phylogenetics toolkit should treat inference as an algorithmic design problem: leverage pruning-style dynamic programming, numerical quadrature, and optimization (including least squares) to build scalable inference pipelines that can move beyond Gaussian assumptions while remaining computationally practical. I will support this thesis by examining (a) the recycled pruning + quadrature framework for non-Gaussian trait likelihoods, (b) least-squares-style objectives for tree/parameter fitting, and (c) robustness-oriented alternatives (e.g., heavier-tailed noise models or threshold/censoring models).

Amara Iverson

Biochemistry, Marshall

Mentored by Yuzhong Liu

Engineering Non-Ribosomal Peptide Synthetases for the Discovery of Novel Antibiotics

Antimicrobial resistance (AMR) is a growing crisis exacerbated by the lack of discovery of new and effective antimicrobials. Our project aims to address this by developing a high throughput platform utilizing non-ribosomal peptide synthetase (NRPS) megaenzymes. Using the antibiotic clovibactin as a model, we will expand chemical diversity by engineering NRPS adenylation domains to incorporate unnatural amino acids. By employing synthetic biology and chemical synthesis, this approach will enable the screening and identification of new antibiotics with novel functions to combat AMR.

Julian Jackson

Astronomy and Astrophysics, Sixth

Mentored by Adam Burgasser

Crazy Cool Quasars: An Infrared Spectra Survey of Quasars

Quasars are compact regions of bright emissions powered by supermassive black holes (106 - 1010 Solar Masses) that are rapidly consuming gas and dust. They have long been observed at optical wavelengths through surveys such as the Sloan Digital Sky Survey (SDSS), with thousands of spectra published. However, there are a far more limited number of quasar spectra covering near-infrared (NIR) wavelengths due to the lack of efficient NIR spectral surveys. NIR observations of quasars is important, as these sources can be very faint and heavily redshifted, making them brighter at longer wavelengths. This project aims to expand the number of NIR quasar spectra by reducing and analyzing data from the IRTF/SpEx archive, a collection of over 20 years of NIR spectral observations that include previously unpublished quasar observations. I will present the process by which these observations were identified and reduced using the newly-developed pypextool package. I will then describe spectral analysis of these data, in particular measurement of redshifts and emission line strengths using the composite spectral template of Glikman et al. (2006). These new spectra will help improve our understanding of the geometry, emission processes, and evolution of quasars over cosmic time.

Pali Jain

Data Science, Sixth

Mentored by Julian Mcauley

Do Hiring Algorithms Treat Everyone Equally? A Study of Bias in Machine Learning

This study investigates whether simple machine learning models produce different outcomes across demographic groups and whether basic fairness adjustments can reduce these disparities. A public recruitment dataset was used to analyze the relationship between applicant features, including age, gender, and race, and hiring outcomes. Initial exploratory analysis involved calculating acceptance rates and visualizing hiring outcomes across demographic groups, revealing differences in selection rates.

A logistic regression model was then developed to predict hiring decisions based on selected features. The model's predicted probabilities were evaluated to determine whether disparities persisted across demographic groups. Results showed that predicted hiring outcomes varied by gender, race, and age, indicating that even simple models can reflect underlying patterns in the data.

To address these differences, a basic fairness adjustment technique was applied to the model's predictions. After adjustment, disparities between groups were reduced, demonstrating that simple methods can improve fairness in machine learning systems. These findings highlight the importance of evaluating algorithmic decisions and suggest that even straightforward approaches can help mitigate bias in real-world applications.

Erin Jang

Neurobiology, Seventh

Mentored by Weg Ongkeko

Identifying Microplastic-Associated Transcriptional Signatures in Human Liver Cancer

Abstract redacted due to proprietary information.

Lily Ji

Microbiology, Revelle

Mentored by Scott Biering

Calprotectin modulates matrix metalloproteinase-9 activity and alleviates dengue virus pathogenesis

Abstract redacted due to proprietary information.

Rayan Jouny

Human Biology BS, ERC

Mentored by Christopher Coyne

Derivation of a Score to Stratify Serious Adverse Outcome Risk in Cancer Patients with Acute Pulmonary Embolism Presenting to the Emergency Department: a Multicenter Study

Cancer patients presenting to the emergency department (ED) with acute pulmonary embolism (PE) represent a high-risk subset of patients. Existing scores are nuanced in their approach to cancer as a comorbidity in stratifying PE by mortality risk, and fail to account for the heterogeneity of different cancer subtypes, their stages, concurrent treatments, and comorbidities, despite these determinants of thrombogenicity being well-established in the literature. In this multicenter retrospective study, we sought to establish associations between PE mortality risk and clinical risk factors pertaining to the cancer, its treatment, or the state of the patient, using a multiple regression analysis, strengthening statistical power by grouping cancer subtypes as appropriate. We derived a weighted cancer-PE Adverse Outcome Score from the multivariable model by assigning integer points proportional to the regression coefficients. The score incorporated ECOG performance status, Charlson Comorbidity Index, recent hospitalization, stage IV disease, high-risk cancer type, and leukocytosis. Scores ranged from 0 to 14 and were categorized as low risk, 0–2; intermediate risk, 3–4; and high risk, ≥ 5 . In the full cohort, the composite adverse outcome occurred in 17.8%, 41.3%, and 62.8% of patients across these strata, respectively. Thirty-day mortality increased from 2.2% in the low-risk group to 34.9% in the high-risk group. Thus, we derive a clinically practical, trichotomous stratification system, fit for use in the emergency department, to score the mortality risk of cancer patients with acute PE whilst accounting for the heterogeneity of cancer presentations.

Eleanor Jung

Neurobiology, Sixth

Mentored by Gabriel Wardi

Capillary Refill Time as an Adjunct to Lactate in Guiding Resuscitation Strategies for Patients with Sepsis

Each year, there are over 1.7 million cases of sepsis in the United States, resulting in over 350,000 deaths annually. Yet, the ideal strategy for initial resuscitation is unclear. Currently, lactate-guided resuscitation is considered the standard of care. Other approaches include capillary refill time (CRT), mottling score (assessing skin discoloration around knees) and other metrics that attempt to measure micro-circulatory changes. In particular, CRT has been compared to lactate as an alternative for guiding resuscitation with encouraging results in a recent international randomized trial. Despite recent efforts to design better protocols, the specifics on how to best implement an approach combining lactate and CRT remains unclear. This review synthesizes recent evidence to clarify how these measures can be integrated in clinical practice. Through primarily searching in the PubMed database and screening for articles (published 2016-present), 12 highly relevant publications were reviewed and synthesized. Data suggest that in early resuscitation, lactate level is dependent on circulation and is an accurate measure of blood perfusion. However, in late resuscitation (>12 hours since ICU admission), lactate becomes more heavily affected by metabolic reprogramming, when immune and parenchymal cells shift from oxidative phosphorylation to aerobic glycolysis, potentially misleading physicians to administer excessive intravenous fluid. Instead, multimodal tissue perfusion assessment methods, including CRT and mottling score, should be used. More research is needed to understand factors contributing to switch from early to late resuscitation. Ultimately, leveraging lactate, continuous lactate monitoring, and CRT may improve patient outcomes and reduce the economic burden of sepsis.

Katelyn Kang

Molecular and Cell Biology/ Biological Sciences, Eighth

Mentored by Andrew Chisholm

Investigating the C. elegans extracellular matrix protein DBD-2 as a model to study pathogenic signal peptide mutations

Abstract redacted due to proprietary information.

Alfred Kao

Molecular and Cell Biology, ERC

Mentored by Weg Ongkeko

Social determinants of California cancer incidence and mortality at the MSSA level: a comprehensive ecological study

Social determinants of health are defined as the “nonmedical factors that impact one’s health”. Factors such as age, gender, demographics, socioeconomic burden, and healthcare accessibility have a substantial impact on disease incidence and outcomes. Importantly, social determinants of health are a major driver of health disparities.

Medical Service Study Areas are subregions within a county with borders drawn based on census tracts, population density, socioeconomics and demographics. It is a California-specific designation used to better analyze healthcare access and identify underserved areas. MSSAs are stratified into rural, urban, and frontier based on population density.

This project aims to leverage MSSA-level cancer incidence and mortality data (from California specifically) for 12 cancers to investigate the role of social determinants of health in cancer disparities. Previous studies focus on cancer incidence/mortality at the country or state level, which neglects the heterogeneity of socioeconomic well-being within the state at the county or city level. Other studies investigating cancer at the county level focus on a single determinant (such as one paper focusing on the role of rurality on cancer disparities).

By leveraging GIS (Geographic information system) data and spatial analyses, as well as regression techniques, this project aims to provide a comprehensive evaluation of the main socioeconomic drivers of cancer disparities in California.

Mridu Karanam

Molecular and Cell Biology / School of Biological Sciences, Marshall

Mentored by Lars Bode

Nutrient Composition of Human Milk for the Premature Infant: Macronutrient Analysis of Pre and Post Enteral Feed

In a neonatal intensive care unit (NICU) setting, continuous enteral tube feeding of human milk can result in nutrient loss, particularly fat, due to separation of milk fat globules and adherence to tubing surfaces (Paulsson et al., 2021). These losses reduce delivery of essential fatty acids and other bioactive components critical for infant development (Zozaya et al., 2018). Through this research, we aimed to characterize the impacts of enteral tube feeding on fat, lactose, protein and human milk oligosaccharides (HMOs). Twenty-five paired clinical samples were collected from the NICU at Jacobs Medical Center in La Jolla. Pre-feeding (prepped) and post-feeding (scavenged) samples were analyzed. Fat was measured by creatamocrit, lactose by Megazyme Lactose Assay, protein by Bicinchoninic Acid Assay, and HMOs by High-Performance Liquid Chromatography with fluorescent detection. Mean fat content was higher in scavenged (4.88 g/dL) compared to prepped sample (3.70 g/dL), indicating that scavenged samples are not representative of the milk that was fed to the baby and that fat is lost during an enteral feed. There were no significant losses of HMOs, range of HMO recovery was between 86-106%. Mean lactose remained the same (5.89 g/dL vs. 5.94 g/dL), as well as mean protein (1.98 g/dL vs. 1.93 g/dL). Losses were most pronounced in triacylglycerol and diacylglycerol lipid classes. Future directions should include optimizing milk preparation and feeding protocols to minimize fat loss and support better health outcomes for NICU infants.

Asha Kent

Political Science-Public Law + Communications, Seventh

Mentored by Christopher Stout

Impact of Mass Incarceration on Youth & Political Participation

How do family experiences with incarceration influence youth political behavior? This study views mass incarceration as a larger social and political institution that alters relationships between people, communities, and the state. I hypothesize that youth whose family members are incarcerated or previously incarcerated have negative perceptions of the state. These negative experiences with incarceration are less civically engaged, vote less in elections, and overall, have weak trust in various forms of government. To test my hypothesis, I will use a nationally representative data set, the 2018 Family History of Incarceration Study. Specifically, I will test how having a family member in prison shapes people's willingness to participate in a variety of activities. This study works to emphasize how mass incarceration leads to uneven patterns of political indoctrination and participation by focusing on youth experiences in both family and local settings.

Jay Keshava

Major: Environmental Systems and Economics, Departments: SIO and ECON, Seventh

Mentored by Katharine Ricke

Quantifying Carbon Sequestration Loss from Climate-Induced Mangrove Decline

This project investigates the relationship between mangrove area loss and carbon dioxide sequestration estimates in blue carbon project (BCP) areas. The BCPs investigated span across Central and South America, Africa, and Asia. Each project is either under validation or registered by Verra's 'Verified Carbon Standard' (VCS). The project types fall under the categories of ARR (Afforestation, Reforestation, and Revegetation) or REDD (Reducing Emissions from Deforestation and Degradation). To research this topic we built upon the projections and results of 'A warming ocean threatens mangrove restoration targets and deepens global inequities in ecosystem service losses' (Bastien-Olvera et al, 2025). Specifically, we used the model equation, preferred values, and sea surface temperature of the hottest month (SSTH) projections for grid cells to estimate area loss in BCPs. Using the equation $\log(\text{Area}) = (\beta_1)\text{SSTH} + \beta_2(\text{SSTH})^2$, mangrove area in a grid cell was calculated based on SSTH. The SSTH projections for each project area were chosen based on the grid cell where the project is located. To quantify the $\Delta\text{CO}_2\text{e}$ sequestered due to climate change, original CO_2e sequestration estimates for BCPs were inputted into our estimation method that connects mangrove area to carbon sequestration. From this, we were able to calculate the $\Delta\text{CO}_2\text{e}$ sequestered. Following the VCS methodology, we applied a buffer value to convert $\Delta\text{CO}_2\text{e}$ (units of tCO_2e) into ΔVCUs (Verified Carbon Credits). After calculating the ΔVCUs , a dollar value per VCU can be used to estimate the economic loss in project areas due to climate change.

Momo Kihara

Cognitive Science, Sixth

Mentored by Noriko Nagata

When Culture Colors the Mind: Possible Acquired Synesthesia and Consistent Color Associations among Competitive Karuta Players

Synesthesia has historically been conceptualized as a perceptual phenomenon that emerges in early childhood, predominantly based on subjective accounts from individuals with innate synesthesia. This study challenges that premise by exploring the possibility that acquired synesthesia can also develop through intensive perceptual learning. The research focuses on experienced participants in Competitive Karuta, a traditional Japanese card game that requires rapid auditory recognition, spatial memory, and motor coordination. Within this culturally structured practice environment, the study investigates whether long-term, consistent training can facilitate the emergence of grapheme-color and/or sound-color synesthesia.

In Competitive Karuta, players are tasked with memorizing the spatial arrangement and involves long-term exposure to consistent auditory, visual, and linguistic stimuli under conditions of high attentional demand. A questionnaire survey was followed by screening tests, which revealed 11 self-reported synesthetes, confirmed through consistency measures. We examined whether the distribution of synesthetic colors showed clustering in color space, as reported in prior studies on innate synesthesia. The findings revealed that both visually presented and auditorily recited stimuli prompted synesthetic colors that formed systematic clusters. The distribution patterns observed in this study closely align with those documented in previous research on innate synesthesia, demonstrating a high degree of consistency. These findings collectively indicate that synesthetic associations developed through extensive training can attain a level of structural stability that is comparable to that found in innate synesthesia. The findings indicate that, at least for specific stimuli, synesthetic associations may develop through experience rather than being solely attributable to innate predispositions.

Chloe Kim

Public Health, Sixth

Mentored by Anne White

Reassurance Across the Care Trajectory: A Longitudinal Case Study of Clinical Interaction

Clinical care often unfolds across multiple encounters, requiring communication practices to adapt over time. Within this longitudinal context, reassurance plays an important role in clinical communication, particularly when reducing patient concern while managing complex health issues. The form and timing of reassurance may be shaped by where patients are in the course of care. While reassurance has been studied within individual encounters, how it is delivered and responded to across repeated visits remains under-

examined. This study explores how physician reassurance is used across a longitudinal care trajectory. Using six video-recorded clinic visits conducted between September 2013 and January 2014 at a rural Texas general surgery practice, Conversation Analysis (CA)—a qualitative method for analyzing naturally occurring interaction—was applied to examine how physician reassurance is delivered and responded to across a series of encounters between a physician and a single patient presenting with multiple health concerns. Instances of reassurance were identified and compared across visits to examine how their form and function vary. Physician reassurance was used in multiple ways, with two prominent uses emerging at key points in the care trajectory: (1) responding to patient overwhelm and uncertainty through explicit, supportive reassurance; and (2) marking the closure of care through explicit, affirmational reassurance emphasizing treatment success. Outside these moments, reassurance occurred less frequently as visits became more routine following treatment. These findings highlight how physician reassurance varies across the course of care, offering insight into how communication can be adapted to patients' needs at different stages of the clinical encounter.

