Master’s Thesis Presentation

Chenyang Lu
Department of Statistics
The University of Chicago

“Association Testing for Multivariate Phenotypes”

Tuesday, February 13, 2024, at 2:00 PM
Jones 111, 5747 S. Ellis Avenue

Abstract

This project, on understanding the genetic underpinnings of complex traits, examines the interplay between Single Nucleotide Polymorphisms (SNPs) and multivariate phenotypes. Diverging from traditional methods that predominantly focus on the principal components of multivariate traits, our study integrates SNPs into the analysis, enriching the investigation of their influence on phenotypic variations. We utilize an adapted form of canonical correlation analysis, designed for categorical variables $X$, and their correlation with phenotypes that are represented as a series of numerical traits $Y$. This approach facilitates the identification of a functional relationship $f(Y)$ with a significant correlation to the analyzed SNPs. Our work contributes to genomic research by introducing a comprehensive significance testing framework for SNP analysis, thereby deepening the understanding of SNP effects on human phenotypes. The paper outlines our methodology, addresses the challenges of analyzing categorical genetic variables, and uses numerical studies to assess their performance.