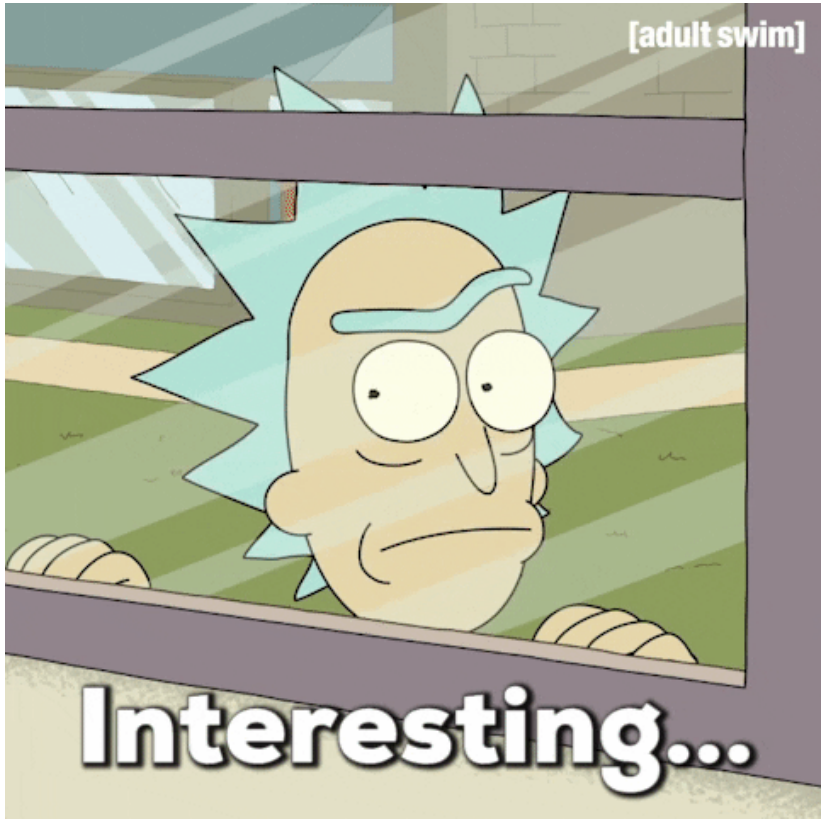
# STA 235 - Causal Inference: Introduction to Observational Studies

## 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:

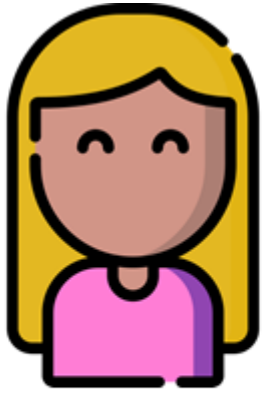
$$Pr(\mathbf{Z}|\mathbf{X}, \mathbf{Y}(0), \mathbf{Y}(1)) = Pr(\mathbf{Z}|\mathbf{X}, \mathbf{Y}'(0), \mathbf{Y}'(1))$$

,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**.

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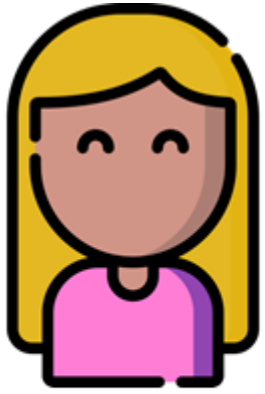
$$\mathbf{X} = \mathbf{X_F}$$



$$(Y_2(0), Y_2(1))$$
$$Z = 0$$
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$$\mathbf{X} = \mathbf{X_F}$$

# 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 $\beta_1$?**

# How do we adjust for observables?

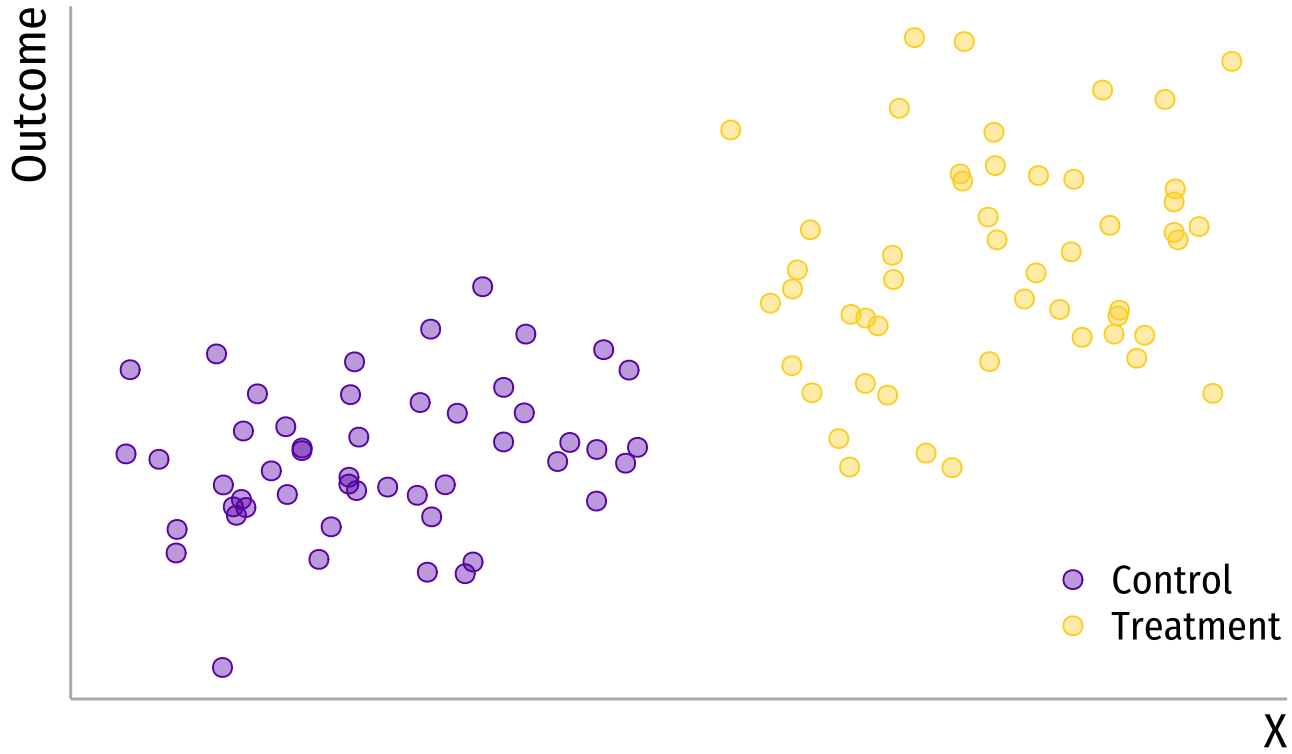
- One way we have seen so far is **regression adjustment**