Elizabeth Kim

Business Psychology, Marshall

Mentored by Weg Ongkeko

Integrative Multi-omic Modeling of Osteosarcoma Prognosis

Osteosarcoma is the most common bone cancer in children and young adults. Many patients develop metastasis, and there is a lack of reliable biomarkers to predict tumor progression. Existing prognostic models perform fairly well, achieving Area Under the Curve (AUC) around 0.85-0.87, but they usually use only one data modality.

Osteosarcoma behavior is influenced by gene expression, immune cell infiltration, microbial signals, and fusion gene events. However, as osteosarcoma tumors are very diverse, relying on one type of data may not capture their full complexities. Although combinations of multiple data types, or multi-omic, methods are gaining interest, the prognostic potential of such combinations remains underexplored.

This project aims to analyze osteosarcoma sequencing datasets to identify multi-omic biomarkers associated with 1-, 3-, and 5-year survival. A machine learning model will be created using gene expression, immune cell composition, microbial abundance, and fusion genes to predict patient survival. By integrating multiple data types, this project will provide a more comprehensive understanding of osteosarcomas and strengthen prognostic predictions to inform treatment strategies.

Sharon Kim

Education Sciences, Muir

Mentored by Amy Bintliff

The Long Road to AP: How EL Designation Shapes Academic Trajectories

This research aims to address the specific challenges EL students face in pursuing advanced-level coursework and curriculum in California secondary schools. It will specifically examine how placement in EL tracks over multiple years shapes students' academic trajectories and access to AP-level coursework, arguing that the EL designation may function as a structural gatekeeping mechanism that negatively affects the opportunities available to these students. It will also investigate EL participation differences across AP subjects to better understand whether language support systems inadvertently contribute to stratified academic pathways. Understanding this relationship is essential for designing more equitable instructional models that support language development while preserving access to rigorous academic opportunities.

Woosik Kim

Computer Science / CSE, Sixth

Mentored by Pengtao Xie

ShowBrand

My research project, ShowBrand, explores how AI-based image recognition systems can identify products and brands from user-uploaded images. The project uses external image recognition models and AI services to analyze product images and return possible product or brand information. Rather than focusing only on whether the system can correctly identify an item, this research also examines how uncertainty affects the reliability of the system.

A key focus of this project is understanding what happens when images are ambiguous, low quality, edited, or visually misleading. These cases can cause AI models to make incorrect predictions or become overly confident in uncertain results. ShowBrand is used as a prototype system to study how confidence scores, unclear model outputs, and API dependency can influence the final result shown to users.

This research connects computer science, security, and system reliability. It considers how manipulated or confusing images may create risks in AI-powered product recognition and how systems can better communicate uncertainty instead of presenting uncertain results as facts. Through this project, I aim to better understand the limitations of AI recognition tools and explore design approaches that make AI-assisted product identification more transparent, reliable, and safer for users.

Sophia Kistler Kistler

Cognitive Science, ERC

Mentored by David Borgo

Creative Cognition: How active creative engagement interacts with daily emotions and wellbeing

This project investigates the psychological and personal impacts of engaging in a consistent creative outlet, specifically music creation, within a college environment. Drawing from both a cognitive science perspective and personal artistic practice, the experience explores the central question: what can be gained from regularly participating in creative expression? Over the course of an academic quarter, I dedicated time each day to songwriting, transcription, recording, and music production using personal instruments, voice, and digital audio software. Throughout this process, I tracked changes in mood, stress, and motivation using daily self-report scales taken at multiple points of the day (morning, pre-practice, and post-practice). This data was compiled and analyzed using excel spreadsheet tools to identify any short-term or long-term trends associated with creative engagement. The results revealed mixed outcomes in emotional changes. There were both positive and negative impacts from the daily practices over the course of a quarter. This could imply certain trade-offs that come with additional commitments as well as how the presence of external factors, such as academic pressure and time constraints, might also play a significant role. Beyond the data, the project resulted in meaningful personal growth and skill development across multiple musical modalities, strengths I am very happy to have grown. The final presentation will include both the completed musical works and a data-driven analysis of the recorded trends. Overall, this

project highlights the complexity of creative expression as both a personal and psychological tool, emphasizing its value while acknowledging the broader context surrounding it.

Seunghee Ko

Sociology, Eighth

Mentored by Vanesa Ribas

Opportunity-Hoarding in the Korean Labor Market: Activist Perceptions and Institutional Demands

This study examines how Korean labor rights activists understand “opportunity-hoarding” within Korean labor market structures. Applying Erik Olin Wright’s integrated theoretical framework, which distinguishes stratification, Weberian market exclusion, and Marxian production relations as sources of opportunity-hoarding mechanisms, this study bridges prominent class theory and labor rights activists’ perceptions. Based on semi-structured interviews with five leaders from notable Korean labor organizations specializing in contingent and platform labor, union and labor relations research, and women’s labor advocacy, the analysis addresses three research questions: how activists perceive opportunity-hoarding, its influence across Wright’s dimensions, and their demands in response.

Findings reveal activists frame wages, precarity, and blocked mobility as relational outcomes of corporate power operating through legal non-recognition and institutional exclusion, rather than individual-deficiency or between-worker competition. The Weberian dimension dominates analyses of regular/non-regular divides, while stratification appears secondary to structural misclassification. The Marxian dimension emerges consistently as a diagnostic frame, but not primarily through control over labor effort; activists emphasize capital’s contestation of the legal boundaries that determine who is recognized as a worker and what claims can be made.

Activists demand institutional reform: expanding the legal “worker” definition and establishing baseline protections for nonstandard employment. Strategic tension exists over broadening the Labor Standards Act versus a Basic Act for Working People. The study illustrates that activists perceive opportunity-hoarding relationally and institutionally, identifying a form of class power operating at the level of institutional

boundary-setting that precedes and conditions Weberian and Marxian relations. Limitations include the small purposive sample.

Yuki Kogane

Exchange Program, Eighth

Mentored by Branislav L. Slantchev

Threat Perception and the Use of Force: Evidence from U.S. Foreign Policy Decision-Making (1947–1988)

How does threat perception shape state behavior in international crises? Although threat perception is central to International Relations theory, its behavioral effects have remained difficult to test due to severe measurement and temporal limitations, leading scholars to rely primarily on structural variables and formal models. This study argues that heightened threat perception tends to produce "strategic inhibition" rather than the intensification of military hostility: as perceived threat rises, decision-makers anticipate higher costs and adopt more cautious strategies to avoid unmanageable escalation. This inhibition occurs more against nations with stronger military power. However, the image one holds regarding adversaries may reverse the dynamics. For example, the U.S. behaved much more aggressively toward countries like the Soviet Union, compared to other nations holding similar capabilities. I test this theory using declassified U.S. foreign policy meeting transcripts and merging them with high-frequency crisis event data. I construct daily measures of U.S. elite threat perception by applying machine learning to the transcripts. Employing Bayesian multinomial logistic regression, this study reveals that the subjective threat perception of national leaders has independent effects on state behavior, even after controlling for objective situational and signaling factors. The analysis shows the primacy of psychological constructs in understanding state behavior, demonstrating that leaders' subjective perceptions possess independent explanatory power beyond objective structural constraints.

Arya Krishna

Microbiology, School of Biological Sciences, ERC

Mentored by Sergey Kryazhimskiy

Fitness effects of spontaneous mutations in budding yeast vary across strains and environments

One of the central suppositions of evolutionary theory is that most mutations decrease fitness of organisms, and only very few mutations increase it. However, recent studies have suggested that instead, most mutations may be deleterious only in relatively well adapted organisms, but become beneficial in poorly adapted organisms. To test this pattern for spontaneous mutations, we conducted a mutation accumulation experiment in yeast *Saccharomyces cerevisiae* in which several strains with varying background fitness were propagated for 61 generations with minimal action of natural selection, allowing each strain to accumulate approximately three to nine new mutations. We then measured how the growth rates of these strains changed during this experiment. We found that in a permissive, nutritionally rich environment, the accumulation of spontaneous mutations led strains that initially grew quickly to lose fitness on average, whereas strains that initially grew slowly gained fitness on average. In contrast, in another more stressful environment, all strains gained or lost fitness by the same amount irrespective of their initial fitness. Overall, these results suggest that the statistical distribution of the effects of random mutations is far more complex and variable than previously thought.

Sanji Kumar

General Biology & Biochemistry, Eighth

Mentored by Alexis Komor

Prime Editing Streamlined Target Optimization (PESTO) of Clinically Relevant Target Genes.

Prime editing (PE) is capable of doing genomic DNA edits without a need for double stranded breaks (DSBs) or a homologous template (HDR). A major bottleneck of Prime Editing technology is the optimization of prime editing guide RNAs (pegRNAs). Prime Editing Streamlined Target Optimization (PESTO) is a high-throughput system that refines gene editing efficiency by decreasing the optimization time of various pegRNAs. PESTO involves constructing a lentiviral library of pegRNAs to test on the same plasmid

containing the respective target genes APP, PSEN1, JAK2, CFTR, and BAP1. With this cellular system, PESTO screens can be designed and executed by testing different prime editor backbones (via cellular transfection) alongside a cell line containing the pegRNAs in mammalian cell lines HEK293T and K562s. After editing, the cells are sorted via fluorescent proteins like GFP and BFP. Genomic DNA from the cell line is amplified for Illumina Next-Generation Sequencing. In optimizing the bioinformatics pipeline for the readout of the screen from NGS, the optimal pegRNA:PE combination that corrects these harmful mutations can be determined in an efficient manner.

Sonija Lam

Chemical Engineering, Marshall

Mentored by Zeinab Jahed

Examining the Use of Nanoelectrodes to Enable Next-Generation Neural Recording Devices

Abstract redacted due to proprietary information.

Kira Lavine

Anthropology, ERC

Mentored by Zachary Dunseth

Camelid Coprolites: Reconstructing Virú Pastoralism through Phytolith Analyses of Chicama Valley Archaeobotanical Taxa

Originating from the Viru Valley of northern Peru, the Virú state (ca. 200 B.C.E. - 700 C.E.) was the earliest state to expand and establish colonies in the Moche and Chicama Valleys (Millaire et al. 2016). Iconic to Andean cultures, camelids such as llamas feature prominently in archaeological faunal assemblages across the region (Szpak et al 2020, 2014; Hultquist et al 2024). In 2023, Proyecto de Investigación Arqueológica de Puerto Malabrigo (PIAPM) excavated household structures at the Virú colony in Puerto Malabrigo, Chicama. As a coastal settlement, the colony had access to various local resources; floodplain crops (e.g., *Capsicum* sp., *Zea mays*, *Phaseolus* sp.), wild desert-dune taxa (e.g., *Solanaceae*, *Prosopis* spp.), and wetland plants (e.g., *Cyperaceae*, *Poaceae*). Opaline microfossils of plant cells, phytoliths, are proxies for diet through

microbotanical analysis of camelid coprolites; the analysis of these coprolites offers insight into Virú agriculture and husbandry practices (Piperno 2006, Shahack-Gross 2011; Billman 2021). Additionally, phytolith reference collections for Andean taxa are improved through extraction and documentation of phytoliths from macrobotanical samples excavated by PIAPM. In this paper, we consider how phytolith insights from camelid coprolites can reveal foddering practices at Virú-Malabrigo (ca. 50 B.C.E. to 223 C.E.) and consider Virú-herder influence on coastal camelid diets. This project aims to reconstruct Virú camelid pastoralism through phytolith analysis, exploring the dynamic human-animal relationship with resource exploitation while contributing to a reconstruction of the paleoenvironment in the archaeological record.

Jayden Lee

Molecular & Cellular Biology, Revelle

Mentored by Enfu Hui

Exploring a novel signaling pathway of the immune checkpoint receptor PD1

PD1 (Programmed cell death protein-1) is an immune checkpoint receptor expressed in T cells and a key target for cancer immunotherapy. Upon binding to its ligand PDL1, PD1 inhibits T cell function, proliferation and survival, reducing immune response. While the PD1:PDL1 interaction is necessary to avoid autoimmune phenotypes, cancer cells take advantage of this pathway by expressing PDL1 to limit natural antitumor activity. PD(L)1 blockade antibodies have been successful across many cancer types by disrupting the PD1:PDL1 interaction, but this approach suffers from limited patient success rate and autoimmune toxicities in some patients, highlighting the need for a better understanding of PD1 mechanism. The PD1 intracellular domain recruits the phosphatase Shp2, which inhibits T cell activation. However, emerging evidence has shown that PD1 still possesses inhibitory effects in the absence of Shp2, suggesting some Shp2-independent pathway(s). In this project, I propose to identify novel PD1 interactors using proximity-labeling proteomics and determine if their deletion impairs PD1 function in both in Shp2 competent and deficient backgrounds. Successful execution of this study will define a new axis of PD1 inhibitory signaling, with implications for novel targets and biomarkers for cancer immunotherapy and autoimmune disease.

Michelle Lee

Cognitive and Behavioral Neuroscience, Seventh

Mentored by Deanna Greene

Characterizing Tic Expression During fMRI Scanning in Pediatric Tourette Syndrome

Tourette syndrome (TS) is a neurodevelopmental disorder characterized by involuntary, repetitive movements and vocalizations in the form of motor and vocal tics. To study the neural mechanisms underlying tics, tics can be observed directly during fMRI scanning, allowing for the assessment of real-time brain activity. However, collecting high-quality fMRI data in pediatric and clinical populations can be challenging. Moreover, tics can vary substantially across different environmental contexts as well as between and within individuals. Therefore, characterizing tic expression during fMRI scanning, including frequency, tic type, and contextual influence, can provide important insight into the feasibility and reliability of fMRI studies in pediatric TS. The current study aims to provide a detailed behavioral tic characterization during fMRI scans in pediatric TS. Tic expression will be examined in two densely-sampled participants: (1) 10-year-old girl with comorbid attention deficit hyperactivity disorder (ADHD) and autism spectrum disorder (ASD), and (2) 15-year-old girl with comorbid generalized anxiety disorder. Video and audio recordings were collected during fMRI scans as well as outside the scanner. We will code the precise timing and type (e.g., eye blink, sniff) of tics across twelve fMRI scan runs (147 minutes of video data) per participant and ten total out-of-scanner sessions (35 minutes of video data). We will quantify the number of tics per minute and types of tics, and compare these metrics for in-scanner vs. out-of-scanner videos. We hypothesize that tic frequency will vary across sessions and within each session, and that tic expression will be unique to each individual.

