Matching

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Soc 114

Winter 2025

Learning goals for today

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

1. Use matching methods for causal effects
    - Select a matching algorithm
    - Define a distance metric for multivariate matching
    - Evaluate matched sets
2. Reason about choosing regression vs matching

Matching: The big idea

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Goal: Sample Average Treatment Effect on the Treated

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Matching: Estimate $\text{E}(Y \mid A=0, \vec{L}=\vec{\ell}_i)$ from one or more untreated units with $\vec{L}$ "near" $\vec{\ell}_i$

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Matching: Estimate $\mathrm{E}(Y \mid A = 0, \vec{L} = \vec{\ell}_i)$ from one or more untreated units with $\vec{L}$ "near" $\vec{\ell}_i$

Debates: What does it mean to be "near"?

A concrete example

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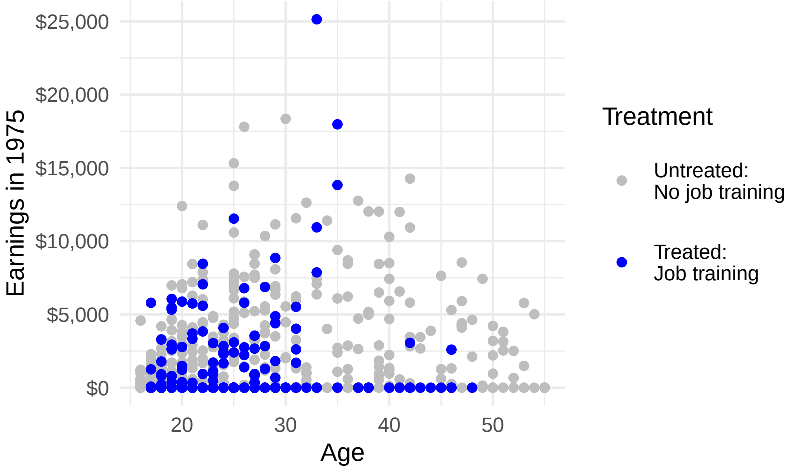
To get the data:

```
install.packages(“MatchIt”)
data(“lalonde”, package = “MatchIt”)
```

A concrete example



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   - We had some treated units
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4. Can assess quality of matches before we look at the outcome
5. Model-free*
   - * but you have to define what makes a match "good"

- Matching overview
    - Matching in univariate settings: Algorithms
    - Matching in multivariate settings: Distance metrics

Matching overview

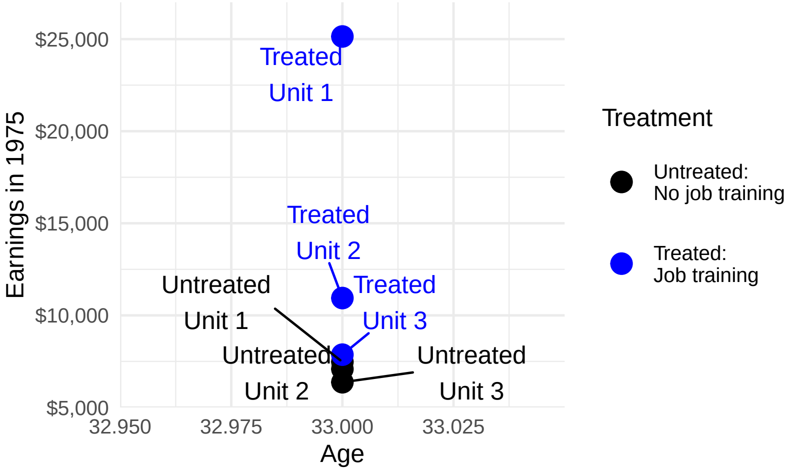
- Matching in univariate settings: Algorithms
- Matching in multivariate settings: Distance metrics

Matching in univariate settings: Algorithms

- Caliper or no caliper
- 1:1 vs k:1
- With replacement vs without replacement
- Greedy vs optimal

Caliper or no caliper matching

Why might I be hesitant to find a match for Treated Unit 1?



