

MICHIGAN STATE UNIVERSITY
Department of Statistics and Probability

COLLOQUIUM

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Multi-loci Linkage Disequilibrium Mapping of Complex Traits

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

Abstract

In genetics, linkage disequilibrium (LD) is a phenomenon arising from the co-inheritance of alleles at nearby loci on the same chromosome, i.e., the alleles at multiple tightly linked genetic loci pass non-randomly from generation to generation in a natural population. Capitalizing on this phenomenon, a group of mapping methods, called LD mapping, have been developed recently for genetic association studies. Unlike traditional association methods, which often treat sampled genetic markers, such as single nucleotide polymorphism (SNP), as independent factors, LD mapping considers linkage information among them and draws inference about unobserved causal genetic variants based on observed markers. However, most current LD mapping methods are mainly based on single-marker analysis, overlooking the rich information contained in a block of linked loci. In this talk, we aim to extend LD mapping to include multiple linked loci and explicitly incorporate their LD information into genetic mapping models. We will focus on the dense SNP data as it represents the major data type in genomewide association studies. We will mainly discuss two statistical methods, including a two-SNP LD mapping model and a neural network based epistasis modeling between SNP blocks. Their detailed statistical properties will be examined and both methods will be applied to real datasets to demonstrate their practical use.

To request an interpreter or other accommodations for people with disabilities, please call the Department of Statistics and Probability at 517-355-9589.