Andrew Liang

Political Science - Data Analytics, Seventh

Mentored by Soichiro Yamauchi

Estimating Dynamic Effects of Strict Voter Identification Laws With Marginal Structural Models

Researchers seek to estimate causal effects from panel data using a variety of methods, like difference-in-differences, synthetic control, or fixed-effects models. While recent

research has addressed issues with using two-way fixed-effects models in estimating the average treatment effect for the treated when treatment adoption is staggered across units, many policies in political science involve treatments that may reverse in later years, preventing us from clearly estimating causal effects with typical difference-in-differences methods. In this paper, we argue that recent difference-in-difference methods designed to address these issues carry assumptions that are unlikely to hold in many political science contexts. Instead, we use a sequential ignorability method - marginal structural models - to estimate dynamic effects of strict voter identification laws on voter turnout in United States House of Representatives Elections. Conditioning on the last four periods of a state's history of enacting strict voter identification laws, we show that for 2020 and 2022, strict voter identification laws decreased overall turnout by approximately 7-9 percentage points.

Elizabeth Lin

Human Biology, Revelle

Mentored by Miles Wilkinson

Improving the Clinical Utility of the Molecular Semen Analysis (MSA) Assay Through Systematic Assay Optimization

The Molecular Semen Analysis (MSA) assay is a highly sensitive, non-invasive diagnostic test designed to support clinical decision-making in men with azoospermia (no semen sperm). By quantifying the expression of stage-specific germ cell markers, the MSA assay identifies the presence of specific germ-cell types, thereby identifying spermatogenic defects. It also predicts the likelihood of successful sperm retrieval by the microdissection testicular sperm extraction (mTESE) method, a procedure that permits fertility for azoospermic men with sperm in their testes.

As a baseline for azoospermic samples, it is critical that the MSA assay also accurately determine sperm counts in “normospermic” men (those with normal semen parameters as defined according to the World Health Organization). An analysis of a large normospermic cohort (n=105) found a high inter-sample variability in expression of sperm gene markers (>1000 fold) despite only a ~10-fold variation in sperm count.

I hypothesized that technical factors including RNA isolation conditions and/or an overload of rate-limiting reagents for RNA isolation, cDNA synthesis, and reverse-transcription polymerase chain reaction (RT-PCR) are responsible for this variation. My dilution experiments with both RNA and cDNA showed the expected linear Ct values from RT-PCR, demonstrating that the “overload hypotheses” are incorrect. My

modifications of lysis conditions improved RNA recovery in select cases but inconsistently across samples.

These and further results provide insights into the factors influencing MSA assay performance, substantially narrowing the likely sources of variability. My ongoing work focuses on further optimization to support the validity and predictive accuracy of the MSA assay.

Connie Liu

Data Science, Sixth

Mentored by Julian McAuley

Data Sonification of Campus Activity

My TRELS project explores how campus activity can be transformed into an interactive audio-visual experience that helps students feel more connected to UC San Diego's shared rhythms and spaces. Using video-derived data from different campus regions, I build a Python pipeline that detects and structures patterns of movement, crowd density, and temporal activity using computer vision and time-series analysis. These patterns are then translated into sound through data sonification, where changes in activity influence musical features such as rhythm, tempo, layering, and intensity.

The project combines technical methods from computer vision, signal processing, audio preprocessing, and interactive 3D visualization. After extracting activity signals, I clean, normalize, and transform the data using tools such as Fourier analysis, then map the resulting patterns into soundscapes that represent the unique energy of different campus locations. These sonified outputs are integrated into an interactive Three.js website featuring custom models of UCSD buildings, allowing users to explore campus spaces visually and sonically.

Beyond representing data, the project emphasizes students' belonging to campus. When multiple locations reach moments of high activity at the same time, the system creates a "chorus" effect, symbolizing how separate routines across campus can align into a shared community experience. Overall, this project uses data sonification and interactive visualization to make invisible patterns of campus life more emotionally meaningful, accessible, and engaging.

Jiaying Liu

Anthropology, Sixth

Mentored by Suzanne A. Brenner

"Market Rejects" as Welfare: How Industrial Food Surplus Shifts Costs onto Recipients

Under neoliberal welfare outsourcing, food insecurity is increasingly addressed through nonprofit redistribution of industrial food surplus—including "ugly produce" rejected for appearance and near-expiry inventory diverted from commercial waste streams. While this model is celebrated for relieving both hunger and corporate disposal costs, less attention has been paid to what recipients actually receive and what they must still supply to make these foods usable. This project, conducted at Feeding San Diego, asks: when "market surplus" becomes welfare, what hidden costs are shifted onto recipients?

Building on Phase I fieldwork examining how fiscal logics shape NGO staff decision-making, this Phase II study turns to the material outcomes of those decisions. Using a standardized material-audit instrument across 6–10 distribution events, I document food composition, freshness, packaging, and "ease-of-use" indicators (trimming required, cooking time, spoilage risk). Short semi-structured interviews with approximately 10–15 recipients capture what is used, discarded, or avoided, and what additional time, storage, equipment, or out-of-pocket spending is required to assemble a meal. Staff interviews link these material outcomes back to donor constraints, sorting rules, and reporting metrics.

Drawing on Jack Goody's work on industrial food and value, I argue that items reclassified from "second-rate" in the market to "help" in nonprofit systems carry an unexamined cost-transfer: welfare expenditure is partially absorbed by recipient households as preparation labor, storage burden, and reduced dietary choice. Findings will inform a reusable audit template and a memo on "hidden costs" in food aid distribution.

Vivian Liu

Physics, Marshall

Mentored by Adam Burgasser

Near-Infrared Spectral Classifications of Previously Unclassified Nearby Low Mass Stars and Brown Dwarfs

Low-mass stars and brown dwarfs ($M < 0.1 M_{\odot}$) comprise most of the stellar population within the Solar Neighborhood, a volume spanning 20 parsecs around the Sun. Despite their proximity, the intrinsic faintness of these objects makes high-quality observations difficult, leaving many sources poorly characterized or without reliable spectral classifications. Using 20 years of archival data from the SpeX spectrograph on the NASA Infrared Telescope Facility, a sample of sources with missing or ambiguous spectral classifications in the SIMBAD astronomical database was compiled, and their associated SpeX spectral data were reduced using the pypextool package. Spectral types for these sources were determined through comparison with established near-infrared spectral standards using the SpeX Prism Library Analysis Toolkit (SPLAT). The findings of this study improves the completeness of the Solar Neighborhood, which provides an empirical basis for broader studies of stellar and substellar populations across the Milky Way.

Carolina Lopez

Psychology B.S., Eighth

Mentored by David Quijada

N/A

Medical school curricula tend to emphasize biomedical knowledge and diagnostic skills, and place less focus on patient-provider relationships. Profound patient-provider relationships are essential for encouraging open communication, particularly when discussing sensitive health topics and for improving culturally sensitive treatment plans. Cultural competence is key to enabling providers to use the tools and knowledge needed to interact with patients from diverse cultural backgrounds and meet their needs. However, differences in cultural competency training in the University of California (UC) medical schools curricula may lead to variations in how well providers are able to engage with patients from diverse backgrounds. It is important to note the implicit bias that can

occur when providers are unable to form close relationships with their patients, due to various factors, including language and cultural barriers. The lack of standardized tools to assess cultural competence further contributes to inconsistent outcomes in patient-centered care. This research examines how variations in UC medical school curricula impact provider preparedness and explores the implications for equitable patient health care.

Maya Madhat

Public Health, Revelle

Mentored by Anne Elizabeth White

A Conversation Analytical Study of General Surgeons Reassuring Patients with Chronic vs Acute Disease

Background & Purpose: Reassurance—defined as removing a patient’s doubts or fears—is a crucial component of the doctor–patient relationship and helps prevent patients from feeling dismissed or untreated. Despite its importance, guidance on how and when physicians should deliver reassurance remains unclear. Little is known about whether reassurance practices differ across clinical contexts, such as chronic versus acute conditions. Studying reassurance through naturalistic, video-recorded clinical interactions is an emerging area of research. This study builds on prior work examining physician reassurance in no-problem diagnoses, extending this line of inquiry to cases requiring active treatment.

Methods: This study uses Conversation Analysis (CA), a qualitative method for examining recurrent patterns in naturally occurring communication. We analyzed 56 video-recorded clinic visits from a rural Texas general surgery practice, identifying and consolidating physician utterances aimed at reassuring patients with chronic or acute conditions requiring treatment. Cases were organized by their sequential position, social action, and interactional design, allowing for systematic comparison across case types.

Results: Physicians provided reassurance for two primary purposes: (1) responding to patients’ explicit expressions of fear by addressing concerns and emphasizing treatment safety or effectiveness; and (2) offering positive assessments of clinical evidence to preempt worry during discussions of results or imaging. Physicians more often incorporated contingency planning in chronic cases, reflecting ongoing care.

Conclusions: These findings clarify how and when physicians deliver reassurance in the surgical context of chronic and acute cases, demonstrating that it is a structured, context-

dependent practice shaped by both interactional dynamics and illness trajectory. Together, they provide practical insight into an essential clinical communication skill and highlight the importance of tailoring reassurance to patient needs, with implications for improving satisfaction, trust, and adherence.

Fabrizio Malatesta

Bioinformatics, Revelle

Mentored by Sandra Sanchez-Roige

The genetic architecture of wisdom: a genome-wide association study in 131,870 individuals

Wisdom is a personality trait composed of self-reflection, pro-social behaviors, emotional regulation, acceptance of diverse perspectives, decisiveness, social advising, and spirituality. Greater levels of wisdom are linked to better overall health, well-being, happiness, life satisfaction, and resilience. However, the underlying genetic architecture of wisdom and its genetic relationships with health remain unexplored. We collected responses to SD-WISE-7, a validated survey measure of wisdom, in 131,870 23andMe research participants and conducted the first large-scale genome-wide association study (GWAS) of this trait. We identified one genome-wide significant locus (rs1028640, $P=3.7e-08$) near the MANEA gene on chromosome 6. Wisdom was heritable ($h^2_{SNP}=0.03\pm 0.004$) and genetically correlated with numerous complex traits, including subjective wellbeing ($r_g=0.34$, $P=1.52e-09$), neuroticism ($r_g=-0.38$, $P=1.87e-16$), loneliness ($r_g=-0.27$, $P=8.45e-07$), other personality traits such as openness ($r_g=0.41$, $P=1.37e-07$) and risk tolerance ($r_g=0.36$, $P=6.94e-11$). Crucially, wisdom was genetically distinct from intelligence ($r_g=0.036$, $P=0.39$) and cognitive educational attainment ($r_g=-0.01$, $P=0.83$). We calculated polygenic scores (PGS) in All of Us ($N\approx 200,000$) and identified significant associations with psychosocial outcomes (e.g., social satisfaction ratings $P=1.16e-12$ and subjective mental health $P=5.93e-10$). This study advances our understanding of wisdom as a biologically-grounded trait that could ultimately be used to develop informed interventions that increase wisdom and improve health and well-being.

Emily Mamou

Public Health, Seventh

Mentored by Anne White

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Amber Marquez

Biochemistry, Sixth

Mentored by Gourisankar Ghosh

Mapping the Longitudinal DNA Damage-Epigenetic Crosstalk Underlying the Progressive Decline of Neural Stem Cell Plasticity causing Alzheimers with Aging

work in progress

Gabrielle Martinez

Cognitive behavioral neuroscience, Eighth

Mentored by Elizabeth Twamley

Differences in Quality of Life and Cognitive Performance in Active Duty Military Personnel and Veterans with a History of Mild TBI

The purpose of this study is to examine differences in cognitive performance and quality of life between active-duty service members and Veterans with a history of mild traumatic brain injury (mTBI). In U.S. military populations mTBI is one of the most common injuries affecting attention, memory, executive functions, emotional regulation, and daily functioning. However, research often treats military personnel as a single group, overlooking important environmental and psychosocial differences between active-duty service members and Veterans. Active-duty service members remain in the military, providing them with identity, belonging, and a daily routine. Veterans may suffer with the transition to civilian life, experiencing many psychological problems after war that have an impact on their quality of life.

This study will use pre-treatment (baseline) data collected from the Personalized Augmented Cognitive Training (PACT) randomized controlled trial. The sample includes 48 active-duty service members and 48 Veterans recruited from Naval Medical Center San Diego and the VA San Diego Healthcare System. All participants had a history of mTBI occurring at least three months prior to enrollment and reported ongoing cognitive difficulties. The independent-samples t-test will be used to examine group differences in cognitive functioning and quality of life measures.

By directly comparing these populations, this study aims to identify improved recovery paths, coping mechanisms, and long-term cognitive and psychosocial outcomes for both

groups. Findings may provide a deeper understanding of mTBI in specific military populations and support the development of targeted interventions to improve cognitive rehabilitation and overall quality of life.

Nikitha Mateti

General Biology, Marshall

Mentored by Karl Willert

The Effect of Piggyback Vector on Wnt Protein Production

The Wnt signaling pathway is critical for embryonic development, stem cell self-renewal and differentiation, and tissue homeostasis. Expression and production of Wnt proteins, which encode secreted growth factors, has proven to be difficult. Recently we found it was possible to increase Wnt protein production using a piggyBac (PB)-based inducible vector system. Cells expressing Wnt5a using this system produced significantly more protein compared to other expression systems. Here we tested to what extent this PB expression system improved expression of another Wnt, Wnt3a. Our experiments are designed to answer the following questions: Can we increase Wnt3a protein output? What effect does this have on cells? Does the PB backbone work universally to increase production of all Wnts?

Noah Mathew

Human Biology/School of Biological Sciences, Seventh

Mentored by Dmitry Lyumkis

Structural Basis of Drug Resistance in HIV-1 Intasomes Revealed by Cryo-EM

Drug resistance in Human Immunodeficiency Virus Type-1 remains a major challenge despite the success of antiretroviral therapy. A key component of treatment uses integrase strand-transfer inhibitors (INSTIs) which target the viral enzyme responsible for inserting viral DNA into the host genome. However, resistance associated mutations at residues E138, G140, and Q148 reduce drug efficacy and compromise therapeutic outcomes. While computational studies have proposed evolutionary pathways for these mutations, the structural mechanisms that underlie resistance remain poorly understood.

This project aims to determine high-resolution structures of drug-resistant HIV-1 intasomes using cryo-electron microscopy. Integrase mutations include clinically relevant variants such as Q148H and G140S are expressed in *E. Coli* and purified using affinity and size exclusion chromatography. These proteins are assembled with viral DNA substrates and the integrase binding domain to form a stable intasome complex in vitro. Complexes are screened by negative-stain electron microscopy prior to high-resolution cryo-EM data collection and structural refinement.

By resolving the structures of mutants intasomes bound to INSTIs, this work will reveal how specific mutations disrupt drug binding while maintaining enzymatic function. These insights will provide a structural framework for understanding the evolution of resistant that can support the rational design of next-generation inhibitors with improved durability against resistant HIV-1 strains.

Ilya Mazalov

Nano Engineering, Revelle

Mentored by Tod Pascal

Coarse-Grained Model of Site-Selective Ligands for Surface Preservation in Noble Metal Nanoparticles

Abstract redacted due to proprietary information.

