

Bayesian Framework for Mendelian Randomization in Mediation Setting

WHEN

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10:00 AM

WHERE

Jones Laboratory, Room 304



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The recent availability of abundant genetic data has sparked the development of new methods to analyze these data. In particular, Mendelian randomization is a technique based on instrumental variables estimation to perform causal inference using observational data from genetic studies. However, methods developed so far have struggled with issues such as violation of model assumptions, noisy observations, and inability to model complex causal networks, such as mediation. We build upon previous work to perform inference under a weaker set of assumptions and in settings with multiple exposure traits. Our Bayesian framework allows for modelling many traits with an arbitrary (acyclic) causal structure, a more robust model for horizontal pleiotropy, and better handling of noisy data. We execute our empirical Bayes-inspired approach using the expectation maximization algorithm and Gibbs sampling. We test our method on simulated data and find that our method has better coverage than previous frequentist methods in more difficult cases.

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