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2026 Columbia Undergraduate Research Symposium



Friday, October 23, 2026
Roone Arledge Auditorium
10:30am-12:00pm



 COLUMBIA UNIVERSITY
IN THE CITY OF NEW YORK

RESEARCH SYMPOSIUM 2026

Research Abstracts:

Aruzhan Abil CC'28, Computer Science and Mathematics

Faculty Mentor(s) or Supervisor(s): Kaveri Thakoor

Title: The Retinal-Glycemic Link: Multimodal Model for Glycemic Variability Prediction

Abstract: Retinal vasculature provides insight into systemic body health. In this work, we characterize and illustrate the potential for early detection of type 2 diabetes mellitus (T2DM) using optical coherence tomography angiography (OCTA) images. Using the AI-READI cohort (N=1062), we extracted vascular metrics from OCTA images and correlate them with diabetic state (based on hemoglobin A1c, HbA1c) as well as continuous glucose monitoring (CGM) variables. Our results show that OCTA features of foveal avascular zone area, roundness of vessels, and degree of branching were most highly correlated with diabetic state and CGM variables. In addition, we also explored the ability of multimodal deep learning models trained on OCTA metrics and additional retinal imaging to classify high vs. low glycemic variability, which has been shown to be an early biomarker of glycemic dysregulation and insulin resistance. We find that combining fundus images with OCTA metrics moderately improves classification performance. These findings highlight the potential of multimodal retinal imaging as a widely deployable tool for early metabolic screening.

Osheen Abraham SEAS'29, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Prasanna Alluri

Title: Histone Lysine Demethylase (KDM) Inhibitors Reduce CDK4/6 Inhibitor-Resistant ER+ Breast Tumors and Rescues Cell Cycle Managers

Abstract: Estrogen receptor positive (ER+) breast cancers (BC) account for 70–80% of BC cases, yet resistance to Cyclin-Dependent Kinase 4/6 inhibitors (CDK4/6i) remains a major therapeutic challenge. Loss of retinoblastoma protein (RB), a key regulator of the G1/S checkpoint, is an established mechanism through which CDK4/6i resistance develops and promotes E2F-driven cell-cycle progression. In this study, we investigated

histone lysine demethylase (KDM) inhibition as a therapeutic strategy for RB-deficient ER+ tumors. A prior high-throughput screen of MCF7-RBKO and T47D-RBKO ER+ cell lines identified JIB-04—a pan-inhibitor of KDM4, 5, and 6 enzymes—as a top therapeutic candidate, and JIB-04 treatment significantly reduced MCF7-RBKO xenograft growth. For this study, bulk RNA-sequencing data were analyzed from (1) JIB-04-treated vs DMSO-treated MCF7-RBKO cells and (2) MCF7-RBKO vs MCF7-Parental cells. Gene Set Enrichment Analysis revealed significant downregulation of E2F Targets, G2M Checkpoint, and Mitotic Spindle pathways following JIB-04 treatment, whereas these pathways were significantly upregulated in MCF7-RBKO vs Parental. Metascape analysis of JIB-04 treated downregulated genes further identified enrichment in Mitotic cell-cycle, DNA-damage response, Chromatin-remodeling and Chromosome-organization. To identify the KDM family driving this effect, a cell viability assay was conducted comparing JIB-04 with KDM4 inhibitor TACH101, KDM5 inhibitor CPI-455, and KDM6 inhibitor GSK-J4. In this, JIB-04 and TACH101 exhibited similarly low IC50 values. For validation, MCF7-RBKO xenografts were treated with TACH101, resulting in significant reduction in tumor volume after three weeks of treatment. Given these findings, KDM inhibition, and namely KDM4i, may be a potential therapeutic strategy for RB-deficient ER+ BC tumors.

Joshua Abrams CC'29, Computational Biology

Faculty Mentor(s) or Supervisor(s): William Robinson

Title: Profiling monoclonal antibodies from Epstein-Barr virus infected B cells in autoimmune diseases of the nervous system

Abstract: Myasthenia gravis, autoimmune encephalitis, myelin oligodendrocyte glycoprotein antibody-associated disease (MOGAD), and neuromyelitis optica spectrum disorder (NMOSD) are autoantibody-mediated autoimmune diseases impacting the nervous system. Epstein-Barr virus (EBV), a gamma herpesvirus that establishes a life-long latent presence in B cells, has been mechanistically implicated in multiple autoimmune diseases, such as multiple sclerosis and systemic lupus erythematosus (SLE). In SLE, EBV-infected autoreactive anti-nuclear antigen B cells are reprogrammed to proliferate and adopt a pathogenic phenotype resistant to tolerance mechanisms. We investigate whether EBV-infected B cells are responsible for producing disease-associated autoantibodies: anti-NMDAR or anti-LGI1 antibodies in their respective autoimmune encephalitis subtypes, anti-AChR or anti-MuSK antibodies in their respective myasthenia gravis subtypes, anti-MOG antibodies in MOGAD, and anti-AQP4 antibodies in NMOSD.

Blood was collected from patients with each disease, and B cells isolated for multi-omic single cell sequencing, yielding transcriptome, B cell receptor, cell-surface protein, and EBV-seq datasets. We found that individuals with each of the six diseases had an increased frequency of EBV-infected B cells as compared to healthy individuals, suggesting poorer control of EBV infection. Antibodies encoded by EBV+ B cells were recombinantly expressed as monoclonal antibodies (mAbs) for study; antibodies derived from matched EBV- B cells were additionally expressed for comparison. Patient mAbs were tested for reactivity against their corresponding disease-associated antigen via cell-based assay (CBA), and their polyreactivity was assessed via enzyme-linked immunosorbent assay (ELISA) against unrelated antigens. We demonstrated that the EBV+ B cell population produces disease-associated autoantibodies with a higher frequency and specificity of binding as compared to the EBV- B cell population. This was observed across all six tested autoimmune diseases, consistent with a pathogenic role for EBV.

Amrita Acharya SEAS'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Benedict Anchang

Title: Predicting Responses to Endocrine-Related Compounds at the Single-Cell Level

Abstract: Due to tumor heterogeneity, cancer treatment has shifted towards precision medicine, where capturing individual cells' gene expression profiles is essential. Single-cell RNA sequencing (scRNA-seq) provides a tool for this, though manually labeling cells is unfeasible due to the sheer volume of data. However, computational methods can predict single cells' drug responses, which this project aims to do using evidence scores calculated from cells' gene expression profiles, and develop an app to automatically label single-cell datasets. The scRNA-seq dataset used was Tahoe-100M. For each endocrine-related drug selected for analysis, treated and control cells were merged and filtered for quality, then preprocessed by cell line and clustered. Four cluster-level evidence scores were calculated, which were used to perform k-means on the clusters to predict their responder status. A logistic regression model was then fitted to the Dexamethasone (Dex) data to be applied to other drug datasets through transfer learning. Lastly, an R Shiny app was created for analysis and visualization. The evidence scores, when used for k-means, were good predictors of responder status and matched the ground truth well. Moreover, the Dex model accurately predicted the ground truth. Further supporting the evidence scores' validity, NR3C1, the GR gene, was differentially expressed between model-predicted responders and

nonresponders. When applied to other drug datasets, differentially expressed genes were found for some drugs – after tailoring evidence scores per drug to their endocrine function – but not for all drugs, implying that this method is valid but needs further work to determine the best way to predict responder status across various drugs.

Kehinde Adekunle GS'28, Sociology

Faculty Mentor(s) or Supervisor(s): John Dennehy, Fabrizio Spagnolo, Monica Trujillo

Title: Evolution of Lambda Phage in an E. coli K-12 Chemostat

Abstract: This study aims to look at the evolution of the lambda phage (λ) lysis time in a continuous-culture chemostat system. We used Escherichia coli MG1655 (JJD 599), a chemostat-adapted, genetically stable host susceptible to λ infection and a twin chemostat setup. A “farm” where host cells are maintained in exponential growth and a “slaughterhouse” where a single inoculum of λ was added. Here we present our exploration of the conditions to study phage lysis time evolution using a chemostat system. First, we added λ to have a multiplicity of infection (MOI) of 0.1. Over 96 hours, bacterial colony-forming units (CFU) and phage plaque-forming units (PFU) were monitored. Plaques were detected only until six hours after inoculation. Our results suggest that phage growth rate in the chemostat is insufficient to maintain the λ population under the current growth conditions. Future work includes changing the dilution rate to increase the time cells stay in the slaughterhouse and/or infecting with a higher MOI. Once we find the conditions for having multiple λ generations in the chemostat system we will study the change in lysis time among them.

Harun Afza CC'27, Psychology

Faculty Mentor(s) or Supervisor(s): Usha Barahmand

Title: Trans Phantom Sensations as Predictors of Desire for Gender-Affirming Surgery: The Role of Gender Dysphoria

Abstract: Trans phantom sensations are sensations of gendered body parts that were physically absent at birth (Langer et al., 2023). Though they are prevalent in nearly 50% of transgender and gender-diverse (TGD) individuals, their impact on medical transition and one's desire for gender-affirming surgery (GAS) has not yet been explored. This study examined whether trans phantom sensations are associated with desire for GAS and whether gender dysphoria mediates these relationships. A total of 286 TGD

participants completed measures assessing current and past phantom sensations of gendered body parts, gender dysphoria, history of GAS, and desire for GAS. Linear regression models examined whether current phantom sensations predicted desire for corresponding surgeries, while mediation analyses tested whether gender dysphoria mediated these relationships. Trans phantom sensations significantly predicted desire for all assessed surgical procedures, including phalloplasty, metoidioplasty, scrotoplasty, vaginoplasty/vulvoplasty, and breast augmentation. Gender dysphoria partially mediated the relationships between trans phantom sensations and desire for phalloplasty and scrotoplasty, but not metoidioplasty, vaginoplasty/vulvoplasty, or breast augmentation. These findings suggest that trans phantom sensations may represent a clinically relevant aspect of gendered embodiment that warrants consideration when discussing GAS care and goals.

Michelle Ahn CC'27, Neuroscience and Behavior

Faculty Mentor(s) or Supervisor(s): Kristin Baldwin

Title: Brain chimeras engineered via in utero reprogramming: Mechanisms of selectivity

Abstract: There is a growing need for relevant research models to study human neurological disease. Recent techniques aim to humanize rodent models by transplanting human cells into immunocompromised animals, an invasive method that prevents exposure of transplanted cells to key developmental processes and limits researcher control over cell fate. Drawing from stem cell reprogramming techniques, where stem cells are genetically induced to become specific neuronal types, it was hypothesized that expressing specific transcription factor genes could control cell identity in a live animal. To explore this, genetically engineered pluripotent stem cells were injected into mouse embryos at an early developmental stage. Upon activation of neuronal genetic programs, a decrease in donor cell abundance was observed in non-neuronal tissues. It was theorized that programmed cell death, apoptosis, could account for this reduction in donor cell representation. To address this, peripheral organs were stained for cleaved caspase 3, a protein involved in the apoptosis molecular cascade. Our preliminary results show that cells stimulated to become inhibitory neurons express higher levels of apoptotic markers in peripheral tissues compared to cells expressing excitatory neuron genetic programs and non-induced donor cells. While the molecular basis for this differential vulnerability remains to be studied, these findings are key to improving our understanding of the interactions between host and donor cells in chimeric animals. Future efforts will focus on

exploring other mechanisms of donor cell death to eventually design chimeric animals reproducibly without donor cell contribution to the germline.

Arda Alisan GS'28, Mathematics, Rafia Hossein BC'28, Mathematics-Computer Science, Sophie Zhang CC'29, Mathematics-Computer Science

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: Neural Mass Dynamics: From Critical Phase Transitions to Reaction-Diffusion Parameter Modulation in Alzheimer's Tau Propagation

Abstract: Currently, no mathematical account fully explains why Alzheimer's tau pathology first targets regions such as the transentorhinal and entorhinal cortex. Hub degree, the leading structural explanation, is confounded with dynamical centrality, so connectivity alone cannot distinguish whether pathology follows a region's wiring or its dynamics. We rank brain regions by their dynamical resistance to destabilization by linearizing a Wilson-Cowan neural mass model near criticality on an 83-region HCP connectome and using network control theory to compute each region's minimum control energy. Across 685 ADNI subjects, tau accumulated preferentially in these hardest-to-tip regions, showing the opposite pattern from amyloid, and the relationship strengthened after controlling for hub degree. We then use this ranking in a personalized Fisher-Kolmogorov reaction-diffusion model calibrated to 43 subjects' longitudinal tau-PET trajectories. Our simulations suggest that suppressing local tau growth outperforms suppressing diffusion, and that protecting regions with the highest baseline tau burden produces greater reductions in simulated tau spread than targeting regions by structural or dynamical vulnerability. These results suggest that burden-informed targeting may better guide future anti-tau interventions.

Imen Alkuraya CC'29, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): Athira Menon

Title: How often do stars merge?: Predicting rates of stellar mergers across cosmic time

Abstract: Massive stars, far more massive than the Sun, are often born with a companion in a binary system. As these binaries evolve, interactions between the two stars can produce a range of observable phenomena, including X-ray binaries, luminous red novae, supernovae, and gravitational waves. Among the most dramatic outcomes is a stellar merger, in which the two stars

combine into one, leaving behind an event that carries clues about the properties of the original pair and the environment in which they formed. Predicting how often mergers occur across cosmic history helps astronomers interpret observations and better understand the history of star formation and chemical enrichment in the universe. This project uses COMPAS, a publicly available simulation code, to model large populations of massive binary stars across a range of chemical compositions and orbital configurations, focusing on the phase of unstable mass transfer, known as a common envelope, that often precedes a merger. A classification scheme was developed to sort these events by the internal structure of the donor star when mass transfer begins, revealing distinct evolutionary pathways toward merger. A data processing and visualization pipeline was also built to combine and analyze the resulting simulation output, allowing merger and common envelope rates to be compared across stellar compositions and mass transfer pathways. These results set the stage for the next phase of the project, which will combine the simulations with star formation history to predict merger rates over cosmic time, followed by detailed modeling of individual mergers using the stellar evolution code MESA.

Areej Al-Mugbil CC'29, Sustainable Development

Faculty Mentor(s) or Supervisor(s): William Roberts

Title: Development of a Novel Contact Liquid for Energy-Efficient Cryogenic Carbon Capture

Abstract: Global carbon dioxide emissions currently exceed 35 billion metric tons annually, surpassing the capacity of existing removal technologies. Cryogenic carbon capture, in which exhaust gas is cooled until carbon dioxide condenses and separates from the stream, represents a promising alternative to conventional methods. However, current systems remain limited to approximately 30 tons of carbon dioxide per day, due to declining efficiency and high evaporative loss in the conventional contact liquid, isopentane, over repeated regeneration. This study developed and evaluated novel contact liquid blends to overcome these limitations. One hundred candidate chemicals were screened, and four blends were characterized and tested across three regeneration cycles. The optimal formulation, an ethyl acetate and isopentane blend, achieved complete carbon dioxide capture across flue gas concentrations of 10, 15, and 20 percent, with peak performance at negative 95 degrees Celsius. Relative to isopentane, which costs 50 to 60 dollars and 470 kilowatt hours per ton, the novel blend reduced costs to 30 to 35 dollars and energy consumption to 280 to 310 kilowatt hours per ton, while fully retaining efficiency across cycles, a property

characterized as phase memory. Field validation at three pilot sites using a mobile capture unit yielded a technology readiness level of six and scalability to 100 tons of carbon dioxide per day, a 233 percent improvement over the current state of the art. These findings establish the feasibility of this contact liquid for improving the efficiency, cost, and scalability of cryogenic carbon capture in power generation, oil refining, and manufacturing.

Ipek Altunyurt CC'29, Physics

Faculty Mentor(s) or Supervisor(s): Kerstin Perez

Title: Optimization of X-Ray Optics Fabrication of International Axion Observatory

Abstract: BabyIAXO helioscope is designed to search for axions generated in the Sun by converting those axions into X-rays inside a man-made magnetic field. X-ray optics play a crucial role in raising the sensitivity by focusing the faint X-ray signal from the large magnetized area onto a small area on the detectors. The performance of these optics, consisting of thousands of tightly nested concentric, ultrathin curved glass segments, depends critically on the accuracy of the glass slumping and mounting processes.

To improve the slumping process, we first assessed the surface quality of slumped glass segments by laser metrology. We adjusted slumping parameters, such as temperature and mandrel positioning inside the slumping oven, to remove the observed surface defects. We increased the slumping yield of inner 2–4 layers from 30% to 76%. The same optimization procedure will be applied for layer 1, the most challenging part of the optic with its smallest radius. To study the redistribution of surface errors during the mounting process, we developed a finite element model in COMSOL Multiphysics, in which the mounting-induced deformation was simulated using spatially varying prescribed displacements. Different geometric matchings between the cylindrical mirrors and conical spacers are investigated to determine the optimal configuration in terms of surface figure error and mechanical stress, and to feed the results back into the selection of the slumping geometry. With the contribution of this project, the innermost 10 layers of the optic will be fabricated and tested by the end of this year as a prototype for the full optic of the International Axion Observatory.

Patricia Arbelaez GS'28, Visual Arts

Faculty Mentor(s) or Supervisor(s): Peter Catalanotto

Title: Ch'aska: Drawing the Morning Star from a Fragmented Archive

Abstract: Knowledge of Ch'aska, an Andean celestial figure associated with Venus as the Morning Star, survives through a fragmented record shaped by oral transmission, colonial accounts, translation, and retelling. This interdisciplinary, practice based project brings creative writing and visual art into conversation with scholarship on Andean history, archaeology, linguistics, cosmology, and material culture. It asks how culturally significant figures can be interpreted from incomplete archives without presenting contemporary reinterpretation as recovered Indigenous tradition or treating Andean cosmology as vanished mythology. The project combined comparative readings of colonial chronicles, scholarship, linguistic sources, material culture, and visual representations with iterative writing and image making. Sources were organized by documentation, scholarly interpretation, remaining uncertainties, and possibilities for responsible creative reinterpretation. These distinctions informed the design, structure, and visual motifs of Ch'aska: The Wandering Star, in which Ch'aska appears as an active presence rather than a distant celestial symbol. The research suggests that contradictions among sources should not be resolved into a single authoritative account. Instead, fragmentation can become an ethical and formal principle: gaps remain visible, creative choices are made transparent, and visual experiments use layering, reflection, and refraction rather than claiming historical reconstruction. Depicting Ch'aska and celestial beings in human form creates intimacy while recognizing that Andean cosmological knowledge persisted after conquest and Christianization and remains present in cultural memory and daily life. By treating creative writing and image making as methods of inquiry, this project proposes a transparent, adaptable framework for contemporary story methods grounded in culturally significant but incompletely documented traditions.

Ashley Armstrong CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Dusan Bogunovic

Title: Establishing Normal: A Dose- and Time-Resolved Baseline of Type I Interferon Signaling in Lung Epithelial Cells

Abstract: When a virus infects the body, cells release signaling proteins called interferons that switch on hundreds of genes to build an antiviral defense. This response must be tightly controlled: too little leaves cells vulnerable to infection, while too much, as seen in certain rare genetic disorders, causes lasting tissue damage. One such disorder arises when a gene called ISG15 is missing, since ISG15 normally helps turn the interferon response off once it is no longer needed. While much research has focused on what goes wrong when this system is overactive, far less is known about how it behaves

normally in a healthy cell. This project addressed that gap by exposing healthy lung cells to interferon at three different strengths and tracking gene activity at eight time points over three days using whole-genome sequencing. The researcher measured a set of protective genes previously linked to interferon deficiency, along with the receptors, signaling proteins, and feedback regulators that control them. The results showed that these genes do not all switch on in the same way. Instead, they fall into four distinct patterns, some responding quickly and fading, others staying active for a sustained period, and some activating only once a certain strength threshold is reached. One signaling protein, STAT2, stood out as uniquely sensitive to the strength of the interferon signal, while a related protein, IRF1, responded faster than any other factor measured. Together, these findings establish a detailed baseline for healthy interferon signaling, offering context for understanding what breaks down in ISG15 deficiency.

Valerie Arreola CC'28, Biophysics

Faculty Mentor(s) or Supervisor(s): Wilfred Chen

Title: Encapsulin Nanoparticle Scaffold Engineering for Enzymatic Carbon Capture

Abstract: Encapsulins are a kind of nanoparticle, originating from prokaryotic agents, that have a wide variety of applications. The attractiveness of the nanoparticles originates from their capacity to encapsulate large protein cargo whilst also being able to be externally decorated by various agents. This project aims to explore such qualities of external decoration through various biomolecular engineering approaches as well as explore previously engineered enzyme pathways for enhanced cofactor regeneration through the nanoparticle scaffold. However, in exploring such pathways for cofactor regeneration enhancement, it must first be assessed that the insertion sites in which the tags utilized to create the enzyme scaffold, SpyTag and DogTag, do not affect the solubility & assembly of the nanoparticle itself or reactivity of each component in the scaffold. Each of the qualities affects how encapsulin nanoparticles will function in a foreign environment and must be analyzed before proceeding with exploring enzyme cofactor regeneration. Solubility and assembly of the nanoparticles were assessed through SDS-Page analysis and ELP purification, respectively. The data gathered from such analyses was able to provide the information needed to determine which insertion variants are most suitable for the implementation of an enzyme pathway that enhances cofactor regeneration. The scaffold will then be subjected to a PK/LDH analysis to determine if cofactor regeneration is enhanced. Overall, this project aims to provide an accurate prediction of how

encapsulin nanoparticles can be explored for various applications, including carbon capture efforts.

Zane Asadi CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Ya-Cheng Liao

Title: Determining if Loss of ALG-2 Affects Kinetics of Post-Synaptic Cargo at ERES

Abstract: Neurons have specialized compartmentalization of organelles involved in protein synthesis and trafficking, enabling functions such as signal transduction and synaptic transmission. By understanding how neurons coordinate protein trafficking to synapses, we can understand the basis of neuronal plasticity, the strengthening or weakening of synaptic connections between neurons. We identified ALG-2, a calcium-binding protein, as a molecule involved in the trafficking of activity-related post-synaptic proteins by gating the secretion of proteins from ER exit sites (ERES) in response to neuronal activity. However, we did not fully understand the mechanism of ALG-2-gated secretion from ERES, and sought to understand how removal of ALG-2 affected the kinetics of protein cargo. We used a RUSH assay, which enables us to control when cargo can move through the trafficking pathway, to assess differences in kinetics between ALG-2 WT and KO mouse hippocampal neurons. We first tested the expression and trafficking of three proteins of interest—Gria2, Abhd6, and Pld3—in HeLa cells and identified that Pld3 was expressed and trafficked properly. We then performed RUSH assays in both ALG-2 WT and KO primary neurons using Pld3 and observed how long it took Pld3 to reach the Golgi; we found that ALG-2 KO neurons slowed the trafficking of Pld3, indicating that the loss of ALG-2 is delaying the trafficking of cargo from the ERES. These findings elucidate a possible method by which neurons can detect neuronal activity and increase the trafficking of proteins that would strengthen synapses, and potentially provide insights into neurodegenerative diseases such as Alzheimer's.

Amina Assefaw SEAS'27, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): Zoltán Harman

Title: Transition Energies in lithium-like Atoms as a Probe of New Forces

Abstract: This research was conducted during a 10-week internship at the Max Planck Institute for Nuclear Physics in Heidelberg, Germany, and sought to establish constraints on the properties of a hypothetical fifth force beyond the four known fundamental forces of the universe. Assuming such a force

exists, the project aimed to determine what strength and range of this force would be compatible with existing precision measurements of atomic energy levels. These constraints provide guidance for experimentalists seeking to design experimental setups for new fundamental interactions. The work employed computational methods to calculate how this hypothetical fifth force would affect the energy levels of electrons in three-electron atoms and ions. Mathematical models were then used to predict how much the energy would shift if this new force existed, and these predictions were then compared with high-precision experimental measurements from the literature. By comparing theoretical predictions with experimental data for atomic lithium and several highly charged lithium-like ions including iron, gold, lead, and uranium, the investigation generated constraints that show the maximum allowed strength of this hypothetical fifth force as a function of the mass of the particle that would carry it. These results help constrain the possible properties of physics beyond the Standard Model.

Rahmat Asuni CC'28, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Christine, Sarah Austin, Trieu
Title: CRP as a Biomarker of Stress: Immunohistochemical Analysis of Inflammatory Markers in Teeth

Abstract: C-Reactive Protein (CRP) is a systemic and biological inflammation marker produced in the liver in response to stress and infection. Teeth grow incrementally, providing a daily record of the biological events that lead to stress and inflammation. This unique property makes them valuable archives for reconstructing early life stress, inflammation, and environmental exposures over time. Utilizing both human and mouse teeth samples, as well as new and burial samples, enabled the potential feasibility of detecting CRP across different preservation conditions and comparing staining patterns between sample types. A standardized two-day immunohistochemistry (IHC) protocol was employed, involving decalcification, cryosectioning, antibody staining with primary and secondary antibodies, and confocal imaging to visualize CRP localization within the tooth structure. CRP was successfully detected in the teeth of both humans and mice, in both newer and burial samples, with staining patterns varying across tooth layers and between sample types. Overall, the study demonstrates that teeth could provide a longitudinal record of inflammatory episodes. In other words, an individual's tooth records information about windows of exposure to stress. Mapping inflammation over the lifespan at specific sites in the developing teeth could inform early interventions and better clarify the relationship between early development, social environment, and long-term health.

Abhinav Avvaru CC'28, English, Financial Economics

Faculty Mentor(s) or Supervisor(s): Tian Zheng
Title: Extending AutoClimDS: A Literature Knowledge Graph and Multi-Agent Pipeline for Linking Climate Science Papers to Validated Code Implementations

Abstract: Machine learning has become central to climate science, but published results are often disconnected from the code that produced them: a paper may describe a method in detail with no way to locate, verify, or rerun the implementation behind it. AutoClimDS partially closes this gap, pairing a curated climate knowledge graph (AWS Neptune) with agentic workflows — an Orchestrator plus Data Discovery, Data Acquisition, and Climate Simulation agents on AWS Bedrock — that interpret natural-language queries, acquire datasets, and run analyses. However, its Knowledge Graph covers datasets and tools, not the literature, and cannot connect a paper to the code behind its results.

My project bridges that gap. Over a 740-paper climate/statistics corpus, I built a knowledge graph of the literature itself: 5,100 typed nodes and 7,900 edges spanning papers, authors, methods, datasets, and findings, with 3,367 authors and shared concepts deduplicated into single nodes. A three-agent pipeline populates its code layer: a KG Agent retrieves a paper's record; a Code Agent searches GitHub but accepts a match only on citation evidence — the paper's own text, author-owned repositories, or an independent README citation — then ranks harvested functions against the paper's methods; an Evaluation Agent runs the notebook in a sandboxed kernel, repairing failing cells before reporting a real pass or fail. All 740 papers were resolved: 38 to verified implementations, 702 marked as having none rather than guessed at, with 35 of 37 notebooks executing clean — a literature-side companion to AutoClimDS's dataset graph.

Busra Aydin CC'28, Anthropology, Biology

Faculty Mentor(s) or Supervisor(s): Oliver Hobert
Title: ceh-27 as a Candidate Regulator of GABAergic Neuron Identity

Abstract: Neuronal identity is maintained through gene expression programs controlled by transcription factors. Most transcription factors involved in establishing and maintaining neuronal identities belong to the homeobox family. Many homeobox transcription factors function as terminal selectors, which activate and preserve genes required for the mature properties of

specific neuron types. This study investigated whether the homeobox gene *ceh-27* contributes to the specification and maintenance of GABAergic neuron identity in *Caenorhabditis elegans* (*C. elegans*). To examine its neuronal function, *ceh-27* was conditionally removed using pan-neuronally expressed *rab-3::Cre* recombinase. Fluorescent reporters were then used to measure *ceh-27* expression and expression of *unc-25*, a well-established marker of GABAergic neurons. Control animals displayed an average of 2.9 neurons with overlapping *unc-25* and *ceh-27* reporter expression, whereas no overlap was detected in animals expressing *rab-3::Cre*, confirming successful neuronal removal of *ceh-27*. However, the mean number of *unc-25* expressing neurons remained similar between experimental and control animals, with no significant difference observed between the two groups. These findings suggest that loss of *ceh-27* alone is insufficient to produce a detectable change in *unc-25* expression and that *ceh-27* may not independently regulate this aspect of GABAergic neuron identity.

Ayodele Ayoola CC'28, Economics

Faculty Mentor(s) or Supervisor(s): Robert Shapiro

Title: Health Equity Deferred: The Legislative Backlog in Combating Health Disparities in the City of New York

Abstract: In the United States, non-White Americans experience disparities in healthcare, resulting in lower health outcomes and higher rates of mortality. Public policy has historically been used to address racial justice, ranging from the emancipation of enslaved people to prohibiting discrimination in public accommodations. However, there has been limited policy action in New York specifically addressing racial health disparities despite historical precedent at the state, local, and federal levels to use legislation to reduce other forms of racial inequality. This research aims to understand the reasons for limited local policy action by the New York City Council in addressing racial health disparities. This study employs a qualitative approach, examining trends in City Council agenda items and priorities, the demographic composition of key committees related to racial disparities, and stories covered by news outlets and campaigns that racial justice organizations center when advocating for social and political change. The lack of policy action appears to result from multiple factors. The Council often prioritizes universal policies over targeted legislation addressing disparities. Racial justice also competes with other policy areas for attention in the media and among community organizers, while, within discourse about racial inequality, health inequality takes a secondary position to other areas of disparity, such as voting rights. Additionally, the Council emphasizes oversight hearings,

commemorations, and resolutions calling on other bodies to act rather than introducing specific anti-medical racism legislation. By understanding how the interactions between media, community networks, and policymakers contribute to limited policy action, the public and legislators can identify and address the root causes of these barriers, allowing for targeted strategies to reduce the factors that limit policy action on racial health disparities.

Maria Sara Baende CC'27, Cognitive Science, Sebastian Cesar Cinco Lumapas CC'28, Environmental Biologist, Savannah Crowder GS'28, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Sarah Ashcroft-Jones

Title: Conversations with AI: Influencing Climate Policy Attitudes Using GenAI Across 24 Countries

Abstract: Costly climate policies have low support, yet interventions to influence climate-policy attitudes have little effect. This study, across 24 countries, tested whether personalized conversations with AI models are an effective alternative for influencing attitudes toward climate policies. Randomly assigned participants ($n \approx 7149$, 19 languages) read 1 of 10 policies, and their baseline support regarding it was measured. Participants engaged in a 3-turn conversation with the chatbot under one of three random conditions: control (sports), positive, or negative persuasion. Some were assigned static prebunking before their conversation (a forewarning of the persuasive methods chatbots use) to see whether it could reduce LLM's persuasive power. Afterward, we measured participants' policy support to assess change of opinion. We hypothesized that participants in the positive condition would increase support relative to baseline, participants in the negative condition would decrease support, and those in the control condition would show no meaningful difference. Consistent with the hypotheses, preliminary results from Study 2 show robust, stable patterns suggesting that positive-persuasion LLMs increase policy support across all tested countries, languages, and policies; negative-persuasion LLMs decrease support; and prebunking seems effective in reducing the persuasive effect across both persuasion conditions. These results can inform policymakers, AI developers, NGOs, journalists, and communicators about how conversational AI can build support for climate action while highlighting the need for transparency and further research into safeguards such as prebunking.

Shay Baer CC'29, Biology, Visual Arts

Faculty Mentor(s) or Supervisor(s): Ken Olive

Title: E. coli-Induced Pancreatitis: Investigating BRCA2-Driven Immune Dysfunction

Abstract: BRCA2 carriers are at an elevated risk of developing pancreatic ductal adenocarcinoma (PDAC), an aggressive and treatment resistant cancer. Emerging research suggests that these individuals may have an altered immune response to inflammation, potentially caused by factors outside of the pancreas. Understanding the mechanisms underlying this immune deficiency may provide insight into how BRCA2 mutations increase susceptibility to PDAC. This project aims to investigate a potential cause of this immune deficiency through a pancreatitis mouse model. Sibling-matched mixed background B6C and BC mice were randomly sorted into control and experimental groups. Experimental mice were dosed weekly with a standardized volume of heat-inactivated E. coli suspended in phosphate-buffered saline (PBS) to induce a controlled inflammatory response, while control mice were dosed with the same volume of PBS. Mice were monitored throughout the study, with body weights recorded at enrollment and at four-week intervals through the study endpoint. Following eight weeks of weekly injections and an additional four-week observation period, the mice were euthanized and organs were collected for downstream analysis. These tissues will be used to characterize differences in inflammatory and immune responses between genotypes and treatment groups. Because the study is ongoing, results and conclusions are not yet available.

Sage Bailey CC'28, Chemistry

Faculty Mentor(s) or Supervisor(s): Asmita Africawala

Title: What the soil says: 3 years of soil health interventions in India

Abstract: Working with the Ambuja Foundation in Jaipur, India, Sage Bailey examined the effectiveness of soil health interventions implemented across seven Indian states, including Himachal Pradesh, Rajasthan, Uttar Pradesh, Punjab, Maharashtra, Uttarakhand, and Gujarat. Indian agriculture has long depended on healthy soil, but decades of intensive farming, crop residue burning, and heavy fertilizer use have degraded soil quality in many rural areas. To rebuild it, the Ambuja Foundation has introduced practices such as composting, crop rotation, mechanized residue management, water conservation systems, and improved soil testing. This project analyzed multiple years of soil testing data, interviewed regional program staff, and visited farming communities directly to evaluate which interventions were producing the strongest results and why. The analysis found that soil organic

carbon, a key measure of soil fertility, was improving in nearly every location with multiple years of data, though it remained below recommended levels everywhere it started low, a pattern consistent with published research showing that soil improvement typically takes many years. The practices with the clearest evidence of success were also the simplest and least expensive: incorporating crop residue back into fields, applying farmyard manure and compost, and regular soil testing. Newer practices such as biochar production showed promise but were limited more by cost and supply chains than by farmer interest. The report concludes that expanding access to affordable inputs and shared equipment, and building institutions that farmers can run themselves, are more effective than additional outreach alone, and recommends closer alignment with existing national soil health programs.

Alanna Belevitch SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Ali Ahmadi

Title: Development of Porous Hydrogel Microbeads for Enhanced T Cell Viability and Proliferation

Abstract: Hydrogels are utilized for immunotherapy administration due to their biomimetic properties and ability to act as 3D culture systems. However, current limitations of T cell-based immunotherapies include the need for cellular localization and persistence of T cells with a therapeutic phenotype. To overcome these limitations, we developed a biocompatible porous hydrogel microbead to support nutrient diffusion and space for proliferation. Two hydrogel formulations were created using alginate, a well-established biocompatible polymer crosslinked with calcium ions, and albumin as a foaming agent, with pectin incorporated into the second formulation to modulate foam structure and crosslinking behavior. To evaluate the effect of porosity on T cell proliferation, an Alamar Blue Proliferation assay was performed on bulk hydrogels of the compositions in foamed and non-foamed forms over 7 days of incubation. At Day 7, the alginate-albumin formulation demonstrated significantly greater Jurkat T cell proliferation compared to all other chemical compositions. The formulations were further evaluated in a microbead architecture. Foamed microbeads demonstrated improved cell viability, proliferation, and colony formation compared to their non-foamed counterparts, as assessed using Calcein-AM/Propidium Iodide Live-Dead assays. Additionally, microbeads were successfully injected through 23G and 25G needles at a 1:6 microbead-to-suspension volume ratio while maintaining cell viability through injection. These results demonstrate that porous microbeads are a promising delivery vehicle and growth matrix for Jurkat T cells.

Amanda Benneh CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Gonzalo Vazquez-Prokopec

Title: Examining the Intergenerational Effects of Larval Nutritional Stress on Fitness and Reproductive Traits in wAlbB-Infected *Aedes aegypti*

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

Uriel Benymon GS'27, Information Science

Faculty Mentor(s) or Supervisor(s): Ansaf Salleb-Aouissi

Title: A Comparative and Interpretable Machine Learning Investigation of Hypertension Prediction Using NHANES Data

Abstract: Hypertension is strongly associated with lifestyle, but does lifestyle information actually improve its prediction once basic demographic and body-measurement data are already known? Using 8,024 adults from the NHANES 2017–March 2020 pre-pandemic release, this study compares demographic, socioeconomic, and anthropometric predictors with an

expanded feature set incorporating physical activity, alcohol use, smoking, and sleep. Five machine-learning models, including Logistic Regression, Random Forest, Gradient Boosting, Bagged Decision Trees, and XGBoost, were evaluated using cross-validation and a separate test set designed to prevent information leakage during model development. Adding lifestyle information did not reliably improve predictive performance for any of the five models. It also reduced agreement among models about which features were most important to their predictions, based on SHAP interpretability analysis. Both findings persisted when the definition of hypertension was changed and when the treatment of class imbalance was modified. These results suggest that additional lifestyle variables may provide little incremental predictive information beyond an already informative demographic and anthropometric baseline while making model explanations less consistent.

Anang Bhagwati SEAS'28, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Kristin Myers

Title: Characterizing the Viscoelasticity of the Murine Cervix Across Gestation

Abstract: Preterm birth, defined as delivery before 37 weeks of gestation, is the leading cause of death among children under 5 and causes about 35 percent of neonatal deaths. Often, preterm birth occurs spontaneously or without any medical indications, usually driven by premature cervical softening. During a normal pregnancy, the cervix also softens, transitioning from a rigid to a compliant structure through remodeling of its extracellular matrix and changes in its mechanical properties, which are important to characterize. Of these, the time-dependent or viscoelastic properties are particularly important, as it deepens understanding of cervical remodeling and provides material parameters for computational models of the cervix that could eventually inform the design of diagnostics and therapies. However, because human cervical tissue cannot ethically be sampled at mid-gestation, animal models are essential for studying how the cervix remodels throughout pregnancy. This project uses a mouse model, whose short, 18-day gestation and human-like remodeling allow efficient collection of cervical tissue across multiple gestational timepoints. It develops an inverse finite element analysis (IFEA) framework to identify viscoelastic material parameters from experimental mechanical testing. In this ring test, cervical specimens from non-pregnant, late-gestation, and postpartum mice undergo repeated stretch-and-hold loading, with force and deformation recorded via digital image correlation and segmented into loading, peak, and relaxation phases for model

calibration. A finite element model of the ring test, using a reactive viscoelastic model, reproduces the experimental protocol. The IFEA adjusts parameters to align simulated and experimental force-time histories using a loss function robust to outliers. These results characterize the time-dependent, viscoelastic nature of the mouse cervix and quantify how its relaxation parameters change across gestation, providing a foundation for understanding cervical remodeling.

Maya Bhaskar CC'28, Biophysics

Faculty Mentor(s) or Supervisor(s): Erin Barnhart

Title: Investigating the effects of perturbing mitochondrial biogenesis in a single neuronal cell type in *Drosophila*

Abstract: Neurons are energetically demanding cells, making efficient energy production essential for neuronal function. Accordingly, deficits in mitochondrial dynamics are linked to neurodegenerative diseases such as Parkinson's. In Parkinson's patients, mitochondrial biogenesis is dysregulated due to reduced expression of the transcriptional coactivator PGC-1 α in dopaminergic neurons. However, it remains unclear how dysregulated mitochondrial biogenesis contributes to vulnerability in specific cell types. Researchers hypothesized that altering PGC-1 α activity in one cell type would disrupt mitochondrial organization and neuronal health. To test this hypothesis, researchers used *Drosophila*, which permits cell-specific manipulation of Spargel, the fly ortholog of PGC-1 α . This project examines spargel knockout and overexpression in a single neuronal cell type of the fly visual system, Mi1. Past work in the lab has shown that Mi1 is susceptible to mitochondrial perturbations, as the knockout of a mitochondrial transport protein caused accumulation of mitochondria in the soma and early onset neurodegeneration. However, this work focused on mitochondrial transport rather than biogenesis, leaving open the question of how regulating mitochondrial production may impact Mi1's overall health and mitochondrial organization. This project uses immunostaining and confocal imaging of Mi1 following spargel knockout and overexpression to quantify mitochondrial density and localization within the neuron. Researchers are imaging at days 7, 28, and 42 post-eclosion to examine if spargel knockout or overexpression leads to accelerated neurodegeneration. At day 7, experimental flies showed no notable deficits in mitochondrial organization or neurodegeneration. These findings may clarify how dysregulated mitochondrial biogenesis contributes to mitochondrial dysfunction and neuronal vulnerability in neurodegenerative diseases.

Ishana Bhattacharya GS'27, Human Rights, Political Science

Faculty Mentor(s) or Supervisor(s): Rebecca A. Lowy

Title: Navigating the climate through law

Abstract: In the context of an accelerating climate emergency, activists and policymakers are turning to a wide range of strategies to drive change, and the law has emerged as a powerful tool among them. This summer's research, conducted with the Sabin Center for Climate Change Law, spanned three projects across the organization's teams. The first project involved developing a typology of parties in climate litigation, drawing from the Sabin Center's database. These cases were organized to create data visualizations that analyze the plaintiffs and defendants of over 3600 cases to identify patterns in the shifting dynamics of climate litigation. The second project produced a research memorandum on how city governments can mitigate the local costs of data center development, focusing on its impacts on energy, water, and public health. As part of the model laws initiative, this memo focused on Community Benefits Ordinances as a way to empower locals in development negotiations. Over four weeks, this involved researching the legal landscape surrounding local government authority, identifying key legal questions that might impede action, and drafting potential policies to protect local communities. Concurrently, the third project supported the Sabin Center's ongoing climate litigation database by incorporating new international cases submitted by a network of rapporteurs, and produced a monthly newsletter summarizing the most consequential developments in climate law.

Joseph Blaine CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Timothy Kuria

Title: Human Splenic Marginal Zone B Cells Across Antigen Response and Age

Abstract: Marginal zone B cells (MZBs) are a subset of immune cells believed to produce antibodies to bacterial infections encountered in the spleen more rapidly than larger, T cell-dependent immune responses. While MZBs are well understood in mice, comparing their function in humans is not feasible, because human splenic microanatomy differs greatly from that of mice. In the past, human biobanks have not been large enough to draw significant conclusions about MZBs. Now, drawing from a biobank containing hundreds of human spleen samples across many ages, the lab has demonstrated novel age- and antigen-associated characteristics of human

MZBs. Previously, based on mouse models, MZBs were thought not to be antigen experienced, meaning shaped by a prior encounter with a specific antigen. This differed from their memory counterparts, which share many MZB markers but are thought to serve a distinct, T cell-dependent function, and were believed to retain memory for a single pathogen while MZBs did not. The lab has now shown that MZBs display response intensities to many tested pathogens similar to those of traditional memory B cells.

Additionally, the lab has further characterized marginal zone splenic structure, which remains difficult to define in humans due to greater structural disorder compared to mice. The researchers have shown that the marginal zone becomes less anatomically distinct with age, as MZBs come to occupy more of the splenic follicle.

Rachel Bochman CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Gerard Karsenty

Title: Digitally Mapping the Brain-Bone Axis

Abstract: Worsening motor coordination is considered one of the hallmarks of aging. Previous work from my host laboratory has provided evidence that this may be due in part to a decline in osteocalcin, a bone hormone involved in motor coordination, among other physiological functions. Once released from the bone, uncarboxylated osteocalcin crosses the blood-brain barrier and reaches Purkinje cells of the cerebellum. This excites the neurons, increasing their firing frequency, and results in improved walking, running, and balance. Unfortunately, the positive effects of osteocalcin only last approximately an hour. This project uses various digital methods to develop a better understanding of the bone-brain axis, with the eventual goal of creating an anti-aging therapeutic based on osteocalcin. Firstly, the structural biology tool AlphaFold was used to model the binding of osteocalcin to its receptor protein, Gpr158. To further understand the role of this receptor, we compared Gpr158 knockdown mouse models to wild-type controls using Noldus Catwalk data. Digitally reconstructing rodent locomotion revealed subtle changes in balance and coordination that were undetectable by the traditional dowel and rotarod tests. This project also utilized light-sheet microscopy to create a 3D reconstruction of the brainstem and tibia, and trace glutamatergic innervation throughout both tissues. These images were then processed using destripping methods in FIJI (ImageJ).

Isabella Bolon SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Isabela Sanches

Title: Examining the Influence of Odontoblast Processes on Dentin Sensitivity and Repair in a Tooth-on-a-Chip Model

Abstract: Human teeth contain specialized cells called odontoblasts that are responsible for the formation and repair of dentin tissue and also function as mechanoreceptors in dentinal pain transduction. However, much remains unclear about the role and behavior of odontoblast processes, the cellular extensions that reside within microscopic channels in dentin called dentinal tubules. Their structure and location make odontoblast processes difficult to study in vivo and recreate in vitro. While previous microfluidic chips have been used to study tooth morphology, few have specifically focused on replicating odontoblast process formation within dentinal tubules. This study aims to simulate the natural structure of the dentin-pulp complex and establish an in vitro model for investigating odontoblast processes. Human dental pulp stem cells (hDPSCs) were differentiated into odontoblast-like cells and seeded onto human dentin slices containing empty dentinal tubules, as well as into a 3D GelMA (gelatin methacrylate) culture, all incorporated onto a PDMS platform. Hydrostatic pressure was applied to promote process extension into the dentinal tubules. Process formation was evaluated using scanning electron microscopy (SEM), which demonstrated cellular processes extending into dentinal tubules, indicating that process formation can be reproduced within the platform. However, the conditions that most reliably promote process formation remain unclear and require further experimentation.

Valeriya Bondarenko SEAS'28, Operations Research

Faculty Mentor(s) or Supervisor(s): Sommer Gentry

Title: Sequence Matters: Quantifying the Impact of No Standardized Multi-Organ Transplant Allocation Order

Abstract: There is currently no organ transplant allocation policy that determines the order in which a donor's organs should be allocated. Thus, candidates who need a multi-organ transplant (MOT) may be disadvantaged although they are often the most medically urgent candidates. We aimed to quantify how often MOT candidates must refuse an organ transplant offer because their co-listed organ has already been allocated. We used 2025 Scientific Registry of Transplant Recipient (SRTR) Standard Analysis Files (SAF) and Potential Transplant Recipient (PTR) data. We identified donors with multiple recovered organs, and linked MOT candidates across organ-specific offer sequences. We identified all instances of refusal code 724, indicating when a multi-organ candidate refused an offer because one of their

required organs was already allocated. In preliminary analysis of July 2025, among donors with multiple recovered organs (n=750), 45.87% (n=344) had at least one MOT who refused via code 724. Among candidates appearing these donors' organ offer sequences (n=12,530), 11.68% (n=1,464) were MOT candidates. Of these MOT candidates, 19.19% (n=281) refused via code 724 at least once. Of the 281 candidates who ever refused via 724, the top three candidate listing types were: liver-kidney candidates (55.9%, n=157), heart-lung candidates (10.0%, n=28), and heart-liver candidates (8.5%, n=24). The absence of a standardized, unified offer sequence across multiple organs appears to measurably disadvantage multi-organ candidates.

Kurt Boone SEAS'28, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Addis Kidane

Title: Developing image-based datasets for ML models of polymer deformation mechanics

Abstract: Image-based experimental methods were employed to investigate the deformation mechanics of polymers and generate high-quality datasets for the development of machine learning-based constitutive models.

Polydimethylsiloxane (PDMS) was selected as the model material due to its well-characterized hyperelastic behavior. Spherical specimens with a diameter of 1 inch were fabricated using a controlled manufacturing process that included precise weighing of the base and curing agent, thorough mixing under a fume hood, vacuum degassing to remove entrapped air bubbles, and oven curing at different temperatures. This procedure produced consistent, high-quality specimens suitable for mechanical testing. The fabricated specimens will be subjected to a range of loading conditions, including quasi-static compression using a universal testing machine, intermediate- to high-strain-rate loading using a drop tower, and high-strain-rate testing using a Split Hopkinson Pressure Bar (SHPB). During testing, digital image correlation (DIC) will be employed to obtain full-field displacement and strain measurements. The resulting experimental data will serve as a benchmark dataset for training and validating machine learning models to predict polymer deformation under a wide range of loading conditions.

Harjaisal Brar SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Elham Azizi

Title: Nympheas: A Cloud-Native, Distributed Computing Framework for the Scalable, End-to-End Analysis of Large, High-Throughput Spatial Transcriptomics and Proteomics Datasets

Abstract: Spatial transcriptomics and proteomics have rapidly advanced our understanding of the tumor microenvironment and other complex biological structures. Recently developed high-plex spatial sequencing technologies have led to the production of massive imaging-based datasets describing complex biology across thousands of patients, creating substantial computational challenges for analysis. Existing tools often struggle to process datasets at this scale, and only do so with substantially increased runtime, memory usage, and storage space, while requiring assay-specific workflows. To address these challenges, we created Nympheas, an easy-to-use, scalable, accelerated framework for automated analysis of large, cross-technology spatial transcriptomics and proteomics datasets. It integrates established tools with performance-enhancing modifications based on distributed computing and GPU acceleration. Nympheas provides an automated workflow which rapidly ingests instrument outputs, and performs segmentation, preprocessing, automated annotation, and downstream analyses. It enables data to stay in the cloud throughout processing, enabling the analysis of tens of millions of cells on a normal computer without downloading big files or maintaining large disk space. A scalable, unified architecture enables the same code to run efficiently across computing environments, from laptops to clusters, while automatically utilizing available resources, including GPUs. We evaluated Nympheas on a publicly-available breast cancer Xenium dataset and a large-scale, 20-sample colorectal cancer CosMx dataset. Across technologies, Nympheas enabled 3-16x faster preprocessing and analysis on a moderately powerful computer, and up to 80x acceleration with GPU, while maintaining ground-truth cell typing and other benchmarks. Therefore, SAP advances rapid, reproducible, and scalable spatial analysis while simplifying workflows and deployment.

Charlotte Bruderly CC'28, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Joseph Lee

Title: TMCC2 Variants and Alzheimer's Disease in Adults with Down syndrome

Abstract: Introduction. People with Down syndrome have a high risk of Alzheimer's Disease (AD), a common cause of dementia, due to the triplication of Chromosome 21, which contains the APP gene. The APP gene and other genes such as the APOE gene have been associated with AD. Another gene of interest is TMCC2; its protein interacts with APP and APOE proteins. Variants in TMCC2 have associations with mean erythrocyte volume (MCV) and mean platelet volume (MPV). The goal of this research is

to understand if rare mutations in TMCC2 could be linked to differences of MCV or MPV, and if these differences are associated with AD or cognitive decline variability. **Methods.** The clinical and whole genome sequencing data from 209 adults with Down syndrome were examined. Genotype-phenotype relationships were analyzed in the context of five variants of TMCC2. **Results.** The investigation of four of the mutations was limited by the presence of only one mutation carrier each in the sample. Data for the fifth variant did not show a statistically significant association between presence of the mutation and MCV or MPV. Only two of the ten carriers of this mutation were classified as having mild cognitive impairment or AD, and these participants were the oldest of their group. **Discussion.** From this preliminary study, it is difficult to draw actionable conclusions. Future areas of exploration include the investigation of more common TMCC2 variants as well as the investigation of the effect of TMCC2 on platelet count or age of onset of AD.

Claire Buchi CC'29, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Sarah Hansen

Title: Metrics of Meaning in Eye-Tracking Research: How Hyper-Personalized Feedback Changes the Face of Chemistry Education

Abstract: When approaching a challenging chemistry problem with diagrams, text, graphs, and equations, an individual's gaze often skips over a critical piece of information. It is unlikely for a learner to answer a problem correctly if they have not viewed the necessary elements. The RevChem Collaborative Research project employs eye-tracking technology to inform artificially intelligent cues and improve problem-solving performance. An eye-tracking system has the unique ability to uncover a participant's viewing strategies. Analyzing where learners look at a chemistry problem illuminates how individuals effectively or ineffectively observe, approach, and persevere through challenging content. RevChem is currently investigating how a Google Sheets "decider" and RStudio can interpret eye-tracking data to identify the greatest gaps between the time a participant fixates on an important element and the time required by the average successful participant. Participants are then presented with a new chemistry question where the format has been preserved. Critical elements that received insufficient attention in the original problem are now boxed in yellow, allowing the decider to provide rapid feedback based on the individual's visual problem-solving strategies. Preliminary findings have already indicated significant changes in participant viewing are possible when learners are cued toward an overlooked element. An artificially intelligent tutor that utilizes eye-tracking

data can provide uniquely personalized student feedback with the potential to instill problem-solving skills and viewing agency. Fuelled by precise fixation counts and pupil-tracking data, these outcomes would be impractical to achieve through observation with the naked eye.

Elif Servi Bulu CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Oliver Hobert

Title: Terminal Selectors Control Dauer-Induced Neuronal Gene Expression Changes in *C. elegans*

Abstract: In *Caenorhabditis elegans*, passing through the stress-induced dauer stage produces persistent changes in neuronal gene expression in post-dauer adults. Previous work has shown that the transcription factors DAF-12 and DAF-16 are required in the nervous system during dauer to establish these changes but they are dispensable in post-dauer animals. This project explored whether terminal selector transcription factors contribute to maintaining dauer-induced changes in post-dauer adults. Using CRISPR/Cas9 transcriptional reporter alleles for cell-specific neuronal identity markers, expression was quantified in control and post-dauer animals across wild-type and terminal selector loss-of-function mutants. Loss of the terminal selectors *unc-86* and *ceh-14* suppressed *flp-10* upregulation in AIM, while the loss of *ttx-3* suppressed the dauer-induced upregulation of *flp-10* in ASK. Loss of *unc-86* also suppressed the dauer-induced upregulation of *trh-1* in IL2, URX, and RIR; affected post-dauer regulation of *flp-32* in IL2 and URA; and abolished *nlp-69* expression in PLM. Results show that across combinations of markers, neurons, and terminal selectors, removing terminal selectors alters post-dauer expression states, suggesting that terminal selectors do play a role in controlling post-dauer-related neuronal gene expression differences in *C. elegans*. In a parallel behavioral analysis, this project characterized differences in locomotory behavior between male control and post-dauer adults, indicating that the effects of having gone through the dauer stage extend beyond neuronal gene expression and into behavioral differences. Notably, the reduction in locomotory speed observed in post-dauer hermaphrodites was not detected in males, suggesting that early life adversity has sexually dimorphic effects on locomotion in *C. elegans*.

Axel Cannon CC'28, Biochemistry, Anna Goldsamt CC'28, Biology, Olivia Young CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Virginia Cornish

Title: Screening R Bodies for Targeted Intracellular Drug Delivery

Abstract: Delivering medicines into specific cells remains a major challenge because many therapeutic molecules cannot efficiently enter cells or escape the compartments that form after cellular uptake. R bodies are naturally occurring bacterial protein structures that can remain tightly coiled under neutral conditions and rapidly extend when exposed to an acidic environment. This behavior makes them a potential tool for carrying therapeutic molecules into cells and releasing them after uptake. This study examined seven different bacterial R body systems to identify a structure small enough to support future targeted delivery. The proteins were produced in bacterial cells, isolated, exposed to neutral and acidic conditions, and examined using scanning electron microscopy. Earlier preparations showed recognizable extended R bodies, demonstrating that the imaging approach could capture their expected structure. However, most structures observed in the larger comparison were rounded particles rather than clearly defined R body coils. Their size, shape, and tendency to cluster suggest that many of these particles may instead represent densely aggregated proteins or remaining cellular material. One preparation showed more elongated structures under acidic conditions than the others, making it a useful candidate for further study, but no system could yet be identified as an optimal delivery platform. These findings show that improving protein production and purification is necessary before the natural diversity of R bodies can be reliably compared. Future work will focus on producing cleaner R body preparations and determining whether their size and acid responsive behavior can be adapted for targeted intracellular drug delivery.

Eleanor Cao CC'29, Political Science

Faculty Mentor(s) or Supervisor(s): Andrew Nathan
Title: "On the Field of Hope": Yan Jiaqi and the Evolution of Chinese Democratic Theory (1978-1996)

Abstract: This paper examines how China's leading political scientist Yan Jiaqi's democratic theory evolved during and beyond the long 1980s. Termed the "decisive decade" by scholar Pei Minxin, China's 1980s was a period of economic reform and failed political change, when public debates about China's political future ended tragically with the 1989 Tiananmen Massacre. Yan Jiaqi was one of the most prominent intellectuals during this "decisive decade": widely read and politically influential, Yan's democratic writings shed light on China's prospect for democratization, helping us envision an alternative future that was curtailed by the Massacre. However, Yan is rarely studied despite his prominence, and this paper fills the gap by (1) chronicling

how Yan's democratic theory changed before and after Tiananmen and (2) evaluating how his vision might be developed further. Drawing from a literature review of primary and secondary sources, this paper argues that Yan's conception of democracy progressed from pure proceduralism before Tiananmen to liberalism after Tiananmen, identifying democracy with rights protection and pluralism in addition to a specific set of institutions and procedures. Yet, this transition opened up questions which Yan did not sufficiently address and which invited further study, especially how China can develop a consciousness of human rights and respect for pluralism, both of which he deemed essential to democracy yet absent in traditional Chinese culture. Ultimately, researching the evolution of Yan's democratic theory matters because only when we understand how Chinese democratic thought emerged and grew can we identify its limitations and future avenues of development. We stand on Yan Jiaqi's shoulders to imagine China's political future.

Aaron Castro CC'27, Urban Studies

Faculty Mentor(s) or Supervisor(s): Noah Allison
Title: Não tá fácil!: Childcare, Employment, and Community Support in São Paulo's Housing Occupations

Abstract: Housing occupations are a defining part of the urban landscape of central Sao Paulo. These communities arise when housing activists organize takeovers of abandoned buildings, refurbishing them into non-profit housing for the city's working families. The organizers and residents of Sao Paulo housing occupations are overwhelmingly women, yet little attention has been paid in English language research to these working mothers. This study examines how working mothers in Sao Paulo's occupations access childcare and how childcare support influences their participation in the workforce. This study utilizes an anonymous survey of mothers living in housing occupations in central Sao Paulo. Participants were recruited at organizational meetings and events, as well as through interactions with organizational leaders. The survey asks about employment, work schedules, childcare arrangements, sources of childcare support, and perceptions of community resources and support. Preliminary findings indicate that mothers generally have some access to childcare through family members, community members, or organized childcare services. At the same time, many respondents report working long hours and identify childcare as a significant barrier to finding and maintaining employment. Respondents also report that access to childcare has a substantial influence on their working lives. Notably, these resources coexist with relatively low levels of trust in neighbors and

other community members. These findings suggest that the presence of community childcare resources does not necessarily mean that mothers can fully benefit from them. Strengthening trust within housing communities may be important for ensuring that existing childcare resources are accessible to residents.