Ketan Mittal

Data Science, ERC

Mentored by Eiman Azim and Talmo Pereira

Unsupervised Behavioral Segmentation for Longitudinal Home Cage Monitoring

Disease progression in amyotrophic lateral sclerosis (ALS) is difficult to track because relevant behavioral changes are distributed across many domains and unfold slowly. By continuously recording group-housed mice undisturbed in their home environment, home-cage monitoring gathers behaviors outside the standard set of ALS markers, including individual and social behavioral data, at a scale that exceeds traditional lab

experiments. Our project has collected over 41,000 hours of video, more than 7.4 billion frames, of group-housed ALS-model mice (SOD1G93A) and controls. A dataset of this size renders manual behavioral annotation impossible, necessitating the use of automated methods to convert raw video data into structured signals about disease progression.

State of the art computer vision softwares like SLEAP can extract detailed animal postures from the video dataset, yet translating these hours of footage into interpretable behaviors remains a strenuous task. Keypoint-MoSeq (KPMS), an unsupervised machine learning algorithm, addresses this by grouping common mouse movements into a small set of recurring behavioral “syllables,” describing the videos as sequences of behaviors. However, KPMS performance is highly sensitive to input data quality. Factors such as keypoint jitter or identity switches between cage-mates degrades the output. We address this with a three-step pipeline. First, a quality-control stage filters out low-quality clips. Second, a CNN model distinguishes visually similar mice, mitigating identity switches. Third, KPMS’s stickiness parameter (κ) was tuned to match syllable duration to natural mouse behavior. Together, this pipeline enables large-scale quantification of behavior and disease progression beyond the limits of a manual workflow.

Omar Mokhashi

Neurobiology, Muir

Mentored by Weg Ongkeko

Excess Epigenetic Clock Dispersion Reveals a Distinct Axis of Tumor Heterogeneity Independent of Purity, Proliferation, and Genomic Instability

Abstract redacted due to proprietary information.

Jordan Montague

Human Biology, Eighth

Mentored by Jing Yang

Investigating the role of TGF- β in Regulating Epithelial Polarity and Invasiveness in Colorectal Cancer

Abstract redacted due to proprietary information.

Megan Muchowski

Biological Sciences, Seventh

Mentored by Alistair Russell

Influenza Excludes Naked RNA from Replication Machinery

In the field of influenza research, a fluorescent reporter cell line that visualizes influenza viral replication would be a valuable tool. Attempts to create such a system have been unsuccessful. When cells are transduced with lentiviral plasmids that mimic influenza viral replication, only a small fraction of the cells produce fluorescent signals. We sought to determine whether creating such a tool is possible or whether some aspect of viral or cellular physiology prevents it.

We found that non-packaged viral RNA is excluded from the influenza viral replication machinery. The lack of fluorescent signals in cells, even after increasing segment concentration, led us to explore more complex approaches. Using a highly diverse synthetic barcoded plasmid library with different viral promoters, we can quantify these barcoded transcripts, revealing that few plasmids load onto the viral polymerase and progress through replication. Flow cytometry further supported this hypothesis by an observed difference between cells producing low fluorescent signals, indicative of transcription, and cells producing high fluorescent signals, indicative of replication.

This suggests that a cellular mechanism somewhere between plasmid transduction and infection with viral replication machinery contributes to the inefficient replication of naked RNA by the viral polymerase.

Vikas Murali

Bioengineering: Biotechnology, Seventh

Mentored by Ludmil Alexandrov

Quality-Control Optimization of a Sequencing-Ready Library Preparation Pipeline for Centenarian Longevity Genomics and Targeted PanCancer Analysis

Studies on exceptionally long-lived individuals are a rare opportunity to gain an insight into the molecular mechanisms driving successful aging, although the scale of necessary genomic research depends largely on the ability to perform stable and reproducible library preparation. The Cilento Initiative on Aging Outcomes (CIAO) study collects blood samples from groups of centenarians and controls assigned to WGS, ultra-deep duplex sequencing, PanCancer hybrid capture, and telomere length measurements. Each assay involves different input DNA conditions and relies heavily on the performance of the preparatory steps performed beforehand.

In this project, we analyze pre-sequencing procedures needed for carrying out these assays in around 149 centenarian samples and matched controls. At each stage of our pipeline, we measure quality control (QC) metrics, including DNA concentration and yield, fragmentation, end repair and ligation, qPCR-based quantification, indexing, hybrid capture, and pool mixing, as well as parameters such as molarity, library concentration, PCR cycles needed, and the frequency of failed/repeated samples. For some samples prepared manually, we compare their metrics to those prepared using a semi-automated Integra VIALAB Assist Plus system.

This study aims to determine which pre-sequencing factors have the greatest impact on successfully preparing libraries for WGS, UDSeq, and PanCancer assays, as well as whether semi-automation can lead to more reproducible and consistent results in population-based longevity studies. With the goal of identifying the best parameters that predict success at the stage of library preparation in each particular assay, this research lays the groundwork for further investigations of centenarian samples in terms of somatic mutation load, clonal heterogeneity, telomere biology, and other molecular features of longevity.

Robert Nasanbat

OB/GYN & Reproductive Sciences, Eighth

Mentored by Kathleen Fisch

Comparing Mesenchymal Stem Cell Proliferation in Preterm and Term Birth Conditions

Preterm birth is a major pregnancy complication associated with increased risk of neonatal morbidity and developmental challenges. Although preterm birth mechanisms are complex, altered placental cell function may contribute to disease progression. Mesenchymal stem cells (MSCs) are involved in tissue repair, immune regulation, and cellular signaling, making them a useful model for studying cellular differences between preterm and term pregnancy conditions. This project examines whether MSCs derived

from the umbilical cords of placenta from preterm and term births differ in proliferation. This work may clarify how gestational timing associates with cell growth and function.

We hypothesize that preterm MSCs will show altered proliferation compared to term MSCs. UC-MSCs (Umbilical Cord-derived MSCs) from preterm and term births (N=7 preterm [n=5 preeclampsia, n=2 normotensive], <37 weeks gestational age; N=3 normotensive term, ≥37 weeks gestational age) will be cultured and assessed using a Click-iT EdU imaging assay. Proliferation is the process by which cells grow and divide, making it an important measure of tissue development. EdU is a thymidine analog incorporated into newly synthesized DNA during DNA replication, allowing proliferating cells to be fluorescently identified. Following EdU incubation, cells will be fixed, permeabilized, labeled using the Click-iT reaction cocktail, and counterstained with Hoechst to visualize total nuclei. Proliferation will be compared by quantifying EdU-positive nuclei relative to total Hoechst-stained nuclei across preterm and term MSC samples.

Understanding how MSC proliferation differs between preterm and term contexts may provide insight into mechanisms of pregnancy complications, placental function, and maternal-fetal health.

Bri Newton

Neurobiology and Psychology: Cognitive and Behavioral Neuroscience, Sixth

Mentored by Miranda Koloski

Individual Differences and Surgical Factors Contribute to Behavioral Performance Post-Injury in Rodent Traumatic Brain Injury Models

Experimentally inducing a traumatic brain injury (TBI) in rodents, leads to deficits in learning, cognition, and memory. Still little is known about how individual differences pre-TBI and surgical factors contribute to behavioral performance after injury. In Long-Evans rats (n=58) split into cohorts based on injury severity (control, mild TBI, and severe TBI) and sex (male and female), we assessed cognition-related behavioral deficits on a probabilistic reversal learning (PRL) task up to 12 weeks post-surgically induced TBI. Using linear mixed models, we assessed if behavior on the PRL task (reversals) was affected by TBI severity across 12 weeks (group x time). Next, we compared our baseline models to two other models: 1.) A model with factors of weight, surgical complications, anesthesia time ($Z_{Perf} \sim 1 + \text{Group} * \text{WeekNum} + (1 | \text{Subject})$) and 2.) A model with only the additional factors ($Z_{Perf} \sim 1 + \text{Group} * \text{WeekNum} + \text{WeekNum} * \text{AnyComp} + \text{WeekNum} * Z_{Weight} + \text{WeekNum} * Z_{Analgesia} + (1 | \text{Subject})$). Surgical complications

were split into three categories: excessive bleeding, anesthesia variations, and impact variations. Model 2 (all factors included) performed the best (AIC=528.53, BIC=578.54; week*complications p=0.003), followed by Model 3 (surgical variables only) (AIC=550.18, BIC=585.9, week*weight p=0.002), and Model 1 (group) last (AIC=559.37, BIC=580.8, p<0.001). Based on the outcomes of these models, weight and surgical variations may serve as an important mediator in the relationship between TBI and behavioral outcomes that should be more formally considered in each study.

Benjamin Ngo

Biological Sciences, Sixth

Mentored by Rommie Amaro

Molecular Dynamics of the SARS-CoV-2 Helicase

The SARS-CoV-2 helicase plays a critical role in viral replication by unwinding RNA during genome transcription and replication. To investigate how RNA binding influences the protein's conformational dynamics, we performed molecular dynamics simulations of the helicase in both its APO (unbound) state and RNA-bound state. Comparative analysis revealed that RNA binding stabilizes key structural regions involved in nucleic acid recognition and unwinding, while increasing flexibility in distal domains that may facilitate translocation along the RNA strand. Additionally, specific residues within the helicase active site and RNA-binding channel were identified as key contributors to RNA interaction through persistent hydrogen bonding and electrostatic contacts. These findings highlight the interactions between structure and function in the helicase and provide insight into how RNA binding modulates its activity. Overall, our studies can be helpful for understanding how protein dynamics can inform novel strategies for inhibiting helicase activity, and how these can be intercepted by small molecule inhibitors.

Kien Ngo

International Business, Marshall

Mentored by Dredge Byung'chu Kang

Recipes for Resilience: The Market-Incubator Model as a Frontier for Innovation and Gender Equity

Vietnam is poised to become a prominent economy in Asia as economic growth structurally shifts labor from agriculture toward manufacturing. Alongside these shifts, state-led formalization policies have reduced informal employment statistics but increased the precariousness of street vending for women through restrictive regulations. However, female vendors remain agile innovators who possess generational craftsmanship who define Vietnamese gastronomy. Despite institutional challenges, street vending remains a dominant feature of Vietnam's brand image, tourism, and urban culture. This research analyzes the socio-economic importance of these women, whose work optimizes culinary skills and fosters vital community relationships. By contrasting the policies of Ho Chi Minh City with the policies of Thailand and South Korea, this study explores how market-incubator models can serve as educational hubs and business infrastructure. Ultimately, implementing such models can enhance the living standards of women street vendors while simultaneously elevating safety standards.

Lester Ngo

Neurobiology, Sixth

Mentored by Richard Childers

Effect of Providing Patients Cost Information on Testing Rates in Urgent Care Patients with Respiratory Infections: A Randomized Trial

Upper respiratory infection (URI) symptoms are highly prevalent and the accessibility of urgent care centers contributes to frequent, and often unnecessary, diagnostic testing. Overuse of such services can result in false positives, adverse side effects, patient discomfort, and increased healthcare costs without meaningful clinical benefits. Price transparency, defined as providing patients with estimated out-of-pocket costs for healthcare services, has emerged as a potential strategy to reduce low-value care. While hospitals have adopted policies to increase cost visibility, similar interventions remain largely unexplored in urgent care settings. This randomized controlled trial evaluates the

effect of cost transparency on diagnostic testing utilization among urgent care patients presenting with URI symptoms. Participants are randomized to receive either a handout including estimated costs of common diagnostic tests alongside information on their risks and benefits or a control handout containing only risks and benefits. The primary outcome includes the amount of diagnostic tests ordered while the secondary outcomes include treatments provided, discharge diagnoses, and return visits to the urgent care or the emergency department. By assessing whether cost information influences testing decisions, this study aims to inform strategies that promote high-value care, reduce unnecessary healthcare spending, and support patient-centered decision-making in urgent care settings.

Haley Nguyen

Molecular and Cell Biology, Seventh

Mentored by Matthew Daugherty

Bioengineering human SERPINs as a targeted mechanism of viral protease inhibition

Viral proteases are ubiquitous amongst a variety of clinically relevant positive-sense single-stranded RNA viruses due to their facilitation of polyprotein processing during viral replication. Due to their critical role in viral maturation, researchers have developed small molecular inhibitors to combat these enzymes. However, it is currently unexplored whether naturally occurring protease inhibitors can be exploited to inhibit viral proteases. In this project, host-encoded serine protease inhibitors (SERPINs) are investigated as an alternative protein-based strategy for inhibiting viral proteases. SERPINs contain a sequence-specific region called the Reactive Center Loop (RCL) which, upon cleavage by a protease, traps the protease in an inactive complex. Though researchers have previously utilized this mechanism to engineer SERPINs against host proteases, employing SERPINs to target viral proteases remains understudied. My research focuses on bioengineering human SERPINs that can inhibit viral proteases by introducing sequence-specific cleavage sites that are recognized and cleaved by viral proteases into the SERPIN RCL. Using this strategy, this project successfully engineers human SERPINs that inhibit proteases from a diversity of viral families, including coronaviruses, picornaviruses, caliciviruses, and arteriviruses. Furthermore, this study investigates determinants of inhibitory function beyond the RCL by engineering cleavage sites into different SERPIN backbones. The success of these SERPINs supports my ongoing effort to expand this model to inhibit proteases from new viral families, starting with the flavivirus Dengue Virus 2. Overall, this project offers a potential model for

engineering SERPINS as virus-specific protease inhibitors capable of halting viral infection, a feat with powerful implications for future antiviral therapies.

Song Nguyen

Neurobiology, Muir

Mentored by Gulcin Pekkurnaz

Metabolic plasticity and neuronal resilience: unraveling adaptive responses to chronic mtDNA damage

Neurons are highly energy-demanding cells that rely on mitochondria to generate ATP through proteins encoded by both nuclear DNA and mitochondrial DNA (mtDNA). During aging, mtDNA is more prone to damage and mutations, which is associated with neurodegenerative diseases such as Alzheimer's and Parkinson's; however, the mechanisms and functions linking mtDNA damage to neuronal dysfunction remain unclear. I hypothesize that mtDNA damage disrupts neuronal ATP production and contributes to age-related neuronal dysfunction. To test this, we engineered cultured neurons to express dominant-negative mutants of the only mtDNA polymerase, polymerase gamma (POLG), therefore inducing mtDNA replication defects. We assessed neuronal morphology using immunocytochemistry and microscopy, with a focus on dendrite branching and spine number as an indicator of synaptic integrity. Additionally, we measured ATP production using the fluorescent sensor iATPSnFR to evaluate metabolic function under baseline, stimulated, and recovery conditions. Together, these approaches aim to examine both the structural integrity and the metabolic health of neurons exposed to mtDNA defects. This study may provide insight into the molecular pathways underlying age-related neurodegenerative diseases.

Nidhi Noronha

Neurobiology, Math-CS, Seventh

Mentored by Leah Dorman

Using high resolution transcriptomics to explore gene expression patterns during flavivirus infection

Flaviviruses are a global health threat, with dengue virus infecting an estimated 390 million people annually and Zika virus causing congenital abnormalities including microcephaly. There are currently zero approved treatments for these infections, highlighting an urgent need for a thorough understanding of viral pathogenesis.

