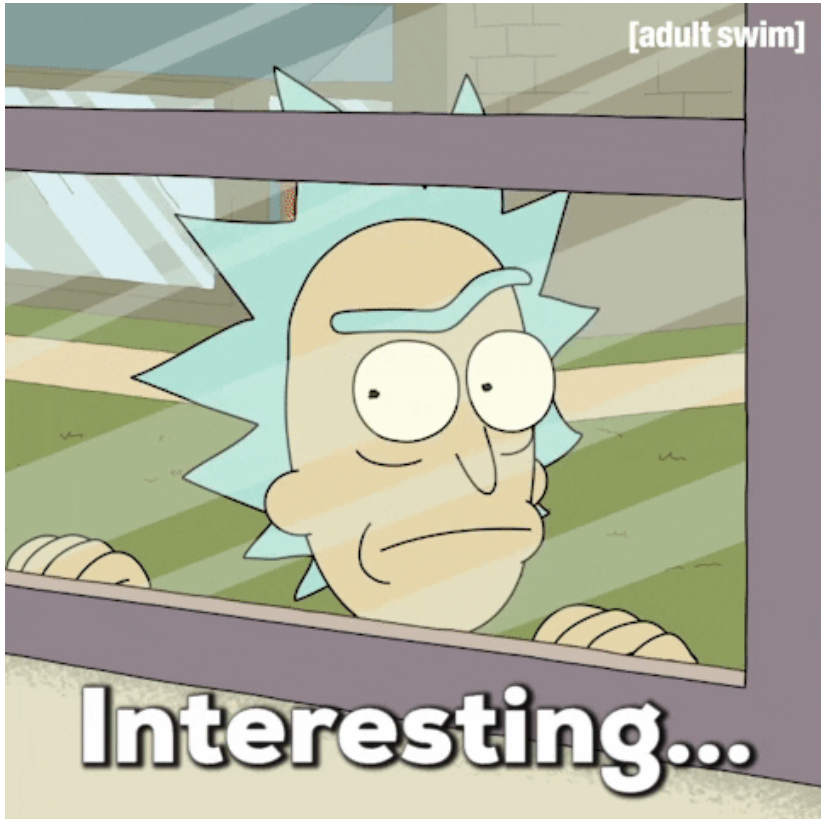
STA 235 - Causal Inference: Introduction to Observational Studies

Spring 2021

McCombs School of Business, UT Austin

Last class

- **Randomized controlled trials**
  - Why is it considered the gold standard?
  - How to analyze an RCT in practice?
  - Assumptions and limitations.
- **Statistical power**:
  - How do sample sizes play a role?
  - Randomized inference.



Today

- **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 **unconfoundnedness** (to a certain extent).

What is that?

Calling in the CIA

- **Unconfoundnedness** 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?**

The assignment mechanism (cont.)

- For now, we will consider 3 assumptions:

Individualistic assignment

Probabilistic assignment

Unconfounded assignment

Individualistic assignment

- Limits the dependence of treatment assignment for unit i on the outcomes and assignments for other units.
- For some function $q(\cdot) \in [0, 1]$:

$$p_i(\mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1)) = q(X_i, Y_i(0), Y_i(1))$$

From last class, can you think of an example where this doesn't hold?

Probabilistic assignment

- Nonzero probability for each treatment value, for each unit.

$$0 < p_i(\mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1)) < 1 \;\; \forall\, i = 1, \ldots, N$$

,for each possible $\mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1)$

When could this assumption fail?

Unconfounded assignment

- The assignment mechanism does not depend on the potential outcomes:

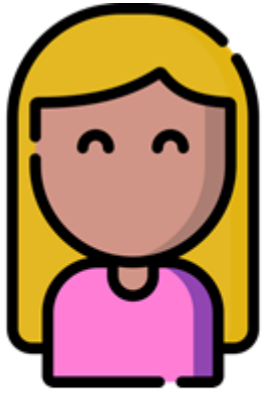
$$Pr(\mathbf{Z}|\mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1)) = Pr(\mathbf{Z}|\mathbf{X}, \mathbf{Y}'(0), \mathbf{Y}'(1))$$

,for all possible $\mathbf{Z}, \mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1), \mathbf{Y}'(0)$, and $\mathbf{Y}'(1)$

Selection on observables

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

$$(Y_1(0), Y_1(1))$$
$$Z = 1$$
$$Y = y_1$$



$$(Y_2(0), Y_2(1))$$
$$Z = 0$$
$$Y = y_2$$

Selection on observables

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

$$(Y_1(0), Y_1(1))$$
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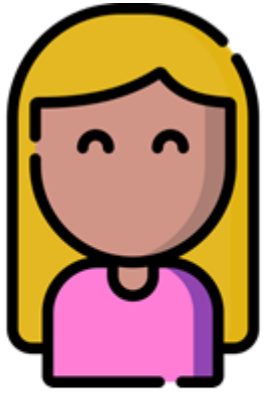
$$\mathbf{X} = \mathbf{X_F}$$



$$(Y_2(0), Y_2(1))$$
$$Z = 0$$
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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?

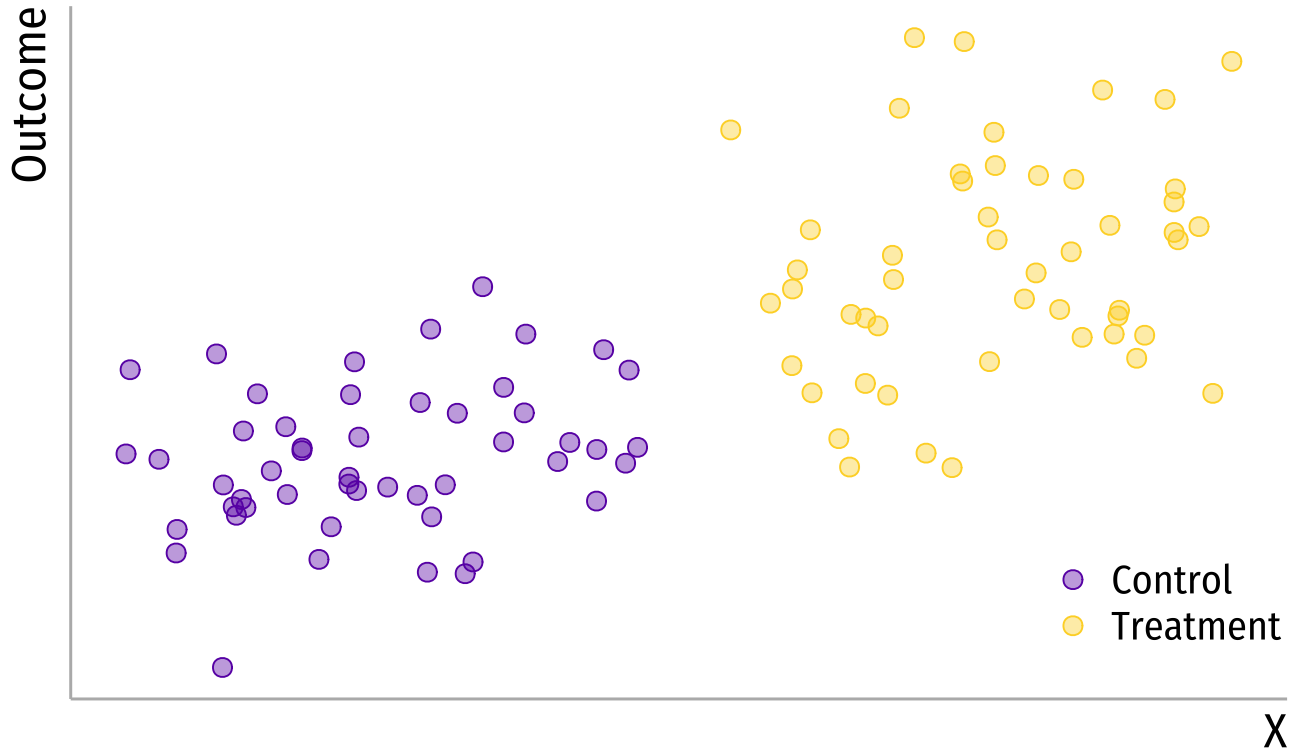
- One way we have seen so far is **regression adjustment**

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

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?



