ABSTRACT

Mendelian Randomization (MR) is a powerful tool in epidemiology that enables us to estimate the causal effect of a risk factor on an outcome using genetic variants as instrumental variables. Although the risk factor is often a time-varying exposure, current MR methods typically present the risk factor as a single variable and interpret its effect as the that of a lifelong intervention. However, in cases where time-varying effects are present, such an approach can lead to biased, unclear and misleading results. To avoid such issues, we propose an alternative approach that evaluates the causal mediation effects of a sequence of exposures in a temporal order on a later outcome. We use linear structural equations to characterize the relationship among traits and propose a Bayesian framework that jointly performs statistical inference on all the causal effects in the structural equations. We implement our approach using EM algorithm and Gibbs Sampler. The effectiveness of our method has been demonstrated on both simulations and real data examples.