

STA 235H - Introduction to Observational Studies I

Fall 2021

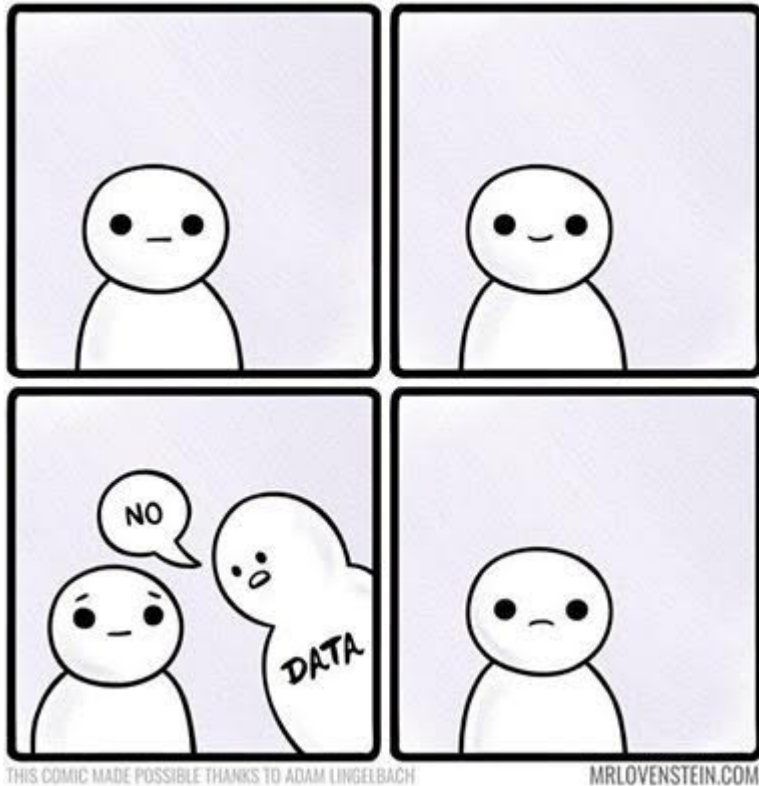
McCombs School of Business, UT Austin

What we just saw...

- **Randomized controlled trials**
 - Why is it considered the gold standard?
 - How to analyze an RCT in practice?
 - Assumptions and limitations.



Now, we're moving forward...



- **Introduction to Observational Studies:**
 - Can we identify causal effects without RCTs?
 - Assumptions
 - Matching vs OLS

No more chance[s]

Introduction to observational studies

- Most times, we will not be able to randomize, and we need to work with **existing data**

Observational data

- Data for which we can't manipulate the treatment assignment, e.g. data in its "natural state".

Can we reasonably assume that the ignorability assumption holds?

Introduction to observational studies (cont.)



- Moving away from the core assumption of RCTs: that **"the probability of treatment assignment is a known function"** (Imbens & Rubin, 2015).

Introduction to observational studies (cont.)



- Moving away from the core assumption of RCTs: that **"the probability of treatment assignment is a known function"** (Imbens & Rubin, 2015).
- We will maintain the assumption of **unconfoundedness** (to a certain extent).

What is that?

Calling in the CIA

- **Unconfoundedness** means that the treatment assignment is independent from the potential outcomes.
- If you recall, the ignorability assumption assumes that:

$$Y(0), Y(1) \perp\!\!\!\perp Z$$

- What if you could assume that this holds **conditional on some covariates**?

Conditional Independence Assumption (CIA)

$$Y(0), Y(1) \perp\!\!\!\perp Z | X$$

The assignment mechanism

- **Key component** in causal analysis:
 - In RCTs, **assignment mechanism** is *known*.
 - But in **observational studies**?



Selection on observables

- Units select into treatment based on characteristics I can observe.



$$\begin{aligned}(Y_1(0), Y_1(1)) \\ Z = 1 \\ Y = y_1 \\ \mathbf{X} = \mathbf{X}_F\end{aligned}$$



$$\begin{aligned}(Y_2(0), Y_2(1)) \\ Z = 0 \\ Y = y_2 \\ \mathbf{X} = \mathbf{X}_F\end{aligned}$$

How do we adjust for observables?

- One way we have seen so far is **regression adjustment**

$$Y_i = \beta_0 + \beta_1 Z_i + \beta_2 X_i + \varepsilon_i$$

Under unconfoundedness, how would we interpret β_1 ?

How do we adjust for observables?

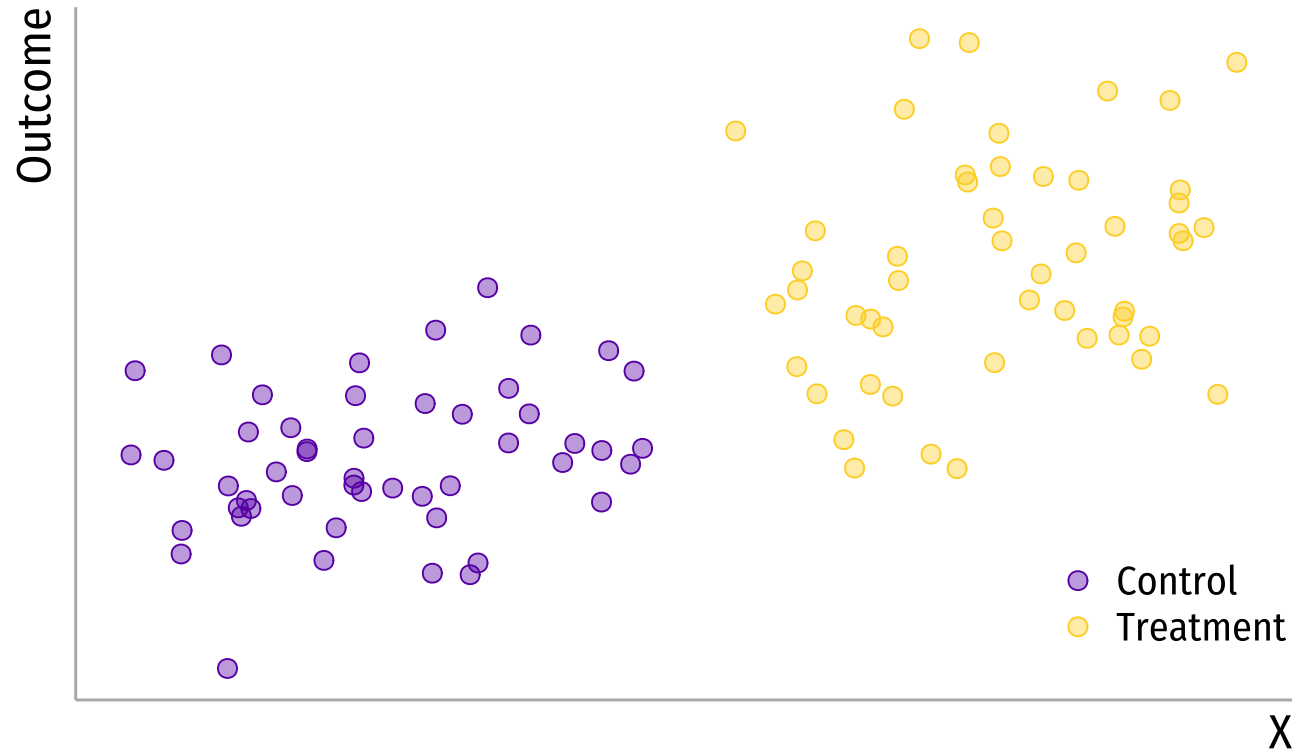
- One way we have seen so far is **regression adjustment**