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

**$\beta_1$ 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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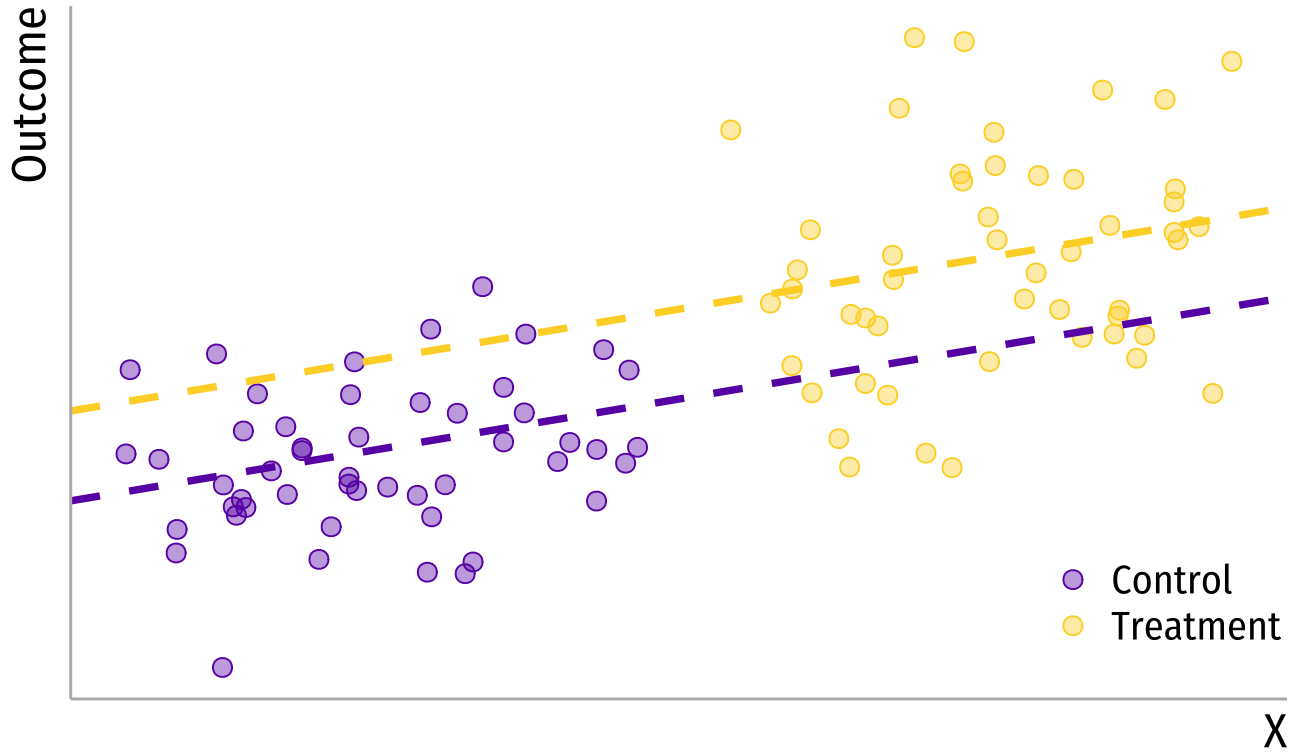

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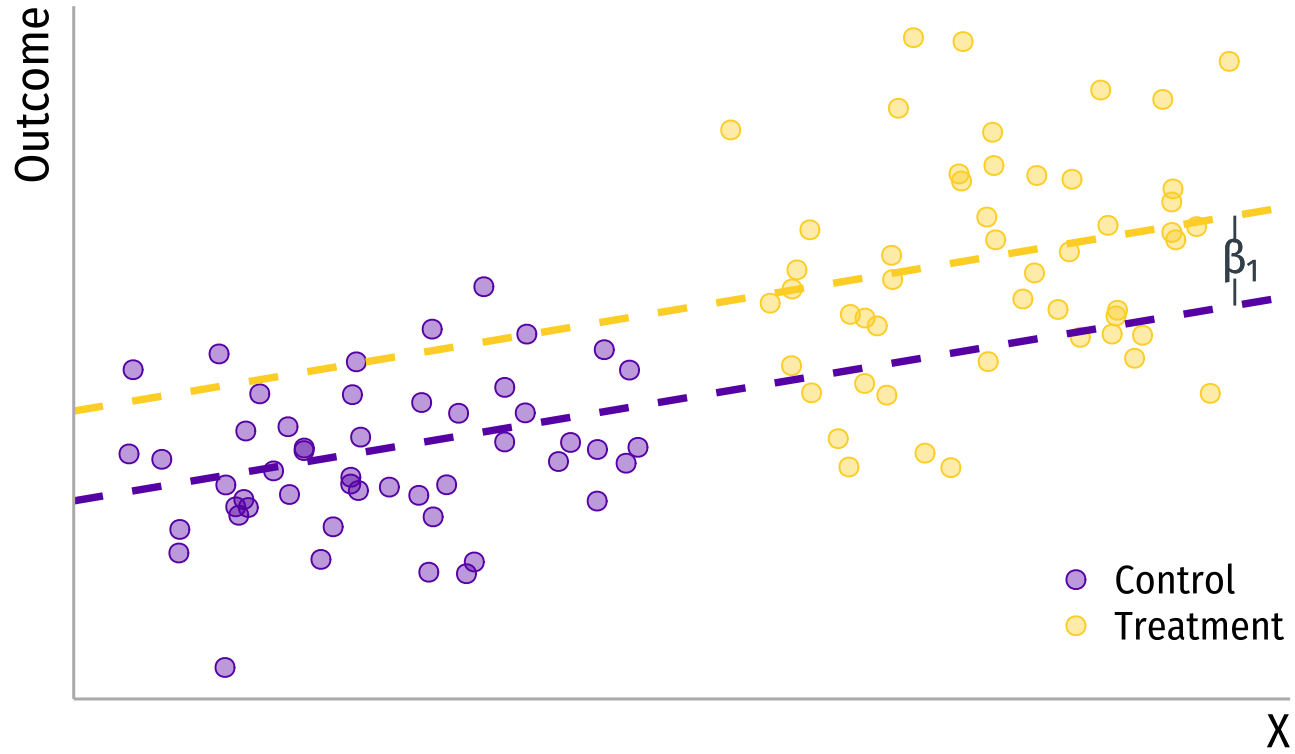

