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

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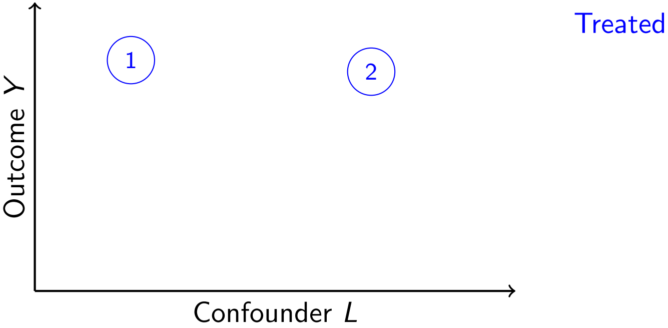
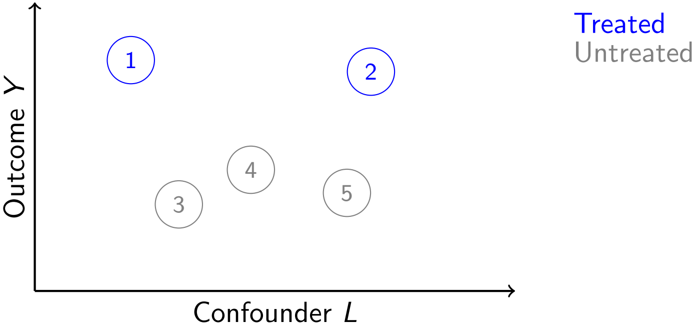
Debates: What does it mean to be "near"?

Matching: The big idea



You have a some treated units.

Matching: The big idea



You go find some untreated units.

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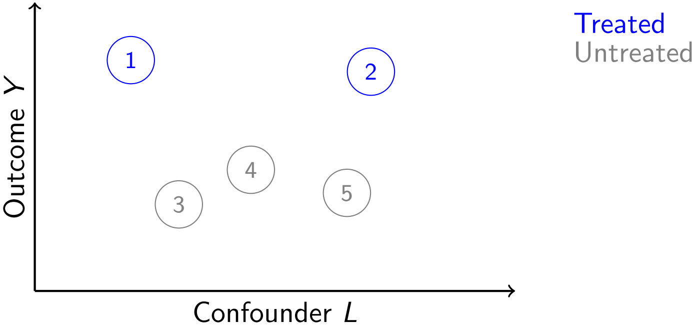
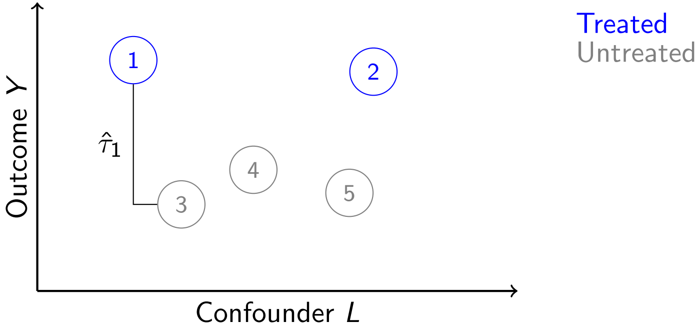


You find the closest matches along L.
You estimate each effect.

Matching: The big idea



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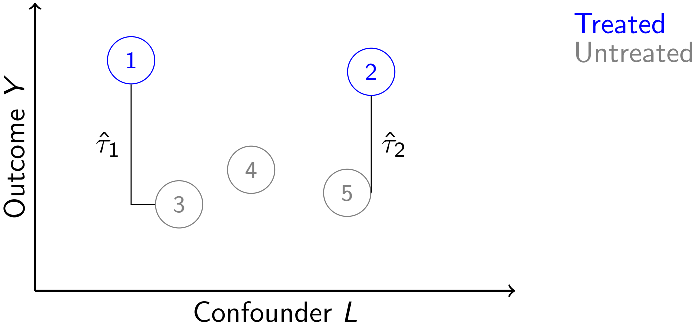