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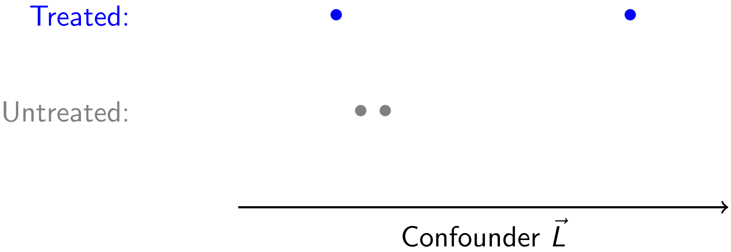
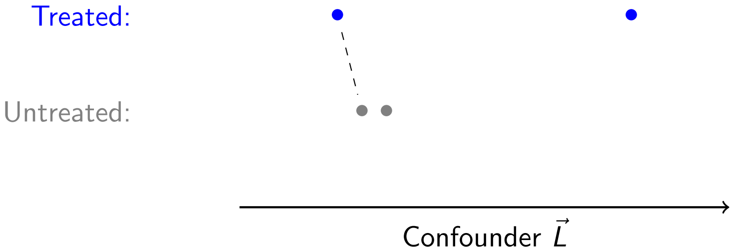


Treated:

Untreated:

Confounder $\vec{L}$

Caliper or no caliper matching



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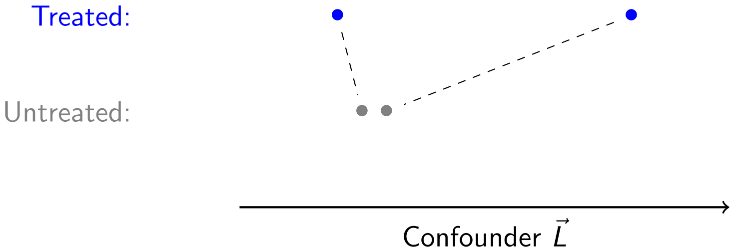

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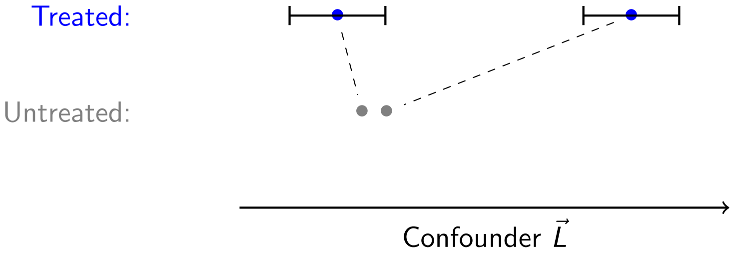

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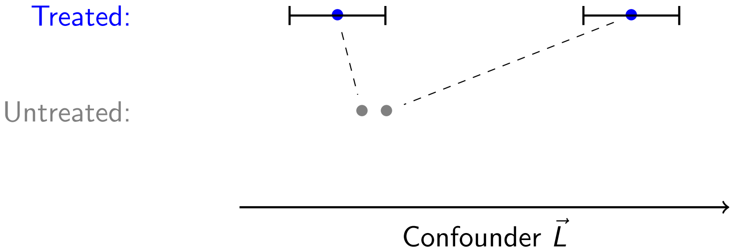
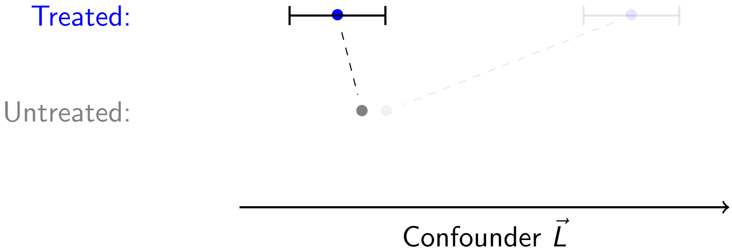


- Caliper: A radius around a treated unit such that we would rather drop the unit than make a match beyond that radius

Caliper or no caliper matching



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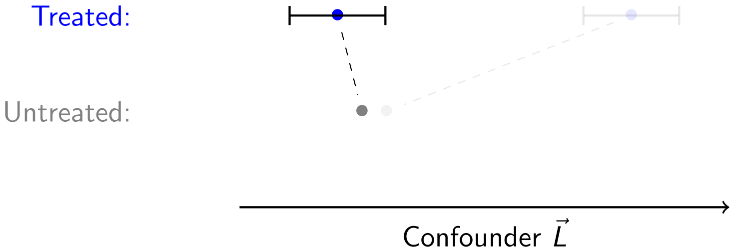
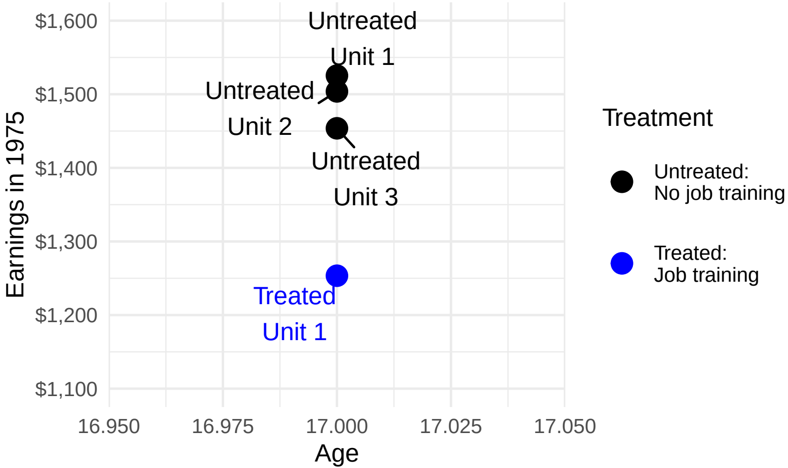