$$Y_i = \beta_0 + \beta_1 Z_i + \beta_2 X_i + \varepsilon_i$$

β_1 is the effect of Z on Y, holding X constant

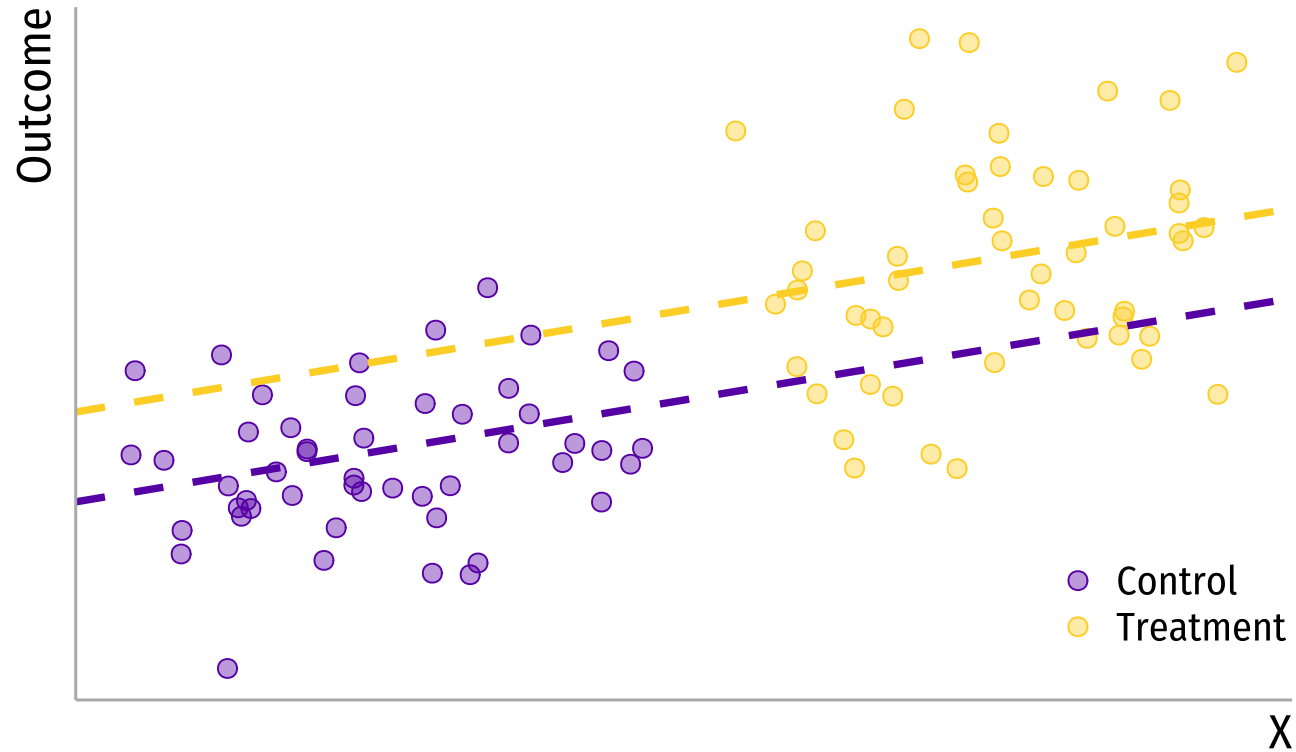
How do we adjust for observables?

- But what if our data looks like this? Do you see a problem?



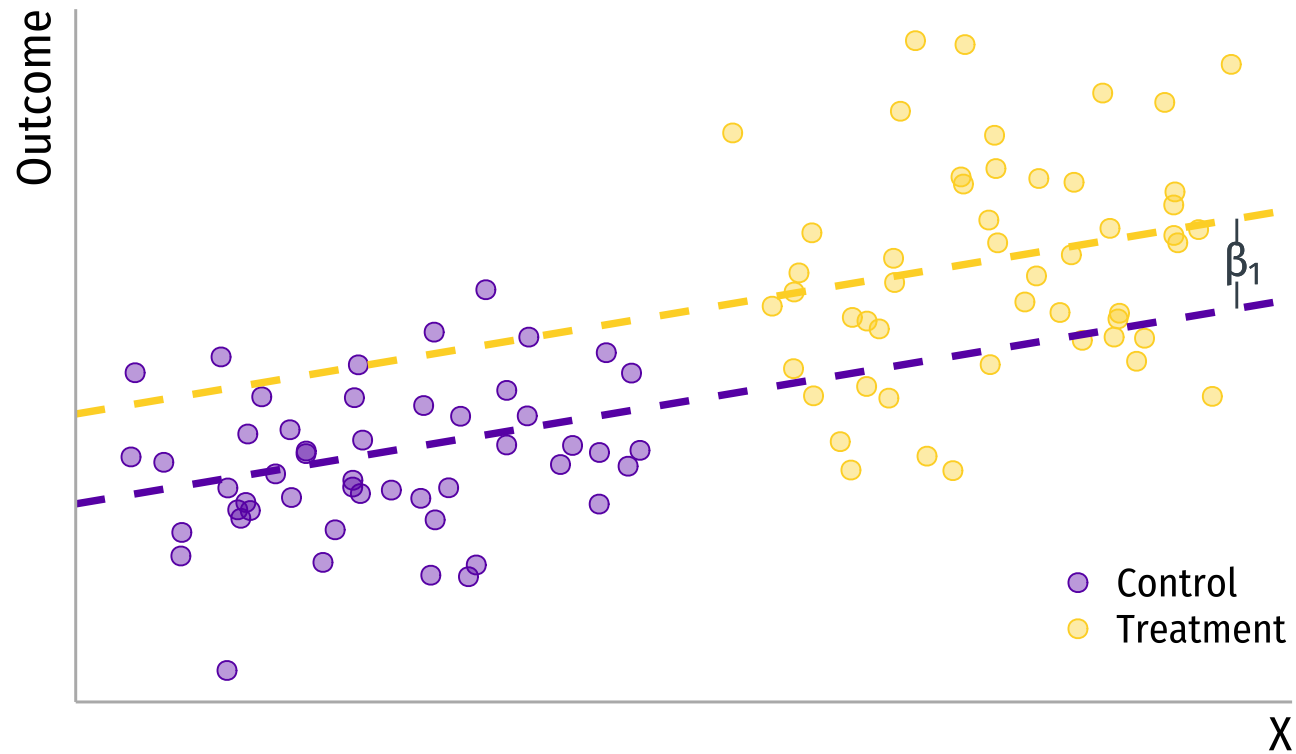
How do we adjust for observables?

- But what if our data looks like this? Do you see a problem?



How do we adjust for observables?

- But what if our data looks like this? Do you see a problem?



Finding your perfect match...

Two peas in a pod

- One other route we could take is to **find similar units** in our sample and **group them together**.
- There are different ways to do it:
 - E.g. subclassification, matching.

.pull-right[



Two peas in a pod

- One other route we could take is to **find similar units** in our sample and **group them together**.
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What do we gain?