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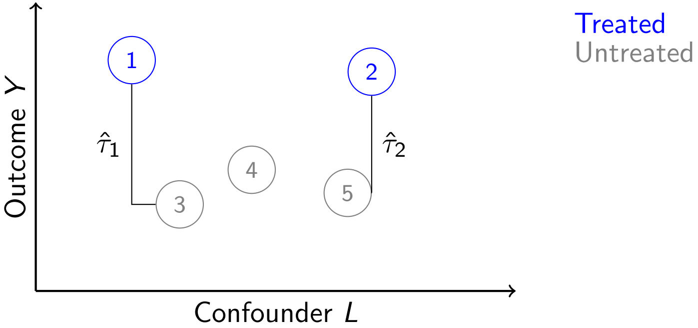

$\widehat{\text{SATT}} = \frac{1}{2}(\hat{\tau}_1 + \hat{\tau}_2)$

(Sample Average Treatment Effect on the Treated)

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5. Model-free*
   - * but you have to define what makes a match "good"

Matching: A word of warning[1]

[1] Sekhon, J. S. (2009). Opiates for the matches: Matching methods for causal inference. Annual Review of Political Science, 12(1), 487-508.

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Matching is an estimation strategy.
It does not solve identification problems.
Matching is only as good as your DAG!

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Matching overview

- Matching in univariate settings: Algorithms
- Matching in multivariate settings: Distance metrics
- After matching: Evaluate matched sets

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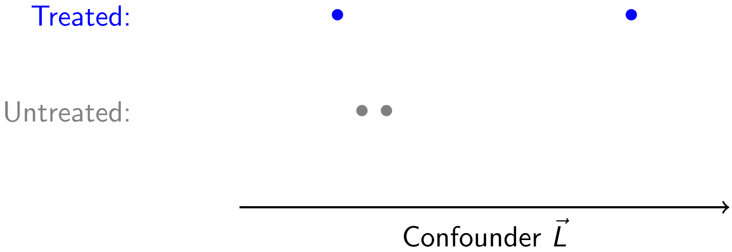
Matching in univariate settings: Algorithms

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

Caliper or no caliper matching



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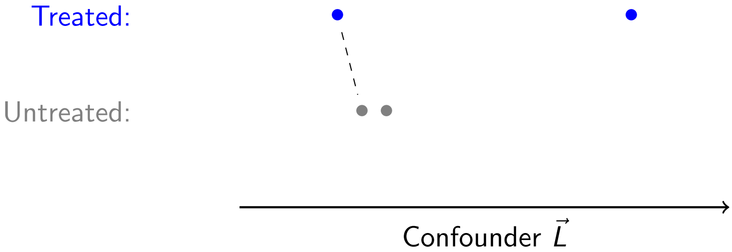

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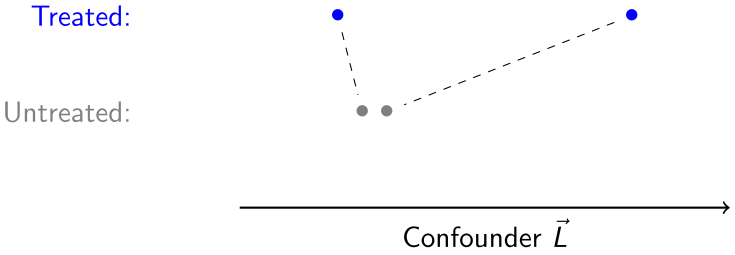

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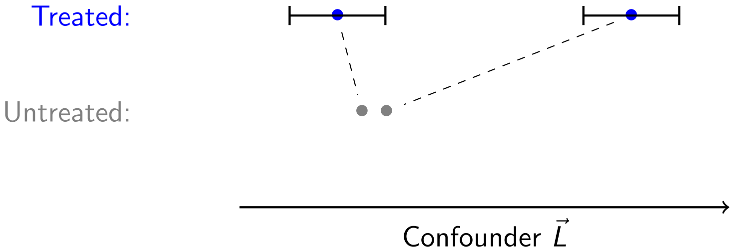

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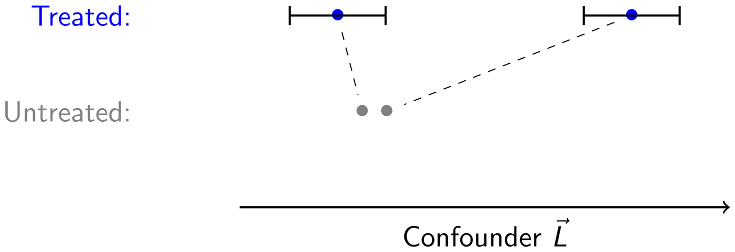

