



香港中文大學統計學系

Department of Statistics

THE CHINESE UNIVERSITY OF HONG KONG

# SEMINAR

## DEPARTMENT OF STATISTICS

### THE CHINESE UNIVERSITY OF HONG KONG

## A Summary Statistics-based Method for Integrating Functional Information into Genetic Association Analysis

### INVITED SPEAKER

Prof. Hsu Li  
Fred Hutch Cancer Center

### TIME

May 17, 2023 (Wed) · 9:00 am - 10:00 am

### VENUE

Zoom ID: 923 1906 4135 · Password: 333257 · [Zoom link](#)

### ABSTRACT

Genome-wide association studies (GWAS) have successfully identified tens of thousands of genetic variants associated with various phenotypes, but together they explain only a fraction of heritability, suggesting many variants have yet to be discovered. This is because the genetic effects are typically very modest, and a much larger sample size will be needed to improve power for detecting these variants. However, it has been increasingly difficult to continue increasing the sample sizes of GWAS. Recently, substantial efforts have been devoted to improving the power by leveraging the functional information of genetic variants (e.g., gene expression) as well as the information from multiple related phenotypes. In this talk, we present a summary statistics-based method for testing genetic association with a set of variants, incorporating the information on genetic regulation of molecular characteristics. Here the summary statistics include the genome-wide marginal association regression coefficient estimates and standard errors, as well as the linkage disequilibrium of genetic variants. I will also show the connection to the popular Mendelian Randomization analysis. Simulation demonstrates that summary statistics-based p-values agree well with those from individual level data, but with substantively improved computational speed. Importantly, a broad application of our method to GWAS is possible, as only GWAS summary statistics are required.