

Matching methods provide simple and intuitive tools for adjusting the distribution of covariates among samples from different populations. Probably because of their transparency and intuitive appeal, matching methods are widely used in evaluation research to estimate treatment effects when all treatment confounders are observed (Rubin, 1973, 1977; Rosenbaum, 2002). In spite of their popularity, the problem of establishing the large sample distribution of matching estimators remains largely unsolved, with the exception of some special cases (see Abadie and Imbens, 2006). The reason is that matching estimators are non-smooth functionals of the data, which makes their large sample theory particularly challenging. This talk will describe a new general method to establish the large sample distribution of matching estimators. As an example of the applicability of the method, we will describe how to derive the distribution of matching estimators when matching is carried out without replacement, a result previously unavailable in the literature. We will also discuss how to adjust the standard errors for propensity score matching estimators to take into account first step estimation of the propensity score, a result also previously unavailable.