

Causal Inference and Matching Techniques

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What is Causal Inference?

Definition

- Causal inference refers to an intellectual discipline that considers the assumptions, study designs, and estimation strategies that allow researchers to draw causal conclusions based on data.^a

^aHill & Stuart 2015

Example

- Suppose you are trying to estimate the causal effect of taking 1 Advil on the strength of your headache.
- You should take the Advil, measure your headache ($Y(1)$), then *reverse time*, not take Advil, and measure your headache ($Y(0)$).
- We need to have the same unit at the same time to avoid *confounding*. If we don't use the same unit at the same time, other covariates may be the source of the treatment effect.

Missing Potential Outcomes

Figure: "Science Table" from Rubin 2005

<i>Units</i>	<i>Covariates</i> X	<i>Potential outcomes</i>		<i>Unit-level</i> <i>Causal effects</i>	<i>Summary</i> <i>Causal effects</i>
		<i>Treatment</i> $Y(1)$	<i>Control</i> $Y(0)$		
1	X_1	$Y_1(1)$	$Y_1(0)$	$Y_1(1)$ v. $Y_1(0)$	Comparison of $Y_i(1)$ v. $Y_i(0)$ for a common set of units
\vdots	\vdots	\vdots	\vdots	\vdots	
i	X_i	$Y_i(1)$	$Y_i(0)$	$Y_i(1)$ v. $Y_i(0)$	
\vdots	\vdots	\vdots	\vdots	\vdots	
N	X_N	$Y_N(1)$	$Y_N(0)$	$Y_N(1)$ v. $Y_N(0)$	

Random Assignment to Solve "Missing" Potential Outcomes

Randomized Controlled Trials

- Randomized Controlled Trials are considered a "gold standard" in providing causal evidence.
- Treatment assignment is independent of potential outcomes *and* covariates.

Definitions

- Y = outcomes, $Y(1)$ is the outcome under treatment, $Y(0)$ is the outcome under the control.
- Z = treatment assignment, 1 = treatment group, 0 = control group.

Deriving the Basic Idea

Comparing Potential Outcomes

$$E[Y(1) - Y(0)] = E[Y(1)] - E[Y(0)]$$

What is $E[Y(1)]$?

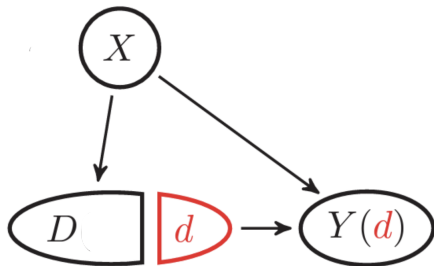
$$E[Y(1)] = E[Y(1) | Z] = E[Y(1) | Z = 1] = E[Y^{\text{obs}} | Z = 1]$$

Following an analogous process for $E[Y(0)]$:

$$\implies E[Y(1) - Y(0)] = E[Y^{\text{obs}} | Z = 1] - E[Y^{\text{obs}} | Z = 0]$$

Directed Acyclic Graphs

We can represent this with a DAG*:



*Wang et. al. 2021

Observational Studies and Matching

Observational Studies

- When an RCT is impossible or unethical, researchers may use matching techniques on an existing data set (i.e. ATE of heart surgery).
- In observational studies, the treatment assignment is not random, and thus, there may be a huge covariate imbalance between the treated and controlled group.
- In a completely randomized experiment, the two covariate distributions are exactly balanced, in expectation.

Matching

- We assume we have a relatively small population of treated units and a large group of potential controls.
- We have N_t units. We wish to select $N_c < N'_c$ so that $N = N_t + N_c$ represents the full sample.

Matching cont.

Setup

- We wish to select a subset of $I'_c = \{N_t + 1, \dots, N_t + N'_c\}$, $I_c \subset I'_c$
- Let I_t be the set of treated units ordered by decreasing propensity score (hardest to match first).
- We want to select a subset that has a better balance of covariates than the whole set of possible controls
- Assume we wish to match one control to each treated unit

For the $i = 1$ unit

$$M_1^c = \{j \in I'_c \mid d(X_1, X_j) = \min_{j' \in I'_c} d(X_1, X_{j'})\}$$

What is the the distance function $d(x, x')$?

Mahalanobis Metric Matching

First, I will provide the intuition behind the Mahalanobis distance.

Mahalanobis Metric Matching

- x and x' are row vectors of covariates.
- $(x - x')$ is a row vector of the difference. We assume a Gaussian distribution with mean $\mu_x = 0$ and covariance matrix $\hat{\Sigma}$.
- If we left multiply, $\hat{\Sigma}^{-\frac{1}{2}}X$, the covariance matrix becomes the identity matrix I .
- We can do the same with the transpose: $(x - x')^T$. Note that the transpose is a column vector.
- Our distance function must output a positive scalar, thus we multiply by the transpose.

Mahalanobis Metric Matching, cont.

