Research Statement

As an Assistant Professor of Statistics, my research focuses on advancing statistical genetics and genomics to better understand the biological mechanisms underlying complex human diseases. My work spans Mendelian randomization, genome-, transcriptome- and proteome-wide association studies (GWAS/TWAS/PWAS), genetic colocalization, fine-mapping, and polygenic risk prediction. These methodologies form a comprehensive framework for identifying and prioritizing causal genes, molecular pathways, and modifiable risk factors that may play an important role in disease risk and progression.

Much of my recent work has focused on developing more robust methods to draw causal conclusions from genetic and omics data, especially in the presence of biases like genetic pleiotropy, which often hinder reliable interpretation of genetic associations. My recent research applies these tools to large-scale genomic and multi-omics datasets to dissect the etiology of age-associated disorders, including Alzheimer's disease and cardiovascular conditions—two of the most pressing public health challenges linked to aging. A core aspect of my research is integrating different types of molecular data to build a more complete picture of disease biology. For example, combining genetic, transcriptomic, and proteomic data can help reveal how genetic variants affect downstream processes in specific tissues or cell types relevant to aging. These insights can ultimately point to new therapeutic targets or biomarkers for early detection.

In alignment with the ISL's mission to understand and counter age-associated declines, I aim to continue building statistically grounded, biologically informed tools that translate complex data into actionable insights for aging research. My long-term goal is to collaborate across disciplines to enable early detection, risk stratification, and targeted prevention strategies that promote cognitive and functional aging.