For favour of Posting

THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

TACO: Leveraging Trans-Ancestry Gene Co-Regulation for Transcriptome-Wide Association Studies

By

Mr. Rijiang ZHOU

Abstract

Transcriptome-wide association studies (TWASs) prioritize trait-associated genes by integrating genome-wide association studies (GWASs) with expression quantitative trait loci (eQTL) reference panels, providing regulatory insights into the genetic basis of complex traits. However, current TWAS methods face two critical challenges. First, as most TWASs have been based on genetic data from individuals of European ancestry, portability and power are limited in under-represented populations due to heterogeneous genetic architectures, including allele frequencies, linkage disequilibrium, and regulatory effects. Second, unmodeled polygenic pleiotropy can severely inflate TWAS test statistics and yield false positives. To address these issues, we developed TACO, a unified framework that enhances TWAS performance in a target ancestry by leveraging shared gene co-regulation patterns from an auxiliary ancestry. TACO effectively adjusts for inflation due to polygenic pleiotropy, ensuring well-calibrated test statistics and reliable gene-level associations. We applied TACO to conduct TWASs for complex traits in East Asian and African populations by integrating data from global biobanks and genomic consortia. TACO not only achieved substantial power gains but also identified high-confidence genes that were reproducible. Leveraging cell-type-level eQTL resources, we demonstrated that TACO enabled high-resolution, cell-type-specific TWASs in diverse populations, offering granular insights into the regulatory mechanisms underlying complex human traits.

Date : 4 May 2026 (Monday)

Time : 10:00am

Venue : Room 1104 (near Lift 19)

All are Welcome!