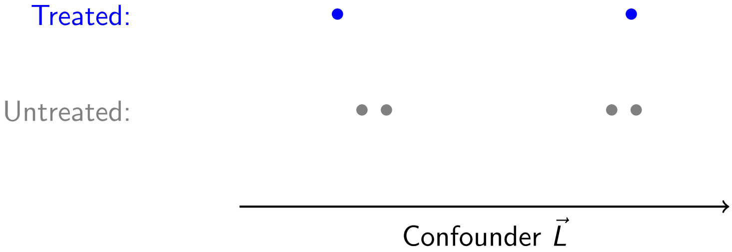
- Caliper: A radius around a treated unit such that we would rather drop the unit than make a match beyond that radius
- Feasible Sample Average Treatment Effect on the Treated (FSATT): Average among treated units for whom an acceptable match exists

1:1 vs *k*:1 matching

Can we make use of Untreated Units 1 and 2?



1:1 vs k:1 matching



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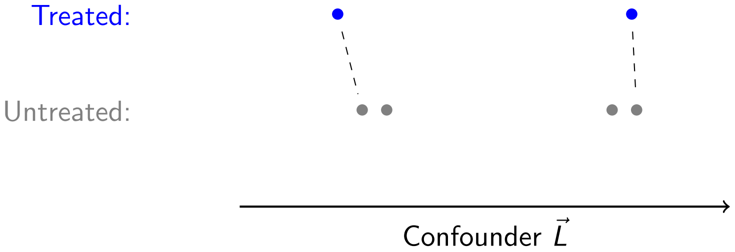
Untreated:

Confounder $\vec{L}$

1:1 vs k:1 matching



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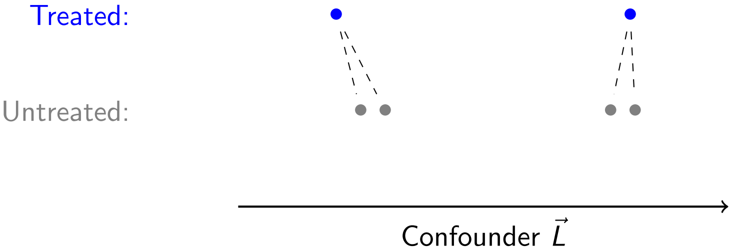

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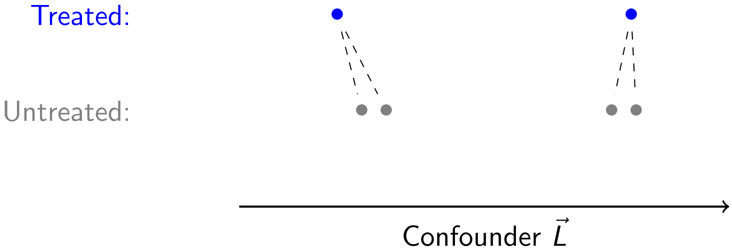
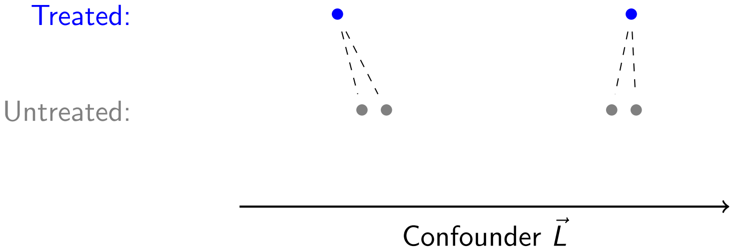


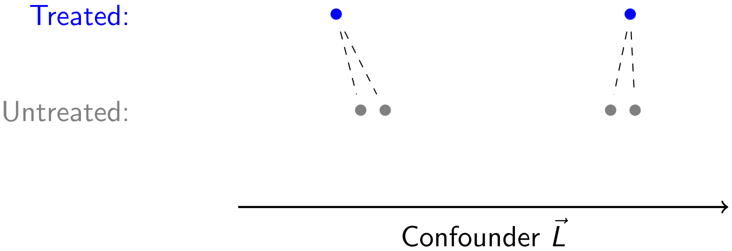
- Benefit of 2:1 matching
- Benefit of 1:1 matching