# Finding your perfect match...

# 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

- 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**

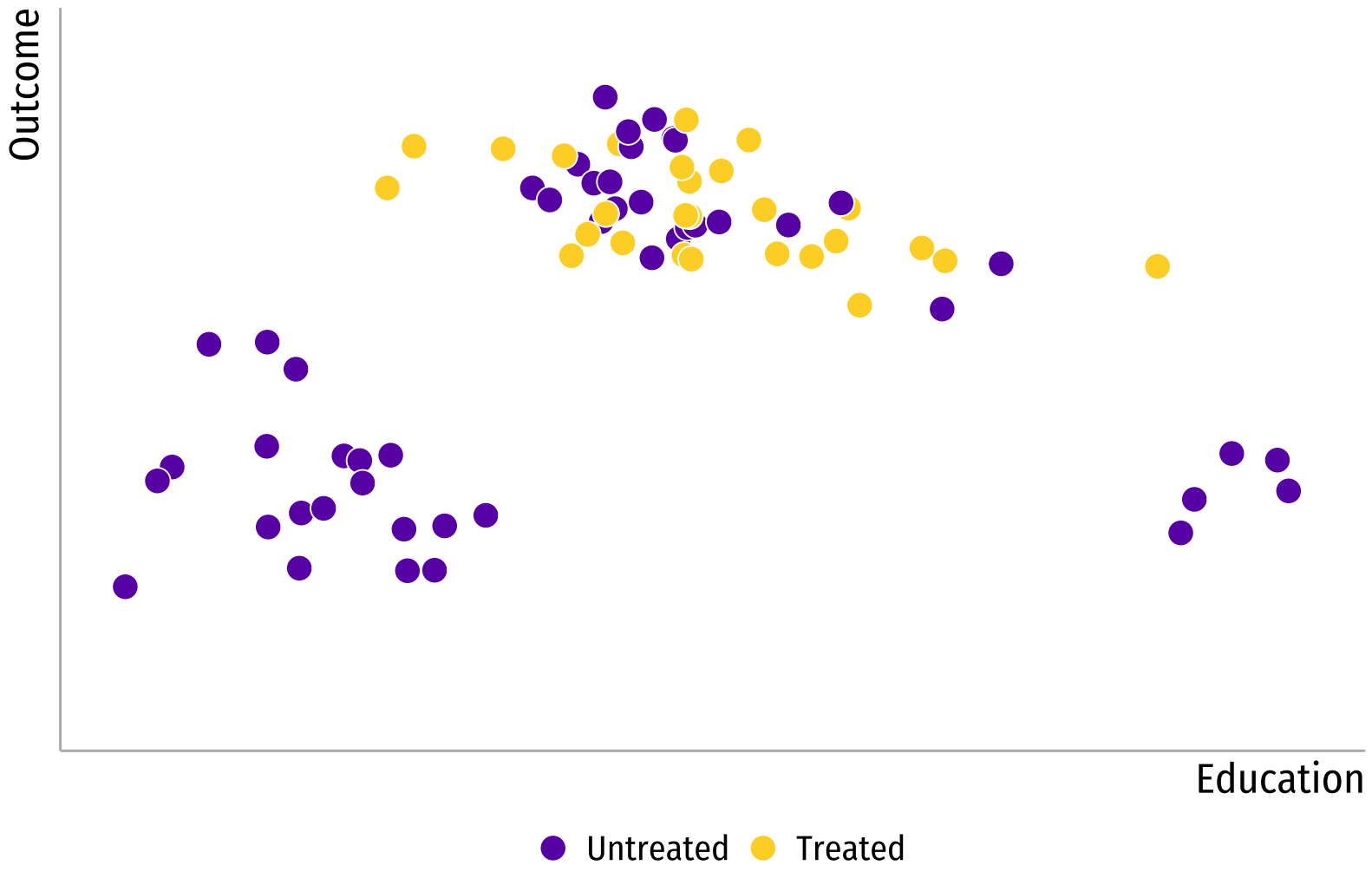
Imbalance → model dependence → researcher discretion → bias

