Optimized matching for retrospective case control: case study in pediatric blood transfusion

Dr. Jack O. Wasey¹, Dr. Steve M. Frank², Dr. Mohamed Rehman¹
1. Dept. Anesthesiology and Critical Care Medicine, Children’s Hospital of Philadelphia, Philadelphia, PA
2. Dept. Anesthesiology and Critical Care Medicine, Johns Hopkins Medical Institutions, Baltimore, MD

Introduction
Pediatric medical research is limited by a more difficult ethical approval and consent process. Meanwhile, large amounts of electronic data are produced by anesthesia, hospital charting and billing. These data have been used for retrospective studies by many authors, but avoiding confounders and attempting causal inference is hard. Case-control is a well established approach, especially using propensity scores. This paper describes a comparison between propensity score matching, and an optimized matching technique using a genetic algorithm which has only recently become practical with increased computing power. A case study in pediatric blood transfusion is given which shows how a retrospective study can better simulate a RCT, and the superiority of optimized matching over propensity matching. The clinical question is: does blood transfusion cause increased in-hospital mortality?

Methods
- Anesthesia data, demographics and admission diagnoses were extracted from the electronic health records, for patients aged under 25 years undergoing any procedure
- ICD-9 codes converted to comorbidities using the icd9 R package
- Covariates chosen that might influence blood transfusion
- Optimized and propensity score matches were performed using R and the GenMatch algorithm, which evolves many combinations of trial treatment-control pairs until a minimum difference between the groups is established. Mahalanobis distance was used.
- Various assessments of balance are made to compare propensity score and genetic algorithm matches.

Discussion
Randomized controlled trials (RCTs) are expensive, time consuming, and often done in strict settings not reflective of real life. Close observation of practitioners affects behavior and outcomes. Retrospective studies have none of these problems, but do not have random treatment assignment. Careful matching can at least partly overcome this problem. Before electronic health records (EHR) and powerful desktop computing, it was impractical to match large numbers of patients on many characteristics. Optimized matching with a genetic algorithm simulates a RCT by generating tightly matched groups, but requires moderate computing power. An optimal matching solution is evolved by thousands of matching trials.

Matching simulates an RCT, providing treatment and control groups with similar characteristics. Traditional multivariable statistics can then be done on these groups, but with less bias. (Stuart, 2010). This technique is widely used in political science where data sets used to be smaller, and with fewer characteristics per person. In medicine, this and similar techniques are increasingly used.

Although this matching technique adds some complexity, it gives better matches and better balance than propensity scores (Diamond and Sekhon, 2012). When seeing the highly non-linear distributions of some of covariates, it is surprising that straightforward multivariable regression is ever attempted on these complex medical data without matching first. Matching should be used for most large retrospective studies, and optimized genetic matching reduces bias.