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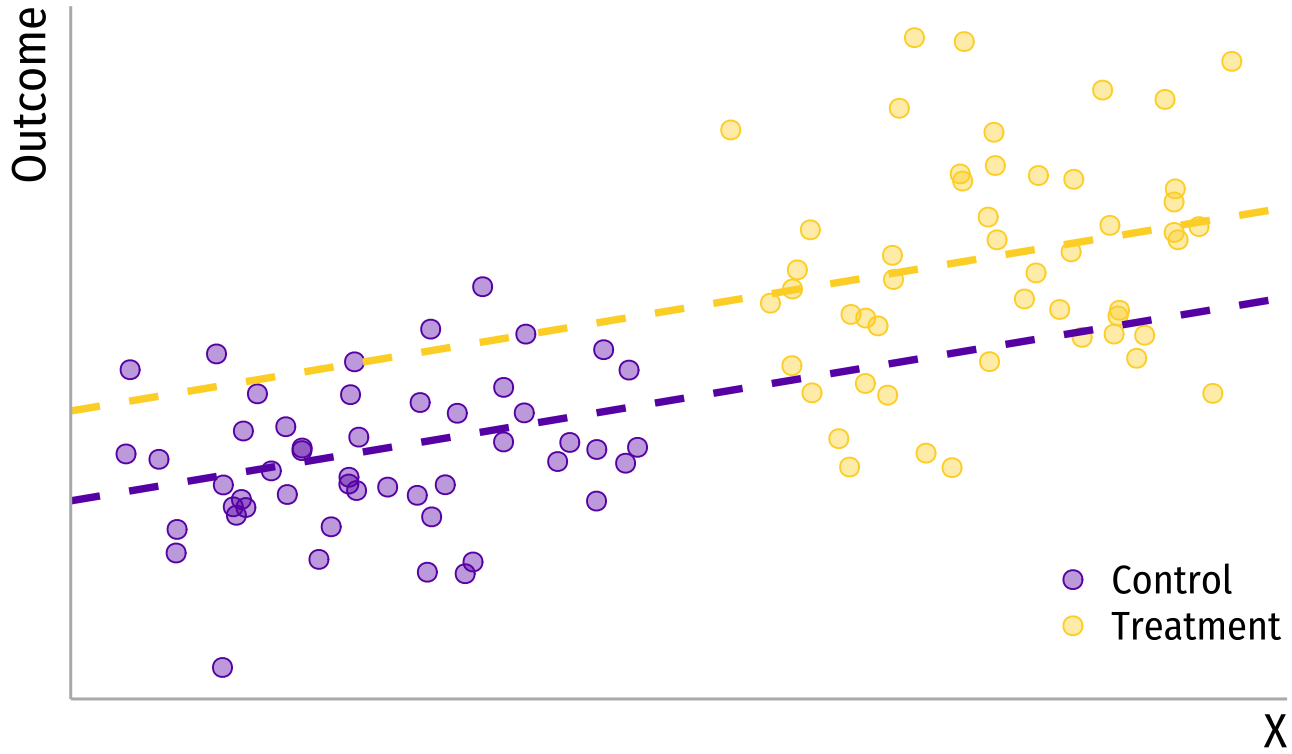

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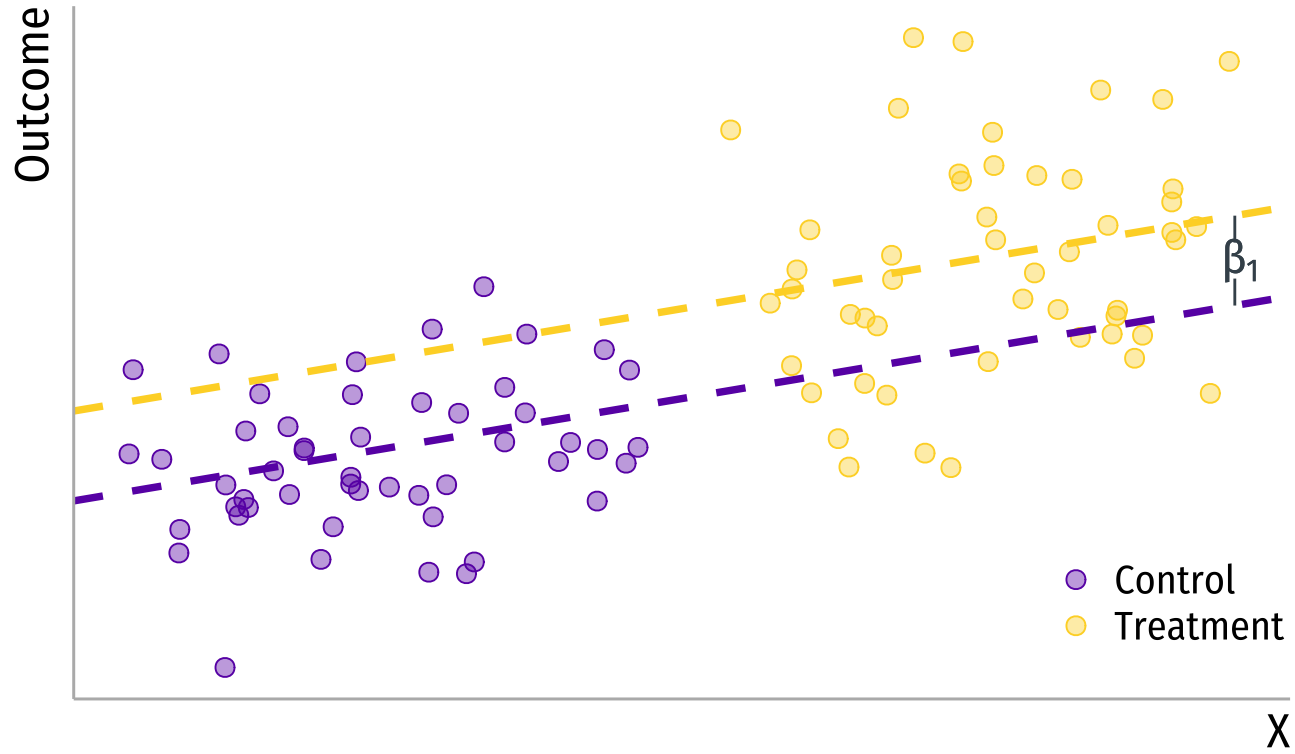

Finding your perfect match...

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.

Two peas in a pod

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- There are different ways to do it:
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What do we gain?

