

TriMatch: An R Package for Propensity Score Matching of Non-Binary Treatments

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The use of propensity score methods (Rosenbaum and Rubin, 1983) have become popular for estimating causal inferences in observational studies in medical research (Austin, 2008) and in the social sciences (Thoemmes and Kim, 2011). In most cases however, the use of propensity score methods have been confined to a single treatment. Several researchers have suggested using propensity score methods with multiple control groups, or to simply perform two separate analyses, one between treatment one and the control and another between treatment two and control. This talk introduces the **TriMatch** package for R that provides a method for determining matched triplets. Examples from educational and medical contexts will be discussed.

Consider two treatments, Tr_1 and Tr_2 , and a control, C . We estimate propensity scores with three separate logistic regression models where model one predicts Tr_1 with C , model two predicts Tr_2 with C , and model three predicts Tr_1 with Tr_2 . The triangle plot in Figure 1 represents the fitted values (i.e. propensity scores) from the three models on each edge. Since each unit has a propensity score in two models, their scores are connected. The **TriMatch** algorithm will find matched triplets where the sum of the distances within each model is minimized. In Figure 1, the black lines illustrate one matched triplet.

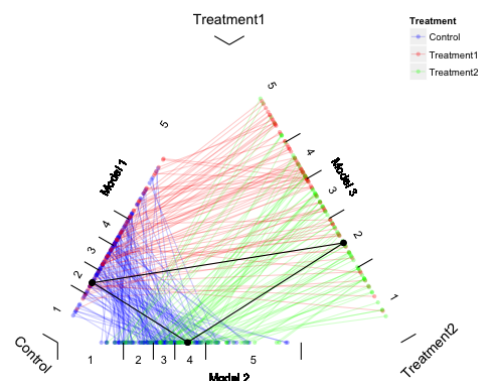


Figure 1: Triangle Plot

Propensity score analysis of two groups typically use dependent sample t -tests. The analogue for matched triplets include repeated measures ANOVA and the Friedman Rank Sum Test. The **TriMatch** package provides utility functions for conducting and visualizing these statistical tests. Moreover, a set of functions extending **PSAgraphics** (Helmreich and Pruzek, 2009) for matched triplets to check covariate balance are provided.

References

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