Advantages of matching methods

Reduce model dependence

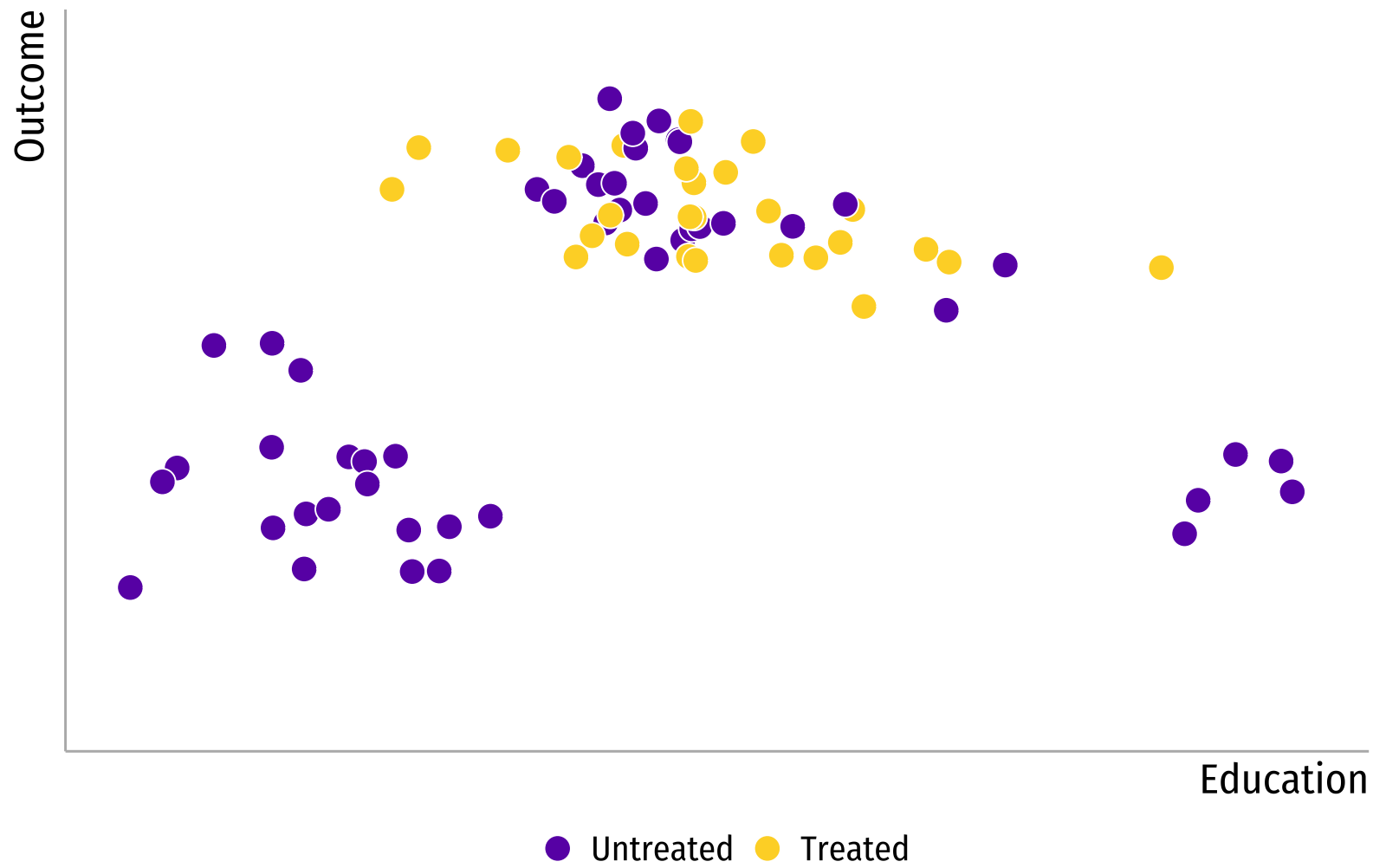
Imbalance → model dependence → researcher discretion → bias

Compare like to like

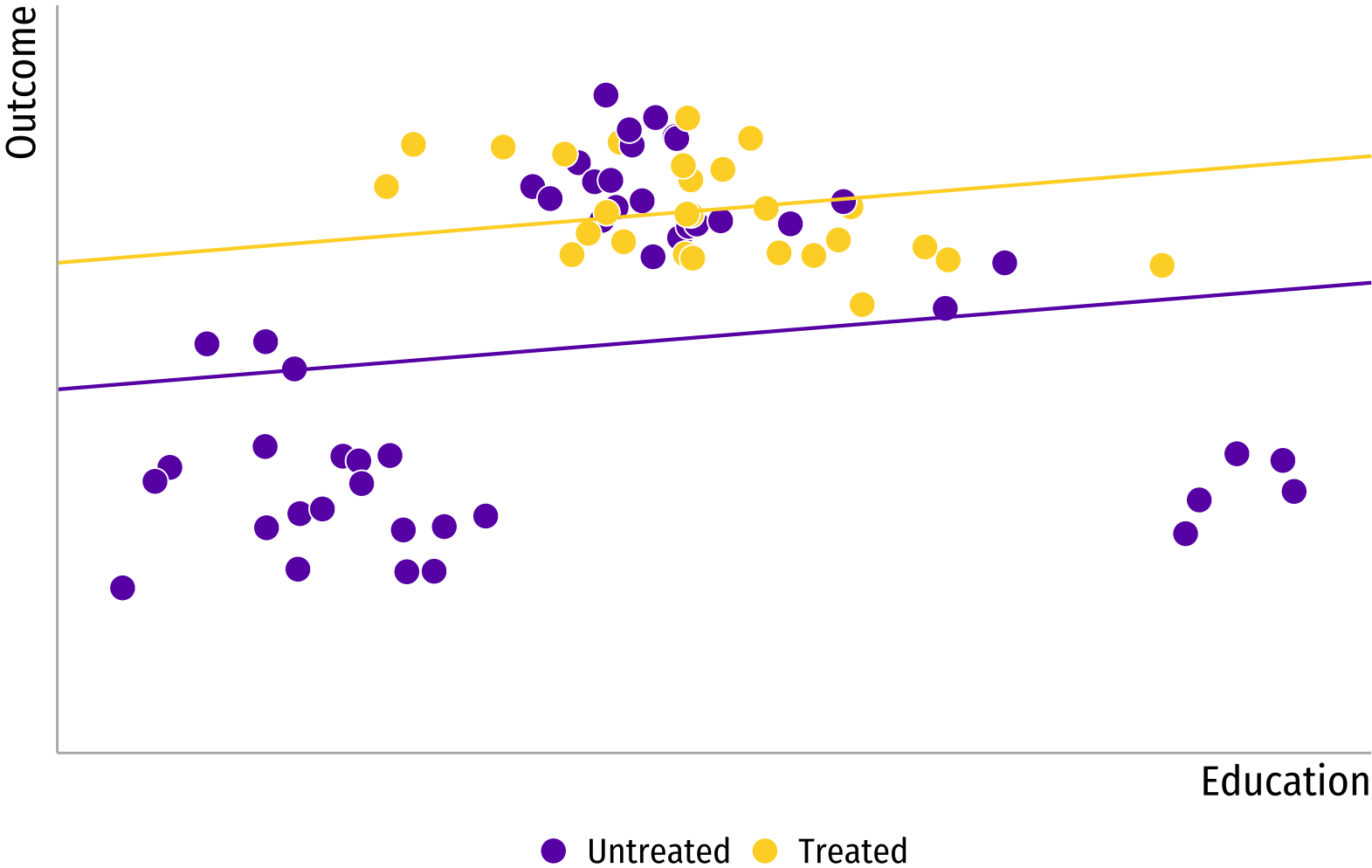
No extrapolation!