Advantages of matching methods

Reduce model dependence

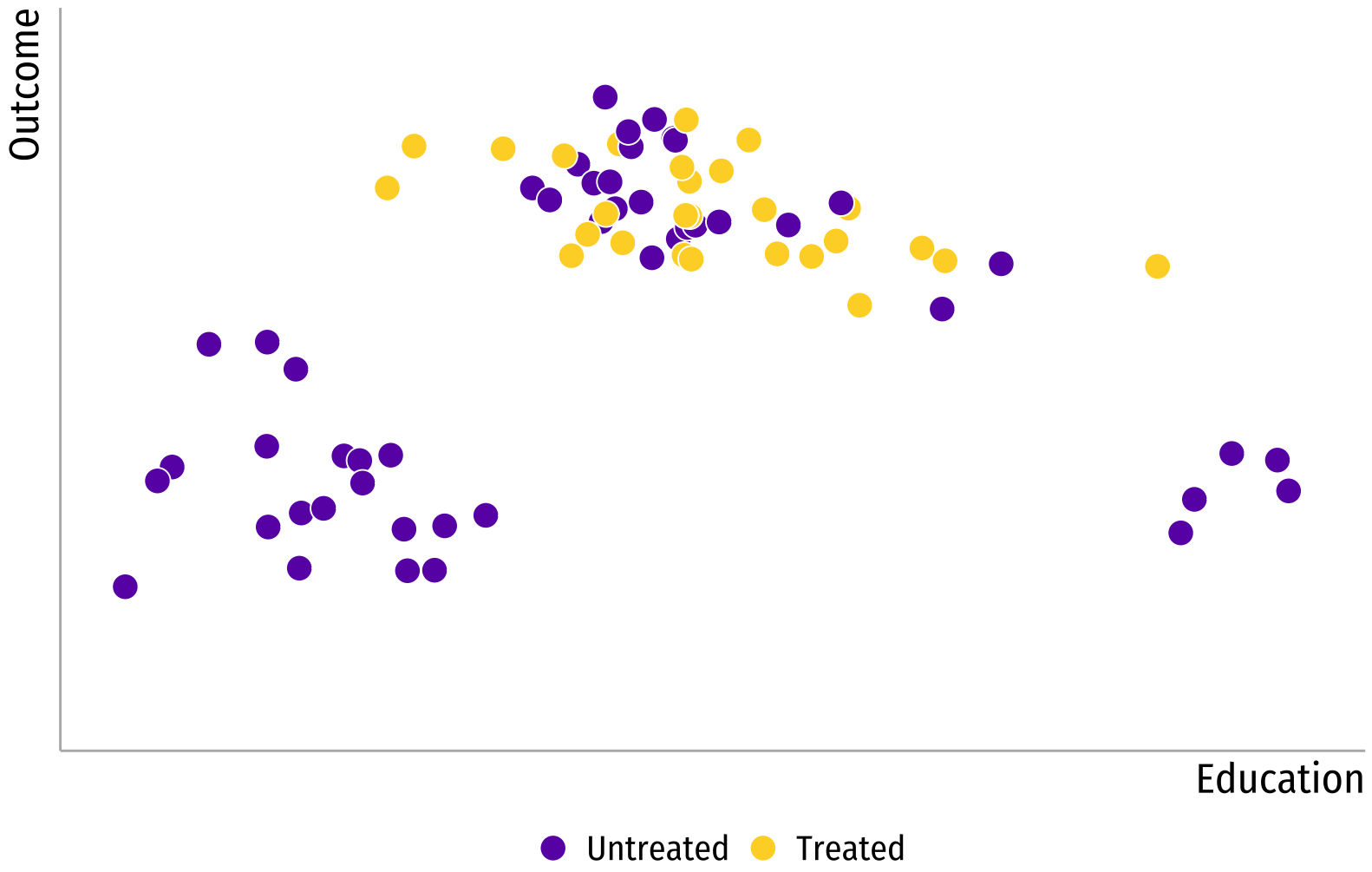
Imbalance → model dependence → researcher discretion → bias

Compare like to like

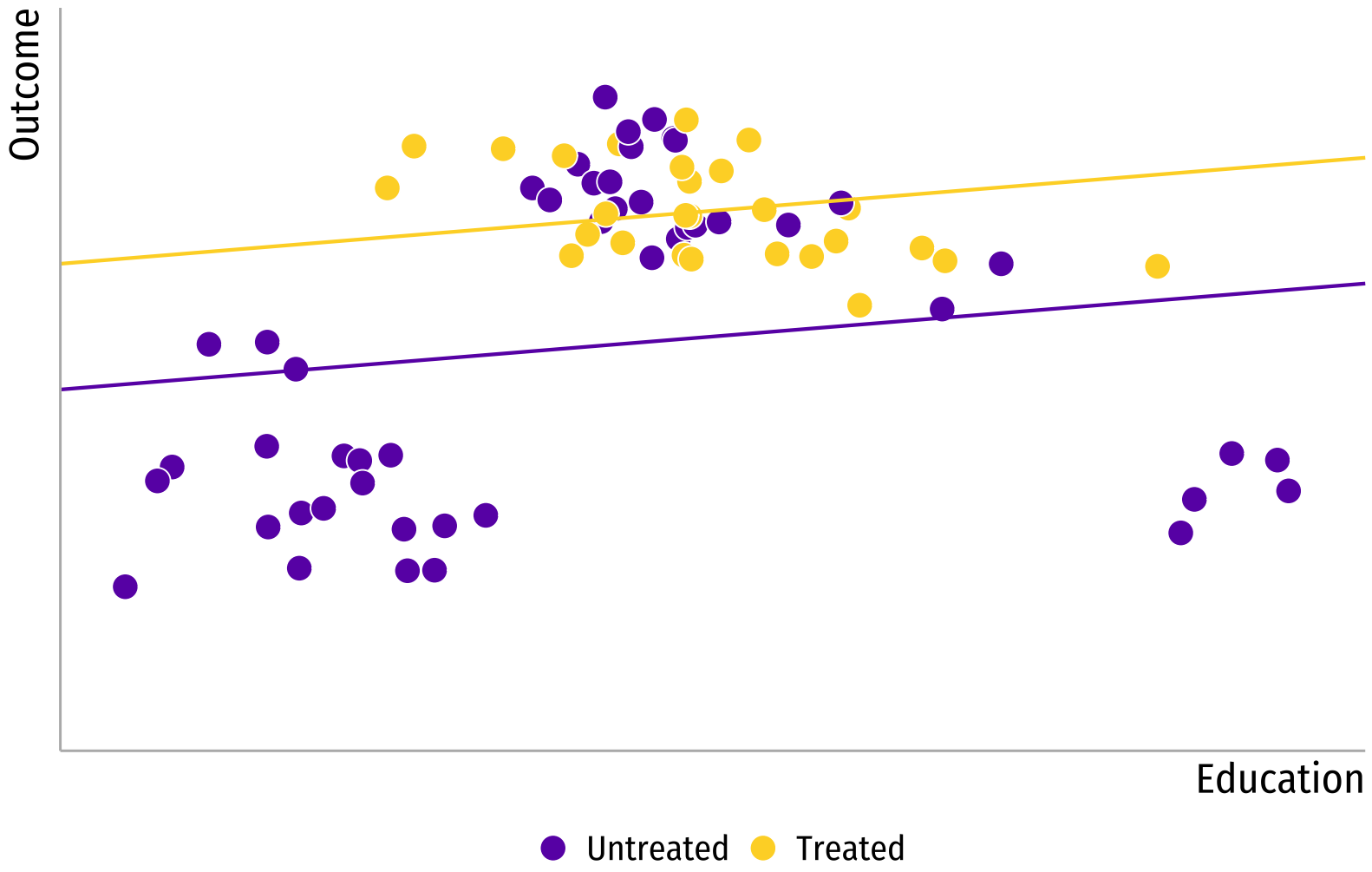
No extrapolation!