1:1 vs k:1 matching



- Benefit of 2:1 matching
  - Lower variance. Averaging over more cases.
- Benefit of 1:1 matching

1:1 vs k:1 matching



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- Benefit of 2:1 matching
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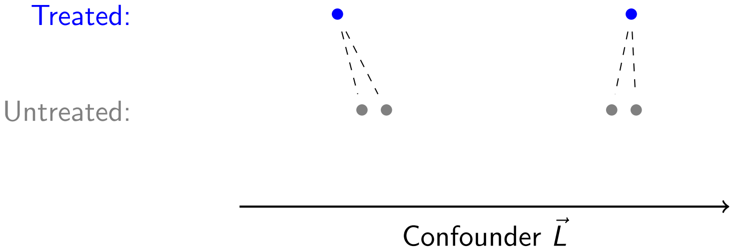
- Benefit of 1:1 matching
    - Lower bias. Only the best matches.

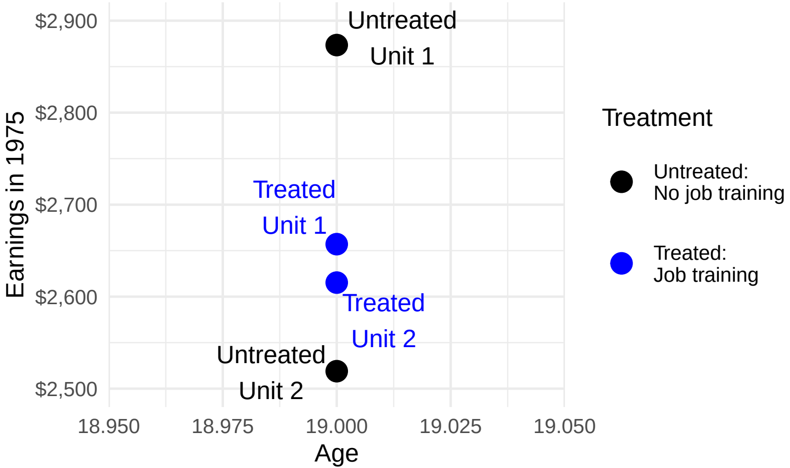
1:1 vs k:1 matching



- Benefit of 2:1 matching
    - Lower variance. Averaging over more cases.
- Benefit of 1:1 matching
    - Lower bias. Only the best matches.
- Greater $k \rightarrow$ lower variance, higher bias

With replacement vs without replacement matching

We match Treated 2 to Untreated 2. Who should be the match for Treated 1?



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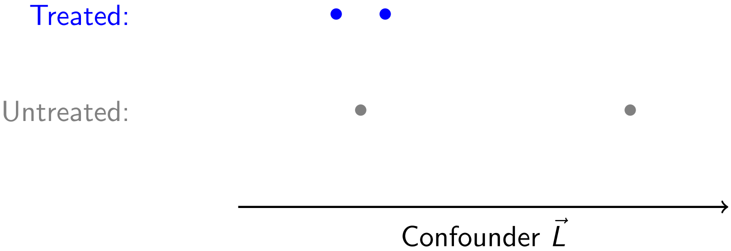

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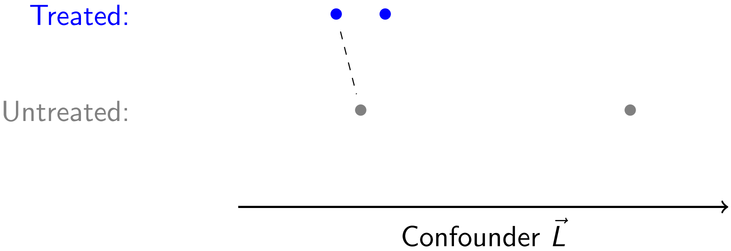

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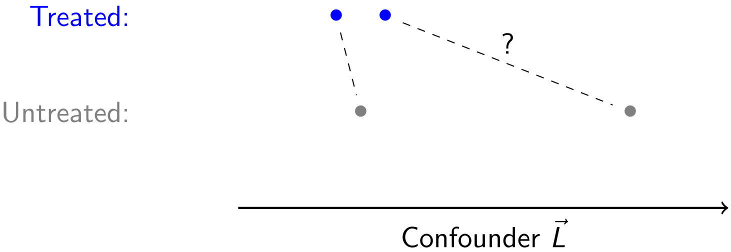

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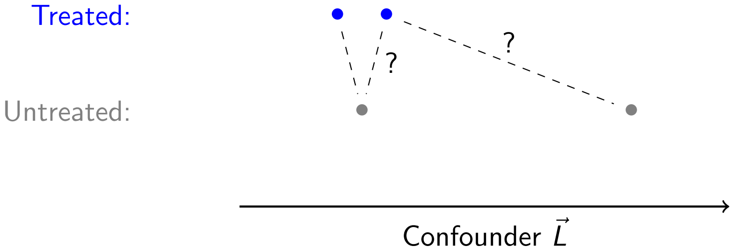

