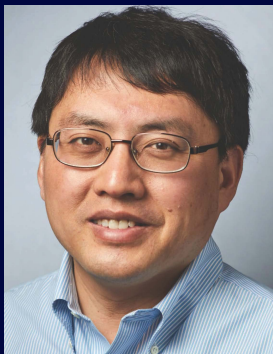


Department of Applied and Computational Mathematics and Statistics Colloquium



Hongyu Zhao

Yale School of Public Health

Genetic Prediction of Disease Risk Across Populations

Polygenic risk score (PRS) has demonstrated its great utility in biomedical research by identifying high-risk individuals for different diseases based on their genotypes, facilitating disease monitoring and prevention. However, the broader application of PRS to the general population is hindered by the limited transferability of PRS developed in Europeans to non-European populations. Many statistical methods have been developed to improve PRS prediction accuracy in non-European populations through integrating results from European populations. In this presentation, I will discuss the statistical models underlying these methods, with a focus on those that use genome-wide association study summary statistics rather than individual-level data from different populations. The performance of these methods will be demonstrated through their applications to various traits in non-European and admixed populations.

Monday, November 17, 2025

3:30 – 4:30 PM

117 Hayes-Healy Center

Colloquium Tea – 3:00 PM in 117 Hayes-Healy