**Compare like to like**

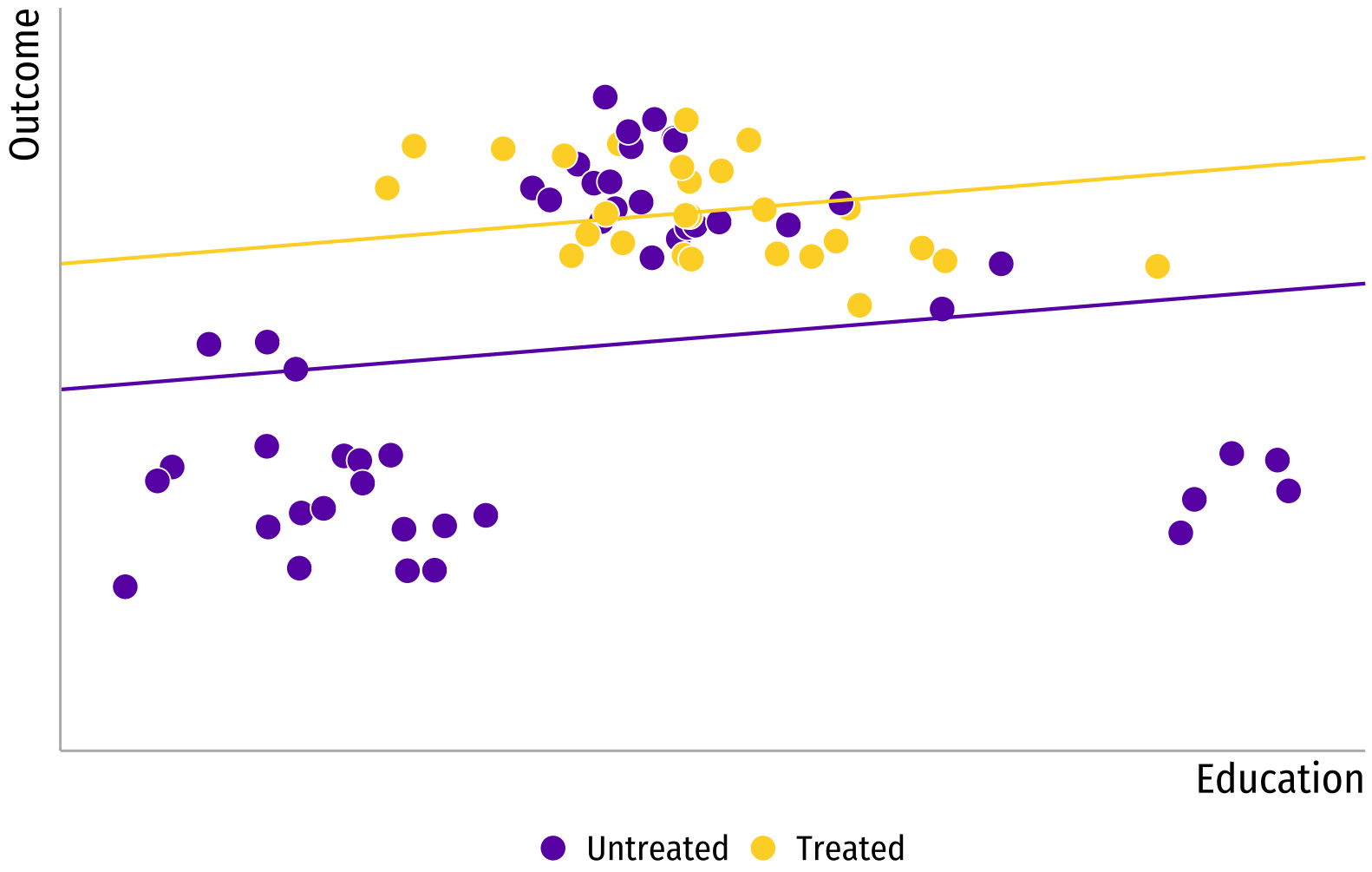
No extrapolation!

**Can adjust closely by covariates**

Exact matching, coarsened exact matching, fine balance..


Outcome
Education
Untreated
Treated

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



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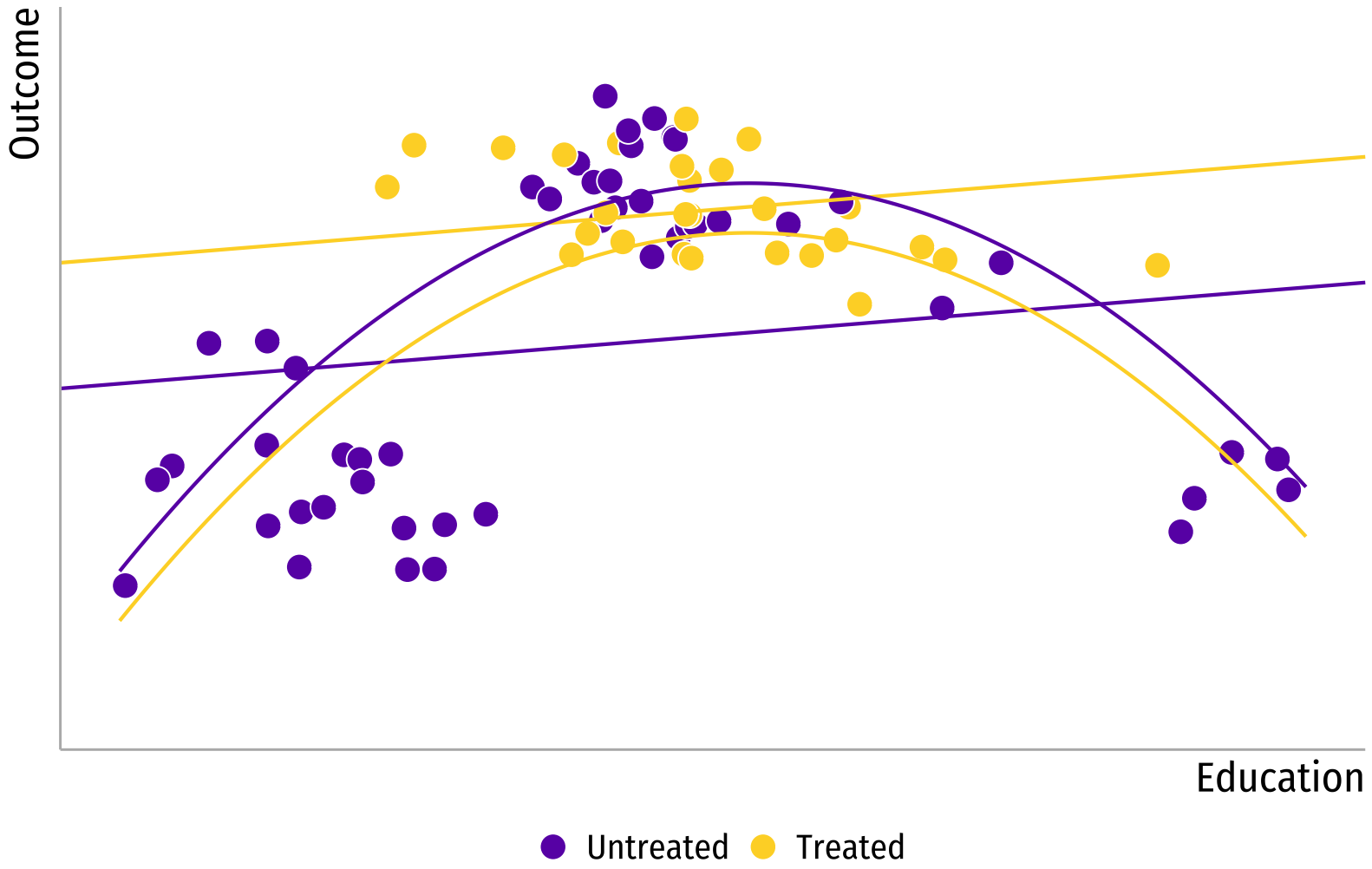

