tumor irradiation. Based on select proteins' surface expression, CITE-Seq generated eight distinct clusters, including three myeloid cell clusters — monocytes, macrophages, and granulocytes. We used VIPER (virtual inference of protein activity by enriched regulon analysis), a machine learning-based algorithm that infers protein activities by taking regulatory gene expression networks and calculating the weighted expression on each protein's targets, to create functional subclusters of the eight immune-cell populations. For subclusters enriched by RT, we used OncoTreat to identify active, druggable proteins. Results: As expected, lymphocytes were depleted with radiation, especially ten days post-irradiation, validating our computational approach. Three subclusters became enriched following tumor irradiation: TAM2, PMN1, and PMN4. Antibody marker analysis have enabled us to define the immunophenotype of the three cell clusters for isolation and functional analyses. Conclusion: Suppressive myeloid subpopulations induced by radiation were identified among the immune cells. We aim to experimentally test whether drugging the aforementioned subpopulations of macrophages and granulocytes improves the overall efficacy of RT by augmenting an anti-tumor immune response.

Ope Lekan CC'23, Biology and Psychology

Faculty Mentor(s) or Supervisor(s): Professor Harris Wang
Title: Restructuring the Mammalian Microbiome Using Fecal Microbiota Transplant (FMT)

Abstract:
The human gut microbiome contains hundreds to thousands of species that interact with each other to create an equilibrium that plays a vital role in human health. Many research groups seek to better understand the nature of this equilibrium and ways in which it could be manipulated to improve human health. Fecal Microbiota Transplantation (FMT) is a therapeutic strategy in which healthy gut microbiomes are transferred to individuals whose microbiomes have entered a state of disequilibrium. In this research we investigate the factors related to Fecal Microbiota Transplant using mice model to better understand ways in which we can alter the gut microbiome. We perform Fecal Microbiota Transplants between mice containing different gut microbiomes to identify factors determining the success of these therapies.. We found a microbiome enriched with Porphyromonadaceae species could robustly engraft in recipient mice. Growth assays revealed that this microbiome carried a vast repertoire of polysaccharide degradation capabilities and this characteristic was conferred to recipient microbiomes via FMT. This study investigates the success rate of fecal microbiota transplant between different mouse microbiomes. This study not only explores factors determining FMT transplant success but also presents questions for further research like the advantage of specialization vs generalization in regards to polysaccharide breakdown across gut microbiome communities.

Zachary Lihn CC'25, Mathematics

Faculty Mentor(s) or Supervisor(s): Professor Lev Borisov
Title: Realizing a Fake Projective Plane as a Degree 25 Surface in Projective 5-Space

Abstract: The Enriques–Kodaira classification splits smooth complex surfaces into several classes that may be studied. While other classes are understood, the class consisting of surfaces of general type still lacks a detailed classification. Fake projective planes (FPPs) are smooth complex surfaces of general type with Betti numbers equal to that of the usual fake projective plane. By the classification of Cartwright-Steger there are exactly 50 conjugate pairs of FPPs, given as quotients of the 2-dimensional complex ball by an explicit group. Explicit constructions of these surfaces as the vanishing locus of polynomial equations (an algebraic variety) have been elusive until recently, when some FPPs were embedded in 9-dimensional projective space via their bicanonical embedding. A natural question is if they may be embedded in lower dimensions. This research studies Keum's fake projective plane and uses the equations of Borisov to construct an embedding of a fake projective plane in 5-dimensional projective space as a system of 56 sextic equations in 6 variables. It also simplifies the 84 cubic equations defining the fake projective plane in 9-dimensional projective space.

