

MICHIGAN STATE UNIVERSITY
Department of Statistics and Probability

COLLOQUIUM

Lin Chen
University of Chicago

Integrative Genomic Association and Mediation Analysis

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10:20 AM - 11:10 AM [Eastern Standard Time](#)
Zoom

Abstract

In the post-GWAS era, tens of thousands of unique associations between single nucleotide polymorphisms (SNPs) and complex diseases/traits were discovered. Most of the trait-associated SNPs reside in non-coding regions with unknown functions. Many of them may affect complex traits through their effects on expression levels and/or other 'omics' traits. Extensive evaluations of genetic effects on omics traits have revealed an abundance of quantitative trait loci for omics traits (omics QTLs), often with effects depending on tissue/cell types and contexts. In order to further understand the biological mechanisms underlying the reported trait-associated SNPs, many efforts have been made to integrate GWAS summary statistics with omics QTL statistics. In this talk, we will discuss several recent works in integrative association and mediation analyses. We proposed methods for analyzing GWAS statistics with multi-tissue eQTL (and multi-tissue meQTL) summary statistics from the Genotype-tissue Expression (GTEx) project, to provide a comprehensive mechanistic interpretation of how known trait-associated SNPs affect complex traits and suggest putative clinically actionable risk factors for diseases.

Zoom details can be found at: <https://stt.natsci.msu.edu/stt-colloquium-zoom-info/>

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