Ana Castro GS'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Michal Schwartzman
Title: Investigating the Role of Ovarian Hormones in GPR75-Mediated Sexual Dimorphism in Diet-Induced Obesity

Abstract: Abstract: Loss-of-function variants in the G-protein coupled receptor 75 (GPR75) are associated with leanness in humans, and Gpr75-deficient mice are protected from diet-induced obesity (DIO). Adipocyte-specific deletion of Gpr75 (adipo-Gpr75^{-/-}) confers protection against high-fat diet (HFD)-induced metabolic dysfunction, with a marked sexual dimorphism in body weight and adiposity. Female adipo-Gpr75^{-/-} mice exhibit substantially reduced weight gain and adiposity compared with wild-type (WT) littermates, whereas male adipo-Gpr75^{-/-} mice gain weight similarly to WT mice. Despite these differences, both male and female adipo-Gpr75^{-/-} mice display improved glucose handling, increased activity and energy expenditure, and reduced adipose tissue inflammation. The mechanisms underlying the greater protection against HFD-induced obesity observed in female adipo-Gpr75^{-/-} mice remain unknown. To investigate the basis of this sexual dimorphism, we hypothesized that ovarian sex hormones contribute to the enhanced protection observed in female adipo-Gpr75^{-/-} mice. Female adipo-Gpr75^{-/-} and WT mice underwent ovariectomy to determine whether removal of ovarian hormones would alter the metabolic phenotype associated with adipocyte-specific Gpr75 deletion and cause female knockout mice to exhibit a phenotype more similar to that observed in males. Following ovariectomy and HFD feeding, metabolic parameters including body weight, adiposity, energy intake and expenditure, activity, and glucose metabolism were assessed. We anticipate that removal of ovarian hormones may attenuate the protective phenotype observed in female adipo-Gpr75^{-/-} mice, supporting a role for sex hormones in mediating the sexual dimorphism. Alternatively, persistence of the female-specific protection following ovariectomy would suggest that other sex-dependent mechanisms contribute to the differential response to adipocyte GPR75 deletion. These findings may provide insight into the mechanisms through which GPR75 regulates adipose tissue function and metabolic health and how these effects are influenced by biological sex.

Alex Cesaretti CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Robert Bauer
Title: CRISPR Cutting of SNP-Dense Region at 8q24 Trib1 Locus Draws Inconclusive Evidence and Points To a Need For Higher Cutting Efficiency

Abstract: The 8q24 locus on the human genome contains the protein coding gene Trib1, which codes for a pseudokinase and has been associated through Genome Wide Association Studies (GWAS) with Coronary Artery Disease (CAD), cholesterol, and triglycerides. Early studies that overexpressed Trib1 in mice showed its therapeutic potential to lower cholesterol and triglycerides, thereby lowering risk for CAD (Burkhardt et al., 2010). Though genetically associated with CAD, the mechanism of the mutations affecting Trib1 to produce the phenotype of CAD is largely unknown. This study aimed to elucidate these mechanisms by first establishing an association with nearby mutations downstream of Trib1 in the genome which were associated with CAD. Using CRISPR technology, this possible regulatory region was entirely cut out along with a positive control targeting the transcription start site of the Trib1 gene and two negative controls. The expression of Trib1 was measured using qPCR. Though our results show that cutting out this region leads to no change in Trib1 transcript levels, our cutting efficiency was near 75%, which is not high enough to draw conclusions on the subtle changes in expression due to regulatory regions. If this data is correct, however, this would imply that Trib1 is not the causal gene for the CAD phenotype at the 8q24 locus. If it were incorrect and Trib1 was the causal gene, we plan to cut out smaller regions of the genome to find where the causal mutation is in this large mutation region. Moving forward, we are implementing single cell colony expansion to avoid the pooled setting as in this experiment so that we can draw more conclusive evidence.

Manas Chan SEAS'29, Computer Engineering

Faculty Mentor(s) or Supervisor(s): WaiChing Sun
Title: ReAct-based 3D Mesh Generation for MVP and FES

Abstract: Generating simulation-ready 3D meshes from raw geometric data remains a complex, multi-stage process that requires expert human intervention to diagnose failures, select corrective operations, and determine mesh suitability. Mesh quality directly affects whether a valid finite-element model can be produced and utilized in simulation.

This project introduces a Reasoning and Acting (ReAct) agent that autonomously manages the mesh-generation workflow by iteratively evaluating the mesh state and selecting subsequent actions. The system converts point-cloud inputs into validated volumetric meshes suitable for finite-element solutions of boundary-value problems, integrating established geometry-processing tools such as Gmsh and MeshLab. At each iteration, the mesh is assessed using metrics that characterize its geometry, topology, and element quality, collectively defining the mesh state observed by the agent. The central focus of the framework is the distinction between deterministic decision-making and large language model (LLM)-based reasoning: states with clear following actions are mapped directly, while the LLM addresses states requiring contextual diagnosis or adaptive action selection. This approach minimizes the human intervention required in the mesh generation workflow, enabling more autonomous and robust processes applicable to domains such as biomedical modeling and structural analysis.

Alicia Chang CC'27, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Kristin Baldwin

Title: Identifying Transcriptional Codes for Neuronal Subtype Specification Using a Barcoded exoTF Library

Abstract: Direct reprogramming enables the conversion of somatic cells into neurons through the ectopic expression of exogenous transcription factors (exoTFs). By overexpressing specific combinations of exoTFs, embryonic mouse fibroblasts (MEFs) can be directly converted into distinct neuronal subtypes. However, identifying the combinations of exoTFs required to generate specific neuronal identities remains a major challenge. To address this, our lab has designed a library of barcoded lentiviral vectors encoding different exoTFs, enabling the simultaneous identification of exoTF combinations and neuronal identities using single-cell RNA sequencing (scRNA-seq). This approach allows us to link the exoTFs expressed during reprogramming with the transcriptional identity of the resulting induced neurons, facilitating the identification of exoTF combinations capable of generating specific neuronal subtypes. However, in the previous exoTF library (v1b), the lentiviral barcode (LBC) was positioned too far upstream for efficient capture by 3' scRNA-seq, limiting exoTF identification. To improve barcode recovery, we redesigned the construct by introducing a second barcode adjacent to the 3' long terminal repeat (LTR), generating Version 4 (v4) of the exoTF library. We first confirmed that viral production and infection efficiency were maintained following the redesign. We then used a pool of 30 exoTF-v4 constructs to reprogram MEFs into induced

neurons. Preliminary analysis demonstrates substantially increased barcode recovery compared with previous library iterations. Ongoing analyses are linking transcriptionally defined neuronal subtypes with their corresponding exoTF combinations to identify candidate transcriptional codes for reliable generation of specific neuronal subtypes.

Nat Chang-Deutsch GS'28, Linguistics

Faculty Mentor(s) or Supervisor(s): William Foley

Title: Pidgin Multilingualism and Social Relations in turn-of-the-century Johannesburg

Abstract: Sometime in the 1890s, a Jewish immigrant to Johannesburg decided to pseudonymously write a glossary between his native Yiddish and what he called "the principle language of Africans." Nothing else is known about this individual. The language he describes is not in fact the native tongue of those around him, but rather Fanakalo, a pidgin associated with the mining industry. The Fanakalo present in the text is very different from the mining companies' standardized version, just as his Yiddish differs from any standard version of the language. By analyzing the 200 odd entries in this brief glossary, an astonishing amount of information may be gained about the life of this person in both Europe and South Africa and about the racial power structure that defined life in Johannesburg. Misspellings in the Yiddish indicate dialect origin down to a specific province of the Russian empire (as well as a lack of education), German influences reveal reading habits, and anglicized terminology for certain items narrows down the list of possible occupations in Europe. His merchant profession is made clear by the sheer quantity of terms for goods, themselves markers of Black mineworkers' engagement with the market economy. These miners' own native languages appear as sources for Fanakalo words in the book. Most interestingly, conspicuous divergences from ordinary Fanakalo seem to result from a concerted attempt by these merchants to linguistically appeal to a (racially reviled) black customer based, something also visible in the behavior of contemporary South Asian merchants in South Africa.

Darrin Charles CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Giorgia Zanetti

Title: The Personalized Immune Mouse Model Recapitulates Type 1 Diabetes-Specific Autoimmunity Against Human β -Cell Grafts

Abstract: Type 1 Diabetes (T1D) is an autoimmune disease in which the body's immune cells mistakenly attack insulin-producing beta cells in the pancreas. T1D research has been limited by the lack of humanized animal models that allow researchers to study how exactly the human immune system attacks beta cells. Megan Sykes' lab at the Columbia Center of Translational Immunology developed the Personalized Immune (PI) mouse model, in which immunodeficient mice are transplanted with CD34+ hematopoietic stem and progenitor cells from T1D patients, as well as healthy controls, along with partially HLA-matched (human leukocyte antigen matched) thymic tissue, allowing the de novo development of the donors' immune system in these mice. These PI mouse models then receive induced pluripotent stem cell (iPSC) derived beta cells generated from the patient's skin fibroblasts, providing target cells for the autoreactive immune response to attack. By analyzing blood, spleen, thymus, and beta cell grafts from these mice, we can better understand how the autoreactive immune system develops and which immune cells contribute to beta-cell destruction in T1D. The future goal for these PI mice is to use these mice to test therapies designed to promote immune tolerance and prevent the human immune system from attacking pancreatic beta cells, treating Type 1 Diabetes.

Brooke Chasalow GS'26, Biology

Faculty Mentor(s) or Supervisor(s): Erin Barnhart

Title: Cell Type-Specific Responses to Disrupted Mitochondrial Transport in the *Drosophila* Visual System

Abstract: Neurons rely on mitochondria to provide ATP and maintain cellular homeostasis, yet different neuronal populations may not depend equally on proper mitochondrial localization. Disruption of mitochondrial transport has been implicated in neurodegenerative disease, but the cellular features that determine neuronal vulnerability remain poorly understood. Here, we investigated how impairing mitochondrial transport affects distinct neuron types in the *Drosophila melanogaster* visual system. Cell type-specific RNA interference was used to knock down the mitochondrial transport adaptor protein Milton, while fluorescent reporters (mitoGFP and TdTomato) were used to visualize mitochondrial localization and neuronal morphology in adult flies. Constitutive Milton knockdown caused mitochondria to accumulate within neuronal somas and reduced mitochondrial localization throughout distal axons and dendrites in both Tm9 and VS neurons, consistent with impaired mitochondrial transport. However, the two neuron types exhibited qualitatively different structural responses. Tm9 neurons showed pronounced axonal and dendritic abnormalities consistent with neurodegeneration,

whereas VS neurons displayed comparatively preserved morphology despite similar mitochondrial mislocalization. Although these observations require quantitative validation, they suggest that neuronal susceptibility to disrupted mitochondrial transport may be cell type-specific. Future studies will quantify these phenotypes across additional neuron types and investigate how the time of Milton KD during the fly lifecycle, neuronal morphology, and metabolic demand contribute to resilience or vulnerability to neurodegeneration following Milton KD. Understanding why some neurons tolerate mitochondrial transport defects while others rapidly degenerate may provide insight into the selective neuronal vulnerability characteristic of neurodegenerative disease.

Sharanya Chatterjee SEAS'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Elham Azizi

Title: COMET: Coupled Statistical Modeling of Gene Regulatory Networks and Cell-State Transitions

Abstract: Cell state transitions underlie fundamental biological processes such as cellular differentiation, development, and disease, yet accurately determining both the direction and regulatory mechanisms of these transitions remains a major challenge. Most trajectory inference methods lack intrinsic directionality, often requiring prior biological knowledge. Methods that do infer direction typically rely on RNA splicing dynamics, which require high coverage unavailable in many datasets. These limitations motivate integrating multi-omic data to gain richer regulatory context, but existing approaches frequently rely on paired data or incur heavy computational costs. Meanwhile, traditional gene regulatory network (GRN) inference methods offer only aggregate, cluster-level views, limiting their ability to resolve regulatory programs driving transitions through intermediate states. Here, we present COMET, a model that integrates unpaired single-cell RNA sequencing (scRNA-seq) and single-cell ATAC sequencing (scATAC-seq) data to learn both the direction and regulatory mechanism of cell state transitions. COMET first learns cell-specific GRNs through a masked reconstruction objective, allowing regulatory programs to vary continuously across cells. It then derives a directional signal from the gap between chromatin accessibility and transcription and propagates this signal through the GRNs to learn cellular displacements—identifying both cell state transitions and their driving regulatory networks. Across diverse biological processes, COMET recovers biologically meaningful trajectories while characterizing distinct regulatory programs driving different cellular fates,

providing an interpretable framework for connecting chromatin dynamics, gene regulation, and cell-state transitions from unpaired data.

**Xinrui Chen CC'27, Economics-Statistics, Aine Reeves
GS'27, Political Science, Meriem Fereva SEAS'28, Financial
Engineering**

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: Private Searches, Public Patterns: Discovering Shapes of Attention with Google Trends

Abstract: Online search behavior provides a rich signal of collective attention, and Google Trends is widely used to study these patterns. Because Google Trends requires search terms to be specified in advance, most studies rely on predefined, topic-specific dictionaries. We instead build a word bank from Google's Top and Rising Queries and analyze the resulting time series using Symbolic Aggregate approXimation (SAX). We then group search terms by the shape of their temporal trajectories using hierarchical clustering. The resulting clusters reveal interpretable categories of attention dynamics, including seasonal interest, gradual growth, and sudden bursts of activity. These recurring attention signatures can be identified across events and time periods and may support downstream applications such as market monitoring and forecasting.

**Anna Chen CC'27, Applied Mathematics, Climate System
Science**

Faculty Mentor(s) or Supervisor(s): Galen McKinley

Title: Evaluating the Impacts of Model Choice on Assessment of Surface Ocean pCO₂ Reconstruction Skill in Climate Model Testbeds

Abstract: Over the past decade, the ocean carbon sink absorbed 29% of total anthropogenic CO₂ emissions. Climate models simulate the global ocean carbon cycle and quantify this sink from sparse observations. Recent assessments of observation-based ocean carbon data products use Global Ocean Biogeochemical Models (GOBMs) and Earth System Models (ESMs) as "testbed" truths: data products sample the testbeds at the spatio-temporal coverage of independent observations, then reconstruct surface ocean pCO₂ using statistical and machine learning techniques. It has not been studied whether differences in the testbed model skill in representing real-world pCO₂ may impact testbed results. Thus, this study assesses the data products

by ensemble-averaging based on their testbed model choice. We use 5 GOBMs over 2001-2021 and 18 ESM members over 1982-2023. Data products are assessed across regional, basin, and global scales against their testbeds. Likewise, the same metrics are computed for each testbed model against real-world data. Results show that sorting the testbed models based on their skill against observations has a minor impact on the assessment of reconstruction skill across 7 data products. Echoing published findings, ensemble-averaging generally improves global and regional reconstruction skill compared to using single-member testbeds. Nonetheless, the equatorial and Southern Ocean subtropical biomes show greater sensitivity to testbed choice, where including certain testbeds can marginally worsen, but not improve, ensemble-averaged skill. This study highlights endorses the use of ensemble-averaging in multi-model testbed experiments, since specific testbed choices can harm regional reconstruction skills, especially in observation-scarce and biogeochemically complex biomes.

Andrew Chen CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Kenneth Olive

Title: RAS inhibition creates a DNA damage-vulnerable state in the context of BRCA2 deficiency in pancreatic ductal adenocarcinoma

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is the most common form of pancreas cancer with an average five-year survival rate of under 10%. Mutations in KRAS account for over 90% of PDAC cases. Germline mutations can elevate the risk of developing PDAC with the most relevant being BRCA2, a gene that holds a critical role in homologous recombination. However, there exists a vulnerability in the mitotic processes of BRCA2 deficient PDAC that platinum-based chemotherapy cisplatin can selectively expose. Tumor selective Ras(ON) inhibitor called RMC-7977 has also recently emerged as a drug to target the active (ON) GTP bound states of the RAS family oncogenes. Genetically engineered mouse models carrying a KRAS LSL G12D/+ mutation, TP53 LSL R172H/+, BRCA2 flox/flox, and pancreas epithelium specific Pdx1-Cre Tg/+ recombinase were used in survival studies to compare efficacy of treatment groups. The groups included RMC-7977, RMC-7977 and cisplatin, cisplatin, gemcitabine and cisplatin, and vehicle. In vivo survival studies show that the RMC-7977 and cisplatin treatment arm possesses a statistically significant higher median overall survival and tumor free progression in the mice compared to other groups. However, immunohistochemistry shows a non-significant difference in CD8 and CD3 T cell markers and the CC3 apoptotic marker among treatments,

pointing to a potential intrinsic process of cell death rather than an external immunoresponse.

Alex Chen CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Christine Chio

Title: Investigating Mechanisms of Labile Iron Pool Expansion During Adipose Differentiation and Browning

Abstract: Adipose tissue is a key regulator of systemic metabolism and primarily exists in two subtypes: white adipose is responsible for energy storage in the form of triglycerides while brown adipose tissue releases energy via thermogenesis. White adipose tissue can undergo metabolic reprogramming to become more similar to brown adipose tissue in a process known as browning, which is regulated by the beta-3 adrenergic receptor signaling pathway. Impairments in white adipose tissue browning lead to systemic metabolic diseases such as cachexia and obesity due to altered energy expenditure. Because iron regulation has previously been reported to be essential for adipocyte function, this project explores how labile iron changes across differentiation and browning. The differentiation of adipocytes leads to an early spike in intracellular iron levels, indicating that free iron ions within the cell may be a contributor to this process. The expansion of the labile iron pool also coincides with an increase in nuclear receptor coactivator 4 levels, suggesting that this protein may drive the iron peak. Interestingly, isoproterenol—an inducer of adipocyte browning—causes an expansion of the labile iron pool. The activation of protein kinase A, a downstream target of the beta-3 adrenergic receptor signaling pathway, was identified to be a key dependency for the regulation of iron upon adipocyte browning. Taken together, these results suggest that adipocyte differentiation and browning in vitro result in iron accumulation, providing more insight on the mechanisms that govern adipose tissue function.

Yiyun Chen GS'28, History

Faculty Mentor(s) or Supervisor(s): Ashley Brown

Title: Religious Writers and their Female Characters

Abstract: England in the twelfth century was not a peaceful kingdom. From 1135 to 1154, the kingdom was defined by a period of civil war, controversially named 'The Anarchy'. For researchers focusing on the representation of women, this period is particularly significant because women played an unusually prominent role in politics and warfare.

Contemporary chronicles portrayed politically influential women within and beyond the kingdom alongside major political events, while hagiographies depicted female saints of considerable religious significance. Despite differences in genre and purpose, these works were all produced by male writers from Christian educational backgrounds who shared common gender values that shaped their portrayal of significant women. This research examines how those writers reconciled portraying specific women with significance with their own understanding of gender norms and expectations. It argues that the writers actively construct women's positionality in their text, whilst consistently attempting to reconcile the actions of women with the writers' own understanding of gender norms and expectations which can be seen across both chronicles and hagiographies. Male writers consistently positioned female characters in the text within perceived gender norms and expectations. When a woman's image contradicted these expectations, the writers sought to reconcile the tension. Where deviation failed to embody masculine virtue, writers reconciled it through simple criticism; where deviation did embody masculine virtue and was praised, writers instead emphasized the exceptionality of these cases, thereby consolidating rather than undermining the hierarchy between the feminine and masculine sexes.

Gigi Chen CC'28, Economics, English

Faculty Mentor(s) or Supervisor(s): Laura Neitzel

Title: Goncharov (1973): Creation and Community on the Post-Canon Internet

Abstract: In late 2022, a viral meme on the social media platform Tumblr emerged where users pretended to be fans of Goncharov (1973)—a mafia movie that had never actually existed—spawning an expansive creative community. Across textposts, fan artwork, fanfiction, archival compilations, meta commentary, and community disputes, tens of thousands of users invented characters, plot points, and film criticism for a movie none of them had seen. Goncharov fans created, joked, and self-regulated in a mimetic representation of a fandom that became a real one. This study examines the Goncharov (1973) fandom as a proxy for patterns of creative labor in online spaces. Goncharov fans, in their self-aware satire of and love letter to fandom and internet behavior, offer an opportunity to situate normative fandom behavior within wider internet culture and shifting perceptions of creative labor. Drawing upon literary media studies, the digital humanities, fan studies, and cultural criticism, this paper argues that internet communities have fundamentally blurred the traditional relationship between the spectators of a media object and its producers or artists. The structure of social media

can transcend the authority of canonical art in favor of communal and rapidly networked storytelling. At the same time, creative works like Goncharov are reliant on the attention economy, sit beyond the reach of commercial copyright, and are beholden to the forms of creative exploitation both might entail. The Goncharov community exemplifies what has always been true about human creation, while embedding the human urges to create and form community into internet-driven media. Modern media engagement requires that storytelling be interpreted holistically alongside sociopolitical considerations, especially as social media algorithms and artificial intelligence exert a growing influence on daily life.

Celine Chien CC'29, Economics-Political Science

Faculty Mentor(s) or Supervisor(s): Patricia Dailey

Title: Taiwanese ecoliterature: camphor trees, colonization, and conflict in ecocritical interpretations

Abstract: Drawing on Chang Ying-min's 血樟腦, or Blood Camphor, (2018), this paper argues that the novel's camphor tree withholds the reciprocity that ecocriticism has taught us to expect from the nonhuman. Rather than registering the Qing settler, and native Atayal people as equal entities to nature, it poses them as merely brief disturbances in a far more extensive timeline that does not recognize them. While the novel initially suggests a mutual interdependence between human bodies and the natural surroundings of the native Atayal peoples, they grow increasingly divergent as the narrative of human conflict moves forward across centuries. In consulting ecocritical theory, English and Chinese literature, and Taiwan-based professors and authors—including Chang Ying-min himself—this research aims to define “Taiwanese ecoliterature” in the larger context of geopolitical and environmental affairs, navigating a space amid overlapping spheres of influence and identity, including Western, Han Chinese, and Austronesian indigenous groups. More specifically, 血樟腦's emphasis on the longevity of the camphor tree suggests the transformation of trees as the primary consumer, with humans as commodities: turning against prevalent anthropocentric relationships between man and nature, and even Western ecocriticism's suggestion of mutual kinship. The paper takes part in a larger ongoing Trees project, which connects narratives of trees with deforestation, colonization, literature, and the environment. Spanning wide time periods, geographic locations, and methodologies, the project provides a different means for conceptualizing climate crises through a consideration of ecocritical theories, narratives, and nonfictional historical documents.

Mari Chikaarashi SEAS'27, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Bahareh Khezri

Title: Electrolyte-driven wetting and CO/H₂ selectivity in commercial gas diffusion layers for CO₂ electrolysis

Abstract: CO₂ electrolysis in gas-fed flow cells requires a stable gas–liquid–solid interface. It is crucial for the CO₂ gas to reach the Ag catalyst without electrolyte flooding in electrodes gas diffusion layers (GDLs). Previous work screened commercial GDLs, however, the influence of electrolyte identity on GDL wetting property and CO/H₂ selectivity remains insufficiently understood. In this study we examined how the electrolyte composition affects CO/H₂ selectivity on Ag-coated gas diffusion electrodes through characterizing GDL wetting properties and electrochemical stability. Ag-coated Sigracets and Torays electrodes were tested with CO₂-saturated electrolytes: 0.5 M KHCO₃, 1 M KOH, and 0.5 M K₂SO₄. GDL wetting was evaluated by water contact-angle measurements before and after the electrolysis, together with the gravimetric electrolyte-uptake. To quantify electrochemical stability, chronopotentiometry was conducted at -50, -100, and -200 mA, while the product gas was quantified by gas chromatography. The results showed strong influences of electrolytes. KOH gave the highest CO selectivity for both GDLs, with CO Faradaic efficiencies of 76–87% for Sigracet and 70–82% for Toray across the tested currents. KHCO₃ provided intermediate CO selectivity, while K₂SO₄ strongly promoted H₂ evolution, increasingly favoring H₂ production at higher current. Post-electrolysis wetting changes and uptake trends indicated electrolyte-dependent flooding propensity under flow-cell operating conditions. Sigracet was more CO-selective and operationally stable than Toray. These results highlight electrolyte–GDL compatibility for a critical design parameter of stable and selective gas-fed CO₂ electrolysis.

Jean Choi CC'29, Biochemistry

Faculty Mentor(s) or Supervisor(s): Harlan Jones

Title: Upregulation of Cyr61 as Molecular Link Between Maternal Separation and Glioblastoma-inducing Microenvironment

Abstract: Background: Early-life stress is a public health concern, with models including maternal separation demonstrating that ELS produces a neuroimmune stress response, leading to heightened pro-inflammatory signaling in brain tissue (1). Adverse childhood experiences, including

maternal separation, have been epidemiologically associated with increased cancer risk in adulthood, positioning early-life stress as a contributor to long-term disease (2). The neuroinflammation induced by ELS shares similar features with the pro-angiogenic, immunosuppressive microenvironment noted in glioblastoma (GBM); thus, we hypothesized that ELS induces a pro-tumorigenic, GBM-permissive environment in brain tissue, notable by upregulation of Cyr61. Cyr61 is overexpressed in the majority of high-grade glioblastoma tumors, where it drives kinase signaling to promote glioma cell growth and angiogenesis (3). Methods: To test this hypothesis, we used a maternal separation (MS) mouse model and performed bulk RNA sequencing on brain and lung tissue from MS and control animals. Mice underwent maternal separation from postnatal day 1 through day 21; brain and lung tissue were collected from MS and control animals at day 63 and frozen until RNA isolation. Tissue was homogenized in TRIzol reagent, followed by chloroform-based phase separation, isopropanol precipitation, and ethanol washing; purified RNA was further processed using the RNeasy Mini Kit (Qiagen, Cat. No. 74106). RNA quality was assessed via Nanodrop spectrophotometry, with samples at a 260:280 ratio of 1.8–2.0 considered acceptable for sequencing. RNA samples were submitted to GENEWIZ (Azenta Life Sciences) for sequencing using the Standard RNA-Seq bundle with PolyA selection, performed as paired-end sequencing at a target depth of 20 million paired-end reads (40 million total reads) per sample. Results: Cyr61 emerged to be significantly upregulated in the maternally separated mice brain tissue. (Brain: $\log_2FC = 1.98$). Conclusion: These findings suggest that ELS reprograms brain expression towards a molecular environment consistent with a glioblastoma-permissive microenvironment, with Malat1 and Cyr61 emerging as a link between early-life adversity and long-term cancer risk.

Irene Choi CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Qing Fan

Title: A Structural Study on GABAB-G Protein Complexes

Abstract: Gamma-aminobutyric acid type B (GABAB) receptors are heterodimeric Class C G protein-coupled receptors (GPCRs) that mediate slow, prolonged inhibitory transmission in the central nervous system via conformational changes. While recent cryo-electron microscopy (cryo-EM) advancements have resolved high-resolution GABAB structures, current models are limited to complexes with the canonical Gi1 subtype from the Gi/o subfamily. Thus, the mechanisms governing how the receptor recruits other transducers — such as Go, the most abundant G-protein in the brain —

remain unresolved. Furthermore, most existing structures rely on detergent micelles, which lack the lateral pressure, fluidity, and native lipid interactions of a phospholipid bilayer.

To address these limitations, we purified the full-length human GABAB1-GABAB2 heterodimer and assembled the active signaling complex with downstream G-proteins. Initial cryo-EM evaluation in detergent yielded particles and reference-free 2D class averages that resolved clear structural features of the extracellular, transmembrane, and intracellular domains as expected. Building on these validation results, ongoing work is transitioning the reconstituted heterodimer into lipid nanodiscs to restore a native-like bilayer environment, an approach previously validated in other Class C GPCRs. These preliminary 2D classifications also demonstrate technical feasibility and establish a foundation for high-resolution 3D reconstructions. Resolving these complexes in a lipid bilayer will clarify the molecular basis of transducer discrimination, advancing our understanding of GABAB signaling diversification in native environments.

Emily Choi CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Cory Abate-Shen

Title: Characterization of Metastatic Phenotypes in Mouse Models of Bladder Cancer

Abstract: Bladder cancer is a urinary system malignancy, with metastasis driving most patient mortality. Metastatic bladder cancer remains understudied due to a lack of in vivo models that naturally develop metastases. To address this gap, a genetically engineered mouse model (GEMM) of bladder cancer with a highly penetrant metastatic phenotype was generated. This research identifies phenotypic differences in metastatic progression between double-knockout (DKO: Pten and p53) and triple-knockout (TKO: Pten, p53, and Arid1a) GEMMs carrying a Rosa26-YFP reporter, using surgically delivered Adeno-Cre to induce bladder tumors. To characterize the metastatic phenotype, hematoxylin and eosin staining outlined tissue architecture and metastatic lesions, while immunohistochemistry evaluated cell lineage (anti-GFP), epithelial-mesenchymal transition (anti-vimentin), and epithelial cells (anti-pan-cytokeratin) across human-relevant metastatic sites: lymph nodes, lungs, and liver. Using two-tailed Mann-Whitney tests, TKO mice showed significantly higher metastasis scores than DKO mice ($P < 0.0001$), reflecting a more aggressive phenotype across lymph nodes ($P = 0.0103$), lungs ($P = 0.0020$), and liver ($P = 0.0005$). Pearson correlation analysis showed that tumor weight was positively correlated with metastasis scores in TKO ($P = 0.0376$) mice

but not in DKO ($P = 0.2095$) mice, confirming that larger TKO tumors directly predicted increased metastatic activity. Metastasis scores were independent of mouse sex. This research confirmed that *Arid1a* loss accelerates the aggressive metastatic phenotype in bladder cancer, particularly in distant organs such as the liver. These findings establish a model that recapitulates the natural evolution of metastatic bladder cancer and provides a platform for studying the mechanisms driving metastatic progression.

Yuli Choi CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Cory Abate-Shen

Title: Genotypes Determine Tumor Lineage Identities in Genetically Engineered Mouse Models of Aggressive Metastatic Prostate Cancer

Abstract: Prostate cancer (PCa) is the most diagnosed cancer among men in the United States, with metastatic prostate cancer accounting for most PCa-related deaths. Metastatic regions remain notably heterogeneous, posing challenges for disease characterization—there are currently only a few standardized frameworks to guide the characterization of metastatic biopsies in clinical practice. To address the limited phenotypical traits of metastatic lesions, we aim to investigate histological differences across primary tumor identities in increasingly aggressive PCa subtypes, whether primary tumor features are conserved at metastatic sites, and how the tumor's identity changes over disease progression. This study generated genetically engineered mouse models (GEMMs) to capture the heterogeneous phenotypes of PCa, modeling indolent to aggressive, metastatic cancer. Across the GEMMs, we analyzed survival, metastasis score, tumor phenotype, and used tissue staining techniques (IHC) to identify proteins associated with different tumor features in the primary tumor, lungs, liver, and bones. The analysis focuses on the presence of androgen receptors (AR), which are involved in PCa growth, along with epithelial, mesenchymal, and neuroendocrine markers. Results show that, across genotypes, AR levels are associated with two divergent routes: 1) an epithelial-to-mesenchymal transition program in AR-high tumors and 2) a neuroendocrine program in AR-low tumors. Moreover, features of primary tumors are conserved in metastatic sites.

Sofia Choudhri CC'28, Chemistry, Earth Science

Faculty Mentor(s) or Supervisor(s): Benjamin Bostick

Title: Photogrammetry: A Novel Technique to Remotely Sense *Phragmites australis* Growth Dynamics in the Piermont Marsh

Abstract: The Piermont Marsh—a brackish tidal marsh in the Hudson river estuary—protects two miles of shoreline, housing a thriving ecosystem and acting as an incredibly effective carbon sink. Over three-quarters of the marsh is dominated by an invasive species called *Phragmites australis*, or the common reed, which varies in height across the marsh. In this study, we combine photogrammetry, a technique to gather measurements from photographs, with data collected in the field to contribute to a more holistic understanding of marsh health and *Phragmites* growth dynamics through time. This summer, we conducted our annual drone survey of the Piermont Marsh [2024–2026]. The drone imagery was then stitched together on Agisoft Metashape to generate an orthomosaic map, or a highly-detailed aerial mosaic refined through the use of overlapping photographs. This also produced a digital surface model [DSM], or a graphic representation of the elevations of the highest visible surface—in this case, the *Phragmites* height—throughout the marsh. This elevation data could then be applied as a proxy to understand physical marsh properties without manual data collection. We hypothesized that areas with taller *Phragmites* would also have higher phosphorus concentrations—a growth-limiting nutrient in this healthy, non-eutrophic marsh. Since the DSM showed that canopy elevation was greater closer to a tidal creek, we collected phosphorus samples along a transect with increasing distance. ICP-MS chemical analysis found that phosphorus concentrations were in fact higher near the creek than further inland ($r^2=0.75$), suggesting that it transports phosphorus to support *Phragmites* growth. The results demonstrate that elevation data can be used to remotely sense nutrient availability in the Piermont Marsh, reducing the need for costly, labor-intensive physical testing to gauge marsh health and eutrophication state.

Wyatt Christlieb CC'29, Cognitive Science, Philosophy

Faculty Mentor(s) or Supervisor(s): Anya Schiffrin

Title: Mapping New York City Influencers and Funding of Public Messaging

Abstract: Since Mamdani's inauguration earlier this year, his social media presence has become ubiquitous. Whether riding a bicycle around the city or answering a question from an influencer on the street, he has continued to use social media to amplify his reach within the New York City community. Drawing on a review of existing literature and the European Union's regulatory approach to political influencers, this research sought to investigate the New York City influencer apparatus that has contributed to this amplification, continuously sharing information about Mayor Mamdani's programs and New York City policies. The paper identifies two types of

relationships currently in place: a Signal group which the Mayor's office uses to communicate with a specific group of influencers, many of them being carried over from the Creators4Zohran campaign group, and pilot programs aimed at using influencers on Instagram and TikTok to promote city services, including immigration rights, public budgeting processes, and tenants' rights, as well as pre-existing campaigns providing information about voting and health care. This research identifies a list of these influencers who appear to have a supportive relationship with the city government, as well as data analysis that seeks to understand the impact that the videos made about Mamdani are having within the community and on the creators' popularity. The paper also differentiates these new quasi-journalistic political influencers from traditional journalists. Lastly, prompted by gaps in the clarity and enforcement of disclosure policies for these relationships, the paper concludes with recommendations for the city government for best practices for increased public transparency.

Grace Chun CC'28, Computational Biology

Faculty Mentor(s) or Supervisor(s): Richard Pan

Title: Investigating the Mechanistic Roles of Mbd3 in Gene Reactivation

Abstract: Epigenetics is the study of how gene activity is regulated without changing the actual DNA sequence. Rather than altering the genetic code, epigenetic mechanisms dictate the accessibility and transcription of specific genes to establish distinct cellular phenotypes. Among the various epigenetic modifications, DNA methylation is widely recognized for its effectiveness in gene silencing. Yet, the opposite— DNA demethylation alone— is often insufficient to reactivate a silenced gene. Understanding the factors that regulate these barriers is critical for advancing epigenetic engineering and potential therapeutics. A CRISPRi screen conducted by the Liu Lab to investigate the factors that facilitate gene reactivation identified the Methyl-CpG-Binding Domain Protein 3 (Mbd3) as a highly significant target. However, it remains unclear whether Mbd3 is directly involved in DNA demethylation or operates in downstream gene reactivation mechanisms. To determine the precise role of Mbd3 in the reactivation pathway, we utilized CRISPR-Cas9 to generate Mbd3 knockout cell lines. Flow cytometry analysis measuring the mCherry fluorescence of knockout cells indicated that Mbd3 functions to repress transcriptional reactivation following DNA demethylation. Furthermore, during the verification of Mbd3 knockout cells, multiple Mbd3 isoforms were observed. This suggests the presence of exon skipping and indicates that Mbd3 undergoes complex post-transcriptional regulation. Ultimately, these findings suggest that Mbd3 acts downstream of

demethylation as a transcriptional repressor, providing new insights into the barriers of gene reactivation.

Josh Corn SEAS'27, Applied Physics

Faculty Mentor(s) or Supervisor(s): Nour Skaf

Title: Photonic Lantern Wavefront Optimization with DrWHO on SCExAO

Abstract: Direct imaging (DI) of young exoplanets offers a powerful route to detecting and characterizing planetary companions by isolating their light directly from the host star, but achieving the wavefront stability required to couple starlight efficiently into high-resolution spectrographs remains a fundamental challenge. Non-common path aberrations (NCPAs) introduce quasi-static speckles that limit the achievable contrast, even after extreme adaptive optics (AO) correction. We present the application of the Direct Reinforcement Wavefront Heuristic Optimization (DrWHO) algorithm to the 19-port photonic lantern (PL) on the FIRST/SCExAO instrument at the Subaru Telescope, using the PL output port intensities as a natural focal-plane wavefront metric. We explore two complementary quality metrics: total intensity across all PL output ports, which maximizes overall coupling efficiency, and H-alpha port concentration, which drives stellar light at 656.3nm into a minimal subset of ports, leaving the remaining ports strictly available for H-alpha emission from a potential accreting planetary companion. We present initial results on pre-collected SCExAO PL data, demonstrating the data synchronization pipeline and both metrics, and outline a pathway toward full on-sky deployment.

Celine Cotran CC'28, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Wesley Asher, Jonathan Javitch

Title: mGluR4's Role in alpha-synuclein internalization in Parkinson's Disease

Abstract: Parkinson's disease is characterized by the progressive loss of dopamine neurons in the brain. The primary driver of this neurodegeneration is the misfolding and aggregation of the protein alpha-synuclein. For these clumps to kill healthy neurons, they must first cross the cell membrane, but the mechanism behind this entry has been unclear. A recent study identified two membrane proteins that bind these clumps very tightly and support their entry into cells. Building on this discovery, we hypothesized that binding of alpha-synuclein clumps to these two proteins, both individually and together, would trigger the receptor's internalization into the cell, with the long-term

goal of determining whether blocking this interaction could slow disease progression. To test this, we used a plate-based antibody assay to measure the signal of each protein present on the cell surface under different experimental conditions, alongside a fluorescent binding assay to assess direct interaction of our receptor to the toxic protein clumps. Our experiment was validated by a clear, concentration-dependent increase in surface signal. However, treatment with the toxic protein clumps produced no measurable change in surface protein levels across conditions. In our binding assay, we also observed non-specific binding of our fluorescent toxin unrelated to the proteins of interest. These results suggest that binding alone may not be sufficient to drive internalization, or that further assay optimization is needed to detect this process. Future work will require refining experimental protocols and incorporate additional controls to clarify this relationship.

Myles Coven CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Leigh Goedeke

Title: Novel Regulation of Low-Density Lipoprotein Receptor (LDLR) by UBOX5

Abstract: Circulating levels of low-density lipoprotein (LDL) cholesterol are a major risk factor for cardiovascular disease (CVD) and are largely determined by hepatic LDL receptor (LDLR)- mediated uptake. Statins and PCSK9 inhibitors have emerged as effective therapies for increasing the abundance of LDLR, yet many patients fail to achieve target lipid levels or experience adverse side effects. LDLR activity is tightly regulated by a family of master transcriptional regulators known as sterol regulatory element-binding proteins (SREBPs). SREBP2 undergoes nuclear translocation to transcriptionally regulate LDLR synthesis, but its own regulation remains incompletely understood, and additional pathways controlling SREBP2, and consequently LDLR, are thought to exist. Here, we identify Ubox-domain containing protein 5 (UBOX5), a novel E3 ubiquitin ligase, as a top regulator of hepatic LDLR activity from an unbiased genome-wide screen. Conversely, knockdown of UBOX5 (siUBOX5) in human hepatic cells (Huh-7) significantly increased LDLR mRNA and protein levels, along with several SREBP2 target genes. However, siUBOX5-mediated increases in LDLR were abolished with pharmacological inhibition of SREBP2 processing, suggesting that UBOX5 modulates LDLR expression through an SREBP2-dependent mechanism. Importantly, siUBOX5 combined with a statin treatment produced an additive, significant increase in LDLR expression. Collectively, these findings identify UBOX5 as a previously unrecognized suppressor of

hepatic LDLR activity and suggest that UBOX5 inhibition could complement existing lipid-lowering therapies. Ongoing studies aim to define the molecular mechanisms by which UBOX5 regulates LDLR expression and to determine its role in hepatic cholesterol metabolism in vivo.

Eva Cullen CC'27, Applied Mathematics, Astrophysics

Faculty Mentor(s) or Supervisor(s): Chen Gu

Title: Distributed Acoustic Sensing for Supershear Earthquake Monitoring

Abstract: Supershear earthquakes rupture unusually fast, with the fault breaking faster than some of the seismic waves produced by the earthquake. This creates strong directional effects that can be difficult to capture with widely spaced seismic instruments. We evaluate whether Distributed Acoustic Sensing (DAS) can improve observations of these earthquakes by using fiber optic cables as large networks of closely spaced sensors. Focusing on the March 28, 2025 magnitude 7.7 Myanmar earthquake and the surrounding region of northern Myanmar and western China, we use a computer model of the Earth to simulate both slower and faster rupture scenarios while keeping other earthquake properties the same. We then compare simulated measurements from a fiber optic cable with measurements from conventional earthquake sensors, examining how well each records when seismic waves arrive, how quickly and in what direction they travel, and how the earthquake rupture itself moves. We also test how the direction and geographic coverage of the fiber optic cable affect the signals it records. Preliminary results show that different sections of the cable record the same earthquake differently depending on their orientation. Sections pointing more directly toward the earthquake record the first arriving waves more strongly, while sections oriented across that direction are more sensitive to later waves. The results also suggest that placing sensors extremely close together cannot fully make up for a network that covers only a small area. Using fiber cables that cover a larger region and extend in multiple directions may therefore improve our ability to determine how an earthquake ruptures and help guide the design of future fiber optic earthquake monitoring networks.

Linh Dang CC'27, Computer Science

Faculty Mentor(s) or Supervisor(s): Gail Kaiser

Title: Behavioral Determinants of Deployed AI Agents in Social Networks: A Multi-Factor Study of Personality, Model, and Guardrail Specification

Abstract: Autonomous AI agents are increasingly deployed in open social environments, yet the relationship between their configuration specifications and their emergent social behavior remains poorly understood. We present a controlled, multi-factor empirical study in which thirteen OpenClaw agents are deployed on Moltbook -- a Reddit-like social network built for AI agents - across three systematically varied independent variables: (1) personality specification, (2) underlying LLM model backbone, and (3) operational rules and memory configuration. A default control agent provides a behavioral baseline. Over a one-week observation window spanning approximately 400 autonomous sessions per agent, we collect behavioral, linguistic, and social metrics to assess how configuration layers predict emergent social behavior. We find that personality specification is the dominant behavioral lever, producing a massive spread in response length across agents, while model backbone and operational rules drive more moderate but still meaningful effects on rhetorical style and topic engagement breadth. Our findings contribute empirical evidence to the emerging literature on deployed multi-agent social systems and offer practical guidance for designing agents intended for collaborative or monitoring tasks in real social environments.

Sebastian David-Mercado CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Aydogan Mustafa

Title: The embryo's emergency brakes: how spermidine shapes the embryonic nucleus

Abstract: Hydrogen Peroxide (H₂O₂) has been implicated as a mitochondrial signaling factor that maintains cellular homeostasis, including the regulation of cell division, growth, and immune response. Previous studies have shown a halt in embryonic development as a result of H₂O₂ depletion. Our lab aims to investigate the mechanisms by which embryonic development is halted under these conditions. A proteomics analysis comparing fold-change protein concentrations in H₂O₂-depleted and anoxic (lacking O₂) embryos (two conditions that independently cause a pause in embryonic development) found that spermidine was consistently unregulated in anoxic and H₂O₂ conditions. Given this similarity, we investigated spermidine, a molecule known to be involved in proliferation, differentiation, apoptosis, and nuclear stability. We found that spermidine injections induce various nuclear phenotypes reminiscent of those seen in anoxic and H₂O₂-depleted embryos. This overlap suggests that spermidine may function as a shared mechanism by which embryos pause development in response to both oxidative and hypoxic stress.

Justin Davis CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Whitney Parker

Title: Low-Intensity Focused Ultrasound in Temporal Lobe Epilepsy Models: Investigating the Effects of Neuromodulation on Mechanosensitive Ion Channel Expression in GABAergic Neurons

Abstract: Mesial temporal lobe epilepsy (MTLE), the predominant form of focal epilepsy, is frequently intractable, highlighting the need for effective, minimally invasive alternatives to surgery. Although low-intensity focused ultrasound (LIFU) reduces seizure severity in animal models, its ability to prevent the pathologic network reorganization underlying epileptogenesis and the cellular mechanisms mediating these effects remains unclear. MTLE epileptogenesis is primarily localized to the hippocampus and involves disruption of excitatory glutamatergic and inhibitory GABAergic signaling during the latent period preceding spontaneous seizures. In our rat model, intrahippocampal kainic acid (KA) induces MTLE with an approximately two-week latent period. Our preliminary work demonstrates that LIFU delivered during this period reduces seizures, increases hippocampal GABAergic signaling, and decreases glutamatergic signaling. We hypothesize that LIFU selectively promotes inhibitory neuronal activity through mechanosensitive ion channels Piezo1, TRPP1, and TRPC1, enhancing GABAergic network development and preventing epileptic network formation. Two cohorts, each comprising four treatment groups (KA, LIFU, KA+LIFU, and untreated control), will investigate this mechanism. In cohort one, immunohistochemistry for Piezo1, TRPP1, TRPC1, GAD1/67, and vGlut will be used to assess ion channel colocalization in hippocampal inhibitory and excitatory neurons. In cohort two, implanted hippocampal electrodes will be used for electrophysiological recordings of neuronal activity and seizure occurrence. Correlation of mechanosensitive ion channel expression with seizure outcomes across treatment groups would support these channels as mediators of LIFU-induced seizure suppression and provide mechanistic evidence for LIFU as a novel, noninvasive strategy to prevent MTLE.

Lucia Dec-Prat CC'27, Biology, History

Faculty Mentor(s) or Supervisor(s): Mark Mazower

Title: Dodecanesian Advocacy and Italian Governance After the First World War

Abstract: The Ottoman-ruled Dodecanese Islands were taken by Italian forces in 1912 in a maneuver designed to help Italy's position in the ongoing Italo-Ottoman War in Libya. Seven years later, at the end of the First World War, the islanders remained under Italian rule and, with military blockade lifted, found themselves navigating new consular systems to hear news of relatives lost across Asia Minor and Europe. In this context of changing borders and a wide Dodecanesian diasporic presence, representatives of the Dodecanese Islands to the Paris Peace Conference understood the islands as an unredeemed Greek territory and, taking inspiration from Wilsonian principles of self-determination, hoped to argue for their union with Greece. They sent hundreds of letters to world leaders and diplomats; Woodrow Wilson seemed sympathetic to their cause, although he and most European heads of state chose not to pressure Italian officials on the issue. Nevertheless, a change in status for the islands appeared imminent: in the Tittoni-Venizelos accord, signed in July 1919, Italy promised to cede the islands to Greece. This treaty was the first of two post-war agreements that would have given control of at least some of the Dodecanese Islands to Greece. The Tittoni-Venizelos accord, and the Bonin-Venizelos agreement a year later, were never enacted. Meanwhile, Italy gained control of Kastellorizo, another island in the Dodecanese, from France. This research examines archival records of Dodecanesian advocacy in the press and in private correspondence with European diplomats at the Paris Peace Conference alongside files documenting local Italian governance of the Dodecanese Islands. It draws on correspondence between the Italian territorial government and the Italian Ministry of Foreign Affairs, which discusses the diplomatic significance of local protests and anti-Italian press coverage in the years immediately following the First World War.

Kristina Isabella Dee SEAS'27, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Vijay Vedula

Title: Multi Patient Evaluation of Computational Models of Uterine Mechanics

Abstract: This research evaluates whether a computational model of uterine and cervical mechanics can be applied consistently across multiple patient anatomies during late pregnancy. The work builds on a previously developed modeling framework that compared two approaches. One approach uses FEBio to represent contact between the uterus, cervix, fetal membrane, and surrounding abdominal tissue. The second uses svMultPhys with simplified boundary conditions that reproduce the effects of surrounding tissues while reducing computational cost. The original study demonstrated close

agreement between the two approaches for one patient and showed substantial savings in simulation time. The current project extends this framework to multiple patients in order to test its robustness and generalizability. For each patient, anatomical models of the uterus and cervix are prepared, assigned consistent tissue properties, and simulated in both FEBio and svMultPhys under the same physiological loading conditions. Predicted deformations are then compared across the two modeling approaches and across patients. Particular attention is given to differences in anatomy, tissue contact, numerical convergence, and local deformation that may affect model performance. By testing the framework across a broader patient group, this study addresses an important limitation of the original single patient model. The results will help determine whether the more efficient svMultPhys approach can reliably reproduce patient specific uterine and cervical deformation and support future studies of pregnancy progression and labor.

Cathy Deng SEAS'29, Applied Mathematics, Sophie He SEAS'29, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: ComfiMap: Multi-Objective Route Optimization for Pedestrian Thermal Comfort in New York City

Abstract: Walking remains one of the most common ways people navigate through cities, yet as global warming intensifies, it is becoming an increasingly dangerous one. This risk is amplified by the Urban Heat Island effect, which makes urban areas significantly warmer than nearby rural areas. Commonplace navigation tools typically optimize for distance alone, and prior efforts to close this gap remain primarily focused on shade or surface air temperature. We propose a novel approach for pedestrian routing by optimizing for both thermal comfort and travel time. The model integrates three distinct microclimatic predictor models—SOLWEIG, URock, and Spatial TC for Mean Radiant Temperature, wind dynamics, and the Universal Thermal Climate Index (UTCI), respectively. The output is a bihourly 2-m resolution pedestrian network graph of Lower Manhattan weighted by two objectives: distance and Cumulative Discomfort (CD), defined as a function of UTCI along the route. For an example study area, we exhaustively conducted a depth-first search for all paths between the shortest path and length of path of lowest CD by Dijkstra's algorithm. From this, we obtained the distance-CD Pareto frontier at each time. At 14:00, the distance-CD trade-off between the shortest and coolest paths was 5.58 m/100°C. This was the

lowest out of all the times, indicating taking an alternative path is most desirable at this time. As LiDAR surface scans are largely complete across the continental United States, this model can be scaled to other regions and offers a means toward increasingly heat-aware urban planning between cities.

Jenny Deng CC'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Katherine Xu

Title: Prioritizing causal candidate genes underlying urinary tract infection (UTI) susceptibility using functional genomic approaches

Abstract: Urinary tract infections (UTIs) are among the most common bacterial infections, yet the genetic factors influencing susceptibility remain poorly understood. A recent genome-wide association (GWAS) of 1.8 million individuals identified 36 genome-wide significant loci associated with UTI risk. This study applies an integrative regulatory genomics framework to link UTI-associated variants to their likely target genes. Four enhancer–gene mapping approaches were used: Open4Gene chromatin–expression links, Activity-By-Contact (ABC) enhancer–promoter interaction scores, single cell enhancer-gene (scE2G) predictions, and promotor AI were used. GWAS SNPs were overlapped with each regulatory model and target genes were identified. Several genes were supported by all three methods including PSCA, ARC, UMOD, GP2, SLC6A18, CLPTM1L, ALDH2, SLC11A2, METTL7A, DNAJC1, FES, and CKB, making them target candidate genes. Of these genes, PSCA was further experimentally validated. Preliminary experiments were conducted to assess PSCA expression in mouse kidney and urine samples and to evaluate the potential effect of PSCA on bacterial growth in urine, although the current findings remain inconclusive. Together, these results provide a regulatory genomics framework for interpreting UTI-associated GWAS loci and prioritizing candidate genes for future functional validation.

Kelly Deng CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Andrew Ji

Title: A transcriptomic atlas of preclinical murine atopic dermatitis models to characterize transcriptionally distinct human disease endotypes

Abstract: Atopic dermatitis (AD; eczema) is a chronic, relapsing, non-contagious condition causing itchy, dry, and inflamed skin, often appearing as red to brown patches in up to 20% of children and 10% of adults worldwide. Currently, many preclinical models broadly classifiable as inducible (happen

or cytokine-driven, MC903 and oxazolone [OXA]), genetically engineered (targeting AD-relevant genes such as IL-4, IL-13), and spontaneous (inbred strains exhibiting AD-like lesions arising from endogenous genetic mutations) exist to recapitulate atopic dermatitis (AD), which itself is a very heterogeneous disease in humans. Despite these individual advances, a comprehensive, cross-species single-cell molecular comparison that systematically maps each preclinical model to specific human AD endotypes remains absent. To address this, we utilize a graph theory and centrality metric-based predictive algorithm, CellChat (Jin et al., 2021), and an unsupervised machine learning method, non-negative matrix factorization (Lin & Boutros, 2020), to uncover cellular and molecular differences across mouse models of AD and relate them to specific subsets and features of human AD patients. Namely, we leverage public and internally generated scRNA-seq, MERFISH, and ATAC-seq data from murine AD models and human AD patient skin, integrated with bulk RNA-seq profiling of a larger AD patient cohort. The present study provides a translational resource enabling researchers to select the most appropriate preclinical model for their specific biological question, while simultaneously informing the identification of new therapeutic targets and the patient subsets most likely to benefit from model-derived translational strategies in AD and related inflammatory skin diseases.

Shreyans Dhamane SEAS'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Tony Dear

Title: Adaptive Loss Balancing for Physics-Informed Imitation Learning of Humanoid Locomotion

Abstract: Imitation learning is increasingly used to generate human-like walking trajectories for humanoid robots from recorded motion. Such models fit the recorded motion but do not enforce the kinematic condition that the support foot remain stationary during contact. The result is foot sliding, in which the support foot translates along the ground while it should be planted. The recordings used in this work are CMU motion capture retargeted onto ergoCub, so they satisfy that condition only approximately. A neural network model trained on them violates it by a considerably larger margin. Recent work reduces sliding with a physics-informed term in the training objective that penalizes support foot velocity during contact. The weight on this term is determined manually, requiring the model to be retrained for each candidate value and the search repeated whenever the robot or the dataset changes. This work examines whether it can instead be determined during training. A mode-adaptive neural network is trained to predict the next state of the robot, and a

rule is introduced that sets each physics weight based on gradients computed during training, updating it multiplicatively so that each term converges to a fixed point. A second physics term penalizes the change in support foot velocity between consecutive contact frames, and the rule is combined with optimizer resets so the weights converge rather than saturate. The rule is evaluated against a swept fixed weight, GradNorm, PCGrad projection, and resets applied alone, with sliding measured on held out ergoCub locomotion data. The results show that this is empirically possible, the rule reducing sliding below the best fixed weight found by a sweep in a single training run.

Evelyn Ding SEAS'29, Computer Science

Faculty Mentor(s) or Supervisor(s): Julia Hirschberg

Title: Investigating Vocal Biomarkers for Health Assessment

Abstract: Vocal biomarkers are a powerful yet underexplored approach for detecting a wide range of health conditions. From mental health disorders to laryngeal cancer, many conditions cause changes to a patient's voice that can be captured by acoustic features. A growing field of research involves training models to understand these complex features and make diagnoses. However, existing studies often rely on models that are limited by their lack of interpretability. This project aims to develop automated diagnostic models that are highly interpretable, providing clinically relevant outputs rather than black-box predictions. First, datasets focused on raw speech audio from patients with various medical conditions were accessed from platforms like Zenodo and PhysioNet. Next, established acoustic feature sets (e.g., eGeMAPS) were extracted to construct interpretable baseline classifiers and to examine which features are most predictive across different conditions. Building upon these baselines, the study explored more advanced speech processing approaches, using self-supervised speech models and recent audio-language models such as Qwen-Audio and Flamingo-Audio. These models were utilized in multiple ways, including the extraction of interpretable speech representations as well as the development of end-to-end systems for automated health assessment. Finally, post hoc explanation techniques, such as SHapley Additive exPlanations (SHAP), were applied to analyze model behavior and to enhance the interpretability of predictions.

Jada Dixon SEAS'27, Computer Science

Faculty Mentor(s) or Supervisor(s): Nikhil Garg

Title: LLM Homogeneity in Peer Reviews

Abstract: As LLM-generated text has become more prevalent in peer reviews, it is important to question whether LLM-generated peer reviews meaningfully differ from their human-written counterparts. Previous research has argued that LLM-generated peer reviews are homogeneous and should not be permitted, but this homogeneity was measured through text embeddings, which do not show the complete picture of homogeneity. This project uses sparse autoencoders (SAEs) as an alternate method of measuring homogeneity in peer reviews by identifying stylistic and semantic features of human-written and LLM-generated peer reviews and analysing any trends that might emerge. After performing regression and doing further analysis to determine the most statistically significant predictive features, it was found that LLM-generated reviews tended to focus on more technical components and quantitative details, while human-written reviews were more specific and focused on clarity.

Jai Dreher SEAS'27, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Carlos Paz Soldan

Title: Building a Tokamak: The Centerstack

Abstract: Abstract: A Tokamak is a donut-shaped ("toroidal") fusion device that uses carefully controlled magnetic fields to confine extremely hot plasma. By keeping this plasma stable, the Tokamak creates conditions similar to those inside stars, allowing nuclear fusion to occur. The machine includes several major components: magnetic coils, a main chamber that holds the plasma, a vacuum system, and a centerstack (a central column that passes through the middle of the "donut" and carries the wiring needed to generate magnetic fields). Because the centerstack must stay precisely aligned while enduring high heat and mechanical forces, supporting it securely is a significant engineering challenge. This project designed a support system using vacuum-sealing O-rings, friction-based clamps, and machined structural supports to stabilize the centerstack inside the main chamber. With these additions, the centerstack became fully self-supporting, removing the need for an external crane or jackstands and making assembly simpler and more efficient.

Alina Du SEAS'29, Financial Engineering, Christopher Lee CC'29, Computer Science, Mathematics, Allison Li CC'29, Computer Science, Mathematics

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: Think Before You Trust: Structure-Aware Verification Budget Allocation in LLM Reasoning

Abstract: Large language models (LLMs) generate reasoning as a growing web of dependent claims, where early errors can contaminate ideas generated downstream. However, verifying every step is too resource-intensive and unrealistic as the questions grow in complexity. Currently, existing verification strategies are limited to scoring complete answers or performing post hoc checks on reasoning chains. We start our address of this problem by modeling the geometry of such generated claims in terms of a tree of nodes for our baseline model, then modeling claims as a directed acyclic graph (DAG) for a more accurate simulation of real LLM reasoning structures. In both models, each claim carries a hidden ground-truth label and a self-reported confidence score. Then, given a fixed verification budget, we compare strategies for selecting which claims to check (random, confidence-based, dependency-aware heuristics, dynamic-programming ceiling for trees, and a submodular Monte Carlo greedy approach for DAGs) and introduce adaptive threshold policies that locally decide whether or not to verify a node based on its estimated downstream damage. The results are tested against eight real LLMs, confirming that models are systematically overconfident on false claims, motivating structure-aware verification over confidence-based checking alone. Furthermore, the true/false confidence gap is narrow (0.03–0.13) and vanishes in the worst case (e.g. Llama-8B with true-false confidence at 0.81–0.82), which reduces confidence-based verification to near random-chance performance. Applying stress tests show that even pressure on the confidence channel can drive it below random while structural signals are immune by construction, which motivates structure-aware verification as a practical alternative.

Sabrina Du CC'29, Psychology

Faculty Mentor(s) or Supervisor(s): Natalie Brito
Title: Examining Infant Relational Memory in the Context of Home Environment and Sleep Patterns

Abstract: Relational memory (RM) is the ability to form associations between individual items and is crucial for producing autobiographical memories (Eichenbaum & Cohen, 2001). While studies have demonstrated the influence of socio-environmental factors on infant memory (e.g., Miquelote et al., 2012), much less is known about their links with specific processes like RM. Thus, this study assessed the implications of the home environment and sleep on RM performance in 4-month-old infants (N = 50). Caregivers completed a

sociodemographic survey and a modified Brief Infant Sleep Questionnaire (Sadeh, 2004). RM was evaluated using an adapted Spatial Relational Memory Task (Richmond & Nelson, 2009). Infants were first shown three distinct face-scene pairs, followed by a test phase where the three familiar faces were superimposed over a previously shown scene. Exhibiting preferential looking at the matching face, measured via webcam-based eye-tracking, suggested evidence of RM ability. Preliminary results indicated that RM was positively associated with the number of children in the home ($B = 0.035$, $p = 0.027$) and daily nap frequency ($B = 0.048$, $p = 0.016$), whereas total sleep duration (nighttime and daytime), average nap duration, and longest sleep period duration were not significantly associated with RM. After adjusting for gestational age, sex, and exact age at assessment, only daily nap frequency remained significant ($B = 0.043$, $p = 0.032$). These findings indicate that sleep frequency may play a more meaningful role in 4-month-old infant RM than sleep duration, suggesting that distinct aspects of infant sleep may be differentially associated with early cognitive development.

