Creating a Matched Pair Randomization Test for Spillover Effect within Two-Stage Observational Data

Tyler Mansfield

November 21, 2022

Consider two-stage observational studies in which treatments are assigned to clusters of individuals, and then units within treated clusters also make an individual decision about whether or not to participate in treatment. Two-stage studies allow us to study the spillover effect, which is the causal effect of treatment on an individual who did not receive the treatment but was affected by the treatment due to being within a treated cluster. In randomized two-stage studies, these effects can be measured by comparing controls in control clusters to controls in treated clusters (Hudgens and Halloran 2008; Basse and Feller 2018), and Barkley et al. (2020) proposed weighting methods for the observational case. However, no matched design has been proposed nor relevant techniques for sensitivity analysis. Sensitivity analysis is especially hard because unobserved confounding may arise from latent differences either between clusters or between individuals within clusters.

Defining spillover effects requires modified potential outcomes. For cluster i with n_i individuals, define length-n_i vectors $\mathbf{Y}_i(\mathbf{0}, 0)$ and $\mathbf{Y}_i(\mathbf{z}_i, 1)$ for all $\mathbf{z}_i \in \{\mathbf{z}_i : P(\mathbf{z}_i) > 0\}$. These potential outcomes depend both on the cluster-level treatment (the final index) and the individual-level treatment values for all individuals in cluster i, which allows for arbitrary spillover structures within clusters, albeit with no spillovers across clusters (Sobel 2006). To test for spillover effects, the following null hypothesis is used:

$$Y_{ij}(\mathbf{0}, 0) = Y_{ij}(\mathbf{z}_i, 1) \text{ for all } \mathbf{z}_i \text{ such that } z_{ij} = 0, \text{ and this holds for all } i. \tag{1}$$

In words, there are no spillover effects of any kind for any individual under the null, although individuals may be affected by their own treatments.

Comparing control individuals in treated clusters to all controls in paired control clusters seems like a logical next step, but poses problems for randomization inference. To compute the randomization distribution of a test statistic under a null hypothesis, the test statistic must be imputable, meaning that its value must be known under each possible treatment assignment (Basse et al. 2019). Here it is not known which individuals in the observed control clusters would have adopted treatment had their clusters been treated (Figure 1).
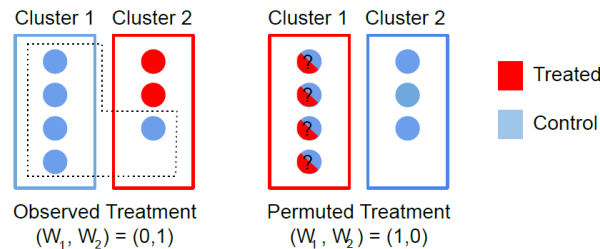
To guarantee imputability, this thesis project proposes an adaption of Basse et al. (2019)'s procedure for randomized trials to construct a matched-pairs randomization test for this null hypothesis. The goal of this project is to demonstrate that in the absence of unmeasured confounding, if we match exactly on the cluster-level propensity score, define our test statistic only using outcomes for pseudo-controls, and conduct randomization inference for cluster-level treatment conditional on individual-level propensity scores, the resulting distribution of the test statistic is uniform under the null hypothesis. Given additional time, the project may extend to a sensitivity analysis for unmeasured confounding.