- Benefit of matching without replacement
- Benefit of matching with replacement

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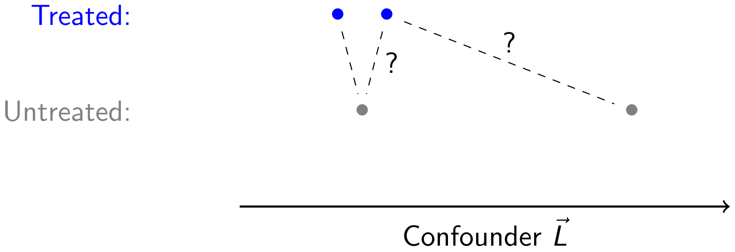

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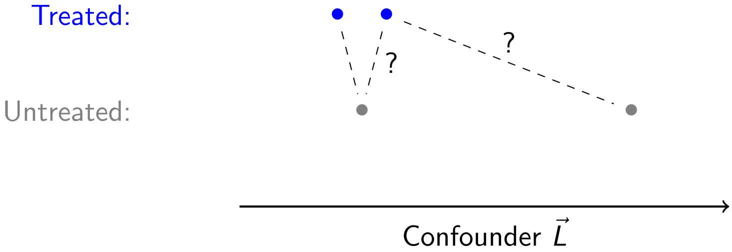
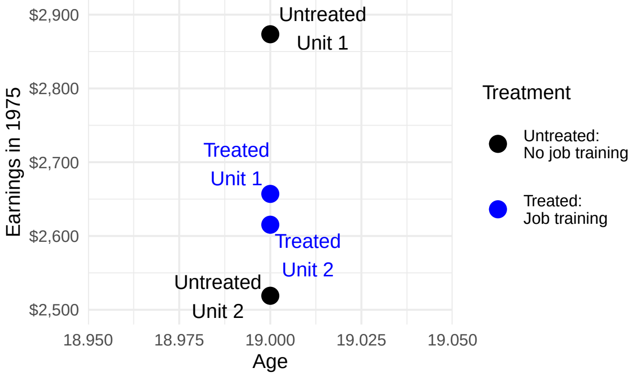


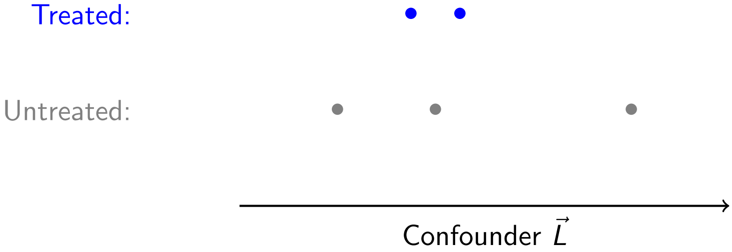
- Benefit of matching without replacement
  - Lower variance. Averaging over more cases.
- Benefit of matching with replacement
  - Lower bias. Better matches.

Greedy vs optimal matching

North side: Start with Treated 1. Find the best match.
South side: Start with Treated 2. Find the best match.
Both sides: Who is left as the match for the other treated unit?



Greedy vs optimal matching[1]



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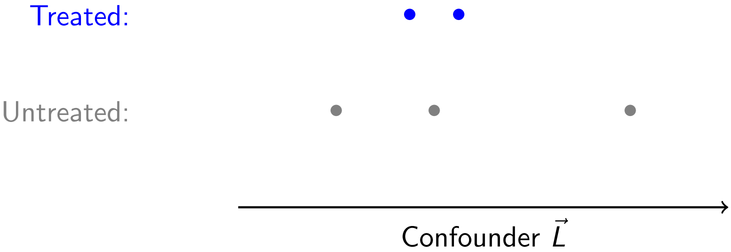
Greedy vs optimal matching[1]

Greedy Matching:
Match sequentially



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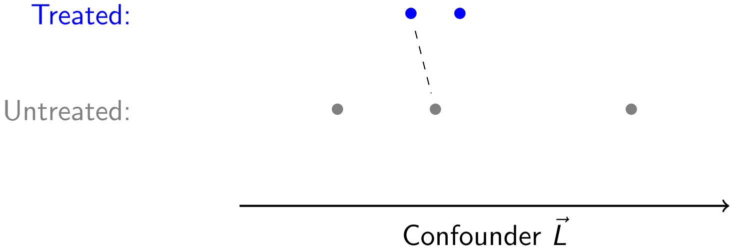

