

Rejoinder: Matched Pairs and the Future of Cluster-Randomized Experiments

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1. INTRODUCTION

We are grateful to our four discussants for their agreement with and contributions to the central points in our article (Imai et al., 2009b). As Zhang and Small (2009) write, “[our article] present[s] 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.” And, as they put it, Hill and Scott (2009) “do not take issue with [our article’s] provocative assertion that one should pair-match in cluster randomized trials ‘whenever feasible.’” Whether denominated in terms of research dollars saved, or additional knowledge learned for the same expenditure, the advantages in any one research project of switching standard experimental protocols from complete randomization to a matched pair designs (along with the accompanying new statistical methods) can be considerable.

In the two sections that follow, we address our discussants’ points regarding ways to pair clusters (Section 2) and the costs and benefits of design- and model-based estimation (Section 3). But first we offer a sense of how many experiments across fields of inquiry can be improved in the ways we discuss in our article. We do this by collecting data from the last 106 cluster-randomized experiments published in 27 leading journals in medicine, public health, political science, economics, and education. We then counted how many experiments used complete randomization, blocking (on some but not all pre-treatment information), or pair-matching—which respectively exploit

none, some and all of the available pre-randomization covariate information. Table 1 gives a summary. Overall, only 19% of cluster-randomized experiments used pair-matching, which means that 81% left at least some pre-randomization covariate information on the table. Indeed, almost 60% of these experiments used complete randomization and so took no advantage of the information in pre-treatment covariates. The table conveys that there is some variation in these figures across fields, but in no field is the use of pair matching in cluster-randomized designs very high, and it never occurs in even as many as 30% of published experiments. Administrative constraints may have prevented some of these experiments from being pair matched, but as using this information involves no modeling risks, the opportunities for improving experimental research across many fields of inquiry seem quite substantial.

2. HOW TO CONSTRUCT MATCHED PAIRS

Zhang and Small (2009) offer some creative ideas on how to construct matched pairs based on minimizing the total (i.e., across pairs) Mahalanobis-based distance metric, which is referred to as an “optimal” method. This procedure can be useful in many situations, and will usually be superior to Mahalanobis-based matching methods that do not consider imbalances for all pairs simultaneously.

This technique, of course, is not always appropriate. For example, the procedure assumes that Mahalanobis distances make sense for the input data, which means that the variance matrix which scales the distances is known or can be estimated, and that the input variables are close to normal. Perhaps even more importantly, the procedure maps all the distances to a scalar to measure balance; this assumes that the researcher is willing to reduce balance within pairs for some pre-treatment variables in order to achieve a larger improvement for other variables. However, if the set of variables having its balance reduced has a bigger impact on the outcome than the other set, then the trade-off implied by the distance metric would be ill advised. One way to avoid these trade-offs is to use a matching method without a

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