# THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

## Department of Mathematics

# PHD STUDENT SEMINAR

## Cross-population genetic prediction by harnessing the shared genetic basis between ancestries

### By

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### Abstract

The polygenic risk score (PRS) derived from the genome-wide association studies (GWASs) predicts the individualized genomic predisposition to complex traits/diseases. Conventional clinical implementations of PRS are constructed from training samples dominated by the European ancestry, hence lose predictive accuracy when applied to minor populations. By modeling the trans-ethnic genetic correlation between Europeans and the target ancestry group, we propose a scalable cross-population analysis framework (XPA) that can effectively harness their shared genetic basis and substantially boost the prediction power in the target population. We apply XPA to analyze a wide range of complex phenotypes, revealing the pervasive existence of genetic basis sharing between Europeans and East Asians. Compared with existing approaches, the PRS constructed by XPA in Chinese population achieves 7.3%-198.0% and 19.5%-313.3% accuracy gain in body height and body mass index (BMI).

Date    : **14 May 2020 (Thursday)**
Time    : **10:00am – 11:00am**
Zoom Meeting  : **https://hkust.zoom.us/j/99688831616**

*All are Welcome!*