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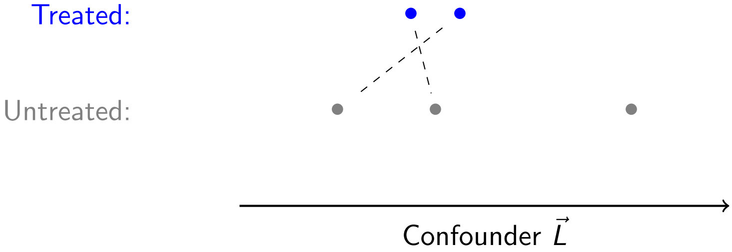

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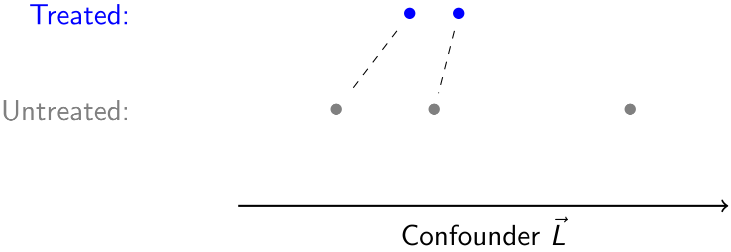
Optimal Matching:
Consider the whole set of matches



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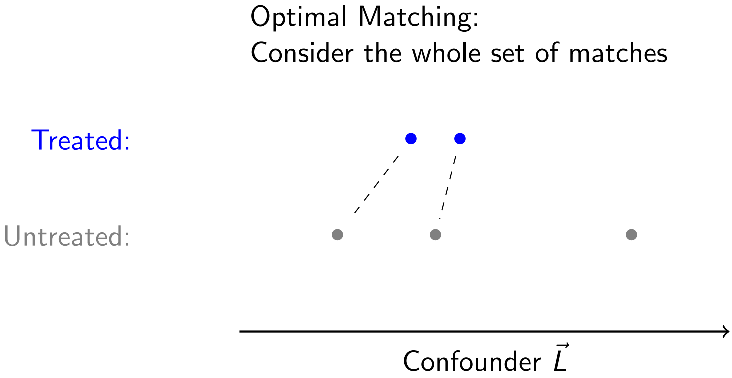

- Optimal is better. Just computationally harder.

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Matching in univariate settings: Algorithms (recap)

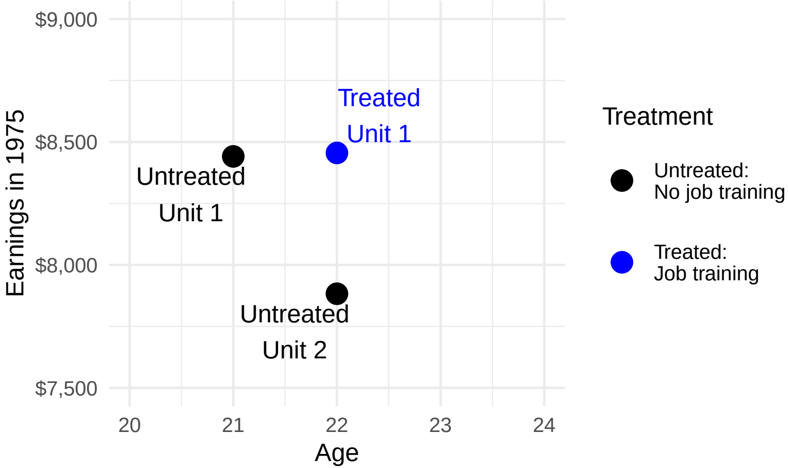
- Caliper or no caliper
- 1:1 vs k:1
- With replacement vs without replacement
- Greedy vs optimal

- Matching overview
  - Matching in univariate settings: Algorithms
  - Matching in multivariate settings: Distance metrics

Matching overview

- Matching in univariate settings: Algorithms
- Matching in multivariate settings: Distance metrics

What if $\vec{L}$ is multivariate?



Key concept: Distance defines who is closer

To find the closest match, we need to define what it means for unit i and j to be **close** to each other.

$$d(\vec{x}_i, \vec{x}_j) = \text{a number}$$

will be the **distance** between confounder vectors $\vec{x}_i$ and $\vec{x}_j$.