Can adjust closely by covariates

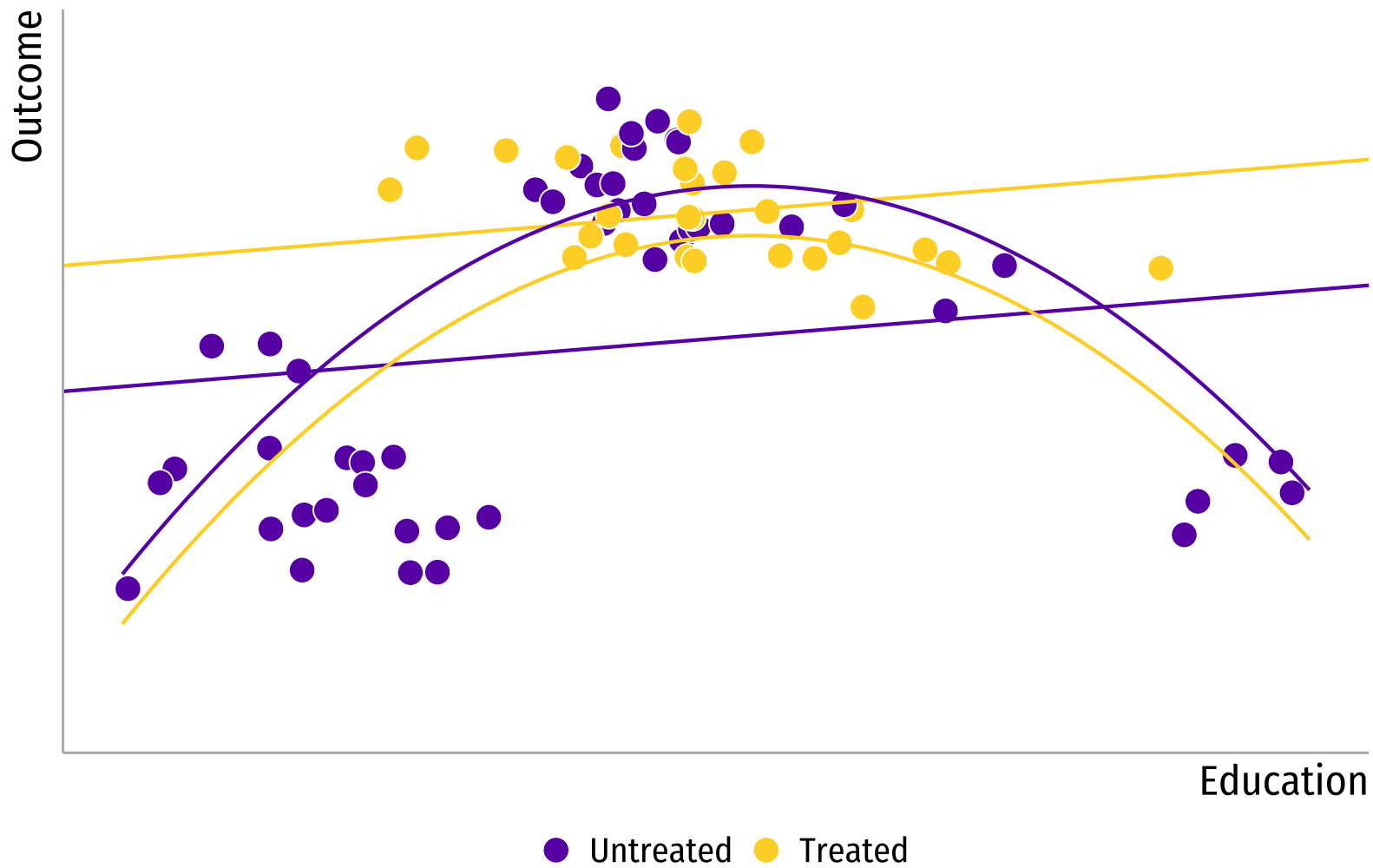
Exact matching, coarsened exact matching, fine balance..

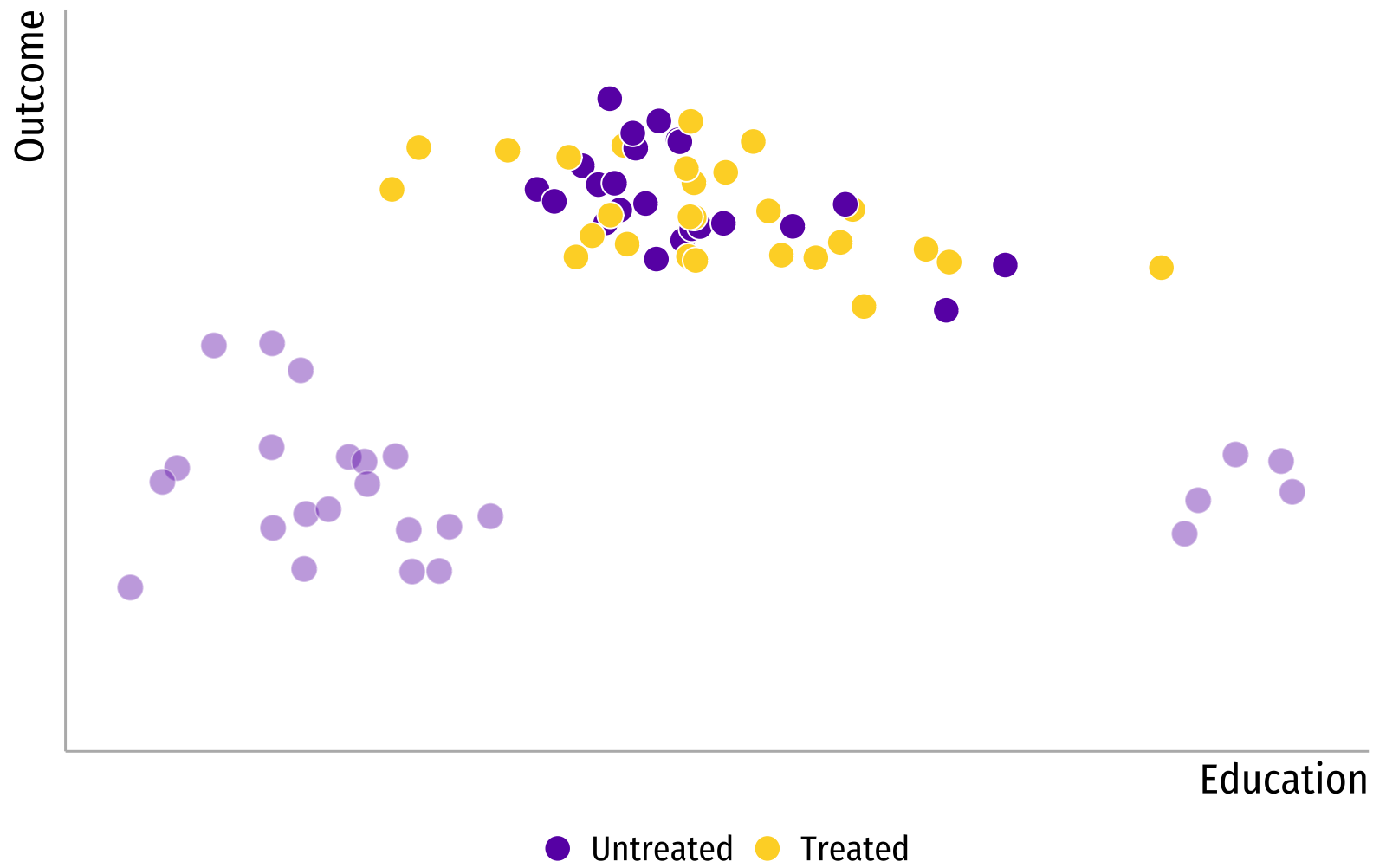


$$\text{Outcome} = \beta_0 + \beta_1 \text{Education} + \beta_2 \text{Treatment}$$