Patrick Dugan CC'28, Political Science

Faculty Mentor(s) or Supervisor(s): Justin Phillips
Title: Political Polarization and "Culture War" Issues

Abstract: This project examines how the McGovern-Fraser reforms reshaped abortion politics in Wisconsin between 1968 and 1972. It contributes anecdotal evidence to a project by Justin Phillips and Gerald Gamm that challenges the conventional narrative that abortion became a partisan issue only after Roe v. Wade, when conservative activists pressured Republican leaders to adopt anti-abortion stances in the late 1970s. Their research instead traces the divide to 1970–72, when women, young people, and minorities mobilized a grassroots liberal movement to pass abortion planks in Democratic state party platforms, enabled by reforms that democratized the party's caucus-and-convention system. Drawing on archival newspaper research, the Wisconsin case supports this account. Democrats adopted an abortion-liberalization plank in 1968 and an abortion-legalization plank in 1970, though office-holders at the statutory convention repeatedly dropped such planks due to concerns about alienating Catholic voters. These debates occurred alongside successful efforts to expand participation, with women and young people faring substantially better in Wisconsin's delegate selection processes. Wisconsin's state party politics between 1968 and 1972 simultaneously complicates the project's core findings. Its voluntary party structure had few institutional barriers prior to the McGovern-Fraser reforms,

and accordingly, liberal insurgents gained political influence earlier than other states. By 1972, key liberal insurgents ossified into party regulars, dominating the state party convention and sacrificing controversial liberal planks. Wisconsin thereby illustrates a two-stage process: liberal activists first gained access to party institutions and pushed abortion onto the Democratic agenda, then they tempered such goals in favor of electoral expediency after gaining power.

Naomi Jo Erny GS'29, Computer Science

Faculty Mentor(s) or Supervisor(s): Sharon Marcus

Title: How are Characters Constructed? Theory of Literary Character

Abstract: Literary scholars have always distinguished major characters from minor ones, but such judgments usually rest on selected passages rather than whole novels. Professor Sharon Marcus, English and Comparative Literature of Columbia University, has addressed this gap by designing a six-component model of character construction, a new approach to understanding the construction of literary characters: name, interiority, communication, discussion by other characters, action, and description by the narrator. In collaboration with the Computer Science Department, literary experts have hand-tagged nineteenth-century Anglophone novels sentence by sentence and produced a tagging manual setting out the logic for computational methods to reproduce the results and scale across a wider corpus. For literary studies, counting every component across an entire novel offers new perspectives about which characters dominate a narrative, and challenges the misconceived 'flatness' of minor characters compared to major ones that can be tested across authors and periods. For computational research, the model offers a richer account of character than the co-occurrence and dialogue networks common in text mining, and the expert tagging provides a benchmark against which results derived by computation can be measured. This project built the benchmark for Dickens's *Oliver Twist*. It aligned the hand-tagged and machine-tagged texts word for word across the novel, then scored how closely the computational results match the human-generated dataset, separating tagging errors from character-attribution errors. The evaluation reveals which components of the model BookNLP can reliably reproduce and where patterns emerge in missed or misclassified tags.

Destiny Estill GS'28, Evolutionary Biology of the Human Species

Faculty Mentor(s) or Supervisor(s): Andreane Lavallee

Title: Does autism affect the observation of synchronicity?

Abstract: Caregiver-child synchrony is an important marker of childhood social development. Synchrony is assessed through behavioral coding of parent-child interactions, such as the Interactional Synchrony/Connection Scale. It is unclear whether coders with Autism Spectrum Disorder (ASD), characterized by persistent social deficits in interaction and synchrony, can achieve inter-rater reliability (IRR) like coders who are typically developing. The study's aim was to investigate whether a formal ASD diagnosis affected observations of caregiver-child synchrony using the InSynC scale. This goal was achieved twofold: By assessing whether an individual with ASD would achieve IRR on the InSynC scale after completing the training process and then whether IRR would generalize to a larger set of videos. The InSync Lab compared the reliability of an ASD coder vs the gold standard. Research assistants coded 149 (70 training set) videos from the COMBO Initiative, a longitudinal study focusing on maternal-child health during the COVID-19 pandemic. Children in 4-48 months, completed 3-5-minute face-to-face interactions with caregivers. Coders evaluated synchrony on 2 measures on a scale ranging from 1(low) to 9(high). IRR is measured using an intraclass-correlation (≥ 0.75 considered reliable) between the ASD coders and the gold-standard score. Results showed that the training process was completed in the same timeframe. The ASD coder achieved, IRR within the acceptable range (0.75 to 0.82), thus suggesting that an ASD diagnosis does not affect observations of caregiver-child synchrony.

Ruby Farmer CC'28, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Robert Bauer

Title: TRIB1 promotes COP1 nuclear localization and reveals a potential novel mechanism of STK40 regulation in hepatocytes

Abstract: Tribbles-1 (TRIB1) is a protein associated with blood lipid levels and coronary artery disease. Previous studies show that increasing TRIB1 levels in the liver can reduce cholesterol and triglyceride levels, suggesting that TRIB1 has potential as a therapeutic target. TRIB1 works with other proteins, including Constitutive Photomorphogenic 1 (COP1) and Serine/Threonine Kinase 40 (STK40), to regulate cellular processes. However, the significance of these interactions and the subcellular localizations of these proteins remain unclear.

This study used fluorescence imaging to examine the locations of TRIB1, COP1, and STK40 in human liver cells. Cells were transfected with different combinations of DNA to regulate protein expression levels and examine how

co-expression affected the subcellular localization of each protein. TRIB1 was consistently found in the nucleus, the part of the cell containing its genetic material. COP1 was primarily found outside the nucleus when expressed alone but moved into the nucleus when co-expressed with TRIB1. This study also provides the first characterization of STK40 localization in liver cells, showing that it is primarily nuclear when expressed alone. Co-expression with COP1 resulted in nuclear localization of both proteins, while co-expression with TRIB1 caused some STK40 to redistribute outside the nucleus. However, all three proteins localized to the nucleus when expressed together. These findings provide new insight into how TRIB1, COP1, and STK40 interact in liver cells. Further studies will investigate these relationships, potentially providing a better understanding of the cellular pathways associated with coronary artery disease and informing prevention and treatment strategies.

Adrienne Ferguson CC'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Anna-Lena Steckelberg
Title: Investigating the Interaction of Exoribonuclease-resistant Viral RNA Structures with Cellular Translation Machinery

Abstract: RNA viruses contain several structured elements in their genomes that enable their dangerous pathogenic processes during infection. One such example are xrRNAs, a conserved class of highly structured, non-coding RNA motifs found across several animal- and plant-infecting viruses that stall RNA degradation by the cellular enzyme Xrn1. This incomplete degradation accumulates a series of subgenomic RNAs, which are critical for viral replication, infectivity, and evasion of host-cell defense mechanisms. Despite their large sequence and structural diversity, xrRNAs in animal- and plant-infecting viral genomes share a common ring-like pseudoknot motif that is required for Xrn1 resistance. Although xrRNAs have been found primarily at the 3' end of viral genomes, recent studies have identified xrRNAs present in both 5' and intergenic regions, suggesting a much broader xrRNA functionality enabled by their interactions with other RNA-associated cellular enzymes. For instance, ribosomes can mechanically unwind RNA secondary structures during translation. Whether xrRNAs in these non-traditional genomic contexts may resist ribosome unwinding remains unclear. Here, we use molecular cloning to install representative xrRNAs into the 5' or intergenic regions ahead of a luciferase reporter gene. Using both in-cell and cell-free translation assays, we demonstrate that xrRNAs installed in the 5' region significantly stall the scanning ribosome, whereas intergenic installed xrRNAs are unwound by the translating ribosome. We further explore the

idea that class 3 xrRNAs, which resemble tRNAs, could act as independent ribosomal entry sites by using a circular RNA translation reporter system.

Amal Fickak CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Erica Rodriguez
Title: Determining the Role of Oxytocin Signaling in the ACC-BLA Pathway During Social Olfactory Processing

Abstract: Social interactions require the brain to recognize and respond to sensory information from other individuals, but how the brain assigns social meaning to these cues is not fully understood. The anterior cingulate cortex (ACC) and basolateral amygdala (BLA) are brain regions involved in social and emotional processing. Previous research in our lab has shown that the ACC-BLA pathway is necessary for rank-dependent and sex-specific olfactory-guided motivated behavior. Oxytocin (OXT), a neuropeptide involved in social behavior, may help regulate how the brain processes these odors. This project investigates whether neurons in the ACC that express oxytocin receptors (OXTR+) are differentially activated by odors from socially dominant and submissive mice. Our hypothesis is that OXTR+ ACC neurons help assign different levels of salience to socially ranked odors and influence communication between the ACC and BLA. To test this hypothesis, mice were first injected with a retrograde virus used to identify ACC neurons that project to the BLA. After injections, mice were assessed for their social ranks using a tube test. Then, mice were exposed to urine odors from dominant or submissive mice. After odor exposure, brain tissue was collected and processed using immunohistochemistry to identify neurons activated by the odors through cFos expression. Finally, imaging and cell-counting analyses were used to determine which OXTR+ neurons project to the BLA and are activated by socially relevant odors. This work will contribute to our understanding of how oxytocin and neural circuits shape social behavior and emotional processing.

Andrés Florentino CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Andrés Bendesky
Title: Application of a Bimodal Fear Assay and Machine Learning in the Investigation of a Novel Motor Cortex Adrenal Gland Circuit

Abstract: Ever get a pit in your stomach before a scary moment and wonder whether your body is reacting to your fear, or your fear is reacting to your body? The link between mind and body is still surprisingly under-explored.

We know that fear can speed up your heart rate, but can changing your body's state on its own trigger a feeling of fear? That is the question behind this project. Our team discovered a brand-new circuit linking the motor cortex (usually seen as just the brain's "move your muscles" center) directly to the adrenal gland, the body's fight-or-flight hormone factory. This suggests the motor cortex might also help generate the feeling of fear itself, possibly through the hormone epinephrine (adrenaline). To test this, we used a "looming stimulus" setup: mice see a scary shadow overhead, mimicking a predator, and we measure how quickly they flee to shelter. We added sound to the classic visual-only version and compared fear responses across several mouse species. AI (YOLO) helped us score the videos automatically, and its results lined up well with human scoring. We also dosed mice with beta-blockers, drugs that block adrenaline's effects, to see if this weakened their fear response. Surprisingly, it made little difference in our main strain, though a second strain proved too intimidated to test reliably. Overall, our results point to a strong, adrenaline-linked fear circuit. However there is more work ahead to fully map how the brain drives this dramatic body-mind feedback loop.

Lily Foroozan SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Umrao Monani

Title: Splicing Modulation Restores SMN Expression in Human SMA Fibroblasts

Abstract: Spinal muscular atrophy (SMA) is a neuromuscular disorder that causes the deterioration of motor neurons in the spinal cord, leading to progressive muscle weakness. SMA results from deletion of the SMN1 gene, which normally produces the functional, full-length SMN (FL-SMN) protein that is essential for motor neuron health. A closely related gene, SMN2, can partially compensate for this loss by producing only 10% of the full-length, functional SMN protein. The remaining transcripts produce a shortened and unstable form known as SMN Δ 7. Current treatments, including risdiplam and oligonucleotide-based therapies, help SMN2 produce more functional SMN protein. However, the extent to which these treatments restore FL-SMN production in humans remains unclear. This study compared fibroblasts from healthy individuals with those from patients with SMA. Untreated SMA fibroblasts showed lower full-length SMN expression and SMN protein levels than healthy fibroblasts. Treatment with risdiplam or an experimental oligonucleotide, SMN-morpholino, increased full-length SMN expression and SMN protein levels while also increasing the ratio of full-length SMN to SMN Δ 7 transcripts. The study further assessed SMN restoration by

measuring nuclear gems, small nuclear structures that contain SMN protein and can serve as biomarkers of SMN function. Untreated SMA fibroblasts had significantly fewer gems than healthy fibroblasts. Both treatments significantly increased gem numbers, with no statistically significant difference between the treatments. These findings demonstrate that patient-derived fibroblasts recapitulate key features of SMA and can be used to study therapies that increase functional SMN protein levels.

Asha Gajraj SEAS'29, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Ngai Yin Yip

Title: Cooperative Synergy in Amine Blends for Enhanced Desalination Selectivity

Abstract: Hypersaline brines from industrial activities are rich in heavy metals that would benefit from critical mineral recovery, and an extraction technique that is both low cost and uses minimal energy is needed. Temperature swing solvent extraction (TSSE) is a nonevaporative desalination method that relies on thermally switchable solvents that act like a chemical sponge, which uptake water and reject salt at a cooler temperature, and release the fresh water when swung to a higher temperature. While previous research has explored the efficacy of single solvents, there is a gap in understanding the behaviors and mechanisms in binary solvent mixtures. This research sought ways to optimize amine mixtures for better desalination performance by analyzing their linear versus synergistic extraction behavior, where synergy is defined as the combination of two or more parts yielding a greater impact than the expected additive effect. Six amine solvents (TEA, TOA, DIPA, DPA, DMCHA, and ECHA) were used to create 15 binary blends, where equal weights of 3M NaCl brine and binary solvent mixture were combined. The blends then sat in a water bath at the designated temperature before separating into two distinct layers, where the organic amine layer was extracted for analysis to assess water percent uptake and salt selectivity. Results showed blends containing TOA demonstrated increased water uptake, with particular blend ratios such as TEA:TOA and TEA:ECHA demonstrating strong synergistic effects in selectivity. Future studies with dynamic light scattering can be done to understand the mechanisms behind solvent molecules' desalination synergy.

Elizabeth Galles GS'27, Philosophy, Psychology

Faculty Mentor(s) or Supervisor(s): David Albert

Title: How Long Is Now?

Abstract: Our experience of time is characterized by a temporally extended present: we perceive motion, change, and succession despite the apparent extensionlessness of the physical present. This creates a longstanding problem for theories of temporal consciousness: how can temporally extended experience arise from a physical reality composed of instantaneous states? Here, I propose that fractal geometry offers a novel framework for addressing this problem. Fractals are characterized by scale invariance, such that their statistical structure remains proportionally constant across different levels of analysis. If temporal consciousness possesses a fractal architecture, then the variability of temporal perception should likewise remain proportionally constant across different temporal scales. To test this prediction, I conducted an exploratory meta-analysis of timing data spanning three established scales of human temporal perception: temporal-order judgment thresholds, temporal windows of integration, and the specious present. Ten reports were randomly sampled at each scale, and the coefficient of variation (CV) was calculated for each report and averaged within scale. The coefficient of variation remained approximately constant across temporal scales, revealing a pattern of scale-invariant variability consistent with the predicted signature of a fractal system. These findings provide preliminary evidence that human temporal perception may exhibit fractal-like organization. More broadly, they suggest a possible framework for reconciling the apparently contradictory properties of physical and psychological time: a static, instantaneous physical reality may give rise to extended temporal phenomenology through a scale-invariant structure in which extension emerges within, rather than across, time.

Karen Garcia SEAS'27, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Anum Glasgow
Title: Designing Tunable Transcription Factors

Abstract: Transcription factors (TFs) regulate gene expression by binding specific DNA sequences. The Lac repressor, for instance, binds the lac operator and blocks transcription, while inducer binding triggers an allosteric change that reduces its DNA-binding affinity. PIGEON-FEATHER uses hydrogen-deuterium exchange mass spectrometry (HX/MS) data to calculate residue-level free energies of opening (ΔG_{op}). These measurements reveal a protein's energetic blueprint, which is the pattern of local stability and flexibility that supports its specific biochemical function. Within LacI/GalR-family TFs, helix H32 is stabilized in the repressed state (DNA-bound) compared to the induced state, suggesting that its energetic properties contribute to allosteric regulation. Building on the foundational work on LacI,

we investigated whether the energetic features that control LacI allostery are conserved across LacI homologs and other transcription factors with related venus flytrap folds. Using AlphaFold3, ProteinMPNN, and Rosetta, we applied a rational design strategy to tune the inducer sensitivity of two *E. coli* sugar-inducible TFs: GalS, and GntR, which are homologs of LacI that have not been structurally and functionally characterized. Our aim is to engineer the H32 helix of these TFs to sample a range of predicted energetic stabilities just as was done with LacI, while determining whether LacI homologs and structurally related transcription factor share conserved energetic blueprints. Through this engineering design project, this work explores whether energetic blueprints can provide a general framework for protein engineering by connecting conformational dynamics to function and guiding the design of poorly characterized proteins using insights from well-studied systems.

Aidan Gavrilu CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Jared Kushner
Title: Exploring the Mechanism of Myogenic Tone Using CaV1.2 and KV1.5 as a Means to Treat Hypertension

Abstract: High blood pressure or hypertension is due to an excessive contraction of certain arteries called resistance arteries and can lead to health complications like stroke and heart failure. Current hypertension medications are not specific to these resistance arteries and can have serious side effects like a lower overall heart function. Vascular contraction is mediated by calcium entry into the cell and as such voltage gated calcium ion channels like CaV1.2 are vital for contraction of these resistance arteries to occur. These channels are negatively regulated by potassium channels. The exit of potassium from the cell causes calcium channels like CaV1.2 to close, thus preventing any further contraction. Whether or not a similar feedback loop occurs with KV1.5 channels, another kind of potassium channel, will be specifically analyzed within this paper as a method to study a vessel specific regulator for hypertension. Unfortunately due to the short time period of this program I was unable to obtain conclusive results but I will utilize our preliminary data to formulate hypotheses. The most exciting possibility is that by removing KV1.5 from the cell will observe unregulated activity of CaV1.2 and thus excessive contraction or even worse hypertension. This would allow a large amount of calcium to enter the cell, continuously stimulating contraction and leading to higher blood pressure. If we found this, not only would it advance our understanding of the mechanism of contraction but it would also enable us to begin synthesizing a vessel specific therapy for hypertension, by increasing vascular expression of KV1.5.

Channels like KV1.5 are far more common in resistance arteries so targeting them specifically, we could hopefully regulate high blood pressure without negatively affecting factors like heart function as a whole.

Maxwell Gaynor CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Edoardo Baldini

Title: What's in a Phase?: A laser-driven study of the semiconductor Nb₃Cl₈

Abstract: The study of strongly-correlated states in 2D materials has grown tremendously in recent years due to its applications in optoelectronics and nanodevices. These applications have intensified the search for new 2D materials with new lattice structures, properties such as ferromagnetism, ferroelectricity, and ferroaxiality, as well as strong electron-electron interactions. However, determining how and when these phases occur in 2D semiconductors remains difficult to predict. Recently, nonlinear optical experiments have quickly become a popular technique to track phase transitions between high-temperature and low-temperature phases. We utilize second harmonic generation micropolarimetry on the material niobium chloride (Nb₃Cl₈) in order to characterize the lattice structure and excitonic response in the material, from cryogenic up to ambient temperatures. The observation of these signals represent the unique changes this material undergoes with light excitation, and the potential for tuning ferroelectricity and excitons within the material. Finally, this study will also provide greater insight into the possible superconducting state occurring in the low temperature phase. The potential for light-induced phases and properties in 2D materials is highly coveted, and future research may entail probing this material optically further in order to discover more about its phases and their relationship with its optical properties.

Dio Gelman CC'29, Germanic Languages, Philosophy

Faculty Mentor(s) or Supervisor(s): Jeremy Dauber

Title: The Historical Necessity of Zionism: Ahad Ha'am and the Limits of Reason

Abstract: The history of modern Jewish thought cannot be separated from the political crises that have shaped modern Jewish life. This paper examines the political philosophy of Ahad Ha'am (Asher Ginsberg), with particular attention to the relationship between reason, history, and national existence in his writings. I argue that Ha'am's account of Zionism rests upon an implicit philosophy of history according to which nations and their characteristic

forms of life emerge through historical development and constitute realities to which political reason must respond. Yet Ha'am does not sufficiently distinguish between historical realities that reason discovers and historical conditions that history itself produces. This ambiguity becomes consequential in his account of Jewish national revival, where the persistence of Jewish national life is treated as a historical necessity without a corresponding argument for why that necessity entails the establishment of a Jewish national center or state. By reconstructing the role of reason in Ha'am's political thought and examining the conception of historical development presupposed by his arguments for Zionism, I argue that his political conclusions depend less upon rational demonstration than upon a Romantic conception of history in which historical development itself acquires normative force. The paper thus situates Ha'am within the history of philosophy while identifying the limits of the philosophical justification he provides for Jewish self-determination.

Alexander Georgiev CC'29, Economics-Statistics

Faculty Mentor(s) or Supervisor(s): Sharon Marcus

Title: A Theory of Literary Character: Character Clustering Methods and Multi-Dimensional Statistical Analysis of Jane Austen's "Pride and Prejudice"

Abstract: Digital humanities often treats narrative attention as a uniform linear construct, frequently compressing the multi-dimensional depth of characters into single-variable word frequencies and simple name mentions. To address this methodological gap, this project models Jane Austen's "Pride and Prejudice" as a closed mathematical system bounded by finite narrative attention. The study projects the novel's cast across a six-dimensional profile space, generating a high-resolution data matrix across all sixty-one chapters. The pipeline integrates Pareto distributions, Principal Component Analysis, and vector clustering to isolate empirical character typologies. These groupings undergo diagnostic testing via multivariate analysis of variance, Mahalanobis distance matrices, and Markov state-transition velocities to evaluate narrative kinetics and structural boundaries. Findings demonstrate that character prominence in "Pride and Prejudice" is not driven by fundamentally different compositional mechanics, but by a direct mathematical function of absolute narrative scaling and multi-component space allocation. Rather than character tiers reflecting distinct qualitative styles, statistical testing confirms clear geometric boundaries across tiers, with localized distance spikes revealing how non-protagonist figures temporarily drive plot transitions. Ultimately, this project introduces a rigorous quantitative methodology to analyze literary structures that have

traditionally been approached through purely qualitative reading. By treating the text as a quantifiable bounded system, this framework offers a reproducible baseline for comparative analysis across broader literary corpora.

David Gima CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Oliver Hobert

Title: Mapping Novel Regulators of Sexually Dimorphic Gene Expression in *C. elegans*

Abstract: Sexually dimorphic gene expression in the nervous system of the nematode *Caenorhabditis elegans* (*C. elegans*) is governed by a well-defined hierarchy of regulatory mechanisms. *nssp-50*, a putative neuropeptide with a sexually dimorphic expression pattern, appears to be regulated independently of these mechanisms. To identify regulators of *nssp-50* expression, complementary candidate-based and unbiased genetic approaches were employed. Mapping crosses were generated between mutagenized strains with disrupted dimorphic expression patterns and the highly polymorphic Hawaiian isolate CB4856, enabling recombination-based mapping to identify candidate causal mutations. In parallel, CRISPR-Cas9 genome editing was used to test candidate mutations in an otherwise wild-type background. This approach identified a point mutation in *ssl-1* that recapitulated the mutant *nssp-50* expression phenotype, establishing *ssl-1* as a regulator of *nssp-50* expression. These findings identify *ssl-1* as a novel component of the regulatory landscape governing sexually dimorphic gene expression in the nervous system of *C. elegans*.

Maria Novella Giobbio GS'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Sheng-Han Kuo

Title: Targeting the Deep Cerebellar Nuclei with Deep Brain Stimulation in the SCA1 Mouse Model ATXN1[82Q] as a Therapeutic Approach to Spinocerebellar Ataxia

Abstract: Spinocerebellar ataxia type 1 (SCA1) is a progressive, autosomal dominant neurodegenerative disorder characterized by cerebellar dysfunction and motor impairment. Currently, no effective treatment exists to alleviate these characteristic motor deficits. This study investigates the therapeutic potential of deep brain stimulation (DBS) targeting the deep cerebellar nuclei (DCN), specifically the dentate, fastigial, and interposed nuclei, to rescue motor deficits in the ATXN1[82Q] mouse model of SCA1. DBS is an

established therapeutic approach for several genetically complex movement disorders, including Parkinson disease, dystonia, and tremor. Additionally, previous DBS studies in animal models and patients with various subtypes of spinocerebellar ataxias (SCAs) have demonstrated motor symptom improvement. However, the lack of standardized stimulation parameters across these studies has hindered the development of effective, translatable clinical protocols.

In this pilot study, an array of five stimulation frequencies (ranging from 10 Hz to 200 Hz) was evaluated in ATXN1[82Q] mice, with motor performance assessed using the balance beam, rotarod, and mirror catwalk assays. Preliminary findings demonstrate that tonic low-frequency stimulation (10 Hz and 30 Hz) produced the most consistent motor recovery, marked by a significant reduction in hind-paw slip count on the balance beam, particularly during fastigial nucleus stimulation. These results suggest that DCN DBS, specifically low-frequency tonic stimulation, represents a viable neuromodulatory strategy to improve cerebellar motor output and provide symptomatic relief in SCA1.

Andrew Glover CC'28, Mathematics

Faculty Mentor(s) or Supervisor(s): Cesar Silva

Title: Exhaustive Weakly Wandering Sets for Group Actions: Tiling a Measure Space

Abstract: Ergodic theory is the study of dynamical systems—a space and a fixed rule, called a transformation, governing how objects in the space change after one unit of time. One can iterate the transformation to see how objects change over the course of time. This research project studies exhaustive weakly wandering sets, which are objects satisfying two key properties. The object never overlaps with past images of itself: the initial object, the object after one iteration of the transformation, the object after two iterations, and the object after, say, one million iterations, are completely disjoint. Secondly, looking at all of the infinitely many copies of the object over the course of time yields the space in its entirety. In this way, an exhaustive weakly wandering set is an infinite tiling of the space. Since to study a dynamical system is to study the iterations of a fixed transformation, a dynamical system can be formalized as what is called a group action, where the group here is the collection of integers. Groups can be much more exotic than the integers—the complex numbers, the group of invertible matrices, and the Heisenberg group are just a few such examples. So, a dynamical system is a group action, where the group can be as strange as one can imagine. It is known, in the classical setting of the integers, that all dynamical systems

admit an exhaustive weakly wandering set. This research project proves that this fact is also true for a large class of groups.

Daniel Gonzalez SEAS'27, Earth and Environmental Engineering

Faculty Mentor(s) or Supervisor(s): Juliana Carneiro

Title: Tuning Carbon Dioxide Hydrogenation Through Nickel Placement and Support Chemistry

Abstract: Carbon dioxide is an abundant greenhouse gas that can also serve as a carbon source for producing useful fuels and chemicals. However, efficiently controlling its conversion remains challenging because catalyst structure and surface chemistry can strongly influence how carbon dioxide reacts with hydrogen. To better understand these effects, we investigated nickel based catalysts using cerium oxide and barium cerate as supporting materials, with nickel either deposited on the surface or incorporated directly into the barium cerate crystal structure. X-ray diffraction was used to examine how nickel changes the structure of each material. While surface deposited nickel produced little change in the underlying supports, nickel incorporated into barium cerate caused a measurable contraction of the crystal lattice, confirming its integration into the structure. Hydrogen temperature programmed reduction was then used to examine how easily each material undergoes reduction. Nickel enhanced the reducibility of cerium oxide, while nickel incorporated into barium cerate produced distinct reduction features associated with changes in nickel state and oxygen vacancy formation. Finally, carbon dioxide temperature programmed desorption showed major differences in surface binding behavior. Cerium oxide displayed mainly weak and medium binding sites, while barium cerate based materials contained substantially stronger sites. Together, these results show how nickel placement and support chemistry can be used to tune the structural, redox, and carbon dioxide binding properties that govern catalytic hydrogenation.

Morgan Greenlaw CC'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Mijo Simunovic

Title: Organoid Model of the Human Yolk Sac Shows Blood Emergence

Abstract: During human development, there are several extraembryonic structures that play a critical role facilitating proper embryonic development, one of which is the yolk sac. The yolk sac is responsible for early gas and nutrient exchange between the mother and fetus, as well as being the site for

hematopoiesis, which is the process in which vasculature and blood cells first develop. Malformations of the yolk sac can lead to miscarriages and blood disorders, but these processes are not yet fully understood because our understanding of the yolk sac is limited. Mouse models present significant physiological differences between mice and humans, and human yolk sac samples are challenging to obtain and pose significant ethical questions. In this study, we established an in vitro organoid model of the human yolk sac by aggregating and differentiating human pluripotent stem cells (hPSCs). Immunofluorescence staining for FOXF1, GATA6, and CD31 revealed an outer FOXF1+ mesodermal layer containing CD31+ vascular structures surrounding an inner GATA6+ endodermal layer, consistent with human yolk sac anatomy. This model could serve as a scaleable, physiologically relevant model of the human yolk sac to further investigate the process in which vasculature and blood cells develop to better understand the underlying mechanisms behind how the yolk sac contributes to miscarriages and blood disorders.

Sherry Guo CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Laura Kaufman

Title: Mapping 2D Morphology to 3D Tissue Fluidity

Abstract: This study investigates whether 2D monolayer morphology can accurately predict 3D tissue fluidity. Nuclear size, shape, and stiffness are known to influence a cell's ability to migrate through confined spaces, making monolayer morphology an attractive but understudied proxy for tissue-scale behavior. Epithelial (MCF10A) and mesenchymal-progressed (MCF10DCIS.com) breast cancer cells were compared, using Trichostatin-A (TSA) to soften nuclei and blebbistatin to reduce actomyosin contractility. Fluidity was assessed via 3D multicellular spheroid coalescence, while morphology was characterized using both standard in-plane and out-of-plane 2D measurements. Results showed that lower 2D nuclear occupancy in DCIS cells successfully predicted their increased 3D spheroid fluidity. Softening 10A nuclei with TSA also enhanced 3D fluidity. However, capturing this TSA-induced deformation required out-of-plane Z-axis quantification, as softened nuclei expanded vertically rather than horizontally in 2D monolayers, a discrepancy not captured by the standard in-plane nuclear aspect ratio. Conversely, reducing contractility with blebbistatin in DCIS cells yielded contradictory 2D morphological markers and resulted in minimal changes to overall 3D spheroid fluidity. The findings indicate that while 2D morphology largely maps to 3D fluidity, out-of-plane morphological quantification is essential due to differing confinement conditions between

monolayer and spheroid systems. These results underscore the need for careful morphological analysis when using 2D systems to predict 3D tissue-scale dynamics.

Tanmay Gupta CC'27, Physics, Mathematics

Faculty Mentor(s) or Supervisor(s): Kerstin Perez

Title: Developing a Lithium Evaporation and Diffusion Process to Fabricate Si(Li) Detectors for the General Antiparticle Spectrometer

Abstract: While astrophysical observations suggest that dark matter makes up a majority of matter in the universe, its identity remains a mystery. The General Antiparticle Spectrometer (GAPS) is the first experiment optimized to search for low-energy cosmic antiparticles as indirect signatures of dark matter. GAPS recently completed its first flight during the 2025/26 NASA Antarctic balloon campaign. At the heart of the GAPS payload is the tracker, assembled from over 1000 custom 8-strip lithium-drifted silicon (Si(Li)) detectors. For future flights, fabricating new detectors will improve the instrument's sensitivity. The Perez Lab is currently developing techniques that will support in-house fabrication of Si(Li) detectors, allowing for the exploration of custom detector geometries and the implementation of cost-saving methods. This work details the development of a custom setup for lithium evaporation and diffusion, one of the first steps in detector fabrication. Under vacuum, a current running through a tungsten boat heats Li, resulting in evaporation. The Li particles condense onto a silicon wafer mounted above the boat. A PID-controlled ohmic heater keeps the wafer at a high temperature, allowing for Li diffusion into the wafer. To validate the process, a copper staining method is used. Through an electrochemical displacement plating process, copper selectively stains regions with greater concentrations of Li, allowing for measurement of the depth of the diffused layer. The development of these techniques will contribute to an optimized and reproducible Si(Li) detector fabrication process, supporting future GAPS flights.

Blake Hammond CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Saravanan Ganesan

Title: Acute Myeloid Leukemia Driver Investigation

Abstract: Fusion oncoproteins are abnormal proteins created when parts of two genes become joined. In some forms of acute myeloid leukemia, these proteins gather into dense cellular compartments called condensates, which

can help control gene activity and support cancer cell growth. Recent work has shown that a small 17-amino-acid peptide, known as a kill switch, can be directed to specific condensates using a protein-targeting nanobody. Once recruited, the kill switch changes the physical behavior of the condensate by reducing protein movement within it. These changes can disrupt gene regulation and slow the growth of leukemia cells.

This project investigates how targeting different leukemia-associated condensates with the kill switch changes the organization and activity of the cancer cell genome. Two acute myeloid leukemia cell lines were developed with VHH05-based and ALFA-based targeting systems, allowing the kill switch to be directed to different condensate-forming proteins. The engineered cell lines were characterized using several molecular biology approaches, including DNA accessibility sequencing, which identifies regions of the genome that are open and available for gene regulation. By comparing cells with and without active kill switch targeting, the study aims to determine how changing condensate properties reshapes DNA accessibility and gene regulatory programs. This work may clarify how condensates support leukemia and could help identify new ways to disrupt cancer-promoting cellular organization.

Isabella Haslinger Johnson CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Christine Chio

Title: PKM2 Oxidation Acts as a Redox Switch Governing PDAC Progression

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is a detrimental disease that develops in a nutrient-poor, poorly perfused microenvironment, driving strong selective metabolic adaptation. Primary PDAC tumors exhibit decreased tricarboxylic acid (TCA) cycle activity compared to metastatic lesions, suggesting metabolic remodeling during progression. Reactive oxygen species, which can act as intracellular messengers in addition to indiscriminate damaging agents, accumulate in tumors and alter target protein function. Oxidation of methionine 239 (M239) stabilizes the high-activity tetrameric form of pyruvate kinase M2 (PKM2), while methionine sulfoxide reductase A (MSRA) reverses this modification via reduction. MSRA loss increases PKM2 activity and metastatic progression. A tissue-specific PKM-M239L knock-in mouse model was crossed with a genetically engineered mouse model of PDAC (KrasG12D;Trp53R172;PdxCre - KPC), and 2D and 3D cells were derived from resulting KPC-PkmM239L animals expressing

the redox-insensitive PKM-M239L leucine mutant specifically in pancreatic epithelial cells. KPC and KPC-PkmM239L cells were examined to determine whether PKM2's methionine redox status regulates glucose metabolism. It is hypothesized that PKM2-M239 oxidation promotes oxidative glucose metabolism and metastasis. Preliminary experiments demonstrate that KPC cells expressing PKM2-M239L have reduced pyruvate kinase activity. [U-¹³C₆]-glucose tracing will determine whether preventing M239 oxidation reduces glucose-derived carbon entry into the TCA cycle. The expectation is that PDAC cells with redox-insensitive PKM2-M239L will exhibit less pyruvate entering the TCA cycle. These studies will establish whether PKM2 methionine oxidation links redox signaling to metabolic reprogramming during PDAC progression.

Jillian Heath SEAS'27, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Vijay Vedula

Title: Coronary Microvascular Resistance and Sex-Based Disparities in the Assessment of Coronary Artery Disease

Abstract: Cardiovascular disease, including coronary artery disease (CAD), is the leading cause of death among women globally and in the US. Accurate patient-specific assessments are required to guide decisions about further tests and surgical interventions, and severe cases can go undiagnosed. Coronary microvascular dysfunction (CMD) is prevalent in patients with CAD, especially in women, leading to restrictions or abnormal flow that can cause ischemia through mismatches in oxygen supply and demand. The increased prevalence of CMD in women may be linked to research showing that women tend to have significantly higher coronary microvascular resistance (CMVR) than men. This study investigates whether sex-related differences in CMVR may influence CAD assessment and contribute to diagnostic disparities. A multiscale 0D-3D coupled model that incorporates myocardial motion from patient-specific CT images is used to simulate hemodynamics and calculate indices such as instantaneous wave-free ratio (iFR), a pressure-based index used in clinical applications to assess the significance of coronary artery stenoses and guide revascularization decisions. CMVR is systematically varied in our model to determine whether higher values alter the proximity of iFR to the clinical threshold for intervention. This ongoing work will characterize iFR sensitivity to CMVR and evaluate whether sex-related differences in coronary microvascular resistance could contribute to disparities in the physiological assessment and diagnosis of CAD.

Mendi Hecht GS'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Chris Murphy

Title: Introducing Generative AI Tools into an Intermediate-Level CS Course

Abstract: Generative AI tools are becoming essential in professional software development, yet most computer science courses prohibit students from using them on programming assignments. This research, conducted under Professor Chris Murphy in Columbia's Department of Computer Science, asked how an intermediate course could teach students to both produce good code with AI and judge whether AI generated code is correct. To answer this, the project developed and tested assignments for COMS 3107W, Software Quality and Design, an intermediate Java course. One assignment has students write detailed instructions for AI to produce a word counting program and then check the result against the course's design principles. A second gives students a program with four planted flaws. One flaw lets other code improperly access internal data. Another causes a bug when items are removed from a list while looping through it. Students write their own tests to catch each flaw before fixing the program with AI help. A comparison of Claude, ChatGPT, and Gemini found no difference on a simpler task, where all three produced correct code. On the larger project, they diverged. Claude and ChatGPT stored data flexibly, without tying it to a specific method, while Gemini used a rigid method that exposed internal details that other code did not need to see, then skipped a safety check and crashed the program on a bad file. The assignments are ready to use in the course. The comparison gives instructors evidence for which AI tools are reliable enough to recommend to students.

Terrance Heng GS'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Rudy Behnia

Title: Establishing and validating a single-hydrogel protein-retention expansion microscopy pipeline for quantifying presynaptic active zones in the *Drosophila* mushroom body

Abstract: Learning is thought to be stored as physical change at synapses, and in the *Drosophila* mushroom body this change is well characterised functionally: reinforcing dopaminergic input depresses the synapses that Kenyon cells make onto mushroom body output neurons. Whether this functional depression is accompanied by a change in the number of synapses is unknown, because existing evidence reports synaptic strength rather than

synapse number, and counting synapses between identified neurons has required low-throughput electron microscopy. Expansion microscopy (ExM) offers an alternative by physically enlarging fixed tissue so that individual presynaptic active zones become resolvable by conventional light microscopy. Here we establish and validate a single-hydrogel, protein-retention ExM pipeline for the whole adult *Drosophila* brain. Hydrogel diameter, brain-to-brain comparison, and feature-to-feature scaling across a five-fold size range converge on a linear expansion factor of 3.93 $\times$, indicating accurate and approximately isotropic expansion. Expansion resolves individual Bruchpilot puncta that are merged in conventional immunohistochemistry and achieves a median effective resolution of $\sim$ 73 nm. Applying a fixed-parameter pipeline for automated three-dimensional counting, we find preliminarily that multisensory-trained brains contain fewer Brp puncta than olfactory-trained brains, based on limited brains. If confirmed against untrained controls, such a reduction would indicate that learning-related synaptic depression is structurally instantiated, and that stronger, multisensory memories are accompanied by greater synapse elimination.

Makaila Hernandez CC'29, Chemistry

Faculty Mentor(s) or Supervisor(s): Jerry McManus

Title: Orbital-Scale Variability in Eastern Equatorial Pacific Thermocline Depth Over the Last 40 ka

Abstract: The depth of the thermocline in the Eastern Equatorial Pacific (EEP) plays a key role in ocean-atmosphere interactions and influences variability in the El Niño Southern Oscillation (ENSO). However, previous reconstructions of EEP thermocline variability may be influenced by their proximity to the South American margin and by the use of different species of planktic foraminifera as thermocline proxies. To investigate this we analyzed the δ 18O in planktic foraminifera species that inhabit the near-surface (*Globigerinoides ruber*) and thermocline (*Neogloboquadrina dutertrei*) depths in the water column, using deep-sea sediment samples spanning the last 40 ka from ODP Site 847D, located west of the Galapagos (0° 11.6' N, 95° 19.2' W, 3335.2 m). The differences in δ 18O between these species were used to reconstruct changes in upper-ocean stratification and thermocline depth. We find that the variance in the EEP thermocline's deep and shallow states broadly correspond to changes in equatorial insolation, suggesting that orbital forcing influenced upper-ocean structure on late Quaternary timescales. Specifically, thermocline shoaling coincides with maxima in equatorial insolation. These variations are accompanied by changes in sea surface

temperature and productivity, indicating a strong relationship to tropical Pacific ocean circulation. Altogether, these findings provide new constraints on thermocline variability in the EEP, and suggest that orbital forcing influenced the ocean conditions that regulate tropical Pacific climate and ENSO variability.

Aiden Hightower CC'28, Physics

Faculty Mentor(s) or Supervisor(s): Raquel Queiroz

Title: Rebuilding a Model of Topological Electrons as Groundwork for Investigating the Quantum Metric of Light-Driven Materials

Abstract: Topological insulators are materials that electrically insulate in their interior while exhibiting conduction without losses on their edges. This edge conduction does not depend on the local details of the material but instead on a global geometric property of its electron states, an integer-valued topological invariant, which is robust against disorder and imperfection. In this project, the original theoretical model that displays this effect, proposed by Duncan Haldane, was computationally rebuilt from first principles on a honeycomb lattice of atoms (graphene). The electronic band structure for a sheet of infinite graphene, a zigzag ribbon geometry, and an armchair ribbon geometry was reproduced, and it was confirmed that the conducting edge states only appear when the model is in the topological phase. This work also mapped out how two deeply related geometric quantities evolve across momentum space: the curvature of electron states (Berry curvature) and the rapidity at which electronic states change (quantum metric). The former property was used to create a phase-space diagram of Chern number—which determines the quantized Hall conductance—which demonstrates the location of phase diagram transitions. These results reproduce an established theoretical model; their purpose was to build a verified computational benchmark and develop a working fluency in topological condensed matter. The next step is to model the same graphene lattice under a periodic drive by circularly polarized light, which can induce a topological phase with no static counterpart, and to determine whether existing definitions of the quantum metric for time-periodic systems accurately describe the system's physics.

Percy Hillier GS'28, Anthropology

Faculty Mentor(s) or Supervisor(s): Judith Pajo

Title: Taking it to the Pews: Faith, Justice, and Activism Amongst Brooklyn's Progressive Christians

Abstract: The Episcopal Church has undergone significant ideological changes that emphasize a liberal theology and social justice since the 1960s regarding issues of race, gender identity, sexuality, and abortion, challenging certain social norms historically commonplace within Christian communities in doing so. To explore how progressive Christians might reconcile the contradictions presumed to exist between their political convictions and faith, I conducted ethnographic research on two Episcopal parishes located in Brooklyn, New York City. Using semi-structured interviews with parishioners and participant observation as my main methodologies, I found that specialty sermons, diversity-focused programming, fundraisers, and volunteer efforts in underserved communities were embraced by parishioners as integral facets of the church experience. Activist modes of faith enriched parishioners' faith by allowing them to actualize their socially informed Christian beliefs in contexts removed from the church building, fostering a holistic spiritual identity wherein the religious and temporal inform one another. Popular assumptions of religious communities as wholly conservative or unconcerned with secular life are thus contested here. Building upon the theory popularized by anthropologist Talal Asad's seminal *Formations of the Secular*, my findings additionally strengthen notions of the "secular" itself as inextricable from faith; in fact, it can be a vital part of a believer's religiosity.

Norie Hirai SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Danwei Huangfu
Title: Temporal Control of Transcription Factor Overexpression to Enhance Human Embryonic Stem Cell-Derived β -Cell Maturation

Abstract: Human embryonic stem cell (hESC)-derived pancreatic β cells offer tremendous potential for disease modeling, drug screening, and regenerative therapies for diabetes. Although current hESC protocols can efficiently generate β -like cells in vitro, these multi-step differentiation protocols are time consuming, and generated cells frequently exhibit functional immaturity and cellular variability, limiting their ability to fully recapitulate adult human β -cell physiology. Transcription factor (TF) directed differentiation in several other cell types has been able to successfully overcome these limitations. Inspired by these, the Huangfu lab has been working on protocols to achieve TF-directed beta cell differentiation. However, the current protocol lacks important genes found in functionally mature beta cells. This project aims to investigate whether temporally overexpressing key transcription factors regulating the expression of these genes can bring us closer to a beta cell transcriptome. To enable precise temporal control of transcription factor

activity, tamoxifen-inducible transcription factor-estrogen receptor (TF-ER) fusion constructs were generated and introduced into human ESCs to establish stable inducible cell lines. This platform allows TF overexpression by controlling its timing of nuclear localization, enabling investigation of the optimal order of TF overexpression. Stable inducible cell lines expressing candidate transcription factors, ISL1 and NKX6.1, have been successfully established. Ongoing work is focused on validating tamoxifen-induced nuclear localization of the TFs, followed by differentiation studies to evaluate the effects of temporally controlled TF activation. Additional inducible constructs, PAX4 and MNX1, are currently being developed to expand the platform. By systematically investigating the timing of transcription factor activation, this platform has the potential to improve the efficiency of generating ESC-derived beta cells for in vitro use.

Margaret Hitt SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Stephen Lantin
Title: Automated Image Analysis for High-Throughput Screening of Microgreen Cultivars for Bioregenerative Life Support

Abstract: NASA's Moon Base initiative aims to establish sustained human presence on the lunar surface; bioregenerative life support systems (BLiSS) offer a promising route to support astronaut dietary health. Microgreens are candidate BLiSS crops for rapid, on-demand food production, harvestable within 1–3 weeks of seed imbibition and containing higher vitamin, mineral, and antioxidant concentrations than their mature counterparts. This project develops a computer vision screening algorithm to identify cultivars compatible with NASA Ames spaceflight hardware, including BioSensor—a microfluidic optical platform for microbial biology beyond low Earth orbit—and Lunar Plant Growth Experiment (LPX) hardware. These platforms activate organisms in small volumes, requiring biocompatible cultivars. Under NASA's Crop Readiness Level (CRL) framework, cultivar selection depends on seed/seedling morphology and on germination and cotyledon rates fast enough to meet mission timelines. These rates serve as a proxy for seed vigor, prioritizing high-vigor cultivars as spaceflight candidates. Fifty-eight microgreen cultivars from a commercial seed company were imbibed in half-strength Murashige and Skoog medium in 96-well half-volume microtiter plates (24 wells/cultivar, 4 cultivars/plate). Plates were incubated at 24 °C under continuous white light (100 $\mu\text{mol m}^{-2} \text{s}^{-1}$ PAR) for 14 days and imaged hourly on a flatbed scanner. A custom high-throughput image-analysis algorithm using nearest-color pixel classification detected germination and cotyledon emergence and calculated the rate of each

transition, validated against ground-truth visual annotation of a subset of plate images. Based on the resulting confusion matrix, the algorithm accurately classified germination of the radicle ($F1 = 0.854$) and cotyledon emergence ($F1 = 0.907$). Computer vision scoring of the cultivar screen identified ten cultivars with early onset and rapid rates of both transitions. This work demonstrates that high-throughput image analysis can accurately pre-screen BLiSS crop candidates and yields image-processing approaches transferable to future space-biology experiments.

Reina Hneidi GS'27, Political Science

Faculty Mentor(s) or Supervisor(s): Khatchig Mouradian
Title: Midwifery and the Birth of the Modern Middle East

Abstract: The history of midwifery and women's health in the modern Middle East is difficult to trace through conventional archival methods. Relevant Arabic-language materials from the nineteenth and early twentieth centuries are scattered across books, newspapers, journals, and medical periodicals, many of which are incompletely digitized or poorly indexed. These limitations can obscure both the historical experiences of women and the ways knowledge about midwifery and maternal care circulated within society. As part of Midwifery and the Birth of the Modern Middle East, this research examined Arabic-language primary sources from approximately 1850 to 1950 relating to midwifery, childbirth, and women's health. Archival materials were identified and evaluated, and relevant passages were extracted and translated into English. The resulting data were systematically recorded. Sources included medical and scientific publications as well as newspapers, journals, books, and other forms of print culture. While explicit references to practicing midwives appeared less frequently than anticipated, discussions of pregnancy, childbirth, breastfeeding, infant care, menstrual health, postpartum recovery, nutrition, and maternal well-being were present across a surprisingly broad range of publications. These findings suggest that, while they cannot always be perfectly reconstructed, the histories of midwifery and reproductive care can be gleaned through the wider circulation of medical, social, and cultural knowledge surrounding women's health. The project also contributed to Connectivity and Individuality in Textual Traditions: Reimagining Scalable and Evidence-Based Approaches for Inclusive and Transformative Humanities Computing, an initiative funded by Schmidt Sciences. Computer scientists were able to use the translated materials to refine a large language model, striving to improve retrieval of foreign-language historical sources. The archival challenges encountered throughout the research—particularly inconsistencies in digitization and poor text

recognition—demonstrate the limitations of conventional keyword-based search for multilingual humanities scholarship. By combining historical analysis and translation with computational methods, this project contributes both to the study of women's health in the modern Middle East and to broader efforts to develop AI tools that can expand access to underrepresented archival materials while remaining attentive to questions of authenticity and cultural representation.

Libby Hod CC'27, Psychology

Faculty Mentor(s) or Supervisor(s): Randy Auerbach
Title: SHIFTing Rumination in Depressed Teens: Preliminary Approaches and Stakeholder Feedback on a CBT-based Smartphone App

Abstract: Rumination consists of repetitive negative thoughts about the past, focused on unachieved goals or negative self-perceptions. In teens with depression, rumination contributes to the onset and maintenance of depression by encouraging avoidance and worsening mood. Contemporary Cognitive Behavioral Therapy (CBT) approaches treat rumination as a modifiable behavior through the lens of functional analysis, examining its antecedents and effects while shifting processing styles toward distraction and problem solving. Engaging teens with these skills in their daily lives requires scalable detection methods; passive language monitoring using natural language processing offers an avenue for identifying shifts in negative self-talk that may signal increased rumination. The present study combines CBT treatment components with these methods to build Smartphone Helper for Individual Flexible Thinking (SHIFT), an app that passively monitors text messages to approximate rumination and deliver guided distractions and problem-solving just-in-time. Following user-centered design principles, Phase 1 of this study focuses on understanding stakeholder needs and perspectives on SHIFT. We designed digital mock-ups of distraction and problem-solving skill trainings and are conducting formative interviews with teens with lived experience of depression as well as providers. Interviews are being analyzed using rapid qualitative methods. Findings will describe how existing therapy components were adapted, how mock-ups were refined, and preliminary quotes and themes from two adolescent interviews, informing design priorities to optimize SHIFT's acceptability and usability. This user-centered approach lays the groundwork for scalable interventions supporting depressed teens when they are ruminating.

Ye min Hong GS'28, Human Rights

Faculty Mentor(s) or Supervisor(s): Ted Perlmutter

Title: What the Press Covered: A Corpus of News Reporting on Federal Immigration Memes

Abstract: In 2025, federal agencies including the Department of Homeland Security and Immigration and Customs Enforcement used internet memes on their official social media accounts to communicate immigration enforcement policy. A research project supervised by Professor Ted Perlmutter at Columbia University's Institute for the Study of Human Rights examines what this shift means for government communication. As a research assistant, the researcher built the record of how the press covered these posts. The researcher ran and logged seventy-three database and archive searches, assembling 119 articles from six news organizations across the political spectrum. Each article was sorted into one of three tiers: coverage of a government post itself, coverage of the debate over "heritage Americans," or coverage of the online nativist movements where they touch immigration or national identity. Queries returning nothing were logged so the search could be reproduced, and the corpus was revised across rounds of faculty review. Sorted this way, the corpus showed that outlets were not covering the same thing. At two conservative publications, fewer than a fifth of the articles addressed a government post directly; the rest took up the heritage debate and the online movements. At two daily papers, more than half addressed the posts themselves. Outlets on opposing sides responded to different aspects of one phenomenon, one treating the posts as government messages to report, the other as a symptom of an argument underway on the right. The corpus makes it possible to compare how these outlets treated the same posts.

Yushi Hu GS'28, Earth Science

Faculty Mentor(s) or Supervisor(s): Matthias Sinnesael

Title: Viability of using Irish pollen records to reconstruct seasonality throughout the Holocene

Abstract: Reconstructions for Holocene climate in Ireland have been attempted from a number of proxy records, but few have been validated against instrumental data recorded during overlapping periods, leaving their validity uncertain. This study, using both weighted average-partial least squares (WA-PLS) and the modern analogue technique (MAT), reconstructs June-July-August (JJA) and December-January-February (DJF) temperature and precipitation across the Holocene from 8 Irish pollen stratigraphic sites and chronologies obtained from the Neotoma Palaeoecology Database, trained on data from version 2 of the European Modern Pollen Database

(EMPD2). These reconstructions are then compared directly to instrumental data from the Armagh Observatory, as well as reconstructions from other proxy records, to assess their validity. Results indicate that JJA temperature is most reliably reconstructed from pollen, despite DJF temperature yielding superior cross-validation performance. Precipitation reconstructions suffer from substantial systematic overestimations, though relative trends show consistencies to that of instrumental and other proxy records. Taxonomic harmonizations of pollen heavily affect WA-PLS reconstructions, leading to considerable systematic deviations. Selecting statistically informative taxa and filtering noise led to improved cross-validation performance, though this fails to produce more accurate reconstructions. MAT suffers from weak analogues and no-analogue sections and does not achieve the same level of precision as WA-PLS. These results show potential for trend-based precipitation reconstructions from pollen using WA-PLS, despite weak cross-validation performance. Further research on alternative reconstruction mechanisms and optimizing training data may provide valuable insight.

Viela Hu CC'27, Art History, Visual Arts

Faculty Mentor(s) or Supervisor(s): Laura Neitzel

Title: Plotting Memory: Recorded Footage and Generative A.I. in Ayoun Kim's AI Mather Plot 1991 (2025)

Abstract: Since the early 2010s, artists such as Trevor Plagen and Hito Steyerl have been using computer image generating tools, especially artificial intelligence (A.I.), to create. At stake now is how generative A.I. redoubles the logic of the traditional archive and production of historical knowledge, especially the erasure or suppression of undesired personal lived histories. Ayoun Kim's single-channel video AI-Mather Plot 1991 (2025) presents a mixture of recorded footage with A.I.-generated image-to-video and image-to-text footage as a novel form of the archive. The recorded and generated materials render visible the underrepresented history of Korea's modernization through international construction projects, which Kim's father was a part of, in Saudi Arabia during the oil crisis of the 1970s. Reading against dominant literature on the work as an interrogation between fiction and non-fiction, Hu focuses on how Kim's video reveals the way the imagined is part of reality, and how AI can be used to visualize memories of unrealized modernizing futures and distant traumatic pasts of war and alienation that continue to make up present subjectivities fused with disillusionment and nostalgia. Employing Michael Rothberg's notion of multidirectional memory, Hu shows that Kim's mixed footage reconnects, her recollections with that of present residents in the AI-Mather apartment complex in Saudi Arabia,

suggesting the present's inseparability from the past across national borders. Kim's archival work evokes past forms of the military-industrial complex to deconstruct the invisible regimes of control that A.I. is a part of and remobilizes A.I. to render visible interconnected lived histories at the threshold of being forgotten.

Mohan Hu CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Amy Rumora

Title: The Effects of Dietary Fatty Acids on Neuroinflammation, Lipid Metabolism, and Cognitive Behavior

Abstract: Alzheimer's disease (AD) is a prevalent neurodegenerative disorder characterized by progressive cognitive decline. Increasing evidence suggests that metabolic dysfunction contributes to AD pathogenesis, and dietary lipids may influence disease risk. However, the distinct effects of saturated fatty acids (SFAs) and monounsaturated fatty acids (MUFAs) on microglial function and AD-related pathology remain poorly understood. To investigate these effects, we used both in vitro and in vivo approaches. Human monocyte-derived microglia-like cells (MDMi) were treated with palmitate (SFA) and oleate (MUFA), while mice fed a high-fat diet (HFD) were used to assess cognitive function. Cell viability was evaluated using the CellTiter-Glo assay, changes in AD-associated lipid metabolism and inflammatory genes were measured by quantitative PCR (qPCR), and lipid droplet formation was visualized using confocal microscopy. Cognitive performance was assessed using the Y-maze test. Our results demonstrate that saturated and monounsaturated fatty acids exert distinct effects on microglial biology. Palmitate induces cytotoxicity, promotes neuroinflammation, and alters the expression of AD-associated lipid metabolism genes, whereas oleate attenuates many of these effects. Furthermore, dietary fatty acid composition is associated with differences in cognitive performance in mice. Together, these findings suggest that fatty acid composition differentially regulates microglial function and may influence AD-related pathology, providing insight into the mechanisms by which dietary fatty acids contribute to AD development.

Jake Huang CC'29, Physics

Faculty Mentor(s) or Supervisor(s): Dmitri Basov

Title: Entangled Photon Microscope for Low-Flux Two-Photon and Non-Local Imaging

Abstract: Two-photon absorption (TPA) uses two longer-wavelength photons absorbed within femtoseconds of each other to excite a sample to a higher energy level rather than a single, shorter-wavelength photon, revealing quantum states and novel material properties typically unobservable with single-photon techniques. However, to ensure photon pairs arrive within a femtosecond window, classical TPA uses high-intensity, short-pulsed lasers that may damage materials or degrade spectral resolution. Entangled photon pairs present an opportunity to overcome many of the disadvantages associated with TPA. Because entangled photons possess strong temporal and spatial correlation, they are predicted to enable excitations at intensities that are orders of magnitude below classical requirements. This work presents the design and construction of an entangled photon microscope that capitalizes on these properties for low-flux fluorescence imaging. In the microscope, correlated photon pairs at 810 nm that are generated by spontaneous parametric down-conversion (SPDC) reach the sample plane through fiber-coupled optics. The resulting fluorescence is then collected on avalanche photodiode (APD) detectors in single-photon counting mode. As a first test, a classical 660 nm pilot laser validates the excitation and detection pathways by exciting emitters that fluoresce around 810 nm, which matches the down-converted entangled photons. In addition to TPA, the entangled photon microscope can perform non-local imaging, or “ghost” imaging, where correlations between a signal photon that probes the material and an idler photon that never directly interacts with the material reconstruct a sample image.

Yuxin Huang CC'27, Anthropology, Political Science-Statistics

Faculty Mentor(s) or Supervisor(s): Maria José de Abreu

Title: A Never-Ending End: The Making of Potential in Portugal's Startup Ecosystem

Abstract: In the aftermath of the 2008 financial crisis, Portugal turned to innovation as the solution to austerity's heavy blow. What followed was the creation of a thriving startup landscape in Lisbon, a process still taking shape a decade later. The goal was said to create not only the landscape, but wealth, abundance, future, and most of all, potential. Where, and out of what, however, could things this intangible be conjured from nothing? While the Latin root of innovation, innovare, refers to the act of renewing, what exactly was being made new? Drawing on ten weeks of fieldwork, this research approaches the intangible promises of Lisbon's startup ecosystem through

their tangible bodies: the biological and digital human bodies surfaced in discussions around longevity, cryonics, and Web3, and the post-industrial body of concrete standing at Lisbon's coastline that is Unicorn Factory Lisboa. It explores the co-constitutive nature of the old and the new as displayed through these bodies. Between them opened a space of passage, suspended and incomplete yet nonetheless generative, full of nothing but potential—where potential itself, rather than what it might realize, has become the wealth, the abundance, the future, and a never-ending end capable of solving the apocalypse the world and individual lives are seeing. The findings of this research are contributing to Professor Maria José de Abreu's project on Portugal's Startup Ecosystem, in hope of providing a grammar for articulating the making of potential and the economics surrounding it at a time of global crises.