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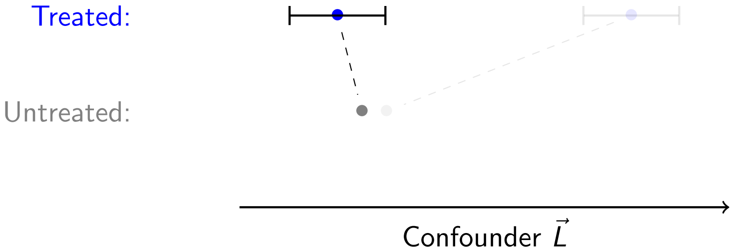

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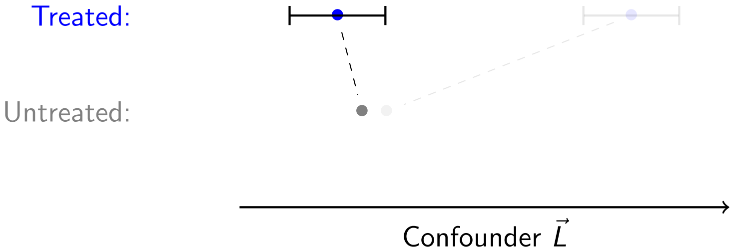
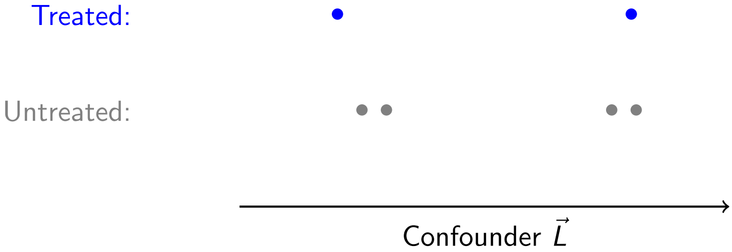


- Caliper: A radius around a treated unit such that we would rather drop the unit than make a match beyond that radius
- Feasible Sample Average Treatment Effect on the Treated (FSATT): Average among treated units for whom an acceptable match exists

1:1 vs k:1 matching



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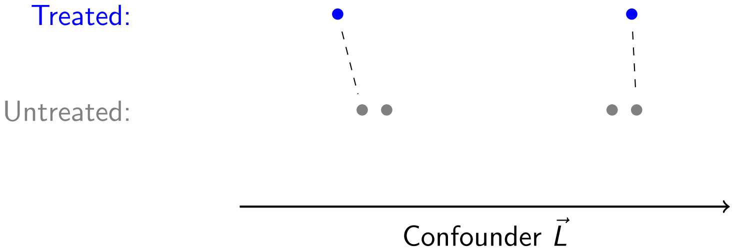

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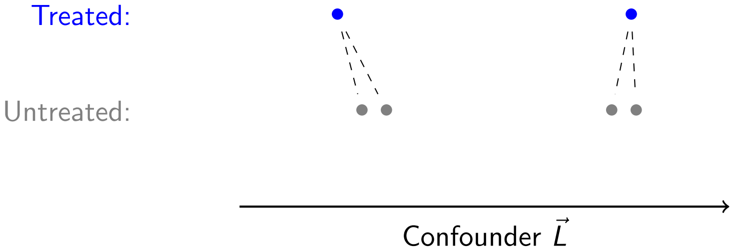

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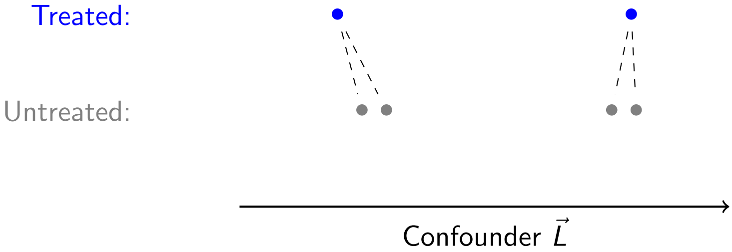