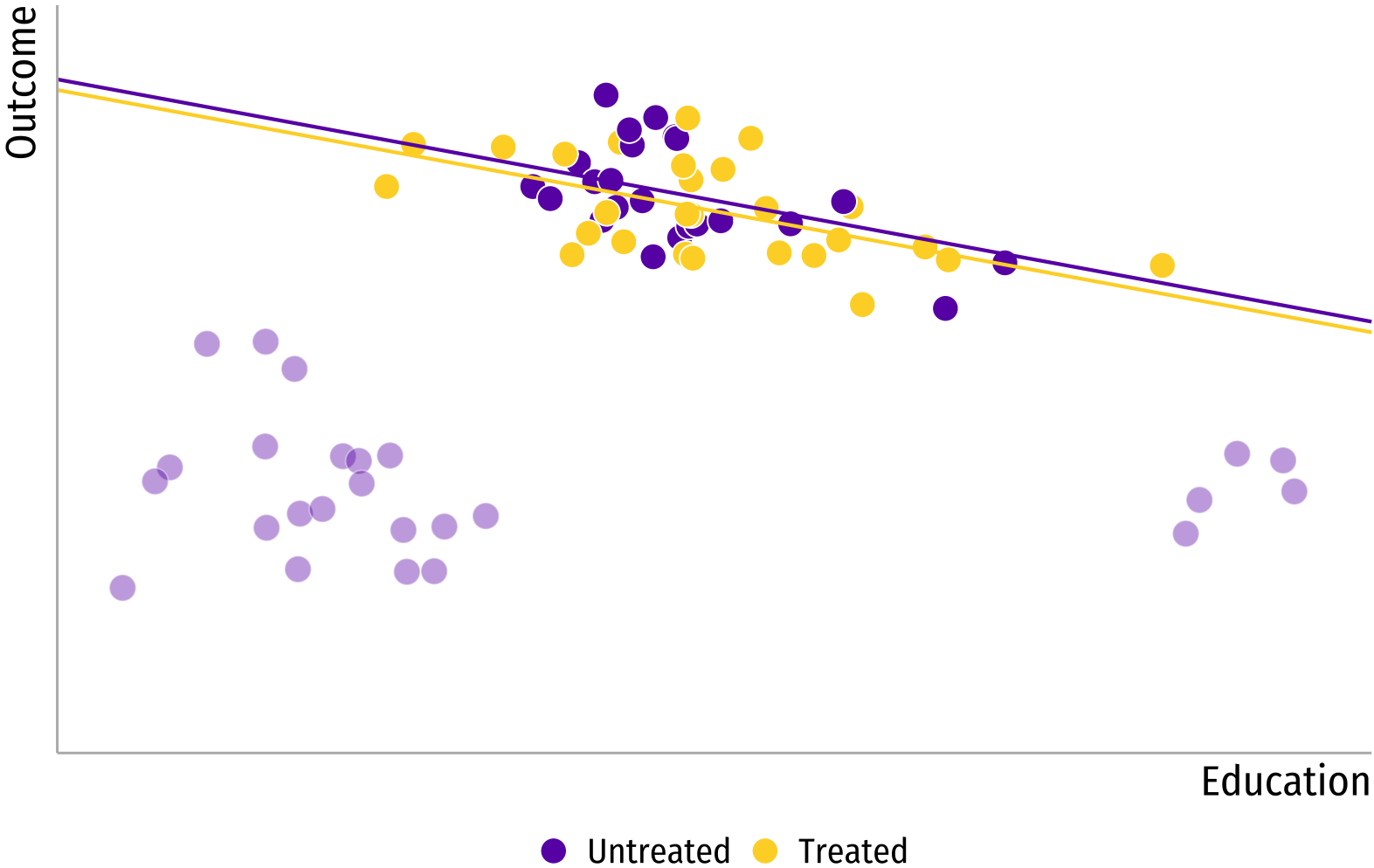


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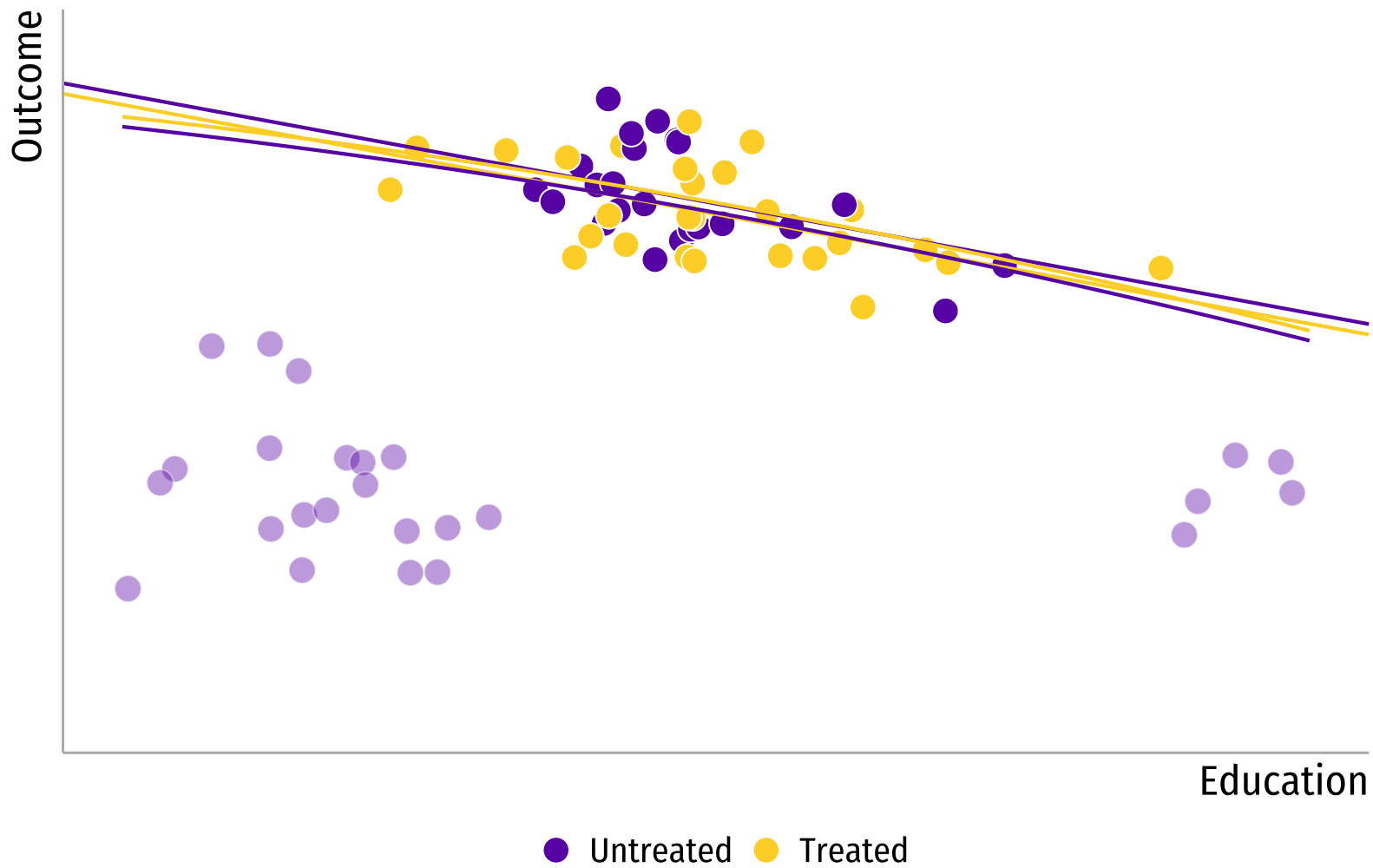




