

Comment: The Essential Role of Pair Matching in Cluster-Randomized Experiments, with Application to the Mexican Universal Health Insurance Evaluation

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1. INTRODUCTION

We congratulate Imai, King and Nall on a valuable paper which will help to improve the design and analysis of cluster randomized studies. The authors make two key contributions: (1) they propose a design-based estimator for matched pair cluster randomized studies that in many circumstances is a better estimator than the harmonic mean estimator; (2) they present convincing evidence that the matched pair design, when accompanied with good inference methods, is more powerful than the unmatched pair design and should be used routinely.

In this discussion, we would like to contribute our thoughts on how to construct the matched pairs. Greevy, Lu, Silber and Rosenbaum (2004) point out that in most randomized studies, only one or two variables are used in constructing the pairs. To remedy this, Greevy et al. present a method for optimal multivariate matching. They demonstrate in an example with 14 covariates and 132 units that the optimal matching achieves substantially better balance on all 14 covariates than an unmatched design. Greevy et al. considered the situation in which we want to use all available units in the experiment. In cluster randomized studies, because of cost considerations, we can often only use some of the clusters, that is, there are $N = 2k$ clusters but we would only like to include $2m$ ($m < k$) clusters in the experiment; see Murray (1998), Chapter 10, for

several examples. How should we choose the best m matched pairs? In our discussion, we compare several methods of constructing matched pairs for this setting.

Our discussion is organized in the following way. We introduce and discuss four methods of matching in the next section. Then we conduct simulations to compare these methods and the results are summarized in Section 3 and 4. Conclusions of our findings are given in Section 5.

2. FOUR METHODS OF MATCHING PAIRS

The goal of matching is to produce a design for the experiment that has high power relative to other designs. Matching methods seek to do this by defining a distance between every pair of units and then making the total distance between the matched units as small as possible. One distance for matching is the Mahalanobis distance (Rubin, 1979). We will compare matching methods by comparing the total Mahalanobis distance between the matched units.

We consider four methods of constructing m matched pairs when there are $N = 2k$ ($k > m$) units. Three of the methods make use of the optimal nonbipartite matching algorithm described by Greevy et al. (2004) which, for a given $2r$ units and a $(2r) \times (2r)$ distance matrix, returns the r pairs which minimize the total distance between the units in the pairs.

1. *The random method.* A simple random sample of $2m$ units from the N units is selected. The selected units are matched optimally using the optimal nonbipartite matching algorithm.
2. *The ranking method.* Optimal nonbipartite matching is applied to construct the k pairs from all $2k$ units which minimize the total distance between matched pairs. Then, the m pairs which have the smallest distance are selected. King et al. (2007) use

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