Lan Huse SEAS'27, Electrical Engineering

Faculty Mentor(s) or Supervisor(s): Eliot Felske

Title: Hardware Setup of Pellet Injection Test Stand to Measure Ablation Characteristics

Abstract: Cryogenic Pellet Injection is used in nuclear fusion experiments for fueling, density control, and mitigating dangerous disruptions. Gas is frozen into a cylindrical “pellet” and fired at high speeds into the hot plasma at the center, where it breaks apart, ionizes, and is incorporated into the reaction. Understanding the methods of how the pellet erodes – or “ablates” – once entering the plasma is essential for the application to larger fusion experiments with higher fueling requirements and disruption risks. Pellets At Columbia (PAC) is a test stand developed to investigate cryogenic pellet ablation in a controlled environment, using an electron beam to emulate plasma conditions. 8.1mm diameter pellets are fired up to 150 m/s under a perpendicularly-positioned electron beam. To characterize pellet ablation, a high-speed camera measures deflection after contact with the electron beam, and pellet volume is quantified before and after the ablation chamber. Both diagnostics are important in determining mass change due to pellet erosion under the electron stream. Ablation characteristics will be observed for both single-species pellets and two-species mixed pellets. Species include Hydrogen and Deuterium, which are important for fueling the reaction, as well as Neon and Argon, which are relevant for disruption mitigation. Reliable mixing, freezing, and firing procedures have been developed across the production of more than 400 Hydrogen and Neon pellets.

Lila Hussein CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Matthias Quick

Title: Establishing an Experimental Framework for the Functional Characterization of Vesicular Glutamate Transporters

Abstract: Glutamate is the major excitatory neurotransmitter in the central nervous system, and dysfunction of its synaptic transmission is implicated in various neurological and psychiatric disorders, including schizophrenia, depression, and compulsive disorders. Vesicular glutamate transporters (VGLUTs) are transmembrane proteins essential for packaging the neurotransmitter glutamate into synaptic vesicles. VGLUTs transport multiple substrates, including glutamate and phosphate. This activity is thought to depend on ion gradients and membrane conditions, but the mechanisms underlying their environment-dependent substrate specificity are not fully understood. Prior work in the Quick Lab demonstrated that *Drosophila* VGLUTs can transport zinc, raising the question of how the proteins recognize and transport different molecules. This study aimed to establish an experimental framework for investigating the biochemical properties of VGLUTs in a controlled membrane environment. Recombinant VGLUT proteins were produced in *Drosophila* cells; initial work focused on validating core techniques required for membrane protein analysis, including protein isolation, detergent-based solubilization, affinity purification, and quantitative absorbance assays. Isolated protein samples were analyzed with gel electrophoresis and color-based protein assays to estimate purity and concentration. These proteins were subsequently concentrated and incorporated into artificial lipid membranes, creating proteoliposomes that provide the controlled membrane environment necessary for further investigation. The study established the framework for purifying, characterizing, concentrating, and preparing VGLUTs for experimentation, allowing for the investigation of the mechanisms VGLUTs employ as they transport various substrates. Understanding these transport mechanisms may provide insight into how membrane proteins regulate communication between neurons and help clarify the role their dysfunction plays in neurological and psychiatric disorders.

Mabel Ince GS'28, Earth Science

Faculty Mentor(s) or Supervisor(s): Andrei Kurbatov

Title: Verifying Automated Hyperspectral Imaging Data Processing for Allan Hills Ice Core 2501

Abstract: Ice cores provide a continuous record of past climate, preserved in layers that accumulate over time. Studying the bubbles and dust trapped within the ice can reveal information about past atmospheric conditions and how the ice formed. Hyperspectral Imaging (HSI) offers continuous, non-destructive, and high-resolution characterization of ice cores by capturing reflectance spectra across hundreds of contiguous wavelength bands, enabling the detection of impurities within the ice. During the July 2026 COLDEX Core Processing Line at the National Science Foundation Ice Core Facility, a HSI system was used to scan the 330-meter ALHIC2501 ice core in meter-long sections. The resulting raw data were processed using an open-source Python algorithm that detects individual air bubbles, measures their size, shape, and spectral properties, and compiles this information into profiles showing how these characteristics change with depth. The program then flags depth intervals that appear statistically unusual compared to their surroundings, based on bubble abundance, shape, and spectral qualities. This project evaluates the accuracy of this automated processing pipeline. Manually cross-checking the flagged anomalies and bubble measurements against the original scan imagery across ALHIC2501 assesses how accurately the program identifies stratigraphic layers, visible layering, and bubble characteristics. Identifying where the algorithm's analysis does and does not align with independently observed features indicates where manual review remains necessary. This quality-control process is essential for building confidence in HSI data processing as a reliable and rapid tool for near-real-time ice core characterization, and for guiding refinements to detection thresholds.

Maryam Isayeva CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Jianlong Wang
Title: Investigating the Role of TEX10 in Maintaining Naive Embryonic Stem Cells

Abstract: Background: Embryonic stem cells can exist in different developmental states, including a naive state that resembles an earlier stage of the embryo and a primed state that is further along toward specialization. TEX10 is a protein known to support stem cell self renewal, but whether it is especially important for maintaining the naive state remains unclear. Methods: This experiment compared human and mouse embryonic stem cell models. Human cells were tested in several culture conditions designed to induce naive characteristics. Because these conditions did not produce stable naive cultures, the effect of TEX10 loss could not be reliably evaluated in the human system. Mouse embryonic stem cells were therefore cultured under

conditions that produced a stable naive state, and TEX10 was then rapidly depleted using an inducible degradation system. Cell appearance, growth, protein levels, and gene expression were examined. Results: Mouse cells lacking TEX10 became flatter, less compact, and appeared to grow more slowly than matched control cells. TEX10 depletion was also associated with reduced levels of OCT4, a key protein involved in maintaining pluripotency, and PELP1, a protein associated with the TEX10 complex. Other pluripotency proteins were largely maintained. Gene expression results were mixed and difficult to interpret because of variation in control samples and possible culture contamination. Conclusions: The findings suggest that TEX10 contributes to maintenance of naive characteristics in mouse embryonic stem cells, but additional experiments using contamination free cultures and stronger controls are needed to determine whether TEX10 is specifically more important in the naive state.

Michael Ishal SEAS'28, Computer Engineering

Faculty Mentor(s) or Supervisor(s): David Park
Title: Detecting Optical Aberrations in Image Data Via CNN-based Autoencoder for Anomaly Detection

Abstract: Optical aberrations degrade scientific image quality, compromising downstream quantitative analysis. Computational methods that estimate aberration coefficients or point spread functions (PSF) can enable image restoration through inverse imaging techniques. However, these methods can be computationally expensive or sensitive to modeling errors. Thus, in cases where high-volume images are captured, discarding images considered anomalous could be preferable to computationally restoring them. A method to quantify anomaly thresholds for image data can be useful in its capacity to reject aberrated data for downstream analysis. In this work, we developed a convolutional neural network-based autoencoder (CNN AE) trained on unaberrated images using mean squared error (MSE) reconstruction loss. Synthetic shift-invariant test image aberrations were generated by modeling wavefronts with Zernike polynomials, constructing PSFs, and convolving them with clean images. Three autoencoder architectures were investigated: a spatial domain model, a frequency domain model operating on shifted log-magnitude Fourier spectra, and a hybrid model combining both representations. Spatial domain reconstruction metrics showed an inverse response to aberration severity with ROC AUC for MSE and 1-SSIM values below 0.11 and 0.059 respectively, suggesting that increasingly aberrated images became easier rather than harder for the autoencoder to reconstruct. In contrast, frequency and hybrid domain latent representations achieved ROC

AUC values of at least 0.97 and 0.99 respectively using OCSVM. These findings demonstrate that the choice of representation domain strongly influences anomaly detection performance and suggests that frequency domain latent representations could be a promising approach for optical image quality assessment and potential rejection.

Talha Islam SEAS'29, Electrical Engineering

Faculty Mentor(s) or Supervisor(s): Ayaskanta Sahu

Title: Electrophoretic Deposition of PbS Colloidal Quantum Dots for Optoelectronic Devices

Abstract: Colloidal quantum dots (CQDs) are nanometer-sized semiconductor particles with size-tunable bandgaps, allowing for optical properties to be easily modified and making them promising candidates for next-generation solar cells and photodetectors. However, conventional film deposition methods such as spin-coating and various layer-by-layer processing are time-consuming, material-wasteful, and dependent on various cleanroom infrastructure. This work investigates electrophoretic deposition (EPD) as a low-cost, scalable alternative for depositing lead sulfide (PbS) CQDs onto zinc oxide and indium tin oxide (ZnO/ITO) substrates. Using a custom 3D-printed apparatus allowed for varying distances between electrodes and therefore controlled variations of electric fields applied to the substrate. PbS CQDs were first synthesized through hot injection and then underwent solution-phase ligand exchange (SPLE), mixing lead bromide, lead iodide, and sodium acetate to replace the native oleic acid capping to render them charged and dispersible in formamide for EPD. Deposition parameters were systematically varied via voltage, time, and distance, where 75 volts applied for 30 minutes at 14cm was identified as the optimal condition, producing a uniform film with confirmed absorbance. Higher voltages (100-200 V) resulted in quantum dot aggregation, while lower voltages (10-30 V) resulted in non-uniform films where the center of the substrate would be left with very few dots compared to the rest of the substrate. These findings demonstrate that high-quality CQD films can be fabricated outside of conventional cleanroom environments, establishing a foundation for more accessible and scalable optoelectronic device manufacturing.

Sonia Ivancic CC'29, Biological Sciences

Faculty Mentor(s) or Supervisor(s): Daniel Kalderon

Title: Follicle Stem Cell organization and differentiation into Follicle Cells is mediated by DE-Cadherin in the Drosophila ovary

Abstract: Follicle Stem Cells (FSCs) in the Drosophila Melanogaster (fruit fly) ovary are a model system to study stem cell differentiation patterns due to their conserved properties with mammalian intestinal stem cells. FSCs differentiate into two kinds of support cells for developing eggs based on their Anterior/Posterior (A/P) position in the germarium, the structure in the ovary where eggs production begins. Since FSC differentiation is dependent on the stem cell's position in the germarium, the adhesion protein DE-cadherin has been studied to investigate its role in governing FSC movement and thus fate determination. We hypothesize that DE-cadherin is expressed by FSCs and their posterior progeny, epithelial Follicle Cells (FCs), and this homophilic adhesion induces posterior movement and ultimate differentiation into FCs. Previous studies have suggested that FSCs produce DE-cadherin for niche retention rather than adhesion-mediated differentiation, but this result may have been due to impaired division rates of FSCs causing stem cell loss. Our findings indicate that cadherin-mutant FSCs do exhibit lower posterior differentiation rates than wild type rates. Germaria with cadherin-mutant FSCs also exhibit abnormal organization implying DE-cadherin's role in proper structuring of the germarium. These findings will help determine cadherin's role in the structure and function of stem cell microenvironments across species.

Jack Jackson SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Tal Danino

Title: Engineered E. coli Nissle Modulates the Glioblastoma Immune Microenvironment to Enhance Antitumor Activity

Abstract: Glioblastoma (GBM) remains a major therapeutic challenge, with a median survival of approximately 9.2 months with the standard of care. Its highly immunosuppressive tumor microenvironment limits treatment efficacy by suppressing antitumor immune responses. Engineered Escherichia coli Nissle (EcN), which preferentially colonizes tumors and can locally produce therapeutic proteins, offers a potential strategy to both stimulate antitumor immunity and deliver targeted therapies within GBM. To evaluate this approach, we investigated how engineered EcN interacts with the GBM immune microenvironment and whether therapeutic payload delivery could enhance its antitumor activity. We hypothesized that EcN would activate local immune responses to promote tumor-cell clearance and that additional therapeutic payloads would improve efficacy in more immunosuppressive tumors. Engineered EcN was evaluated across multiple human and murine cell lines using assays of microglial activation, tumor-cell phagocytosis, and

therapeutic response, with selected payloads subsequently evaluated in orthotopic GBM models. EcN activated microglia, increased tumor-cell phagocytosis, and improved outcomes in an immunologically responsive GL261 model, but showed limited efficacy in a more immunosuppressive APCL model. Engineering EcN to express a CD47-targeting nanobody enhanced microglia-mediated tumor-cell clearance and improved efficacy in APCL tumors. Furthermore, the standard of care chemotherapy temozolomide was compatible with engineered EcN. Together, these findings demonstrate the potential of engineered EcN as a modular GBM therapeutic that combines local immune activation with targeted therapeutic delivery to address heterogeneous tumor immune environments.

Emilia Jacome CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): David Sulzer

Title: Investigating the Spatial Localization of Epstein-Barr Virus Gene Expression in the Human Brain

Abstract: Epstein-Barr virus (EBV) is one of the most common human viruses, infecting the majority of people worldwide and remaining latent in the body for life. It has long been considered harmless outside of its role in certain cancers, but recent studies have linked it to neurological conditions such as multiple sclerosis, raising the question of whether EBV also plays a role in neurodegenerative diseases like Alzheimer's disease. Prior work in this laboratory found that latent EBV RNA transcripts are widespread in postmortem brain tissue from older adults, with no significant difference in overall levels between Alzheimer's disease and age-matched control subjects. This study built on that finding by asking a more specific question: is latent viral gene expression distributed differently across compartments of the brain? Using RNA in situ hybridization, EBNA1 transcripts, a marker of latent EBV gene expression, were measured separately in the brain parenchyma, containing neurons and glial cells, and the vascular compartment, containing endothelial and perivascular cells, in twelve subjects with and without Alzheimer's disease. No significant enrichment of viral transcripts was found in either compartment or diagnostic group, suggesting that latent EBV gene expression is not compartment-specific in the aging brain, though the small number of Alzheimer's disease subjects analyzed limits how far this conclusion can be drawn. Future work will build on these results by looking at the cells and structures immediately surrounding virus-positive nuclei to better understand whether the local environment around latent EBV, rather than its abundance or location alone, may be relevant to neuroinflammation.

Rinaz Jamal CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Franck Polleux

Title: Activity-Dependent Transcription of Nuclear-Encoded Mitochondrial Genes in Parvalbumin-Positive Interneurons

Abstract: Parvalbumin-positive interneurons (PV-INs) play a crucial role in maintaining the balance between excitation and inhibition in the brain. These neurons depict fast-spiking properties that represent a metabolic burden, which likely render them more susceptible to disease. It has been shown that certain nuclear-encoded mitochondrial genes, such as Cox6a2 and Me3, are upregulated in PV-INs, both at the transcriptional and translational levels. Moreover, in preliminary results from the Polleux group, it was shown that PV-IN activity regulates the expression of some of these mitochondrial proteins. However, whether such regulation occurs at the transcriptional level remains unknown. Here, we employed fluorescence in-situ hybridization, using RNAscope technology, combined with intra-cortical delivery of the inward rectifying potassium channel Kir2.1 to assess whether the expression of nuclear-encoded mitochondrial mRNAs is dependent on neuronal activity. Our preliminary results suggest that Me3 mRNA levels are regulated by neuronal activity in cortical PV-INs from adult C57BL6/J mice. These findings suggest that activity plays an important role in regulating transcription of nuclear-encoded mitochondrial genes in PV-INs. Since altered transcription and dysfunction of PV-INs are early events in Alzheimer's disease progression, the development of targeted interventions to rescue the expression of activity-dependent genes in PV-INs has the potential to improve outcomes earlier in this pathology.

Linden James GS'27, Political Science, Statistics

Faculty Mentor(s) or Supervisor(s): Sandra Lee

Title: Impacts of Actions Against Federal Bioethics Advisory Bodies

Abstract: Since January 2025, the second Trump administration has terminated, rendered administratively inactive, and reconstituted the membership of 71 bioethics-related federal advisory committees, actions justified as necessary to reduce the scope of federal bureaucracy in line with Executive Order 14217. Analysis of the FACA Database, Federal Register, and public media revealed that such dismantling did little to streamline the policy recommendations and grant evaluations produced by these committees, instead concentrating authority in the hands of very few individuals, namely

Secretary of Health and Human Services Robert F. Kennedy, Jr. and National Institutes of Health Director Jay Bhattacharya. The effects of these changes were assessed: members of the public have lost avenues for engagement with federal decision-making on bioethics governance; certain highly-publicized topics such as autism and vaccination have received lots of attention and priority among public health organizations and state departments of health, while other marginalized topics such as Long COVID and rural healthcare have received much less support; and the formation of independent advisory groups and establishment of legal precedent via cases against RFK Jr. points towards a future where bioethical expertise is sourced less from the government and more from independent coalitions.

Zach Jeon CC'28, Applied Mathematics, Lily Pham CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Wes Grueber

Title: Behavioral analysis of an airway sensory system for internal chemosensation

Abstract: Internal sensory neurons monitor the chemical and physical state of the body, providing critical feedback to the central nervous system to maintain body homeostasis and promote survival. The circuit and molecular basis for these interoceptive senses remain under active investigation. In *Drosophila* larvae, tracheal dendrite sensory neurons (TDSNs) reside along peripheral respiratory organs in a segmental pattern. TDSNs express reporters for a variety of gustatory receptors (GRs), oxygen sensors, and ionotropic receptors (IRs) with cell type and body segment specificity, suggesting diverse roles in internal chemosensation. Prior results showed that partially overlapping subsets of TDSNs respond to decreases in O₂ and increases in CO₂ and identified the receptors required for these responses. However, most TDSNs roles are unknown. We developed a two-choice assay to examine larval behaviors upon CsChrimson-based optogenetic activation of molecularly-defined TDSN subsets. Activation of neurons labeled by three GR reporters (Gr89a, Gr33a, and Gr28a-Gal4) and another TDSN driver (260-Gal4) all led to larval avoidance of illuminated quadrants. In contrast, optogenetic activation of two downstream synaptic targets of TDSNs, the DH44 and GPB5 peptidergic neurons, produced no significant shift from the unstimulated controls. Since both DH44 and GPB5 mediate water balance, we propose that TDSNs mediate activity in two distinct circuits for homeostasis; an aversive behavioral response that ultimately leads to downregulation of TDSN activity, and a distinct physiological pathway that

does not cause observable behavioral changes but that may lead to physiological adjustments in circulating hemolymph (blood). Future work will probe these circuits and characterize the diversity of behavioral and physiological roles of TDSNs along the body axis, to reveal general insights into interoceptive mechanisms.

Alexandru Jerpelea CC'29, Applied Mathematics, Computer Science

Faculty Mentor(s) or Supervisor(s): Eugene Wu

Title: Lost in Propagation: Communication Failure in Multi-Agent Systems

Abstract: Large language models are increasingly deployed autonomously as agents, and multi-agent systems take this further on the premise that more intelligence might emerge from interaction, where agents communicate and divide labor. In practice, adding more agents helps inconsistently, for reasons not fully understood. This study identifies one such reason, coined loss-in-propagation, where task-relevant information held by one agent fails to reach the agents that depend on it, compounding as the system grows. It identifies two forms of this loss: 1. external, where an agent omits information it possesses (whether discovered by itself or inherited from earlier agents), and 2. internal, where agents hold priors (understood as "beliefs") about their environment that are never expressed in tokens, and thus never shared. To quantify both, the paper introduces an evaluation protocol over two topologies, namely a chain, where each agent sees only what its predecessor hands over, and a star, where a central agent coordinates several workers, the design most common in deployed systems. Beyond correlating agent count with loss-in-propagation, the protocol provides causal experiments by isolating agents at the point of failure and letting them continue the trace with near-perfect information, meaning everything earlier agents had found but failed to pass on, and by instilling divergent beliefs across agents and then aligning them. Across several benchmarks, such as FanOutQA, external loss scales with the number of agents, falling hardest on later agents, while aligning beliefs increases performance. The paper also explores solutions, including training a monitor LLM to anticipate what later agents will need, and belief-sharing systems inspired by Theory-of-Mind and mechanistic interpretability research.

Amy Ji CC'28, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Lynn Yap

Title: Circuit Mechanism Supporting Behavioral Flexibility During Extinction Learning in the Medial Prefrontal Cortex

Abstract: Learning allows animals to form associations between cues and meaningful outcomes, but survival also requires the flexibility to change behavior when those associations are no longer useful. This study examines how the brain balances these demands during extinction learning, a process in which a previously learned response decreases when an expected outcome no longer occurs. The work focuses on the medial prefrontal cortex, a brain region involved in learning, decision-making, and behavioral flexibility. Mice will first learn that certain odors predict a reward while other odors do not. Their behavior and brain activity will be monitored throughout learning to identify groups of neurons that respond differently to rewarded and unrewarded cues. The same neurons will then be tracked as previously rewarded odors stop predicting a reward, allowing changes in brain activity to be compared with changes in behavior. Previous findings suggest that neurons associated with unrewarded cues may become active during this process and could help suppress the neural activity associated with the original learned response. Advanced imaging and stimulation techniques will be used to test whether these neurons actively contribute to behavioral change. By selectively activating neurons associated with unrewarded cues, the study will determine whether they can alter the activity of reward-associated neurons and influence the animals' behavior. Understanding these interactions may reveal how the brain can preserve previously learned information while still adapting behavior when circumstances change. More broadly, these findings could provide insight into the neural mechanisms that allow learning to remain both stable and flexible.

Chris Ji CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Xueyue (Sherry) Zhang
Title: Photonic device design and measurement for silicon T center

Abstract: Quantum computers and quantum networks will need a way to store information and send it over long distances. One promising approach uses the T center, a defect in silicon that emits light at a wavelengths already used by fiber optic communication networks. Because these emitters are faint, they must be surrounded by purposefully designed structures that trap and direct their light. This project focuses on designing and testing such structures on silicon chips. The work centers on a mirror built directly into a chip, a photonic crystal, formed by etching a repeating pattern into a narrow light guiding channel. The pattern reflects a different wavelengths of light

differently. Measuring how well the photonic crystals required high precision because the light must first be delivered into a channel with nanometer dimensions. Chris built and operated a measurement system that does this at room temperature. A laser whose wavelength can be swept across a range is guided through optical fiber and focused onto the edge of the chip using a lensed fiber held by motorized stages. Light returning from the chip is collected by a photodiode, and the resulting spectrum is a key metric for the performance of the mirror. Using this system, Chris successfully coupled light into the device and recorded reflection spectra that closely match simulations. Additional work prepared the hardware for future operation at cryogenic temperatures, including splicing optical fibers, installing them through a vacuum chamber, and confirming that the chamber still holds vacuum.

Paula Jimenez CC'28, Comparative Literature, Political Science

Faculty Mentor(s) or Supervisor(s): Tracey Holland
Title: Children's Rights and the Arms Industry: the Impact of Weapons in Conflict Affected and High Risk Areas

Abstract: Weapon deployment has caused an overwhelming degree of immediate destruction and long-term harm to civilian populations, particularly children. Explosive weapons alone accounted for nearly seventy percent of child casualties in 2024, up from about half in 2020, illustrating how quickly this risk has accelerated. Although the vulnerability of children in armed conflict has been long established and internationally recognized, little has been done to incorporate their protection into the arms industry's corporate policies, due diligence, and risk assessment procedures, and any assessments that occur happen without public visibility. This project responds to that gap by developing the Arms Sales Risk to Children's Rights framework, ASRCR, to help conduct a risk assessment based on the weapon made, the end user who receives it, and the region of deployment. The ASRCR score combines ten measures of a recipient country's conditions, including a newly created Previous Human Rights Violations score, tracking a country's history of grave violations against children, and a Legal Compliance Score, measuring ratification of treaties protecting children in conflict alongside documented violations. This score is combined with the developed Weapon Harm Potential Score, which rates each weapon type defined by the Arms Trade Treaty, on factors such as lethality, area of effect, and diversion risk, to produce a final Child Risk Score. The resulting score

offers arms manufacturers, states, and policymakers a quantifiable reference point to weigh before a weapon is made, sold, or deployed, in relation to its potential impact on children.

Sara John SEAS'28, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Carlos Paz-Soldan

Title: Design of a Force Sensing System for Cryogenic Pellet Injection

Abstract: Sara worked as a Research Intern with the Pellets at Columbia group at the Columbia Fusion Research Center, contributing to research on cryogenic pellet injection for fusion energy. Her project focused on designing a new force sensing system to better understand what happens as frozen pellets are released from an injector. Current pellet injectors have limited ability to directly observe the mechanical forces involved during pellet release. To address this, Sara worked to integrate a load cell, a sensor used to measure force, into the pneumatic punch that releases pellets from the injection chamber. The resulting system is designed to produce force measurements throughout the punch process, providing a new way to identify when a pellet begins to move, fractures, shatters, and fully releases. These measurements may also help researchers understand how pellet composition and impurities affect pellet strength and injection behavior. Sara's work involved evaluating the existing punch assembly, using previous force and buckling calculations, selecting an appropriate load sensor, developing computer aided design models, and designing supporting components needed to incorporate the sensor while accounting for the mechanical and space constraints of the existing system. Future work will involve fabricating and installing the redesigned components, validating the instrumented punch under operating conditions, and collecting force data during pellet experiments. Ultimately, this diagnostic could improve researchers' understanding of cryogenic pellet injection and contribute to the development of more reliable pellet systems for fusion energy research.

Adrian Karras CC'29, Physics

Faculty Mentor(s) or Supervisor(s): Jeffrey Levesque

Title: Low Resistance Joints for the Hybrid HBT-EP Banana Coils

Abstract: Fusion reactors come in two main designs called stellarators and tokamaks. Stellarators use a complex configuration of coils that give them the desired magnetic field geometry, while tokamaks compensate for their relatively simple coil geometry by inducing a current in the plasma. While the

HBT-EP has previously done this, we will be adding a third type called the banana coils. We aim to achieve currents of at least $\sim 4\text{kA}$ – 7kA in the new banana coils, which requires minimizing circuit resistance to limit coil heating. With nine joints connecting the banana coils, each carrying potential for imperfect contact, we expected these joints to be a significant contributor to overall circuit resistance. We modeled two joint designs, the first being an insulated bracket (Design A) and the second a conducting barrel (Design B) using Holm's contact resistance theory, using contact force, real contact area, material resistivity and hardness, all of which is available for these designs. We calculated contact force at both the spec sheet's maximum recommended torque and at a more practical 80% maximum torque. The resulting contact force allows us to solve for total contact resistance, which is combined with the non-contact resistance. For the 80% models, total resistance was $11.62\text{ m}\Omega$ for Design A and $11.64\text{ m}\Omega$ for Design B, making the contact resistance negligible. RLC modeling of the circuit, using the power bank capacitance, inductance, and this resistance, projects currents above the targeted amperage. Thus, these results suggest a design decision that prioritizes ease of installation.

Samhita Kashyap Kiran SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Barclay Morrison

Title: Region-Dependent Mechanical Properties of Bovine Cerebellum White and Grey Matter via Inverse Finite Element Optimization of Microindentation Data

Abstract: The goal of this analysis is to use manual fitting with inverse Finite Element (FE) optimization to match simulation to experimental indentation data to determine the varying mechanical properties of the white and grey matter subregions and the impact of direction in the cerebellum of the bovine brain. Experimental microindentation was performed on fresh tissue from the bovine brain. Manual fitting and optimization using the Ogden constitutive formulation and Prony series allowed an understanding of the mechanical differences between the two tissue regions. Optimized parameters indicated that white matter stiffness moduli are significantly greater than grey matter, indicating white matter to be stiffer than grey matter. No statistically significant difference was found between the directions. This understanding is foundational to increasing accuracy in modeling strain fields caused by large deformations of brain tissue during a Traumatic Brain Injury (TBI).

Jennifer Kava GS'29, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): Sharon Di

Title: Preserving Spectral Structure and Statistics in Diffusion Models

Abstract: Standard diffusion models (DMs) rely on the total destruction of data into non-informative white noise, forcing the backward process to denoise from a fully unstructured noise state. While ensuring diversity, this results in a cumbersome and computationally intensive image generation task. We address this challenge by proposing new forward and backward process within a mathematically tractable spectral space. Unlike pixel-based DMs, our forward process converges towards an informative Gaussian prior $N(\mu_{\text{hat}}, \Sigma_{\text{hat}})$ rather than white noise. Our method, termed Preserving Spectral Structure and Statistics (PreSS) in diffusion models, guides spectral components toward this informative prior while ensuring that corresponding structural signals remain intact at terminal time. This provides a principled starting point for the backward process, enabling high-quality image reconstruction that builds upon preserved spectral structure while maintaining high generative diversity. Experimental results on CIFAR-10, CelebA and CelebA-HQ demonstrate significant reductions in computational complexity, improved visual diversity, less drift, and a smoother diffusion process compared to pixel-based DMs.

Bradley Kelton CC'28, Earth Science, Physics

Faculty Mentor(s) or Supervisor(s): Laura Schaefer

Title: Tracing Carbon Loss in Planetary Populations

Abstract: Carbon is an element vital to the habitability and atmospheric processes of Earth and other terrestrial planets. Despite this, the source of Earth's carbon reservoir remains poorly understood. One proposal attributes the Earth's C budget to inner Solar System non-carbonaceous material (NCs) during the Earth's main accretion stage, which requires a moderate C depletion from the source material. Alternatively, C can be delivered by a small addition of outer Solar System, volatile-rich, carbonaceous materials (CCs), possibly over a longer timescale. This work aims to probe the possible pathways of C reservoir evolution in populations of NC and CC planetary bodies, the feedstock of terrestrial planet accretion. The Planetary Outgassing Evolution Model (POEM), a thermal-chemical-mechanical model that simulates the C depletion history of individual planetary bodies, was used to construct a library of planetary evolution across wide ranges of masses, formation times and compositions. A population synthesis pipeline then simulated random sampling from proposed distributions in this parameter space. Mock outgassing data were generated to test this pipeline, which

created a 2D interpolation program that calculates relative bulk carbon abundance for each sampled population. Finally, Monte Carlo simulations obtained a mean outgassing curve for planetary populations, and the relative abundances of each chondrite composition were adjusted to compare these simulated results to the bulk carbon content of Earth. Constraints can therefore be placed on the population characteristics of the initial building blocks of terrestrial planets.

Bryce Key CC'28, Biochemistry, Music

Faculty Mentor(s) or Supervisor(s): Myles Smith

Title: Synthetic Studies Toward Penicillolide A

Abstract: Penicillolide A is an indole alkaloid metabolite of *Penicillium* sp. OUCMDZ-77 that exhibits antifouling activity, preventing the buildup of marine organisms on submerged surfaces. The initial structure, proposed by the isolation team, contains an unstable and unlikely twist amide at a bridgehead position. We propose a more chemically reasonable structure, which instead contains a triazaspirocyclic core. The goal of this work is to synthesize our proposed structure and compare its spectral elements with those of the isolation team, directly testing our proposal against the original assignment. Efforts to synthesize the tricyclic core proved difficult because numerous cyclization attempts have led to decomposition, so protection at the C3 position was explored to overcome this. The triazaspirocyclic core, protected with an allyl ester, was prepared in 6 steps from methyl 2-(1H-indol-3-yl)acetate. Various efforts to deprotect this species were unsuccessful, including ruthenium-catalyzed isomerizations and hydrolysis attempts. Simultaneously, a separate route employing phenylsulfenyl protection at the same carbon was investigated. Indole acetic acid was allylated at its carboxyl, oxidized to yield an oxindole, and sulfenylated, prior to an amide coupling and two intramolecular cyclizations. Despite the low-yielding character of the final cyclization, this route successfully afforded the phenylsulfenyl-protected tricyclic scaffold, confirmed by ¹H NMR and LC-MS analysis. Both deallylation and desulfenylation to unmask the triazaspirocyclic core of penicillolide A are ongoing. Once the core is obtained, its spectral data will be compared with that of the isolation team, providing an initial test of our proposed structural reassignment en route to the complete molecule.

Mazen Khalil CC'27, Statistics

Faculty Mentor(s) or Supervisor(s): Talha Malik

Title: Advanced Medical Therapies for Oral and Orofacial Crohn's Disease and Related Oral Granulomatous Conditions: A Systematic Review of Clinical Outcomes

Abstract: Background: Orofacial Crohn's disease, orofacial granulomatosis, granulomatous cheilitis, and Melkersson-Rosenthal syndrome, often grouped under orofacial granulomatosis (OFG), can cause pain, swelling, disfigurement, impaired eating and speech, and substantial morbidity. Although advanced therapies are widely used for Crohn disease, evidence for OFG remains limited and inconsistently defined. We systematically reviewed the reported effectiveness of advanced therapies for these conditions. **Methods:** We conducted a systematic review in accordance with PRISMA 2020. Electronic databases were searched from inception through August 2026, supplemented by searches of recent relevant conference proceedings. We included observational studies and case series with at least two eligible patients reporting a defined oral/orofacial manifestation or diagnosis before treatment, a named advanced therapy, and a post-treatment manifestation-specific outcome. Given the substantial clinical and methodological heterogeneity of the studies included and the inconsistent definitions and reporting of outcomes, findings were synthesized descriptively rather than meta-analyzed. Risk of bias was assessed using the JBI critical appraisal tool for case series. **Results:** Seventeen studies comprising of at least 193 unique eligible patients and 289 reported treatment courses were included. Outcomes were classified as complete, partial, no, or unclear response. Complete or partial response occurred in 223/289 exposures (77.2%), comprising 149 complete responses (51.6%) and 74 partial responses (25.6%). Tumor necrosis factor- α inhibitors constituted the largest intervention group 208/289 exposures (72.0%), with complete or partial response reported in 161/208 (77.4%). The highest response proportion was observed with JAK1 inhibitors (10/11; 90.9%), although this is based on very sparse data.

Zoya Khan CC'27, Cognitive Science, Computer Science

Faculty Mentor(s) or Supervisor(s): Stefano Fusi

Title: Hippocampus and neocortex compress experience through rapid but distinct population reorganization

Abstract: Efficient learning requires the brain to rapidly encode new experiences while leveraging shared structure across related episodes. Hippocampal CA1 and posterior parietal cortex (PPC) both contribute to navigational decision-making, yet how their computations jointly support learning remains unclear. We used two-photon calcium imaging to record

population activity in CA1 and PPC as mice navigated three sequential virtual-reality corridors: one familiar and two novel. Mice rapidly learned corridor-specific reward locations despite unique visual cues, consistent with meta-learning across environments. We find that neurons in both regions show place-field-like tuning, but each population relates positions differently: CA1 continuously, PPC within discrete cue-defined blocks. To quantify how these encodings reorganize, we developed a representational-geometry metric of experience-dependent changes in population similarity. We find that both regions exhibit increases in local similarity but decreases in distal similarity over learning, consistent with compression of experience. CA1 integrates positions across cue boundaries, whereas PPC integrates only within blocks. Further, in CA1, but not PPC, local integration width scales with running speed, a population signature of behavioral-timescale synaptic plasticity (BTSP). Such restructuring emerges most strongly in CA1 within the familiar environment and in PPC upon exposure to novelty. Neither decorrelates distal positions in the second novel environment, suggesting a physiological limit to rapid plasticity. Together, we show that both hippocampus and neocortex rapidly reconfigure their population codes: CA1 temporally indexes space, consistent with BTSP as a mechanism for efficient memory encoding, whereas PPC reorganizes around the structure of the world, consistent with robust encoding of sensory experience.

Elaheh Khazi CC'27, Middle Eastern, South Asian, and African Studies, History

Faculty Mentor(s) or Supervisor(s): Ali Karjoo-Ravary

Title: Reclaiming Our Narrative: A Deeper Look into Afghan and Afghan American Muslim Traditions (my research this summer is a part of my larger project that has been IRB certified which looks at different parts of the Afghan-American diaspora)

Abstract: The United States is home to one of the largest Afghan populations outside of Afghanistan. Especially since the onset of the Soviet-Afghan War in 1979, a proxy war of the Cold War, the Afghan American diaspora has grown significantly. However, since the onset of the War on Terror, the Muslim religion and Afghan identity have become synonymous with "terrorism," as Afghans and Afghan Americans are often described with vilified and negative imagery in mass media. This project presents the background of Muslim Afghan religious traditions, which are much older and richer in history than modern narratives of geopolitics and the weaponization of religion through archival research and oral history interviews. This project

looks more deeply into Afghan religious traditions, including ziyarat (pilgrimage to holy figures' burial places) and nazr (praying for desires to be accepted in exchange for votive offerings), which, despite the diversity of religious beliefs in the country and diaspora, many Muslim Afghans partake in, unlike many modern Muslim communities, which have conflicting opinions on these practices. By bringing light to these traditions and looking into Afghan American spaces of worship, this project highlights Afghan voices and stories that are often forgotten and undermined in conversations about the community and the larger country of Afghanistan. This project contributes to reclaiming the narrative of the Afghan American diaspora.

Thaddaeus Kiker CC'27, Astrophysics

Faculty Mentor(s) or Supervisor(s): Ethan Peterson

Title: Harder, Better, Faster, Stronger: Physics-Informed Neutron Sources and Automated Magnet-Shield Optimization for Stellarators and Tokamaks in OpenMC

Abstract: Superconducting magnets are the most radiation-sensitive and costly components of a fusion power plant, and protecting them from the intense 14 MeV neutron flux requires shielding tuned inside Monte Carlo transport simulations that can take hours per design. This work confronts a harder version of that problem than standard axisymmetric tools allow, adding physics-informed fusion neutron sources to the open-source OpenMC code that capture both the true, twisting three-dimensional geometry of stellarator and tokamak plasmas (a native VMEC-fluxmap StellaratorSource) and the anisotropic, spin-steered emission of spin-polarized fuel (a Schwartz-kernel birth-direction sampler). These sources give a better, higher-fidelity account of where neutrons are born and aimed: the polarized kernel reproduces the analytic angular limits of Schwartz (2025) and, unlike precomputed-point approaches, evaluates the local magnetic-field direction natively and composes with any device geometry. Building on them, we develop a faster, direct-forward automated shield-optimization loop that resolves the per-magnet neutron load to a few percent in minutes—removing the variance-reduction machinery previously assumed necessary—and drives an attribution-guided redesign of the shield. The outcome is stronger magnet protection from the same footprint: concentrating shielding where neutron attribution directs it cut the peak coil fast-neutron load roughly fourfold (4.2×) versus a uniform baseline at fixed envelope, while an exact volume-calculation pipeline reveals that identical nominal shield thickness varies 2.4× in mass by location—and that the tightest engineering clearances fall exactly

where protection is most needed. Together these tools reframe fusion-magnet shielding as a problem of placement, not bulk.

Natalie Kim CC'27, Sociology

Faculty Mentor(s) or Supervisor(s): Amy Zhou

Title: Stop AAPI Hate: Brokering Between AAPIs and the Carceral State

Abstract: This study examines the relationship between the nonprofit organization Stop AAPI Hate (SAH) and carceral state institutions. During the COVID-19 pandemic, SAH began as an online platform for Asian Americans and Pacific Islanders (AAPI) to document experiences of anti-AAPI hate without interacting with law enforcement. SAH claims to champion non-carceral solutions, given that the U.S. carceral system disproportionately harms communities of color and leaves the root causes of anti-AAPI hate intact. At the same time, SAH leaders have supported hiring more hate crime investigators within police departments, hiring FBI personnel with diverse backgrounds, reporting anti-AAPI hate to the police, and increasing penalties for hate crimes. What is the underlying logic of SAH's relationship with carceral state institutions, even as it insists upon non-carceral solutions? Drawing from literature on the carceral state, social closure theory, network theory, and in-depth interviews with SAH leaders, this study finds that social brokerage is the logic by which SAH aims to redistribute a valuable resource: state protection against bias-related harm. In other words, SAH serves as a bridge between AAPIs and state institutions, deciding what information about AAPIs to relay to state actors (and vice versa) and how. For SAH, the anticipated return on their social brokerage is state protection against anti-AAPI hate. Yet, for carceral state institutions, the return on SAH's social brokerage is their continued material and ideological influence. As such, this study offers insight into the limits of social brokerage with carceral state institutions as a strategy for dismantling racism.

Graysen Kirk Linn CC'27, Human Rights

Faculty Mentor(s) or Supervisor(s): Dr. Gyula Csurgai

Title: From Testimony to Impact: Dignity, Agency and the Ethics of Using Survivors' Stories in Humanitarian Research and Advocacy

Abstract: This study examines testimony collection of survivors of gender based violence in post-conflict settings for the purpose of international humanitarian policy and advocacy projects. To do this, I am looking at the questions that arise around dignity, ethics, and saviorism when Geneva-based

humanitarian and human rights actors are collecting, evaluating, publishing, and circulating information from survivors. Using theoretical frameworks such as violent recognitions, human security, voyeurism, and victimhood, my research calls for a shift in the conversation from victims and subjects of war to agents of change and strong survivors. Findings suggest that more holistic, long-term, and community-based projects create fertile ground for more dignified approaches that focus on amplification and upliftment rather than extraction. Ultimately, this study underscores the importance of dignity-centered approaches to testimony-based work at each stage of the process that do not instrumentalize suffering or re-traumatize survivors but rather close the gap between advocacy aims and survivor benefits.

Nicholas Koch CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Kazuhiro Fujita

Title: Development and Characterization of Shot Noise Detection System

Abstract: Shot noise, the discreteness of electron charge, arises as electrons tunnel through vacuum-sample junctions. This noise provides a visualization of electron charge in quantum tunneling and reflects the intrinsic properties of quantum materials at the atomic level. Detecting this characteristic provides insight into phenomena such as unconventional/topological superconductors and Quantum Hall systems. However, this noise is very small, so it must be amplified and isolated from all other interference. This study employs a radio-frequency amplification circuit using the high electron mobility transistor (HEMT) with an array of high-pass and low-pass filters to achieve voltage amplification and frequency filtering, thereby isolating shot noise. This circuit was assembled using various soldering techniques and tested with a lock-in amplifier, demonstrating its ability to amplify the voltage at a specific frequency. From simulations, the circuit design exhibited a voltage amplification gain of approximately 240 times at a frequency of approximately 1.7 MHz. During testing at room temperature, a prototype circuit exhibited a gain of 1.2 times at 1.94 MHz with 68 uH inductors, and at 4 MHz with 16 uH inductors. For measurements at cryogenic temperatures, a cryogenic insert was developed and assembled using a 1 Kelvin pot, a sub-vessel used for evaporative cooling. Once the insert is submerged in liquid helium, the circuit can be characterized at 300K, 77K, 4K, and 1K. With the system fully assembled, testing at these temperatures will soon begin, followed by tests using a niobium junction sample.

Eftychia Kotsiou CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Mark Ross-Lonergan

Title: MicroBooNE/PROSPECT comparative neutrino disappearance analysis using PROfit

Abstract: Neutrinos are massless, abundant particles, produced as a result of nuclear reactions. They couple to the three main charged leptons, giving us three, so-called, “flavors”. Neutrinos can “oscillate” between the three flavors given the right conditions of energy and distance. These conditions are simulated in neutrino beamlines, like the Booster Neutrino Beamline at FermiLab. MicroBooNE is one of three experiments on this beamline, 470 meters from the target. The target produces muon neutrinos, and the larger the distance, the more likely an oscillation is observed between the original flavor and others. This is in the mission to observe a fourth flavor: a massive, “sterile” neutrino that was favoured as an explanation of dark matter. This is why tracking the “appearance” and “disappearance” of all the flavors is important. In the context of MicroBooNE, the oscillations make it particularly difficult to properly plot the disappearance of electron neutrinos. Here is where PROSPECT, a short-baseline reactor experiment enters the picture. This experiment is set up on the order of 10 meters away from the HFIR reactor at Oak Ridge National Lab. Due to the proximity of the detector, the emitted anti-electron neutrinos can’t oscillate and are detected immediately, breaking the degeneracy in MicroBooNE’s data. In this study, the data from both experiments is analysed concurrently using PROfit, a fit framework designed for short-baseline neutrino experiments. While still in progress, the hope is to show increased sensitivity is shown in electron neutrino disappearance plots.

Nat Kpodonu CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Gisette Reyes-Soffer

Title: KIV-2 VNTR Length Is Associated With Broad Lipidomic Shifts and Selective Remodeling Signatures in Human Lipoprotein(a)

Abstract: Lipoprotein(a) [Lp(a)] is a strong genetically determined independent cardiovascular risk factor primarily regulated by copy number variation in the kringle IV type 2 (KIV-2) domain of the LPA gene. Shorter KIV-2 alleles are classically associated with smaller apo(a) isoforms, elevated circulating Lp(a), and greater atherosclerotic cardiovascular disease (ASCVD) risk, while longer alleles generally correspond with lower plasma concentrations. Although the inverse relationship between KIV-2 length and Lp(a) quantity is well established, it remains unclear whether variation in Lp(a) particle size associated with KIV-2 copy number may also correspond

with differences in lipid component composition and related regulatory lipidomic mechanisms. To address this, we analyzed quantitative lipidomic data from plasma samples within a subset of the Washington Heights-Inwood Community Aging Project (WHICAP), integrating KIV-2 VNTR estimates with analyses of lipid class patterns and the strongest lipid species associations. Broad comparisons demonstrated that KIV-2 variation corresponded with widespread differences across multiple lipid groups rather than isolated changes in a single phenotype. Specifically, species-level ranking showed that shorter or longer KIV-2 repeat size was most strongly associated with monoacylglycerols (MG), diacylglycerols (DG), ceramides (Cer), phosphatidylcholines (PC), plasmalogens, and phospholipid-associated species-lipid groups integral to membrane biology, signaling pathways, and phospholipid remodeling. These findings suggest that KIV-2 variation influences molecular lipid environments beyond its established role in determining Lp(a) concentration. This supports an expanded framework in which differences in Lp(a) particle size related to KIV-2 repeat number correspond with distinct lipidomic signatures relevant to cardiovascular biology.

David Kramer CC'28, Art History, Visual Arts

Faculty Mentor(s) or Supervisor(s): Mark Santolucito

Title: The Protector: Cryptographic Proof of Authenticity in Photographs and Video

Abstract: David Kramer designed and built The Protector, a wearable device that lets anyone verify whether a video in question shows a real person or a deepfake of a person. Motivated by the lack of autonomy and inherent vulnerability individuals face as the most massive tech companies build deepfake software for public misuse, Kramer was inspired by his mentor, Professor Mark Santolucito of the Barnard Computer Science Department, to build a solution. Kramer spent the spring and summer of 2026 researching deepfake detection methods and training local artificial intelligence models before designing and building the device from scratch. The Protector generates a unique light pattern once every second using cryptography. Anyone in the world can record a video of a person wearing the device. Independent researchers can then check that video against The Protector Network at iamnotfake.com by entering the light pattern frame by frame. The website confirms whether the pattern matches what the device would have produced at that exact moment. Consider the following relevant use case: A video of a politician giving an offensive speech is circulating on the internet and the politician claims it is fake. The politician always wears a Protector,

and indeed, in this video he is wearing one. Independent researchers take the light sequence in the video and compare it to the possible light sequences that could have occurred during a reasonable time frame. The sequences do not match, meaning the video has been altered. The Protector is patent pending, and Kramer is pursuing federal funding to continue its development.

Morlyne Kwekeh CC'27, Neuroscience and Behavior

Faculty Mentor(s) or Supervisor(s): Yuki Utsugi

Title: Using Engineered Deubiquitinases to Stabilize ATM Protein in Ataxia-Telangiectasia

Abstract: Ataxia-Telangiectasia (A-T) is a rare genetic disorder caused by mutations in the ATM gene. It is an autosomal recessive condition with early onset in children aged 2 to 5 years old. Patients with A-T have reduced ATM protein expression. ATM is a primary protein kinase involved in activating the DNA damage response. Reduced ATM expression impairs downstream signaling through p53 and checkpoint kinase 2, compromising cell-cycle checkpoint regulation and DNA damage repair, contributing to genomic instability, cerebellar neurodegeneration, immunodeficiency, and increased cancer risk. In this research, we aimed to investigate whether the ATM protein could be stabilized through the use of engineered deubiquitinases and determine which ubiquitin chain modification had the greatest effect on ATM protein expression. Following transfection of Venus-ATM with five engineered deubiquitinases, nanoOTUD1, nanoOTUD4, nanoCezanne, nanoTRABID, and nanoUSP21, flow cytometry was used to compare Venus-ATM fluorescence across the different conditions. Unexpectedly, cleavage of K63-linked ubiquitin chains on ATM by nanoOTUD1 produced the greatest increase in Venus-ATM fluorescence, raising the possibility that K63-linked ubiquitination may contribute to ATM destabilization. In contrast, cleavage of K48-linked ubiquitin chains by nanoOTUD4 produced the lowest Venus-ATM fluorescence. Because K48-linked ubiquitination is canonically associated with proteasomal degradation, this unexpected decrease suggests that K48-linked ubiquitination may have an alternative role in regulating ATM stability beyond its canonical function. Future studies will use Western blotting and immunoprecipitation to further investigate ATM deubiquitination, protein levels, and stability. Additionally, endogenous binders for native ATM will be designed using AlphaFold and ProteinHunter.

Michelle Kwon CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Kristen Baldwin

Title: Developing iPSC-Derived Neuronal Models for Studying SETD1A

Abstract: SETD1A is a gene involved in regulating the activity of other genes and has been linked to schizophrenia and other neurodevelopmental disorders. Understanding how changes in SETD1A affect human neurons requires reliable laboratory models that reproduce important features of these cells. This project focused on developing and characterizing human neuronal models that can be used to study the effects of SETD1A. Human induced pluripotent stem cells, which can develop into many different cell types, were grown and differentiated into neurons. The stem cell lines contained different combinations of transcription factors, proteins that help control which genes are active and can guide cells toward specific neuronal identities. Individual stem cell colonies, known as clones, were isolated and expanded to establish new cell lines. These clones were then tested for their ability to successfully develop into neurons. Through this process, additional clones capable of producing neurons were identified and differentiated for further study. The resulting cells were monitored throughout differentiation and assessed using fluorescent staining and microscopy to confirm neuronal identity, alongside molecular techniques used to characterize the lines and investigate SETD1A. By establishing and validating new stem cell clones capable of reliably generating human neurons, this work expands the set of models available for studying the role of SETD1A in neuronal development and function. These models may ultimately help clarify the cellular changes underlying neuropsychiatric disease.

Tara Lago CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Alex Dranovsky

Title: Automated labeling of behavioral outputs in control and early-life stressed mice

Abstract: Early life stress (ELS) is a risk factor for mood and anxiety disorders, the most common mental health issues in the US. The limited nesting and bedding paradigm (LBN) is a common experimental rodent model to study ELS but has produced inconsistent results in behavioral tasks. Recent advances in technology for automated labeling are potential solutions to the variability from human scoring. Different tasks measure diverse aspects of behavior, from location to interaction. We have constructed two computational pipelines to automate scoring in mice (n = 62) performing a working memory and a social interaction task. To maximize consistency, behavioral tasks were recorded from a top view camera and performed at the same time of day. The videos were processed with DeepLabCut (DLC) until

tracking reached a 60% confidence threshold. We then used custom scripts in MATLAB and Python to measure behaviors and found that while this approach yielded robust results for studying navigation, it fell short in detecting interaction behaviors. We turned to Simple Behavioral Analysis (SimBA), a machine learning software that we trained to detect social interaction. Following validation against a subsample using human expert scoring, the pipelines were applied to a large dataset of ELS and control mice. This approach allowed us to unambiguously demonstrate the effects of ELS across behavioral tasks using a standardized method. Overall, this work solidifies and extends our understanding of ELS on behavior while dramatically increasing throughput for behavioral analysis. It also underscores the value of automated, data-driven approaches in behavioral neuroscience research.

Isabella Lala CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Sandra Soo-Jin Lee

Title: Administrative Grant Terminations and Their Impact on the NSF Ethics, ELSI, and STS Portfolio: A Portfolio Analysis of Federally Funded Research

Abstract: Federal funding shapes the direction of scientific discovery, yet little is known about how recent administrative grant terminations have affected bioethics-related research supported by the U.S. National Science Foundation (NSF). This project examined how changes in federal funding priorities since January 2025 have influenced NSF programs that support ethics, the Ethical, Legal, and Social Implications (ELSI) of science, and Science and Technology Studies (STS). Using publicly available NSF award records, agency announcements, institutional statements, and grant tracking resources, the study conducted a longitudinal analysis of active and expired awards across five major NSF programs. Each award was classified according to its research focus, ethical relevance, and administrative status to identify broader patterns in the agency's evolving portfolio. The analysis found that administrative grant terminations were concentrated in programs historically associated with ethics, social inquiry, governance, and research integrity, while large technology-focused initiatives, particularly those related to artificial intelligence, remained comparatively well funded. The findings suggest that the impact of these funding changes extends beyond the loss of individual grants, influencing the broader ecosystem that supports ethical reflection in science and technology. Many affected projects incorporated ethics as an integral component of interdisciplinary research rather than as their primary focus, demonstrating that bioethical inquiry often exists beyond

traditionally defined bioethics programs. By documenting these shifts, this research provides one of the first systematic examinations of how administrative grant terminations may be reshaping the NSF's ethics portfolio and identifies important questions for future research and science policy.

Audrey Lam CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Yi Fan

Title: Understanding Vascular Niche-Mediated Dendritic Cell Dysfunction in Glioblastoma

Abstract: Glioblastoma is the deadliest primary brain cancer in adults, with a five-year survival rate of less than 7%. Although immunotherapies such as chimeric antigen receptor (CAR) T cells have transformed treatment for some cancers, glioblastoma remains highly resistant and frequently relapses. One major contributor to this therapeutic resistance is the immunosuppressive tumor vascular niche, where tumor endothelial cells secrete factors that inhibit antitumor immune responses of macrophages (Yang et al., 2024). As professional antigen presenting cells play a critical role in initiating anti-tumor immunity, dendritic cells (DCs) may be particularly susceptible to this suppressive microenvironment. This study investigates whether the tumor vascular niche impairs DC antigen uptake, co-stimulatory molecule expression, and subsequent T-cell proliferation and activation. Monocyte-derived dendritic cells were treated with tumor endothelial cell conditioned media (TEC-CM) and analyzed by flow cytometry for their ability to uptake model antigens and express co-stimulatory molecules. To assess functional significance, T cells were co-cultured with media-treated DCs and assessed for proliferation and activation markers by flow cytometry. Compared with normal endothelial cell conditioned media (NEC-CM), TEC-CM treatment significantly reduced antigen uptake, expression of co-stimulatory molecules, and DC-mediated T-cell activation following TLR4 (LPS) stimulation. The findings suggest that the tumor vascular niche alters dendritic cell function. If further studies support an immunosuppressive relationship, future work will use RNA sequencing to investigate the molecular mechanisms underlying this modulation and identify potential therapeutic targets to restore antitumor immunity and improve immunotherapy outcomes in glioblastoma.

Eliza Lamster CC'28, Biochemistry

Faculty Mentor(s) or Supervisor(s): Laura Kaufman

Title: Understanding Local Mechanical Properties of Extracellular Matrix Materials via Cell Induced Deformations

Abstract: Prior to metastasis, the cells in breast cancer tumors pull the collagen-I fibers of their local extracellular environment into radial alignment, a geometry which promotes cancer cell invasion. The ability of cells to irreversibly remodel their environment is, in part, a result of collagen-I's plasticity, which is the tendency for a material to maintain stress-induced deformations after the deforming force is removed. The biological importance of plasticity remains an area of interest, and previous work from the Kaufman Group has aimed to characterize collagen-I plasticity at a microscopic scale using multicellular tumor spheroid-embedded hydrogel systems. These measurements suggested that the network plasticity is extremely heterogeneous, a finding which was attributed in part to the fact that collagen-I shows stress-dependent plasticity. This property is unique to collagen-I and can complicate interpretation of cell-based plasticity measurements. Here, spheroids are embedded in gels exhibiting stress-independent plasticity: if previously the observed spatial heterogeneity is a result of collagen-I's stress-dependent plasticity, a stress-independent network should exhibit reduced correlation between cell-induced deformation and local plasticity. A composite gel network of 1mg/mL collagen-I and 3mg/mL Matrigel was found to exhibit stress-independent plasticity in bulk and to be susceptible to cell pulling. When spheroids were embedded into composite networks using systems analogous to prior experiments, the networks displayed different patterns of plasticity compared to pure collagen-I gels. Specifically, there was a positive correlation between plasticity and radial distance from the spheroid. Further optimization and experimentation are necessary to fully understand these patterns and their origins. Nevertheless, this work characterizes interactions between cells and their extracellular matrices, providing context about how cell-environmental reciprocal interactions can promote cancer progression.

Victor Lee CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Kore Liow

Title: Cardiac Autonomic Context Moderates the Association Between EEG Alpha Reactivity and Reaction Time in Mild Cognitive Impairment

Abstract: Mild cognitive impairment (MCI) is defined by changes in memory and thinking, yet there is substantial variability in its underlying physiology and diagnostic trajectory. This drives the need for accessible biomarkers to better characterize this heterogeneity. Alpha reactivity—the difference between eyes-closed and eyes-open alpha power on resting electroencephalography (EEG)—has shown a graded association with

cognitive status, differentiating healthy controls, MCI, and dementia; we therefore explored its association with reaction time and ERP latency (the interval between stimulus onset and its associated brain-wave peak). We conducted a cross-sectional chart review of 182 patients with MCI who underwent Biomarker-Based Electrophysiology for Advanced Monitoring (BEAM), which provided resting-state EEG and heart rate variability (HRV) measures alongside task-based EEG and behavioral data from three cognitive assessments: an auditory oddball task, a standard image recognition task, and a 3-choice vigilance task. Although alpha reactivity was not directly correlated with either reaction time or ERP latency, the LF/HF ratio—a measure reflecting the balance between faster, breathing-linked and slower, blood-pressure-linked fluctuations in heart rate—significantly modulated the relationship between alpha reactivity and reaction time, particularly in the 3-choice vigilance task. This interaction may reflect competition between internally directed (interoceptive) and externally directed (exteroceptive) attention. Our findings support the potential of combined EEG-HRV assessment as a non-invasive, portable, resource-efficient tool for characterizing physiologic variability in MCI, helping to clarify diagnoses and inform prevention protocols.

Madeline Lee CC'29, Chemistry, Earth Science

Faculty Mentor(s) or Supervisor(s): Molleigh Preefer

Title: Quantifying Amorphous Content in HERMES Feedstocks to Streamline Critical Minerals Extraction

Abstract: Critical minerals and materials (CMMs) are essential for building renewable energy technologies like batteries and hastening the green transition, yet these materials face threatened supply chains due to a lack of production in the US. To identify a reliable domestic source of CMMs, the Department of Energy launched HERMES (Hastening the Exploration & Recovery of Minerals from Earth & Energy Systems), a national initiative that aims to characterize and extract critical materials from unconventional sources like the byproducts of coal combustion. Two key feedstocks HERMES is studying are coal fly ash and coal refuse due to their wide availability in waste piles across the country. Better understanding the percentage of amorphous (non-crystalline) content in these samples can improve researchers' understanding of the spatial distribution of CMMs. This project used X-ray diffraction at the Stanford/SLAC synchrotron to characterize key features about each sample and manually calculate the percentage of amorphous content, with the goal of building an amorphous calibration curve for future HERMES researchers to use. To develop the

calibration curve, samples were prepared for X-ray diffraction containing varying percentages of 100% amorphous coal fly ash or coal refuse and 100% crystalline zinc oxide standard. The diffraction data was refined using GSAS-II software and the Internal Standard Method was used for the amorphous calculation. Being able to quickly calibrate the amorphous percentage in feedstocks will reduce the amount of time spent on lengthy data refinement and manual calculations, overall streamlining extraction procedures for critical minerals and materials from a domestic source.