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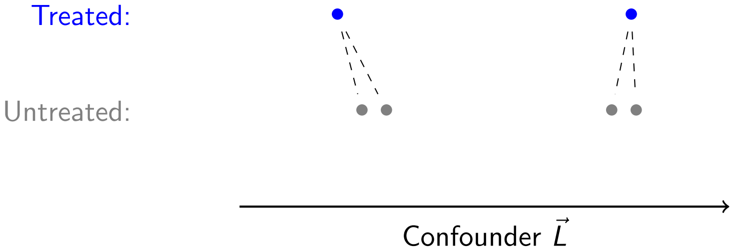

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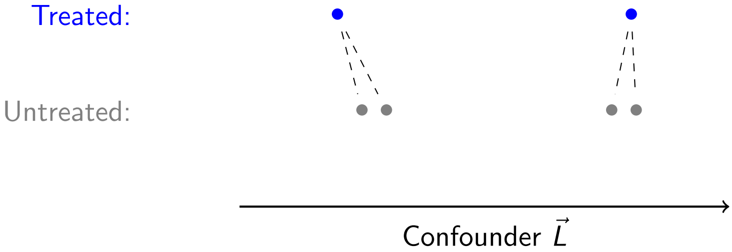

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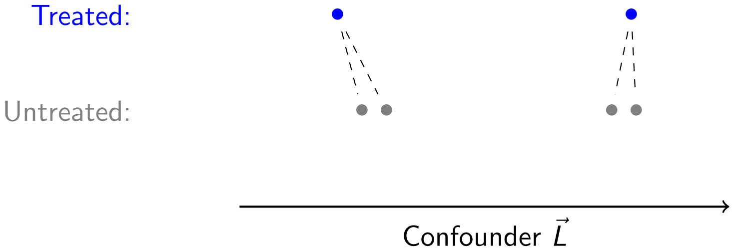

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- Benefit of 1:1 matching
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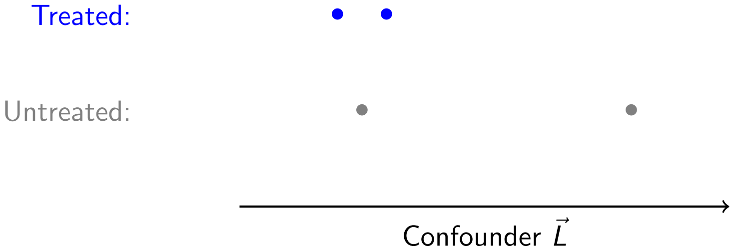
- Greater $k \rightarrow$ lower variance, higher bias

With replacement vs without replacement matching



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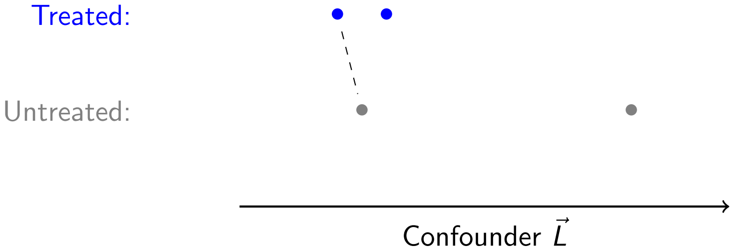

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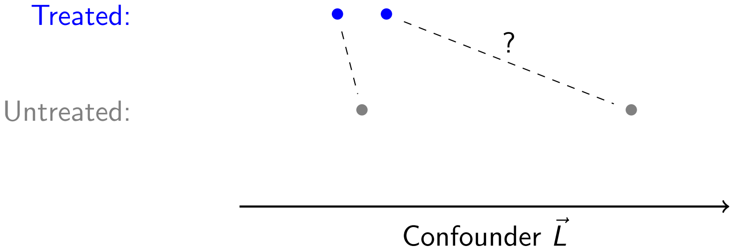

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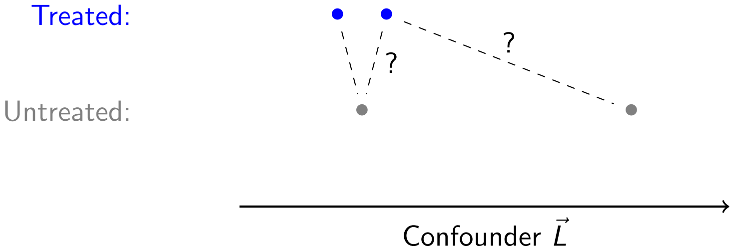