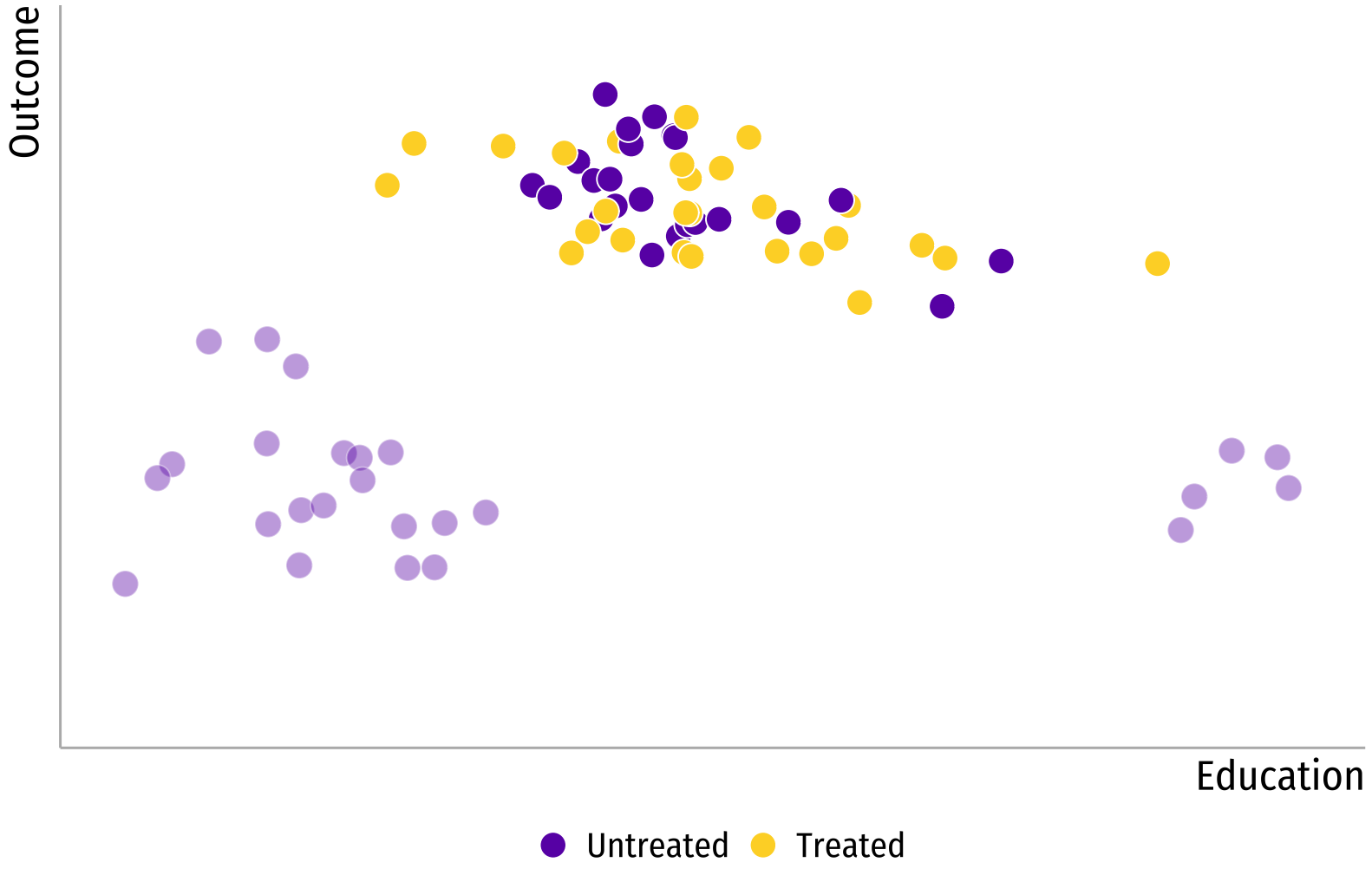
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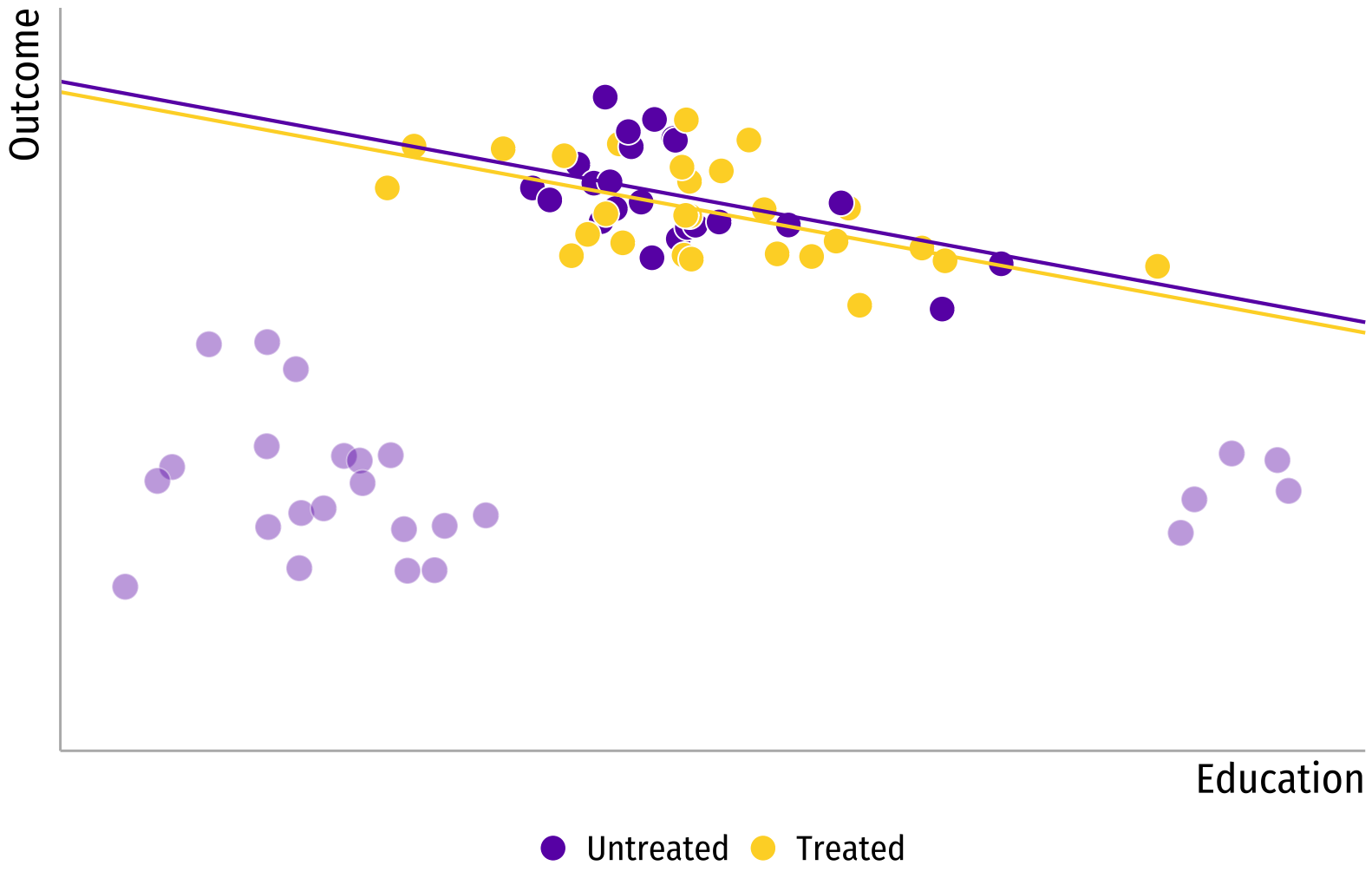

