

Mendelian Randomization for Causal inference of heritable phenotypic risk factors



Jingshu Wang, PhD
Assistant Professor in Statistics
University of Chicago

Mendelian randomization (MR) is a method of exploiting genetic variation to unbiasedly estimate a causal effect in the 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 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, Dr. Wang will discuss a series of developments using a new comprehensive framework that they developed for MR that can deal with pervasive horizontal pleiotropy, weak genetic instruments, and the temporal relationship between the risk factors and disease progression. She'll also illustrate a few case studies at the end of the talk.

Thursday January 12, 2023, 3:30-4:30 PM Eastern

133 Rosenau Hall

Virtual using link and info below.

<https://unc.zoom.us/j/91249030964?pwd=UXloTWIHajdQbkRqd1d5TnRaMitYdz09>

Meeting ID: 912 4903 0964

Passcode: 884852