- Benefit of matching without replacement
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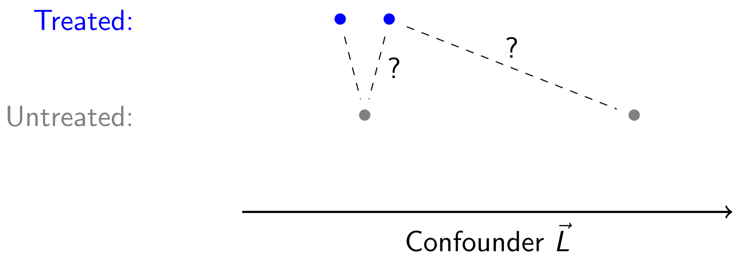

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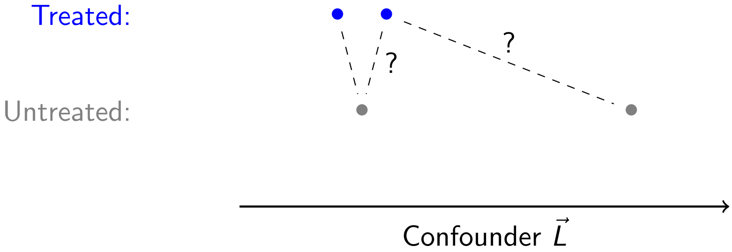
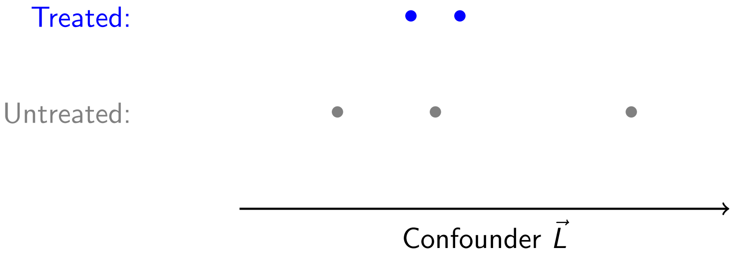


- Benefit of matching without replacement
  - Lower variance. Averaging over more cases.
- Benefit of matching with replacement
  - Lower bias. Better matches.

Greedy vs optimal matching[2]



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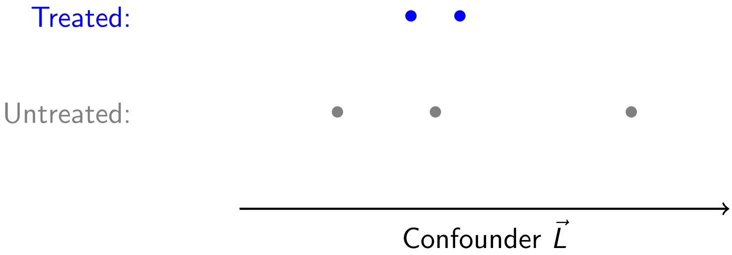
Greedy vs optimal matching[2]

Greedy Matching:
Match sequentially



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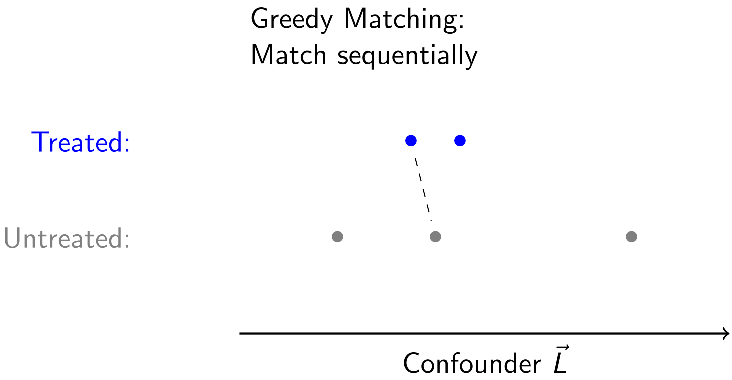

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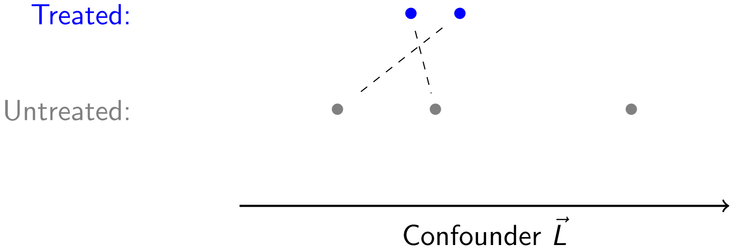

