University of California, Irvine
Statistics Seminar

Statistical Modeling and Inference in GWAS Data-based Mendelian Randomization Analysis

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By leveraging publicly available summary statistics from many large-scale genome-wide association studies (GWAS), Mendelian randomization (MR) has become a popular and cost-effective approach to exploiting genetic variation to study the potential causal effect of various risk factors on health outcomes in the presence of unmeasured confounding. However, due to the omni-genic nature of most complex traits and the widespread pleiotropic effects of genetic variants, the exclusion restriction assumption in conventional MR analysis (i.e. no horizontal pleiotropy in genetic terms) is likely violated for some genetic variants, and poses challenges for modeling and inference.

In this talk, we will discuss some of our recent research efforts to develop statistical models that can flexibly accommodate genetic variants with and without pleiotropic variation to best extract information for robust and efficient inference of MR analysis. We will discuss a powerful and unified inference framework with appropriately controlled type I errors. We demonstrate the robustness and efficiency of the proposed methods by simulation studies and applications to GWAS summary data to investigate the causal effects of cardiometabolic risk factors on various health outcomes.