Joshua Lee CC'28, Education, Biochemistry

Faculty Mentor(s) or Supervisor(s): Dr. Matthew Yousefzadeh Yousefzadeh

Title: Investigating the Effects of Rapamycin on Age-related Gene Expression

Abstract: A central goal of modern biomedical aging research is not merely to extend lifespan, which is defined by the total number of years an individual lives, but to extend healthspan, the proportion of life spent in good health and away from chronic disease. Although the average lifespan has increased by about 26 years since 1950, there is still a gap between the average lifespan and average healthspan, which is about 9 years. By targeting biological aging, age-associated outcomes of chronic diseases can be minimized. Aging is viewed as being driven by the accumulation of cellular damage over time; furthermore, the immune system is especially vulnerable to the direct effects of aging as older adults become more prone to infection and less responsive to vaccination, making immune decline a promising target for healthspan-extending interventions. Rapamycin, an inhibitor of the mechanistic target of rapamycin pathway, is one of the most well-studied aging interventions shown to extend healthspan and, by extension, lifespan. In this study, we determine whether rapamycin treatment alters gene expression across immune cell populations through single-nucleus RNA sequencing, and if so, whether these changes are broadly distributed across the genome or within specific pathways. To address these questions, 18-month-old mice were fed either rapamycin-encapsulated or control chow, alongside 5-month-old young controls for 7 months. By characterizing the specificity of rapamycin-induced changes, this study also aims to investigate whether rapamycin actively restores lost immune function or dampens aberrant immune activity, a distinction with direct implications for its viability as a healthspan-extending therapeutic.

Simon Leton CC'28, Political Science - Statistics

Faculty Mentor(s) or Supervisor(s): Justin Phillips
Title: Partisan Polarization in 1970s Vermont

Abstract: Over the last generation, partisan polarization on “culture war” issues has become a defining feature of American politics, with the Democratic Party embracing social liberalism and the Republican Party embracing social conservatism. This was not always the case; for much of the twentieth century, social issues such as abortion rights and LGBT rights played virtually no role in politics. Today, of course, they are central to partisan conflict. Despite its importance, this transformation is not well understood. In fact, there is little consensus among political scientists about its timing, sequence, or causes. This research examines how these changes occurred through a focused case study of Vermont’s political transformation between 1968 and 1970. It then compares developments in Vermont with national shifts to determine whether the state’s political transformation during this period resulted from broader forces or from characteristics unique to the Green Mountain State. To do so, this research evaluates hundreds of articles from local newspapers across Vermont to understand how and why this transformation took place.

Hayden Leung SEAS’28, Computer Science, Austin Wijaya SEAS’28, Computer Science

Faculty Mentor(s) or Supervisor(s): Cassandra Burdziak
Title: MINA: linear probes reveal coding-sequence family signal in frozen DNA encoders up to protein composition

Abstract: Frozen DNA encoders are widely used as feature extractors, but fine-tuning hides what their fixed embeddings already make linearly accessible. We introduce MINA (Model Interrogation of Nucleotide Architectures), a lightweight benchmark testing whether frozen DNA embeddings can recover (i) a 5-way protein-family label and (ii) the 1,536-d GenePT natural-language embedding for each gene, comparing coding-sequence (CDS) and transcription-start-site (TSS) contexts under a homology-aware split, against translated-composition and protein-language-model baselines. Across 3,244 human genes from five families, the best DNA encoder recovers CDS family labels above 4-mer composition (NT-v2 macro-F1 0.727 vs. 0.633) but only reaches translated amino-acid composition (AA 2-mer 0.735), far below ESM-2 on translated proteins (0.960). GenePT recovery is weak (best DNA R2 = 0.077), and TSS family recovery collapses under homology control (NT-v2 0.447 → 0.313). Pooling and encoder choice

matter as much, so encoders are not interchangeable: frozen DNA encoders expose coding-sequence protein-compositional signal from raw nucleotides, not robust gene-function signal from arbitrary genomic context.

Terran Li CC’28, Economics, Maraki Tamrat CC’27 Cognitive Science, Tommaso Vincenzo Tricamo CC’28, Political Science, Anjelica Anyango Young CC’28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Sarah Ashcroft-Jones
Title: Green policy around the globe: consensus and variability in adoption, implementation, and efficacy

Abstract: In this study, nine green policies with global relevance underwent systematic review, assessing implementation status and economic, behavioral, environmental, and social outcomes. The policies were chosen due to their inclusion in a recent large-scale study across 23 countries. These policies included: product carbon taxation, a ban on fossil fuel ads, presence of green infrastructure programs, participation in the Global Climate Fund, a ban on food waste, presence of energy-efficient building standards, a consumer flight tax, implemented nature-based solutions, and subsidies for renewable energy. Using a systematic consensus-based approach, these policies were reviewed in the 23 sample countries, assessing both current empirical evidence and theoretical projections for impact and efficacy. A high degree of heterogeneity was revealed across all nine policies, both in terms of effectiveness and the scope of impact under the four outcome dimensions: economic, environmental, social, and behavioral. There were promising results on all outcome dimensions beyond environmental benefits, yet some of the policies lack proper implementation. The results and successes of these policies proved context-dependent, highlighting the importance of institutional theory, governance, transparency, and legitimacy as determinants of policy success. The review of the policies shows promising results across all outcome dimensions, especially when adopted as policy mixes, while demonstrating the variability in implementation status and approach across countries and policy types. Challenges to implementation, country variability, the need for greater empirical evidence, and next steps are discussed as relevant to future green policy decisions.

Leo Li CC’27, Biology

Faculty Mentor(s) or Supervisor(s): Shah Ali

Title: Coupling and uncoupling proteins regulate Cardiomyocyte development and key to achieving heart regeneration

Abstract: Heart disease is the leading cause of death in the US, primarily due to our heart's inability to regenerate. In mammals, cardiac regeneration is possible before birth. These cardiomyocytes obtain additional DNA after birth, becoming polyploid due to cytokinesis failure, which is connected to a loss of regenerative potential. Zebrafish have mononucleated cardiomyocytes yet have regenerative capabilities. To identify the missing pieces of heart regeneration, uncovering the mechanisms behind polyploidization is necessary. In *Drosophila*, cytokinesis occurs before DNA replication during the embryonic stage, showing evidence of the uncoupling of the two cell cycles. From this screen, 4 proteins (CHORDC1, Melusin, PTS, and Nemuri) were identified as their protein levels significantly changed during this uncoupling. Utilizing wild-type mice, we investigated the presence of these 4 proteins across three time points (embryonic day 18.5, postnatal day 8, and postnatal day 60) using immunofluorescence and microscopy. Localization of all four proteins shifts dynamically across these time points, representing the shift in function throughout development. Chordc1 and PTS are significantly more prevalent during embryonic development compared to binucleation development and homeostasis of the heart, further implicating their role as coupling proteins that regulate the cell cycle. Meanwhile, Melusin and Nemuri were significantly more prevalent at P8, when binucleation occurs, implicating their role in uncoupling cell division and preventing cytokinesis. Our findings suggest a revolutionary coupling and uncoupling of the nuclear and cellular cell cycles as regulated by these 4 proteins, which can provide new targets to improve heart regeneration with significant clinical potential.

Eric Li CC'28, History

Faculty Mentor(s) or Supervisor(s): Xiaobo Lu

Title: Greasing the Machine, Inverted: Corruption as an Intermediary of Informal Governance in Developing Economies

Abstract: Why does corruption often coincide with rapid economic progress in developing economies? Various scholastic traditions have conceptualized corruption differently. Some characterized it as a moral issue with disastrous economic consequences, still others have characterized corruption as a “lubricant” that speeds up processes and bypasses red tape in inefficient bureaucracies. Depending on how one characterizes the nature of corruption, one could interpret its consequences— and thus the appropriate mitigation strategy— if desirable at all— very differently if the end goal is rapid economic

development. This specific project uses developing economies— particularly those with limited oversight via formal institutions or accountability mechanisms due to material or historical reasons— as case studies to move beyond the simplistic dichotomy of “corruption is bad” versus “corruption is good”. Rather, it attempts to demonstrate that the structural functions corruption performs must be understood in the context of the historical institutions it inhabited. The project conducted an extensive literature survey over three major threads of thought and concluded that informal institutions could, in their own right, perform governance functions — such as coordinating exchange, providing credible commitment, allocating access to scarce resources — when no formal institution counterpart was yet available. The project then suggests that corruption is, under these constrained, specific conditions, one of the intermediaries that permits informal institutions to function. In other words, corruption could be understood as a mechanism whose effects are empirical, that is, could be simultaneously beneficial or harmful not only dependent on one's metric but contingent on the ecosystem. A more fruitful way to conceptualize the nature of corruption, therefore, is to consider the counterfactual of its absence: if this intermediary were removed, would the substitute, if there were one at all, positively or negatively affect development?

Andrew Li CC'27, Astronomy

Faculty Mentor(s) or Supervisor(s): Marcel Agueros

Title: The ZTF-TESS ZuMB Project: 600+ New rotation periods in the open cluster M34

Abstract: Determining the spin periods of stars across different stellar ages is vital to understanding how young and old stars evolve. For single stars, there is no way of determining a star's age with complete certainty, but for stars which share a common origin in a cluster, the age can be determined quite easily. In this project, I use archival data from the Palomar ZTF night sky survey and TESS space telescope to determine new stellar rotation periods for 600+ stars in the bright star cluster M34, most of which have no previously reported spin period in the literature. With this, the sample of rotation periods in M34 has been expanded by at least a factor of six, and I compare these new results to similar previous results in other star clusters of different ages.

Manfred Lim CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Hugo Fernandes

Title: Modulating Lipid Droplet Homeostasis and Neuronal Cytotoxicity in Human iPSC-Derived Cortical Neurons

Abstract: Lipid dysregulation is increasingly implicated in neurodegenerative disease, emphasizing the importance of understanding how neurons maintain lipid homeostasis. Although neurons were once thought to lack lipid droplets (LDs) entirely, recent studies have shown that neuronal LDs are involved in lipid trafficking and energy metabolism. How neuronal LD abundance is regulated through pathways controlling LD formation and turnover remains unclear. Here, human induced pluripotent stem cell-derived cortical neurons were used to investigate how pharmacological modulation of LD formation, lipolysis, and lipophagy affects neuronal lipid accumulation and cytotoxicity. LD formation was promoted with oleic acid, lipolysis was inhibited with CAY10499, an inhibitor of MAGL and HSL, and lysosome-dependent lipophagy was disrupted with bafilomycin. LD abundance, cytotoxicity, and lipid-metabolism-associated gene expression were assessed by high-content imaging, ToxiLight, and qPCR, respectively. Oleic acid increased the number of BODIPY-positive LDs and total LD area. Inhibition of lipolysis with CAY10499 increased LD-associated measurements at higher concentrations, with cytotoxicity observed at the highest concentration. Inhibition of lipophagy with bafilomycin increased the number of PLIN3-positive LDs and total LD area. qPCR identified treatment-associated changes in genes involved in LD biology and lipid metabolism. Together, these findings suggest that lipolysis and lipophagy contribute to neuronal LD turnover and are important for maintaining LD homeostasis by limiting excessive accumulation. Pharmacological modulation of LD formation and turnover therefore provides a direct approach to investigate the physiological and pathological consequences of neuronal LD accumulation.

Bridget Liu CC'28, Biochemistry, Computer Science

Faculty Mentor(s) or Supervisor(s): Richard Friesner

Title: Disentangling the Black Box: Interpretable Protein-Ligand Docking

Abstract: Protein-ligand docking pipelines based on variational autoencoders (VAEs) achieve strong predictive performance but produce opaque latent representations, while the large number of candidate poses generated per complex imposes substantial computational cost as each undergoes expensive energy minimization and refinement regardless of quality. Physics-informed generative pipelines like BRAID ground predictions in thermodynamic principles, making their learned representations more likely to encode physically meaningful features and making interpretability both more

tractable and more scientifically valuable than in end-to-end learned models. We apply sparse autoencoders (SAEs) to the VAE latent space of BRAID, training on 435,069 poses across 36 protein systems. At a 4Å threshold SAE-derived features filter 29% of poor poses prior to refinement while retaining 93.6% of native-like conformations, far outperforming BRAID's own energy score. Fraction-of-variance-explained (FVE) analysis shows the top SAE retains 62% of latent variance while still supporting a high-precision filter. Feature analysis reveals sparse features activating exclusively on failed docking attempts corresponding to distinct structural failure modes and providing interpretable windows into what generative models learn about binding physics. As machine learning models take on greater roles in drug discovery, these results demonstrate that SAEs can simultaneously serve as practical computational filters and interpretability tools for building trustworthy, explainable systems.

Lisa Liu CC'29, Economics-Mathematics

Faculty Mentor(s) or Supervisor(s): Kexin Zhao

Title: Stablecoin Value Adjustment (SVA) for Financial Contracts with Stablecoin Payments

Abstract: This research investigates the financial risks associated with stablecoins, with a particular focus on issuer default risk. Although stablecoins are designed to maintain a stable value relative to the U.S. dollar, holders may still incur losses if the issuer defaults. These losses may arise from delayed redemption or declines in the value of the reserve collateral during the recovery period. The project develops a quantitative framework for measuring stablecoin issuer default risk for stablecoins that comply with the GENIUS Act regulatory framework. The research introduces the concept of Stablecoin Value Adjustment (SVA) for hypothetical stablecoin-denominated financial contracts. Analogous to Credit Valuation Adjustment (CVA) in derivatives pricing, SVA represents the fair-value adjustment to account for the risk of stablecoin issuer default. Within this framework, the fair value of a stablecoin-denominated financial contract is expressed as the value of the equivalent U.S. dollar-denominated risk-free contract, adjusted for both counterparty credit risk through CVA and stablecoin issuer default risk through SVA. The research defines stablecoin-denominated bonds and interest rate swaps, and demonstrates how issuer default risk can be incorporated into standard valuation frameworks similar to CVA calculation. Under simplified assumption of constant discount rate and constant issuer hazard rate, the research derives closed-form SVA analytical formula for unit stablecoin redemption and for stablecoin bonds. To capture more realistic

market dynamics, the study further incorporates the one-factor Hull–White interest rate model and Monte Carlo simulation to model stochastic interest-rate evolution. Numerical integration techniques are used to evaluate expected exposures along each simulated interest-rate path, and the resulting exposures are aggregated to compute SVA for stablecoin swaps. This computational framework provides a practical methodology for valuing financial contracts settled in stablecoins while explicitly accounting for issuer default risk.

Coco Liu CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Elisa Konofagou

Title: Automated Focused Ultrasound Lesion Segmentation on Harmonic Motion Imaging Validated Against Gross Pathology

Abstract: High-intensity focused ultrasound (HIFU) offers a noninvasive alternative for treating breast tumors but requires reliable lesion monitoring. Harmonic Motion Imaging-guided Focused Ultrasound (HMIgFUS) tracks ablation through tissue stiffness rather than B-mode echo intensity. This study evaluated whether HMI lesion maps agree with gross pathology. A chicken breast specimen was ablated in vitro under continuous HMI monitoring. Displacement maps were generated by subtracting post-coagulation minimum from pre-coagulation maximum displacement. The specimen was sectioned and photographed. Both were segmented by thresholding pixel values against untreated tissue baseline standard deviations. The gross pathology pipeline achieved a Dice similarity coefficient of 0.89 against manual tracing, with a margin of error of 14.5% in area (~1 mm). The HMI margin of error was about 1.5 mm in width from threshold placement and 2.0 mm in depth, as coupling gel obscures the depth reference. Width measured 11.7 mm on HMI versus 12.3 mm on pathology, a 0.6 mm difference against a combined margin of error of 1.7 mm. Depth measured 14.1 mm versus 13.0 mm, a 1.1 mm difference against 2.2 mm. Both fall within the combined margin of error, so the modalities agree. HMI-measured stiffness reflects pathology, separating benign from malignant and ablated from non-ablated tissue, so intraoperative lesion maps could verify ablation coverage and guide further sonication. Though limited to one lesion, these findings show feasibility. Future work will expand sample size and register the acoustic plane to pathology.

Cindy Liu CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Kerstin Perez

Title: Testing the Effects of Airborne Organics Contaminants on Lithium-Drifted Silicon Detectors

Abstract: Dark matter accounts for approximately 85 percent of the universe's matter, yet it has never been observed beyond its gravitational effects. The General AntiParticle Spectrometer, or GAPS, is an Antarctic balloon experiment designed to search for low-energy cosmic ray antiparticles as unique signatures of dark matter. The GAPS particle tracking system relies on over 1,000 lithium-drifted silicon detectors to measure particle trajectories and energy levels. A major concern, however, is that exposed silicon on detector surfaces contains dangling bonds that react with airborne contaminants, risking performance degradation. To neutralize these dangling bonds during the first GAPS flight in December 2025, a protective polyimide coating was applied to exposed silicon surfaces via passivation. In preparation for the next GAPS flight, we are determining whether the detectors require re-passivation. This project evaluates how effectively the detectors' previous passivation protects against airborne organic contaminants. Current testing focuses on identifying organic airborne contaminants that cause substantial, irrecoverable harm to unpassivated detectors. We select candidate contaminants based on common modes of contamination on silicon semiconductors, then expose unpassivated detectors to them in controlled environments for varying durations. Detector performance is measured before and after exposure via leakage current tests. If the performance degrades, we apply recovery procedures and re-assess detector performance to test recoverability. Contaminants causing irrecoverable harm will then be tested against previously passivated and newly passivated detectors to evaluate the original passivation's strength. Ultimately, these results will help determine whether re-passivating all 1,000-plus detectors is necessary for the next GAPS flight.

Viktor Loh GS'28, Atrophysics, Climate Systems Science

Faculty Mentor(s) or Supervisor(s): Danielle Su

Title: Mesoscale Eddy Energetics in the South China Sea - A Case Study

Abstract: Oceanic mesoscale eddies are a key process in the distribution of heat, energy and nutrient transport throughout the global ocean. Eddies can typically be observed via satellite altimetry and in-situ observations. However, in the South China Sea (SCS) these methods are limited due to its complex bathymetry and strong tides; regional eddy scales are also below the effective resolution of available satellite data. Recent literature suggests SCS eddy formation may be more strongly driven by barotropic instability than the

typical baroclinic instability driving eddy formation elsewhere. To investigate the processes driving SCS eddy formation, we analyzed 20 years (1995-2014) of high-resolution (1/12°) model output using the Nucleus for European Modelling of the Ocean (NEMO) framework. The configuration is forced by the Centre of Climate Research Singapore's SINGV regional atmospheric product, and tides. It also implements a multi-envelope sigma vertical coordinate system to account for the region's unique bathymetry. First, seasonal and spatial distributions of eddy kinetic energy (EKE) were mapped to identify seasonal EKE hotspots in the SCS. Next, the vertical distribution of EKE was examined and the relative contributions of barotropic conversion, baroclinic conversion and wind work to the eddy energy budget were quantified. We also assessed the variability of these energy budget terms with extreme years, selecting the 1997 (El Niño) and 2010 (La Niña) extreme years against 2005 as a reference. The study provides new insights into seasonal SCS eddy dynamics and their driving mechanisms, which can guide future observational studies in this data-sparse region.

Matthew Lombardi CC'29, Computational Biology

Faculty Mentor(s) or Supervisor(s): Marko Jovanovic

Title: Informing RNAi Therapeutics: Evaluating General-Purpose RNA Language Models for shRNA Design

Abstract: Micro-RNA mimicking short-hairpin RNA (shRNAmir), a form of gene-interfering RNA, shows promise in treating neurodegenerative disorders such as Huntington's disease and ALS through its ability to produce long-lasting effects while minimizing unintended interference. However, identifying the appropriate RNA sequences via experiment is a time-consuming task with billions of combinatorial possibilities. Researchers have employed machine learning models in an effort to improve the efficiency and accuracy of this process. However, it remains unclear if large, general foundation models can gain a deep enough understanding of RNA biology to match or surpass the predictive performance of specialized prediction models. This project sought to understand how accurately general-purpose RNA models like RiNALMo can predict short hairpin RNA potency compared to specialized models like shRNAi. To answer that question, this project evaluated the predictive accuracy of the RiNALMo foundation model on the same dataset used to evaluate shRNAi, which contains experimentally validated information regarding various shRNAmir sequences and their potencies. The results demonstrated that baseline variants of RiNALMo across different model sizes performed comparably to the prediction ability of shRNAi. However, fine-tuning the general model for this task allowed for

RiNALMo to outperform shRNAi. Analysis of the model's internal representations suggested that RiNALMo attends to biophysical sequence features, such as guide sequence AU nucleotide content, when considering sequence potency. Ultimately, this shows that broad, trained knowledge combined with specialized sequence exposure can yield more reliable sequence potency prediction.

Aaron Ly GS'27, Postbaccalaureate Premedical

Faculty Mentor(s) or Supervisor(s): Son Duong

Title: Using Electrocardiograms to Assess Right Ventricular Health

Abstract: Right ventricular abnormalities are important markers of pulmonary hypertension, heart failure, congenital heart disease, and other serious cardiovascular conditions. Detecting these changes typically requires echocardiography or cardiac magnetic resonance imaging, which depend on specialized equipment and expertise. Electrocardiograms, however, are inexpensive, rapid, and among the most widely available clinical tests worldwide. This project developed an artificial intelligence model that transforms the electrocardiogram into a tool for assessing right ventricular health. Using electrocardiograms paired with clinical interpretations from echocardiograms, the model learned to identify normal, mild, moderate, and severe abnormalities in right ventricular size and function. The approach recognized that these categories represent a meaningful progression of disease severity, allowing the model to learn both the presence and degree of abnormality. The completed model establishes a foundation for extracting clinically valuable structural and functional information from electrical signals alone. Its performance was evaluated across patient populations, and the electrical patterns driving its predictions were examined to support clinical interpretation. This work could enable earlier recognition of right heart disease, guide decisions about advanced imaging, and expand cardiac assessment in settings where imaging is unavailable or difficult to obtain. The next phase will integrate information learned independently from electrocardiograms and echocardiograms. By connecting the heart's electrical activity with its mechanical structure and motion, this future system aims to create a more comprehensive and accessible assessment of cardiovascular function.

Rachel Jiayi Lyons GS'27, Music

Faculty Mentor(s) or Supervisor(s): Julia Doe

Title: And the Rest Is History: Louise Farrenc and the Historiographical Construction of Nineteenth-Century Musical Authority

Abstract: Louise Farrenc (1804-1875) was a Parisian composer, pianist, and scholar who received sustained critical praise and held an elite institutional position as Professor of Piano at the Paris Conservatoire. Yet that acclaim did not secure her music a lasting place in the repertoire after her death. This project asks how nineteenth-century critical and institutional systems established Farrenc as a serious composer without producing the repeated practices necessary to sustain her music, and what her later recovery reveals about the construction of musical value. Drawing principally upon nineteenth-century concert reviews, institutional reports, biographical writing, and other criticism from the French and international press, this study traces recurring critical vocabulary across genres and professional contexts, asking how gender shaped its use and comparing these patterns with changing interpretations in modern scholarship. It argues that Farrenc's marginalization emerged from inequalities in how musical authority was constructed, sustained, and later reinterpreted. Critics praised her technical learning, expressive elegance, Classical discipline, command of large-scale instrumental writing, and professional authority while treating such qualities in a woman as exceptional. During her lifetime, Farrenc's musical authority accumulated through comparison to canonical composers, performance, pedagogy, scholarship, professional networks, and institutional prestige, but did not generate the repeated programming, performance, and historical transmission necessary for lasting presence in the musical repertoire. Modern scholarship has reassessed Farrenc's significance while sometimes reproducing inherited hierarchies of genre and canonical value. Farrenc's history therefore demonstrates that recovering neglected women requires interrogating the categories through which musical authority and historical legacies are constructed.

Yinfu Lyu CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Lixia Gao

Title: An Automated and Adaptive Quality-Control Pipeline for 128-Channel Neuroscroll Probe Recordings in Awake Common Marmoset Auditory and Auditory-Association Cortices

Abstract: Electrophysiological recordings from the auditory and auditory association regions in awake common marmosets (*Callithrix jacchus*) provide valuable insights into the neural mechanisms of auditory processing. Current chronic recordings with a 128-channel Neuroscroll probe, an ultra-flexible

high-density microelectrode array, are inevitably affected by cross-session drift and baseline noise. Unfortunately, these studies depend heavily on manual spike curation, introducing subjectivity and hindering reproducibility. Hence, standardizing an automated, adaptive quality-control (QC) paradigm is crucial for data processing. The work relies on Kilosort 4 (Ks4) to sort neuronal spikes in the primary auditory cortex (A1) and insula. Subsequently, Spike interface 0.104.7 is used to evaluate the consistency and robustness of the sorting results. Unlike fixed thresholds, which may not account for variability within and across recording sessions, the quality control framework combines seven complementary quality metrics into a normalized and weighted total score. Thresholds are determined using the 2.5-fold Median Absolute Deviation (MAD) and fixed bounds. Waveform traces from peak windows show effective preservation of real, high-quality spikes and removal of noise artifacts under both single-session and whole-day conditions across A1 and insula. Specifically, the Pearson and Spearman correlations reflect highly similar temporal structures after whole-day QC compared with single-session QC. The raster plot and Wilcoxon test demonstrate a visible and statistically significant reduction in spikes after QC. Without ground truth, QC performance is evaluated indirectly through waveform diagnostics and within-recording temporal consistency. Overall, the study provides a generalizable framework for multi-channel chronic recordings and a reproducible alternative to manual spike curation.

Jasmine Ma CC'29, Computer Science, Mathematics

Faculty Mentor(s) or Supervisor(s): Jacob New

Title: RET Fusion Partner as a Prognostic Biomarker in Non-Small Cell Lung Cancer: A Real-World Cohort Analysis

Abstract: RET gene fusions occur in a small subset of non-small cell lung cancer (NSCLC) patients and can be treated with targeted therapies, but it remains unclear whether the specific gene fused to RET affects how patients respond to treatment. This study examined real-world data from 415 patients with RET fusion-positive NSCLC to compare outcomes between the two most common fusion partners, CCDC6 and KIF5B. Using a large real-world oncology database, clinical outcomes and tumor gene expression patterns were analyzed for patients with each fusion type, with a focus on the 290 patients diagnosed with Stage IV disease. Patients with CCDC6-RET fusions were found to have substantially better survival outcomes than those with KIF5B-RET fusions. Gene expression analysis also revealed that tumors with each fusion type activate different biological pathways, where CCDC6-RET tumors showed patterns associated with normal cell structure and function,

while KIF5B-RET tumors showed patterns linked to more aggressive tumor behavior and spread. Additionally, patients treated with the drug seliparitinib had better outcomes than those treated with pralsetinib, another RET-targeted therapy. These findings suggest that a patient's specific RET fusion partner may be clinically meaningful and could help inform more personalized treatment strategies for RET-positive lung cancer patients.

Maxwell Ma CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Osama Al-Dalahmah

Title: Identifying Transcriptomic Regulators of Metallothioneins in Huntington's Disease

Abstract: Huntington's disease (HD) is a neurodegenerative disorder caused by buildup of mutant huntingtin protein that eventually leads to neuronal dysfunction. These mutant huntingtin proteins begin to cause neurodegeneration once they aggregate together, a process that requires metal ions. In healthy brains, these metal ions are controlled by proteins called metallothioneins (MTs). Previous studies have shown that increasing the level of MTs improves symptoms of mouse models of HD, providing support for their important role in stopping the progression of HD. Studies from our lab have demonstrated that MTs are downregulated in the most severely affected regions of the brain in HD, indicating dysfunction in the pathways that normally control MT levels. Currently, the field's understanding of how MTs are regulated in HD is limited, which this project addresses using transcriptomic data and experimental validation. Using a technique that analyzes the levels of MTs and other molecules in individual cells called single-cell RNA sequencing, I obtained data from tens of thousands of individual brain cells. Using the pySCENIC algorithm, I found candidates for molecules that are associated with an increase or decrease of MTs in HD. I then performed experiments that modified the levels of these molecules in astrocytes to observe the effects of MTs. The pathways that this research uncovered improves our understanding of the regulation of MTs in HD. Future research will be done in which we use these pathways to increase the levels of MTs in mouse models of HD to determine if they improve symptoms.

Karthik Mahakala CC'29, Environmental Biology

Faculty Mentor(s) or Supervisor(s): Adana Llanos

Title: Chemicals of Concern in Skin Lightening Products Available in Northern Manhattan: Label Accuracy and Packaging Patterns

Abstract: Introduction: Skin lightening products (SLPs) frequently contain chemicals of concern (CoCs) — substances linked to toxicity and bioaccumulation — often undisclosed. SLP use is widespread among women of color, rendering New York City's (NYC) diverse communities especially vulnerable. Unregulated SLPs remain commercially available, leaving consumers to rely on packaging information despite limited research on SLP safety and packaging patterns. Methods: Retailers across four Northern Manhattan neighborhoods were surveyed to build a database of unique SLPs, from which 30 were proportionally purchased. Subsequently, products were screened for CoCs via two-dimensional gas chromatography-mass spectrometry (GCxGC-MS). CoCs on ingredient labels were classified as 'disclosed', and those identified via NTA but not disclosed were classified as 'undisclosed'. Association between packaging characteristics and total CoC count were assessed using univariate tests. Results: 65 total CoCs were identified across the 30 products: 37 disclosed on labels and 28 exclusively via NTA. Products averaged 3.8 disclosed and 7.2 undisclosed CoCs each. Although five products disclosed hydroquinone, detectable levels were identified in only four of these products and in an additional five products that did not disclose hydroquinone. No packaging characteristic was significantly associated with total CoC count ($p > .05$). Conclusions: This study reveals substantial discrepancies between ingredient labels and actual SLP chemical composition, and the persistence of hydroquinone-containing products despite regulatory bans underscores ongoing enforcement gaps. The lack of association between packaging and CoC count highlights the unreliability of packaging as a safety indicator. These findings can be used to inform targeted market surveillance and risk exposure assessments.

Namya Manghnani CC'27, History, Political Science

Faculty Mentor(s) or Supervisor(s): Kalyani Ramnath

Title: South Asian Student Life, Visas, and Pathways to U.S. Citizenship in Mid-Twentieth-Century New York

Abstract: As the student visa system faces renewed scrutiny with heightened ideological vetting, rising denials, and public debate over international students' place in American life, this research returns to the system's origins to understand its founding purpose and the lived experience it produced for South Asians. Between the 1940s and 60s, the student visa evolved into a Cold War instrument, advancing American scientific ambition and extending U.S. influence abroad, while gradually opening pathways to citizenship. This project traces that transformation through South Asian students in New York,

particularly at Columbia University. Drawing on Columbia's archives alongside existing oral histories, exhibition work, legal records, and current news coverage, this research examines how the 1948 Smith-Mundt Act, the 1952 Immigration and Nationality Act, and the 1965 Hart-Celler Act reshaped South Asian student migration. Findings suggest South Asian student growth in this period was a direct expression of Cold War policy. Students were absorbed into an emerging "highly skilled labor" category, a political construction shaped by Cold War competition for scientific dominance. However, increased access did not translate into social acceptance. Indian students were held apart from broader "Asian" categorization, and in turn forged their own terms of belonging. An entirely new identity — the South Asian American, and more specifically the Indian American — took shape in this period, often expressed within student organizations. These findings suggest the "model minority" framing later applied to South Asian Americans was a narrative actively produced through Cold War-era legal categories.

Ruchi Mangtani CC'29, Political Science

Faculty Mentor(s) or Supervisor(s): Shana Redmond

Title: The Intimacies of Solidarity: George Jackson and Eldridge Cleaver's Prison Love Letters

Abstract: George Jackson's Soledad Brother and Eldridge Cleaver's Soul on Ice make up two major published collections of prison letters from the 1960s and '70s. Jackson and Cleaver's writings to their loved ones and allies trace their radicalization in prison as they took on leading roles in the prisoners' rights movement. While their expressly revolutionary writings have received the greatest attention in public discourse and existing scholarship, this project explores the significance of their intimate and ostensibly apolitical love letters. Written in real time and constantly at risk of censorship, delay, or destruction, the letters have in many ways undergone incarceration itself. They are liminal and unstable, varying in tense, genre, and length. They are a creation of the carceral experience, and they are a lifeline: letter-writing was one of the few means for Jackson and Cleaver to maintain bonds across prison walls and insist upon their humanity. Their intimate writings thus went beyond documenting affection; they fortified who Jackson and Cleaver knew themselves to be and strengthened their will to survive in totalizing and brutalizing conditions. As a result, their love letters reveal the intimacies and romance of solidarity while pursuing the most material aim of escape. The personal and the political thus emerge not as opposed spheres but mutually

reinforcing, with intimacy being a practice through which revolutionary politics — and the people who held them — could be sustained.

Eliza Manny CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Philippe Batut

Title: Mechanisms of Long-range Gene Regulation in Drosophila Embryos and Neurons

Abstract: The spatial organization of the genome is recognized as an important regulator of gene expression, but the mechanisms by which it shapes transcriptional dynamics in differentiated cell types remain poorly understood. Genome organization is established by architectural DNA elements, including tethering elements (TEs), whose pairing forms long-range chromatin loops that bring distant enhancers into proximity with target gene promoters, facilitating rapid activation of developmental genes. Polycomb factors associate with tethering element sequences genome-wide and are candidate complexes responsible for establishing these loops. Neurons offer a compelling system for studying these mechanisms: they depend on tightly regulated gene expression to establish and maintain cell identity, synaptic function, and plasticity, and display markedly more complex 3D genome organization than other cell types. Disruptions to neuronal chromatin architecture have been implicated in developmental and psychiatric disorders as well as aging. To determine whether TE-mediated long-range interactions and their associated protein complexes operate in neurons of the adult Drosophila brain, Micro-C will be used to map chromatin contacts at nucleosome resolution in genetically defined neuronal populations isolated by INTACT, combined with a chemically inducible degron system to acutely deplete candidate architectural proteins. Endogenous CRISPR alleles have been generated encoding multiple subunits of PRC1 and MKM tagged with a degron and GFP. Several of the tagged alleles for these essential genes are homozygous viable, indicating that the tags do not interfere with protein function. These validated lines provide the foundation for cell-type-specific dissection of long-range chromatin interactions in neurons of the adult Drosophila brain.

Stella Manyan CC'27, Astrophysics, Germanic Languages

Faculty Mentor(s) or Supervisor(s): Nathan Lourie

Title: Optomechanical Design and Construction of an Optical and Infrared Dual Camera Port

Abstract: This project focuses on the design, engineering, and development of a specialized camera mount supporting simultaneous dual-imaging capabilities for future astronomical follow-up observations. Time-domain astronomy requires the rapid characterization of fast-fading cosmic phenomena, making multi-wavelength data collection vital to understanding transient events. The proposed mounting system successfully integrates two distinct instruments: the SUMMER optical camera and the SPRING infrared camera. These instruments are engineered to work simultaneously to provide focused, swift follow-up observations for the Wide-field Infrared Transient Explorer (WINTER) survey. To ensure a precise, diffraction-limited system capable of reliable imaging, the dual optical pathways were optimized using Zemax optical design software. Following the optical analysis, the physical assembly was modeled in SolidWorks to ensure structural integrity under varying gravitational loads, minimize thermal impacts, and guarantee precise alignment. The detailed engineering workflow prioritized overall ease of maintenance and accessibility for servicing, incorporating custom aluminum filterwheel-to-camera adapters to isolate key design components. The resulting integrated mount enables the precise, long-term co-alignment of both camera systems. This instrument will be permanently deployed at the Palomar Mountain Observatory, with initial on-sky testing successfully completed in August 2026. This development ultimately enhances the follow-up capabilities of the WINTER survey by allowing for immediate, real-time, multi-wavelength tracking of short-lived transient astronomical events.

Emilia Marshall SEAS'27, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Juliana Carneiro

Title: Investigating the Activation Kinetics and Surface Reduction Behavior of Pt-BCO in Non-Oxidative Methane Coupling

Abstract: Platinum-barium cerate (Pt-BCO) serves as a critical anode material in non-oxidative coupling of methane (NOCM), facilitating C–H bond cleavage, methyl radical coupling to form ethane and ethylene, and the transport of protons and electrons. However, optimizing its catalytic performance requires a deeper understanding of its temperature and flow-dependent activation mechanisms, which exhibit complex kinetic behavior beyond simple thermodynamics. In this study, the temperature-programmed reduction behavior of Pt-BCO was evaluated at a heating rate of 10 °C/min across operational temperatures of 650 °C, 700 °C, and 750 °C. TPR profiles revealed distinct reduction regimes: a low-temperature peak between 100 °C and 300 °C, followed by higher-temperature reduction events at ~500 °C and 600 - 750 °C. These features correspond to specific electronic and structural

transformations, including the reduction of matrix Ce⁴⁺ to Ce²⁺ and sequential noble metal reductions Pt⁴⁺ to Pt²⁺ to Pt⁰. To correlate these reduction events with active site evolution, CO diffuse reflectance infrared fourier transform spectroscopy (CO-DRIFTS) was employed to probe Platinum coordination and oxidation states, transmission electron microscopy (TEM) evaluated surface morphology, and X-ray photoelectron spectroscopy (XPS) quantified element valence states. Together, these complementary techniques clarify how active site structure evolves under thermal and reductive conditions, offering a pathway toward catalyst design for NOCM applications.

Theo Martien CC'27, Sociology

Faculty Mentor(s) or Supervisor(s): Tey Meadow

Title: Confronting the “bully-in-chief”: Defensive Adaptations in Trans Rights Organizations Under Trump 2.0

Abstract: Trans rights organizations in the United States are currently operating under a fraught environment. In 2025, President Trump unleashed his pernicious anti-trans agenda and shuttered opportunities for advocates. The resulting political landscape sharply contrasted with that under the Biden administration, which ushered in movement progress. This investigation of public documents released by 20 trans rights organizations between 2021 and 2025 employs content analysis to illuminate how the movement adapted to the profound upset. Building on literature that would predict a transition from proactive to defensive advocacy, this study finds that trans rights organizations also supplanted statements of pressure with statements of criticism. Further, trans rights organizations reallocated resources across political arenas in surprising ways: despite the jarring rise in anti-trans bills introduced to state legislatures, trans rights organizations all but neglected state-level advocacy in favor of federal-level advocacy. Trans advocates lost not only the opportunity for federal-level proactivity but also the capacity for state-level defensiveness. Taken together, these shifts engendered a movement concentrated on holding ground against federal attacks, deprioritizing strategies that could effectuate immediate change. The political ferment in 2025 triggered a transformation unlike the trans rights movement has yet seen: from exerting active political pressure to performing reactive, passive work. This research contributes to social movement literature by theorizing how rights movements react to such sudden and comprehensive political loss.

Phoebe Matthew CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Steven Siegelbaum

Title: The Role of Ventral Hippocampal CA1 Region in Memory of Acute Social Defeat

Abstract: Social memory is impaired in several psychiatric conditions, including anxiety, autism spectrum disorder, and schizophrenia, making it important to understand the neural circuits underlying this process. Several hippocampal subregions have been implicated in this process. In particular, hippocampal area CA2 plays an important role in valence-associated social memory, whereas ventral CA1 (vCA1), a major downstream target of CA2, has been implicated in the regulation of fear-related behavior. However, whether vCA1 is required for social memory associated with negative valence remains unclear. Here, we investigated the role of vCA1 neurons in the memory of acute social defeat in mice. Acute social defeat was used as a naturalistic paradigm to associate negative valence with an individual through an attack by an aggressive mouse. Chemogenetic techniques and stereotaxic surgeries were used to silence vCA1 neurons, and social memory was assessed through behavioral analysis using a machine learning pose tracking model. Inhibition of vCA1 excitatory neurons did not impair the ability of mice to discriminate against an individual associated with negative valence. However, mice in the experimental group exhibited significantly increased freezing behavior compared to the control, suggesting that vCA1 activity may contribute more strongly to fear-like regulation than to the formation of social memories associated with a negative valence. These findings provide insight into the role of vCA1 in social and emotional processing and may contribute to understanding neural mechanisms involved in psychiatric disorders that impair social memory.

Dean Mayo GS'27, Physics

Faculty Mentor(s) or Supervisor(s): James McIver

Title: Electromagnetic Quantum Field fluctuations in a Chiral Cavity

Abstract: Empty space is not truly empty. Even in a perfect vacuum with no light present, the electromagnetic field flickers with faint random fluctuations predicted by quantum theory, with measurable effects on matter. A cavity, two mirrors facing each other, traps and reshapes these fluctuations. The McIver Lab at Columbia, in collaboration with Rice University, is building a chiral cavity, one whose mirrors treat light circulating clockwise and counterclockwise differently, to test whether these shaped fluctuations can

change the electrical behavior of a material placed inside, in the dark, with no light applied. Rice builds the cavity. Dean Mayo's work this summer was building the sensor that goes inside it. The sensor is a stack of four crystal layers, each only a few atoms thick: a single sheet of carbon called graphene, protected above and below by insulating boron nitride, resting on a thin graphite layer that lets the device be tuned with a voltage. He peeled bulk crystals down to atomic thickness with adhesive tape, searched the resulting flakes under a microscope for pieces of the right size and thickness, and assembled them one at a time with a soft polymer stamp, aligning each layer to within a few millionths of a meter. He completed two full stacks that meet the requirements of the experiment, diagnosing why an intermediate attempt failed at its final step and refining the process accordingly. Finished devices will be placed inside the cavity for its first measurements.

Alijandro Mendoza CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Dmitri Basov

Title: Fabricating Magnetic Force Microscopy Probes

Abstract: This project focuses on improving the reliability of Magnetic Force Microscopy, a technique used to study tiny magnetic patterns in advanced materials. MFM requires extremely sensitive probes made from small silicon cantilevers coated with a magnetic material. These coatings can degrade quickly when exposed to air, and commercially produced probes often spend several days in transit before reaching a laboratory. By the time they arrive, the magnetic coating may already be damaged, which reduces the quality and consistency of measurements. To address this challenge, the Basov Infrared Group at Columbia University began developing a method for fabricating these probes directly inside the laboratory. The goal is to coat and use the probes on the same day, preventing oxidation and improving performance. The project involves depositing thin magnetic films onto the cantilevers using high vacuum equipment and carefully controlling factors such as pressure, temperature, and the relative angle of the probe during coating. The probes are then examined with scanning electron microscopy to confirm that the coating is smooth and that the tip shape is preserved before moving into further testing. Early results show that in house techniques can produce coatings with uniformity comparable to commercial probes, while also being more cost effective and available same day. This work establishes the foundation for a reliable in house fabrication process that will allow researchers to create high quality MFM probes whenever they are needed. The project supports future studies of magnetic behavior in quantum

materials by improving one of the most important tools used to investigate them.

Joshua Mendoza SEAS'29, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Shaina Kelly

Title: Decoupling physical-chemical controls on REE leaching in soils and ores with low-field NMR

Abstract: Rare Earth Elements (REEs) play a critical role in modern technology, defense, and clean energy systems. However, conventional REE mining has significant environmental impacts, motivating more sustainable extraction methods. Phytomining offers an alternative by using plants to accumulate REEs from enriched soils, but faces challenges in REE mobility and bioavailability. Organic acids may accelerate REE leaching through interactions with soil mineral components amended with crushed ores. This project investigates the use of low-field Nuclear Magnetic Resonance (NMR) to characterize changes in REE-enriched substrate following acid treatment and develop a reproducible workflow for evaluating fluid-mineral interactions in these systems. Artificial substrates consisting of 30% field soil, 20% ore, 15% sand, 25% vermiculite, and 10% perlite were treated with citric, malic, oxalic, tartaric, acetic, and nitrilotriacetic acids. Three duplicates of each acid were tested at 1, 5, and 10 mmol/L concentrations. NMR analysis was performed on the samples after treatment, with a focus on T2 relaxation responses relative to untreated controls. Preliminary measurements show a leftward shift in T2 peak positions following treatment, indicating faster relaxation times compatible with paramagnetic influence on the decay of magnetized pore water at fluid-mineral interfaces. Ongoing work is focused on controlling saturation and sample preparation, time-lapse NMR (with leaching), and integration with thin section analysis to distinguish chemical effects from physical changes in pore-water distribution. These results support NMR's potential as a complementary tool to fluid chemical analysis (i.e., ICP-MS) for characterizing REE source, mobilization, and sinks within soils and other porous media environments.

Amy Meng CC'29, Political Science

Faculty Mentor(s) or Supervisor(s): Sonya Chen

Title: Asian American Environmental Advocacy in New York City

Abstract: Although existing literature reflects high levels of concern for environmental issues among Asian Americans, their contributions to

environmental advocacy receive comparatively low scholarly and public attention. This research examines how Asian Americans in New York City, with particular focus on Manhattan Chinatown and Flushing in Queens, as well as neighborhoods in Brooklyn and the Bronx, advocate for environmental and political justice in their communities. Over six weeks, the study used a qualitative approach consisting of a literature review, neighborhood walk-throughs and documentation, research on fourteen Asian American nonprofit organizations, and semi-structured interviews with organization members and residents. The research identifies four primary avenues of advocacy: youth leadership and education, artistic activism, digital community organizing, and environmental stewardship. Grassroots organizations such as The W.O.W. Project, Welcome to Chinatown, Chinatown Youth Initiatives, and Neighbors United Below Canal reveal that environmental advocacy is often deeply intertwined with housing security, public health, gentrification, and cultural identity. The research also finds that various forms of Asian American environmental advocacy may not always be recognized as political participation, including educational workshops, public art projects, social media engagement, neighborhood cleanups, and community gardens. These forms of engagement may vary across generations, with younger interview participants describing social media as a key avenue for learning about and sharing community issues, while perceiving older generations to be less active on social platforms. The diversity of community-centered approaches to advocacy challenges common perceptions that Asian Americans are politically inactive in environmental movements.

Arjun Menon CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Andres Bendesky

Title: Identification of molecular markers of Adrenal gland-projecting cells in the brains of *Peromyscus polionotus* and *maniculatus*

Abstract: Stress-related psychiatric and cardiovascular conditions, including PTSD, major depressive disorder, and hypertension, have been linked to dysregulation of sympathetic circuits controlling epinephrine release. The adrenal medulla, a primary source of circulating epinephrine during stress responses, receives descending input from the hypothalamus, but the specific neuronal populations driving this connection have remained poorly characterized. Using monosynaptic rabies virus tracing from the adrenal medulla in *Peromyscus polionotus* and *maniculatus*, adrenal-projecting cells were identified in the paraventricular hypothalamus (PVH), and single-cell RNA sequencing was performed to define their molecular identity. Rabies-

labeled neurons were significantly enriched in a discrete transcriptomic cluster (cluster 2367), comprising approximately 40% of labeled cells compared to roughly 3% of general spinal-projecting PVH neurons. Differential expression analysis identified combinatorial molecular markers distinguishing this population, including *Ecm1* and *Slc22a23* within cluster 2367, and *Retreg3* paired with *Slc22a23* across the broader adrenal-projecting population. Notably, the ion channel *Piezo2* was enriched 9.1-fold in cluster 2367, distinguishing it clearly from surrounding hypothalamic populations. These findings establish a molecularly distinct hypothalamic population with a defined projection target to the adrenal medulla, offering candidate markers for a stress-responsive circuit relevant to sympathetic dysregulation in disease. Ongoing work focuses on validating these markers in situ and confirming the projection identity of cluster 2367 through complementary anatomical and genetic approaches.

Lydia Mhando CC'29, Human Rights

Faculty Mentor(s) or Supervisor(s): Tracey Holland
Title: Children's Rights and the Arms Industry

Abstract: For the longest time, the human rights framework has placed almost full responsibility on sovereign states to respect, protect, and fulfil individuals' rights. Consequently, significant gaps in accountability have emerged for non-state actors, particularly corporations, which have faced less scrutiny than states. UNICEF recognizes children as a vulnerable group, making them inherently dependent on others for their survival, well-being, and development. They are therefore entitled to special protection, and all actors are responsible for ensuring this. This research examines how children living in conflict-affected regions are affected by the products and services produced by arms companies. To do so, this research investigates the corporate policies of arms companies to understand how they publicly address the rights of children living in conflict-affected areas. The companies examined were drawn from SIPRI's 2024 list of the world's top 100 arms-producing companies. Publicly available corporate documents, including codes of conduct, annual reports, supplier regulations, and sustainability reports, were analyzed. The analysis focused on the presence of children's rights, human rights due diligence, risk assessment, investigation and remediation, and end-use monitoring. Some of the findings indicate that while companies have relatively robust monitoring processes within their supply chains, there are limited mechanisms for monitoring the end use of their products. Few companies explicitly refer to affected populations, and where they do, such as Kongsberg Gruppen, these references are not made in the

context of violence or war. These findings highlight gaps between corporate human rights commitments and the risks faced by children in conflict-affected settings.

Eugene Miller GS'27, Postbaccalaureate Premedical

Faculty Mentor(s) or Supervisor(s): Anne-Catrin Uhlemann
Title: Body Site Does Not Predict Phage Susceptibility in Drug-Resistant *Klebsiella Pneumoniae*

Abstract: Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is a priority pathogen and a leading cause of antibiotic treatment failure. Bacteriophage (phage) therapy has been proposed as an alternative treatment. Our previous work suggested that phage defense systems, the bacterial immune systems against phage infection, were less diverse in isolates collected from urine. Our hypothesis was that phage susceptibility also differed by body site. We tested 34 diverse CRKP isolates from urine, blood, and respiratory sources against a core panel of 12 varied phages given to every isolate (384 pairs). We then challenged the five isolates that resisted the entire core with 8 additional phages. A typical isolate was lysed by about three quarters of the core panel and rates of lysis did not significantly differ between body sites (median 0.80 blood, 0.75 urine, 0.67 respiratory). Lysis varied more by phage than bacterium, with individual phages that lysed 6 to 85 percent of tested isolates. Two isolates, one from blood and one from urine, resisted all 20 phages tested against them. Effective phage therapy requires a phage able to lyse the infecting strain. Body site alone did not predict susceptibility, but most isolates had several lytic options. The resistant isolates identified provide a means to define the mechanisms of phage resistance. These findings suggest that lower defense-system diversity in urine may reflect a narrower range of phage threats at that site rather than a site-level difference in susceptibility.

Jake Miller CC'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Alice Prince
Title: SigX Regulates Bacterial Metabolism to Suppress the Host NAD⁺–NMNAT1–SIRT6 Metabolic Axis and Drive Host Dysfunction During *Pseudomonas aeruginosa* Pulmonary Infection

Abstract: *Pseudomonas aeruginosa*, a gram-negative bacterium, is an opportunistic pathogen associated with pneumonia, burn and wound infections, and chronic airway infections found in cystic fibrosis patients. This bacterium exhibits exceptional adaptability due to its large number of

regulatory elements, including various sigma factors that modulate its response to environmental stresses. Sigma factors, particularly extracytoplasmic function sigma factors, are crucial for transcriptional regulation in response to extracellular signals. Here, we show that the sigma factor sigX is vital for managing bacterial growth and host interactions during airway infections. Comparative analyses of wild-type and sigX mutant strains revealed that although the wild type showed greater growth in complex media outside of a living host, infection with the sigX mutant resulted in much higher bacterial loads but a decreased host response. After conducting a comprehensive analysis of gene expression in the bacterial and host cells, we identified significant changes in genes responsible for maintaining the energy pool of the host cells during infection. The presence of sigX suppresses the production of NAD, a key energy molecule, and the function of the SIRT6 protein. SIRT6 helps regulate cell metabolism by promoting efficient energy use, supporting mitochondrial energy production, reducing excessive inflammation, and helping cells adapt to stress. Together, these effects can help cells maintain normal function and limit tissue damage during infection. We therefore propose that the sigX mutant can reach higher bacterial loads without causing more severe disease because increased NAD and SIRT6 activity allow host cells to better tolerate the infection.

Yordan Mintz CC'27, Computational Biology

Faculty Mentor(s) or Supervisor(s): Tim Lantin

Title: Brain-wide, cell-type-specific locus coeruleus modulation of the transcriptome

Abstract: The locus coeruleus is the brain's main source of norepinephrine, a chemical messenger that influences arousal, attention, learning, and neuroplasticity. Although changes in norepinephrine signaling are common in major depression, post traumatic stress disorder, and anxiety, it remains unclear how long term changes in locus coeruleus activity affect gene expression in different types of brain cells.

This study repeatedly increased or decreased the activity of norepinephrine producing locus coeruleus neurons over three days and then measured gene expression in individual cell nuclei across the brain. In total, 108823 nuclei representing 32 major non cerebellar brain cell classes were analyzed. The effects of locus coeruleus activity varied greatly between cell types and were strongest in a small number of cortical cell populations, particularly excitatory neurons. Increasing locus coeruleus activity primarily increased gene programs involved in postsynaptic neurotransmitter receptors. Decreasing activity instead increased programs involved in presynaptic

neurotransmitter release and synaptic structure. These opposite manipulations therefore affected largely different parts of the synaptic machinery rather than simply increasing or decreasing the same processes.

Parvalbumin interneurons showed a particularly distinct response, with reduced expression of genes involved in cellular energy production during increased locus coeruleus activity. The response to prolonged inhibition also suggested that brain cells actively compensate for reduced norepinephrine signaling. These findings show that sustained locus coeruleus activity can reshape synaptic gene programs throughout the brain in highly specific and direction dependent ways.

Saba Mirafzal SEAS'29, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Dr. Michal Levo

Title: Development of an Automated Imaging Analysis Pipeline to Quantify Single mRNA Transcripts During Cellular Differentiation

Abstract: Cell fate specification during development relies on precise spatial and temporal gene expression, governed by a multitude of regulatory elements scattered in the genome. To decipher how these elements work together to dynamically tune the activation of often distal genes, we need the capacity to engineer these sequences and to assess the consequences to the target gene activity (mRNA production). The latter can be obtained by single-molecule fluorescence in situ hybridization (smFISH), in which mRNA transcripts of a gene of interest are fluorescently labeled, but precise quantification requires robust and automated image analysis pipelines, applicable in the right cellular contexts. During the summer, an automated end-to-end Python image-analysis pipeline was developed with lab members to process high-throughput smFISH microscopy images from mouse embryonic stem cells. The pipeline incorporates 3D nuclear segmentation via the machine-learning algorithm Cellpose and subpixel RNA spot detection using BIG-FISH. Quality control scripts were written to report nuclear volumes, validate spot intensities and quantify spot density.

Moving into the upcoming academic year, this quantitative imaging workflow will be deployed to characterize the expression of Isl1, a gene critical for motor neuron identity that is controlled by distal enhancers located 200 and 600 kilobases away; how these elements regulate its timely activation in cells remain unclear. To address this, we will perform smFISH to evaluate transcription across sequential differentiation time points, in CRISPR/Cas9-engineered cell lines carrying combinatorial enhancer perturbations. Combining genome engineering with single-cell transcript quantification will

provide insight into how distal non-coding elements govern cell fate decisions.

Joel Montano Angulo SEAS'27, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Addis Kidane

Title: Design of a Bulge Testing System for Investigating Material Behavior Under Complex Loading

Abstract: This research focused on the design and development of a custom bulge-testing system to investigate the deformation behavior of materials under complex loading conditions. Bulge testing provides a method for studying how thin specimens deform under pressure and can be used to better understand material behavior under these conditions that are difficult to reproduce using conventional testing methods. Drawing on existing experimental methods and published research, a new bulge-testing apparatus was designed entirely in-house. The system was modeled and CNC programmed using Fusion360 and manufactured from 6061 aluminum down to 0.001" tolerance, leveraging the CNC Mills provided in the Mechanical Engineering Teaching Lab. This process involved developing the mechanical design, revising designs for fabrication, and integrating the system into a full-fledged experimental setup capable of consistent and controlled material testing. A major focus of the research was the development and testing of specialized specimens designed to experience complex loading. The apparatus will be used to study the deformation behavior of complex geometries compared with that of specimens subjected to uniform loading, providing insight into how different loading conditions influence the material response. High-speed Photon cameras will be used alongside digital image correlation to capture and quantify specimen deformation during testing, measuring strain localizations. Together, these efforts combined mechanical design, machining, experimental testing, and high-speed optical measurement to establish new experimental capabilities for studying material behavior in both controlled and dynamic loading conditions.

Margaux Moos CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Megan Sykes

Title: Using Mixed Lymphocyte Reactions to Select Pig-Reactive T Cells To Investigate Positive and Negative Thymic Selection in a Humanized Mouse Model

Abstract: Xenotransplantation of genetically modified pig kidneys is a promising solution to the rapidly increasing organ shortage facing patients suffering from kidney failure. However, T cell mediated immune rejection through both direct and indirect pathways poses a barrier to widespread clinical adoption, making induction of immune tolerance a desirable goal. Two approaches to inducing human T cell tolerance to the pig have been developed, both involving selection of a tolerant T cell repertoire in the thymus. The precise mechanisms of tolerance of pig-reactive human T cells in these models remain unclear, so this study aims to develop T cell receptor (TCR) transgenic tools to investigate the thymic fate of pig-reactive T cells in humanized mice. Xenogeneic donor-reactive T cell clones were identified from direct and indirect mixed lymphocyte reactions, and TCRs of interest were selected based on clonal expansion and phenotype via bulk TCR beta and single cell RNA/TCR sequencing. A viral vector carrying the DNA of a pig-reactive TCR of interest was used to transduce human CD34+ hematopoietic stem cells (HSCs) that were then injected into irradiated thymectomized immunodeficient mice transplanted with a fragment of HLA-matched human fetal thymus. While sufficient immune reconstitution was not achieved, useful information regarding HSC quality and number was identified, and will be used to optimize future experimentation. This project successfully characterized pig-reactive human T cells and generated the tools necessary for future thymic selection experiments. Tracking positive and negative selection will advance the understanding of the mechanisms underlying xenograft tolerance induction.

Jesus Morales Santos GS'27, Biology

Faculty Mentor(s) or Supervisor(s): Anna-Lena Steckelberg

Title: Acute degradation of DDX6 decreases Zika virus replication and infectivity

Abstract: Mosquito-borne flaviviruses are positive-sense, single-stranded RNA viruses that cause an estimated 400 million infections worldwide each year. Zika virus (ZIKV), a member of the Orthoflavivirus genus, can cause congenital abnormalities, including microcephaly. Despite their global health burden, no antiviral therapies are available against flaviviruses, and the available vaccines are not broadly used. The flaviviral RNA contains untranslated regions (UTRs) at both the 5' and 3' ends that flank a single open reading frame. Tertiary RNA structures within the 3'UTR resist degradation by cellular 5' to 3' exoribonucleases such as XRN1, leading to XRN1 stalling and the accumulation of subgenomic flaviviral RNAs (sfRNAs). sfRNAs play important roles in immune modulation and cellular

toxicity. DDX6, a DEAD-box RNA helicase, has been identified as one of the few host proteins that interact with sfRNAs in both human and mosquito cells, but its specific role in ZIKV infection remains to be fully elucidated. Here, we investigate the role of DDX6 in ZIKV infection using a degron-mediated protein depletion system. We hypothesize that acute DDX6 depletion will impair viral RNA replication and reduce viral infectivity, demonstrating that DDX6 is required for efficient ZIKV replication. These findings would identify the viability of DDX6 as a potential target for antiviral therapy. Because host-targeted therapies are less susceptible to viral escape mutations than direct-acting antivirals, this approach may represent a promising strategy for combating flaviviral infections.