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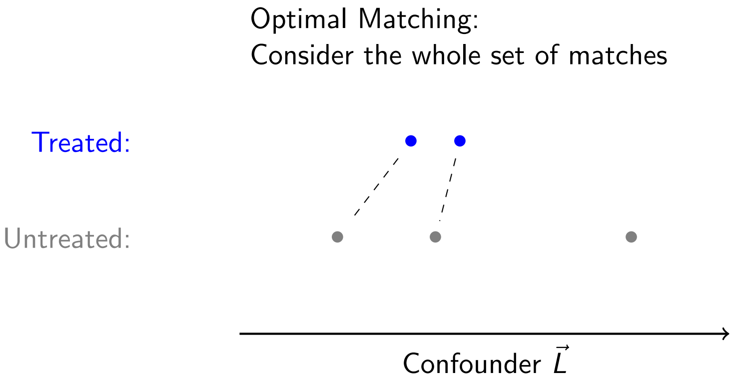

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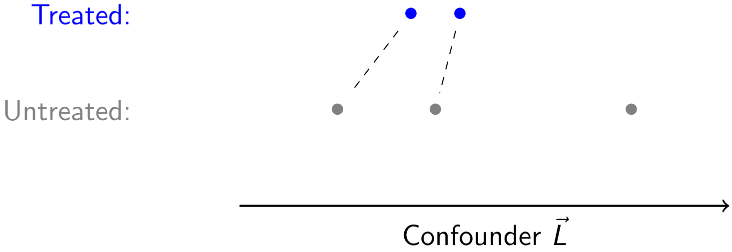
Optimal Matching:
Consider the whole set of matches



- Optimal is better. Just computationally harder.

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Matching in univariate settings: Algorithms (recap)

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- 1:1 vs k:1
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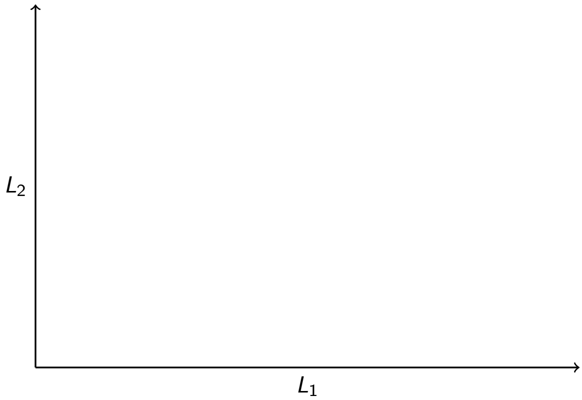

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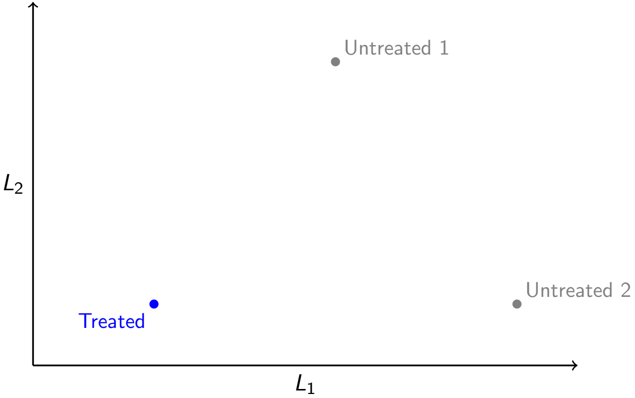

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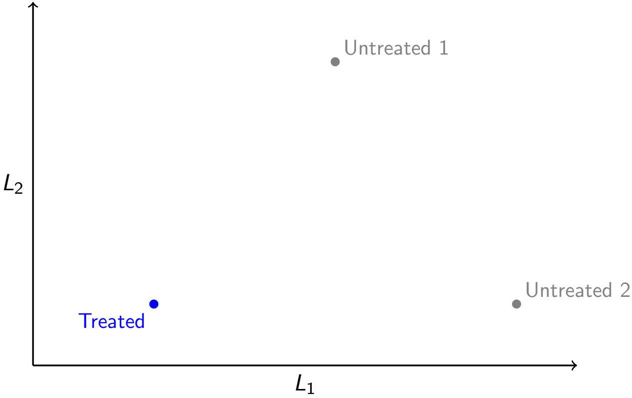

