THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

XMR: A cross-population Mendelian randomization method for causal inference using genome-wide summary statistics

By

Miss Xinrui HUANG

Abstract

Mendelian randomization (MR) is a powerful approach for inferring causal relationships between traits using genome-wide association study (GWAS) summary statistics. However, most large-scale GWAS datasets are derived from European populations, while non-European populations, such as Central/South Asian, East Asian, and African groups, suffer from limited sample sizes, challenging the robustness and precision of causal effect estimation when using MR. To address this issue, we propose XMR, a novel cross-population Mendelian randomization method which integrates data from larger populations to enhance causal inference for underrepresented groups. By leveraging genetic correlations between populations, XMR identifies more valid IVs and accurately estimates causal effects within a variational EM framework. Through extensive simulations and real-world data applications, we demonstrate that XMR significantly improves statistical power while maintaining well-calibrated p-values under negative control experiments.

Date : **7 May 2025 (Wednesday)**
Time : **4:00pm**
Venue : **Room 2612B (near Lifts 31/32)**

All are Welcome!