Leonardo Moreno CC'29, Economics-Political Science

Faculty Mentor(s) or Supervisor(s): Justin Phillips

Title: Party Reform and the Origins of Abortion Politics in the State of Idaho

Abstract: This paper tests the theory developed by Gerald Gamm and Justin H. Phillips that Democratic Party reforms of the late 1960s and early 1970s transformed state party organizations by expanding participation and empowering previously marginalized activists, particularly young and liberal Democrats. Gamm and Phillips argue that reforms focused on delegate selection produced broader consequences for party politics by changing who participated in party institutions and enabling activists to influence Democratic platforms, including on abortion before *Roe v. Wade*. This paper examines Idaho as a state-level test of their theory, tracing changes in Democratic participation, delegate selection, and platform politics from 1968 to 1972. Drawing primarily on contemporary newspaper coverage of party meetings, precinct caucuses, state conventions, and platform debates, it examines the relationship between institutional reform, participation, and ideological change. The evidence is broadly consistent with Gamm and Phillips's theory. In 1968, Idaho's Democratic Party showed limited evidence of significant youth influence and remained largely shaped by established party actors. By 1970, younger Democrats increasingly challenged party leadership and sought greater participation in determining the party's direction. Following the adoption of a more open delegate-selection process in 1972, participation expanded dramatically, and young delegates became a significant force within the state convention and platform debates. Their influence extended to abortion, sex education, voting rights, and the Vietnam War. The Idaho case demonstrates how changes in party organization can reshape both the composition of party institutions and the policies they advance.

Nikhil Mudumbi CC'27, Mathematics

Faculty Mentor(s) or Supervisor(s): Ivan Corwin

Title: Hole Probability Asymptotics for Free Fermions via the Stochastic Bessel Operator

Abstract: Recent work in the physics literature on systems of many identical quantum particles, known as fermions, examined the probability that a region of space is completely empty of particles -- specifically, the probability that no particle occupies a ball of a given radius, broken down by angular momentum. The researchers proposed an approximate formula for this probability, but their derivation relied on a heuristic argument that was never rigorously justified. This work provides a rigorous derivation of that formula using a different strategy. The physics problem is recast as a probability problem in which all of the randomness comes from a single evolving random process. Within this framework, the author first gives a heuristic argument that recovers the formula predicted in the physics literature, then works to make it rigorous by proving matching lower and upper bounds. The lower bound has been proven; the upper bound remains ongoing.

Van Muller CC'29, Classics and Political Science

Faculty Mentor(s) or Supervisor(s): Katharina Volk

Title: "An Empire for Liberty:" The Impact of the Classical Canon on Imperialism in the United States Constitution

Abstract: This research project argues that the American Framers' classical background and knowledge of ancient constitutionalism provide a lens through which to view the development of United States constitutional provisions for territorial expansion. Although classicist Carl J. Richards has previously demonstrated that the Framers' classical education considerably influenced the drafting of the United States Constitution, and legal historian Benjamin Straumann has theorized both on the nature of classical constitutionalism and imperialism, neither completely connected the matters together nor considered the United States Constitution a beneficiary of the unique combination of these ideas. First, this project introduces relevant scholarship in a literature review and reaches an understanding of the classics during America's founding era. Then, the project transitions to the Framers' ancient inspirations, namely Polybius and Cicero, to determine that classical constitutionalism presupposes and thus relies on the imperial state. Finally, the project transitions back to the 18th century to evaluate that there is a

correlation between classical depictions of good constitutions depending on imperialism and the admissions, property, sweeping, general welfare, and territory clauses of the United States Constitution. These findings are significant for the purpose of evaluating the United States Constitution both historically and with reference to modern constitutional interpretation, and reveals that classical thought has played no small role in shaping modern regimes.

Jackson Myers GS'28, English, Mathematics

Faculty Mentor(s) or Supervisor(s): Andrew Blumberg

Title: Anomaly

Abstract: Jackson's research occupies the intersection between mathematics, philosophy, literature, and literary criticism. During the summer, he investigated and developed ideas in the philosophy of science and information theory, beginning specifically with the problem of anomaly detection and characterization—the question of how extraordinary phenomena can be inferred to exist and how they are integrated into the scientific literature. He began by studying the mathematical and information-theoretical underpinnings of knowledge and inference and continued to trace relevant ideas into the field of scientific philosophy, delineating a conceptual framework of ideas in association with prominent theorists concerned with the nature of how scientific communities recognize, delineate, and reckon with the unfamiliar. He continued to follow relevant concepts into the realm of literature and literary criticism, focusing mainly on the use of poetry as a metaphysical tool for inference and the incitement of novelty. Since Jackson is, himself, a poet, his research became entwined with the creative act, culminating in a short collection of poetry that gives literary form to the questions of hiddenness and emergence that motivate his more technical study.

Aung Myint GS'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Dalibor Sames

Title: Kinetic Fingerprints of Inhibition: Resolving the Mechanistic Basis of VMAT2 Blockade by Ibogaine Alkaloids and Tetrabenazine

Abstract: The vesicular monoamine transporter 2 (VMAT2) governs the loading of dopamine, serotonin, and norepinephrine into synaptic vesicles, making it a central node in both therapeutic intervention and substance-use pharmacology. While tetrabenazine (TBZ) is a clinically approved VMAT2

inhibitor and ibogaine-class alkaloids have drawn renewed interest for their anti-addictive and neuroplastic properties, the precise kinetic mechanisms by which these structurally distinct compounds inhibit VMAT2 remain incompletely characterized. This project aims to define the Michaelis-Menten kinetic parameters (K_m , V_{max}) of substrate transport at hVMAT2 in the presence of four pharmacologically significant inhibitors which are ibogaine, noribogaine, TBZ, and N-ethylnoribogaine by using a fluorescence-based vesicular uptake assay with appropriate nonspecific-binding correction (reserpine-defined floor). By systematically varying substrate concentration across a fixed range of inhibitor concentrations, Lineweaver-Burk and nonlinear regression fits are generated to classify each compound's inhibition mode as competitive, noncompetitive, uncompetitive, or mixed, and derive corresponding K_i values. We hypothesize that the ibogaine-derived alkaloids, despite sharing a core indole scaffold with divergent basicity and lipophilicity from TBZ's benzoquinolizine structure, will exhibit distinct binding kinetics reflecting differential engagement of the transporter's substrate-translocation versus allosteric sites. Elucidating these mechanistic differences will clarify structure-kinetic relationships within this inhibitor class and inform the rational design of next-generation ibogaine analogs with improved selectivity and reduced cardiotoxic liability.

Ahalya Nambiar CC'29, Neuroscience, Baifern Boondoungprasert BC'28 Cognitive Science, Economics, Uma Laroia BC'29, Neuroscience & Behavior, Neomi Li Simoni GS'27, Biology

Faculty Mentor(s) or Supervisor(s): Sarah Ashcroft-Jones

Title: 24 Countries, 20 Languages, One Study: Challenges and Lessons Learned from Global Research

Abstract: Cells use immune defense mechanisms in order to recognize viral infections and limit their viral spread. Some of these defenses detect double stranded RNA, which is a molecule commonly associated with viruses. However, our cells can also naturally produce double stranded RNA, therefore tight regulation of these immune pathways is needed. When this regulation is disrupted, immune proteins may become overactive and contribute to disease. This project investigated an innate immune protein called Protein Kinase R, or PKR, that responds to double stranded RNA by reducing protein production within the cell. Genetic mutations affecting PKR have recently been identified in patients with inflammatory and neurological diseases, but how these changes alter PKR activity remains unknown. The

study examined several disease associated PKR mutations using cell based experiments. Their activity was compared with normal PKR to determine whether disease associated genetic changes could alter activation of the protein and its downstream signaling pathways. The project also explored whether similar genetic changes could be studied in an animal model, which may eventually help better understand how altered PKR activity contributes to disease. The findings suggest that disease associated changes in PKR can affect its activity and support further investigation into how abnormal regulation of this antiviral pathway may contribute to human disease. This work also highlights important considerations in developing experimental models for studying altered PKR signaling.

Melnick Nebart CC'27, Astrophysics

Faculty Mentor(s) or Supervisor(s): Paul Schenk

Title: Mapping Surface Roughness Across Europa, Ganymede, and Enceladus

Abstract: Europa, Ganymede, and Enceladus are icy moons whose landscapes preserve evidence of impacts, fractures, ridges, and possible geologic activity. This project investigates how rough each surface is and how that roughness changes when measured over different distances. Melnick Nebart conducted the research at the Lunar and Planetary Institute under the supervision of planetary scientist Paul Schenk. The study used digital terrain models, which are three dimensional maps of surface elevation created from spacecraft images. Regions representing different terrain types were selected and checked for missing data and image processing artifacts. A computer based analysis then measured differences in elevation over progressively larger distances. This approach revealed whether small features, such as closely spaced ridges and troughs, or broader landforms contributed more strongly to the shape of each surface. Preliminary results show that roughness often grows rapidly over short distances and more slowly over longer distances. On Europa, the average change in behavior occurred near five hundred meters. Bands, ridged plains, and impact debris showed especially strong shifts, while chaotic and cratered terrains retained more large scale relief. Ganymede and Enceladus showed similar patterns, although differences in image resolution and the number of sampled regions require caution. Understanding Europa's surface roughness may help scientists interpret radar observations from NASA's Europa Clipper mission, because surface features can produce echoes that resemble signals from beneath the ice. The project also provides a reproducible method for comparing landscapes across icy worlds.

Simon Nemeh SEAS'28, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Christopher Chen

Title: From Remote Kitchens to the Lab: Continuation of a Low Cost, Take-Home Fermentation Lab for First-Year Engineering Students Using Sourdough and Kombucha

Abstract: During the COVID-19 lockdown, a first-year chemical engineering laboratory course was redesigned so students could complete experiments safely at home using common, inexpensive materials. The six-week module used sourdough fermentation to teach students how engineers track the movement and transformation of materials and study the rate of chemical and biological processes. Because sourdough starters can behave differently depending on factors such as flour type, temperature, or feeding schedule, students also learned how to design experiments when conditions are not perfectly controlled and subsequently interpret real experimental variation rather than working only with idealized data. The laboratory continued after courses returned to campus and was later adapted for high school programs where a similar protocol was developed for students to explore kombucha as another fermentation system. Unlike dough, kombucha is a liquid, making it possible for students to directly measure changes in acidity and sugar concentration as fermentation progresses. This project describes the development of these fermentation experiments, along with lessons from their use. In general, running the slower fermentation steps outside class time gives students more time in class to compare results, identify sources of error, and troubleshoot unexpected outcomes, all while discussing how engineers improve experiments. Overall, the project shows how familiar fermentation systems such as sourdough and kombucha can be used to make introductory chemical engineering concepts more concrete and accessible while giving students hands-on experience with experimental design and data analysis.

Ray Nobuhara SEAS'27, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Ben O'Shaughnessy

Title: Learning the pathway of membrane fusion for neurotransmitter release in the brain

Abstract: The arrival of an action potential at the axon terminal is sensed by a complex molecular machinery with SNARE complexes at its core, which fuse synaptic vesicles with the presynaptic plasma membrane in milliseconds. This triggers the release of neurotransmitters that bind to postsynaptic receptors.

Simulating membrane fusion under physiological conditions is computationally challenging, since atomistic methods are limited to microseconds. To address this, we previously developed ultra coarse-grained molecular dynamics simulations of SNARE-mediated fusion that enabled us to access physiological millisecond fusion timescales. In simulations, SNAREs drive fusion by generating forces that squeeze the membranes together (Butu et al., 2025). Fusion begins with the formation of a stalk, a hemifusion intermediate in which the outer leaflets of the two membranes have merged. The stalk then expands and ruptures to form a fusion pore between the membranes, allowing content release. A related challenge, however, is visualizing these pathways which involve many complex molecular rearrangements and large energy barriers. Here, we study the hemifusion pathway in greater detail by collecting transition paths from the unhemifused to the stalk state. We find that hemifusion begins with local defects at the membrane-membrane interface, in which lipids from both vesicles protrude from their respective bilayers towards each other and become tilted relative to the membranes. Furthermore, by measuring the probability that a membrane state proceeds to hemifusion, and ordering states accordingly, we obtain a representative hemifusion pathway that reveals the early lipid rearrangement patterns preceding stalk formation, obscured in individual stochastic trajectories.

Isabel Norman GS'27, English, Environmental Biology

Faculty Mentor(s) or Supervisor(s): Alexander Van Geen (faculty, but worked more closely w PhD student Jennifer Angel-Amaya)

Title: Mining the Madre: A Physical Analysis of Gold Mining's Environmental Impacts in the Amazon

Abstract: The Madre de Dios Basin of southeastern Peru is a biodiversity hotspot and one of the most severely gold mining affected landscapes in the Amazon. Legal and illegal artisanal and small-scale gold mining (ASGM) has deforested approximately 300,000 acres in the basin since 2001, converting forest into excavated mining ponds. However, the resulting basins' sedimentology is poorly understood given the novel surge in mining and access difficulties. This study analyzed the sedimentology of four sites across a gradient of mining intensity, pond age, and disturbance history to examine the effect of ASGM on Amazon lacustrine systems. 23 sediment cores were sectioned into intervals every 1-2 cm, resulting in 453 sections that were then analyzed through loss of ignition (LOI), x-ray fluorescence (XRF), and grain size. LOI at 550°C was measured as a proxy for organic matter content. Elemental composition was measured using a handheld Nitron XRF analyzer,

focusing on iron and titanium as redox indicators. Grain size was analyzed by visual analysis calibrated to a method of wet-sieving at a 63 µm threshold using a washing station. Results demonstrate that oxbow lakes have higher organic matter and intact redox profiles by depth compared to mining ponds. Legal concessions in the Huepetuhe site, which retain topsoil and actively revegetate, had improvements in organic matter and redox profiles compared to illegal mining sites. This study contextualizes the ongoing biogeochemical work studying heavy metals in the basin and provides a physical analysis of mining disturbance as ASGM expands in the Amazon.

Yuki Ogawa CC'27, Computational Biology

Faculty Mentor(s) or Supervisor(s): Megan weivoda

Title: Light Chain Fibrils in Bone Marrow Macrophages: Generation, Clearance and Myeloid Effects

Abstract: Amyloid light-chain (AL) amyloidosis is a hematologic disorder caused by clonal plasma cells in the bone marrow producing aberrant free light chains (LCs). LCs accumulate and aggregate as toxic amyloid fibrils, resulting in progressive organ dysfunction and eventual failure. Previous studies have shown that low pH environments promote LC misfolding and fibril formation in certain LC variants. However, it remains unknown how LC exposure to low pH environments within cells, such as late endosomes and lysosomes, may be contributing to the fibril formation process. Similarly, the immune effects of chronic LC and fibril exposure on myeloid cells, including phagocytes, are poorly characterized. Here, we cultured macrophages from mice with free LCs for 4 weeks and observed the formation of fibril-like structures via transmission electron microscopy. More work will be required to confirm the presence of β -sheet fibrils. With fluorescent fibrils, we also showed how external fibrils are endocytosed and trafficked to lysosomes inside macrophages. Lastly, we showed that exposure to LCs and insoluble fibrils affected myeloid cell differentiation and osteoclast activity. Enhanced osteoclastogenesis and cell viability were observed, suggesting that LCs and fibrils may enhance differentiation and activation of myeloid lineage cells. A better understanding of how fibrils are generated, trafficked, and affect immune cells in the bone marrow environment will shed light on mechanisms of pathogenesis, potentially leading to the uncovering of new therapeutic strategies.

Eunseo Oh CC'27, Physics

Faculty Mentor(s) or Supervisor(s): Sebastian Will

Title: Probing the Interaction Symmetry in Dipolar Ultracold Molecules

Abstract: Beyond the four familiar states of matter—solid, liquid, gas, plasma—lies an entire regime in which quantum statistics govern the macroscopic behavior of a system. Exemplified by the Bose-Einstein condensate, these quantum phases provide a diverse platform for exploring many-body physics. Particularly, strongly dipolar ultracold molecules, with their long-range and anisotropic dipole-dipole interactions, offer a rich phase diagram, hosting self-bound droplets, supersolids, and roton excitations. Double microwave shielding is a powerful means of suppressing two- and three-body collisional losses in such ultracold polar molecules. By coupling different rotational states, it produces a time-averaged dipolar interaction that can also be continuously tuned. Using elliptically and linearly polarized microwave fields, the interaction is controlled through coefficients associated with different spherical-harmonic components of the interaction potential, and the resulting symmetries are explored across the (a_{d0}, a_{d2}) parameter space. The corresponding energy landscape offers a window into the stability and collective behavior of the dressed molecular gas. We first apply the variational principle with a Gaussian ansatz to map this landscape, then solve the extended Gross-Pitaevskii equation to determine the ground state and analyze its energy and expansion dynamics during time of flight. Finally, by validating these simulations against experimental measurements, we connect microscopic control of the molecular interactions to the macroscopic stability and dynamics of the quantum gas.

Ezinne Okonkwo CC'28, Information Science, Valeria Olguin BC'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Christian Murphy

Title: Student perspectives on policies governing the use of generative AI in computer science courses

Abstract: The use of generative artificial intelligence, or generative AI, in computer science courses has drawn significant attention in recent years, particularly regarding its effects on student learning, skill development, and academic honesty. However, policies restricting the use of these tools may also have unintended effects on the student experience, such as making students anxious about being falsely accused of using AI or even leading them to consider changing majors. On the other hand, when students have input on AI course policies or feel encouraged to use AI, they may feel more welcome and more supported by their instructors. To understand the effects

of policies governing the use of generative AI in computer science courses, the researchers surveyed 97 students at a private research university in the Northeastern United States (Columbia). The study found that both having input on AI policies and being encouraged to use AI lead students to feel more supported, and that these experiences are associated with lower levels of impostor syndrome and less anxiety about being falsely accused of using AI. While the majority of students reported high levels of anxiety about false accusations, this finding was consistent regardless of school or major, gender, or level of programming experience, indicating that this is a concern shared by students broadly. This presentation will share the details of the study and its findings, and offers recommendations to computer science instructors on how to create generative AI course policies that make students feel welcome and supported.

Oyenike Oladapo-Ekundayo CC'29, Sociology

Faculty Mentor(s) or Supervisor(s): Shana Redmond

Title: Finding Humanity Beyond the Headlines:

Abstract: Sean Bell, Philando Castile, and Amir Locke are just a few of the many Black lives that were stripped at the hands of America's violent vigilante police force. Professor Shana Redmond's experimental piece "The Dark Prelude: Black Life Before Mourning" promotes the recovery of Black life through an analysis of individual music choices and instances of joy. In response to the sensationalized and dehumanizing nature of media reports on traffic stops and no-knock warrant home invasions, this creative non-fiction explores the musical choices made by Black individuals as a response to and refusal of destructive power structures. As the first part of Oyenike Oladapo's Laidlaw Scholars Research project, "Finding Humanity Beyond the Headlines" contributes to the development of "Dark Prelude" by further examining the lives of Amir Locke, Sean Bell, and others who were murdered through inexplicable state violence. It demonstrates how these specific victims of fatal traffic stops and no-knock home invasions enjoyed music in their daily lives, or left a subsequent impact on the music scene following their death. An investigation of internet and social media sources from each victim's family members reveals the stories they have told before and after the death of their loved ones. Archives of music platforms, blogs, interviews, and podcasts hint at the stories not yet told; the ones that represent individual humanity. In this way, this research serves as a powerful and novel form of resistance against the narratives sanctioned by those whose lives were not intertwined with the subjects.

Ryan Ouardaoui SEAS'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Houda Chakiri

Title: From Geographic Shortcut to Temporal Ranking: Evaluating Frozen Prithvi Representations for Recorded Wildfire Dates

Abstract: Predicting wildfires from satellite imagery is difficult because geography can make a model look smarter than it is. This study examined whether Prithvi, an artificial intelligence model developed by IBM and NASA for Earth observation, could detect patterns in images collected before recorded fires in Morocco rather than recognize places where fires are common. The first models performed well, yet latitude and longitude alone nearly matched them. That result changed the study. The experiment was redesigned to compare dates within the same ten kilometer grid cell and year, asking whether a model could rank a recorded fire date above dates without a recorded fire. Across 347 comparison groups, Prithvi analyzed four Landsat and Sentinel images collected during the previous three months. Its output was tested alone and with calendar information. Data from 2020 were used for training, 2021 for model selection, and unseen 2022 data for final testing. The combined model performed best, placing the recorded fire date first in about half of the final comparisons and ranking it nearer the top than Prithvi alone. This gain remained reliable after linked observations were analyzed together. Exact locations still differed within each grid cell, so fine scale geography may still influence the result. Even so, the redesigned analysis indicates that Prithvi can extract useful information from satellite imagery collected before each date once the broad geographic shortcut is reduced. The signal is more modest than the original scores suggested, but more meaningful for evaluating satellite models in wildfire research.

Been Park GS'27, Mathematics-Statistics

Faculty Mentor(s) or Supervisor(s): Bianca M.Dumitrascu

Title: Cell Trajectory Similarity: Quantitative Evaluation and Interactive Exploration

Abstract: Comparing cell trajectories can help reveal movement patterns during embryonic development, but what counts as similar depends on how trajectories are represented and how distances are calculated. Different approaches emphasize spatial position, path geometry, or temporal dynamics and may therefore identify different trajectories as similar. We present a

framework for comparing these approaches and interpreting their similarity judgments in cell tracking data. The framework evaluates classical geometric and sequence based distances alongside self-supervised representations learned using Joint Embedding Predictive Architecture (JEPA) and contrastive learning. We hold out non-overlapping sparse subsamples from the same trajectory to assess robustness to sparse sampling and compare retrieved neighbors to identify where the methods agree and differ. We developed Trajectory Similarity Explorer, a napari plugin that connects these comparisons to interactive exploration of two- and three-dimensional cell tracks. Researchers can select a query trajectory, compare method-specific rankings, and inspect retrieved paths in their original spatial context or with starting positions aligned. The plugin also supports trajectory grouping and comparison with imported results from learned representations. Illustrative cases show that different methods can return different neighbors for the same query. This framework combines quantitative evaluation with visual analysis to help select appropriate trajectory comparison methods and interpret differences in cell movement.

Milani Payne CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Francesca Bartolini

Title: α -Synuclein and γ -Tubulin Cooperatively Regulate Activity-Evoked Presynaptic Microtubule Nucleation

Abstract: Dopamine- neurons depend on efficient movement of synaptic vesicles between presynaptic boutons, where neurotransmitters are released. Previous work from this laboratory showed that neuronal activation increases microtubule nucleation at synaptic boutons through gamma-tubulin, a protein that helps initiate microtubule formation. These microtubules promote vesicle exchange between neighboring boutons and help sustain dopamine release. Alpha-synuclein, a protein linked to Parkinson's disease (PD), is required for this response, but the mechanism remains unclear. This study tested whether phosphorylation of alpha-synuclein at serine 129, induced by neuronal activity, regulates its association with gamma-tubulin in cultured dopaminergic neurons. Proximity ligation assays detected alpha-synuclein and gamma-tubulin in close proximity at presynaptic terminals under control and stimulated conditions. Importantly, activation with bicuculline increased the synaptic proximity signal between serine 129-phosphorylated alpha-synuclein and gamma-tubulin. Live imaging and kymograph analysis further

showed that a phosphorylation-mimicking alpha-synuclein mutant increased microtubule growth without stimulation, whereas a mutant that cannot be phosphorylated prevented activity-induced increase in microtubule nucleation, as did pharmacological inhibition of phosphorylation. Analysis of three PD-associated alpha-synuclein mutants, A30P, E46K, and A53T, showed that each impaired the normal activity-dependent regulation of microtubule dynamics. Together, these results support a model in which neuronal activity promotes serine 129 phosphorylation, increasing alpha-synuclein proximity to gamma-tubulin at presynaptic terminals and stimulating microtubule nucleation required for vesicle exchange. They further suggest that PD-associated mutations may disrupt this process, potentially altering dopamine release through microtubule-dependent mechanisms.

Darya Petina CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Laura Benoit

Title: Volitional Control of VTA Dopamine Activity Through Closed-Loop Neurofeedback in Mice: Implications for Psychiatric Disorder Treatment

Abstract: Major depressive disorder (MDD) affects millions worldwide and is characterized by anhedonia - the loss of motivation and pleasure - driven by disrupted dopamine signaling in the reward circuit. Specifically, chronic stress selectively impairs dopamine activity in the nucleus accumbens (NAc) during reward anticipation while leaving responses to reward receipt relatively intact. Current antidepressant treatments fail to adequately address this circuit-level dysfunction in approximately half of patients, highlighting the need for novel therapeutic approaches.

This study investigates whether mice can learn to volitionally upregulate their own ventral tegmental area (VTA) dopamine activity through a closed-loop neurofeedback paradigm. DAT-Cre mice expressing GCaMP in dopamine neurons via AAV-FLEX viral injection undergo fiber photometry recording of real-time VTA dopamine activity. In a closed-loop behavioral paradigm, the dopamine signal is continuously converted into an auditory tone whose pitch reflects moment-to-moment dopamine activity. Mice learn that crossing a pre-defined dopamine threshold during neurofeedback trials - indicated by tone pitch - results in a 0.1% saccharine water reward, thereby creating a contingency that may drive volitional dopamine upregulation.

Behavioral performance is quantified across training sessions through success rate, response latency, and threshold crossing patterns. Preliminary findings suggest that response latency decreases significantly across early training days, consistent with mice learning to engage with the neurofeedback cue.

These findings advance understanding of whether closed-loop dopamine neurofeedback can serve as a circuit-targeted intervention for depression-related psychiatric disorders.

Daiane Quicine GS'27, Film & Media Studies

Faculty Mentor(s) or Supervisor(s): Laura Neitzel

Title: When Acting Becomes Data: Synthetic Performers, Digital Replicas, and the Future of Human Acting

Abstract: This project examines how artificial intelligence is changing the meaning of acting in contemporary film culture. It focuses on synthetic performers, digital replicas, posthumous reconstructions, and AI-assisted performances, with special attention to cases such as Tilly Norwood and other recent debates about AI actors. Rather than asking only whether AI can create convincing screen images, the project asks how audiences, actors, unions, critics, and media industries decide when a synthetic performance still feels connected to human acting. The research places current AI debates within a longer history of mediated performance, from theatre and film to CGI, motion capture, digital doubles, and generative AI. It draws on performance theory, digital media theory, film studies, industry reporting, and public reception. The project also analyzes audience comments, entertainment journalism, and industry statements to identify recurring concerns about labor, consent, authorship, ownership, authenticity, and replacement. The central argument is that AI-generated performance becomes most controversial when it separates the visible signs of acting, such as face, voice, gesture, and emotion, from the embodied labor and agency of a human performer. At the same time, the project recognizes that AI is not always rejected. Some uses are accepted when they support human creativity, restore or extend performance with consent, or fit specific media formats. By studying both rejection and conditional acceptance, this project shows how film culture is actively drawing boundaries around the future of human acting.

Christina Quiñones CC'27, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Claudia Lugo-Candelas

Title: How Do Extreme Weather Events Effect Family Dynamics

Abstract: Limited literature suggests climate change may increase risk of adverse childhood experiences (ACES) via lack of resources and changes in family dynamics. Previous studies found that extreme weather events such as extreme heat and floods positively correlated with child maltreatment,

disciplinary violence, and internalizing symptoms. For example, in Bangladesh, floods exacerbated child sexual abuse, and in Haiti children were exposed to elevated levels of intimate partner violence and abuse during hurricanes. However, research has yet to investigate the mechanism by which extreme events may increase ACEs risk in early childhood. The present pilot study investigates the relationship between extreme weather events, family dynamics, and risk for early childhood adversity. Our sample includes Puerto Rican mothers with children between the ages of 1-3, who reside in upper Manhattan and the Metropolitan area of Puerto Rico. Latinos are disproportionately exposed to extreme weather and ACEs, compared to their non-Latino counterparts, and thus our study focused on this highly exposed population. We conducted a thematic analysis of ten in-depth semi-structured interviews that examined how extreme weather affected family functioning and dynamics. Our code included parenting, coping strategies, emotional, cognitive and mental health repercussions among other related variables. Preliminary analyses suggest extreme weather disrupts family routines as mothers adopt various coping and parenting practices. Furthermore, these events impact access to basic needs, and negatively affect the physical, mental and emotional well-being of family members. Overall, these factors interact with one another changing family functioning and thus may increase children's risk of ACEs.

Conner Radke CC'27, Sociology

Faculty Mentor(s) or Supervisor(s): Chris Wimer

Title: Experience of Disadvantage and Hardship for Lesbian, Gay, and Bisexual New Yorkers

Abstract: Do lesbian, gay, and/or bisexual New Yorkers experience different rates of disadvantage (severe material hardship, SPM poverty, deep SPM poverty, poor health) or hardship (food, housing, bills, financial, medical) compared to their heterosexual counterparts? And how do these forms of disadvantage persist over time? This report builds on a 2016 analysis of lesbian, gay, and bisexual New Yorkers experiences of hardship and disadvantage with updated methodology, a larger sample size, and updated measures (like persistence of disadvantage). By using weighted logistic regression models and unweighted comparisons to analyze different sexual orientations of New Yorkers compared to their heterosexual counterparts, it gives insight into how demographic influences affect the experiences of disadvantage and hardship among non-heterosexual New Yorkers. The results of this research maintain that bisexual New Yorkers face levels of disadvantage that cannot be fully explained by the demographic composition

that we have accounted for, presenting certain advantages and disadvantages to the group. Furthermore, the demographic composition of gay/lesbian New Yorkers showcases statuses of advantage (white, older, more college educated, etc.) that lead to less disadvantage and hardship. Yet, as our recent data suggests, these demographics are shifting from past forms of advantage. Understanding the unique rates and experiences of disadvantage and hardship for lesbian, gay, and bisexual New Yorkers across their demographic identities, allows for policymakers and government officials to better implement research-based solutions for these minoritized groups of people.

Iniya Raja CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Jack Grinband

Title: Shared Monitoring, Distributed Control: The Task-Dependent Architecture of Cognitive Conflict Resolution

Abstract: Cognitive control is the everyday ability to behave in a goal-oriented manner despite distracting or competing input. Despite decades of research on the topic, it remains unclear whether cognitive control operates through a common mechanism or depends substantially on the situation that produces conflict. The present study examined whether cognitive control ability generalizes across six cognitive conflict tasks involving different types of visual, spatial, auditory, emotional, and language-based conflict. Ultimately, the tasks elicited the expected effects of cognitive control and conflict, and there was a strong general relationship in overall performance across tasks. However, despite examining multiple components of conflict and control, including interference, facilitation, and several measures of adaptive control, a participant who showed a relatively large effect in one task did not necessarily show a large effect in another. Trial-level statistical analyses also showed that allowing each person's conflict effect to vary depending on the specific task explained the data substantially better than assuming that each person had one general conflict tendency across all tasks. These results were then replicated in a larger independent dataset and using drift-diffusion modeling (DDM) to separate conflict- and control-specific elements from nonspecific processing. Together, these findings suggest that cognitive control may not be best understood as one ability that is expressed in the same way across every situation, with implications for how cognitive control impairments are measured today in psychiatric research.

Tamila Rakhimbayeva SEAS'29, Applied Physics

Faculty Mentor(s) or Supervisor(s): Xavier Roy

Title: Synthesis of first rare-earth metals intercalated transition metal dichalcogenides

Abstract: Two-dimensional materials are layered crystalline solids in which strongly bonded atomic sheets are held together by weak van der Waals interactions. These weak interlayer forces create spaces where additional atoms can be inserted without destroying the overall host structure, a process known as intercalation. Intercalation provides a powerful way to tune the electronic, structural, and magnetic properties of layered materials, making it particularly relevant for the study of transition metal dichalcogenides (TMDs) and other quantum materials. In this work, we investigate rare-earth intercalation in layered TMDs, focusing on europium-intercalated compounds with approximately 1/3 Eu occupancy. Single crystals were synthesized using chemical vapor transport and characterized using complementary structural, compositional, and spectroscopic techniques. The study examines how ordered Eu insertion modifies the host lattice, crystal symmetry, and vibrational behavior. Structural measurements confirm approximately 0.29 Eu incorporation, while diffraction reveals a superlattice associated with ordered intercalation. Raman spectroscopy further shows changes in phonon modes consistent with electron doping and possible symmetry modification. Together, these results demonstrate how controlled rare-earth intercalation can reshape the physical behavior of layered materials and provide a platform for exploring new electronic, magnetic, and collective phenomena in low-dimensional systems.

Rohan Ramachandran SEAS'29, Computer Science

Faculty Mentor(s) or Supervisor(s): Nathan McDonald

Title: Beyond Object Detection: Lightweight, Few-Shot Visual Task Reasoning at the Edge

Abstract: Small uncrewed aircraft operating under size, weight, and power constraints cannot host large vision-language models or rely on cloud inference, yet missions such as search and rescue, environmental monitoring, and reconnaissance require task-driven object detection: identifying which object in a scene can accomplish a stated task, including tasks and object classes absent from training. This work presents Task-Image Prototype Learning (TIPL), a lightweight architecture that pairs frozen foundation encoders for vision and language, large pretrained models that map images and text into a shared numerical space, with a small trainable projection into an associative prototype memory. Each task is represented by a single prototype vector initialized from its encoded text description, and inference

reduces to a constant-time nearest-prototype lookup over detected objects, completing in under a millisecond per query. Adaptation requires no gradient computation: a bounded arithmetic update pulls a prototype toward encoded representations of objects that satisfied the task and away from objects mistakenly ranked first, so ten labeled scenes nearly doubled accuracy on a novel task, and adding a task appends a single row to memory. Compact task graphs, generated offline by a language model and folded into each task encoding, further improve accuracy by up to eight points and sample efficiency sevenfold. On the COCO-Tasks benchmark, TIPL matches or exceeds TaskCLIP, the prior accuracy-efficiency frontier, while training thirteen times fewer parameters. Together, these results demonstrate that open-vocabulary task reasoning can run, and continually learn, onboard resource-constrained platforms in real time.

Amrutha Rao SEAS'28, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): Micah Goldblum

Title: Recovering Wasted Compute in Autoresearch Agents

Abstract: Recent advances in artificial intelligence have led to agents that can independently solve machine learning research problems from start to finish. These agents have the potential to automate time-consuming human labor and customize machine learning solutions for specialized applications. This paper studies the modeling pipeline at the core of these systems, identifies problems they currently face, and develops solutions to address them. The four common failure modes of these agents are that they waste computing resources resolving the same bugs repeatedly, fail to tune model settings, known as hyperparameters, even when additional computing resources are available, do not effectively explore different approaches, and analyze their data without using those findings to guide later decisions. The research explores targeted changes to the agents' design to address these problems and finds that a global debugging system that shares discovered constraints across the search process, prompt-level changes and changes to the agents' decision-making process that reliably drive agents to perform hyperparameter tuning, and more effective search strategies can successfully recover wasted computing resources. These findings demonstrate that autonomous machine learning systems can become significantly more effective through improvements to their design alone, without changing the underlying language model. This work moves autonomous research systems closer to conducting machine learning research independently and at scale.

Arjun Ratan CC'28, Classics

Faculty Mentor(s) or Supervisor(s): Maya Arianti

Title: Community Engagement through Youth Education at Empathy School International

Abstract: For Arjun Ratan's Leadership in Action project in the second summer of his participation in the Laidlaw Scholars Program, he spent six weeks in Bali, Indonesia working with young students at Empathy School International. Empathy School International's educational philosophy states "that through exposure to nature, individualized focus, and a strong foundation in social-emotional learning [their] students will grow to become the compassionate leaders and change-makers of tomorrow." Founded by one Harvard and one Stanford graduate, the school utilizes Montessori principles and a project-based learning methodology. Ratan contributed to Empathy School's six-week summer camp, where he helped lead visual arts and movement courses and developed lessons incorporating Latin instruction, building on his first-year Laidlaw research examining the impact of Latin instruction on youth literacy. While there, Ratan documented his qualitative observations through weekly posts on the Laidlaw Network, a social interface platform where all of the Laidlaw scholars share updates on their individual experience. Ratan spent his time learning about and putting into practice the alternative learning methodologies of Empathy School's nature-focused framework and student leadership initiatives. This manifested itself through greater independence granted to the students when doing activities like harvesting coconuts, planting flowers and seeds in the community garden, and building clay and painting. Ratan ultimately developed strong relationships in the program with both his students and fellow co-workers.

Christian Rebolledo CC'29, Medical Humanities, Political Science

Faculty Mentor(s) or Supervisor(s): Carmela Alcántara

Title: Characterizing the Social Determinants of Health in ICE Detention from Postmortem Data

Abstract: Following the Trump Administration's rapid expansion of Immigration and Customs Enforcement (ICE), immigrant communities across the United States continue to face heightened instability. Threats of deportation, detainment, and even death have impacted Black and Brown communities nationwide creating a virulent pathogen of fear. The current "immigration crackdown" in the US has raised concerns regarding human

rights violations against those placed in ICE detention. This study is concerned with understanding mortality in detention centers as a result of compounding factors through social justice and public health lenses. By leveraging the transparency requirements of the Department of Homeland Security Appropriations Act of 2018, this research uses ICE's Detainee Death Reports (DDR's) to understand multivariate patterns or trends in the stories that led up to decedent deaths. Limited research has systematically examined these records beyond clinical features—here, the social determinants of health framework is applied to suggest that detainee mortality is influenced not only by biological factors but also by social, environmental, institutional, and structural conditions. The National Institute on Minority Health and Health Disparities (NIMHD) Research Framework provides a useful model for examining these multilevel influences. By adapting the NIMHD model, this study characterizes over 80 variables of interest across biological, behavioral, physical, sociocultural, health system, and carceral domains for 113 detainee deaths occurring between 2018 and 2026 across the country. This work describes government data on ethical grounds. By generating a dataset that describes the bigger picture behind immigrant death in detention, this research aims to inform future advocacy.

Simon Reich CC'28, History

Faculty Mentor(s) or Supervisor(s): Rebecca Kobrin

Title: In 1930, Columbia University Hired a Nazi to Teach its Jewish Students: Friedrich Ernst Auhagen and the Seth Low Junior College

Abstract: The establishment of the Seth Low Junior College in Brooklyn, extant from 1928 to 1938, was Columbia University's main response to the increase in qualified Jewish first- and second-generation immigrant applicants to Columbia College. The student body of the Seth Low Junior College consisted almost entirely of Jewish applicants who may have been qualified for admission to Columbia College but would not be let in because of the administration's reticence to admit Jews to the College. Ironically, one of the longest-serving teachers at Seth Low, effectively Columbia's Jewish College, was Friedrich Ernst Auhagen, who was accused in 1937, convicted in 1941, and deported to Germany in 1947 on charges of having failed to register in America as an agent of the Nazi German government. Auhagen's support of the Nazi cause during his employment at Columbia and afterwards emerges from an analysis of the pro-Nazi columns he wrote in the Seth Low student newspaper. Auhagen also founded the American Fellowship Forum, a pseudo-patriotic front for German Americans sympathetic to the Nazi cause, which he directed from 1939 to 1941. Notwithstanding the charges, the nature

of Auhagen's work for the Nazi government was unclear—despite the years of pay stubs from an operative in Hamburg. Indeed, a subsequent trial at Nuremberg in 1947 found him innocent. The case of Auhagen at Columbia speaks to the unpredictable and incongruous consequences of setting up an institution motivated by exclusion. As Auhagen said upon his arrest in Los Angeles, “this is all a misunderstanding.”

Nadia Reichman CC'29, Biochemistry

Faculty Mentor(s) or Supervisor(s): Peter Sims

Title: Targeting ecDNA-Driven Gene Expression in Glioblastoma: A Novel Therapeutic Approach

Abstract: Glioblastoma (GBM) is a highly aggressive brain cancer that, despite ongoing research, remains largely incurable. In recent years, research has revealed that extrachromosomal DNA (ecDNA) is especially prevalent in GBM, contributing to increased oncogenic transcription and cancer heterogeneity. In this study, we aim to target ecDNA-derived RNAs using Cas13d, a CRISPR enzyme known to induce collateral cleavage when targeting abundant transcripts. Given that ecDNA promotes high levels of oncogene expression, targeting these abundant transcripts with Cas13d may provide a novel way to selectively weaken aggressive, ecDNA-harboring GBM cells. A critical step in this approach is the development of suitable guide RNAs (gRNAs) targeting transcripts that are highly upregulated, consistently expressed, and cancer-specific. Here, we propose a novel pipeline that identifies such ecDNA intervals, assesses their biological validity, and uses these intervals to design effective gRNAs. When applied retrospectively to 42 tested Cas13d gRNAs, our method preferentially selected guides associated with lower average cell viability than previously reported (16.61% to 30.76%, $p = 0.0002$). When implemented in our TS543 GBM cell line, 52 candidate intervals were found. Notably, 36 (69.23%) of these identified intervals directly overlapped with documented GBM-associated oncogenes, including PDGFRA, CDK4, TSPAN31, and PVT1, providing further support for our selection criteria. From these intervals, 17 high-confidence candidate gRNAs were identified, with the top 5 currently undergoing cell-viability testing. Together, these results support our computational pipeline as an effective, biologically informed strategy for identifying both target intervals and candidate gRNAs for future Cas13d experiments.

Eric Ren SEAS'28, Mechanical Engineering

Faculty Mentor(s) or Supervisor(s): Sinisa Vukelic

Title: Toward Reliable Corneal Topography from Volumetric Optical Coherence Tomography

Abstract: Placido disk corneal topographers primarily measure the anterior corneal surface and use its geometry to generate elevation and power maps for assessing conditions such as keratoconus. In contrast, volumetric optical coherence tomography, or OCT, captures both the anterior and posterior corneal surfaces across hundreds of cross sectional images. Assembling these images enables three dimensional reconstruction of both surfaces and measurement of corneal thickness, potentially supporting a combined power estimate rather than one based on the anterior surface alone. Because OCT records images in scanner coordinates, quantitative mapping requires boundary detection, spatial calibration, distortion correction, and compensation for how light bends within the cornea. This project developed a Python program to process rabbit corneal volumes containing 512 images, trace both surfaces, generate elevation maps, and calculate power from surface curvature. The platform was calibrated using a sphere of known curvature and evaluated against Placido disk topography. It recovered plausible average corneal power but revealed systematic distortions resembling astigmatism: maps with similar averages could differ markedly in spatial pattern. This finding showed that accurate boundary tracing alone is insufficient and identified scanner geometry, frame spacing, refraction, and motion as major error sources. The study therefore introduced Zernike polynomial modeling as a potential correction framework for quantifying astigmatism and other structured aberrations. Although matched calibration data are still needed, the project established a method for reconstructing both corneal surfaces, demonstrated why reasonable power values can conceal inaccurate geometry, and defined a path toward OCT based corneal topography.

Abril Rodriguez Calle CC'29, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Sandra Lee

Title: The Human Side of Genomics: Designing Tools for Better Research Partnerships

Abstract: As genomic research becomes increasingly global and collaborative, partnerships among researchers, institutions, governments, funders, and communities have become essential to generating and sharing large-scale genomic datasets. Yet these collaborations also introduce complex questions of governance, data access, intellectual property, benefit-sharing,

and institutional responsibility. While genomic research has produced significant scientific and public health advances, comparatively less attention has been given to the processes through which the partnerships underlying this work are negotiated and maintained. As part of the NIH-funded Pathways to Negotiating Genomics Research Partnerships study, this project examined existing playbooks to inform the development of a negotiation resource for genomics stakeholders. More than thirty resources spanning public health, cross-sector collaboration, data sharing, genomic surveillance, health equity, and artificial intelligence governance were compiled. Seven playbooks were selected for comparative review, with three analyzed in depth based on their relevance and applicability to genomics partnerships. The analysis identified key design principles for a genomics-specific negotiation playbook. Effective resources define diverse audiences, provide intuitive navigation, organize complex material through modular, thematic, or phased structures, and use case studies and interactive tools to support decision-making. These findings establish a framework for developing a flexible resource that can address different negotiation challenges across the lifecycle of a research partnership. The framework will inform the next phase of the project, in which stakeholder interviews and observations will guide the playbook's development and validation.

Sebastian Rojas SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Scott Banta

Title: Development of an Iron-Responsive Gene Expression System in *Acidithiobacillus ferrooxidans* Using the Ferric Uptake Regulator

Abstract: *Acidithiobacillus ferrooxidans* (AF) is a bacterium that thrives in acidic, metal rich environments and is relevant to biomining because it oxidizes iron and sulfur compounds. Biotechnology applications within biomining systems are limited, however, by the lack of well characterized genetic tools for controlling protein expression. Current heterologous expression systems in AF are largely restricted to constitutive promoters, such as the *tac* promoter, or weak inducible systems, such as arabinose-responsive expression. This work aims to develop an iron-responsive expression system based on the ferric uptake regulator (Fur), a transcription factor native to AF that can regulate gene expression in response to iron availability. By coupling protein expression directly to iron, a central species in bioleaching environments, this system could provide a self-regulating platform for engineering enhanced biomining functions. As a first step, the AF fur gene was cloned into an *Escherichia coli* expression system, sequence verified, expressed, and the resulting Fur protein purified for biochemical

characterization. To investigate metal-binding behavior underlying Fur activation, a fluorescence-based competition assay using the metal-sensitive dye Mag-Fura-2 was evaluated to establish metal conditions for regulatory experiments. In parallel, bioinformatic analysis identified Fur-responsive DNA regulatory sequences, which were incorporated upstream of GFP reporter constructs to evaluate Fur-dependent transcriptional control. Future work will introduce these constructs into AF and quantify GFP expression across iron concentrations to characterize the dynamic range and iron responsiveness of the system. Ultimately, Fur-responsive promoters will be used to control genes relevant to bioleaching, enabling autonomous, environmentally responsive engineering of AF for biomining applications.

Anacorina Romero CC'28, Physics

Faculty Mentor(s) or Supervisor(s): Kerstin Perez

Title: The First Flight of the GAPS Antarctic Balloon Experiment

Abstract: The nature of dark matter is still unknown and remains an open question in modern physics. Low-energy cosmic-ray antideuterons are a promising dark matter detection channel because conventional astrophysical processes rarely produce them at kinetic energies below approximately 1 GeV/n, resulting in a uniquely low-background window for new physics. The General Antiparticle Spectrometer (GAPS) is a long-duration Antarctic balloon experiment designed to study low-energy cosmic-ray antinuclei, with a particular focus on antideuterons. GAPS combines large acceptance with strong background rejection for this rare-event search. GAPS is composed of a plastic scintillator time-of-flight (TOF) system and a 10-layer Si(Li) tracker, consisting of more than 1,000 custom lithium-drifted silicon detectors cooled by an oscillating heat pipe thermal system. GAPS uses a novel and unique exotic-atom detection technique: incoming antiparticles are slowed and captured in the detector material, produce characteristic de-excitation X-rays, and then annihilate with the nucleus, producing secondary particles. GAPS will provide a high-statistics measurement of the antiproton spectrum in the 0.1–0.3 GeV/n energy range, extending below the reach of previous experiments, while also offering unique sensitivity to cosmic antihelium. The GAPS payload launched on its first flight from Antarctica on December 16, 2025, and flew for approximately 25 days, collecting the experiment's first in-flight science data. This work provides an overview of the first GAPS flight, including the characterization of data quality across the full flight and the selection of a dataset suitable for further science analysis.

Gregory Ronel CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Dr. Eunhee Choi

Title: Discovering the Biological Mechanisms of Metabolically Obese, Normal Weight (MONW)

Abstract: MONW, or Metabolically Obese, Normal Weight, is a condition in which patients present with normal body weight but have high body fat, hyperinsulinemia, and hyperglycemia. This predisposes them to metabolic disease and higher mortality. Moreover, it is estimated that about 30% of the world's lean population may suffer from MONW. Despite this, MONW is not well studied and the physiological and genetic mechanisms responsible for the condition are unknown. This study aimed to correct that by using a Refined Carbohydrate Purified diet (purified diet) to model MONW in mice and investigate its effects on basal and refed insulin receptor (IR) activation in metabolically important tissues. First, we confirmed that chronic exposure to purified diet had increased body fat in mice without increasing their body weight. Next, we found that mice who were chronically treated with purified diet had significantly higher basal IR activation in visceral adipose tissue depots but did not have higher basal IR activation in subcutaneous adipose tissue, liver, or muscle. Lastly, we found that acute exposure to purified diet caused significantly higher IR activation in visceral adipose tissue compared to the control chow diet. Overall, this study found that the purified diet, and MONW in general, may cause alterations to the IR activation pathway and broader metabolism in visceral adipose tissue, thereby illustrating this as a possible mechanism involved with MONW.

Gavin Rubin GS'27, History

Faculty Mentor(s) or Supervisor(s): Rebecca Kobrin

Title: Columbia's Forgotten Seth Low Junior College 1928-1936

Abstract: In 1928, Columbia University felt that they had a problem. As opposed to the archetypal "Columbia Man," an athletic, well-to-do socialite with knickerbocker roots, they were receiving an influx of the Jews and Italians that made up large swaths of the city applying to Columbia. These new students were considered socially undesirable by then-President Butler. In order to keep such undesirable young men as Isaac Asimov, Herbert Aptheker, and Red Auerbach out of Morningside Heights, Columbia built Seth Low Junior College, a two year junior commuter college on Pearl Street, later to be expanded into Brooklyn, where able young men of the wrong backgrounds could earn a second-class education. Despite their sidelining, the

students of Seth Low built, Ex Nihilo, an athletic program where a young Red Auerbach developed the Fast Break that brought Boston 16 NBA titles, political organizations that shaped the mind of WEB Du Bois's eventual literary executor, and literary societies that shaped the mind of one of Science Fiction's greatest writers. New analysis of materials from Seth Low provides both valuable insights into Columbia's relationship with a changing city, and new chapters in the biographies of some towering historical figures.

Kwangje Sa GS'27, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): Parijat Dube

Title: Not All Complexity Is Equal: Cross Application of Parameter- and Data-Driven Approaches to Model Complexity

Abstract: In classical machine learning, model complexity can be defined as the ratio of the number of model parameters to the size of the model training set. This implies that there are two distinct methods for manipulating model complexity. The first method is through manipulating the number of model parameters and the second is through manipulating the size of the training set. This paper investigates whether these two approaches of manipulating model complexity are empirically interchangeable, that is whether they have the same effect on model evaluation metrics. Both methodologies are then extended and applied to a classification problem. It is found that sweeping the number of model parameters reliably reproduces the expected results across most cases. On the other hand, sweeping the size of the training set reproduces only a fraction of the expected results and needs to be combined with proper constraints to avoid model instability. In the classification setting, it is found that the two methods affect model performance differently. These results suggest that the ratio-based definition of model complexity alone is an incomplete descriptor of model behavior, and that sweeping the number of model parameters and sweeping the size of the training set are not interchangeable methods of manipulating model complexity.

Evalina Sain CC'29, Sustainable Development, Political Science

Faculty Mentor(s) or Supervisor(s): Michael Gerrard

Title: Legislating the Grid: How States Are Balancing Data Center Growth, Ratepayer Protection, and Energy Infrastructure—A 50-State Analysis

Abstract: As AI-driven computing pushes electricity demand to unprecedented levels that utilities are ill-equipped to confront, state

legislatures have become the primary arena where the costs and benefits of data-center expansion are allocated. Emerging from environmental and ratepayer advocacy in Nebraska, where a single proposed facility would draw more power than the population of the state capital, this study examines how states legislate the tradeoff between power and its expense. It conducts a 50-state analysis of hundreds of bills introduced or enacted during the 2025–2026 legislative sessions, typologizing legislation across dimensions including cost allocation, energy sources, environmental and economic objectives, water use, siting, utility involvement, and load thresholds. This legislative analysis is combined with a composite scoring framework to map and characterize emerging state approaches to data-center governance, centered on a publicly accessible, universal database equipped with tools for cross-state comparison and supplemented by research on state energy systems, political dynamics, and community impacts to further contextualize the complex national energy ecosystem. The analysis suggests that state responses cannot be adequately understood along a simple pro-growth–restrictive spectrum. Instead, states are experimenting with distinct governance models—including tax incentives conditioned on environmental and labor requirements, utility expansion, self-supply arrangements, transparency mandates, and moratoria. Preliminary findings also indicate pronounced regional and partisan differences, alongside cross-partisan concern over ratepayer exposure. By analyzing, mapping, quantifying, and comparing divergent state approaches, this research identifies data-center expansion as a novel test of how states govern competing corporate and community interests, infrastructure development, and environmental externalities amid rapidly accelerating technological innovation.

Luna Salinas CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Huguet Landa-Galvan

Title: Evaluation of in-vivo Beta Cell Proliferation in Response to ATF6 and CDK4 Activation

Abstract: Diabetes is a growing global health concern affecting approximately 589 million adults worldwide, and estimates suggest that this number will rise to 853 million by 2050. In diabetes, function and number of beta cells are impaired. Since current treatments do not restore beta cell mass, identifying mechanisms that promote beta cell division is an important area of diabetes research. In high glucose conditions, beta cells increase insulin synthesis and the endoplasmic reticulum experiences stress which activates the unfolded protein response. One of the three unfolded protein response branches is the activating transcription factor 6 (ATF6). The lab reported that ex-vivo

activation of ATF6 in high glucose conditions or overexpression of a non-inhibitable form of cyclin-dependent kinase 4 (CDK4R24C) increases beta cell proliferation. However, it remains unknown whether this mechanism induces replication in-vivo. We hypothesize that in-vivo activation of ATF6 and CDK4R24C will increase beta cell proliferation and mass. To evaluate this, we will use a mouse model that expresses a misfolded form of dihydrofolate reductase (DHFR) bound to ATF6 in beta cells. This construct undergoes degradation in the proteasome but when trimethoprim is administered via a sulfatrim diet, it binds to DHFR, stabilizes it and activates ATF6. The mice will undergo 5 intermittent feeding pulses of trimethoprim. We will perform immunostaining to detect insulin and BrdU. Beta cell proliferation will be measured as the percentage of BrdU+ insulin+ cells. Beta cell mass will be estimated by the ratio of insulin area to total pancreas area, multiplied by the pancreas weight.

Param Sampat CC'28, Biology, Sustainable Development

Faculty Mentor(s) or Supervisor(s): Robbie Parks

Title: Temperature, certification, and the rise in heat- and cold-related deaths in the United States

Abstract: Deaths certified as heat- or cold-related are widely used to gauge how a warming climate affects human health, and the recorded numbers have risen sharply since 1999. But the count depends on two factors: how often dangerous temperatures occur and how reliably a physician or coroner records temperature as a contributing cause on the death certificate. Sampat built statistical models to separate them, drawing on records of heat- and cold-related deaths across the United States from 1999 to 2024, together with daily temperatures for every county. The models estimate each state's sensitivity to extreme temperature, then recreate what mortality would have looked like had the warming trend not occurred. The difference is the share attributable to temperature, and the remainder is a change that temperature does not account for. Temperature accounted for a minority of the recorded rise across all eight groups examined. For heat-related deaths in men, roughly two-fifths of the increase was attributable to temperature, and the rest was not. Cold gave the clearest result: extremely cold days have become less frequent, so warming alone predicts fewer cold deaths, yet recorded cold deaths rose. Repeating the analysis under five different definitions of extreme temperature substantially changed the attributable share but never its direction. The results indicate that a widely used indicator of climate-related mortality partly measures something other than the hazard it is taken to represent, and that the rise is not mainly explained by temperature.

Tomás Sanabria CC'29, Medical Humanities

Faculty Mentor(s) or Supervisor(s): Sandra Soo-Jin Lee

Title: The Future of Bioethics: Developing a Methodology for the International Comparison of Bioethics Funding

Abstract: Recent federal changes in the United States have weakened advisory bodies, reduced funding streams, and threatened the infrastructure supporting bioethics research, training, and oversight. These disruptions raise broader questions about which forms of expertise society values and how scientific institutions remain accountable to the public. To help assess the resilience of American bioethics and better understand global medical ethics efforts, this project examines how bioethics research is produced and funded in international settings. Using Elsevier's Scopus database, a broad longitudinal search identified countries with high volumes of bioethics-related publications. The United States, the United Kingdom, and China emerged as the most publication-active countries, while South Africa was added as a comparative case from the Global South. A refined search was then used to construct country-specific datasets for 2020 and compare frequently mentioned funders, funding origins, and funder types. The results reveal distinct national profiles. China's system was predominantly domestic and government-centered. South African research was strongly connected to international funding networks, particularly those based in the United States and the United Kingdom. The United Kingdom displayed the most pluralistic structure, combining government, charitable, international, academic, and health-system support. The United States showed the strongest single-funder concentration, with the National Institutes of Health dominating funder mentions. These findings demonstrate that bioethics is not politically or institutionally neutral. Its development reflects the priorities and infrastructures of the societies that support it. The project establishes a reproducible baseline for future longitudinal comparison and identifies topic classification options for the next stage of analysis.

Ricardo Sanchez Cortes SEAS'28, Chemical Engineering, Yuri Sasamoto SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Parisa Yousefpour

Title: Tuning Self-Amplifying RNA Replication to Improve Cell Viability

Abstract: Self-amplifying RNA (saRNA) technologies are an emerging alternative to conventional mRNA therapeutics, offering robust and durable

gene expression at lower doses. Derived from alphaviruses, saRNA vectors encode viral non-structural proteins (nsP1-4) that form a replication complex, which amplifies the saRNA molecule within the host cell. Additionally, the gene of interest is encoded in a subgenomic open reading frame under the control of the subgenomic promoter, allowing for increased levels of subgenomic RNA, resulting in enhanced protein translation. However, excessive replication can trigger innate immune overactivation and cause cellular toxicity, reducing therapeutic efficacy. As such, there is a critical need to modulate the immunogenicity while preserving gene expression. This study addresses this need by introducing targeted sequence modifications into the nsP coding regions to modulate saRNA amplification. Modified saRNAs encoding the reporter protein mCherry were synthesized by in vitro transcription and electroporated into B16F10 melanoma cells. Cell viability and transgene expression were assessed by flow cytometry at 24 and 72 hours post-transfection. Type I interferon activity in culture supernatants was measured at both time points using RAW-Lucia-ISG reporter cells. Preliminary results demonstrate improved viability relative to standard saRNA replicons while maintaining substantial transgene expression. Future work will further optimize the balance between saRNA tolerability and transgene expression to enhance the platform's therapeutic potential.

Jacques Sangwa CC'28, Political Science

Faculty Mentor(s) or Supervisor(s): Vira Ameli

Title: Governing Digital Health: A Toolkit for Responsible AI and Health Technology Adoption

Abstract: Countries across the globe are digitalizing their infrastructures for several reasons. Most of these reasons are aligned with system efficiency, like being able to communicate across different departments, have information placed in one shared system, enhance record keeping and overall consolidation. Health systems have naturally become part of the digitalization process as it is also a public service and there are always improvements to be made. The key to ensuring digitalization creates a future of prosperity and not a future of concern is through governance and regulations. These two terms allow for the safeguarding of health systems, healthcare providers, and the citizens themselves to proceed with digitalization in a way that protects everyone involved. Several countries have begun this process, and have created both regulations and legal precedents to ensure that future technology procurement and integration are tales of success and health optimization. This toolkit serves to play a role in this through the inclusion of regulation briefs and more. This manuscript, which will be further developed through

co-design with healthcare system decision-makers for better nuance, is meant to help in the decision to adopt technologies that affect the expanding digitized health systems and recognize the rights of the citizens under these digital systems. Alongside these briefings are cases and questions for these decision makers to think about when moving in the direction of procurement to make sure that this technology adoption is not a hindrance, but a helper in the progression of a country's national health status. It is also important to mention that the toolkit has been informed by the NASSS framework, but expands to incorporate governance, procurement and legal considerations as identified through the cases.

