



The Hong Kong University of Science and Technology

Department of Mathematics

Seminar on Statistics and Data Science

**Integrative genomic association
and mediation analysis**

By

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Abstract

To date, genome-wide association studies (GWAS) have identified many thousands of unique SNP-trait associations, but the functional mechanisms underlying many of these associations remain unknown. The analysis of the joint associations of a SNP to complex trait(s) and omics-phenotypes (e.g., mRNA expression, DNA methylation, and protein abundance) has the potential to elucidate mechanisms underlying known associations or to reveal novel relationships between genetic variants and complex traits. In this work, we first propose an integrative genomics approach for mapping multi-trait associations using summary statistics from correlated, overlapping or independent samples, and develop an R package: “primo.” Different than existing methods in the literature, primo can analyze the joint associations of more than three sets of summary statistics. Primo estimates the probability that a SNP is associated with any arbitrary combination of (e.g. at least 1, at least 2, some but not others, or all) traits and omics-phenotypes of interest. Empirical false discovery rates are estimated and controlled through permutation of test statistics. We apply this method to jointly analyze multiple sets of GWAS summary statistics and eQTL summary statistics in disease-relevant tissue types from the Genotype-Tissue Expression (GTEx) project. Moreover, based on the primo framework, we further propose to study genomic mediation across many human tissues. That is, we estimate the probability of a cis-SNP affecting a cis-gene transcript and the cis-transcript acts as a mediator further affecting a trans-gene transcript in multiple tissues, i.e., $P(\text{cis SNP} \rightarrow \text{cis-gene expression} \rightarrow \text{trans-gene expression in multiple tissues})$. We apply the proposed cross-tissue mediation analysis method to the multi-tissue GTEx data to detect the cis-expression mediated trans-associations across tissue types.

Date: Monday, 17 December 2018

Time: 4:00p.m.-5:00p.m.

**Venue: Room 4582 (lifts 27 & 28),
Academic Building, HKUST**

All are welcome!