THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

Cross-population trait prediction using genetic data

By

Mr. Mingxuan CAI

Abstract

The genetic data has been extensively used to construct phenotype prediction, which was proved useful to stratify the general European population into different risk groups. However, genetic data-based predictions are less accurate in non-European populations due to genetic differences across different populations. To improve the prediction accuracy in non-European populations, we propose a cross-population analysis framework for genetic prediction with both individual-level (XPA) and summary-level (XPASS) GWAS data. By leveraging trans-ancestry genetic correlation, our methods can borrow information from the large-scale European population data to improve risk prediction in the non-European populations. With innovations in data structure and algorithm design, our methods provide a substantial saving in computational time and memory usage. Through comprehensive simulation studies, we show that our framework provides accurate, efficient, and robust prediction across a range of genetic architectures. In a Chinese cohort, our methods achieved 7.3%–198.0% accuracy gain for height and 19.5%–313.3% accuracy gain for body mass index (BMI) in terms of predictive R^2 compared to existing prediction models.

Date : 5 May 2021 (Wednesday)
Time : 2:00pm
Zoom Meeting : https://hkust.zoom.us/j/97732958524 **(Passcode: 606288)**

All are Welcome!