

Observational Studies

Assume ‘regular assignment mechanisms,’ meaning the following three restrictions hold: individualistic assignment, probabilistic assignment, and unconfounded assignment. Essentially, each unit has some probability of being assigned the treatment independent of the assignment for other units or its own potential outcomes. Unconfoundedness is usually the key assumption.

Definition of Propensity Score

Propensity score = $e(x)$ = average assignment probability for units with $X_i = x$

$$e(x) = \frac{1}{N_x} \sum_{i: X_i=x} P_i(X, Y(0), Y(1))$$

If operating under the assumptions from the regular assignment mechanisms, above, $P_i(X, Y(0), Y(1)) = Pr(W_i = 1 | X, Y(0), Y(1)) = q(X_i) \in (0, 1)$. The propensity score then simplifies to $e(x) = \frac{1}{N_x} \sum_{i: X_i=x} q(X_i) = q(x)$. Unlike $e(x)$, $q(x)$ can be estimated with X_i data so under regular assignment mechanisms where $e(x)=q(x)$, we can estimate $e(x)$ which has desirable properties.

In observational studies, there are two common estimands:

Average Treatment Effect (ATE) $\tau = \frac{1}{N} \sum_{i=1}^N (Y_i(1) - Y_i(0))$

Average Treatment Effect on Treated (ATT) $\tau_t = \frac{1}{N_t} \sum_{i=1}^N W_i (Y_i(1) - Y_i(0))$

Note: Superpopulation estimands would be written with expectation notation; ATT estimand written in terms for comparison to ATE but there are, of course, multiple ways to write it.

Matching for Causal Inference (Chapters 14, 15, 18, and Stuart and Imbens papers)

Two settings:

1. Outcomes (Y) not yet collected
 - identified treatment group (ex. people accepted into treatment program)
 - large number of possible controls (ex. applicants not accepted to program, survey)
2. Post-study
 - have X and Y on all units and match to get good estimates

Note: Critical to not use Y to match; can use several matching strategies and choose one that works best, meaning best X matches... not Y.

Intuition for matching is that if the units match perfectly (in the case of categorical covariates), the study resembles a stratified randomized experiment (Ch 9) in which the treatment effect would be estimated within blocks/strata as follows:

$$\hat{\tau}_x = \frac{1}{N_{tx}} \sum_{\substack{i=1 \\ X_i=x}}^N W_i Y_i^{obs} - \frac{1}{N_{cx}} \sum_{\substack{i=1 \\ X_i=x}}^N (1 - W_i) Y_i^{obs}$$

$$\hat{\tau}_{ATE} = \sum_x \left(\frac{N_{tx} + N_{cx}}{N} \right) \hat{\tau}_x \qquad \hat{\tau}_{ATT} = \sum_x \left(\frac{N_{tx}}{N_t} \right) \hat{\tau}_x$$

Matching in Practice (Stuart paper)

1. Define 'close' (Ch 15,18)
2. Strategy for matching (Ch 18)
3. Assess quality of match (Ch 14)
 - If not ok, return to step 2; otherwise; continue to step 4.
4. Analysis (Ch 18)

1. Defining 'close'

- Which variables to include
 - only covariates related to assignment and outcome
 - include more rather than less
 - do not include any effected by treatment (intermediate outcomes)
- How to measure distance where D_{ij} = distance between X_i and X_j , $p \times 1$ vectors of quantitative covariates
 - exact matching $D_{ij} = 0$ if $X_i = X_j$, ∞ otherwise
 - Euclidean $D_{ij} = (X_i - X_j)'(X_i - X_j)$
 - standardized Euclidean $D_{ij} = (X_i - X_j)'V^{-1}(X_i - X_j)$ where

$$V = \begin{pmatrix} Var(X_{i1}) & 0 & \dots & 0 \\ 0 & Var(X_{i2}) & \dots & 0 \\ \dots & \dots & \dots & \dots \\ 0 & 0 & \dots & Var(X_{ip}) \end{pmatrix}$$
 - Mahalanobis $D_{ij} = (X_i - X_j)'\Sigma^{-1}(X_i - X_j)$ where $\Sigma = \frac{\sum_{i=1}^N (X_i - \bar{X})(X_i - \bar{X})'}{N}$, pooled over treatment and control
 - propensity score $D_{ij} = |e_i - e_j|$
 - combination of things
 - * require exact match on some and D_{ij} within groups
 - * add weight to D_{ij}
 - * 'calipers' on key variable, k , $|X_{ik} - X_{jk}| < c$ and D_{ij} within caliper

Note: Mahalanobis and propensity score methods primarily used and recommended.