SEMINAR

DEPARTMENT OF STATISTICS
THE CHINESE UNIVERSITY OF HONG KONG

Causal Inference with Possibly Invalid Instruments

INVITED SPEAKER

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TIME

June 18, 2024 (Tue) · 2:30 pm - 3:30 pm

VENUE

LSB LT2 · Lady Shaw Building - LT2 · CUHK

ABSTRACT

Mendelian randomization (MR) uses genetic variants as instrument variables (IV) to identify and estimate causal effects in the presence of unmeasured confounding. However, violations of core IV assumptions threaten the validity of MR in biomedical studies. In this talk, I will introduce two methods to address such violations. First, in the multiple IV framework, we proposed to use genetic interactions to remove the bias due to violations of the IV independence and exclusion restriction assumptions; and estimation can be easily carried out using existing off-the-shelf software. Second, in the single IV framework, we proposed a mixed-scale robust identification strategy by leveraging outcome heteroskedasticity in conjunction with two homogeneity assumptions: (i) homogeneous causal effect on the additive scale; and (ii) homogeneous confounding bias on the odds ratio scale. The two proposed methods are illustrated using UK Biobank data.