

Matching Continued

INFO/STSCI/ILRST 3900: Causal Inference

3 Oct 2023

Learning goals for today

At the end of class, you will be able to:

1. Understand propensity score matching and coarsened exact matching
2. Use matching methods to estimate causal effects

Matching: so far

Goal: Sample Average Treatment Effect on the Treated

$$E(Y^{a=1} | A = 1) - E(Y^{a=0} | A = 1)$$

Potential Solution: Create a group of untreated individuals, \mathcal{M} , which have a **similar distribution of L** to the treated group

$$\frac{1}{n_m} \sum_{i \in \mathcal{M}} Y_i \approx \frac{1}{n_t} \sum_{i: A_i=1} Y_i^{a=0} \approx E(Y^{a=0} | A = 1)$$

How:

- ▶ Find untreated unit(s) which are similar to each treated unit

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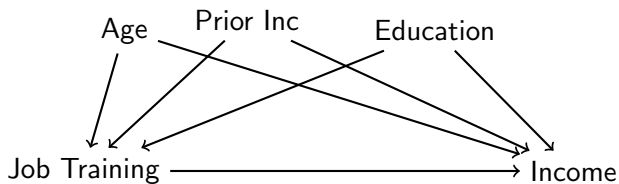
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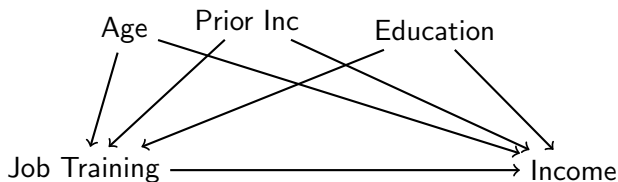
How:

- ▶ Find untreated unit(s) which are similar to each treated unit
- ▶ Define “similar”

A common distance metric: Propensity scores



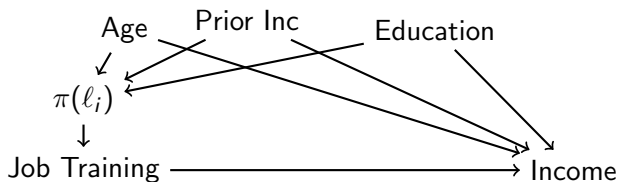
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Suppose \vec{L} only affects A through a probability of treatment

$$\pi_i = \pi(\vec{\ell}_i) = P(A_i = 1 \mid \vec{L} = \vec{\ell})$$

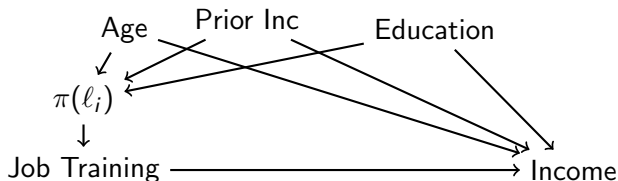
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Conditional exchangeability holds given $\pi(\ell_i)$

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- ▶ Intuitive: Prioritizes covariates that predict treatment
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 - ▶ If our DAG is correct
 - ▶ If our matches are good
 - ▶ We should **on average** get a matched group which looks like the the treatment group

$$P(L \mid \pi_i, A_i = 1) = P(L \mid \pi_i, A_i = 0)$$

A common distance metric: Exact matching

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- ▶ Ideally, we find an exact match for each treated unit

$$d(i, j) = \begin{cases} 0 & \text{if } \vec{L}_i = \vec{L}_j \\ \infty & \text{if } \vec{L}_i \neq \vec{L}_j \end{cases}$$

Often leads to **no matches at all**

A common distance metric: Coarsened exact matching¹

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Multivariate distances: Recap

When matching on multivariate \vec{L} , you have to define the distance between each pair of confounder values $\vec{\ell}_j$ and $\vec{\ell}_i$

- ▶ Manhattan distance
- ▶ Euclidean distance
- ▶ Mahalanobis distance
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There is no right answer! Depends on the setting.

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Evaluate the matched sets

Whatever method, you should check that it worked

- ▶ Compare means of \vec{L} (propensity scores) across groups
- ▶ Possibly compare interaction cells; e.g., race \times age

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- ▶ Compare means of \vec{L} (propensity scores) across groups
- ▶ Possibly compare interaction cells; e.g., race \times age
- ▶ Visually assess distribution

Overlap

- ▶ Lack of overlap may indicate violation of positivity assumption

$$P(A = a \mid L = \ell) > 0 \text{ for all } a$$

- ▶ Ex: Sarah has no MD training. Would Sarah earn more money if she were a surgeon?

$$P(A = \text{Surgeon} \mid \text{No MD}) = 0$$

- ▶ If no good match exists, could be that $P(A = 0 \mid L = \ell) = 0$

Matching: A word of warning²

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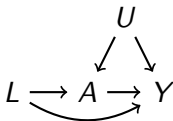


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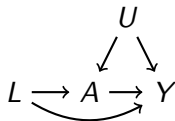


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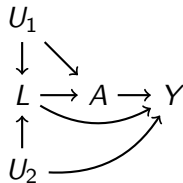
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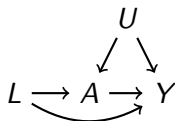
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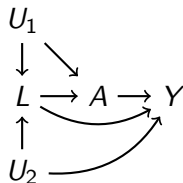
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Matching is an estimation strategy.

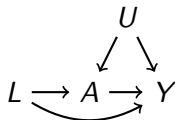
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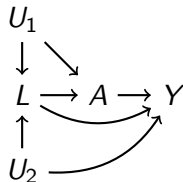
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Matching is an estimation strategy.
It does not solve identification problems.

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Estimating a causal effect

- ▶ If we've matched everything well, we can compare the means

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 - ▶ Combining can reduce bias
 - ▶ Reduces model sensitivity³

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Code

Let's try this out in R!

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