

# Matching and Balance

October 19, 2012

## Recap: Neyman-Rubin Model, Estimating ATE, ATT

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- Under the Neyman-Rubin model, we observe

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- Problem: For each unit, we only observe one of the pair  $Y_i(1), Y_i(0)$ .

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$$\begin{aligned}\widehat{ATE} &= \frac{\sum T_i}{N} \left( \frac{\sum_{i=1}^N (Y_i(1) - Y_{i'}(0)) T_i}{\sum T_i} \right) \\ &+ \frac{N - \sum T_i}{N} \left( \frac{\sum_{i=1}^N (Y_{i'}(1) - Y_i(0)) (1 - T_i)}{N - \sum T_i} \right) \\ \widehat{ATT} &= \frac{\sum_{i=1}^N (Y_i(1) - Y_{i'}(0)) T_i}{\sum T_i}\end{aligned}$$

- Here,  $i'$  denotes an observed unit similar to unit  $i$  where the treatment indicators satisfy  $T_i = 1 - T_{i'}$ .

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- GenMatch.
- We're going to focus on Mahalanobis distance today.

## Mahalanobis distance

- Suppose we have  $X_1, \dots, X_n$ , with each variable  $X_i$  having  $k$  components (covariates):  $X_i = (X_{i1}, X_{i2}, \dots, X_{ik})$ .
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- Suppose we have the  $k \times k$  covariance matrix of these covariates. (either by estimating this matrix, or given to us). Call this covariance matrix  $S$ .
- The Mahalanobis distance between  $X_i$  and  $X_j$  is

$$md(X_i, X_j) = [(X_i - X_j)' S^{-1} (X_i - X_j)]^{1/2}$$

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- Suppose covariates are ellipsoidal (in a crude sense, the data looks like an oval).
- Special case of ellipsoidal: Multivariate normal.
- Transform the covariates into a circle, where the marginal SD is 1 for any covariate.
- Equivalent to “Eliminating the correlation between covariates and scaling all covariates so that they are on the same scale.”
- Calculate the distance within this circle.
- Mahalanobis distance can be computed for any other original shape of data... but nice properties can be had if the data is ellipsoidal.

## EPBR

- Suppose we are matching treated units to control units.
- A matching method is Equal Percent Bias Reducing (EPBR) if, for ALL covariates  $X$ :

$$\begin{aligned} & E(X|T = 1) - E(X|\text{Matched Controls}) \\ &= \gamma(E(X|T = 1) - E(X|T = 0)) \end{aligned}$$

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- In words, the average covariate imbalance shrinks a little bit for each covariate.
- If data is ellipsoidal, then the matching with the Mahalanobis distance is EPBR.
- EPBR may not be that attractive of a property; especially if you think that balance over some covariates (height, weight) is more important than others (number of hair follicles).

## Quick teaser: How can you tell if matching worked?

- Recall, the whole point of matching is to find people in the control group that look like people that are treated.
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- If data is quantitative, compare means of covariates between the treatment group and the matched control group ( $t$ -test).
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- These methods compare single points (a mean or proportion) between these two groups. This is sufficient for categorical data, but not for quantitative data.
- Kolmogorov-Smirnov test can test if there's discrepancies across the entire distribution (for next time).