

The Hong Kong University of Science and Technology

Department of Mathematics

PhD THESIS EXAMINATION

Improving Association Mapping and Polygenic Prediction in Trans-ancestry Analysis

By

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<u>ABSTRACT</u>

Over the past two decades, genome-wide association studies (GWASs) have successfully advanced our understanding of the genetic basis of complex traits. Despite the fruitful discovery of GWASs, current GWASs were often criticized for their lack of ancestry diversity as most samples are collected from European populations. There is a pressing need to improve association mapping and polygenic prediction in trans-ancestry analysis. To fill the gap of disparities in genetic studies between non-Europeans and Europeans, we propose a statistical method, LOG-TRAM, to leverage the local genetic architecture for trans-ancestry association mapping (TRAM). By using biobank-scale datasets, we showed that LOG-TRAM could greatly improve the statistical power of identifying risk variants in under-represented populations while producing well-calibrated p-values. We applied LOG-TRAM to the GWAS summary statistics of various complex traits/diseases from BioBank Japan, UK Biobank, and Africans. Our method obtained substantial gains in power and achieved effective correction of confounding biases. GWAS-derived polygenic risk scores (PRS) have shown great potential in stratifying patients into differences across populations. To address this issue, we propose a cross-population and cross-phenotype (XPXP) method for the construction of PRSs in trans-ancestry analysis. By leveraging biobank-scale datasets in European populations and multiple GWASs of genetically correlated phenotypes, we showed that XPXP could substantially improve predictive power in identifying high-risk groups of type 2 diabetes for East Asians.

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(Open to all faculty and students)

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