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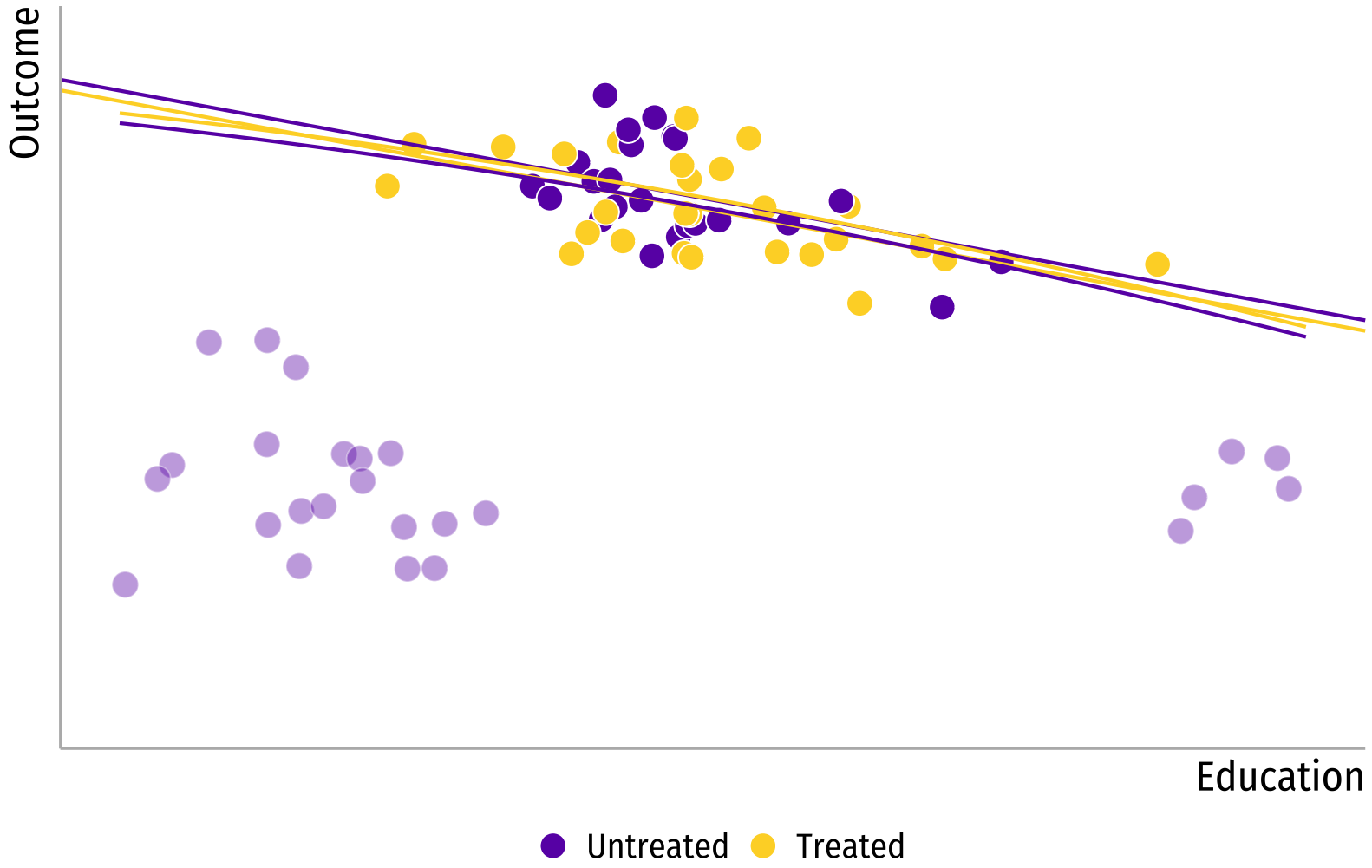