Jacob Sanning CC'27, Linguistics

Faculty Mentor(s) or Supervisor(s): Meredith Landman

Title: Sociolinguistic Dialect Blending within Oirat Mongol

Abstract: Since the introduction of Khalkha Mongolian as the national written standard in the early 1940s, formerly distinct lects of the Oirat subfamily of the Mongolic languages have begun to “Khalkhasize,” or resemble their more culturally dominant counterpart in grammatical and lexical structure. Despite some academic research claiming that Khalkha has completely displaced local dialects within the region, leaving only individual colloquialisms behind, speakers of Oirat dialects within semi-urbanized regions retain key features of Oirat speech. Rather than supplanting the local dialect, Khalkha Mongolian has instead begun to merge with it, producing a continuum of gradient dialects situated between Oirat and Khalkha, varying based on the speaker's gender, socioeconomic status, and level of education. This project utilizes linguistic analysis to identify distinct levels of transition between the two dialects, using morphological and lexical markers from Oirat as evidence of mixture. Comparisons are made between contact in the Oirat-Khalkha area and contact within Ukraine, where Russification efforts led to the emergence of Surzhyk, a Russo-Ukrainian mixed language. Both Surzhyk and Oirat display variation based upon the socioeconomic status of speakers, and both languages are the result of prolonged periods of contact between closely related languages. Ultimately, researchers posit that contact between closely related (or typologically aligned) languages can produce transitional ways of speech which are distributed in a gradient based upon the socioeconomic status of speaker groups.

Anand Schwabe CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Nicholas Arpaia

Title: TGF- β inhibition and its impact on anti-tumor immunity

Abstract: In recent years, the TGF-beta signaling pathway has received increasing attention as a target for cancer therapy. TGF-beta inhibitors have shown strong preclinical success, but clinical trials have reported numerous challenges from off-target toxic effects on healthy tissues. Here, we sought to address this issue by developing a tumor-targeted bacterial TGF-beta inhibitor that acts locally within tumors while reducing systemic side effects. By integrating a synchronized lysis circuit and a plasmid containing a mutant TGF-beta gene into the genome of *E. coli* Nissle 1917, we engineered a bacterial strain that locally inhibits TGF-beta signaling in the tumor microenvironment. Results from mouse models of colorectal cancer reveal the potential of these bacteria for use as a cancer therapy. Ongoing studies are optimizing the strain's plasmid production to further improve its therapeutic efficacy. Beyond developing a cancer therapeutic, we also used our strain to investigate how TGF-beta inhibition and tumor fibrosis shape the anti-cancer immune response. We hypothesized that TGF-beta inhibition reduces tumor fibrosis, or scar-like tissue buildup, allowing antigen-presenting cells, which help activate other immune cells, to migrate more effectively to tumor-draining lymph nodes. This may improve CD8-positive T cell activation and strengthen the immune response against the tumor. Past studies in the lab have supported this hypothesis, and ongoing experiments are being conducted to gain a more complete mechanistic understanding of TGF-beta inhibition in the context of cancer immunotherapy.

Nicole Serrano CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Franck Polleux

Title: Whole-Brain Registration Pipeline Optimization for Mapping Layer 5 Pyramidal Neuron Projection in the Developing Mouse Brain

Abstract: Understanding how neurons are able to project to multiple specific projection targets is crucial for uncovering how circuit formation goes awry in neurodevelopmental disorders. While previous studies have characterized axonal projection patterns, the molecular mechanisms enabling a single neuron to establish multiple specific targets remain incompletely understood. Two theories for specification have emerged: either specification is determined before axon branching or at individual synaptic complexes. Axon projection development must be labeled, mapped, and quantified across timepoints to verify which model is the best approximation. Current methods for analyzing serially sliced brain images are developed around 3D adult atlases. However, due to shifting brain morphology throughout development,

these methods do not translate to developing brains. Because of their diverse cortical and subcortical targets, Layer 5 pyramidal neurons (L5PNs) are ideal for studying target-specific connectivity throughout development. To start to track and quantify L5PN development across timepoints, a novel semi-automatic mapping and segmentation pipeline for fluorescence-based projection mapping in Fezf2 Cre-ER driver mice was developed. The 4D atlas Developmental Mouse Brain Atlas (DeMBA) with Aligning Big Brains & Atlases (ABBA) for semi-automatic landmark-based registration was used for mapping. Then, with machine learning toolkit Ilastik, semi-automatic binary segmentation of fluorescent signal was performed, followed by manual clean-up in FIJI. These images then trained a model which automatically warped and mapped a reference atlas onto brain regions, then quantified fluorescence intensity normalized against background signal per atlas region. This pipeline provides the foundation for future comparison of L5PN projections across developmental stages and experimental conditions.

Diya Shah CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Rafael Yuste

Title: Using SLEAP Pose Tracking to Compare Contraction, Expansion, and Shared Behavioral Patterns in Hydra During Sensory Stimulation

Abstract: Hydra vulgaris is a small freshwater animal with a simple nerve net that produces clear whole body behaviors, making it a useful model for studying how nervous systems coordinate movement and respond to changes in the environment. This project uses SLEAP, a machine learning program for animal pose tracking, to measure and compare contraction and expansion patterns across multiple Hydra during sensory stimulation. Three body points, the head, center, and foot, are labeled so that SLEAP can track changes in body position and length across video frames. Preliminary analysis shows that several Hydra often change body length within the same time periods. During the strongest contraction event analyzed so far, 80.0 percent of the Hydra showed substantial shortening, with an average positive decrease in body length of approximately 30.0 percent. Expansion events also showed strong similarities between animals. In one recording, 100.0 percent of the Hydra expanded by at least 8.0 percent during the same time window, with an average expansion of approximately 25.1 percent. In another recording, all five Hydra expanded together during a candidate event, with an average increase of approximately 27.7 percent. Additional videos will be analyzed to determine how consistent these patterns are across animals and repeated stimulation. Because Hydra has a much simpler nervous system than humans,

it allows basic relationships between neural activity and behavior to be studied more directly. Understanding these fundamental principles may contribute to broader neuroscience research on how networks of neurons coordinate behavior, adapt to repeated stimulation, and organize activity in more complex nervous systems.

Trisha Sharan CC'27, Environmental Science

Faculty Mentor(s) or Supervisor(s): Dhruv Balwada

Title: Characterizing Ocean Eddy Heat Fluxes and Kinetic Energy Cascades Across Scales Using High-Resolution Satellite Altimetry

Abstract: Eddies are circular water motions that break off from larger ocean currents and travel independently for days to months before dissipating. They occur in the ocean across spatial scales of tens to hundreds of kilometers, with kinetic energy generally transferring from smaller to larger scales and impact basin-wide patterns such as gyres. Eddies are also the primary drivers of heat transport, making them a key component of the ocean's role in climate. Using high-resolution satellite and machine-learning-derived observations from 2010–2024, this study examines how heat transported by these eddies relates to their energy transfer across spatial scales. We quantified the cross-scale energy transfer by calculating kinetic energy cascade at scales from 50-500 km. Heat flux was similarly derived across scale, and we analyzed the two measures independently and in tandem to reveal how cross-scale dynamics shape heat transport and to identify inter- and sub-annual trends. In the Gulf Stream, interannual variability in kinetic energy cascade appeared larger in magnitude than the seasonal cycle, challenging the assumption that subannual variability dominates. In an energetic region of the Antarctic Circumpolar Current, the strongest current in the world, we analyzed heat flux and kinetic energy cascades jointly to assess their relationship with poleward ocean heat transport, the global pattern driving increased warming and glacial melt at the poles. These analyses develop a stronger understanding of the ocean's role in global heat transport and how that role evolves under climate change, offering a foundation for future work on the ocean-climate system and its feedbacks.

Anvesha Sharda SEAS'28, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Elisa Konofagou

Title: A 3D Multimodal Primate Brain Framework for Understanding Focused Ultrasound Effects

Abstract: Focused Ultrasound Stimulation (FUS) allows us to noninvasively sonicate the brain to stimulate and engage different brain regions. FUS's ability to do so with extreme precision and at high penetration depths has established it as a promising tool for both therapy and the advancement of neuroscience. However, given the complex nature of the brain itself, understanding the effects of FUS on different systems within the brain is still underexplored. The effects of ultrasound vary across different brain tissue types. During propagation, the FUS beam interacts with ventricles and other cerebrospinal fluid spaces, gray and white matter, vasculature, and fiber tracts, each of which influences the brain's response and potential treatment efficacy. To better understand the effects of FUS on each of these brain regions, we developed a 3D multimodal tool that integrates Magnetic Resonance Imaging (MRI), Magnetic Resonance Angiography (MRA), and cortical and subcortical anatomical regions, grey and white matter segmentations, as well as diffusion-based tractographies, focused ultrasound simulations, and functional ultrasound imaging. The 3D nature of the model enables simultaneous visualizations of multiple brain systems within the same anatomical subspace. This allows us to understand the interaction of FUS with each system independently and also contextualize its effects at a whole-brain level. Using this framework, we can visualize and analyze how FUS engages distributed neural networks, interacts with major blood vessels, and produces functional responses shaped by its interaction with the neuro-vascular-ventricular systems it encounters.

Ethan Sharma SEAS'29, Electrical Engineering, Raymond Zhao CC'29, Applied Mathematics, Emma Jia BC'29 Mathematics-Statistics

Faculty Mentor(s) or Supervisor(s): George Dragomir
Title: Uncovering Our Galaxy's Darkest Secret: Improving Black Hole Video Reconstruction with Optimal Transport Regularization

Abstract: Sagittarius A*, the black hole at the center of our galaxy, moves on short, intrahour timescales and thus data used for image reconstruction is particularly sparse. When dealing with underconstrained inverse problems like this, regularization functions are often added to encode prior information and, ideally, ensure a unique solution. Optimal Transport Theory focuses on finding the minimal-cost transport between mass distributions, and has connections to physical laws of conservation. We propose novel optimal transport-based regularization schemes aiming to penalize brightness movement that deviates from conservation of flux, using an unbalanced

formulation to allow for local brightness creation or destruction in the case of black hole flares. We simulated black hole data with physically motivated models and sampled it with realistic Event Horizon Telescope sparsity and noise before testing existing static and dynamic reconstruction methods, as well as our optimal transport-based regularization. Our results show that signed residual unbalanced optimal transport can improve normalized root mean squared error by 20-40%, structural similarity by 5-10%, and spatiotemporal gradient error by 20-25% without sacrificing chi-squared data fit when compared to existing reconstruction methods. We also developed a novel evaluation metric called Optimal Transport Path Consistency (OTPC), which can be used to evaluate temporal coherence in a way that explicitly considers source motion. This supports optimal transport as a promising temporal regularization approach for Event Horizon Telescope imaging on very sparse data sets.
preventative treatment.

Richa Shukla CC'28, Chemistry, Economics

Faculty Mentor(s) or Supervisor(s): Venkat Venkatasubramanian
Title: Human-In-The-Loop AI for Pharmaceutical Information Extraction and Representation

Abstract: Pharmaceutical process literature contains detailed information on reaction conditions, intermediates, unit operations, and manufacturing workflows, but this information is often distributed across text, reaction schemes, and process-flow diagrams. We present an artificial intelligence pipeline that converts pharmaceutical research articles into structured representations of drug manufacturing processes. The pipeline combines image extraction, domain-informed natural language processing, and reaction and molecular recognition. It leverages tools such as OpenChemIE, molecular representations and pattern languages such as SMILES and SMARTS, and large language models, including Qwen and Llama. Particular attention was given to reactant and intermediate identities, reagent quantities, addition order, temperature, reaction time, workup, phase separation, purification, and final product isolation. While LLMs are powerful at processing text, they often struggle with accuracy in scientific and mathematical tasks. As such, a human-in-the-loop is critical during training to define rules that support explainability. Human review identified and corrected recurring errors, including hallucinations, reversal of reagent-addition order, missing functional groups, and confusion between optimization experiments and manufacturing steps. Our model training strategy integrates expert feedback

on compound identity, process order, and multimodal consistency to transform natural language text into a machine-readable format.

Gabriela Sicre CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Dr. Maria Monzon-Medina

Title: Empowering At-Risk Communities Through Blood Pressure Awareness

Abstract: Hypertension affects 48.1% of U.S. adults and 1 in 4 men and 1 in 5 women globally; prevalence has doubled in the past 30 years. Only 25% of adults with hypertension have their condition under control, highlighting gaps in awareness and management. Culturally and linguistically tailored mobile health apps may support hypertension self-management, yet gaps in culturally relevant resources for Hispanic communities highlight the need for tailored digital interventions. A literature review investigated barriers to home blood pressure management and informed the development of a bilingual mobile application prototype designed to deliver motivational notifications that support sustained self-management, informed by findings from the literature review. Key barriers to blood pressure control included limited health knowledge, improper cuff use, low motivation, and lack of social support. Evidence suggests that blood pressure self-management applications achieve high user satisfaction, with meta-analyses reporting average reductions of 4–6 mm Hg in systolic blood pressure and 2–3 mm Hg in diastolic blood pressure compared to controls. Given that approximately 85% of U.S. adults have access to internet-connected devices, app-based tracking represents a scalable intervention. In response, a bilingual blood pressure tracking application was developed featuring educational resources, trend visualization, and a simplified logging interface. Future research will evaluate real-world effectiveness, long-term adherence, and refinement of features such as reminders, visual feedback, and stress-support tools to enhance engagement and clinical outcomes.

Neomi Li Simoni GS'27, Biology

Faculty Mentor(s) or Supervisor(s): Hachung Chung

Title: Understanding the Role of PKR in Neurodegeneration

Abstract: Cells rely on immune defenses to detect viral infections, including viral double-stranded RNA (dsRNA). However, host cells also naturally produce dsRNA, so tight regulation of these immune defenses is required to avoid aberrant activation against self-dsRNA. When this regulation is disrupted, immune proteins can become overactive and contribute to disease.

Protein kinase R, or PKR, is one such immune protein that detects double-stranded RNA and responds by shutting down protein production in the cell as a defense mechanism to limit viral spread to neighboring cells. Recent clinical data have identified PKR variants in patients with autoinflammatory and neurodevelopmental disorders, but the functional effects of these mutations remain unclear. In this research, several disease-associated PKR variants were examined by comparing them with wild-type PKR and a previously characterized hyperactive PKR mutant. Using an overexpression system in PKR-knockout human embryonic kidney (HEK293T) cells, PKR activation and downstream signaling were measured by western blot. All patient-associated variants showed increased PKR activation and downstream signaling compared with wild-type PKR, suggesting gain-of-function activity. To further investigate PKR hyperactivation in a mouse model, human patient-associated PKR mutations were expressed in mouse fibroblast cells to identify variants that could be used to generate a hyperactive mouse model. Because wild-type mouse PKR already contains four residues corresponding to human patient-associated mutations and shows relatively high PKR activity, identifying an additional hyperactivating mutation was challenging. Based on preliminary results, several variants may alter downstream signaling compared with wild-type mouse PKR.

Alexander Skrypek SEAS'27, Applied Physics

Faculty Mentor(s) or Supervisor(s): Michele Simoncelli

Title: Thermal Transport in PBTTT with Quantum Accuracy at Foundation Model Cost

Abstract: Organic thermoelectrics convert waste heat into electricity and, unlike many of their inorganic counterparts, are non-toxic and solution-processable, but designing them requires understanding how their structure determines thermal conductivity. First-principles density functional theory (DFT) can predict atomic interactions in thermoelectric conjugated polymers with quantum-mechanical accuracy, yet the full pipeline from forces to vibrational frequencies to thermal conductivity requires simulation cells on a scale that renders direct DFT computationally infeasible. Here, we show that fine-tuning the NEP89 foundation model on a small training set of hybrid-DFT configurations enables prediction of the thermal conductivity of the crystalline phase of the conjugated polymer PBTTT-C14. We first find that the hybrid functional B3LYP with Grimme D3 dispersion corrections (B3LYP-D3), evaluated in ABACUS, reproduces the semiconducting band gap and mass density of PBTTT. In contrast, the generalized-gradient-approximation functional BLYP collapses the gap and predicts a metal. We

then fine-tune NEP89 in GPU-MD using B3LYP-D3 energies, forces, and stresses for 138 frames rattled from the relaxed structure. The resulting potential agrees with reference forces within 15 meV/Å and predicts a thermal conductivity above that measured for disordered films. This fine-tuned potential makes structural relaxation, phonon calculations, and thermal-transport predictions feasible at a level of theory otherwise out of reach.

Luke Smith CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Bianca Jones Marlin

Title: Fatherhood on the Brain: Characterizing Whole-Brain Oxytocin Circuitry

Abstract: Although the transition to motherhood is marked by vast changes in physiology, males do not undergo pregnancy or parturition, thus removing any obvious physiological event to induce potential changes in behavior. Yet, the onset of fatherhood is accompanied by behavioral changes to care for offspring. The neuropeptide oxytocin is involved in the onset of maternal behavior, and it has also been shown that hypothalamic oxytocinergic neurons are important for paternal behavior. However, there remains a gap in characterizing oxytocinergic projections across the entire paternal mouse brain. Therefore, this project aims to characterize the whole-brain oxytocinergic circuitry of fathers and naïve males to determine whether this circuitry changes with the onset of fatherhood. To achieve this, we have fathers who have raised two litters and age-matched naïve virgin males. Both groups were screened for pup retrieval to assess parental caregiving, and we found that fathers, like mothers, retrieve while naïve males do not. We have also included two-litter mothers and naïve females to enable a comparison between maternal and paternal oxytocin circuitry. We will use the iDISCO+ method for whole-brain clearing and light-sheet microscopy at 5x resolution to visualize oxytocinergic projections. We will then use a consolidated deep-learning pipeline developed in our lab to automatically preprocess, segment, and quantify these projections following alignment to the Allen Brain Atlas. By imaging these groups at a higher resolution, we will be able to definitively characterize whole-brain oxytocinergic projections across sex and parental experience.

Jennifer Song CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Haotian Wu

Title: Overcoming Heparin Interference for Extracellular Vesicle Small RNA Sequencing in Archived Plasma

Abstract: Plasma extracellular vesicle (EV) small RNAs are promising non-invasive biomarkers, but archived clinical plasma often contains heparin anticoagulants that interfere with downstream applications. Heparin creates severe false-positive fluorescence during fluorometric RNA quantification and inhibits enzymatic reactions required for small RNA sequencing. Overcoming this barrier would unlock vast repositories of archived clinical plasma for novel biomarker discovery. To resolve this issue, this study evaluated whether heparinase-treated EV RNA is compatible with small RNA sequencing. The EV RNA was isolated from 45 archived plasma samples in the Columbia Center for Children's Environmental Health cohort and treated with Heparinase I prior to library preparation. RNA recovery, target integrity, and final library quality were evaluated using Qubit fluorometry, RT-qPCR targeting reference microRNA hsa-miR-16-5p, and High Sensitivity DNA Bioanalyzer chips. Initial Qubit measurements of untreated EV RNA showed heavily inflated small RNA concentrations ranging from 7.92 to 14.90 ng/uL due to heparin interference. Following Heparinase I digestion, apparent small RNA concentrations decreased by over 95% to between 0.16 and 0.38 ng/uL. Crucially, RT-qPCR confirmed that endogenous microRNA detection remained stable across samples (Cq 20.02 to 23.46), proving enzymatic digestion removed heparin without causing RNA loss. Downstream library preparation using Heparinase I-treated RNA successfully yielded high-quality sequencing libraries, characterized by clear, narrow size distribution peaks centered between 149 bp and 172 bp on Bioanalyzer profiles. Ultimately, integrating a Heparinase I treatment step eliminates heparin-induced quantification artifacts while maintaining RNA integrity, offering a reliable, standardized pipeline for small RNA sequencing from archived clinical plasma cohorts.

Abigail Song CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Aaron Gitler

Title: Investigating the Methods of TMEM106B C-Terminal Fragmentation in Disease

Abstract: TMEM106B is a lysosomal transmembrane protein strongly associated with the risk and development of frontotemporal dementia (FTD). Structurally, TMEM106B is made up of three domains: a cytoplasmic N-terminal, a transmembrane region, and a luminal C-terminal domain, which is susceptible to cleavage. Recent studies have shown that the cleaved C-terminal domain turns into smaller C-terminal fragments (CTF) which form amyloid fibrils that accumulate in the brains of patients with FTD. However,

the molecular mechanisms behind the generation and accumulation of this fragment as well as the functional consequences of CTF accumulation is unknown. Here, we investigated the molecular determinants and potential consequences of CTF accumulation. Firstly, in order to understand how exactly the CTF is generated, we designed and tested different TMEM106B mutants targeting the residues within the predicted cleavage region and checked their effects on CTF production. These mutants allowed us to identify a region of TMEM106B that is crucial for CTF generation and to narrow down possible sites of proteolytic processing. Additionally, since TMEM106B is a heavily glycosylated protein, we created glycosylation-deficient mutants to determine whether glycosylation is needed to regulate TMEM106B processing and CTF abundance. Lastly, we overexpressed TMEM106B in human iPSC-derived neurons (iNeurons) to examine the effects of increased TMEM106B and CTF abundance in a neuronal context.

Tyler Sotomayor GS'27, Economics – Mathematics, Gabriel Uceda-Sosa CC'28, Computer Science and Mathematics

Faculty Mentor(s) or Supervisor(s): Seyhan Erden

Title: Tipping the Tax

Abstract: New York taxi screens suggest tips as percentages of the fee-inclusive total, so every government surcharge on the meter raises every suggested tip. We estimate the causal pass-through of statutory charges into gratuities: eleven cents of each legislated surcharge dollar becomes tip, about four-fifths of the rate at which riders tip the fare itself. Identification comes from six sources of quasi-experimental variation: surcharges that switch on and off at fixed clock times, the holiday calendar, a large repricing, a flat fare, and the spatial boundary of the 2025 congestion toll. The per-dollar estimate is stable across doses from \$0.50 to \$5.00 and in both directions, and riders absorb the charges rather than re-optimize. At the 2025 schedule, \$141 million of government charges flow through the tip base each year, generating \$15–21 million in gratuities that no legislature enacted; ignoring tips misstates the incidence of these charges.

Coumba Sow CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Chao Lu

Title: Inhibition of NSD1 reveals H3K36 di-methylation regulates the epithelial-to-mesenchymal transition in head and neck squamous cell carcinoma

Abstract: Metastasis remains a major cause of morbidity and mortality in head and neck squamous cell carcinoma (HNSCC), with the epithelial-to-mesenchymal transition (EMT) playing a central role in tumor invasion. In 2015, The Cancer Genome Atlas network provided a comprehensive genomic characterization of 279 HNSCC carcinomas, identifying mutations in several tumor suppressor genes; namely, they discovered loss-of-function alterations of the chromatin-modifier NSD1 (methyltransferase). This project aimed to validate an investigational drug known as KTX-1001, an inhibitor of NSD1/2, functional units of the NSD family that mono- and dimethylate histone 3 lysine 36 (H3K36). Previous work from our lab has shown that K36 dimethylation is correlated with transcriptional activation of genes, including those that control EMT. Dose-response analysis showed decreased viability in FaDu and UM-SCC17B, both invasive HNSCC cell lines, at higher KTX concentrations. Similarly, for both, Western blot analysis revealed a decrease in H3K36me2 at higher treatment concentrations. RT-qPCR showed decreased expression of EMT regulatory genes in cells treated with KTX under TGF- β stimulation. Additionally, we observed a decrease in mesenchymal markers and the rescue of E-cadherin, an epithelial marker, when treated with KTX under the same stimulation. These results reveal the implication of NSD1-mediated H3K36 dimethylation on HNSCC metastasis and the potential of targeting the modifier pharmacologically to reduce migration.

Katherine Speer CC'27, Climate System Science

Faculty Mentor(s) or Supervisor(s): Jerry McManus

Title: Reconstructing Heinrich events at the Iberian Margin over the past 40,000 years

Abstract: Earth's last ice age and deglaciation were punctuated by Heinrich events, periods when armadas of icebergs flooded the North Atlantic, influencing the Atlantic Meridional Overturning Circulation and rapid global climate change. Drifting icebergs leave behind terrigenous fragments, called ice-rafted debris (IRD), which are preserved in deep-sea sediments. We present a 40,000-year history of IRD deposition at two sites along the Iberian Margin (IODP Expedition 397 sites U1586 and U1587), where exceptionally high-resolution sediment cores enable precise observation of the farthest extents of iceberg passage. We quantify IRD using grain counting and ^{230}Th -normalized bulk sediment flux, comparing these with $\delta^{18}\text{O}$, a proxy for temperature and ice volume; $\delta^{13}\text{C}$, a proxy for ocean circulation; and known values from other North Atlantic sites. Results reveal that icebergs traveled as far as the Iberian Margin during Heinrich events, with distinct signatures of

the first (H1), second (H2), and fourth (H4) events at ~15, ~24, and ~40 thousand years ago, respectively. Signals are particularly pronounced at site U1586, reaching 80% (H1), 59% (H2), and 95% (H4) IRD relative to foraminifera. This study yields IRD fluxes orders of magnitude lower than those calculated elsewhere in the North Atlantic, supporting the sensitivity and fidelity of the proxies used. H1 and H2 align with intervals of decreasing $\delta^{18}O$, indicating a connection to concurrent abrupt climate changes. Refining our understanding of when and how Heinrich events transpired lends us insight into the mechanisms underlying past rapid climate changes, which in turn improves our assessments of future climate variability.

Aaron Springer CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Hans Snoeck

Title: Mapping the Regenerative Potential of Pulmonary Neuroendocrine Cells into Alveolar Lineages

Abstract: Isolated epithelial cells in the distal airway of the lungs have been observed to express genes relating to a previously observed cell type in murine models, the pulmonary neuroendocrine cell. PNECs have many unique and understudied functions, including the possibility to proliferate after a lung airway epithelium injury. However, this has not yet been proven in a human model. This paper details the attempts to build a base of PNEC-like cells that can be sustained and developed while maintaining the genes that mark PNECs, principally ASCL1. ASCL1 is an oscillatory gene on the Notch pathway, whose expression was found to be able to be sustained by nirogacestat, a drug inhibiting the Notch pathway. Additionally, insulin-like growth factor expression was found to increase proliferation of PNECs. Developing a protocol to differentiate PNECs in vitro will provide a platform to study both idiopathic pulmonary fibrosis and small cell lung cancer, as both of these diseases implicate PNECs in the distal airways as a cause.

Peter Steinmetz SEAS'29, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Ryan Gaudet

Title: IDO1 and WARS1 Restriction of Trypanosoma cruzi

Abstract: Chagas disease is caused by infection by the parasite Trypanosoma cruzi and affects an estimated 8 million people a year. However, there is no current effective treatment for chronic Chagas disease. Data from Dominic Ritacco of Gaudet Lab, indicates that interferon-gamma stimulation confers protection against T. cruzi to endothelial cells, not to cardiomyocytes. From a

CRISPR-CAS12a knockout screen, 36 candidate genes were identified that may be responsible for the protective phenotype. Validation of the candidate was done by knocking out candidates using lentiviral vectors, analyzing parasite burden with flow cytometry for multiple replicates. WARS1 and IDO1 were two knockouts that resulted in a significant increase in parasite burden, both involving cytosolic tryptophan depletion. To examine the mechanisms, a study with tryptophan addition in both endothelial and smooth muscle cells with IDO1 and WARS1 knockouts was done in which tryptophan addition restored the protection in muscle cells, but not endothelial cells. Additional studies with the IDO1 inhibitors Epacadostat and 1-methyl-tryptophan and WARS1 inhibitor tryptamine in T. cruzi infected smooth muscle cells were done to support these findings. This confounding result may be due to differences in tryptophan uptake in muscle versus endothelial cells which are not well enough understood. To further examine uptake of tryptophan in endothelial cells versus smooth muscle, GRIT, a novel tryptophan biosensor was tested, validated, and cloned into both inducible and constitutive expression lentiviral plasmids for future studies to determine the mechanism of IDO1 and WARS1 as protective genes against T. cruzi.

Aria Suchak CC'29, Biology

Faculty Mentor(s) or Supervisor(s): Anne-Catrin Uhlemann

Title: Genetic analysis of untyped blaKPC-harboring Plasmids in Gram-negative bacterial species

Abstract: Antimicrobial resistance (AMR) is one of the most important public health crises in our current world. A major driver of this crisis is the ability of bacteria to share resistance genes with one another through small, transferable pieces of DNA called plasmids. Scientists have classified plasmids into groups based on how they copy themselves, which helps track how resistance spreads in clinical settings. This summer, research was conducted in the Uhlemann Lab at Columbia University Medical Center to study a group of plasmids found across multiple antibiotic-resistant bacteria that have not yet been classified and appear to move between bacterial cells at unusually high rates. To understand how efficiently these plasmids spread, experiments were performed to quantify the rate at which the plasmid transfer occurred among bacterial cells. The transferred plasmids were then genetically sequenced and computational analysis was used to compare the genetic makeup of the original bacteria and the ones that received the plasmids. Plasmids in the group varied considerably in how efficiently they transferred, with some spreading more readily than others. The central question driving the project is understanding what genetic differences account for this variation. This fall, a

more refined sequencing dataset will be generated and work will begin to build a tool that will allow specific genes to be selectively turned off. This will be a critical next step toward identifying exactly which genes are responsible for making these plasmids spread so effectively.

Tiffany Suen CC'28, Mathematics, Physics

Faculty Mentor(s) or Supervisor(s): Lynne Hillenbrand

Title: Extreme Long-Duration Be Star Outbursts Discovered with NEOWISE

Abstract: B-type stars are hot, luminous stars that are several times more massive than the Sun. Be stars are defined as B-type stars that exhibit Balmer line emission, which is indicative of circumstellar gas. They rotate very rapidly, often at a substantial fraction of their breakup velocity. As a result, gas is ejected from their equatorial regions to form a circumstellar disk called a decretion disk. A subset of Be stars undergoes outbursts associated with disk formation and dissipation, typically with amplitudes of 0.5-1 magnitude and durations of less than 1-2 years. This project identifies a new class of extreme Be star outbursts using NEOWISE light curves, characterized by larger amplitudes (up to 2.5 magnitudes) and significantly longer durations (5-15 years). Multiwavelength light curves from optical and infrared surveys are used to characterize their variability. Most sources become redder as they brighten in the infrared, which is consistent with circumstellar disk formation. Optical behavior ranges from correlated brightening to anti-correlated dimming, suggesting inclination-dependent effects. Additional evidence for circumstellar material includes H alpha emission and infrared excess that increases with wavelength. Optical and infrared spectroscopic data, including Gaia XP and ground-based observations, support early-type classifications and the presence of emission-line features. These results suggest that the observed variability is driven by sustained mass injection and long-term disk growth, representing an extreme and previously underexplored regime of Be star activity.

Lauren Suh CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Yousin Suh

Title: Understanding ZNF518A Expression in Ovarian Aging

Abstract: Women are born with a finite reserve of ovarian cells, which is continuously depleted throughout reproductive life until menopause. As more women choose to have children later in life, early menopause is becoming a prominent cause of infertility. When considering ovarian aging, people tend

to consider only infertility and reproductive health. However, its consequences extend well beyond reproduction, contributing to postmenopausal conditions like osteoporosis, cardiovascular disease, immunosenescence, and neurodegenerative disorders. Despite women comprising roughly half of the global population, women's health has historically been under-researched and underfunded. Understanding female reproductive aging is essential to extending the health-span for women, but the underlying mechanisms are poorly understood. Age at natural menopause, or ANM, can be used as a proxy for the rate of reproductive aging. Genome studies have shown that ANM is highly heritable; in fact, genetics account for 50% of the variation in ANM. Through genome-wide association studies, hundreds of variants associated with ANM have been linked to DNA damage response and repair pathways, suggesting that certain variants may be linked to earlier ANM. Earlier studies have identified several genes with large effects on ANM, and Lauren's research focuses on one gene in particular: ZNF518A. It has been observed that the ZNF518A locus contains variants for later female puberty timing and age at menarche years, or a female's first menstrual period. To understand what the physiological functions of ZNF518A are, it is necessary to determine what ovarian cell types express ZNF518A, which Lauren's research intends to do.

Solon Sun CC'29, Mathematics, Manni Lin BC'28, Mathematics and Statistics, Lara Urteaga SEAS'28, Applied Mathematics

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: Take the Gamble Out of Gambling: Using Financial Data to Estimate Dynamic Fair Value in Prediction Markets

Abstract: This project aims to assess the information signalling between traditional financial markets and prediction markets, specifically estimating fair value prices that can be used to exploit edges on prediction markets. Existing work primarily focuses on leveraging prediction markets to inform financial market strategies, based on the concept of "wisdom of crowds." We choose to focus on the inverse relationship to investigate whether traditional financial market data can inform trading strategies in prediction markets. Our trading strategies explore two distinct pathways, single series allocation and multi-series allocation. Single series allocation uses a Sharpe ratio optimization algorithm. The multi-series allocation model uses a dynamic portfolio based on Granger causality in combination with fair value estimations from financial signals.

Zhuorong Tang CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Iva Greenwald

Title: Investigating Mechanisms of Pulling-Force Generation for GLP-1 Notch Activation in *C. elegans*

Abstract: Notch signaling regulates cell fate decisions and is implicated in human diseases, including cancer. In *C. elegans*, distal tip cells (DTC) maintain germline cell proliferation and prevent premature entry into meiosis. DTC express LAG-2, which activates GLP-1 receptors on germ cells. In *D. melanogaster* and vertebrates, Notch activation requires Epsin-dependent, Clathrin-mediated ligand endocytosis, which generates a pulling force on the receptor, exposes protease cleavage sites, and allows shedding of the receptor intracellular domain. However, previous studies suggest that Notch activation in *C. elegans* can occur independently of Epsin and that the two receptor types, GLP-1 and LIN-12, have different activation force requirements. Hence, the endocytic requirements of *C. elegans* Notch activation remain unclear. This study investigates whether Notch activation requires clathrin-mediated endocytosis and whether cellular properties such as membrane rigidity also influence Notch activation. Chimeric LAG-2 ligands containing a functional Myc epitope will be designed to allow for LAG-2 endocytosis. Animals expressing chimeric LAG-2 ligands will be evaluated for progenitor-zone length and cell number as readouts of GLP-1 signaling levels. In addition, we successfully generated three *C. elegans* strains: GS10280, GS10281, and GS10293. GS10280 enables RNAi specifically in distal tip cells (DTC), GS10281 contains an mCherry fluorescent DTC marker, and GS10293 combines both genotypes. We verified strains through PCR genotyping, antibiotic selection, and fluorescence microscopy. Strains will be used to knock down genes involved in endocytosis and lipid metabolism, such as *fld-1*.

Sonali Teja Rao CC'27, Philosophy, Xavier Terminello GS'28, Cognitive Science

Faculty Mentor(s) or Supervisor(s): Joshua Kramer

Title: The Machine In the Mirror: Self-Attribution of Minds in LLM's

Abstract: Language models produce reports about their own internal states, and these reports are often viewed as evidence. However, what produces these reports is unknown. We ask whether self-reports are generated by the same mind-attribution machinery that the model applies to third parties. In

this case, these reports would be inferences rather than readouts. Using Gemma-2-2B, we extract a mind-attribution direction from 210 third-person contrast pairs spanning 7 entities, 6 mental claims, and 5 counterbalanced sentence templates. The direction is able to separate held-out sentence frames at 0.923(0.577 chance band), is not directly explained by negation, and is not aligned with placebo in comparison to other contrasts. When applied to first-person claims under a referent swap, it classifies the model's own assertions about mind relatively high at 0.933, yet does not separate experiential from mundane self-description, although this separation exists elsewhere in the model. With two referent ladders and a Jacobian lens, we find the boundary of self-attribution is grammatical rather than structural. Self-reports appear to be produced by mind-attribution machinery keyed to conversational cues rather than systematic facts. This bears on how welfare evaluations should be conditioned.

Emerald Tellez CC'29, Biochemistry

Faculty Mentor(s) or Supervisor(s): Alexis Tapanes-Castillo

Title: Benchmarking Genomic DNA Extraction Protocols Across Diverse Biological Samples

Abstract: High-quality genomic DNA serves as the foundation for biomedical research and clinical findings. Since biological samples, derived from blood, buccal swabs, nasal swabs, and saliva, differ in biomass concentration and contaminants, laboratories optimize DNA extraction through extraction chemistry protocols. This study evaluated the efficacy of DNA extraction protocols across six biological sample types: whole blood, blood clots, lymphoblasts, wet buccal swabs, wet nasal swabs stored in beta-mercaptoethanol, and saliva. While buccal swab samples were fresh, the others were frozen legacy samples. In total, twenty-five human samples were processed according to IRB approved protocols. Two different ThermoFisher kits, MagMax Ultra 2.0 and MagMAX HMW, were utilized to extract DNA on an automated KingFisher Instrument. DNA concentrations were assessed using a Qubit fluorometer. For each chemistry and sample type, individual averages and standard deviations were calculated. The mean across sample types for Ultra 2.0 chemistry was 116 ng/ μ L, n=7 individual samples obtained from whole blood, blood clots, buccal swabs, or saliva. Comparably, the mean across sample types for HMW chemistry was 120 ng/ μ L, n=18 individual samples obtained from whole blood, blood clots, lymphoblasts, buccal swabs, or nasal swabs. Hence, both chemistries yielded adequate DNA concentrations across diverse biological samples for downstream workflows,

including next generation sequencing. Future work will assess DNA purity and fragment length sizes.

Gabriel Thin CC'27, History

Faculty Mentor(s) or Supervisor(s): Richard John

Title: "Steam Reconstruction": Railroad Politics and Anti-Monopoly Thought in the Era of the Second Founding

Abstract: The controversy surrounding New Jersey's Camden and Amboy Railroad and Transportation Company, which enjoyed a state-chartered monopoly on railway traffic between New York and Philadelphia from 1832 to 1869, is well understood within the scope of New Jersey political and transportation history. However, the Camden and Amboy disputes have rarely been considered in the political context of the Civil War and Reconstruction. Throughout the antebellum period, the Company's control over commerce in the Northeast was an area of contention within the larger debate over states' rights and federal power. During the Civil War, when the railroad was accused of providing insufficient transportation for Union troops and goods moving southward, arguments against the monopoly became infused with the rhetoric of Unionism: the Camden and Amboy monopoly threatened the political unity of the nation by subjecting the Union war effort to the dictates of an unconstitutional monopoly born of the commercial jealousy of New Jersey and protected by the reviled doctrine of states' rights. During the 38th and 39th Congresses, the Camden and Amboy monopoly and the attendant issue of interstate commerce were closely intertwined with disputes over citizenship, civil rights, and Congressional authority. Integral to Republicans' vision of a reconstructed Union was an interstate railroad system that protected the constitutional right of unrestricted commerce between states. The Camden and Amboy disputes, therefore, illuminate a strand of anti-monopoly thought—grounded in the use of federal power to curb special privilege—reaching from antebellum free-labor ideology into the era of the "Second Founding."

Mallory Thomas SEAS'27, Earth and Environmental Engineering

Faculty Mentor(s) or Supervisor(s): Laura Neitzel

Title: For the People, For the Birds: Migratory bird window collision surveying as an intervention for mental health challenges on university campuses

Abstract: Bird-window collisions are a major source of anthropogenic avian mortality, yet campus mitigation programs often face persistent challenges related to funding, volunteer turnover, and coordination among institutional stakeholders. This paper examines bird-window collision research and mitigation at Columbia University through a "For the Birds, For the People" framework that links avian conservation with student well-being. We synthesize three connected initiatives: a Facilities-funded work-study monitoring program on Columbia's Morningside campus, staff-led window mitigation at the Lamont-Doherty Earth Observatory, and the Columbia Birding Troupe's role in building student engagement and conservation partnerships. Student surveys identified Avery Hall and the Northwest Corner Building as major collision hotspots and informed installation of bird-safe window markers, while Lamont staff implemented FeatherFriendly markers and low-cost Acopian BirdSavers. We argue that student birdwatching organizations can strengthen these efforts by providing a recurring volunteer base, preserving institutional knowledge, connecting stakeholders, and expanding access to external funding and training. At the same time, birdwatching and related conservation activities may support student well-being through time outdoors, social connection, attention restoration, and purposeful environmental action. Columbia's emerging Lifestyle Subscription Program provides one pathway for integrating bird walks and collision monitoring into campus social-prescribing efforts. Together, these initiatives illustrate a scalable model in which universities can align biodiversity protection, paid undergraduate research, student engagement, and non-clinical well-being support.

Skylar Tian CC'29, Mathematics

Faculty Mentor(s) or Supervisor(s): George Dragomir

Title: Routing for Fairness: Adaptive Allocation in Urban Food Rescue Under Capacity Constraints

Abstract: Food insecurity in New York City is spatially unequal, while the vehicle capacity, donor supply, and recipient operating windows available to redistribute rescued food are inherently limited. This research frames urban food-rescue routing as an adaptive allocation problem and develops a three-layer modeling framework: a baseline pickup-and-delivery vehicle-routing problem with time windows to capture operational efficiency, a cold-chain layer to account for perishable handling and freshness, and an equity-weighted valuation of recipient service to represent distributive priorities. Using a New York City transportation network constructed from public recipient-location data and clearly labeled synthetic operating parameters, the

study compares routing strategies under identical vehicle, time, and supply constraints while varying a single parameter governing the strength of equity prioritization. Increasing this weight systematically shifts service toward high-need, low-access communities, but at a measurable cost in the total number of recipients served. The results also reveal diminishing marginal equity gains beyond a moderate weighting level, with the direction of these trade-offs remaining stable under perturbations to demand, travel times, operating windows, and donation availability.

These findings demonstrate that routing objectives do more than optimize logistics: they implicitly encode distributive choices about who receives scarce resources. By making those choices explicit, measurable, and comparable, this research provides a strategic decision-support framework that can inform locally calibrated operational planning and help food-rescue organizations evaluate trade-offs among efficiency, freshness, and equity.

Chaipat Tirapongprasert CC'27, Astrophysics

Faculty Mentor(s) or Supervisor(s): Parijat Dube

Title: Internal World Models Drive Decision in LLM Reasoning Traces

Abstract: Large language model (LLM) agents achieve state-of-the-art performance across domains through chain-of-thought (CoT) reasoning. Despite their ubiquitous use, little is known about the LLMs' cognitive processes. We address this by investigating how these agents make decisions in iterative games with incomplete information. Using a series of mechanistic interpretability techniques, we find that the model forms and iteratively revises an internal representation of the game throughout the CoT.

We also demonstrate that once the model prematurely commits to an incorrect belief, it rarely recovers, resulting in self-reinforcing errors that drive game-theoretically suboptimal play. Ultimately, our work opens the door to a more focused diagnosis of strategic reasoning errors in deployed agents.

Natalia Tobar Aldana CC'28, Environmental Chemistry

Faculty Mentor(s) or Supervisor(s): Gisela Winckler

Title: The Extent and Impact of the 2025 Canadian Wildfires Through Aerosol and Sediment Analysis

Abstract: The 2025 Canadian wildfires were the second worst on record in the nation's history, starting in May and involving numerous waves that ended in late August, with plumes of smoke that reached as far as Europe. Wildfire smoke is composed primarily of PM2.5, particulate matter 2.5 microns or

smaller, and has numerous environmental impacts and harms to human health. This study characterizes the chemical composition of wildfire biomass and documents how it travels over space and time. We collected aerosol and sediment samples from the Labrador Sea aboard the R/V Roger Revelle during cruise RR2504 between June and July 2025, at the height of the summer wildfires. Utilizing aerosol sample mass, PM2.5 equivalent values were calculated to ground truth satellite reanalysis data. The observed data followed similar trends to satellite data, but moderately underestimated the amount of PM2.5 in the atmosphere. Aerosol samples were investigated using XRF (X-Ray Fluorescence) to characterize bulk elemental composition and SRX (Sub-micron X-Ray Fluorescence) for particle-level analysis. Aerosol samples from the Labrador Shelf, open ocean, and Greenland Shelf all showed consistently high levels of Ti, S, K, and Cr, implying contributions from multiple sources, including continental dust, anthropogenic combustion, and wildfire biomass. Samples from the Greenland Shelf had the highest markers of biomass burning, with 20–30% K by mass, demonstrating a transport of approximately 4,000 km. Particle-level analysis shows more diversity in element aggregates at coastal sites compared to open ocean sites. Aerosol particulate loading rates were also compared to 230Th-normalized 232Th flux in co-located core-top (0–1 cm) sediment samples as a proxy for background lithogenic input into modern (past ~1-5 yrs) ocean sediment. As the intensity of the summer Canadian wildfires increases in both frequency and magnitude, these findings suggest wildfires will continue to spread hazardous particulates across land and sea and impact Arctic communities.

Kim Tong GS'27, Postbaccalaureate Premedical

Faculty Mentor(s) or Supervisor(s): Rebecca Haeusler

Title: The Role of Manganese in Regulation of AKT and Insulin Signaling Pathway

Abstract: Diabetes mellitus is a chronic disease with high prevalence in the US. According to the American Diabetes Association, nearly one in two Americans has diabetes or pre-diabetes. There is no known cure for diabetes besides lifelong symptom management. This underscores the importance of understanding the deeper mechanisms of the insulin signaling pathway and its dysregulation for better clinical application. AKT, a serine/threonine kinase also known as protein kinase B (PKB), is one of the primary regulators of the insulin pathway, regulating glucose uptake, glycogen synthesis, and metabolic homeostasis downstream of insulin receptor activation. AKT is canonically understood to be activated exclusively through insulin-stimulated phosphorylation, proceeding via the PI3K/PIP₃ axis and subsequent

recruitment of PDK1 and mTORC2. However, we have found that, even in the absence of insulin or insulin-related stimulation, AKT in mouse primary hepatocytes can be activated by manganese ions (Mn^{2+}) alone and can trigger its typical downstream activities. We also hypothesize that E314, Q352, D353, H354, and E355 on AKT constitute the direct binding sites of Mn^{2+} . We tested this hypothesis by transfecting HCT116 and HepG2-C3A cell lines with mutant AKT and treating the cells with Mn^{2+} . Simultaneously, we genetically modified B6 mice with the same mutant using adeno-associated virus (AAV) gene therapy and isolated primary hepatocytes for further analysis. The phosphorylation of the downstream enzyme glycogen synthase kinase 3 β (GSK3 β) served as our indirect measurement of both wild-type control and mutant AKT activity. Our findings challenge the long-standing assumption that AKT activation is strictly insulin-dependent, revealing manganese as a novel, non-canonical activator of this key metabolic kinase.

Rokhyatou Toure CC'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Erika Stewart

Title: Characterizing Behavioral Responses to Acute and Chronic Social Defeat Stress in Male and Female Mice

Abstract: Stressful events can trigger the onset of neuropsychiatric disorders in vulnerable individuals, yet there is substantial individual variability in stress response. A major goal of stress research is to understand why some individuals are susceptible to behavioral and emotional disturbance following stress and others remain resilient. Furthermore, there are well-documented sex differences in the incidence and symptomatology of neuropsychiatric disorders that highlight the importance of understanding sex differences in stress responses. Yet, the historic exclusion of female subjects and standard use of male-defined criteria has led to a gap in our understanding of female-specific stress responses. In this study, we used a paired male-female social defeat stress model to explore sex differences in stress responses. Here, mice experienced either acute or chronic social defeat stress, in addition to a “two-hit” group that experienced both acute and chronic stress. We aim to quantify traditional social approach/avoidance behavior and characterize other behaviors that might better capture female-specific stress responses. Using EthoVision XT, we conducted automated and manual video analysis of mouse behavior in a social interaction test following social defeat stress. We quantified sociability, locomotor activity, grooming, and rearing behaviors. Our findings expand the behavioral characterization of acute and chronic social defeat stress by demonstrating that grooming and rearing provide complementary measures to the classical Social Interaction Ratio. By directly

comparing male and female mice, these findings contribute to a more comprehensive understanding of stress-related behavioral adaptations and support the inclusion of both sexes in preclinical stress research.

Emnet Tsegaye CC'28, Computer Science, Financial Economics

Faculty Mentor(s) or Supervisor(s): Parijat Dube

Title: Cognitive Maps or Recitation? A Teacher-Student Paradigm Inspired by Human Spatial Cognition, Applied to Language Models

Abstract: When a language model is taught the layout of a space, does anything like a stable mental map form, or is the model simply reciting what it was just told? Human spatial cognition treats a learned environment as a Euclidean map, a relational graph, or, ordinarily, both at once. We test this in a language model: a Teacher model teaches a Student model the layout of five rooms, and the Student is scored on metric knowledge (where each room is) and relational knowledge (which direction one room is from another), against three scripted baseline agents. Teaching format determines what the Student can later demonstrate, and asymmetrically: coordinate teaching gives near-perfect position and chance-level direction, while relative-offset teaching improves both measures but unevenly, in a pattern that differs by which model is doing the learning, and no format produces a Student good at both. None of this knowledge survives once the teaching leaves the context window, and returning the Student's own notes, probing them, or fine-tuning on the taught facts directly all fail to restore it, the last of these leaving the Student worse off than if it had never been taught at all.

The pattern is more consistent with the model reading an answer out of text still in front of it than with anything resembling the stable maps or graphs described in the human literature. Teacher and Student are the simplest possible case of a pattern now central to the multi-agent systems being built for real deployment, where one agent routinely has to transfer what it knows to another; if that transfer is recitation rather than representation here, the same test is worth running before trusting it elsewhere.

Joy Udoh CC'29, English

Faculty Mentor(s) or Supervisor(s): Nyle Fort

Title: The Social World in the Digital Age: Technology and the Transformation of Social Life

Abstract: The Social World in the Digital Age: Technology and the Transformation of Social Life examines how the rise of the internet and smartphone technology has transformed the ways people communicate, form relationships, navigate daily life, and participate in society. The project uses life before the internet as a point of comparison for understanding the social changes brought about by constant digital connectivity. Through archival research, interviews, and engagement with scholarship on technology and society, the research considers both what digital technology has made possible and what forms of social interaction may have been diminished or displaced. Particular attention is given to changes in communication, including the shift from handwritten letters and landline telephone calls to texting, social media, and constant accessibility. The project also considers the growing role of smartphones as infrastructure for everyday life, from navigation and banking to education and social connection, and examines emerging efforts to reduce dependence on these technologies through phone-free communities and movements focused on reclaiming attention. A central goal of the project is to collect and preserve firsthand accounts of technological change across generations, with particular emphasis on older people who experienced life before the internet while also incorporating perspectives from the general population and younger generations. These interviews will document not only what life was like before widespread connectivity, but how people's relationships with technology have evolved. Ultimately, the project asks what is gained and lost as technology becomes increasingly embedded in social life and how understanding these changes can help people think more intentionally about their digital future.

Oscar Uhalde CC'28, Sociology

Faculty Mentor(s) or Supervisor(s): Frank Guridy

Title: A Culture of Change: Legal Accessibility and Collective Action in Appalachian Ohio

Abstract: Despite Appalachia's long history of organizing and resistance, the region is often portrayed as politically passive. This paper asks how Appalachia's political economy constrains or enables sustained mobilization for structural change. Using the seven-county service area of Legal Aid of Southeast and Central Ohio's office in Athens, Ohio as a case study, it asks how access to legal institutions shapes the ability of communities to recognize and organize around shared grievances. Drawing on scholarship on the Appalachian region, political sociology, and legal aid history, as well as data on legal accessibility and socioeconomic conditions, the paper examines a crisis of legal inaccessibility in Southeast Ohio within Appalachia's broader

history of exploitation and marginalization. The findings illustrate that poor people in the region face significant barriers to accessing legal help, including attorney scarcity, overwhelming legal needs, and ongoing underfunding of legal aid. However, this paper argues that access to justice is not just a legal issue. Rather, legal institutions function as a mechanism through which people translate individual problems into shared ones and challenge unequal systems. When this mechanism is inaccessible or ineffective, systems of political disempowerment go unaddressed, reinforcing or even strengthening patterns of inequality. By contextualizing legal inaccessibility in Southeast Ohio within Appalachia's extractive political economy, this paper aims to offer a new perspective on the persistence of marginalization and inequality in Appalachian communities, while also illustrating the continued commitment of legal aid advocates and possibilities for collective action and structural change.

Bailey Van SEAS'28, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Nicholas Hou

Title: Constitutive Cdkn2a Loss in the Dual Screen Alters the State and Composition of Patchwork Tumor-Associated T Cells

Abstract: Glioblastoma is the most common and aggressive primary brain cancer, with no cure despite multi-modality treatment. The disease's poor prognosis can be largely attributed to significant inter- and intratumoral heterogeneity. Although immunotherapy has transformed treatment for several other cancers, clinical trials in glioblastoma have largely failed. This may result from limited immune cell access to the brain, an immunosuppressive tumor microenvironment (TME), and tumor cells' ability to adapt to treatment.

To investigate how specific mutations impact individual tumor cells and their surrounding environment, Patchwork was developed as a single-cell CRISPR screening platform that enables glioma initiation in mice using a pool of tumor suppressor gene (TSG) perturbations. Two screens were performed, each containing eight tumors. The dual screen delivered the same set of perturbations as the single screen but with an additional fixed Cdkn2a perturbation, a TSG commonly deleted in glioblastoma. Comparing the two screens isolates how TSG loss reshapes the tumor and its microenvironment within a permissive and common glioblastoma background.

This study focused on characterizing T cell behavior across screens to determine how fixed Cdkn2a loss reshapes the T cell compartment of the TME. A deep generative model identified enrichment of regulatory T cells and upregulation of checkpoint inhibitor receptors under Cdkn2a co-

perturbation. Cell-cell communication analysis further identified increased myeloid-recruitment chemokines linked specifically to Trp53 loss tumor cells within the dual screen. Together, these findings indicate that Cdkn2a loss reshapes the immune environment of glioblastoma and may create a vulnerability that could be targeted therapeutically.

Gabriel Vega Troncoso CC'27, Biophysics

Faculty Mentor(s) or Supervisor(s): Michael Argenziano

Title: Changing Anatomic Sources of Bleeding at Reexploration After Cardiac Surgery: Predictors, Findings, and Outcomes

Abstract: After heart surgery, a small number of patients bleed enough that surgeons must reopen the chest to locate and control the source. This second operation carries substantial risk of death and complications. Over the past decade, hospitals have widely adopted blood conservation practices, and transfusion rates have fallen considerably. It has generally been assumed that these same practices would also reduce the need to reoperate for bleeding. Investigators at a large academic heart surgery program reviewed every adult cardiac operation performed at their institution between 2015 and 2026, more than twelve thousand cases in total. They identified each patient who returned to the operating room for bleeding and read the operative report from every one of those procedures to determine precisely what the surgeon encountered and where the bleeding originated. Transfusion declined by roughly a quarter across the study period. Despite this, the proportion of patients requiring reoperation for bleeding did not fall. What changed instead was the anatomy of the bleeding itself. Early in the study, bleeding most commonly arose from the sutured connections between blood vessels created during the original operation. By the end, these accounted for far fewer cases, while bleeding from raw tissue surfaces, cut bone edges, and the tracts left behind by chest tubes and sternal wires had become the predominant finding. These findings suggest that further progress may depend less on medications and blood products than on surgical technique at the sites where instruments, tubes, and wires pass through the chest.

Maya Velasco CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Wesley Grueber

Title: Identification of a gate control circuit mediating the stability of a nocifensive behavioral sequence

Abstract: An internal representation of the outside world is constructed by integration of multiple sensory modalities to drive appropriate behaviors. One influential model of multisensory integration in somatosensory systems is the gate theory of pain of Melzack and Wall (1965) in which the perception of pain arising from nociceptive C-fibers is “gated”, or modulated, by touch or vibration. More generally, gate control has been a highly influential model to understand how sensory signals can be modified on their way to the brain to generate context-appropriate behavior. To study possible roles for gate control circuits in *Drosophila* larval nociception, we used a synapse-level connectome of the *Drosophila* larval nervous system to examine circuits underlying escape behavior induced by peripheral nociceptors. In flies, noxious stimuli lead to a rapid bend and roll response followed by transition to escape forward crawling. We hypothesized that the transition from bend & roll to crawling involves modulation of input from nociceptors to downstream circuitry by accumulated tactile signals received during rolling. We thus searched the connectome for possible links between tactile and nociceptive circuitry, primarily focusing on a population of body wall tactile hairs innervated by external sensory neurons (ESNs). We find that ESNs form synapses onto an uncharacterized, likely inhibitory, interneuron in the ventral nerve cord called A19b. A19b, in turn, synapses onto an excitatory nociceptive interneuron called Basin-4 that receives direct input from nociceptive sensory neurons and promotes escape rolling behavior. The anatomy of this circuit raises the possibility of cross-modal modulation, in which tactile input could gate nociceptive input through A19b and Basin-4 interneurons, perhaps promoting a switch from rolling to crawling behavior. The experiments described were designed to test this hypothesis by singly and jointly manipulating ESNs and nociceptive pathways and analyzing resulting behavioral responses. Together, our results point to a new nociceptive gating circuit that contributes to a stable transition between successive nocifensive behaviors.

Sindhu Vemulapalli CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Carol Troy

Title: Assessing Neurodegeneration in the Visual Relay of the Brain in a Mitochondrial Disease Model

Abstract: Leigh syndrome is a mitochondrial disorder that produces progressive neurodegeneration, yet its consequences for the central visual pathway remain poorly defined. Particularly vulnerable may be the dorsal lateral geniculate nucleus (dLGN), the thalamic relay conveying retinal input to the visual cortex, whose metabolically demanding neurons depend heavily

on bioenergetics. This project characterizes synaptic and cellular degeneration in the dLGN of a Leigh syndrome mouse model, a necessary step toward testing whether our laboratory's eye-drop therapy, shown to resolve retinal vein occlusion and prevent blindness, can also protect visual circuitry in this more severe disease model. To characterize degeneration, coronal sections from a cohort of 10 affected and control animals were cryosectioned, stained with DAPI, PSD95, VGLUT1, and Tuj1 following optimization of an antibody panel for reliable colocalization, and imaged by confocal microscopy. Synaptic integrity was assessed from colocalization of the presynaptic marker VGLUT1 and postsynaptic marker PSD95, and neuronal density was quantified from DAPI-labeled nuclei under a self-established protocol, with a shape-based filter excluding non-neuronal nuclei such as vascular endothelial cells. Synaptic colocalization did not differ significantly between affected and control tissue; neuronal density, however, was reduced in affected animals, revealing a dissociation between preserved synaptic content and diminished cell number in the same region. These findings establish cell density as a more sensitive early index of degeneration than synaptic markers and suggest that surviving neurons maintain synaptic connectivity despite cell loss, defining a quantitative baseline for an upcoming study of whether our eye-drop therapy attenuates this neuronal loss.