Can adjust closely by covariates

Exact matching, coarsened exact matching, fine balance..


Outcome
Education
Untreated
Treated

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



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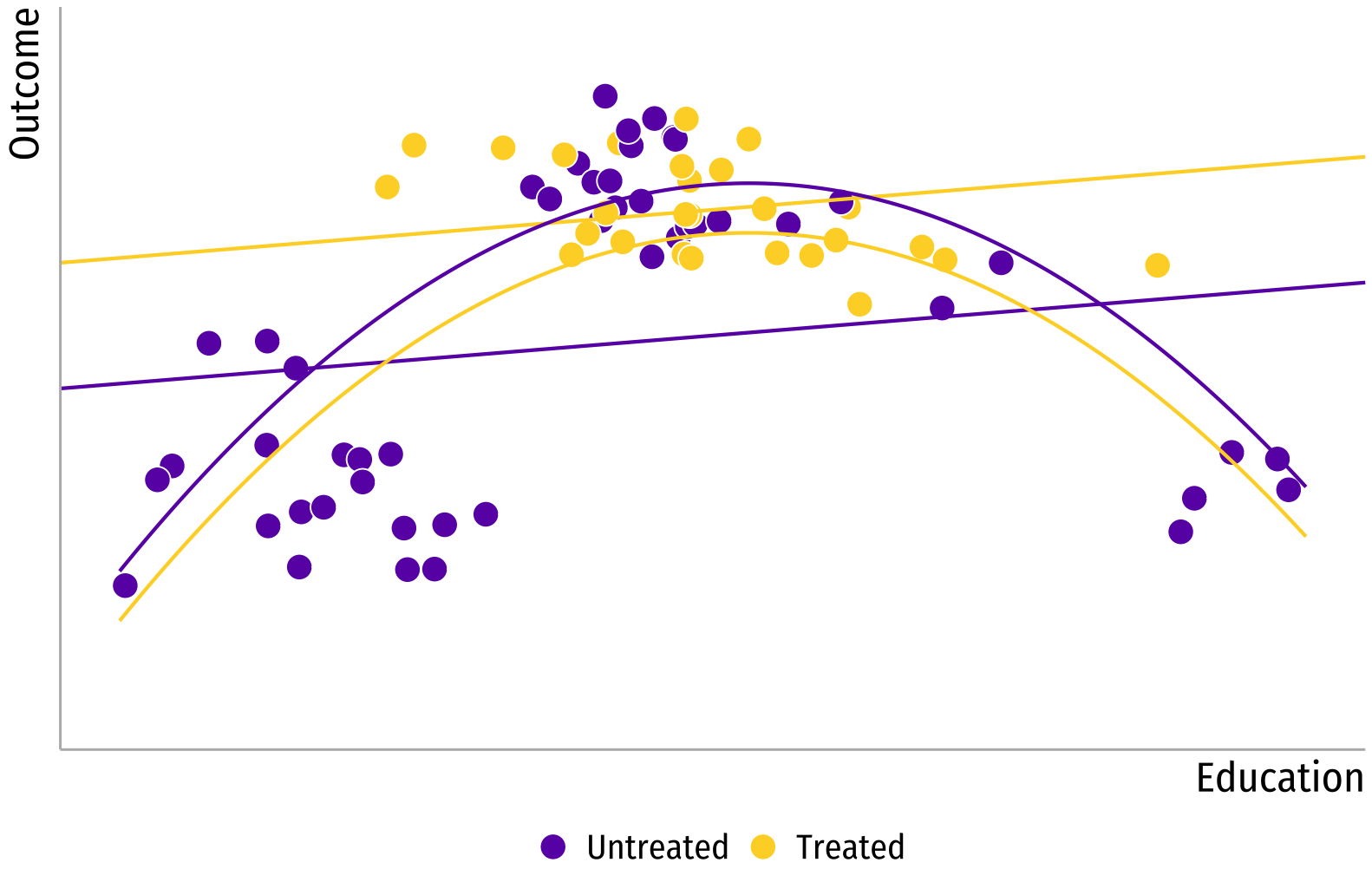