Mahalanobis Metric Matching

$$d_M(x, x') = (x - x') \left(\frac{N_c \Sigma_c + N_t \Sigma_t}{N_c + N_t} \right)^{-1} (x - x')^T$$

- The middle term represents the weighed sum of the covariance matrices of the treatment and control group.
- Since the middle term also makes $(x - x')$ and $(x - x')^T$ have the identity matrix as their covariances, then the distance metric is a simple sum of squared terms.

Propensity Score

What is the Propensity Score

- Since treatment assignment is nonrandom, we want to express the likelihood of assignment to the treatment group as a function of the covariates
- We do this by estimating the logistic regression function of a subset of the covariates.
- There is an algorithmic way to select the subset: Selecting basic terms, additional linear terms, and quadratic and interaction terms.

Propensity Score Example

Variable	EST	(s. e.)	t-Stat
Intercept	-2.38	(0.06)	-41.0
sex	-0.01	(0.08)	-0.2
lmotage	0.48	(0.04)	11.7
ses	0.10	(0.04)	2.6

Figure: Rubin & Imbens, 2015

- lmotage is the log of the mother's age.
- ses is socioeconomic status

Propensity Score Distance Metric

Note that in the previous example the propensity score $e(x)^\dagger$ is a linear combination of variables. Thus, $\ln\left(\frac{e(x)}{1-e(x)}\right) = X^T \beta$

Propensity Score Matching

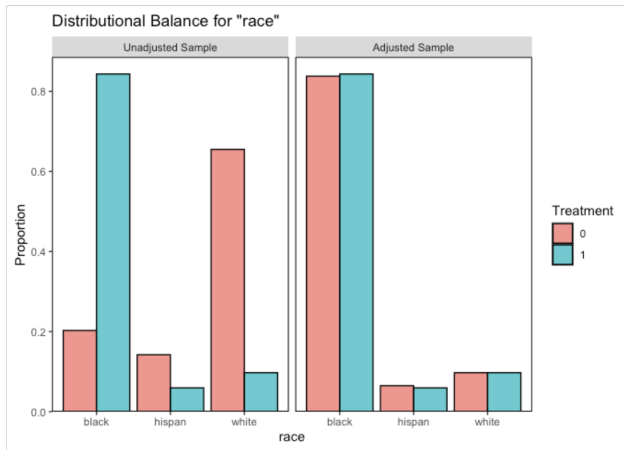
$$d_\ell(x, x') = (\ell(x) - \ell(x'))^2 = \left(\ln\left(\frac{e(x)}{1-e(x)}\right) - \ln\left(\frac{e(x')}{1-e(x')}\right)\right)^2$$

- We use the linearized propensity score to take into account the fact that a (0.10 - 0.05) difference has a larger effect on outcomes than (0.55-0.50)

[†]In practice, we do not actually know the propensity score, so we use the estimated propensity score ($\hat{e}(x)$).

Results of Matching

This is from the LaLonde dataset of the National Supported Work Study, which sought to evaluate the effectiveness of an employment training program on wage increases. Here we see the balance of *race* after 1-1 propensity score matching (Greifer, 2022).



Comparing the Distance Metrics

The difference between the distance metrics matters most when the distribution of the covariates is normal. We are concerned with reducing the *bias* in the distribution of the covariates.

Difference

- Propensity score matching only considers covariates with a difference in distribution between treatment and control groups
- Mahalanobis matches in addition on a set of covariates whose distributions are identical in both the treatment and control groups

Pros and Cons

- Emphasizing already balanced covariates is bad because 1) it has less bias reduction on unbalanced covariates and 2) may compromise balance that already exists in the population
- However, even if a covariate is balanced in expectation, Mahalanobis might remove random variation

Conclusion

- In causal inference, researchers consider study design and assumptions that allow researchers to make causal conclusions.
- Matching is a valuable strategy for researchers to make causal conclusions from observational studies.
- Matching finds a control group with a minimum covariate distance from the treatment group.
- There are choices of the distance metric, each with pros and cons.

Bibliography I

- Greifer, Noah. *Assessing Balance*. <https://cran.r-project.org/web/packages/MatchIt/vignettes/assessing-balance.html#references>. 2022.
- Hill, Jennifer and Elizabeth A. Stuart. "Causal Inference: Overview". In: *International Encyclopedia of the Social Behavioral Sciences (Second Edition)*. Ed. by James D. Wright. Second Edition. Oxford: Elsevier, 2015, pp. 255–260. ISBN: 978-0-08-097087-5.
- Rubin, Donald. "Causal Inference Using Potential Outcomes". In: *Journal of the American Statistical Association* 100.469 (Dec. 2005), pp. 322–331. DOI: 10.1198/016214504000001880.
- Rubin, Donald and Imbens, Guido. "Causal Inference for Statistics, Social, and Biomedical Sciences: An Introduction". In: Cambridge: Cambridge University Press, 2015.

Bibliography II

- Wang, Linbo et al. "Estimation of local treatment effects under the binary instrumental variable model". In: *Biometrika* 108.4 (Feb. 2021), pp. 881–894. ISSN: 0006-3444. DOI: 10.1093/biomet/asab003. eprint: <https://academic.oup.com/biomet/article-pdf/108/4/881/41153672/asab003.pdf>. URL: <https://doi.org/10.1093/biomet/asab003>.