Viral infections hijack host cell machinery to replicate and evade immune responses. These changes happen rapidly, with key viral-host interactions occurring within hours of infection. Traditional transcriptomic studies sample at long intervals (24-48 hours or days), missing critical early events that determine infection outcomes and represent prime therapeutic targets.

High-resolution temporal profiling allows tracking of viral infection dynamics by measuring gene expression changes at frequent intervals throughout infection. This approach reveals how gene expression changes during infection, revealing pathways that flaviviruses target. By combining bulk and single-cell transcriptomics with protein analysis, we can identify key molecular mechanisms underlying infection progression.

Danny Ortega

Biochemistry / Department of Chemistry and Biochemistry, Revelle

Mentored by Brian Zid

Mitochondrial mRNA Tethering Enhances Protein Expression in Saccharomyces cerevisiae

Abstract redacted due to proprietary information.

Yazmin Ortega

Cognitive Science, Neuroscience, Sixth

Mentored by Lara Rangel

Foundations of Social Communication: Normative USV-Behavior Profiles Across Social Relationship and Group Structure

Social communication reveals affiliative bonding, motivation, and emotional valence integral to mammalian behavior. Rodents emit ultrasonic vocalizations (USVs), high-frequency sounds (22-90kHz), that encode social intent and emotional state. Vocalizations >50 kHz are associated with prosocial engagement, whereas ~22kHz calls indicate distress. Although rats exhibit rich affiliative behaviors paralleling human social reciprocity, their translational potential is limited by inconsistent characterization metrics and a poor understanding of emotional and temporal communication foundations. This gap is relevant to neurodevelopmental disorders, which are marked by variability in timing, reciprocity, prosody, and social drive. While most research focuses on speech and language, fewer studies examine affective cues and temporal structures underlying social interaction.

This study aims to establish normative USV-behavior profiles across multiple social contexts, examining how vocal patterns shift with relationship type and social group complexity. Specifically, we assess how familiarity (cagemates and same-strain strangers) and increasing social group size shape USV features such as frequency, amplitude, duration, calling rates, and motif structure. These USV parameters are analyzed in relation to prosocial behaviors (sniffing, following, grooming) to identify calls signaling prosocial intent. This project integrates ultra high-frequency microphone recordings with video-based behavioral scoring. Deep learning-based tools are used to detect and classify motifs. Synchronizing audio and behavioral data reveals how communication patterns vary with social familiarity and context, generating normative profiles that link affect state, observable behavior, and group structure. These findings aim to provide a foundation for improving translational models of communication deficits in neurodevelopmental disorders.

Keshvi Patel

Human Biology, Warren

Mentored by Alice Chen

Effect of TNF- α -Induced Inflammation on Endothelial Cell Expression of Syndecan-1 in Human Umbilical Vein Endothelial Cells (HUVECs)

Sepsis is the third most common cause of death in US hospitals, yet early diagnosis in the Emergency Department remains difficult due to the limitations of current clinical scoring systems. Emerging evidence suggests that sepsis is fundamentally a disease of early endothelial dysfunction, particularly involving disruption of the endothelial glycocalyx. Syndecan-1, a key membrane-bound proteoglycan of this glycocalyx, is shed when the

endothelium gets activated and is a marker of vascular injury. However, the relationship between inflammatory signaling and cell-surface Syndecan-1 expression remains poorly understood. The objective of this study is to determine whether TNF- α -induced inflammatory activation alters cell-surface expression of Syndecan-1 in human umbilical vein endothelial cells (HUVECs). We hypothesize that TNF- α -induced endothelial activation decreases cell-surface Syndecan-1 expression in HUVECs, serving as a marker of endothelial activation and dysfunction. To study this, HUVECs were cultured to 70–80% confluence, serum starved for 24 hours. Cells were divided into three experimental conditions: untreated control (no TNF- α), solvent control, and TNF- α -stimulated positive control (25 ng/mL for 24 hours). Following treatment, cells were stained with antibodies targeting surface Syndecan-1 and a live/dead viability marker for accurate analysis of viable cells. Flow cytometry was used to quantify changes in cell-surface Syndecan-1 expression across conditions. By integrating cellular analysis, this study aims to clarify the role of Syndecan-1 in inflammation and its potential as a biomarker for sepsis identification. These findings may improve understanding of vascular injury in sepsis and contribute more accurate identification of high-risk patients in clinical settings.

Richie Pham

Biochemistry, Seventh

Mentored by Neville Bethel

De novo protein design of tale-based protein binders to target non-canonical DNA forms

Z-DNA is a left-handed DNA conformer with demonstrated biological roles, including association with neurodegenerative diseases such as Alzheimer's and regulation of downstream genomic transcription. Despite its biological relevance, the functional role of Z-DNA remains poorly understood, largely due to the scarcity of high resolution Z-DNA-protein structures. This gap reflects the limited repertoire of existing Z-DNA binding proteins. De novo protein design has recently yielded novel binders to a range of protein and DNA targets, but this methodology has yet to be applied to target alternative DNA conformations. We chose Transcription Activator-Like Effectors (TALEs) as our design scaffold, given their modular architecture in which each repeat unit independently recognizes a single base pair through both specific sequence recognition and geometric shape complementarity. By reparametrizing these repeat modules to match Z-DNA backbone geometry and using the resulting designs as input seeds for deep-learning protein design models, we generated a set of TALE-based Z-DNA binders (zTALEs) with sequence-specific recognition capability and geometric complementarity to the Z-DNA backbone. Computational evaluation indicates structural viability and favorable predicted

binding geometry, and these designs are now poised for experimental validation. If successful, zTALEs would provide a robust, programmable platform for detecting and investigating Z-DNA in biologically relevant contexts.

Garabuning Pongpun

Psychology, Muir

Mentored by Gail Heyman, Maura White (preferred contact)

Understanding AI Moralization: Contextual and Demographic Variation in College Students' Moral Views of AI

Artificial intelligence (AI) is increasingly shaping classroom environments, fueling ongoing debates about the ethics of its use. Students are at the center of these debates, holding a range of perspectives as advocates, critics, and observers. As they develop their understanding of AI and its implications for their learning, students actively construct moral and ethical frameworks to make sense of these technologies. In this study, we refer to this process as “AI moralization,” emphasizing the ongoing, dialectical formation of students’ identities and beliefs about AI. We examine this process by tracing how students’ moral beliefs shift across different contexts, showing how students actively make sense of and position themselves in relation to AI. Building on this foundation, the present study investigates the relationship between students’ characteristics and their perceptions of AI. Using a correlational mixed-methods approach that combines Likert-scale items with open-ended responses, the study examines how students’ AI-related moral stances vary by context and how demographic characteristics relate to their perceptions of AI users.

Khang Quach

Cognitive Science, Warren

Mentored by Lucy Lai

Policy Compression as an Account of Reduced Exploration in Autism

This project investigates how differences in cognitive constraints, such as reward sensitivity and working memory, influence exploratory decision-making across individuals with varying levels of autism traits. While prior scientific literature

documented behavioral differences in autism, less is understood about the underlying mechanisms that shape how individuals explore and navigate changing environments. This work aims to bridge that gap by whether these exploratory decisions are guided by reward dynamics.

We will reanalyze the truffle-task dataset from Goetmaeckers et al. (2025) to test whether autism-related differences in exploration are better explained as differences in policy compression than as differences in reward learning. The original paper reported that the diagnosed ASD group made fewer novel clicks, more high-value clicks, sampled more locally, and showed reduced uncertainty-guided exploration, while not differing in average reward, generalization, or random exploration. Our central hypothesis is that ASD is associated with a more compressed mapping from state to action: participants with ASD rely less on uncertainty-sensitive state information and more on reusable local/exploitative action tendencies.

Bowen Quan

Human Biology, Sixth

Mentored by Karl Willert

The Effect of Piggyback Vector on Wnt Protein Production

The Wnt signaling pathway is critical for embryonic development, stem cell self-renewal and differentiation, and tissue homeostasis. Expression and production of Wnt proteins, which encode secreted growth factors, has proven to be difficult. Recently we found it was possible to increase Wnt protein production using a piggyBac (PB)-based inducible vector system. Cells expressing Wnt5a using this system produced significantly more protein compared to other expression systems. Here we tested to what extent this PB expression system improved expression of another Wnt, Wnt3a. Our experiments are designed to answer the following questions: Can we increase Wnt3a protein output? What effect does this have on cells? Does the PB backbone work universally to increase production of all Wnts?

Jayne Quezada

Psychology, Sixth

Mentored by Gail Heyman

Understanding high school students' anticipated feelings of belonging and college decision-making

Research on students' university-going decisions has overlooked sociocultural factors such as diversity cues, which have been shown to increase feelings of belonging in undergraduates. However, little is known about how these cues might translate into students' university decisions.

The present research aimed to examine the importance of diversity cues in students' university-going decisions and understand the relationship between diversity messaging, belonging, and students' university-going decisions.

In Study 1, undergraduates (current $n = 127$) completed an online survey reflecting on being high schoolers considering which university to attend. The survey assessed factors students consider when choosing a university, and answered questions about a hypothetical university brochure. In a between-subjects experimental design, participants saw either a brochure that emphasized racial-ethnic diversity (diversity-conscious) or a brochure that did not (diversity-neutral).

Findings showed students rated the importance of athletic teams very low, while they cared more about having people of the same race as them in the student and faculty population. Students cared more about having diverse student and faculty populations, though not as much as the quality of education. Notably, the diversity-conscious condition increased belonging and predicted greater likelihood of students choosing to attend the university. This mediation effect was significant, suggesting belonging is a mechanism in the relationship between diversity cues and university-going decisions.

Study 2 builds on this work by administering the same survey to high schoolers (current $n = 28$), providing greater ecological validity into university-going decisions.

These findings will advance our understanding of the psychological processes behind university decision-making.

Emilio Ramos

Anthropology (Sociocultural concentration)/Anthropology, Sixth

Mentored by Jana Fortier

Monastic Perceptions of Sacred Landscape Change in the Khumbu Region of Nepal

The Khumbu region of Nepal is increasingly affected by shifting precipitation patterns and rapid glacial recession, leading to growing water scarcity and heightened vulnerability to Glacial Lake Outburst Floods (GLOF). Past research has examined the perceptions and interpretations of laypeople and tourism-involved workers regarding climate change and its effects, identifying concerns such as declining stream flows, tourism pressure, and GLOF risk. However, little attention has been given to monastic communities as a distinct group with their own epistemic construction of environmental knowledge, despite evidence that monks and laypeople interpret shared landscapes in significantly different ways. This study investigates how the monks of Thame and Tengboche monasteries perceive environmental change through a Buddhist cosmological lens. While past research focuses on local residents and tourists, I address the lack of monastic perspectives by conducting ethnographic fieldwork in the Khumbu region. Using semi-structured interviews and transect walks, I will document how monastic memories of the landscape inform their understanding of current glacial recession and water scarcity. I will use GIS software to map specific environmental changes identified by the community, such as altered stream flows and glacier retreat, to correlate monastic observations with scientific climate data. This research prioritizes data sovereignty, with copies for monastery leaders to help guide decision-making about environmental changes. Discussions of buddhist ideas about Karma, knowledge, and sacred sites will inform the ethnographic narrative, but no sensitive or private sacred geography will be digitally mapped to ensure the protection of the sacred landscapes in the area. Preliminary findings from the consulted literature suggest that monks interpret sacred landscape transformations through moral and cosmological frameworks, linking landscape change to karmic decline and to the preservation of the Beyul, both of which have been perturbed by tourism. The findings of this project will contribute to more culturally grounded understandings of climate change in Khumbu.

Zidane Reyes Gomez

Cognitive Science, ERC

Mentored by Neil Smith

Geometric Deep Learning for 3D Modeling

This research explores the development of adaptive 3D mesh representations for real time extended reality (XR) systems using geometric deep learning. Traditional mesh based modeling methods rely on fixed levels of detail, creating a trade off between visual

fidelity and computational efficiency. High resolution meshes improve realism but are computationally expensive, while simplified meshes enhance performance at the cost of quality. Existing approaches, such as heuristic based level of detail techniques, lack the ability to dynamically adjust to changing runtime conditions. To address this limitation, this project proposes a learning based framework that represents 3D meshes as graph structures, enabling the use of Graph Neural Networks (GNNs) to analyze mesh topology. The model predicts vertex level importance scores using geometric and contextual features such as curvature, visibility, and distance to the camera. These predictions guide adaptive refinement, where important regions are subdivided and less critical areas are simplified, producing a mesh that balances performance and visual quality in real time. The system will be implemented using PyTorch Geometric and integrated into an Unreal Engine environment for evaluation. Performance will be assessed through computational metrics such as frame rate and resource usage, alongside geometric accuracy measures like Chamfer Distance and user based evaluations of visual realism. This work aims to advance intelligent, data driven 3D modeling pipelines that enhance scalability and interactivity in XR environments.

Kyle Rich

Biochemistry/ Chemistry and Biochemistry, Muir

Mentored by Michael Burkart

Solvatochromic probes capture inter-domain interactions in carrier protein-dependent biosynthesis

Carrier protein (CP)-dependent biosynthesis pathways produce a broad range of important metabolites, including many clinically relevant natural products. These pathways rely on a carefully orchestrated series of enzymatic reactions mediated by a central carrier protein and multiple partner proteins. However, the protein-substrate and protein-protein interactions that enable these processes are often subtle, transient, and difficult to monitor in situ. Solvatochromic fluorophores offer a promising strategy to probe these interactions. These fluorescent molecules exhibit shifts in emission wavelength and intensity depending on their local chemical environment, allowing them to report changes in protein interactions. Such probes can be chemically synthesized, selectively attached to carrier proteins, and used to visualize CP-dependent pathways involving partner proteins such as fatty acid synthases (FAS), polyketide synthases (PKS), and nonribosomal peptide synthetases (NRPS). In this work, we demonstrate the application of solvatochromic probes to monitor inter-domain interactions within type I NRPS system. Using mutagenesis at the peptidyl carrier protein-epimerization (PCP-E)

domain interface, interactions were detected with the solvatochromic 5-(4''-dimethylaminophenyl)-2-(4'-phenyl)oxazole (dapoxy) pantetheinamide probe. These findings highlight the utility of solvatochromic probes for detecting dynamic inter-domain protein interactions and suggest broader applications for studying carrier protein-mediated biosynthetic pathways.

Jeff Richmond

Psychology, Sixth

Mentored by Hilary Gould

Social Conditions, Psychological Consequences: The Impact of Food Insecurity and Housing Instability on Depression and Anxiety Severity

Background

A growing body of research underscores the important role that social determinants of health (SDoH) play in shaping mental health outcomes. This study focused on two SDoHs: food insecurity and housing instability, and examined their relationship to severity of depression and anxiety symptoms in a health system's general ambulatory clinics.

Methods

This study utilized electronic medical record data from UCSD Health System. Depression and anxiety scores were measured using the Patient Health Questionnaire (PHQ-2 and/or PHQ-9) and Generalized Anxiety Disorder scale (GAD-7). Patients also completed screening for SDoH and were categorized as "At Risk" or "Not At Risk."

