



## Statistics and Actuarial Science Seminar

**Title:** Pooled vs. meta-analytic models in multi-ancestry genome-wide association studies: Power, population structure, and prac

**Speaker:** Julie-Alexia Dias (Harvard University)

**Date:** Thu 15th January 2026 at 3:00PM

**Location:** E0.32 (beside Pi restaurant)

**Abstract:** Multi-ancestry biobanks now make it possible to conduct genome-wide association studies (GWAS) across diverse populations, but there remains no consensus on the most statistically powerful and robust analytical strategy. Two dominant approaches are widely used: pooled analysis, which jointly models individuals from all ancestries with population-structure adjustment (typically via principal components), and meta-analysis, which fits ancestry-specific GWAS followed by summary-statistic aggregation. Each approach has advantages and potential pitfalls arising from sample size imbalance, allele frequency differences, and the complexity of population structure. In this talk, I will compare these strategies using large-scale simulations spanning a range of ancestry compositions and sample sizes, as well as empirical analyses of eight continuous and five binary traits from the UK Biobank (N324,000) and the All of Us Research Program (N207,000). Our findings show that pooled analysis consistently achieves higher statistical power while adequately controlling for population stratification. I will also introduce a theoretical framework that links the observed power differences to cross-population allele frequency variation. Together, these results—replicated across both biobanks—demonstrate that pooled analysis offers a robust and scalable approach for multi-ancestry GWAS, improving discovery while maintaining rigorous control of confounding. If time permits, I will present my

new research in developing a survival PRS (polygenic risk score) method, leveraging time-to-event data.