

Colloquium
Michigan State University
Department of Statistics and Probability

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A Fast Algorithm for Detecting Gene-Gene Interactions in Genome-Wide Association Studie

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10:20 a.m. - 11:10 am
Refreshments 10:00 am
C405 Wells Hall

Abstract:

With the recent advent of high-throughput genotyping techniques, genetic data for genome-wide association studies (GWAS) have become increasingly available. Although many statistical approaches have been developed and used to identify single-nucleotide polymorphisms (SNPs) that are associated with complex traits or diseases, few are able to detect gene-gene interactions due to an extremely large number of SNP-SNP combinations in GWAS. In this talk, we present a statistical framework for characterizing main genetic effects and epistatic interactions in a GWAS study. Specifically, we first propose a two-stage sure independence screening (TS-SIS) procedure and generate a pool of candidate SNPs and interactions, which serve as predictors to explain and predict the phenotypes of a complex trait. We also propose a rates adjusted thresholding estimation (RATE) approach to control the false positive rate of the selected model by a general independent screening procedure. Regularization regression methods, such as LASSO or SCAD, are then applied to further identify important genetic effects. The simulation studies show that the TS-SIS procedure is computationally efficient and has an outstanding finite sample performance in selecting potential SNPs as well as gene-gene interactions. We apply the proposed framework to a real GWAS dataset from the Framingham Heart Study.

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