Results

The final sample included 13,298 individuals. Housing instability was significantly associated with higher rates of positive depression screening (49.5% vs 26.8%, $\chi^2 = 84.09$, $p < .001$) and anxiety screening (33.1% vs. 20.4%, $\chi^2 = 21.64$, $p < .001$) compared to those not at risk. Similarly, food insecurity was significantly associated with higher rates of positive depression screening (54.3% vs. 26.4%, $\chi^2 = 76.25$, $p < .001$) and anxiety screening (42.2% vs. 19.3%, $\chi^2 = 76.23$, $p < .001$) compared to those not at risk.

Conclusions

The results of this study suggest that individuals at risk of food insecurity and housing instability have a higher likelihood of screening positive for anxiety or depression

symptoms. Limitations include significant missing data across screening measures. This study supports SDoH screening at the healthcare level and addresses the progression of mental health conditions.

Kati Richter

Bioengineering, ERC

Mentored by Brian Aguado

Decoupling sex chromosome and sex hormone regulation of cardiac myofibroblast activation

Abstract redacted due to proprietary information.

Carina Rocha Rocha

Neurobiology, Revelle

Mentored by Roberto Baccala

Endosomal, but not cytosolic, nucleic acid sensing drives lupus-like autoimmunity in low-predisposition mice after viral infection and airway silica exposure.

Systemic lupus erythematosus (SLE) is an autoimmune disease characterized by production of autoantibodies against nucleic acids and associated self-antigens, leading to immune complex-mediated tissue damage. Both genetic and environmental factors contribute to disease development. Among environmental triggers, viral infection and exposure to respirable crystalline silica – a major component of rocks and soil that promotes lung inflammation and silicosis – have been linked to lupus. We previously showed that lymphocytic choriomeningitis virus (LCMV) and silica can each promote lupus in mice with moderate to high genetic predisposition, but in combination these factors synergize to induce disease even in non-autoimmune C57BL/6 (B6) mice. However, the mechanisms underlying this synergy remain unclear.

Nucleic acid sensing by endosomal TLRs is central to lupus pathogenesis. LCMV, an RNA virus, can induce endosomal TLR7 signaling via TASL or activate cytosolic RNA sensing through MAVS. Silica promotes lung cell injury and release of self-nucleic acids, leading to stimulation of TLR7 and in some contexts cytosolic cGAS–STING pathways, while also inducing NLRP3 inflammasome activation. To define the contribution of these pathways, B6 mice deficient in TLR7, TASL, MAVS, cGAS, STING, or NLRP3 were exposed to LCMV and silica. TLR7 or TASL deficiency significantly reduced anti-chromatin and anti-nuclear autoantibodies, whereas deficiency in MAVS, cGAS, STING, or NLRP3 had no measurable effect. However, none of these mutations altered lung inflammation.

These findings dissociate the inflammatory response from tolerance breaking and identify TLR7/TASL-mediated endosomal sensing as a nonredundant checkpoint for autoantibody production in this low-predisposition, multi-hit environmental model of lupus pathogenesis.

Giovanni Rodriguez

Cognitive & Behavioral Neuroscience, Muir

Mentored by Isabella Maita

Impact of Classroom Uncertainty on Student Feelings and Coping Mechanisms in STEM Education

Uncertainty within undergraduate STEM courses can cause students to experience a variety of different emotions and coping mechanisms responding to the uncertainty. The ambiguity of what qualifies as success in the classroom is a common issue students face, which causes unnecessary stress to a student's academic performance within the classroom. To subside this, the Transparency in Learning and Teaching (TILT) framework promotes instructors to be communicative to students about what the purpose of learning certain material is, the reasoning as to why certain tasks are assigned as coursework, and what grading criteria they are being evaluated on. This study seeks to investigate this phenomenon of how students feel when they are uncertain on how to succeed in a class by conducting group interviews with 24 undergraduate STEM students and conducting qualitative analysis. Participants were asked how they felt when they were unsure on how to succeed in a class and how this affected their learning experience. We used qualitative coding to detail the effects of students' reported emotions and coping mechanisms to uncertainty in the classroom. After, we conducted qualitative analysis to categorize the

responses of students in order to find any trends within the data. Preliminary trends predict that students will experience a wide range of negative feelings towards classroom uncertainty and will use different methods to cope with this uncertainty. These results may help identify where uncertainty in the classroom arises from and what steps can be taken to address it and foster student success in the classroom.

Elijah Khalil Rosales

Biochemistry, Marshall

Mentored by Gene Yeo

Benchmarking Therapeutic mRNA Translation using Ribo-STAMP

Abstract redacted due to proprietary information.

Sofia Ruiz-Murphy

Astronomy & Astrophysics, Sixth

Mentored by Quinn Konopacky

Probing the planetary mass function in the Orion Nebula with kinematic membership from JWST astrometry

The modern astronomical understanding of the planetary mass function breaks down on both extremes. We seek to probe the full mass function of the Trapezium cluster in the Orion Nebula by connecting previous deep observations of the cluster along with newer data from JWST. The Orion Nebula is an ideal location to test these extremes due to its proximity, diverse population of stars, and recent star formation activity. We utilized archival JWST data (12561), specifically using the F187N and F212N filters, which detect cool stars, brown dwarfs, and planetary mass objects. Our goal is to create a JWST source catalog with precise astrometry that can be used to update the proper motions of sources in the cluster and thereby vet sources for membership without reliance on photometry alone. By adapting PSF-fitting algorithms originally developed for the densely populated Galactic Center, we performed source detection on the sparser field of

the Trapezium Cluster. We refine detection parameters to reduce over-detections near saturated stars while preserving faint sources. Our new precise positional information from JWST is then cross-matched with previous catalogs from HST to compute new proper motions. We perform updated analysis of the cluster motion, including an exploration of previously noticed kinematic patterns in the ONC. Our ultimate goal is to thoroughly vet the cluster membership in the planetary mass regime (<13 Jupiter Masses).

Vivian Sanchez

Public Health, Muir

Mentored by Karl Willert

Purifying the Signal: WNT9A-FZD9 Pathway Activation for Reproducible Hematopoietic Differentiation

Pluripotent stem cells (PSCs) are a promising starting point for generating hematopoietic stem cells (HSCs), but the differentiation protocols we currently rely on use undefined, variable inputs that make it difficult to reproduce results or control which cell lineages develop. Wnt9a, a lipid-modified signaling protein, plays a critical role in the emergence of definitive HSCs through its interaction with the Frizzled 9 (FZD9) receptor. In this study, I am using inducible CHO cells to produce WNT9A, which I am enriching from CHO conditioned medium (CM) using Blue Sepharose affinity chromatography (FPLC). Fractions containing WNT9A will be identified via Western blot and functionally validated using β -catenin stabilization assays in FZD9-expressing L cells, which will allow me to confirm that the WNT9A signal is specifically transduced through FZD9. I anticipate that this work will establish a reproducible workflow for enriching, and eventually purifying, bioactive WNT9A, with the goal of improving PSC differentiation toward the hematopoietic lineage and laying the groundwork for more reliable, donor-independent stem cell therapies.

Chantal Sandoval

Biological Sciences, Muir

Mentored by John Chang

The Role of TCF1 in Regulating Tissue-Resident Memory T Cell Formation within the Small Intestine and Colon.

Abstract redacted due to proprietary information.

Haya sattar

public health, Sixth

Mentored by Corry Root

Brain Dysregulation After Traumatic Brain Injury: Explaining Mood, Impulse Control, and Executive Function Changes Through a Systems-Level Lens

Traumatic brain injury is often understood as a localized physical injury, but this view does not fully explain the long term cognitive, emotional, and behavioral changes many individuals experience. This literature review reframes TBI as a disorder of brain dysregulation, focusing on disruptions in large scale neural networks rather than isolated structural damage. The central research question explores how changes in brain connectivity after injury contribute to lasting impairments in mood, impulse control, and executive functioning. Using peer reviewed neuroimaging and neuropsychological studies, this review highlights diffuse axonal injury and reduced white matter integrity as key mechanisms that disrupt communication between brain regions. These disruptions affect systems responsible for self regulation, especially frontal and frontal limbic networks, leading to difficulties with emotional control, decision making, and behavior. Research also shows that altered interactions between executive and salience networks are linked to emotional instability and reduced cognitive flexibility. By integrating findings across brain connectivity, executive dysfunction, and emotional regulation, this review presents a systems level framework for understanding TBI. This perspective helps explain how different symptoms are connected and emphasizes the importance of recognizing TBI as a disorder of brain regulation to improve understanding, reduce stigma, and support better treatment outcomes.

Shauna Schiffman

Bioinformatics/Biology, Eighth

Mentored by Vu Nguyen

Deciphering Functional Disorder of Nuclear Proteins with Deep Learning

Over 80% of nuclear proteins harbor intrinsically disordered regions (IDRs), whose lack of stable structure prevents prediction of function using traditional sequence-to-structure paradigms. IDRs regulate protein localization and condensate interactions through multivalent, sequence-encoded properties, but how sequence composition shapes dynamic nuclear motion remains unknown. I propose to test whether an “IDR code” links amino acid sequence directly to dynamic behavior in living cells.

I analyzed a yeast transcription protein whose real-time motion was captured by live-cell, single-molecule microscopy. To dissect thousands of complex trajectories, I have developed an unsupervised Long Short-Term Memory (LSTM)-based autoencoder that clusters trajectories into dynamically distinct populations. This approach resolved DNA-bound and free diffusive states, demonstrating that protein motion partitions into discrete, learnable categories.

To link sequence to motion, I will implement a multimodal, multitask autoencoder that integrates IDR sequence features with trajectory-derived motion features. Separate encoders will generate modality-specific embeddings that fuse into a shared latent space. A multitask framework will jointly reconstruct features and predict motion state labels. Critically, I will compare multimodal and sequence-only prediction performance to determine whether sequence features alone can predict dynamic state.

This project provides the first quantitative framework linking IDR sequence composition to quantitative motion states. By establishing motion as a predictable and sequence-encoded property, this work lays the groundwork for transforming disordered protein dynamics from a descriptive phenomenon into a controllable design principle.

Angela Sheng

Human Biology, Muir

Mentored by Thomas James Kipps

Targeting ROR1 to Restore APR-246-Induced Ferroptosis in ROR1-Positive B-Cell Malignancies

Abstract redacted due to proprietary information.

Hanxiao Shi

Structural Engineering, Sixth

Mentored by Joel Conte

No textbook? No problem!: Creating a reader for SE 105: Statistics, Probability, and Reliability

Abstract redacted due to proprietary information.

Shreya Singh

Math-CS/Econ, Revelle

Mentored by Isabel Trevino

Visual Interface Design and Behavioral Bias in Novice Trading

Financial markets are often described through the lens of rational decision making, but in practice traders deviate from this ideal in predictable ways. Two of the most well documented sources of deviation are herding, where investors imitate others rather than acting on their own information, and overconfidence, where investors overestimate the quality of their own signals and trade more than is optimal. What remains less understood is whether the design of the platforms through which people trade plays a role in how strong these biases are. This project investigates how altering visual features on stock trading platforms affects herding, overconfidence, risk taking, and trading outcomes among novice investors.

To study this, a controlled laboratory experiment is designed using oTree's Zurich Trading Simulator. The key design principle is that financial fundamentals stay identical across all participants, so any differences in behavior can be attributed to visual

presentation alone. Participants first trade under a standard interface to establish baseline bias levels, then are randomly assigned to either keep that interface or receive one with modified visual features such as neutral color schemes instead of red and green framing, adjusted chart displays, and changes to how rankings are shown.

This paper hypothesizes that visually salient design features amplify both herding and overconfidence, leading to higher trading frequency and weaker payoffs, and that reducing salience through neutral design choices will moderate these effects. Ultimately this research aims to produce causal evidence with direct implications for platform regulation and retail investor protection.

Tanya Singh

Molecular Biology, Seventh

Mentored by Guillaume Urtecho

Functional Variation of Bile Salt Hydrolase Enzymes Across Human Gut Microbiome

Bile acids (BAs) are important for lipid digestion and signaling between the host and gut microbiota. While microbial bile salt hydrolases have been widely known to hydrolyze amino acid-conjugated bile acids, it was recently discovered that these enzymes also perform acyltransfer, conjugating diverse functional groups to BAs. However, given the comprehensive diversity of these enzymes, the extent to which BSH hydrolytic or acyltransferase activity varies across different members of the human microbiome has not yet been comprehensively understood. This project will investigate how BSH activity differs across the human microbiome by evaluating the substrate specificity and conjugation properties across BSH variants. To address the research question, we will use in vitro assays and targeted metabolomics-based approaches. Bacterial clones expressing diverse BSH genes will be cultured in 96-well plates to allow for high-throughput screening of growth rate under different bile acid conditions. Enzymatic activity will be measured across wells containing different bile acid substrates. Samples demonstrating bile salt hydrolase activity will be selected for DNA extraction and sequencing to identify gene variants associated with bile salt hydrolase activity.

Grecia Paola Siono Gutierrez

Electrical Engineering/ ECE Department, Marshall

Mentored by Oscar Vazquez-Mena

Ligand Exchange Strategies for Enhanced Sensitivity in Quantum Dot Photodetectors

Colloidal Quantum Dots are semiconductor nanocrystals that can be processed in solution, making them a primary focus for next-generation optoelectronics. Because their electronic properties can be tuned by adjusting their physical size, they are ideal for use in photodetectors. These devices function by capturing light and converting it into electrical signals, serving as critical components in technologies such as autonomous vehicle navigation, medical imaging, and infrared night vision systems.

Currently, a significant challenge involves the long, insulating organic ligands used during the initial synthesis of these dots. These bulky molecules act as barriers that hinder charge transport and create "trap states" on the surface where electrons become stuck. This results in increased electrical noise and a loss of sensor sensitivity. This research focuses on identifying optimal ligand exchange strategies to replace these organic chains with compact inorganic alternatives. By engineering the surface chemistry and the way these nanocrystals are packed, we can minimize noise and facilitate more efficient carrier mobility.

Establishing a protocol for surface passivation is essential for transitioning from disordered thin films to highly organized architectures. This project evaluates various chemical treatments and assembly techniques to determine which creates the most effective interface between individual dots. Ultimately, this work seeks to bridge the gap between laboratory-scale chemistry and the development of high-performance, low-noise infrared sensors.

Alexa Solis

Education Sciences, ERC

Mentored by Makeba Jones

Conversations on the Table: a Literature Review on School Choice, Zone Boundaries, and Educational Opportunities

School choice policies have increasingly shaped the landscape of public education in the United States, raising concerning questions about equity, access, and the distribution of resources among schools in districts. This literature review examines a slight history and ongoing scholarly conversations surrounding school choice and school zone boundaries, with a specific focus on how these policies influence students' access to educational opportunities within the public school system. Drawing from peer-reviewed research, empirical studies, and journalistic and media sources, this review seeks to synthesize key themes including the relationships between residential zoning and school resource allocation, the role of school choice programs such as magnet schools and charter schools, and their implications for educational equity across socioeconomic and racial lines.

Harry Song

Human Biology/School of Biological Science, Eighth

Mentored by Cole Ferguson

Possible role of H2Ak119ub in regulating other chromatin identity markers

Abstract redacted due to proprietary information.