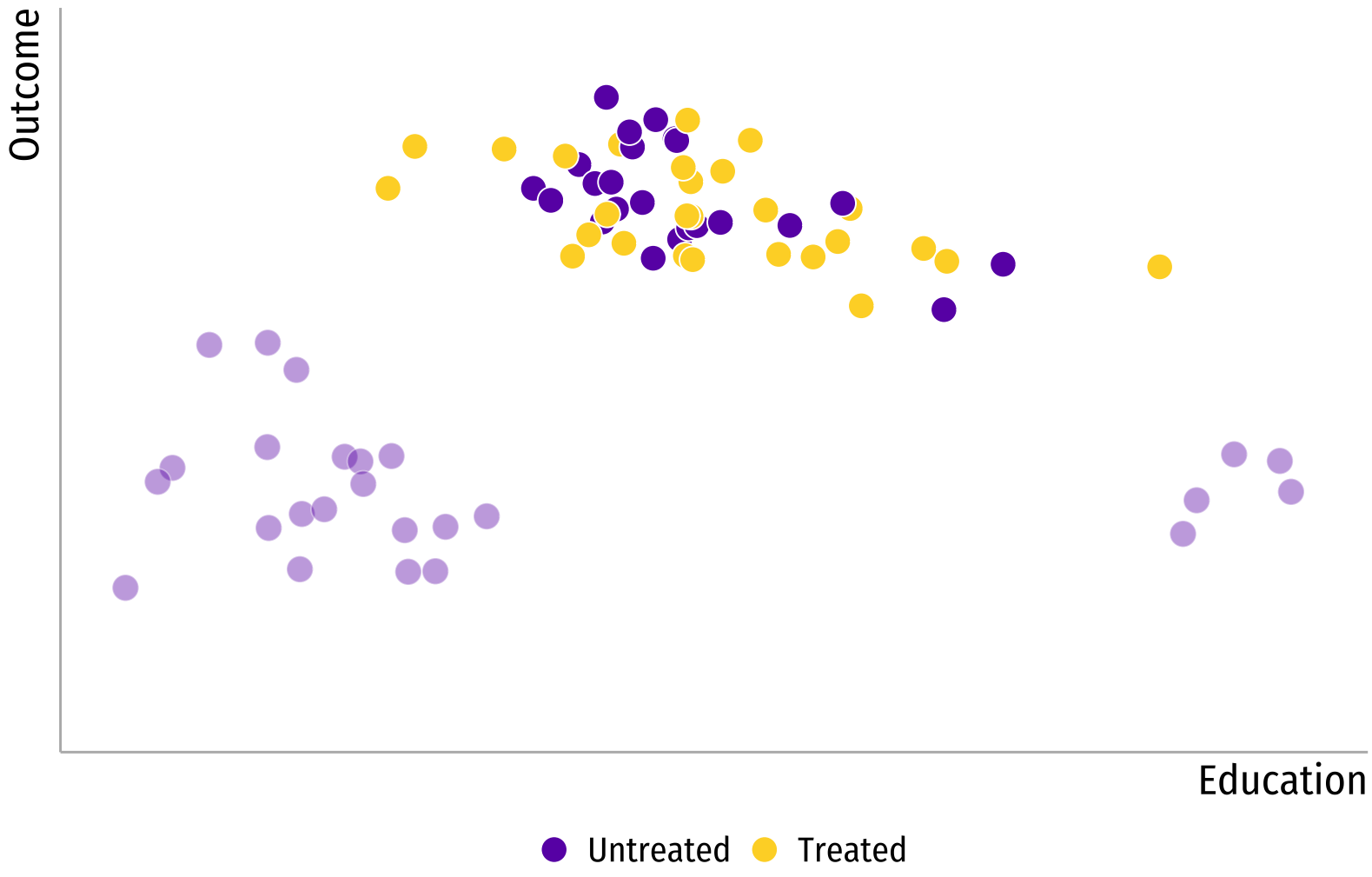
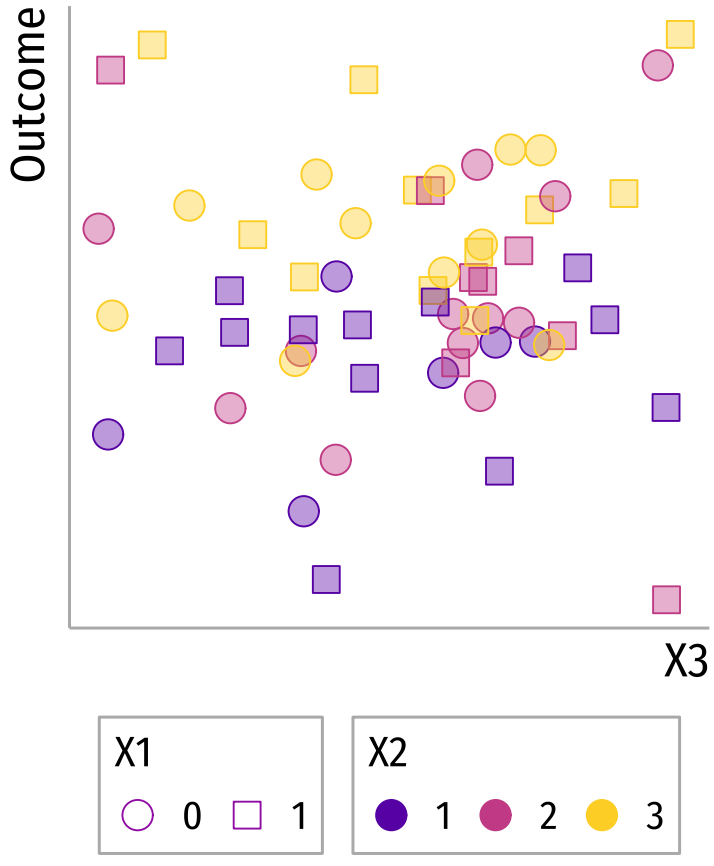