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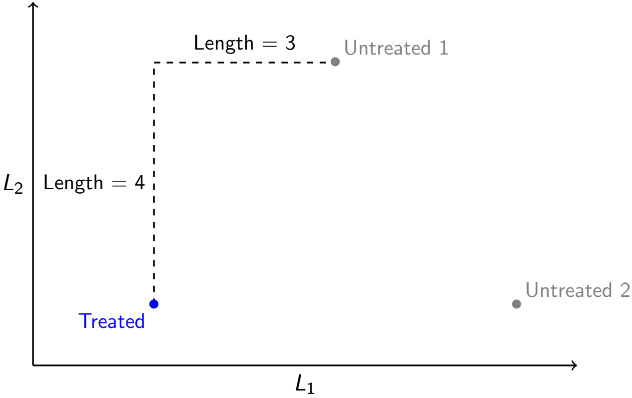

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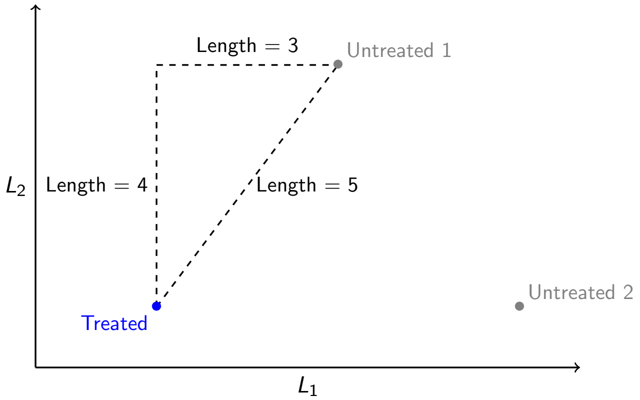

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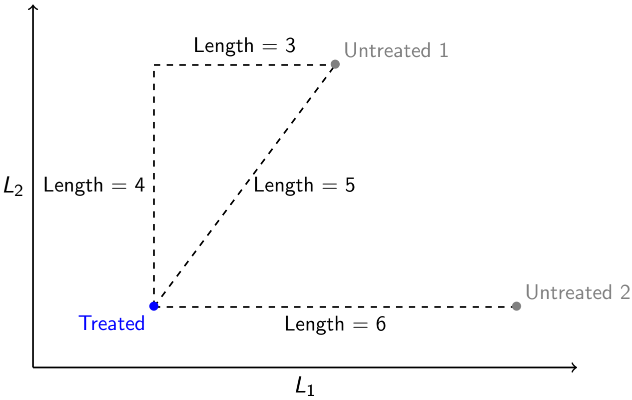

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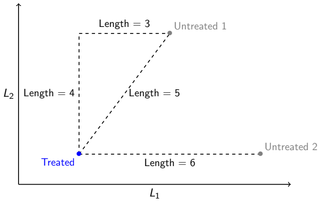

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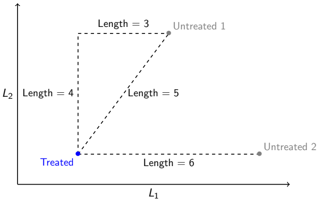

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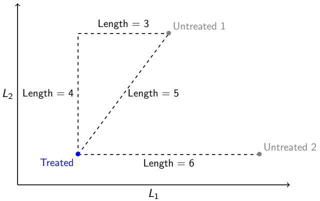

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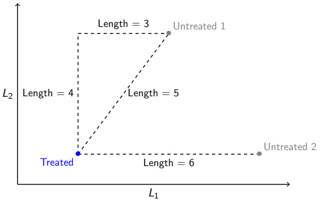

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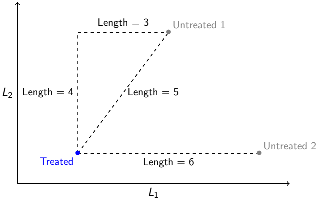

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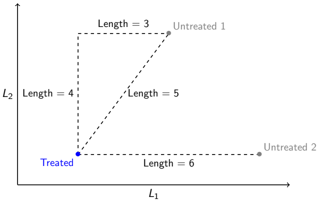

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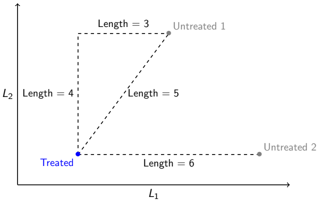

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- It depends on the distance metric!