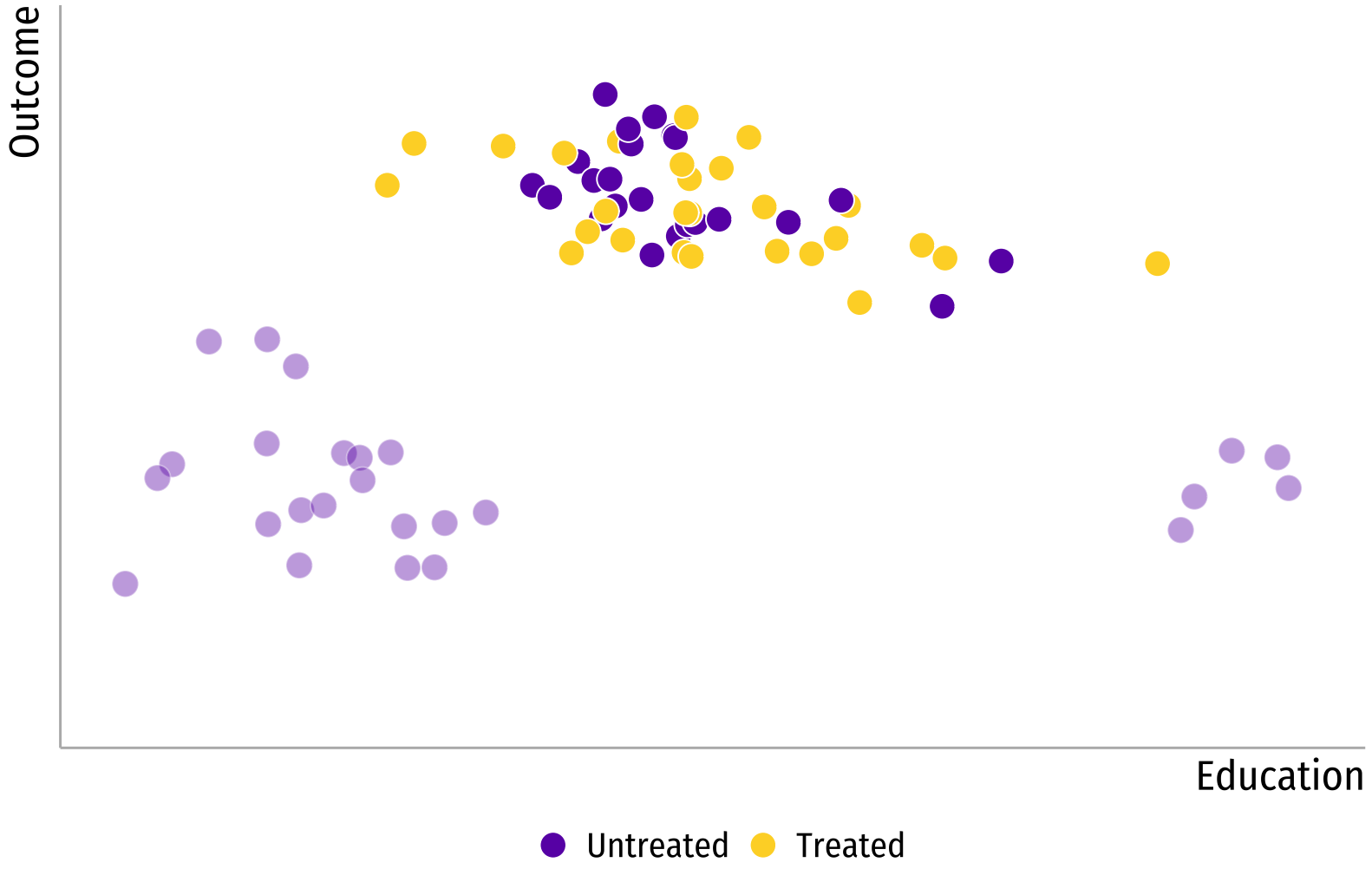
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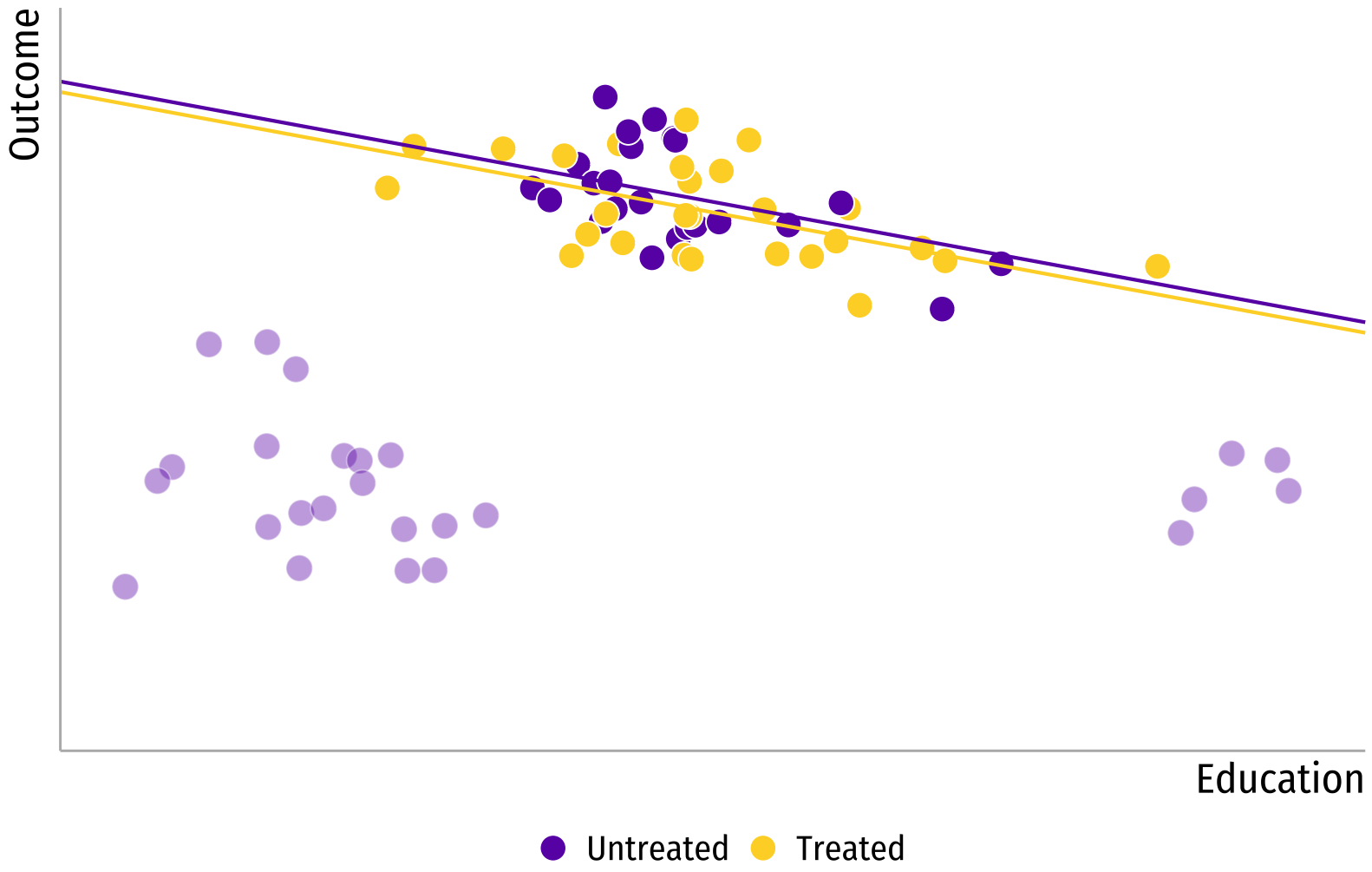