Avellana Vigil-Villalobos CC'29, Computational Biology

Faculty Mentor(s) or Supervisor(s): Charles Shuster

Title: Development of a novel computer-vision tool to track cancer cell fates from low-resolution data sets

Abstract: Machine learning tools and Generative AI have vastly improved the ability to track movements from subcellular structures to whole tissues in living organisms. For high-resolution imaging applications such as confocal microscopy, open-source (CellPose) and commercial (Imaris) packages afford efficient tracking and quantification of fluorescent structures within 4D data sets. However, these packages are not useful for analyzing transmitted light images. Our lab seeks to understand the variability of cancer cell responses to mitotic arrest when cells are unable to complete mitosis. Cancer cells display a high degree of heterogeneity in response to mitotic arrest, where some cells die by apoptosis while others slip out of mitosis to die later or attempt another cell cycle. The Sartorius Incucyte high-throughput imaging system monitors cells over time and can quantify apoptosis with a fluorescent reporter.

However, the system also generates a phase contrast image for each time point, enabling us to quantify all possible cell fates manually. To automate

the identification of different cell fates from these low-resolution image stacks, we developed a Python-based computer-vision workflow to label and track cells over time. This pipeline consists of multiple python libraries including matplotlib, scikit-image, trackpy, and a RandomForestClassifier machine learning model. Our tool currently labels and categorizes cells undergoing mitosis, measuring parameters including size, shape, movement, and fate prediction data for each cell in a tiff image stack. Current efforts are focused on improving the mitosis timing feature as well as training our machine learning model to more precisely predict complex cell fates.

Enzo Visintin CC'29, Physics

Faculty Mentor(s) or Supervisor(s): Marcelo Cunha

Title: A Simulation Approach Toward a Definition of Catalytic Power in Entanglement-Assisted Local Transformations

Abstract: Enzo was a summer research scholar at the Mathematical Foundations of Quantum Theory Group, led by Professor Marcelo Cunha at UNICAMP, the State University of Campinas, in Sao Paulo, Brazil. He led a computational project on quantum catalysis, which studies, from the lens of information theory, the implications of quantum entanglement, defined as the deep correlation that can exist between the states of two systems held by separated parties, conventionally called Alice and Bob.

The project investigates a class of manipulation procedures known as local operations and classical communication, or LOCC, in which each party may freely act or measure their own system and communicate with the other only classically, sharing the results they obtain. Within this framework, Nielsen's theorem establishes which pairs of entangled states can be converted into one another with certainty, using an algebraic ordering relation called majorization. Surprisingly, some conversions that are only probabilistic under LOCC alone become certain if both parties are temporarily lent an additional entangled state from a third one. This auxiliary state, remarkably, is returned unchanged once the conversion is complete, much like a catalyst in a chemical reaction, from which the effect borrows its name.

Enzo's research focuses on developing simulation algorithms, written in Julia, that sample large numbers of quantum states to measure how often a catalyst can enable a conversion that would otherwise be uncertain under only LOCC protocols. The goal is to contribute to an ongoing effort to define catalytic power and thus rank catalysts by their effectiveness.

Ashling Walshe SEAS'28, Electrical Engineering

Faculty Mentor(s) or Supervisor(s): Savannah Eisner

Title: GaN Hall Sensors for Steady State Plasma Diagnostics

Abstract: Magnetic field diagnostics in fusion environments, such as Tokamaks, require sensors that are capable of operating in extreme conditions. Current diagnostic technologies such as B-dot probes often face limitations in durability and precision. We present the development and deployment of Gallium Nitride (GaN) Hall effect sensors designed for ex-vessel magnetic diagnostics on the HBT-EP Tokamak. Experimental results demonstrate a linear Hall voltage response to applied magnetic fields, verifying the sensor's operational integrity during vacuum and plasma shots. These results validate the feasibility of using wide-bandgap semiconductor sensors for robust magnetic diagnostics in future high-beta fusion research.

Celeste Wang GS'28, Political Science

Faculty Mentor(s) or Supervisor(s): Justin Phillips

Title: Party Reform and the Origins of Abortion Politics

Abstract: The partisan divide over abortion has often been attributed to the Republican party and conservative activists in the 1980s, yet recent research suggests that this divide began as early as the late 1960s, through Democratic party reforms and issue activists mobilized by the democratizing McGovern-Fraser reforms. This research project, through novel digitized newspaper archives and state party platforms, examines Delaware between 1968 and 1972 as a case study of emergent theories on party reforms' effects on abortion politics. By tracing changes in the state's party rules, conventions, platforms, and delegate selection processes, with particular focus on the increased participation of previously underrepresented groups such as students and women, Delaware exposes the complexity of abortion's inclusion into national politics. In Delaware, reforms both directly the cause of the McGovern-Fraser Commission and those inspired by it, opened up the party to minority activists, reducing structural barriers. In 1972, abortion appeared in Delaware's proposed state platform for the first time, yet failed to pass, remaining contingent on party leaders who indirectly resisted abortion's entry onto party agendas, through contesting political reforms, rather than directly abortion-related planks. Research into Delaware's role suggested that not only did the democratization of party institutions produce new leadership opportunities, but also a struggle for authority: a conflict between established leadership and minority activists that bolstered the weight of issue politics on state platform committees before the transformative national partisanship following Roe v. Wade.

Ben Wang CC'28, Data Science

Faculty Mentor(s) or Supervisor(s): Ensheng Weng

Title: Modeling and Attributing Forest Carbon Tipping Points Under Climate Change

Abstract: Forests absorb approximately 30% of anthropogenic carbon dioxide emissions, but rising CO₂, temperatures and altered precipitation may weaken the global land carbon sink and tip vulnerable ecosystems from net carbon uptake to release. Identifying where and when these tipping points occur under different emissions scenarios is critical because widespread sink loss could amplify climate change through a positive carbon-cycle feedback loop. To address this issue, we developed a machine learning emulator for NASA GISS's demographic vegetation model BiomeE, which is currently a useful but computationally expensive tool for simulating ecosystem dynamics. The emulator allows us to rapidly simulate realistic carbon-flux responses across different future climate conditions and emissions scenarios. We trained it on 2.8 million BiomeE-generated samples using XGBoost to calculate net ecosystem exchange (NEE) by predicting gross primary production (GPP) and ecosystem respiration across a global forest grid. To evaluate the emulator performance, we used CMIP6 Shared Socioeconomic Pathway (SSP) climate data from the GFDL ESM4 model as inputs into BiomeE. We then applied SHAP analysis to reveal that precipitation and humidity are the main drivers of NEE. Both BiomeE simulations and emulator results suggest that forest NEE increases with time and higher-emissions pathways. Even under the intermediate-emissions pathway SSP2-4.5, global mean forest NEE will dangerously approach carbon neutrality by 2100. The results highlight the importance of emissions reductions in reducing the risk that forests lose their carbon-uptake capacity and increasingly amplify climate change through a positive feedback loop.

Taeyoung Wang SEAS'27, Materials Science and Engineering

Faculty Mentor(s) or Supervisor(s): Yuan Yang

Title: Probing Salt Partitioning and Low Temperature Transport in Gel Polymer Electrolytes

Abstract: Gel polymer electrolytes can improve cycling stability and safety in lithium batteries, but the mechanisms behind these benefits remain uncertain. Some designs attribute these benefits to salt-phobic polymer regions that

exclude lithium salts and create locally anion-rich solvation environments. Although spectroscopy and simulations support this mechanism, equilibrium salt partitioning between gel and liquid has not been quantified, leaving its contribution hard to isolate. This study examined three linked signatures: spatial composition near an electrode, equilibrium gel-liquid partitioning, and low-temperature phase behavior and ion transport. Raman depth profiles through a polypropylene separator toward a nickel-manganese-cobalt oxide cathode were analyzed using a custom-developed program that reduced operator dependence in baseline selection. Lithium coordination by ethylene carbonate remained essentially unchanged toward the cathode. One band ratio increased from 0.67 to 0.85, but overlap with the separator prevents definitive assignment. Gel-liquid partitioning was assessed by quantitative NMR of the initial dual salt electrolyte, equilibrated liquid, and gel extract. No clear compositional difference was resolved between the equilibrated liquid and gel extract. Differential scanning calorimetry showed that gelation lowered melting and crystallization temperatures relative to the corresponding liquid, yet none of the tested gel formulations exhibited improved low-temperature ionic conductivity. Together, these findings constrain proposed explanations for gel electrolyte performance: equilibrium salt partitioning was not measurably resolved under the tested conditions, and lower phase-transition temperatures did not translate into improved low-temperature ion transport.

Sirius Wang CC'29, Biochemistry

Faculty Mentor(s) or Supervisor(s): Anne-Catrin Uhlemann

Title: SDIC3, a prophage encoded phage-defense system, in carbapenem-resistant *K. pneumoniae* and *S. marcescens*

Abstract: Prophage-encoded anti-phage defense systems are widespread contributors to bacterial fitness, as prophages often protect their bacterial hosts from superinfection by competing phages, in order to secure their own persistence. *Serratia marcescens*, an opportunistic pathogen with intrinsic resistance to polymyxin B, is a leading cause of nosocomial infections and a WHO-designated critical priority for alternative treatment development. Its genome possesses environmental plasticity, making it highly flexible to environmental changes. Thus, the understanding of its phage defense mechanism is crucial for the development of an alternative combat approach for antibiotic-resistant infections. Here, we aimed to characterize SDIC3, a defense system located within *S. marcescens*. Surprisingly, this system is also found in *Klebsiella pneumoniae*, another gram-negative pathogen associated with human gut infections. Thus, the question focuses on why this *S. marcescens* system is present in *K. pneumoniae* and how these two variants

work differently. To compare their function, we heterologously expressed the *Serratia*- and *Klebsiella*-derived systems in *E. coli* and found that they exhibit distinct activity. The *Serratia* variant additionally encodes two extra gene components that are not present in the *Klebsiella* system, which may underlie this difference in functionality. The exact function of those two gene components is yet to be elucidated, as the future step of this project.

Vika Wei SEAS'28, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Dan Steingart

Title: Stabilizing Effect of Iron on Lead Anodes for Aqueous Metallurgy

Abstract: Traditional methods of metal processing face challenges including requiring high-grade ores and contributing a meaningful proportion of global carbon emissions. In response to these issues, electrowinning, a process in which metals are electrolytically deposited from ores, has emerged as a more sustainable solution for metal processing. Sulfate-based electrowinning systems often use lead-based anodes to extract metals such as zinc and copper, and there is growing interest in expanding electrowinning to other metals, like iron. Lead-based anodes are oxidatively stable, inexpensive, and earth-abundant, but a major downside lies in lead's toxicity. Shedding and contamination arise as significant environmental and health hazards. This project examines the impact of two particular metal ions, iron and manganese, on lead anode stability. Manganese is a common contaminant in ore inputs, while iron is relevant to new electrowinning processes and is commonly present in other metal ores. Electrolysis was performed in the presence of both ions individually as well as together, in order to understand how they interact simultaneously in the same system. In experiments with no metal cation and with manganese alone, anode mass loss increased linearly with time, where manganese electrolytes led to slightly higher mass loss at longer timescales. The presence of iron, even alongside manganese, entirely mitigated any mass loss. Additionally, presence of manganese caused experiments to generate solid "sludge," which, at scale, would require plants to stop operation and clean cells more often. Sludge disposal also raises concerns for the handling of hazardous, lead-containing waste. It was found that iron also decreases the amount of sludge produced in experiments. Iron thus shows promise in stabilizing lead anodes, opening many possibilities in the continued development of sustainable metallurgical practices.

Shira Weiss-Ishai GS'27, Biochemistry

Faculty Mentor(s) or Supervisor(s): Brent Stockwell

Title: Synthetic development of novel 3-alkyltetrahydro- β -carbolines as GPX4 inhibitors

Abstract: This project conducted in the Stockwell Lab focuses on developing new drug candidates that target a protein called GPX4, which plays a central role in protecting cells from a cell death called ferroptosis. Ferroptosis occurs when cells are damaged by excessive oxidation, and this type of cell death has been linked to diseases such as cancer and neurodegenerative disorders. Researchers from this lab have been working on small-molecules that can inhibit GPX4, therefore inducing ferroptosis and potentially killing cancer cells that have become resistant to other forms of treatment. While these initial small-molecule GPX4-inhibitors have been able to selectively induce ferroptosis in cancer cells, they lack the drug-like properties that would make them sufficient for clinical application.

This work focused on modifying existing GPX4 inhibitors to improve their potential for clinical translation. This summer, the project focused on modifying a particular portion of an existing GPX4 inhibitor that may be easily broken down in the body. An unstable chemical group was replaced with a more stable carbon chain with the goal of improving the compound's stability while maintaining its ability to target GPX4. The modified core structure was produced through a series of chemical reactions, several of which required optimization in order to improve their success and yield. The final modified structure was successfully synthesized and chemically characterized. This new core can now be used to create a broader set of GPX4 inhibitor candidates, which can be tested in cancer cells to determine how the structural change affects their stability, potency, and ability to induce ferroptosis.

Ari Wen CC'28, Applied Mathematics, Psychology

Faculty Mentor(s) or Supervisor(s): Gaurav Patel

Title: Individual Heterogeneity in the Retinotopic and Functional Organization of the Intraparietal Sulcus

Abstract: The human cortex exhibits highly organized topographic representations of the visual field, which can be mapped retinotopically using functional magnetic resonance imaging (fMRI) on an individual basis. However, much of today's progress on visual neuroscience relies on interpreting population-average data, potentially obscuring meaningful heterogeneity in cortical organization. In this study, we developed a novel task to map retinotopy that required peripheral attention while maintaining fixation and used fMRI to measure retinotopic maps of 25 healthy controls.

We further collected 22 minutes of resting-state fMRI (rsfMRI) to allow us to assess functional connectivity in the same individuals. After annotating the maps to identify distinct areas (IPS0-IPS5 maps) in each individual using a consensus procedure, we found that in some individuals there were prominent spatial discontinuities between in the maps IPS2 and IPS4 (12/25 left hemisphere, 10/25 right hemisphere), while the rest show a more compact structure. We then used the rsfMRI data to construct subject-specific functional connectivity matrices to determine whether the discontinuities found in the retinotopic maps were related functional network organization in the IPS. We found that discontinuities in the retinotopic maps were mirrored in the functional connectivity. By examining retinotopic organization and functional connectivity at the individual level, we identified a previously unreported heterogeneity of intraparietal neural networks in a healthy population.

Cynthia Wen SEAS'28, Materials Science

Faculty Mentor(s) or Supervisor(s): Arkadiy Simonov

Title: Modeling Disorder in a Binary Fe-20 at.% Al Alloy

Abstract: Atomic disorder controls many technologically important properties, from the thermoelectric efficiency of half-Heuslers to the relaxor behavior of ferroelectrics. Such disorder can be measured with single-crystal diffuse scattering from X-ray and neutron diffraction, but interpreting these signals remains difficult, as contributions from short-range order (SRO), size-effect strain, and thermal diffuse scattering overlap in a single diffraction map. Here, a workflow is proposed to separate these contributions using a binary Fe-20 at.% Al alloy as a model system. Chemical SRO correlations are refined against synchrotron data using the three-dimensional difference pair distribution function (3D- Δ PDF). Shell-resolved interaction parameters are then fitted to reproduce them by histogram reweighting and used to drive Monte Carlo simulations of a 16,000-atom crystal. The static displacements that give rise to the size effect are introduced by relaxing these configurations with a universal machine-learned interatomic potential. Pre-trained on large quantum-mechanical databases, such potentials reach near density-functional accuracy at a cost low enough to relax tens of thousands of atoms, removing the scaling barrier that has limited first-principles relaxation in disordered crystals. Thermal motion is included only through an isotropic approximation, leaving explicit modeling of correlated vibrations to future work. The resulting model reproduces the experimental diffuse scattering well across multiple reciprocal-space planes, and this approach should extend to more complex materials with similar disorder.

Margaret Whelan GS'28, History

Faculty Mentor(s) or Supervisor(s): Seema Chauhan

Title: Value and Vulnerability: Sex Work in Thai Theravāda Buddhism

Abstract: Western frameworks typically interpret women's status through individual autonomy, reducing prostitutes to a binary of women who choose sex work or victims of exploitation. Commercial sex work within Thai society occupies a distinctive position, where Theravāda Buddhist ethics inform understandings of gender, duty, and social value. This research reframes sex workers' position through an emic analysis of Thai Theravāda Buddhist socio-religious relations. Central is the male bhikkhu (monk), whose authority has reinforced gender hierarchy, subordinating women while depending upon their economic and religious contributions. Excluded from religious authority, women can use commercial sex work to accumulate more merit, or "bun", than other available work because its higher earnings allow them to contribute to their families and the Buddhist community—acts that constitute bun. Ethnographic accounts from northern Thailand reveal less stigma toward sex workers than Western frameworks predict.

Yet the same structures that give sex workers value in Buddhist ideology can heighten their vulnerability to exploitation. Thai social and religious expectations, economic inequality, and inadequate legal protections can make sexual coercion difficult to recognize and resist. Neither Western individualism nor cultural relativism adequately explains this tension. Imposing Western assumptions about agency risks cultural imperialism, while romanticizing culturally specific duty and merit can obscure trafficking and coercion. As demonstrated by the bhikkhunī movement, reform can emerge from within Theravāda Buddhism itself. Thai sex workers' vulnerability cannot be addressed by treating Western ideals of liberation as universally applicable; reform must instead engage the Theravāda Buddhist structures shaping both their value and vulnerability.

Marcella Willett CC'28, Environmental Biology

Faculty Mentor(s) or Supervisor(s): Caitlin Wells

Title: Impact of Litter Emergence Timing on Pup Growth Rate of Golden-Mantled Ground Squirrels

Abstract: Phenological mismatch has been shown to impact juvenile growth and body condition in several species of birds, but its effects on juvenile growth in small mammals are less well- documented. Golden-mantled ground

squirrels (*Callospermophilus lateralis*, GMGS) are a small, hibernating mammal to whom body mass is particularly important for survival during their first winter. Using historic data from 1996-2021 from long-term studies at the Rocky Mountain Biological Laboratory, I investigated how GMGS pup growth rate is affected by litter emergence timing relative to the timing of peak abundance of common dandelions (*Taraxacum officinale*), a key diet item for GMGS. I found that pups emerging slightly later relative to peak dandelion abundance (greater mismatch) showed lower growth rates within two-weeks of emergence, with weaker effects of emergence timing on four and six-week growth rates, suggesting that older pups are better able to buffer against the effects of mismatch.

Wiann Wilson CC'28, English, Ethnicity & Race Studies

Faculty Mentor(s) or Supervisor(s): Alessandra Cianetti

Title: Decolonial Art History Resource Development

Abstract: Wiann Wilson's Laidlaw Leadership in Action project at Art History Link Up (AHLU) in London, UK explored how decolonial approaches can support the development of more inclusive art history education. The project examined how overlooked histories and excluded perspectives could be incorporated into educational resources without requiring the replacement of established curriculum content. The project drew on the practice of close reading, or "reading against the grain," to teach existing artworks and materials through more nuanced historical perspectives. Rather than changing the objects being studied, the project asked new questions of them to uncover overlooked histories and perspectives that have remained untold. Wiann's research included reviewing teaching specifications and educational materials, observing classes at The Courtauld Gallery, and consulting with AHLU's resource development team to identify areas where new resources could have the greatest impact. The project resulted in Wiann developing two resource databases. The first supports the Higher Project Qualification by bringing together existing decolonial pedagogical practices, student resources, supplementary lesson plans, and novel lesson ideas that incorporate decolonial practices and perspectives from the Global Majority while remaining grounded in British historical contexts. The second similarly supports Art History A Level and Extended Project Qualification. Together, these resources provide teachers and students with practical ways to engage with existing art history curricula while considering a wider range of historical interpretations. The project demonstrates how small shifts in the questions asked of familiar artworks can

open up space for perspectives that are often absent from traditional art historical narratives.

Fiona Witty-Daugherty CC'28, Environmental Chemistry

Faculty Mentor(s) or Supervisor(s): Benjamin Bostick

Title: Field Testing an Iron Oxide Bioreactor for Arsenic and Uranium Removal in Drinking Water

Abstract: In the United States, rural and Indigenous communities face elevated health risks from arsenic and uranium in drinking water. Water treatment for uranium is challenging, and is often insufficient for arsenic. We have been developing water treatment technologies that overcome these limitations through active microbial iron cycling. Bioreactors containing cultures with iron oxidizing and reducing microorganisms continuously generate adsorption media and can reduce uranium to insoluble forms. In this study, we examine the efficacy of iron-containing bioreactors installed on private wells impacted by arsenic and uranium (greater than 10 ppb) to establish if such systems work effectively under real-world conditions. Synchrotron-based spectroscopy indicates that the iron minerals formed are ferrihydrite and lepidocrosite, both of which have strong affinity for metal adsorption. The composition of untreated groundwater and treated water samples were collected daily, with measured flow rates and composition, determined by inductively coupled plasma mass spectrometry, to evaluate bioreactor performance. Field data indicates that reactors achieved up to eighty percent removal of arsenic, with removal increasing as flow rates decreased. Measured rate constants (0.02 min^{-1}) are consistent with residence times of about 1h to achieve two parts per billion arsenic target effluent levels. Uranium removal was minimal under experimental conditions. Our data demonstrate sufficient arsenic removal for water treatment, but suggest reactors need to maintain Fe(II) levels to improve uranium removal. Understanding conditions under which the system treats water effectively will inform future steps in optimizing the system, ultimately improving sustainable access to clean water in rural areas.

Audrey Wolk CC'28, Computational Biology

Faculty Mentor(s) or Supervisor(s): Clarice Weinberg

Title: An Enduring Mark: Epigenetic Consequences of Maternal Smoking During Pregnancy

Abstract: In-utero exposure to maternal smoking is associated with differential DNA methylation during childhood, but whether these changes persist throughout the lifespan remains unclear. Additionally, women exposed to maternal smoking in-utero are at increased risk of later experiencing a miscarriage. This study examined whether epigenetic changes related to in-utero smoke exposure persist into late adulthood and could explain differences in health outcomes. To do this, whole-blood methylation data from 2,878 women enrolled in the Sister Study were analyzed.

A total of 12,568 previously identified maternal smoking-associated CpG sites, four epigenetic clocks, 12 SystemsAge clocks, and 108 protein EpiScores were evaluated. Robust linear regression was used to assess associations between in-utero smoking exposure and CpG methylation, while linear regression evaluated associations with aging measures, protein EpiScores, and miscarriage risk. Persistent differential methylation at 110 CpG sites associated with in-utero smoking exposure was identified; these CpGs were enriched in fetal and embryonic regulatory elements and bivalent chromatin regions. Women exposed to maternal smoking in-utero also exhibited accelerated biological aging, including faster heart, lung, and immune system aging, as well as altered levels of 27 protein EpiScores. Among these measures, accelerated biological aging, six immune-related protein EpiScores, and one vascular signaling related protein EpiScore were also associated with miscarriage risk. These findings suggest that in-utero exposure to maternal smoking is associated with persistent epigenetic effects that extend into late adulthood. Alterations in immune and respiratory function may contribute to the association between in-utero smoking exposure and miscarriage risk, warranting further investigation.

Brooklyn Wright CC'27, Earth Science

Faculty Mentor(s) or Supervisor(s): Winnie Chu

Title: Evaluating the Effect of a Soft Basal Ice Unit On Glacier Flow

Abstract: Marine-terminating glaciers are the largest source of uncertainty in projections of modern sea-level rise. These projections are generated using ice-flow models, most of which assume the ice throughout the glacier deforms uniformly in response to an applied stress. In other words, the ice rheology is constant across the glacial domain. This assumption is at odds with borehole observations and geophysical data suggesting a variable rheology, with ice near the bed of the glacier being warmer, softer, and rheologically distinct from the ice above. To investigate the influence of soft, basal ice on glacier flow, we derive a multilayer ice-flow model using the icepack Python library. The model implements vertical layers, each with

independent rheologies that are coupled to describe depth-dependent, non-uniform deformation. We evaluated the model using a suite of depth-varying rheology experiments inspired by benchmarks from the Ice Sheet Model Intercomparison Project for Higher-Order Models (ISMIP-HOM). We present ISMIP-HOM sensitivity tests for both frictional and rheological properties, and vary the thickness of the soft basal ice layer. We find that a soft basal ice layer significantly increases the surface-to-bed velocity ratio relative to a uniform rheology model. However, once present, increasing basal ice thickness decreases surface velocities relative to basal velocities. Future work will expand the application to realistic modeling domains where a basal ice unit has been detected.

Claire Wu SEAS'29, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Santiago Correa

Title: Liposome Lyophilization Maintains the Viscoelasticity and Injectability of Liposome-Cross-Linked Supramolecular Hydrogels

Abstract: Supramolecular hydrogels are dynamic biomaterials used in medicine and the environment, from drug delivery and wound healing to water purification and energy storage, that are formed as hydrated networks from the reversible self-assembly of macromolecules. Configured from non-covalent interactions, supramolecular hydrogels exhibit properties including viscoelasticity, self-healing, and injectability. Supramolecular hydrogels can be formed from a polymer system cross-linked by liposomes, vesicles consisting of a phospholipid bilayer surrounding an aqueous core that create the structural cohesion of hydrogels. With the advancement of supramolecular hydrogel applications, it is increasingly important to optimize the shelf-life of these materials for long-term storage, distribution, and readiness for use across clinics and laboratories. The lyophilization of liposomes is investigated as a storage method for liposome-cross-linked supramolecular hydrogels. Liposomes created using the lipids, DMPC, DMPG, and cholesterol, were frozen with a cryoprotectant of 20% sucrose after extrusion at two rates: gradually at -80° C and flash-frozen in liquid nitrogen. After freezing for at least 24 hours, the liposomes were lyophilized, reconstituted, and incorporated with HPMC-C12 polymer to form a hydrogel. Liposome size and charge were measured after extrusion and lyophilization using dynamic light scattering to compare fresh, unfrozen liposomes to lyophilized and

reconstituted ones. Liposome-cross-linked supramolecular hydrogels made from fresh and lyophilized liposomes were then characterized via gel rheometry to determine differences in the viscoelasticity, self-healing, yield strain, and injectability of the hydrogels. Hydrogels made with lyophilized and reconstituted liposomes were generally softer than those consisting of fresh liposomes, while self-healing capabilities of the hydrogels were preserved after liposome lyophilization. Hydrogels formed using lyophilized and reconstituted liposomes maintained the viscoelasticity and injectability of hydrogels containing fresh liposomes. The stability of hydrogel characteristics before and after lyophilization promote liposome lyophilization as a promising method to improve the storage and distribution of liposome-cross-linked supramolecular hydrogel systems for biomedical translation.

Erin Xia GS'27, Computer Science

Faculty Mentor(s) or Supervisor(s): Kathleen McKeown

Title: Perspective-Taking: A Multi-Task Benchmark for Perspective-Aware Spatial Reasoning

Abstract: Vision-language models (VLMs) have made remarkable progress in understanding visual scenes, yet they still struggle with basic spatial reasoning from a human-centered perspective. In particular, perspective-aware reasoning requires models to interpret a scene from the viewpoint of an entity within the scene, rather than from the image's global perspective. To systematically study this capability, we develop a Blender-based synthetic data generation pipeline covering five key tasks: left/right positioning, near/far positioning, occlusion visibility, out-of-view visibility, and facing direction. Using this pipeline, we construct a benchmark of 3.8K image-question pairs for evaluating perspective-aware spatial reasoning, together with 10K synthetic scenes containing paired ground-truth perspective data for supervised training. Our datasets provide a controlled framework for analyzing and improving VLMs' ability to reason about spatial relationships from different perspectives.

Teresa Xiao CC'28, Biology

Faculty Mentor(s) or Supervisor(s): Stavroula Kousteni

Title: Serum Amyloid A1 Promotes Competitive Fitness and Clonal Expansion in Acute Myeloid Leukemia and Myelodysplastic Syndromes

Abstract: Acute myeloid leukemia (AML) and myelodysplastic syndromes (MDS) are blood disorders characterized by the rapid expansion of abnormal blood cells, which can outcompete healthy blood cells and disrupt normal function. These conditions have poor outcomes and limited therapeutic options. The surrounding bone marrow microenvironment plays a significant role in disease progression. Recent evidence has suggested that the Kynurenine-HTR1B-SAA1 pathway is a driver of AML by reshaping the bone marrow microenvironment. This study investigates the role of Serum Amyloid A1 (SAA1) using cell proliferation assays, colony-forming unit assays, competitive growth models, and cell population analysis. Using the OCI-AML3, SC, and MDS-L cell lines as leukemic models, the study shows that SAA1 promotes cell division and reduces markers of DNA damage. Additionally, blood-forming CD34+ cells were genetically edited to create an early human model of MDS and AML. SAA1 increased the competitive fitness and self-renewal capacity of CD34+ cells modeling early MDS and AML compared with control cells. Together, these results indicate that SAA1 promotes clonal expansion of abnormal blood cell populations. This suggests a potential link between inflammatory signaling and the enhanced growth and survival of abnormal blood cell populations, providing a foundation for further investigation into the mechanisms of SAA1 signaling. Further investigation of these mechanisms may lead to the development of therapeutics that target and inhibit SAA1 activity.

Qizheng Xie SEAS'27, Electrical Engineering

Faculty Mentor(s) or Supervisor(s): Xiang Meng

Title: Athermal Mach-Zehnder Interferometer Design on Aluminum Nitride

Abstract: As semiconductor foundries explore novel materials for next-generation computing, aluminum nitride (AlN), with its promising optical properties for nonlinear and quantum photonic devices, has emerged as a potential platform. However, photonic devices such as Mach-Zehnder Interferometers (MZIs) are sensitive to ambient temperature variations, which can undesirably shift the device's resonance and worsen performance. Thus, robust design methodologies are needed to ensure that AlN-based photonic devices maintain stable performance under practical operating thermal conditions. This project investigates the design of athermal MZIs on AlN. Instead of relying on external circuits for active thermal control, this approach passively and robustly engineers the MZI's temperature-dependent optical properties by modifying its geometry. Specifically, waveguide widths are asymmetrically designed to control how light propagates in the MZI arms.

This balances the phase accumulated in each arm due to temperature, making the resonance profile practically invariant over the operating temperature range. While this athermal design methodology has been demonstrated on silicon platforms, its application to AlN is novel. The design process combines analytical modeling with numerical simulations in Lumerical MODE and INTERCONNECT. Python-based optimization then selects the design that minimizes temperature-dependent frequency shifts. The optimized structures are then converted into fabrication-ready layouts with GDSFactory. The design is submitted for commercial fabrication for experimental validation and tolerance testing.

Eric Xin GS'28, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Hitesh Tewari

Title: Tamper-Resilient Authentication with Cross-modal Evidence

Abstract: TRACE is a system for verifying whether a digital image has been altered and for recording who first registered it. Rather than relying on a single method of image analysis, TRACE examines three different kinds of evidence at the same time. These methods look for changes in the visual structure, frequency patterns, and overall meaning of an image. The system then compares the results across these methods. Differences between them can reveal manipulation that might be missed when each method is used alone. To protect privacy, TRACE converts the image analysis results into compact digital fingerprints that allow similarity checks without revealing the original fingerprint data. It then records a secure summary of these fingerprints on a blockchain, creating a permanent record linked to the image. TRACE also uses a privacy preserving proof system to allow the original registrant to demonstrate ownership without revealing the private secret used during registration. This prevents someone who simply obtains a copy of the image from recreating the same ownership proof. The prototype was evaluated on a collection of images containing different types of edits. TRACE distinguished altered images from unchanged images more accurately than approaches based on only one type of evidence. Its combined method achieved an area under the curve score of 0.91, compared with 0.82 for the strongest single method. Ownership proofs were also generated within seconds.

Katie Xu CC'29, Biochemistry

Faculty Mentor(s) or Supervisor(s): Samuel Sternberg

Title: Elucidating G2L RTs as novel anti-phage systems in bacteria

Abstract: Bacteria have coevolved under the selective pressure of diverse bacteriophages (phages), driving the evolution of a vast array of robust anti-phage systems. Despite recent expansions of the known repertoire of anti-phage systems, their distinct mechanisms of action remain unknown. Prokaryotic reverse transcriptases (RTs) have recently emerged as novel effectors of anti-phage activity. Here, we studied diverse homologs of a largely understudied family of RTs, group II intron-like (G2L) RTs and screened homologs for phage defense activity. Several representative homologs conferred resistance to phage infection in plaque assays; however, mutating the G2L RT active site completely abolished defense activity, demonstrating that RT activity is required for immunity. Preliminary time-course and growth-curve experiments suggest that G2L RT activity restricts phage propagation without a major cost to host growth, though these results require further validation. RNA immunoprecipitation sequencing (RIP-seq) experiments identified a noncoding RNA (ncRNA) associated with the RT immediately upstream of its open reading frame. Interestingly, complementary DNA immunoprecipitation sequencing (cDIP-seq) experiments identified two distinct regions enriched for cDNA within the putative ncRNA region upstream of the RT. The relationship between G2L RT-mediated reverse transcription of a ncRNA into a cDNA product and its observed anti-phage activity are objects of further study.

Yu Duo Xu GS'27, Political Science

Faculty Mentor(s) or Supervisor(s): Jayme Schlesinger
Title: Derogation of Rights in Times of Crisis: A Comparative Analysis of Emergency Powers in Democracies

Abstract: How do democracies protect their citizens during moments of crisis without undermining the rights and institutions they seek to defend? This project examines how the United States, France, and the United Kingdom responded to major terrorist attacks in the early twenty-first century, focusing on the expansion and use of emergency powers. Although all three countries are established democracies committed to civil and political rights, their responses differed considerably in the scope, duration, and form of government action. The study examines whether these differences can be explained by variations in four factors: military capacity, judicial constraints, legislative constraints, and international legal oversight. Using data from the Varieties of Democracy (V-Dem) project and the Global Militarization Index, the quantitative analysis compares these factors across the three countries over five-year periods beginning with the relevant security crisis. The

measures are standardized to account for differences in scale and incorporated into several models that examine the factors individually, add them together, and explore how military capacity and institutional constraints operate in combination. The quantitative findings are then combined with qualitative analysis of each country's emergency policies, legal decisions, and existing scholarship. This approach allows the study to assess whether patterns identified by the quantitative models correspond with how governments actually exercised and constrained emergency powers. The findings suggest that the three countries occupy distinct positions across military capacity and institutional constraints, and that these patterns change depending on how the factors are combined. In particular, the interaction models reveal relationships that are less apparent when military capacity or institutional constraints are considered independently. The qualitative analysis further evaluates how these patterns correspond with the actual development and use of emergency powers in each case. Taken together, the quantitative and qualitative findings offer a comparative explanation for why democracies facing comparable security threats can make different choices about the balance between national security and individual rights.

Ariana Yahia SEAS'27, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Ann Iturra-Mena
Title: Audio-Only Adaptation of the Exposure Process Coding System in Pediatric Exposure Therapy

Abstract: Exposure-based cognitive-behavioral therapy (CBT) is a well-established treatment for pediatric anxiety disorders and obsessive-compulsive disorder (OCD). However, clinicians have limited tools to evaluate exposure quality during sessions. Progress is commonly monitored with symptom measures collected across treatment, which may not capture whether the exposures are delivered in ways that support learning. This limits timely feedback for training, supervision, and treatment quality improvement. The Exposure Process Coding System (EPCS; Benito et al. 2018) addresses this gap with microanalytic observer ratings of exposure timing, patient fear, approach and avoidance, and therapist behaviors that support or interfere with exposure. EPCS was developed for video-based coding, which is costly, raises privacy concerns, and is often unavailable in routine clinical or training settings. This preliminary study examined the feasibility and inter-rater reliability of an audio-only EPCS adaptation. Audio recordings of exposure-based CBT sessions with 24 youth ages 7–18 were double-coded by three independent trained raters using ELAN. Coders marked exposure start and end times and coded audio-identifiable exposure variables, including

Subjective Units of Distress (SUDS) ratings when available, therapist and patient statements, and fear-decrease events. Reliability was evaluated using intraclass correlations for continuous variables and Cohen's kappa and percent agreement for categorical variables. Inter-rater reliability was excellent for exposure timing and SUDS ratings. Agreement was more variable for habituation and several therapist and client statement categories, suggesting a need for further coder calibration. A reliable, audio-only EPCS adaptation could enable exposure-process measurement where video is unavailable, potentially improving exposure quality and treatment outcomes.

Roger Yang CC'28, Mathematics, Physics

Faculty Mentor(s) or Supervisor(s): Cory Dean

Title: Fabrication of twisted bilayer graphene using laminated hBN pulling

Abstract: The study of twisted bilayer graphene (tBG) has generated great interest in condensed matter physics over recent years. As with any moire material, rotational interference effects change the band gap structure of tBG, leading to a host of novel electronic qualities. Most interesting of all was the discovery that 1 degree ("magic angle") twisted bilayer graphene may superconduct at low (~2 K) temperatures. The traditional way of synthesizing tBG is a method called "tear-and-stack," in which a single atom-layer thick graphene sheet is punctured using a stamp and then re-copied at a slight twist angle. This technique, though simple, can produce significant disorder during the copying process as the edges of the stamp must be torn from the surrounding graphene. In this study, we experiment with a new approach to synthesizing tBG's that involves the fabrication of an intermediate, 3-layer device consisting of two twisted sheets of graphene and a sheet of hexagonal boron nitride (hBN) sandwiched in between. Using traditional mechanical pulling, the hBN layer is pulled out causing the two layers of graphene to laminate on top of each other, leading to the formation of a large tBG region with more uniformity and stability than those made from the "tear-and-stack" method. With this approach, we have been able to fabricate tBG devices down to 2 degrees twist angle with robust moire, although we have not yet been able to target the 1 degree magic angle.

Daniel Ye SEAS'28, Electrical Engineering

Faculty Mentor(s) or Supervisor(s): Ioannis Kymissis

Title: Capacitive Proximity Sensing for Pre-Contact Awareness in Dexterous Robotic Hand

Abstract: Autonomous robotic hands often rely on cameras for long-range vision and on tactile sensors for physical contact. However, when a hand gets incredibly close to an object without touching the object, it blocks the camera view and creates a blind spot in robotic sensory data. To bridge the gap between vision and touch, capacitive proximity sensors provide the sensory data needed for safe and reactive object manipulation. This work presents the design, fabrication, and control of a parallel gripper integrated with capacitive proximity sensors, establishing a practical framework toward full pre-contact awareness in robot hands. The system uses an embedded Cypress microcontroller with built-in capacitive sensors to detect capacitive changes as a conductive object approaches. The detection thresholds were fine-tuned across materials with varying dielectric properties, encompassing both metallic conductors and ionic conductors like human hands. Using a custom Python control script, the system translates these proximity measurements in real time to adjust the gripper's motors. This enables the fingers to close rapidly from a distance and automatically slow down as they near the target, preventing harsh collisions and ensuring a soft grasp. Transitioning beyond breadboard prototypes, a PCB was designed to make the electronics compact and reliable. Ultimately, this project hopes to offer a scalable foundation for both safer human-robot collaboration and intelligent robotic manipulation.

Erin Yoo CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Ishmail Abdus-Saboor

Title: Establishing the Effects of Chronic Corticosterone Treatment in Dorsal Root Ganglia (DRG) Cell Culture in Adult C57 Mice

Abstract: Chronic stress is known to heighten pain sensitivity, yet the cellular mechanisms that link stress to altered nociception remain poorly defined. This project investigated whether glucocorticoid exposure elevates activity-dependent gene expression in dorsal root ganglion (DRG) neurons, thereby identifying the transcriptional activity underlying stress-induced hyperexcitability. Primary DRG neurons were treated with corticosterone in vitro for 6 days. At the end of the treatment, the neurons were stimulated with KCl for 30 minutes before final collection, depolarizing and thus activating them. The expression of a potential activity-dependent gene, Gene X*, was quantified by quantitative PCR (qPCR) for gene expression and by immunohistochemistry (IHC) for protein expression. The results revealed that KCL stimulation upregulates Gene X* expression and corticosterone exposure downregulates Nr3c1 expression in vitro, which responds to corticosterone treatment as the glucocorticoid receptor. Further studies are needed to determine whether this biological effect applies in vivo.

Tyler Young CC'27, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Itamar Kahn

Title: Relating Behavioral Repertoire to Resting-State fMRI Network Organization Longitudinally in Mice

Abstract: System segregation is a measure of modular organization of large-scale brain networks, and it declines with age in both humans and mice (Winter-Nelson et al., PNAS, 2026). Reduced system segregation has been associated with poorer cognitive performance across adulthood (Chan et al., PNAS, 2014), and declines in system segregation in individuals is predictive of subsequent cognitive and functional impairment as we get older (Chan et al., Nature Aging, 2021). However, how within-individual changes in functional network organization relate to behavioral trajectories throughout aging remains poorly understood and difficult to investigate in humans. Here, we established a longitudinal study that combined whole-brain functional imaging (resting-state fMRI) with multidimensional behavioral phenotyping across the mouse lifespan. Twenty C57bl/6J mice (10 male, 10 female) underwent fMRI and behavioral testing at 3 and 9 months of age, with 15 of the 20 mice (8 male, 7 female) undergoing testing at 15 months. We used fMRI to assess system segregation and within- and between-network functional connectivity. Behavioral phenotyping included traditional open-field exploration and novel object recognition tests, with machine learning-based approaches providing higher-resolution insight into the underlying behavioral repertoire and characterizing age-related behavioral changes. By integrating fine-grained behavioral phenotyping with longitudinal fMRI, we reveal individual brain-behavior trajectories throughout aging and how changes in large-scale functional network organization relate to preserved or changing behavioral function with age.

Sabrina Yu CC'28, Computer Science and Mathematics

Faculty Mentor(s) or Supervisor(s): Jonathan Simone

Title: Alternating Braid Closures, Dehn Surgery Involutions, and QB^4 s

Abstract: The study of knots and links is an important part of topology, providing ways to construct and study higher dimensional manifolds. Our research is motivated by the 45th problem in Kirby's Problems in Low Dimensional Manifold Theory, which asks which rational homology 3-spheres bound rational homology 4-balls. We investigate this question for a family of rational homology 3-spheres arising as branched double covers of

closed alternating braids. These manifolds are indexed by the number of strands and repetitions in the braid. We use two complementary approaches. First, we study algebraic obstructions arising from the intersection forms of associated four dimensional manifolds. Donaldson's theorem implies that if one of these rational homology 3-spheres bounds a rational homology 4-ball, then its intersection form must admit an associated ubiquitous lattice embedding. We determine when a necessary determinant condition is satisfied and construct the corresponding lattice embeddings for several families. Second, we use orientation reversing involutions to construct rational homology 4-balls directly. Combining these approaches, we prove that when the number of strands is odd and not seven, the associated rational homology 3-sphere bounds a rational homology 4-ball if and only if the number of repetitions is odd. The seven strand case is exceptional: we construct a rational homology 4-ball when there are two repetitions, while the general even repetition case remains open.

Theresa Yu CC'28, Mathematics, Philosophy

Faculty Mentor(s) or Supervisor(s): Kiyohito Iigaya

Title: Formation of sparse graph representations

Abstract: Humans move about the world experiencing complex events happening all the time and infer relationships between events. Some events are associated with others to varying degrees; for instance, cutting onions is sometimes associated with your eyes tearing up, and touching burning hot items is sometimes associated with getting a burn on your skin. The Sparse Cognitive Graph (SCG) framework proposes that these statistical associations are used to construct simplified graphs that guide human behavior. In this model, statistical relationships are accumulated and transformed into binary associations once a threshold is crossed. This project explores some behavioral predictions of this framework: 1) participants present abrupt learning due to the presence of non-linearities in the construction of the sparse graph (threshold), 2) participants display behavior aligned with a binary representation of the associations, i.e., all-or-nothing association instead of a probabilistic representation. Specifically, I designed and implemented a behavioral task consisting of streams of icons being displayed, varying the condition of transitional frequency between icons. The participants are probed on their perception of the relationship between the icons using 2 methods: dynamic button pressing (which captures the online recognition of the associations), as well as question probes (that identify specific association between items). These methods assess if and when the participant has formed a predictive relationship, allowing us to determine

when the statistical associations between icons enter the sparse graph for participants. Pilot data suggests an abrupt transition in behavior during learning and participants choices may reflect binary representations of the items associations conforming the graphs.

Sarah Yuh CC'29, Astrophysics, Mathematics

Faculty Mentor(s) or Supervisor(s): Maximiliano Isi

Title: Analyzing the Ringdown of Precessing Binary Black Holes

Abstract: Gravitational waves were first detected by the Laser Interferometer Gravitational-wave Observatory (LIGO) in 2015. Gravitational waves from black hole coalescences encode valuable information about the black holes themselves and, more generally, the nature of gravity. In the final stage of coalescence, the remnant black hole rings down by emitting gravitational waves that can be described as a sum of quasi-normal modes (QNMs). Notably, the signals emitted in ringdown depend on the states of the progenitors at the moment of collision. This research examines how precessing binary black hole systems can be distinguished from non-precessing systems in ringdown analyses. Previous works have shown that the two scenarios can excite different sets of QNMs in ringdown. Consequently, this work aims to study the conditions under which the existence of different modes can be determined. Ringdown signals consistent with precessing and non-precessing systems were simulated. Next, the signal was layered with noise computed from a LIGO power spectral density. In both precessing and non-precessing cases, the data were fit to various models, and the recovered parameters were compared to the truth. This was achieved by varying model assumptions regarding the modes present, as well as the relationship between the polarization amplitudes and phases of the signal. Ultimately, this work characterizes the manifestations of different systems in ringdown data and identifies possible systematic errors that can bias its analysis.

Julia Zang CC'28, Computational Biology

Faculty Mentor(s) or Supervisor(s): David Knowles

Title: Building Genetic Prediction Models of Alternative Splicing for Alzheimer's Disease TWAS

Abstract: Alternative splicing is a biological process that allows a single gene to produce different RNA products. Genetic differences between individuals can influence how RNA is spliced, and some of these genetically driven changes may contribute to complex diseases such as Alzheimer's disease.

This study developed a framework to predict differences in RNA splicing using genetic information. These predictions can later be used in a transcriptome-wide association study, or TWAS, to investigate whether genetically regulated differences in RNA splicing are associated with Alzheimer's disease. The researchers used BigBrain, a large collection of datasets containing both genetic and RNA sequencing data. For each splicing event, prediction models learned how nearby genetic differences relate to how frequently that event occurs. Different methods of processing the RNA data and building the prediction models were applied. The models were then evaluated and compared in a held-out set of brain samples to test how well they could predict RNA splicing from genetic data. Among the three prediction models evaluated, Bayesian ridge regression showed the strongest overall performance and was selected for the final framework. The resulting models will next be applied to genetic data from the Alzheimer's Disease Sequencing Project, a study including individuals with and without Alzheimer's disease. This will enable the researchers to test whether genetically predicted differences in RNA splicing are associated with Alzheimer's disease, without requiring brain RNA measurements from every individual.

Sarah Zhang CC'29, Biophysics

Faculty Mentor(s) or Supervisor(s): Mary Teena Joy

Title: A Pipeline for Volumetric Mapping of Axonal Sprouting Post-Stroke

Abstract: Stroke is a leading cause of disability, yet the brain enters a critical window of rare and heightened plasticity soon afterward, during which axonal sprouting rewires brain structure. Specifically, the axonal sprouting patterns of intratelencephalic (IT) and pyramidal tract (PT) neurons after stroke remains poorly understood, obscuring the crucial link between how microscale sprouting produces macroscale changes in cortical circuitry. Such investigation requires imaging that preserves both axonal resolution and whole-brain structure, as well as an optimized pipeline to process the resulting data. We combined the recently published VIVIT tissue-clearing protocol with mesoSPIM light-sheet microscopy to acquire whole-brain volumes of control and photothrombotic-stroke mouse brains. To segment axons from these volumes, we adapted TrailMap, a 3D convolutional neural network, and evaluated both transfer learning on our annotated data and DeepTraCE's pre-trained models. Transfer learning was constrained by image quality and labeling limitations, whereas DeepTraCE's Model 3 provided segmentations effective for further skeletonization and spatial analysis. A preliminary comparison of one control and one stroke brain localized regional

differences in axonal projections, revealing cortical axonal loss and denser striatal bundles after stroke. Completing atlas registration and expanding sample size will enable statistically robust, region-resolved mapping of post-stroke axonal reorganization.

Ray Zhang CC'27, Biology

Faculty Mentor(s) or Supervisor(s): Martin Chalfie

Title: Identifying Genes Involved in *C. elegans* Touch Sensitivity

Abstract: *C. elegans* is a small nematode with a fully mapped nervous system, making it a powerful model for studying how nerve cells sense touch. Previous screening of the Million Mutation Project library, a fully sequenced collection of 2,006 mutagenized strains, identified several touch insensitive strains with no connection to established mechanosensory genes. This project focused on three of these strains, VC40527, VC40782, and VC40359, to identify their causative mutations. Sequencing of VC40527 revealed a nonsense mutation in *unc-2*, a gene encoding a voltage-gated calcium channel subunit essential for synaptic transmission and neuronal excitability. A complementation test against a reference *unc-2* mutant produced touch-insensitive progeny, supporting *unc-2* as the affected gene. VC40782 displayed a weaker touch-insensitive phenotype, and complementation tests implicated *mec-1*, a chromosome V gene, as the likely causative locus; whole-genome sequencing of homozygous mutant progeny is underway to confirm *mec-1* as the affected gene. VC40359 showed strong touch insensitivity, and whole-genome sequencing of pooled homozygous mutants identified *kin-9*, a gene predicted to function in transmembrane receptor tyrosine kinase signaling, as a candidate mutation. Because *kin-9* is not expressed in the gentle-touch receptor neurons themselves, it may act through a downstream neuronal signaling pathway. Future work will directly test *kin-9* through complementation analysis and complete analysis of the VC40782 sequencing data. These results extend the known genetic basis of the *C. elegans* touch circuit and may reveal mechanosensory mechanisms conserved across the nervous systems of other animals.

David Zhang CC'29, Neuroscience & Behavior

Faculty Mentor(s) or Supervisor(s): Charalampos Brakatselos

Title: Striatal Dopamine Dynamics and Spontaneous Behavior in a Mouse Model of 22q11.2 Deletion Syndrome

Abstract: Schizophrenia is a chronic mental condition that affects almost 1% of the global population. Dysregulation of dopamine signaling, particularly in the striatal region, plays a major role in schizophrenia. A particularly important genetic risk factor for schizophrenia is the 22q11.2 deletion syndrome. Its strong association with schizophrenia makes 22q11.2 (Df16) mice models a useful genetic model for investigating the biological mechanisms underlying the disorder. Although dopamine-related abnormalities have been identified in Df16 mice models, in vivo dynamics during freely expressed behavior have not been well characterized. Df16 mutant and wild-type mice were studied using fiber photometry to examine changes in dopamine signaling in the dorsomedial striatum (DMS) during spontaneous behavior. Mice were surgically manipulated to enable the recording of a dopamine sensor (dLight1.3b). A bottom-view camera recorded the animals' movements synchronizing behavioral and dopamine data. Behavioral analysis using pose estimation and unsupervised behavioral clustering identified recurring patterns of movement, or behavioral syllables. Many syllables showed distinct differences in terms of velocity and frequency between wild-type and mutant mice. Alignment of behavioral syllables with fiber photometry revealed group differences in the onset and amplitude of dopamine responses associated with specific behaviors. Pharmacological manipulation of dopamine signaling and behavior utilizing d-amphetamine, DETQ and Metyrosine further altered behavior and signal transience. Together, these findings demonstrate how the relationship between behavior and dopamine signaling in Df16 mice may provide insights into schizophrenia-related phenotypes

Ruimian Zheng CC'27, Mathematics, Physics

Faculty Mentor(s) or Supervisor(s): Yuri Levin

Title: Searching for Individual Cosmic String Loops in the Milky Way with Pulsar Timing Arrays

Abstract: Pulsars are fast-spinning neutron stars with beamed radio emissions that we can measure regular pulses and use as good clocks. These pulses can vary due to background disturbances such as gravitational waves. Cosmic strings are theoretically well-motivated relics of the early universe and may survive today as oscillating loops that emit gravitational waves. Most studies searching for cosmic strings using pulsar timing arrays (PTAs) focus on the stochastic gravitational wave background generated by an ensemble of loops. In this project, we explore the possibility of searching for an individual cosmic string loop captured by the Milky Way, whose periodic oscillation produces a deterministic signal. We constructed an improved signal model

based on evaporated loops from a simulation result from another group. Breaking the timing residues into Fourier components, we developed a framework to efficiently search over loop period, sky position, signal amplitude, and noise parameters to fit for potential signals from an individual cosmic string that is captured in our galaxy. We then tested signal detectability on mocked data sets. This work will provide a new way to use PTA data to probe cosmic strings, complementing existing stochastic background searches and broadening the range of new physics signals accessible to pulsar timing arrays.

Yanchi Zheng CC'27, Linguistics

Faculty Mentor(s) or Supervisor(s): Stathis Gourgouris

Title: Einai Ola Kinezika Yia Mena: Deconstructing Rituals of Misunderstanding in Athens Chinatown

Abstract: This study is a linguistic and anthropological survey on the Chinese immigrant population in Athens, Greece that examines the level of language contact between Mandarin and Modern Greek. According to estimates by various online sources, there are around 20,000-35,000 Chinese immigrants living in Greece, with most residing in Athens. After Greece's entry into the Eurozone in 2001, the Athens Olympics in 2004, and the introduction of the new Golden Visa in 2013, sudden influxes of Chinese merchants, capital, and commodities entered Greece, with the population peaking around 2010. While there has been a significant Chinese population since the late 1980s, little to no anthropological or demographic research conducted. Through a combination of on-site observation and interviews, it was found that there has been little to no language contact between Mandarin and Greek, with most adult immigrants rating their Greek language skills and interest in learning the language as very low or non-existent. Children bilingual in Mandarin and Greek seem to observe a rigid system of code-switching in which the two languages are used in very separate contexts. Furthermore, the results suggest the existence of complex hierarchical relationships within the Chinese community that are built upon dialectal differences and socioeconomic status.

Alex Zhong SEAS'29, Biomedical Engineering

Faculty Mentor(s) or Supervisor(s): Elisa Konofagou

Title: Predicting AAV Gene Expression in the Brain using MRI and Ultrasound Cavitation Imaging

Abstract: Neurodegenerative diseases like Parkinson's Disease affect millions of individuals each year there are currently no effective treatments. Gene therapies such as those using adeno-associated viruses (AAV) are a promising treatment route, however, their efficacy in the brain is largely limited by the blood-brain barrier (BBB). Our lab has developed a novel method utilizing focused ultrasound with microbubbles to temporarily open the BBB, allowing AAV to cross. Currently, evaluating the efficacy of gene delivery requires invasive procedures which are not feasible in human clinical trials. In this study, we employ imaging methods during and after the ultrasound treatment to predict the levels of gene expression in the brain. Power cavitation imaging (PCI), which maps the microbubble activity in the brain, and contrast-enhanced magnetic resonance imaging (MRI), which can help assess the volume of the BBB opening (BBBO), were combined in a machine learning model (ElasticNet) to predict the resulting gene expression in the brain. Our results show a significant correlation between AAV expression and BBBO Volume ($R^2=0.399$, $p<0.001$) and a weaker correlation between AAV expression and PCI ($R^2=0.099$, $p=0.039$). From these findings, we then applied an ElasticNet model ($\alpha=0.01$, $l1_ratio=0.8$) to PCI, MRI, and key experimental variables including AAV dose and serotype, obtaining an R^2 of 0.56. This demonstrates the initial feasibility of non-invasively assessing the amount of gene expression in the brain and can pave the way towards clinical translation of ultrasound-mediated gene therapies for neurodegenerative diseases.

Kyle Zhou SEAS'28, Computer Science

Faculty Mentor(s) or Supervisor(s): Saeed Tavazoie

Title: Reconstruction of Bacterial Proteomes from Protein Language Model Embeddings

Abstract: Bacterial functions are carried out by coordinated protein systems, but proteins are commonly interpreted one at a time. This leaves an important biological question: does the rest of a proteome contain enough organism-level context to identify functions that are missing from a partial genome? To test this question, bacterial genomes were represented as variable-size, unordered sets of 480-dimensional ESM-2 protein embeddings and modeled with a hierarchical set variational autoencoder (SetVAE). The model was trained on 13,840 bacterial genomes and evaluated on held-out whole-genome reconstruction and targeted protein-set completion in *Escherichia coli* K-12 MG1655. In a 100-genome benchmark with 100,000 background proteins, exact source-protein recovery was enriched over random expectation at top-1 (3.12x) and top-10 (1.60x). One-to-one bipartite matching assigned

71.09% of source proteins to unique reconstructed embeddings at cosine similarity at least 0.95, whereas only 0.66% exceeded 0.99, indicating neighborhood-level rather than near-exact reconstruction. After targeted pathway removal, top-25 recovery exceeded same-size model-run random controls for tryptophan biosynthesis (2.15x) and histidine biosynthesis (1.75). Recovery was generally stronger for conserved metabolic and informational systems than for heterogeneous accessory functions. Thus, whole-proteome composition contains recoverable biological signal that can prioritize missing conserved functions.

Sophie Zhu SEAS'28, Chemical Engineering

Faculty Mentor(s) or Supervisor(s): Jingguang Chen

Title: Technoeconomic Analysis and Energy Modeling for CO₂ Valorization Schemes

Abstract: Anthropogenic carbon dioxide (CO₂) emissions continue to accelerate climate change. Recent efforts to convert CO₂ into value-added chemicals focus on single-use plastics and fuels with short-term carbon storage potential. This study evaluates the economics and emissions of two alternative products derived from CO₂ electrolysis. In the first, CO₂ and water are converted to synthesis gas by electrolysis, which is then converted to carbon nanotubes in a thermochemical flow reactor. In the second, CO₂ is electrochemically reduced directly to formate, with the analysis exploring the effect of inlet CO₂ concentration. For each process, a physics-based model was developed in Python from fundamental thermodynamic relations, transport phenomena, and mass balances, and its results used as the basis for a techno-economic analysis. Net emissions for carbon nanotube production can become negative as the share of renewable energy grows and the grid CO₂ emissions factor falls. Formate produced by CO₂ electrolysis shows potential to be cheaper and less carbon-intensive than fossil-fuel-derived routes, reducing the carbon emissions from 2.2 to 0.5 kg CO₂/kg formate. Future work will use the models to conduct a cradle-to-gate life cycle assessment to determine how the energy cost and carbon footprint of both technologies change at a commercial scale.

Zoey Zhu CC'29, Computer Science and Mathematics

Faculty Mentor(s) or Supervisor(s): Frits Paerels

Title: Searching for X-ray Counterparts to Gravitational Wave Events in eRASS1

Abstract: It is difficult to pinpoint the source of gravitational wave events solely from gravitational wave data because localization relies on triangulating the small differences in signal arrival time, amplitude, and phase across the detector network (LIGO, Virgo, KAGRA), which typically constrains the source to a region tens to hundreds of square degrees in size. A strategy to more precisely locate a binary black hole event is to look for an x-ray halo produced by dust scattering of x-ray emissions from the event. Dust grains in the interstellar medium scatter X-rays at small angles, so an X-ray transient occurring behind a sufficiently large column of dust can produce a halo of scattered photons centered on its true position. If a binary black hole merger is accompanied by an X-ray-bright event, searching archival X-ray survey data for such a halo offers a way to pin down the source location beyond what gravitational-wave data alone can provide. This project discusses where x-ray halos would be most easily detectable, which binary black hole gravitational wave events may be most likely to produce a detectable x-ray halo, and conducts a preliminary search for x-ray halos on data from eRASS1. Although a validated halo did not emerge, this paper invites further study as more data is released.