Michelle Tang

Human Biology, Marshall

Mentored by Mark Ginsberg

Effects of Anti-CD25 Antibody mPC61 on Regulatory T Cell Differentiation

Treg (T-regulatory) cells are a special subset of immune cells that suppress excessive or misdirected immune responses, preventing autoimmune diseases. Tregs arise through the differentiation of naive CD4⁺ T cells. CD25 is a protein expressed on the surface of CD4⁺ T cells, and the binding of the anti-CD25 antibody mPC61 to this receptor can initiate a novel IL-2 signaling pathway in Tregs. Previous studies in the Ginsberg Lab have shown that the mPC61 anti-CD25 antibody enhances the suppressive function of Treg cells through this novel signaling pathway. Building on this work, our project aims to investigate the effects of mPC61 on Treg differentiation in vitro. Specifically, we hypothesize that mPC61 increases Treg differentiation.

Naive CD4⁺ cells were isolated from C57BL/6 Foxp3GFP mouse spleens and cultured under standard conditions for Treg differentiation, with mPC61 or an isotype control. After 5 days of incubation, the cells were analyzed by flow cytometry to assess the percentage of Tregs, defined by Foxp3-GFP expression, for both groups and compared via a paired t-test. The mPC61-treated group showed a significant increase in the proportion of Tregs compared to the control group, indicating that CD25 signaling induced by mPC61 promotes greater differentiation of naive CD4⁺ T cells into Tregs. These findings highlight the potential of mPC61 as a therapy for autoimmune diseases involving Treg dysregulation.

Tue Thai

MAE, ERC

Mentored by Christopher Theissen

pySpex Analysis: A New Way to Analyze

Analysis of near-infrared spectroscopic data is often limited by fragmented workflows and manual intervention, which limit efficiency and reproducibility. From 2000-2022 alone, almost 43TB of data is available to IRSA and Legacy Archive, yet only 10% of said data has been utilized in publishing. The large volume of data, combined with reliance on prior reduction approaches based on proprietary software and significant user intervention, has limited widespread analysis. To address these challenges, pySpextool has been designed for the SpeX instrument on the NASA Infrared Telescope Facility and its associated archives (including the IRSA SpeX Archive and the IRTF SpeX Legacy Archive). This pipeline is an open-source data reduction pipeline developed by a collaboration of scientists with the goal to standardize reduction procedures while minimizing user-dependent variability through automated routines.

In our work, we apply pySpextool to reduce spectral data and evaluate its performance relative to prior methods based on proprietary software. Our results demonstrate improved consistency in spectral extraction and increased processing efficiency. These advances support ongoing efforts to uniformly reprocess the extensive SpeX archival dataset, most spanning decades of observations with much of which remains unpublished, and to build consistent spectral libraries for low-mass stellar and substellar objects.

Anh Tong

Biochemistry/ Medicine, Muir

Mentored by Shyamanga Borooah

Investigation of Base Editing on EFEMP Mutations in Sorsby Fundus Dystrophy

Abstract redacted due to proprietary information.

Annika Torres

Human Biology/Biological Sciences, ERC

Mentored by Daniel Bayless

Characterizing the Role of LSvEsr1 Population in Aggression and its Sex Dimorphisms

Aggression is a natural, critical behavior throughout the animal kingdom, governing survival from predators or threatening situations. When excessive or poorly controlled, this high-energy cost behavior can be detrimental to one's health. Increased aggression or irritability are also common symptoms of many neurological disorders, including PTSD, bipolar disorder, and dementia. Current pharmaceutical treatments often suppress neural activity and impair cognition, highlighting the need to target the specific mechanisms that inhibit aggressive impulses. Compounding this issue, most neurobiological mechanistic studies on aggression have historically focused on male subjects, despite evident sex differences in this behavior.

To investigate this, I will focus on a key region, the lateral septum (LS), known from previous studies to act as a “brake” on the ventromedial hypothalamus (VMHvl), another brain region known to trigger aggressive attacks. In the Bayless Lab, we have identified a potential sexually dimorphic neural population in the ventral lateral septum (LSv) labeled by estrogen receptor 1 (Esr1) that differs in the amount of projections from the LSv to the VMHvl between male and female mice. Therefore, I hypothesize that the LSvEsr1 neurons suppress aggressive behavior and that their modulation differs between sexes. To support this, I will investigate the functional role of the LSvEsr1 neural population by neuronal ablation, then characterize their aggressive behavior from perturbing these cells, and validate targeting specificity with immunohistochemistry. This project will provide

cell-type-specific evidence for a neural circuit that naturally inhibits aggression, establishing a foundation for sex-specific therapeutic strategies.

Alexandra Tuff

Art History and Criticism/Visual Arts, Sixth

Mentored by Mariana Wardwell

Modernity in Crescendo: Ernst Ludwig Kirchner and Modern Germany

The competing pressures fueling Germany's modernization in the early twentieth century shaped the experience of modern life for the individual. On one hand, this transformation enabled broader cultural and political participation, evident in the rise of the avant-garde and the largest socialist party in the world at the time. On the other hand, Germany's expansion was driven by a narrowly self-interested nationalism that contributed to the outbreak of the two world wars—the most catastrophic conflicts in human history. The speed and scale of these developments catapulted individuals into a radically transformed modern world. This environment was louder, more crowded, and increasingly commercialized and mechanized, forcing individuals to adapt. The tension of this adaptation, and the overstimulation it produced, emerged as defining conditions of modern life and central concerns of German Expressionism.

Ernst Ludwig Kirchner's paintings directly register these pressures. Kirchner's evolving approach to color and form traces the crescendo of German modernity, as individual expression emerges alongside the conditions that ultimately undermine it. Focusing on paintings across three periods—his early work in Dresden (1905–1911), his Berlin years, including work produced around his military service and subsequent breakdown (1911–1917), and his later period in Switzerland after his relocation to Davos (1917–1920s)—this project traces his development within German modernity. These phases chart both Germany's transformation and Kirchner's psychological response. Through visual analysis within a critical theory framework, this paper examines the acidity of his color palette and the compression of space and form under the pressures of German modernity.

Michael Vasandani

Data Science, Seventh

Mentored by Benjamin Smarr

Wearable-Derived Aberrant Sleep Patterns and Their Association with Depression

Sleep and mental health are closely linked; however, most existing knowledge is derived from controlled clinical studies, which may not adequately reflect the complexity of sleep behavior in real-world contexts. The proliferation of wearable devices such as Fitbit enables the collection of large-scale, continuous sleep data in everyday environments, presenting a unique opportunity to investigate natural sleep patterns. This study utilizes a data-driven framework to identify atypical sleep behaviors and examine their association with depression severity.

High-dimensional nightly sleep data are projected into a two-dimensional space using Uniform Manifold Approximation and Projection (UMAP), which facilitates visualization and comparison of behavioral patterns across nights. The relative frequency of each night is quantified by estimating local point density within this space, and 'outlier nights' are defined as those occurring in low-density, less typical regions.

To ensure interpretability, density thresholds are calibrated so that a fixed proportion of nights are classified as outliers. Both global thresholds, based on all available data, and label-informed thresholds, derived from nights with PHQ-9 depression scores, are evaluated. Generalized estimating equations are used to account for repeated observations within individuals, enabling robust analysis of associations between sleep behavior and depression severity.

This framework offers a scalable and flexible method for characterizing real-world sleep variability and enables systematic investigation of the relationship between deviations in natural sleep patterns and mental health outcomes.

Izabella Vasquez

Neurobiology, ERC

Mentored by Amy Bintliff

Biology Education and Engagement in East Africa

This research project focuses on providing hands-on biology education kits for children in Kenya and Uganda, with the goal of increasing interest in the biological sciences. East Africa has a high percentage of students lacking basic educational skills, many of whom are also underperforming in biology. I conducted a curricular review of the Uganda Ministry of Education and Sports science curriculum and identified the following findings: 1) Biology material was based on the memorization of material; 2) there was a lack of hands-on learning, which left little room for conceptual understanding or imagination; 3) the curriculum did not include resources for teachers to implement the lessons. Implementing hands-on activities for students to visualize biology concepts, practice making connections, and interact with their classmates would allow students to use their curiosity and learn in ways that are engaging. I built three biology kits, including lessons and materials, used by our international partners, Africa Education and Leadership Initiative, and Teule Kenya. Last summer, I taught and implemented the pilot curriculum in Kenya for children in primary grades 1-7. I also received feedback from students. Results from participant responses and modifications to the curriculum will be discussed.

Sergio Veliz

Physics, Revelle

Mentored by Simon Bott-Suzuki

Single Wire Z-pinch experiments with and without a plane

The plasma formation and dynamics of single wire Z-pinchs without a plane have been extensively studied. However, as of recent interest, the dynamical behaviors of those with a plane has been considered. A pulsed plasma machine named Bertha (200kA, 1 microsecond) in the P3 laboratory produced these plasmas. This experiment simulates important aspects of a new inertial confinement scheme in Sandia National Labs. The optical diagnostic method used on Bertha was interferometry, in order to recover the density profile of the plasma as a function of time. The interferometry was set up in a

Mach-Zehnder configuration, in which one beam travels through the vacuum chamber and the other around it. The experimental results show the differences between those with and without a plane, comparing simulations at Sandia National Labs.

Aditya Verma

Biology with a Specialization in Bioinformatics, Marshall

Mentored by Shiri Gur-Cohen

Lymphatic Signaling Promotes Tumor Plasticity in Squamous Cell Carcinoma

The aggressiveness of cancer cells can be attributed in part to their ability to adopt distinct identities, including a more invasive and mesenchymal phenotype, a behavior known as plasticity. Growing evidence suggests the tumor microenvironment, including the vasculature and immune milieu, plays a key role in shaping cancer cell plasticity and metastatic potential. Recent work from our lab demonstrated that lymphatic vessels interact with epithelial stem cells to maintain tissue homeostasis. Despite evidence linking lymphatic vessels to heightened risks of tumor metastasis, the mechanisms by which lymphatic vessels shape the plastic potential of cancer-initiating cells remain unknown. In this study, we investigated how lymphatic function affects tumor plasticity in cutaneous squamous cell carcinoma (SCC), a common and invasive skin cancer. Using a genetically engineered mouse model of SCC using Sox9-CreER; KRAS; p53fl/fl; YFPfl/fl mice, tumors were analyzed comparing endogenous lymphatic conditions to intratumor lymphatic dysfunction using VEGFR3-Fc, a chimeric antibody that blocks lymphatic vessel growth and signaling. To build a comprehensive transcriptomic profile of cancer cells with and without lymphatic integration and examine how gene expression changes when lymphatics are dysfunctional, tumor cells were sorted and profiled using scRNA sequencing. The analysis revealed that lymphatic regressed tumors had reduced expression of epithelial-to-mesenchymal transition (EMT)-associated genes and shifted

toward an epithelial cell state characterized by increased EpCAM expression. Together, these findings suggest that lymphatic signaling promotes tumor cell plasticity and EMT in SCC, whereas lymphatic regression constrains these programs and maintains tumor cells in a more epithelial state.

Araceli Villarreal

Education Studies, Sixth

Mentored by Shana Cohen

A Case Study: Early Intervention for Neurodivergent Children

Early language development is critical for children's academic and social success, however children with Autism Spectrum Disorder (ASD) or speech and language delays often experience barriers to acquiring expressive vocabulary. Even within the ASD diagnosis a child's journey to learning language is vastly different across families. Some differences to take into consideration is that every child's home environment provides different amounts of language exposure and access to resources. These resources are crucial in a child's ability to get an early diagnosis and early interventions. This study will ask, does vocabulary knowledge increase after using Sing and Speak for Kids for four weeks? And is there a difference in daily music engagement before and after using the Sing and Speak for Kids Program? The child's expressive vocabulary growth and levels of music engagement are measured before and after participation using a list of target words and parent interviews. Findings within this study may contribute to research on accessible, music-based interventions that support early language development for preschool-aged children.

Aarya Vishnu

Biology: Bioinformatics, School of Biological Sciences, Eighth

Mentored by Matthew Daugherty

Assessing the bacterial origins and functions of lysozyme-like proteins in metazoans

Horizontal gene transfer (HGT) is the transfer of genetic information between species rather than the inheritance of genetic information from parent to offspring. While known to be common among bacteria, the extent to which HGT occurs between bacteria and metazoans (animals) is unknown. In addition, the functions that metazoans may have acquired by HGT from bacteria are also unknown. A prior undergraduate student at the Daugherty Lab developed a computational pipeline to comprehensively detect cases between bacteria and metazoans, revealing 100+ potential instances of HGT. Interestingly, around 20 of these putative HGT events were tentatively annotated as lysozyme-like proteins, which are enzymes that hydrolyze peptidoglycan found in bacterial cell walls. This data leads us to hypothesize that there is a large number of bacteria-to-metazoan events that provide metazoans with antibacterial properties through the expression of lysozyme-like proteins. This project hopes to test the nature of these hits and involves both wet lab experiments and dry lab analysis. The analysis will involve searches using BlastP, as well as the Geneious Prime software, to provide further phylogenetic evidence to support that these are truly HGT events and to support the lysozyme-like nature of these sequences. Afterwards, the sequences that have “passed” the analysis will be tested on bacteria to verify their functionality as cell-wall degrading and, therefore, antibacterial proteins. In short, this study aims to identify the functionality of these genes, as well as provide insight into their genetic origins.

Zelda Waite

CH25/ IN29 Chemistry Department, Marshall

Mentored by Brian Cross

SUBHUMAN – A Photographic Vernacular of Autistic Perception (II)

SUBHUMAN lives in that split second when the darkroom tray is still quiet and an image is only beginning to appear. In that lingering breath, light is not yet fixed; it pools, bends, and hesitates. That threshold where light is neither fixed nor entirely seen is the emotional and perceptual ground for this research-based analog photography project. Using darkroom techniques SUBHUMAN is a black-and-white 35 mm film series that treats the darkroom as a site of perceptual research and science communication: a place where autistic experience, masking, and miscommunication can be translated into the slow grammar of light instead of clinical language. The work uses layered exposures, photograms, and deliberate light manipulation to render perception through an autistic lens. The photographic surface becomes both mask and mirror: a protective, distorting veil that reveals how sensory entanglement and cognitive structure can be misread as “disorder” when viewed too quickly. Autism here is framed as a difference in how light

moves through the mind—variations in sensitivity, connectivity, and how signal becomes sense. Masking, or camouflaging to appear “legible,” becomes a visual problem inside the darkroom: which layers are allowed to show, which are burned back, which are left as ghosts in the emulsion. Each print rehearses the fragile instant before meaning hardens into a single interpretation. Rather than smoothing that moment over, SUBHUMAN slows it down so viewers can feel the effort of perception itself.