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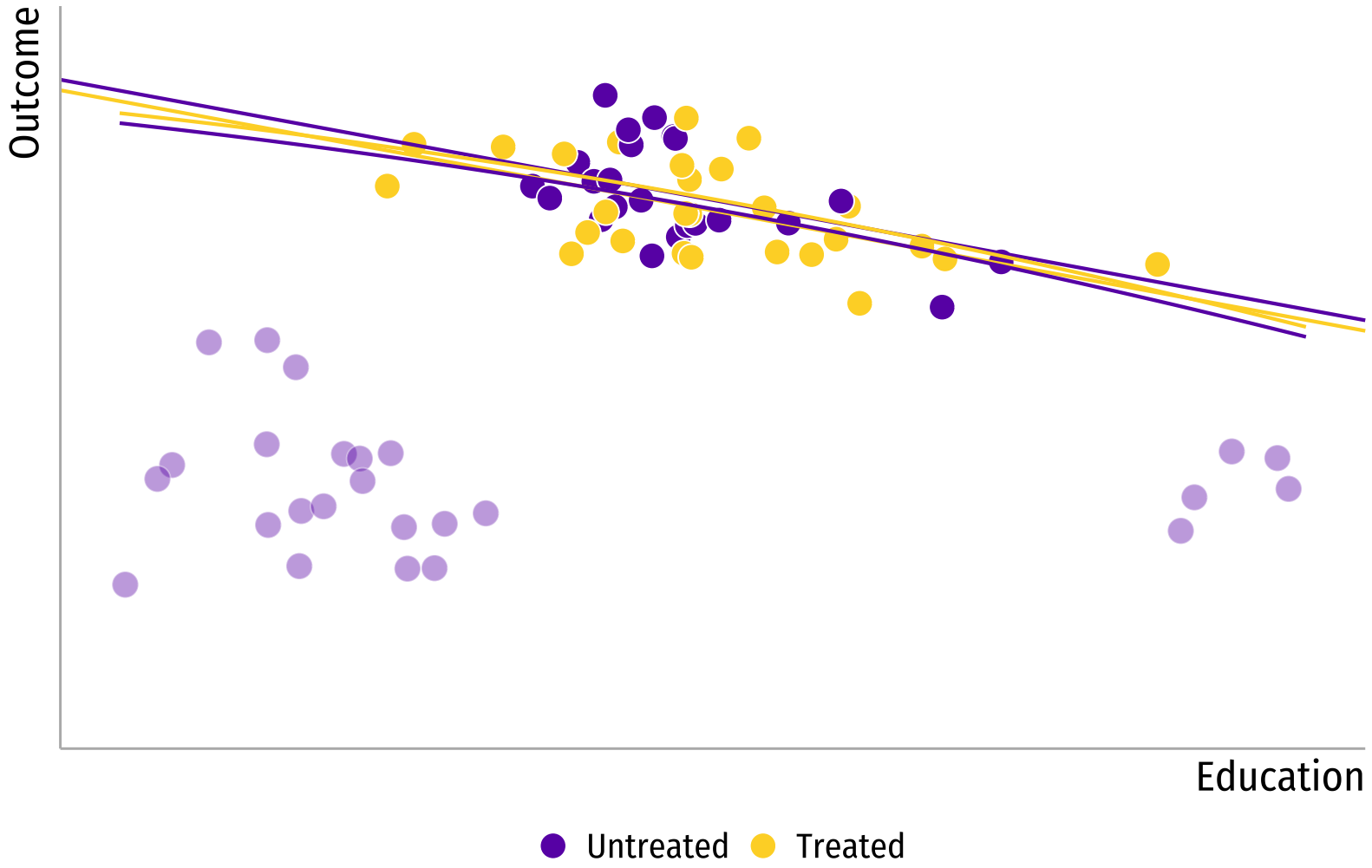
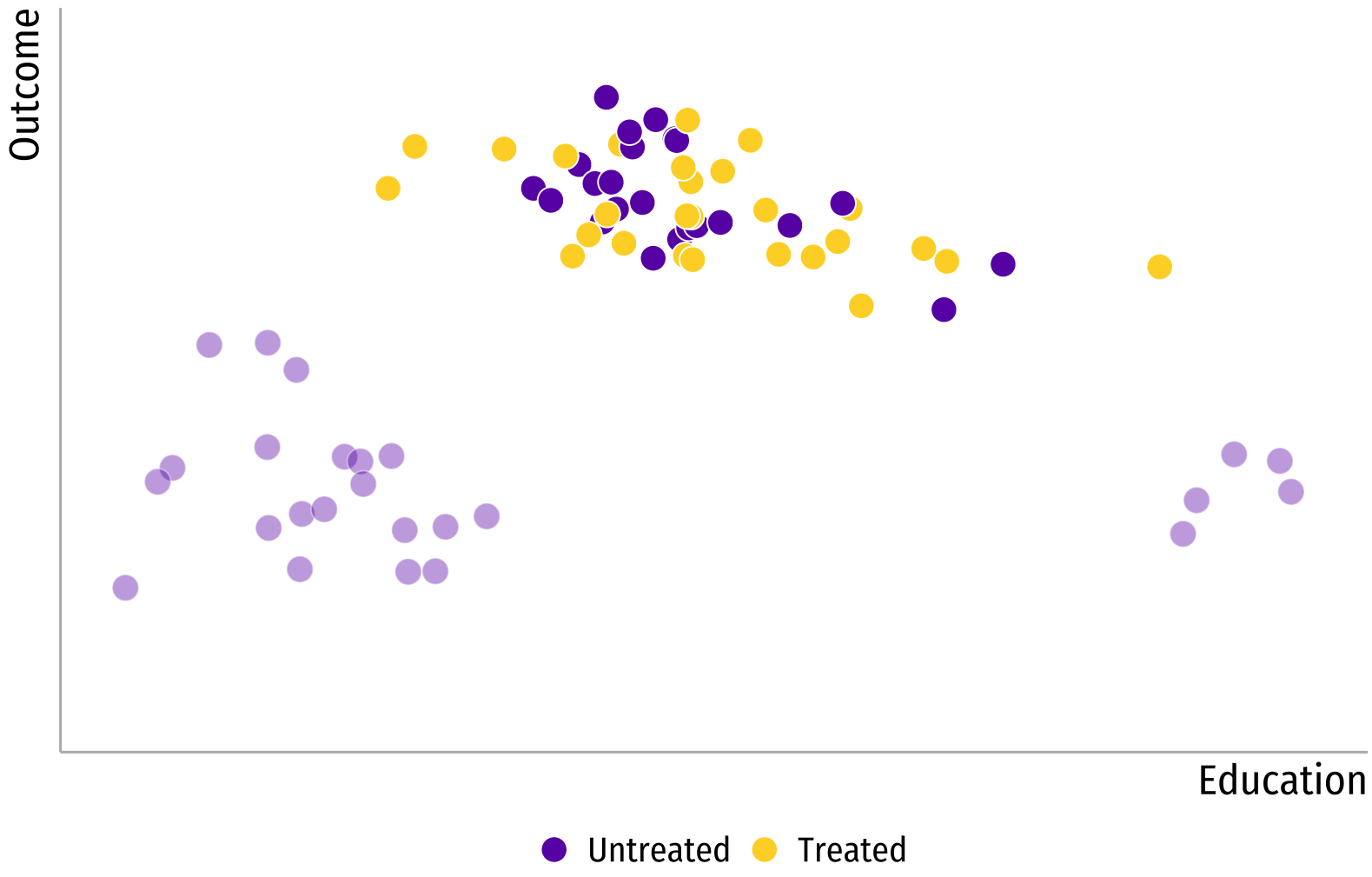
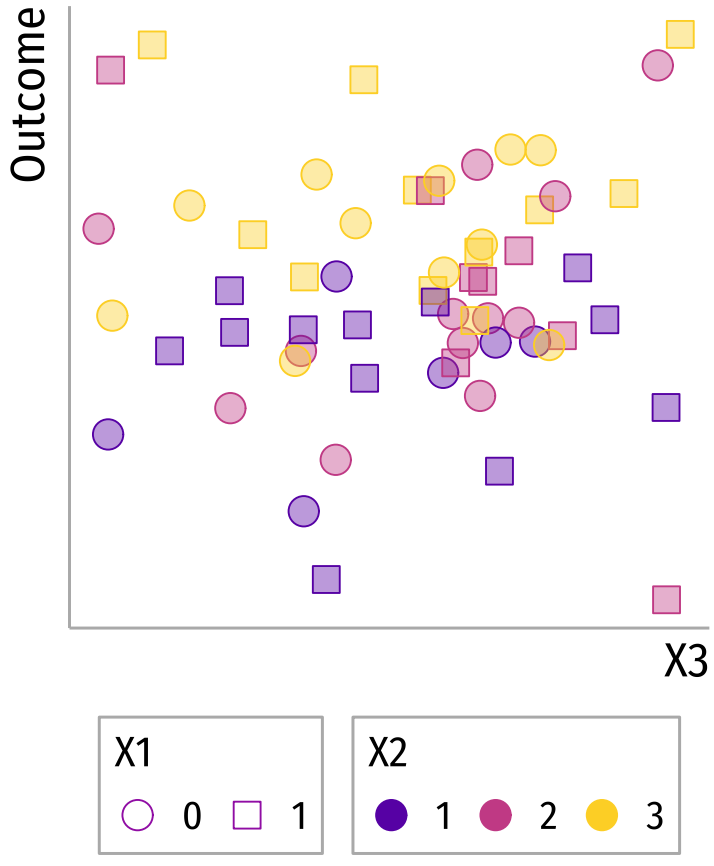


How do we know we can remove those observations?



Subclassification

- Very similar to **stratifying**.