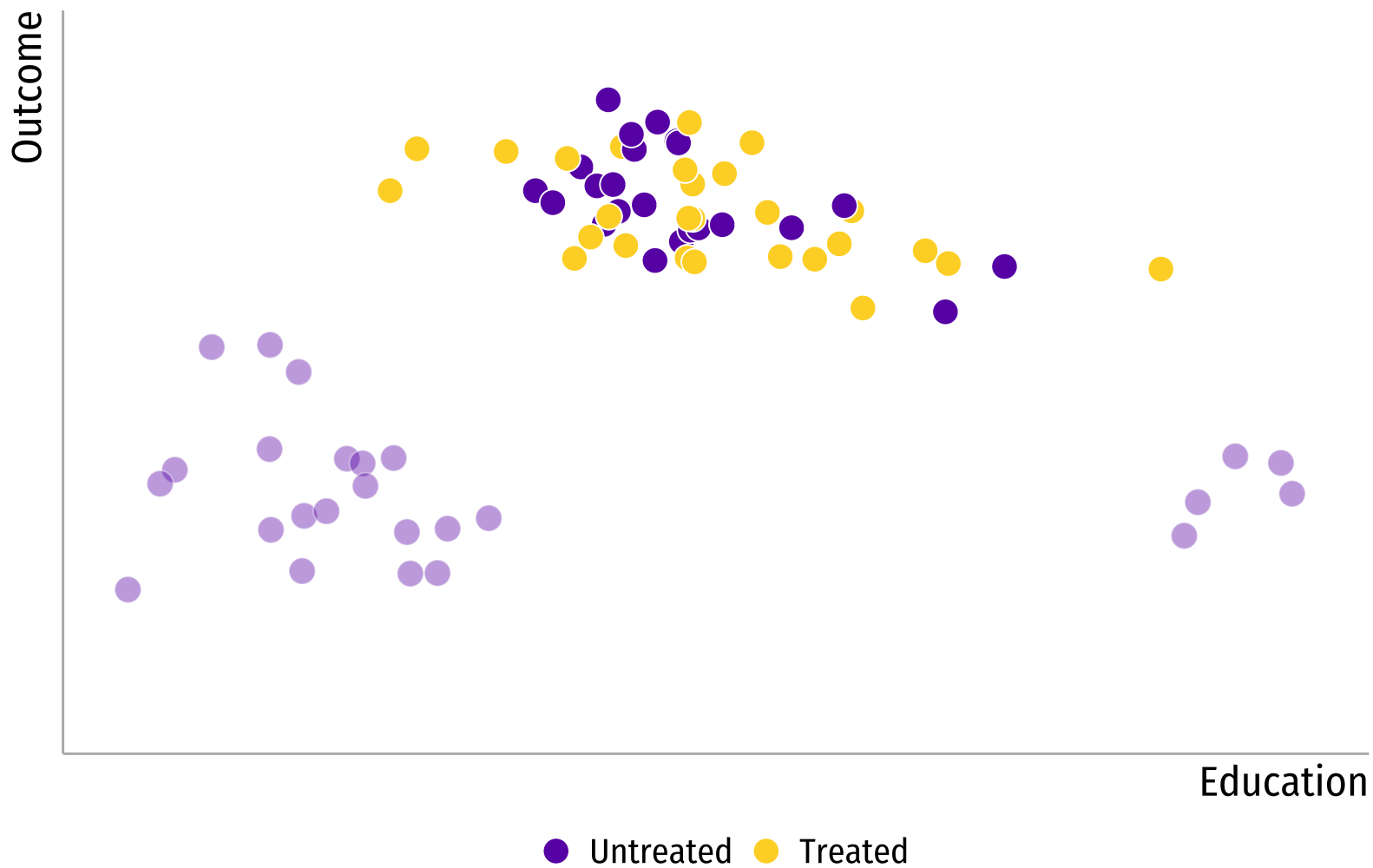
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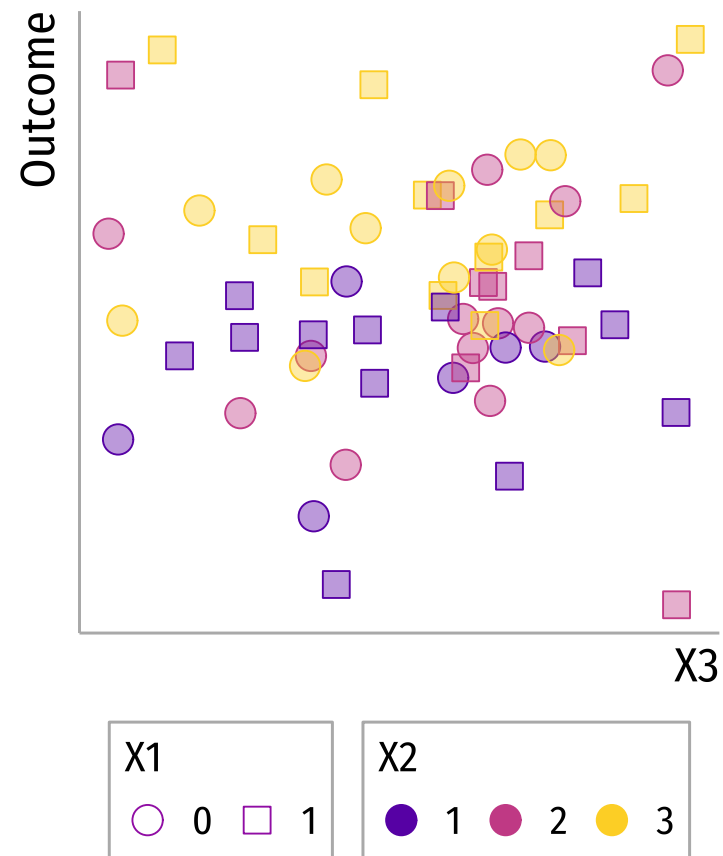


How do we know we can remove those observations?



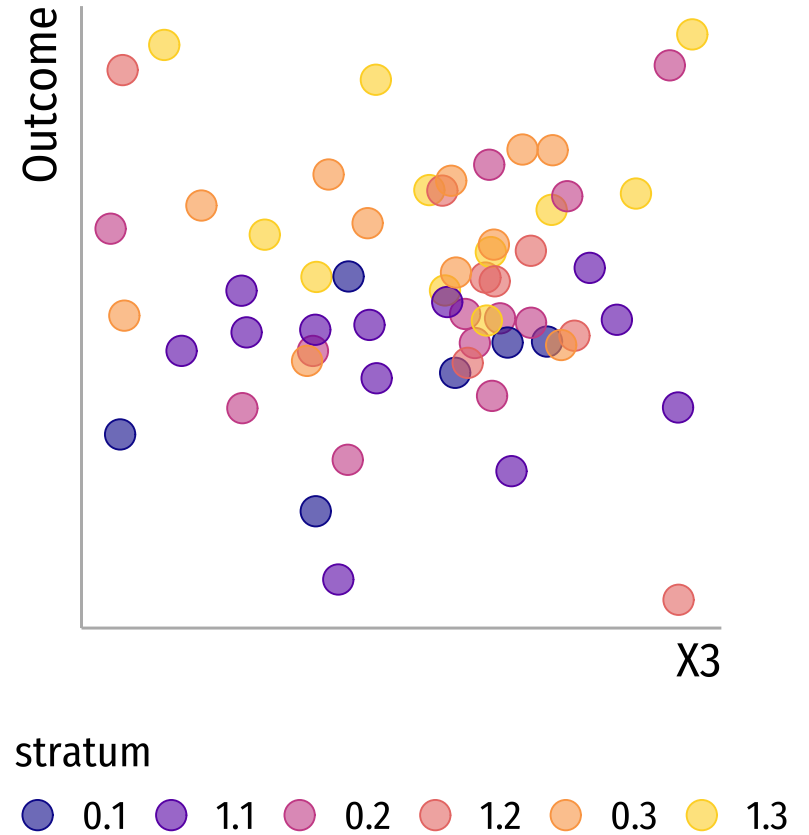
Subclassification

- Very similar to **stratifying**.



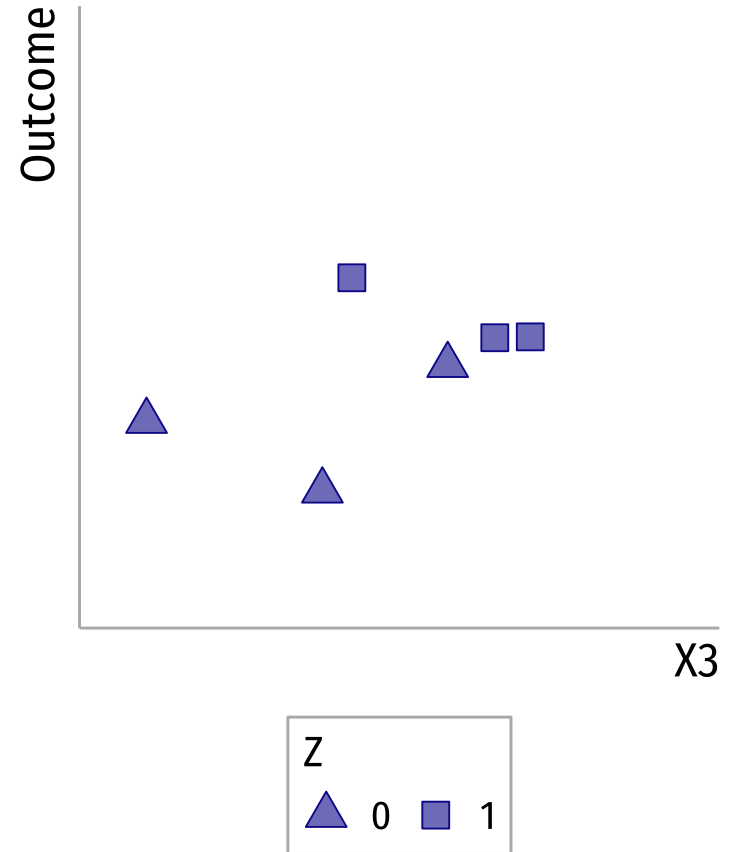
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- Very similar to **stratifying**.
- Build **combination** of X1 and X2 (strata).