Eleanor Lin CC'24, Computer Science and Linguistics

Faculty Mentor(s) or Supervisor(s): Professor Vicente Ordóñez Román
*Title:*Text-Based Prediction of Visual Complexity

Abstract: Visual complexity is of interest across cognitive science, computer science, advertising, web design, and other areas, due to the increased difficulty both computers and humans encounter in processing complex visuals. Intuitively, one might expect biases in how complex visuals are described: e.g., using adjectives like "busy" or "cluttered." This work explores the relationship between linguistic and visual complexity by asking if it is possible to predict an image's visual complexity based on its textual description alone. This text-based approach contrasts with the majority of past work, which focuses on the images themselves, rather than their descriptions. A new automated complexity metric is introduced, number of distinct regions per image, which serves as an effective predictor of human judgments of visual complexity. Using this metric to identify complex and non-complex images from the Microsoft COCO Dataset, the authors fine-tune BERT base (a machine learning model pretrained to understand English-language text) to predict visual complexity from image captions. They find that the model is able to predict visual complexity with a high degree of accuracy, and appears to rely on vocabulary and sentence structure clues in making its predictions. This study suggests a relationship between visual complexity of images and linguistic complexity of image descriptions, which may be leveraged by machine learning models to better identify complex images. Additionally, tasks that involve both vision and language, such as automatic caption generation, may benefit from continued investigation of the relationship between visual and linguistic complexity.

Jonathan Liu CC’25, Computer Science

Faculty Mentor(s) or Supervisor(s): Professor Henning Schulzrinne
Title: Researching the benefits of a Django Web Framework over no-code alternatives for Web Applications.

Abstract: The principle goal of my research with Dr. Henning Schulzrinne was to explore optimal web application architecture for an application requiring advanced form checking and internationalization functionalities. To carry out this project, our research group developed a Django web application capable of handling the pre-approval applications for three Habitat for Humanity affiliates, with target users in low-income demographics from around the country. There were three phases to the research progression: 1) building a full-stack app with a Django frontend and API connected to a PostgreSQL database, 2) implementing sanity checking, error messages, and django form-cleaning to prevent database corruption or incorrect application processing, and 3) gauging optimal implementation of multilingual functionality using Django’s gettext and translation models. In seeking to answer the question of whether to use PostgreSQL or MySQL with the Django application, we found PostgreSQL’s more intensive constraints and migrations setup to better serve our relational schema, and ultimately opted for PostgreSQL. We also discovered Django’s GNU gettext functionality to be a crucial component to the success of our project with a wider target audience, an advantage over many alternatives offered by “no code” movement alternatives such as Webflow. These research findings collectively impacted the non-profit organization Habitat for Humanity by providing them with functional mortgage pre-approval software, catered to the diverse demographics of its applicants. They also provide support for the use of frameworks like Django for creating websites requiring internationalization, localization, and an accommodative UI and form experience over no code/low code development alternatives.

Luke Llaurado CC’22, Biochemistry

Faculty Mentor(s) or Supervisor(s): Professor Jellert Gaublomme
Title: CRISPR-Facilitated Genetic Screening of SARS-CoV-2 Host and Viral Factors

Abstract: This summer, Luke performed host-genome wide perturbation screenings for genes necessary for SARS-COV-2 viral entry and replication to contribute to existing knowledge of the COVID-19 virus life cycle and reveal potential therapeutic drug targets for COVID-19 patients. Employing a spatial transcriptomics approach, he utilized CRISPR knockout screenings in A549 human lung carcinoma. Preliminary experiments have revealed host cell mRNA production is halted in infected cells at 48 hours post infection, making these molecules elusive to detection. Immunofluorescent staining sheds light on this phenomenon, indicating this production halt begins during early stages of viral replication as noted by formation of double stranded RNA viral replication complexes, then continues through later stages of the viral life cycle such as exocytosis of mature, replicated virus.

Andrew Lu CC’24, Computer Science

Faculty Mentor(s) or Supervisor(s): Professor Shih-Fu Change
Title: In Defense of Structural Symbolic Representation for Video Event-Relation Prediction

Abstract: Understanding the relationship between events in videos requires a model to have both factual knowledge and reasoning ability. Compared to structural symbolic representation (SSR) based methods that only use event types and argument roles of the events as inputs, existing approaches with continuous video features achieve much better performance. However, it remains an open question why even oracle event type and argument roles cannot help predict the event relation. In this project, they answer this question by bootstrapping state-of-the-art video event-relation prediction