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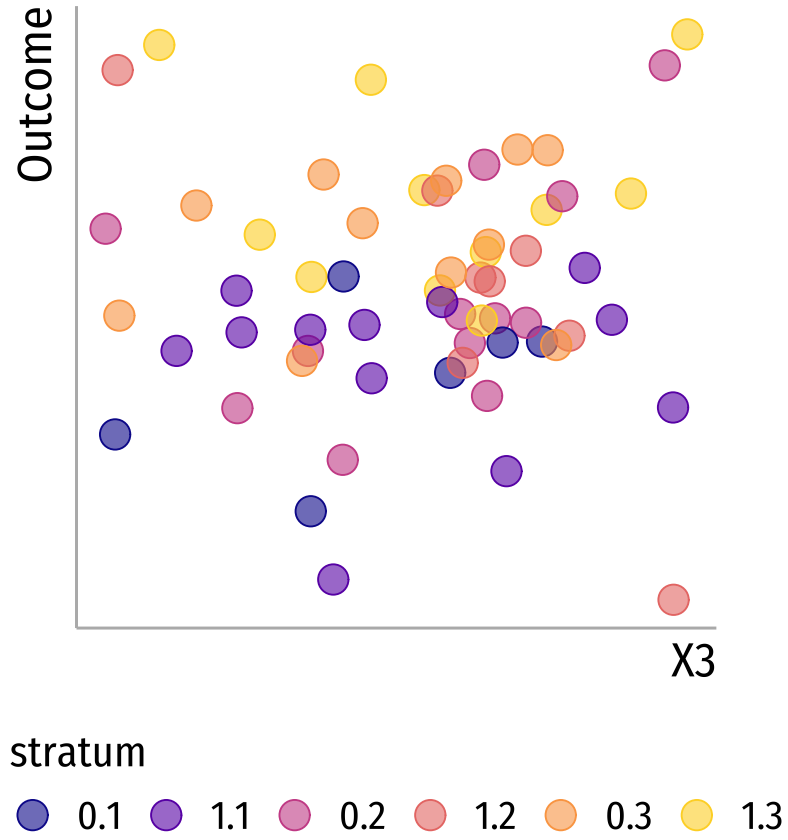

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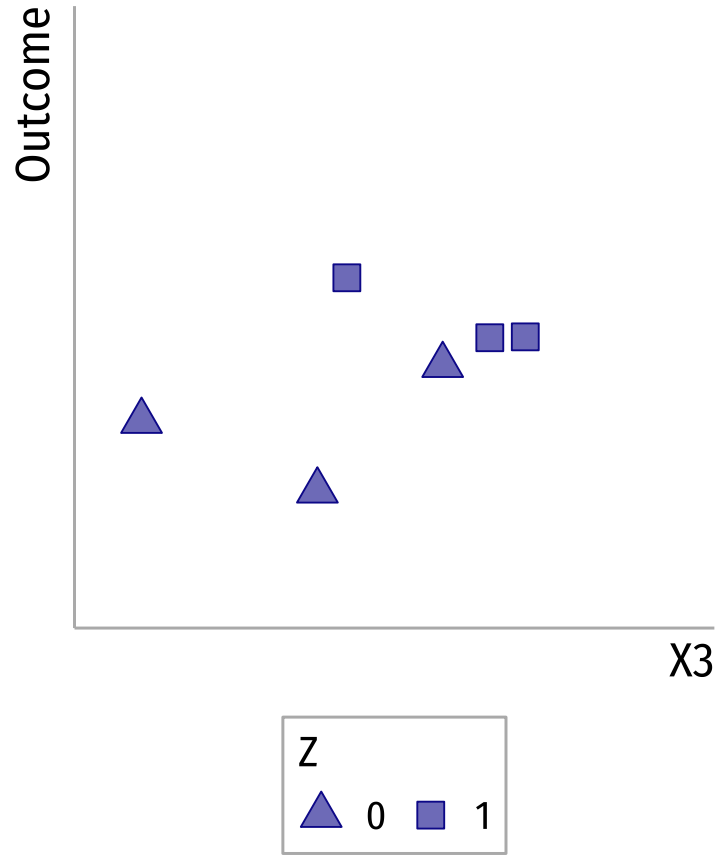

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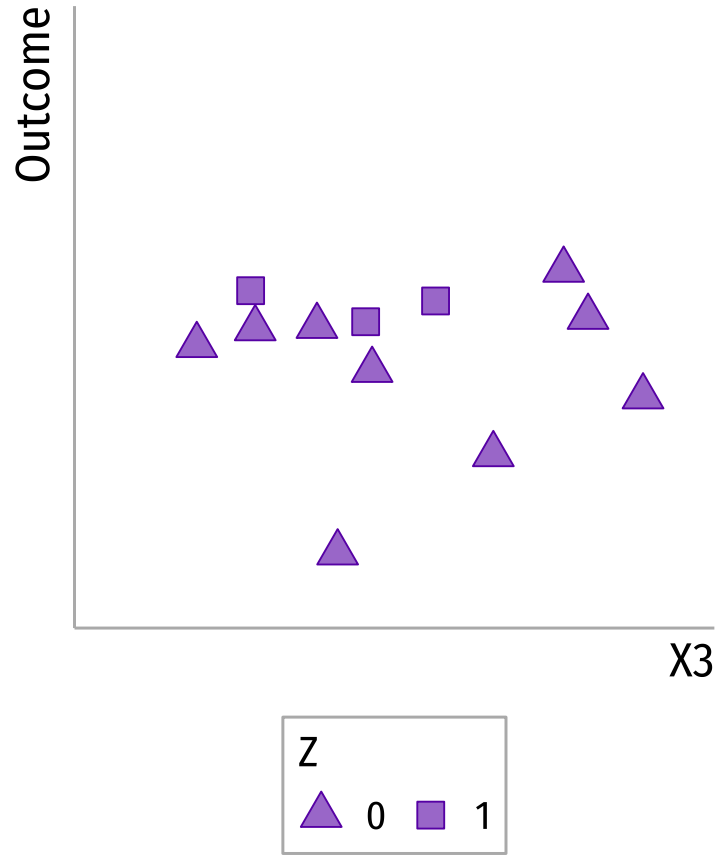

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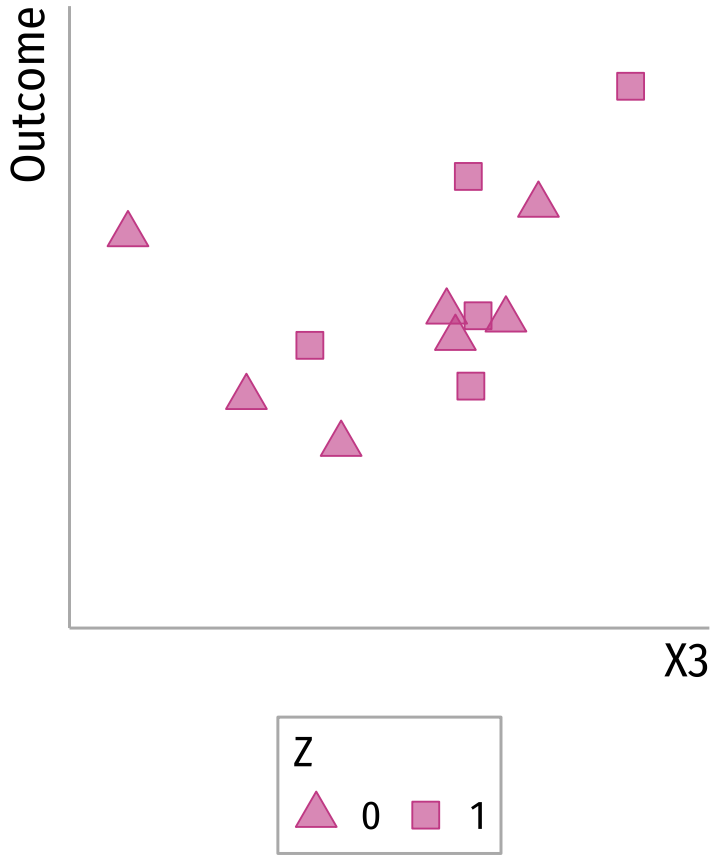