Who is closer? Euclidean and Manhattan distance

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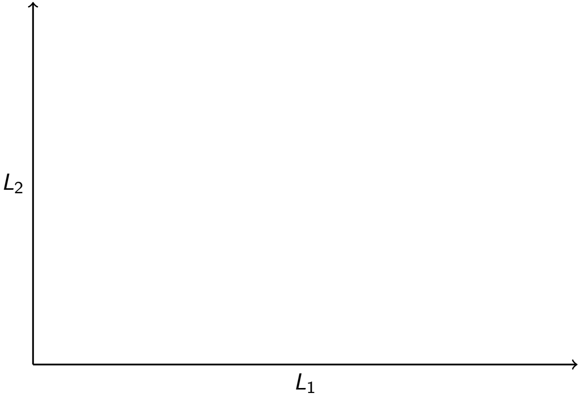

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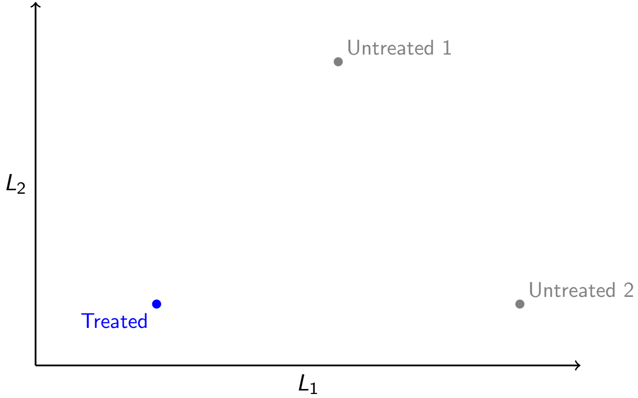

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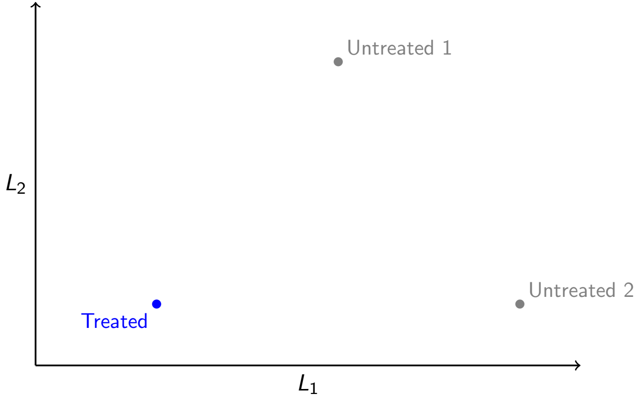
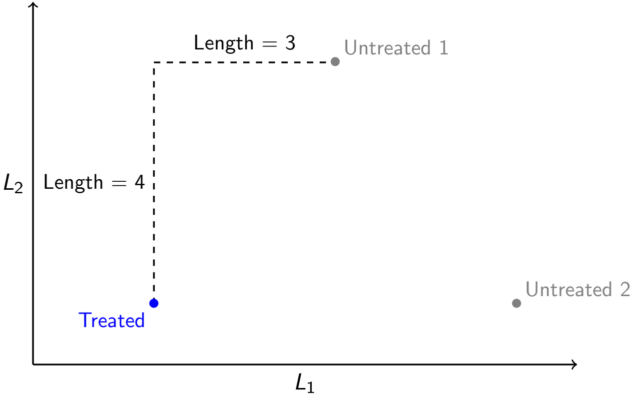


Which untreated unit should be the match?

Who is closer? Euclidean and Manhattan distance



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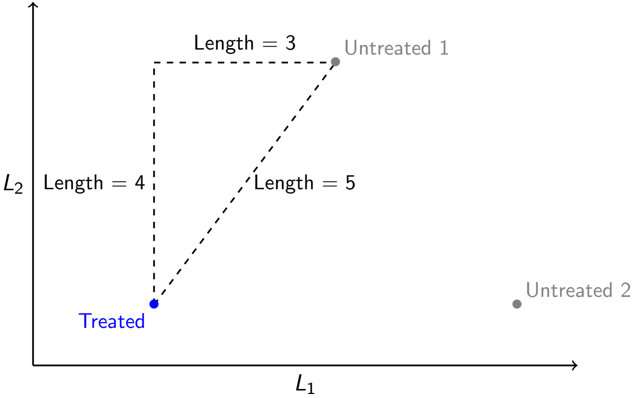

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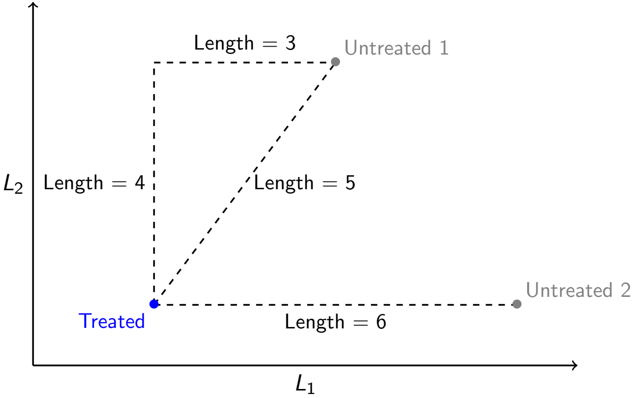