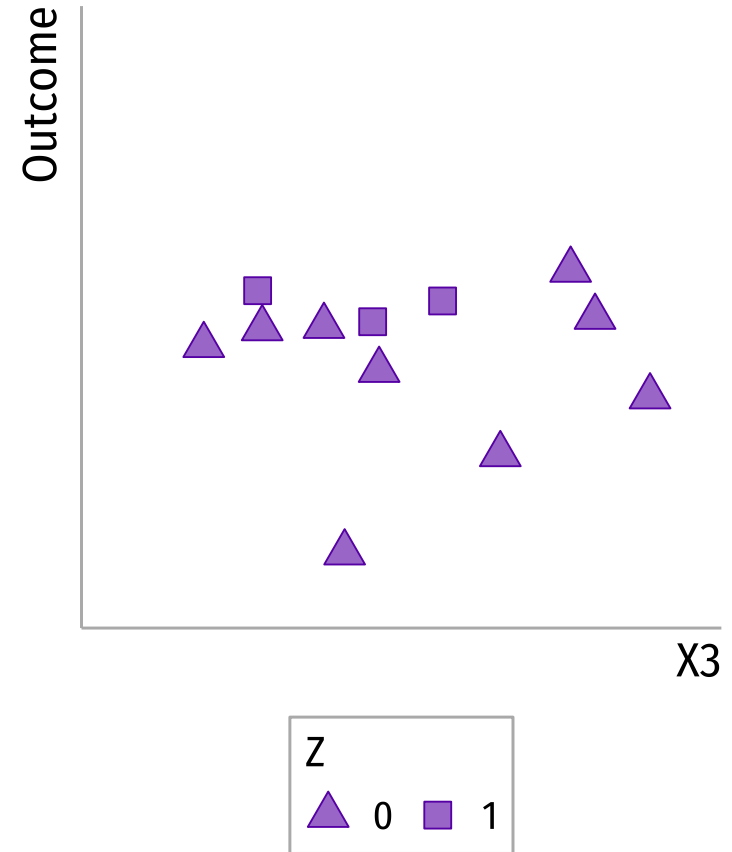
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- Very similar to **stratifying**.
- Build **combination** of X_1 and X_2 (strata).
- Compare **within stratum**.



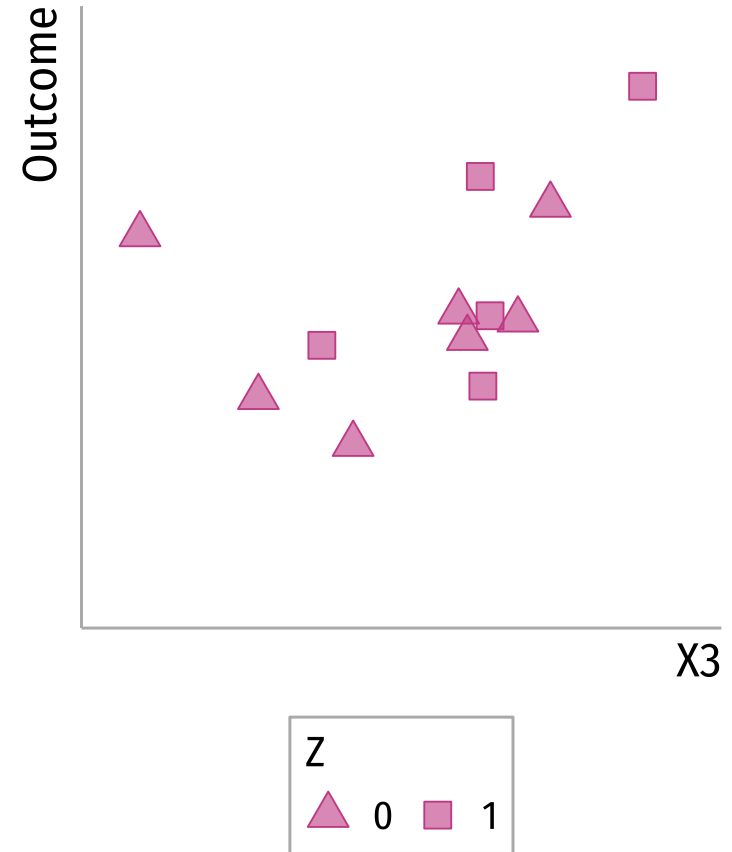
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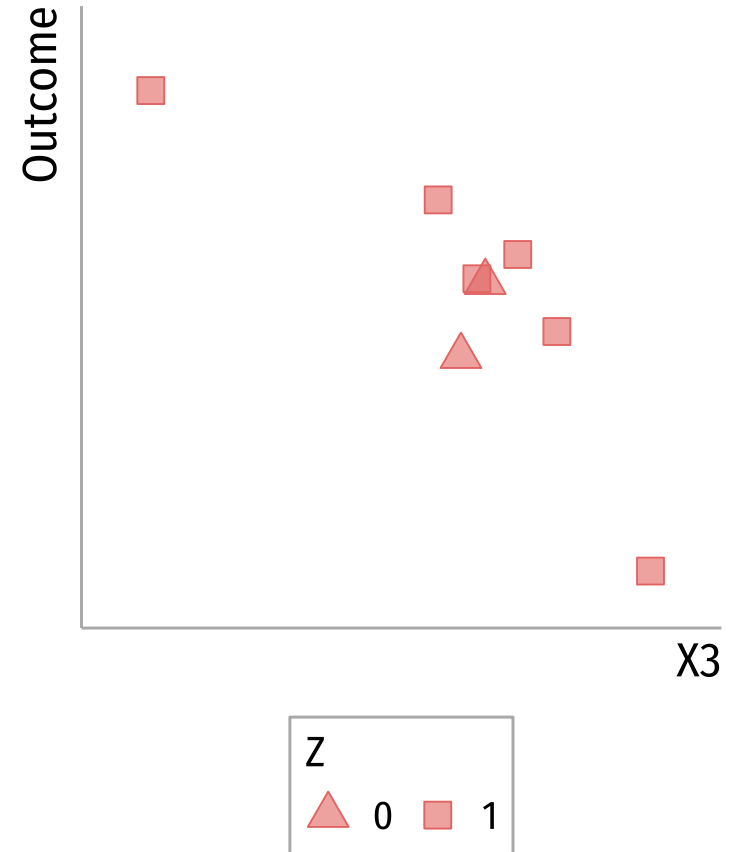
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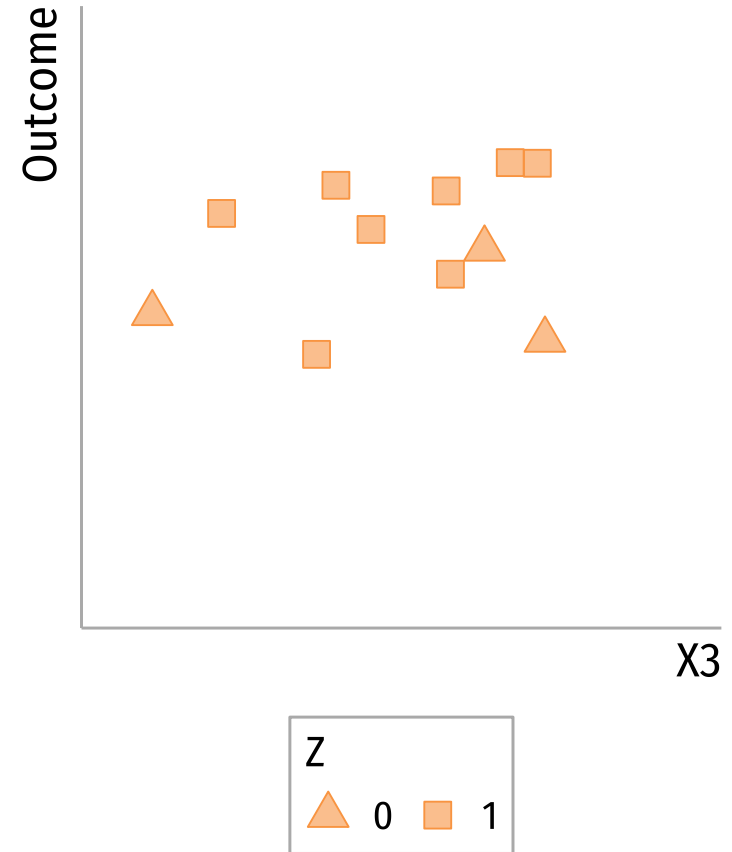
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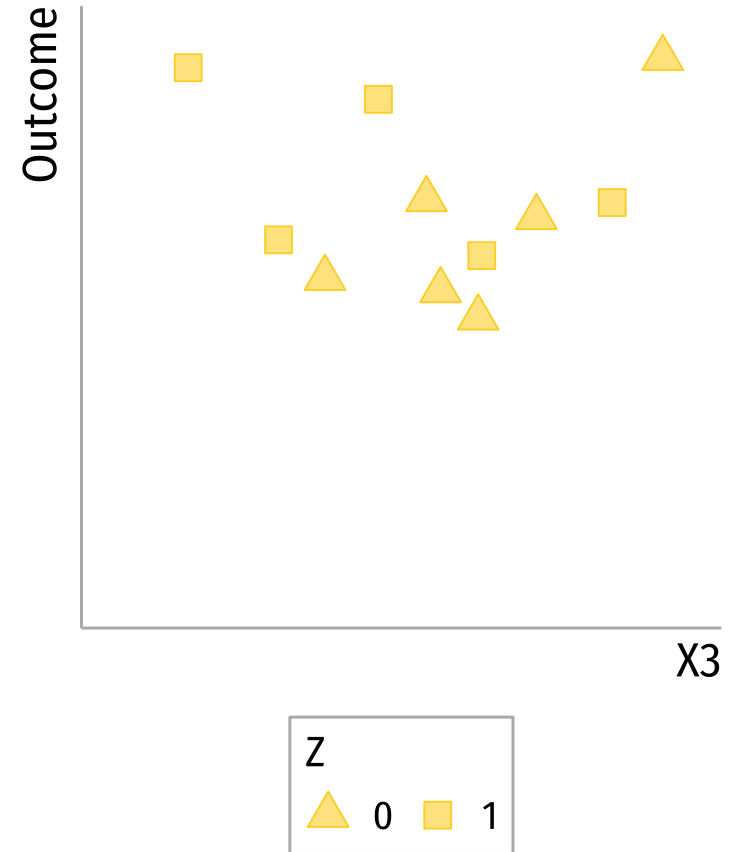
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Subclassification