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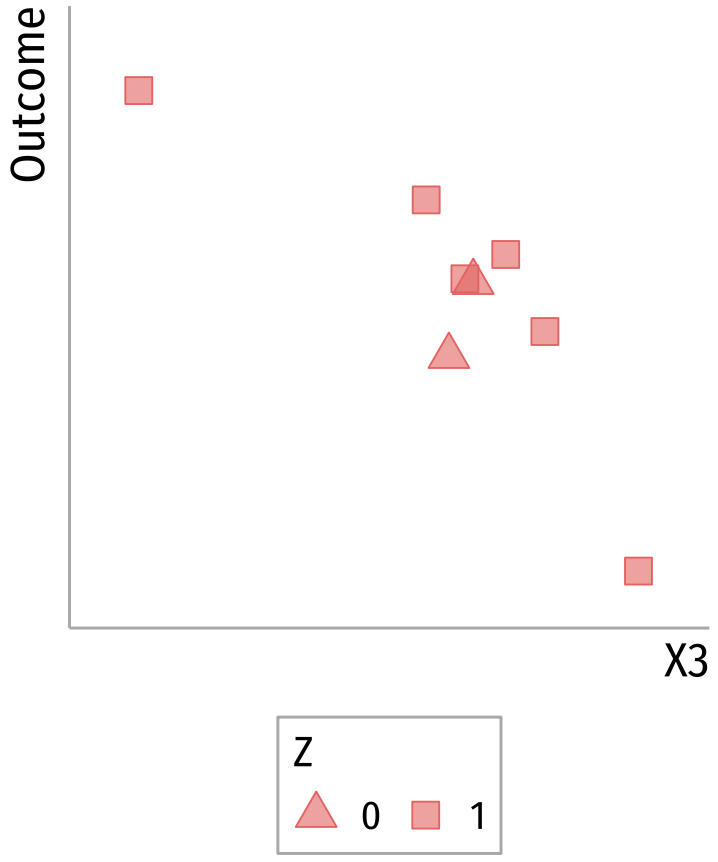

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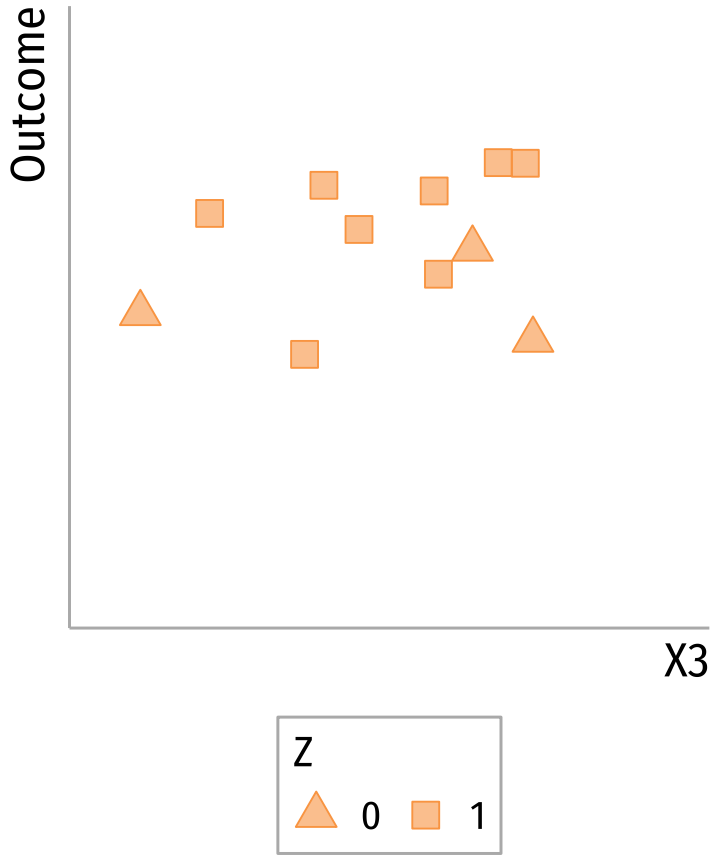

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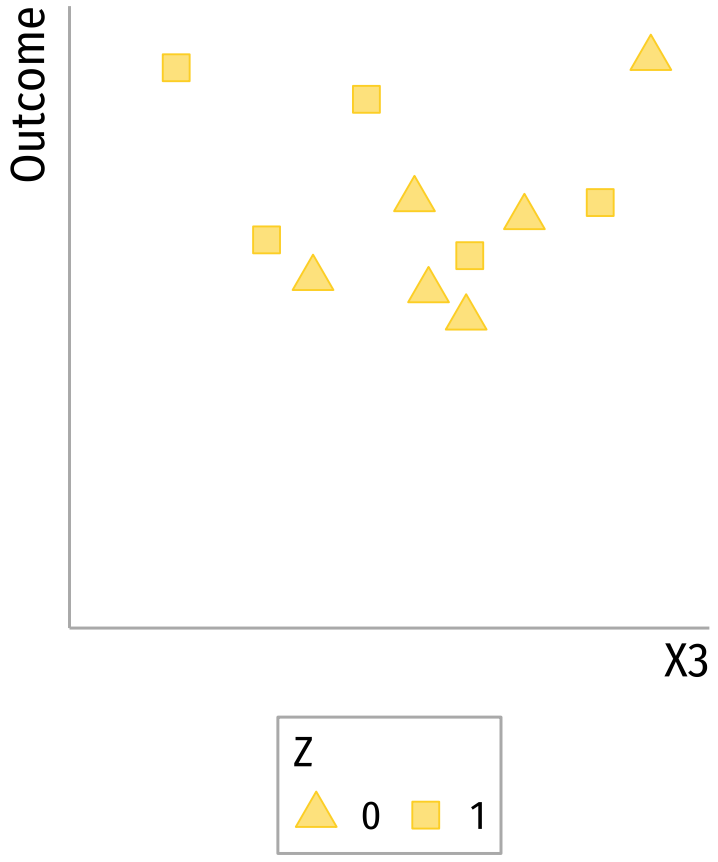

Subclassification

- 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 dimentionality

- 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 dimentionality

- 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 dimentionality** 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

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

where $p = Pr(Z = 1)$

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

Estimating balancing scores

Mahalanobis Distance

$$D_M(\mathbf{x}) = \sqrt{(\mathbf{x} - \mu)^T S^{-1} (\mathbf{x} - \mu)}$$

where $\mathbf{x}$ is the covariate vector for observation i, μ is the mean vector of covariates for the sample, and S is the covariance matrix.

```
Sx <- cov(x)
D <- mahalanobis(x, colMeans(x), Sx)

# We can also use a rank-based Mahalanobis distance matrix
library(designmatch)

D <- distmat(z, x)
```

How matchy-matchy

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

You need other source of exogeneous 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*