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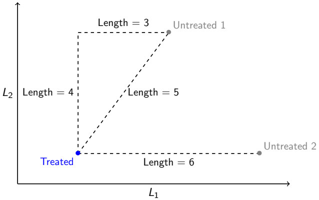

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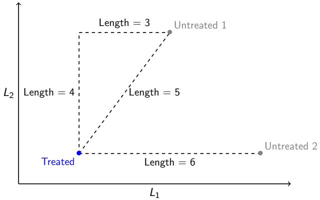

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- Euclidean distance:

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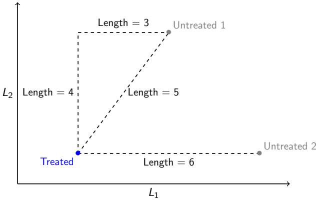

- Manhattan distance: $d(i,j) = \sum_p |L_{pi} - L_{pj}|$

- Euclidean distance:

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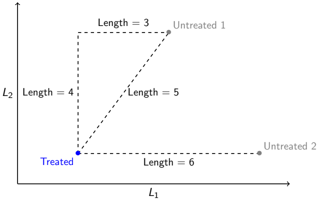

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  - $d(\text{Treated, Untreated 1}) = 3 + 4 = 7$
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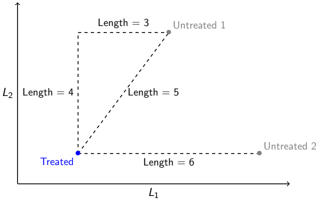
- Euclidean distance:

Who is closer? Euclidean and Manhattan distance



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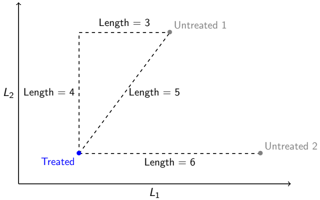

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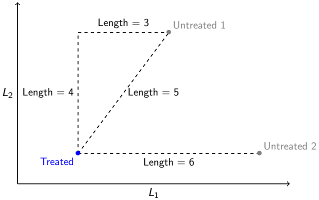

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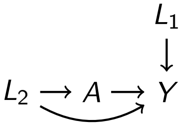
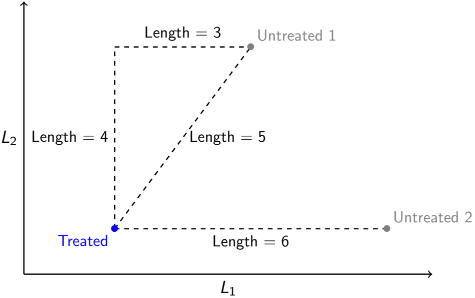
- It depends on the distance metric!

A common distance metric: Propensity scores

Now suppose only L_2 is related to treatment.



Which match do you pick?



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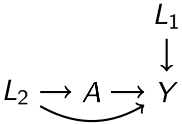
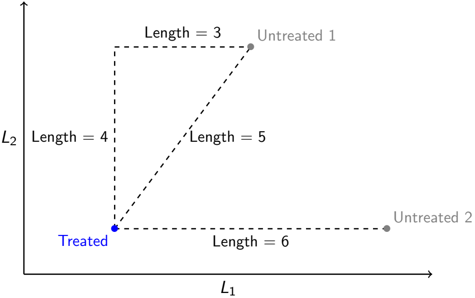


Which match do you pick? Untreated 2! Perfect match.



A common distance metric: Propensity scores

Propensity score: $\pi_i = \mathrm{P}(A = 1 \mid \vec{L} = \vec{\ell}_i)$

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[2] Rosenbaum, P. R., & Rubin, D. B. (1983). The central role of the propensity score in observational studies for causal effects. Biometrika, 70(1), 41-55.

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- Univariate summary of all confounders
- In expectation, a sample balanced on π is balanced on $\vec{L}$
  - Rosenbaum & Rubin theorem[2]

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Propensity score distance for matching:

$$d(i,j) = |\hat{\pi}_i - \hat{\pi}_j|$$

Workflow for matching

- Draw a DAG
- Select a sufficient adjustment set $\vec{X}$
- Define a distance: how far apart $\vec{x}_i$ and $\vec{x}_j$ are
- Choose a matching algorithm
  - 1:1 without replacement, greedy
- Conduct matching
- Estimate ATE by outcome modeling on the matched set

The **MatchIt** package makes it easy

Discuss: Why regression? Why matching?

Learning goals for today

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

1. Use matching methods for causal effects
    - Select a matching algorithm
    - Define a distance metric for multivariate matching
    - Evaluate matched sets
2. Reason about choosing regression vs matching