MICHIGAN STATE UNIVERSITY
Department of Statistics and Probability

COLLOQUIUM

Jingshu Wang
University of Chicago

Causal Inference for Heritable Phenotypic Risk Factors Using Heterogeneous Genetic Instruments

Tuesday, October 5, 2021
10:20 AM - 11:10 AM Eastern Time
Zoom

Abstract

Mendelian randomization (MR) is a method of exploiting genetic variation to unbiasedly estimate a causal effect in presence of unmeasured confounding. In MR, natural genetic variations are used as instrumental variables to perform causal inference on the effect of heritable risk factors. Because of its convenience, MR has been being widely used in epidemiology and other related areas of population science. However, the phenomenon that "all genes affect every complex trait" complicates Mendelian Randomization (MR) studies as most genetic variants will then be invalid instruments.

In the talk, I'll discuss the assumptions of existing MR methods and show how they need to be clarified to allow for pervasive horizontal pleiotropy and heterogeneous effect sizes. I'll present a comprehensive framework that we have developed for MR. By using GWAS summary statistics, we can efficiently use both strong and weak genetic instruments, detect the existence of multiple pleiotropic pathways, determine the causal direction and perform multivariable MR to adjust for confounding risk factors. I'll also illustrate a few case studies at the end of the talk.

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

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