Emmy Wei

Electrical Engineering/Department of Electrical and Computer Engineering, Seventh

Mentored by Yu-Hwa Lo

Improving Lateral Flow Assay Sensitivity Using Advanced Signal Processing

Lateral flow assays (LFAs) are widely used for rapid, low-cost, and accessible disease diagnostics, but they remain limited by low sensitivity and binary outputs compared to the gold standard, Polymerase Chain Reaction (PCR). This work presents a signal processing framework that improves detection sensitivity for low analyte concentrations and enables quantitative analysis from standard test strip images. A cross-correlation-based algorithm uses the control line as a positional reference to segment the strip and generate position-dependent correlation curves, allowing extremely faint test lines that are normally undetectable to the human eye to produce consistent peaks and be reliably classified as positive. However, at high dilution levels, noise-induced correlations can introduce false positives and decrease detection performance. To address this limitation, large-scale synthetic datasets of test strips are generated with controlled variations in signal amplitude, noise, line thickness, and spatial positioning, enabling systematic evaluation under low signal-to-noise conditions. These datasets are used to refine the detection algorithm and lay the groundwork for integrating machine learning models to improve robustness and reduce false detections. Overall, this work advances LFAs toward sensitive, quantitative, and scalable diagnostic tools suitable for point-of-care and large-scale testing applications.

Ivan Wong

Political Science, Sixth

Mentored by Kwai Ng

One City, Two Systems: The Rule of Law in Hong Kong Under the National Security Law

How did the changes made by the National Security Law (NSL) to Hong Kong's legal system reshape civil liberties in the region? I analyze legislation, court cases, and scholarly articles on how the law uprooted the city's political culture. The NSL created a special police force and prosecutor's office solely responsible for national security cases, mandated they be heard by designated judges, and denied defendants their due process rights. Hong Kong judges permitted those special provisions even though they circumvented the rule of law, and their broad interpretations of the NSL effectively warned Hongkongers that anything that could be considered political opposition would be scrutinized. This had significant effects on Hong Kong's civil society, including the suppression of the media and education, closure of NGOs, and decrease in investor confidence. These changes bear striking similarity to the courts in authoritarian regimes, whose dictators often divert politically sensitive cases to specially-created security courts or bend the existing courts into compliance in light of extraordinary circumstances so they can claim to follow the letter of the law while silencing opposition to their rule. This suggests the courts are among the targeted victims of Hong Kong's democratic backsliding.

Allison Woo

Biochemistry/Chemistry and Biochemistry, Marshall

Mentored by Lalit Deshmukh

Ubiquitination of HIV-1 p6 Enhances ALIX Recruitment via Avidity-Driven Interactions

Human immunodeficiency virus type 1 (HIV-1) hijacks the host Endosomal Sorting Complex Required for Transport (ESCRT) machinery to facilitate viral budding and membrane scission. This recruitment is primarily mediated by the interaction between the p6 domain of the viral Gag polyprotein and the host adaptor protein ALIX. While Gag ubiquitination is known to occur during budding, its precise biophysical impact on ALIX recruitment has remained unclear. In this study, we utilized fluorescence anisotropy to quantify the binding dynamics between ALIX and a recombinant ubiquitin-p6 fusion

protein. Our results demonstrate that the presence of ubiquitin increases the binding affinity for ALIX by approximately 3-fold compared to p6 alone. This enhancement is driven by an avidity effect, suggesting that ubiquitin provides a secondary docking site that stabilizes the ALIX–Gag complex. These findings highlight how post-translational modifications can cooperatively regulate host-pathogen interfaces, providing a biochemical basis for how ubiquitination may accelerate HIV-1 release.

Ellen Wu

Molecular and Cell Biology, School of Biological Sciences, Revelle

Mentored by George Sen

Investigating the Role of HDAC Inhibition in Restoring Foxp3 Stability in Hnrnpu-Deficient Treg Cells

Regulatory T cells (Tregs) maintain immune tolerance through stable expression of the transcription factor Foxp3. Disruption of Foxp3 expression destabilizes Tregs and promotes autoimmune inflammation. Prior work in the Sen Lab demonstrated that deletion of heterogeneous nuclear ribonucleoprotein U (Hnrnpu) in Tregs causes chromatin closure at the Foxp3 conserved non-coding sequence 2 (CNS2) enhancer, leading to reduced Foxp3 expression, loss of Treg identity, and autoimmune disease.

This project investigates whether histone deacetylase (HDAC) inhibition can restore Foxp3 expression and stabilize Tregs in Hnrnpu-deficient mice. Because HDACs remove acetyl groups from histones and promote chromatin compaction, pharmacologic inhibition may increase histone acetylation and reopen chromatin at regulatory loci controlling Foxp3 transcription. Hnrnpu-deficient and control mice were treated in vivo with the HDAC inhibitor Trichostatin A (TSA), and immune cell populations were analyzed using flow cytometry.

Initial pilot experiments established a safe dosing regimen for TSA treatment and confirmed the feasibility of the experimental workflow. In a subsequent higher-dose trial, TSA-treated knockout mice exhibited partial restoration of Foxp3⁺ Treg populations compared with vehicle-treated knockouts. TSA-treated knockouts showed a tissue-specific rescue of Foxp3⁺ Tregs in lymph nodes, with frequencies approaching wild-type levels, while splenic Tregs remained unrescued. Treated mice also displayed reduced lymphadenopathy and splenomegaly relative to untreated knockouts, suggesting an improvement in autoimmune pathology. These findings suggest that HDAC inhibition partially rescues Foxp3 expression and Treg stability, supporting a role for histone acetylation in maintaining Treg identity.

Stephanie Wu

Biochemistry/Chemistry and Biochemistry, Sixth

Mentored by Erik Romero

One-pot synthesis of 1,1-aminoboranes

1,1-aminoboranes compounds are highly valuable motifs because they unite a nitrogen-containing functionality with a synthetically versatile boron handle in a single scaffold. Their importance is further emphasized by their role in medically important boron-containing enzyme inhibitors, including Bortezomib and Ixazomib, and therefore, new methods to access this structural motif have become attractive. Herein, we report a one-pot multicomponent bora-Petasis-type reaction that couples ubiquitous starting aldehydes, secondary amines, bis(pinacolato)diboron (B₂Pin₂), and N-heterocyclic carbene (NHC), as well as cyclic(alkyl)(amino)carbene (CAAC)-ligated copper catalysts under mild, base-free conditions. This transformation provides direct access to >50 isolable 1,1-aminoboranes with broad functional group compatibility and synthetic utility for downstream derivatization. Additionally, this strategy facilitates the efficient synthesis of the aminoboronic acid drug, Bortezomib, an FDA-approved treatment for multiple myeloma and lymphoma. Mechanistic insights support that this transformation does not proceed via a Cu-boryl intermediate, indicating an alternative pathway that adheres more towards a Cu-boronate/iminium ion-pair reminiscent of Petasis-type chemistry to forge the carbon-boron bond.

Overall, this work demonstrates an efficient synthetic approach to synthesizing 1,1-aminoboranes with commercially available starting material, low catalyst loading, and mild reaction conditions.

Derek Xu

Psychology, Marshall

Mentored by Leslie Carver

Politics in Plain Sight? Organizing and Interpreting Neurophysiological Asymmetries Between Liberals and Conservatives Using the Elective Affinities Model

Research on personality differences between liberals and conservatives has increasingly turned to neurophysiological methods, with many studies reporting that individuals of different ideological orientations show different neurophysiological responses to nonpolitical stimuli. Yet, this literature remains fragmented, with substantial variation in methods, ideological operationalizations, and interpretive frameworks. My project recruits John Jost's Elective Affinities Model (EAM), which posits that distinct psychological needs in epistemic, existential, and relational domains motivate ideological belief, as a framework for organizing and interpreting studies that report neurophysiological differences between liberals and conservatives. Based on their stimuli, reviewed studies are categorized as dealing with epistemic, existential, and relational personality domains. Then, each category is assessed for consistency with the EAM's claim that liberal and conservative personalities differ in the corresponding domain. For epistemic and relational domains, I found clear neurophysiological support for liberal and conservative asymmetries, though there are fewer-than-ideal studies on these two domains. In contrast, evidence for liberal and conservative personality differences in the existential domain is more contentious, partially due to methodological debates. Prospects for future research are discussed, touching on the uses/limits of using neurophysiological methods to investigate ideological asymmetries, how the operationalization of ideology shapes a study's methods and interpretation of results, what the reviewed literature reveals about the dimensional structure of political ideology, and alternative ways in which this seemingly disparate topic could be organized.

Christina Yang

Clinical Psychology, Seventh

Mentored by William Pelham

Examining the Relationship Between Adolescent Depression and Parental Knowledge of Adolescent Cannabis Use

Abstract redacted due to proprietary information.

Desiree Yang

Cognitive Science, Sixth

Mentored by Bitna Joo

Prefrontal Encoding of Social Rank Dependent Strategies

Social hierarchies occur in numerous social species, and rank within them profoundly shapes physiological stress, motivation, and long-term health outcomes. Downward social mobility in particular is associated with depression and stress vulnerability, yet the neural

mechanisms linking rank change to altered behavioral strategy remain unknown. While the medial prefrontal cortex (mPFC) is established as a key regulator of social dominance, how it encodes rank-dependent behavioral strategies, particularly during individual performance outside of direct competitive interaction, remains poorly understood. To address this gap, we developed the climbing beta task, a modular vertical pegboard assay that captures multidimensional behavioral readouts, including latency, tortuosity, path selection, and climbing strategy across configurable board layouts. Using SLEAP-based pose tracking, we will extract continuous behavioral manifolds to characterize rank-dependent strategies across dominant, intermediate, and subordinate animals, and critically, test whether these strategies update following experimental rank change through rehousing. Simultaneous Neuropixels recordings across mPFC subregions will test whether rank occupies a separable dimension within population geometry during individual task performance, and whether this geometry remaps after rehousing-induced rank change. Establishing how social reorganization reshapes both behavior and its neural substrates provides a mechanistic foundation for understanding how rank change translates into altered motivation and health vulnerability.

Joyce Yang

Anthropology, Eighth

Mentored by Amy Non

Preterm Birth Risk and the Role of Maternal and Paternal Race, Ethnicity, and Nativity

Preterm birth (<37 weeks gestation) increased by 13% from 2014 to 2023, with persistent racial disparities. Black women in the U.S. experience significantly higher rates of preterm birth than non-Hispanic White women, a pattern that has persisted for decades, but less is known about how paternal race/ethnicity influences preterm births. This study analyzed all live singleton births in the U.S. from 2019 to 2024 (n=16,187,903) to examine associations between maternal and paternal race, ethnicity, nativity, and preterm birth. Logistic regression models adjusted for age, education, insurance, and WIC status estimated odds of preterm birth across racial, ethnic, and nativity groups, using US-born non-Hispanic White mothers as the reference. All maternal racial and ethnic groups had a higher rate of preterm birth compared to White mothers. Among fathers, all groups except Asian fathers had higher rates relative to White fathers. Foreign-born mothers had a lower risk of preterm birth, with the exception of Native Hawaiian or Pacific Islander individuals. Compared to same-race White parents, all same-race parents across all other groups had higher preterm birth risk, with Black same-race parents having the greatest risk overall. Among those with more than high school education, mothers and fathers from non-White groups have higher risk compared to White parents. These findings highlight how structural inequities rather than inherent biological differences drive racial and ethnic disparities in reproductive health, highlighting the need to address social determinants to advance reproductive justice among minorities groups.

Minshen Yang

Bio: Bioinformatics, Warren

Mentored by Guillaume Urtecho

Validation of a Putative Insulin Receptor in a Gut Microbe via CRISPR-associated transposases (CAST)

Current evidence has shown that gut microbiota plays an important role in regulating host metabolism and metabolic health. However, the mechanisms directly linking bacterial and host physiology remain understudied. Here, we identified that *Bacteroides uniformis*

expresses a membrane bound protein with sequence and structural homology to mammalian insulin receptor (INSR). Moreover, in *B. uniformis* strains containing this protein, insulin accelerates growth and glucose absorption in vitro. We hypothesize that this identified and yet uncharacterized protein mediates a direct insulin-sensing response in *B. uniformis*. To test this, we are using CRISPR-associated transposases (CAST) to create a knock-out strain of the *B. uniformis* putative INSR protein. We expect that interrupting this gene will result in the bacteria losing its response to insulin. The necessity of this sequence will demonstrate the first example of a gut commensal microbe directly responding to a human endocrine hormone. We hope this finding of a direct host-bacteria interaction may provide a new lens in the research of gut microbiome and ultimately contribute to the development of new treatments for metabolic diseases such as diabetes.

Madison Yu

Neurobiology, Eighth

Mentored by Kay Tye

Prefrontal Encoding of Rank Dependent Strategies

Social hierarchies occur in numerous social species, and rank within them profoundly shapes physiological stress, motivation, and long-term health outcomes. Downward social mobility in particular is associated with depression and stress vulnerability, yet the neural mechanisms linking rank change to altered behavioral strategy remain unknown. While the medial prefrontal cortex (mPFC) is established as a key regulator of social dominance, how it encodes rank-dependent behavioral strategies, particularly during individual performance outside of direct competitive interaction, remains poorly understood. To address this gap, we developed the climbing beta task, a modular vertical pegboard assay that captures multidimensional behavioral readouts, including latency, tortuosity, path selection, and climbing strategy across configurable board layouts. Using SLEAP-based pose tracking, we will extract continuous behavioral manifolds to characterize rank-dependent strategies across dominant, intermediate, and subordinate animals, and critically, test whether these strategies update following experimental rank change through rehousing. Simultaneous Neuropixels recordings across mPFC subregions will test whether rank occupies a separable dimension within population geometry during individual task performance, and whether this geometry remaps after rehousing-induced rank change. Establishing how social reorganization reshapes both

behavior and its neural substrates provides a mechanistic foundation for understanding how rank change translates into altered motivation and health vulnerability.

Daniel Zhang

Bioengineering: Biotechnology, Revelle

Mentored by Kolade Adebawale

Modeling Mechanical Stimulation of Cancer in High Sugar Tissue

Throughout 2025, 30,000 people died of liver cancer in the U.S. Furthermore, global liver cancer incidence is projected to increase, and type 2 diabetes is implicated. Excessive sugar in tissue, a symptom of type 2 diabetes, can react with proteins to form advanced glycation end products (AGEs). These AGEs crosslink collagen to modulate the tissue's viscoelasticity, or its balance between being a viscous fluid and elastic solid. Recent findings suggest such viscoelastic modulation then alters cancer and immune cell behavior in the tumor microenvironment, but responsible mechanisms are underexplored – especially in a type 2 diabetes context. Hence, there is a need for quick-to-produce experimental models to study cell behavior in high-sugar, viscoelastic environments. Ultimately, the objective of this project is to develop said model as a collagen hydrogel. Collagen is first tested with treatments of prepared AGEs or methylglyoxal to induce glycation. The effect is evaluated through high resolution microscopy, and the viscoelastic properties of the hydrogels are measured via shear rheology. After the optimal treatment is determined, cancer cells and macrophages are seeded into the finalized hydrogel, and confocal imaging tracks behavior. Based on literature, sugar crosslinking is expected to maintain stiffness while accelerating hydrogel stress relaxation rate, or the rate which resistance to deformation decreases over time. The cells are expected to be more motile in this fast relaxation setting, reflecting a dangerous tumor microenvironment. Overall, this investigation will produce a hydrogel model that elucidates the impact of viscoelasticity on cancer in high sugar tissue.

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