A common distance metric: Mahalanobis distance

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Motivated by two principles

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$$d(i,j) = \sqrt{\left(\vec{L}_i - \vec{L}_j\right)^T \Sigma^{-1} \left(\vec{L}_i - \vec{L}_j\right)}$$

where $\Sigma = \text{V}(\vec{L})$, the variance-covariance matrix

A common distance metric: Exact matching

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- Equivalent to nonparametric stratification

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- Equivalent to nonparametric stratification
- Infinite distance if any confounder is different!

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

Often leads to **no matches at all**

A common distance metric: Coarsened exact matching[3]

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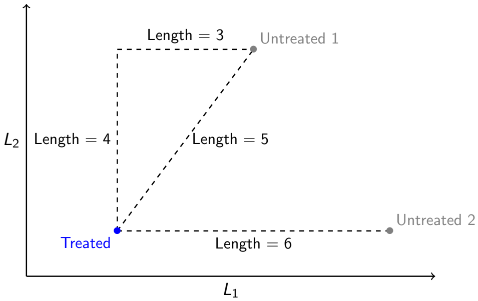
A common distance metric: Propensity scores



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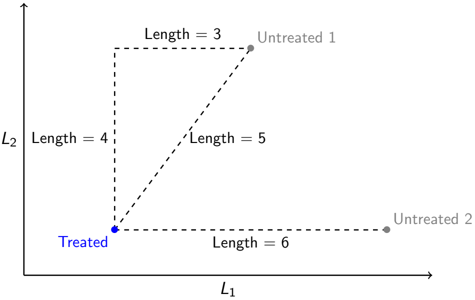

Now suppose only L_2 is related to treatment. L_1 doesn't matter.

$$\begin{tikzcd}
 & & L_1 \arrow[d] \\
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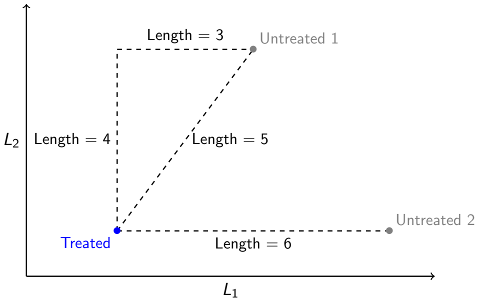

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Which match do you pick?

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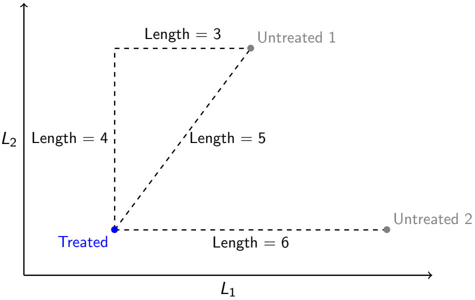

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Which match do you pick? Untreated 2! Perfect match.

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

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- Univariate summary of all confounders
- In expectation, a sample balanced on π is balanced on $\vec{L}$
  - Rosenbaum & Rubin theorem[4]

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Propensity score distance for matching:

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

Why propensity scores are nice

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- Mathematical guarantees in expectation
- Intuitive: Prioritizes covariates that predict treatment

Multivariate distances: Recap

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

- Manhattan distance
- Euclidean distanace
- Mahalanobis distance
- Exact distance
- Coarsened exact distance
- Propensity score distance

There is no right answer! Depends on the setting.

Matching overview
- Matching in univariate settings: Algorithms
- Matching in multivariate settings: Distance metrics
- After matching: Evaluate matched sets

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Evaluate the matched sets

Why we match: So $\vec{L}$ follows a similar distribution

- in the treated sample
- in the untreated sample

Whatever method, you should check that.

- Compare means of $\vec{L}$ across groups
- Possibly compare interactive cells
- Ideally, before looking at Y!

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