- To estimate the Average Treatment Effect, we take a **weighted average**:

$$\hat{ATE} = \sum_{s=1}^S \frac{N_s}{N} (\bar{Y}_{1s} - \bar{Y}_{0s})$$

What happens when we have too many variables to build strata?

The curse of dimensionality

- When we have too many covariates, the number of strata or groups grow **exponentially**!
 - E.g. with 4 covariates, each with 5 categories, we have **625 combinations**!
- Very possible that a stratum only has treatment or control units.



The curse of dimensionality

- When we have too many covariates, the number of strata or groups grow **exponentially**!
 - E.g. with 4 covariates, each with 5 categories, we have **625 combinations**!
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What to do?



Breaking the curse: Balancing scores

- Want to **reduce the dimensionality** of our covariates
- A balancing score $b(x)$ is a function of the covariates such that:

$$Z_i \perp\!\!\!\perp X_i | b(X_i)$$

- This means that conditioning on the balancing score is **enough to remove bias** associated to the covariates.
- Under unconfoundedness:

$$Z_i \perp\!\!\!\perp Y_i(0), Y_i(1) | b(X_i)$$

- There are different balancing scores:
 - E.g. propensity scores, mahalanobis distance.

Estimating balancing scores

Propensity score

$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_p X_p + \varepsilon$$

where $p = Pr(Z = 1)$

```
e <- predict(glm(z ~ x1 + x2 + x3, data = d, family = binomial(link="logit")),  
             type="response")
```

Estimating balancing scores

Propensity score

- Importance of overlap region

Making groups comparable

- Using the previous balancing scores (or covariates directly!) we can **match observations between the treatment and control group**

Step 1: Preprocessing

Try to model the treatment assignment

Step 2: Estimation

Use the new trimmed/preprocessed data to build a model, calculate difference in means, etc.

How matchy-matchy

- There are different matching methods (and different ways to use them!)

Nearest neighbor (NN)

Use balancing scores; Greedy algorithm

Optimal matching

Solves an optimization problem; slow on large samples

Mixed Integer Programming (MIP) matching

Balances covariates directly; can generate smaller samples

Let's go to R

Weighting, the cousin of matching

- We can also use **weights** to make two samples look alike.

Inverse Probability Weighting (IPW)

- Make some observations more important than others.

Weighting, the cousin of matching

- You can make the treatment and the control group look more like each other:

$$w_{ATE} = \frac{Z_i}{e_i} + \frac{1 - Z_i}{1 - e_i}$$

- Observations in the control group will have a weight of $\frac{1}{1-e_i}$, while observations in the treatment group will have weights of $\frac{1}{e_i}$

What happens with obs that are very likely to be in the treatment group?

Weighting, the cousin of matching

- You can make the treatment and the control group look more like each other:

$$w_{ATT} = \frac{e_i \cdot Z_i}{e_i} + \frac{e_i(1 - Z_i)}{1 - e_i}$$

- Observations in the control group will have a weight of $\frac{e_i}{1-e_i}$, while observations in the treatment group will have weights of 1

Why do observations in the treatment group get a weight of 1?

Weighting for approximating a population

- If we assume that our sample was selected on observables, and we want it to **look more like a population of interest**, we can also do that!
- We can use the same formula for ATT , but now e_i is not the probability of being assigned to treatment, but the probability of **being in the population sample**.
- For this type of weighting, we only need population covariates.

Let's go to R

The shortcomings of matching

- Many researchers misuse matching and **confuse it with an identification strategy**
- In terms of identification, **matching still relies on selection on observables**

You need other source of exogenous variation!

- Claiming that you can identify a **causal effect** just by using matching is almost the same as claiming this using a regression approach.

Not a good idea...

Don't get it twisted

- Matching works great as an **adjustment method**.
- Combined with **other identification strategies**, it can improve results!



Main takeaways



- Matching and weighting methods can be great tools for your analysis.
 - Create more similar groups of comparisons.
 - Reduce model dependence
 - Even help with external validity (under assumptions)

Next week

- We will look at some **identification strategies** for observational studies:
 - Natural experiments and differences-in-differences.
- What **assumptions** need to hold?
- How do we **identify a natural experiment**?
- What does **DD** buy us?

References

- Angrist, J. and S. Pischke. (2015). "Mastering Metrics". *Chapter 2*.
- Heiss, A. (2020). "Program Evaluation for Public Policy". *Class 7: Randomization and Matching, Course at BYU*
- Imbens, G. and D. Rubin. (2015). "Causal Inference for Statistics, Social, and Biomedical Sciences: An Introduction". *Chapter 3*
- Cunningham, S. (2021). "Causal Inference: The Mixtape". *Chapter 5*