# How do we know we can remove those observations?



# Subclassification

- Very similar to **stratifying**.



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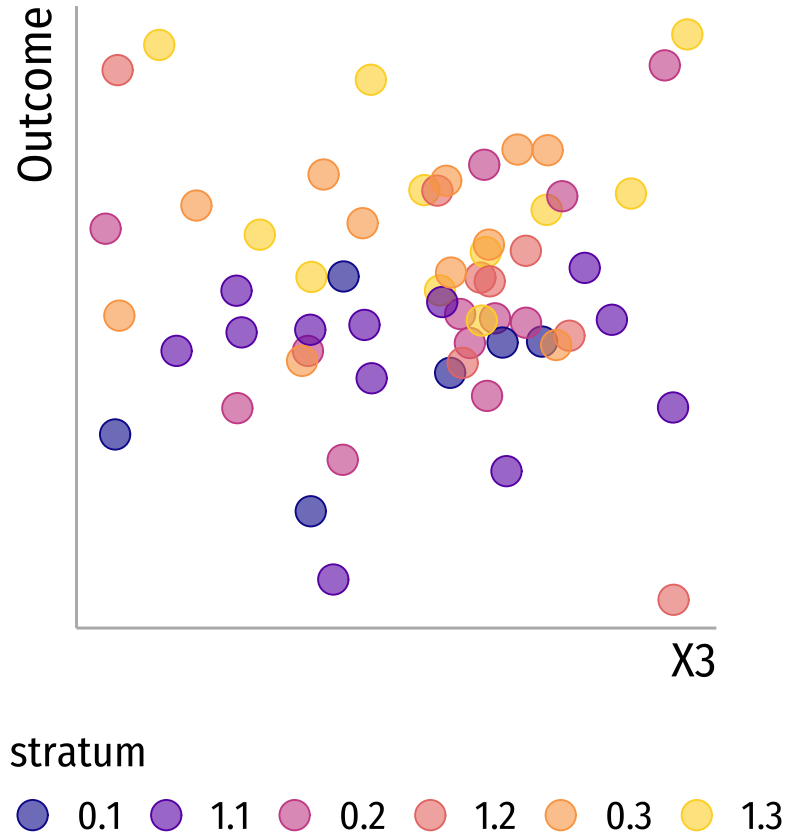

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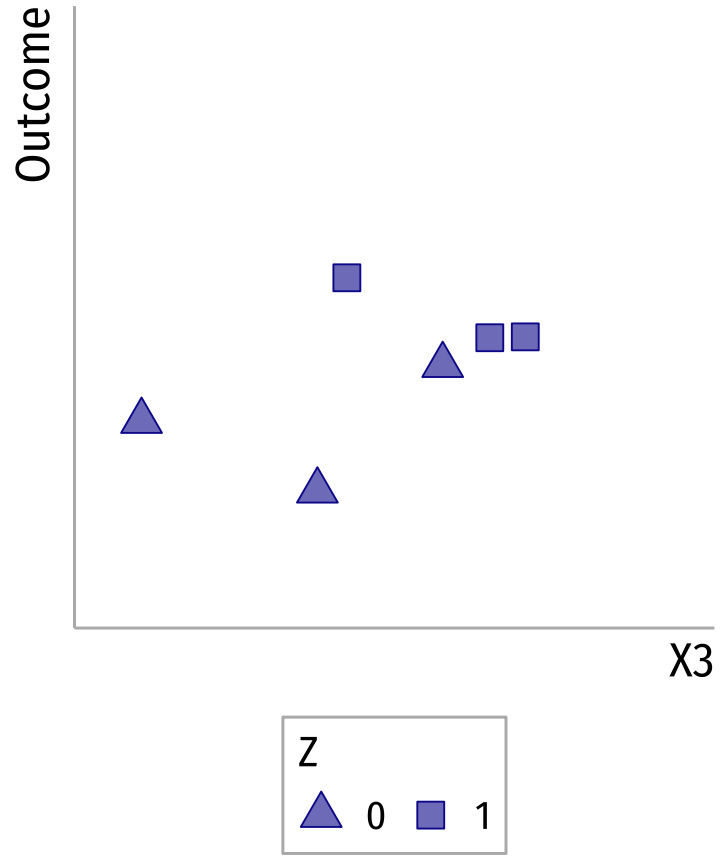

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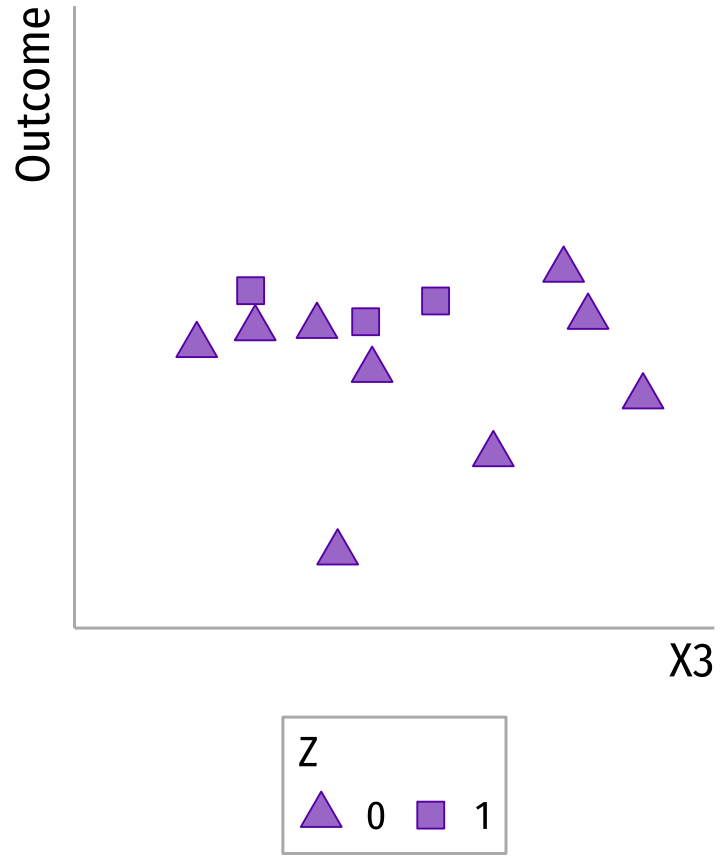

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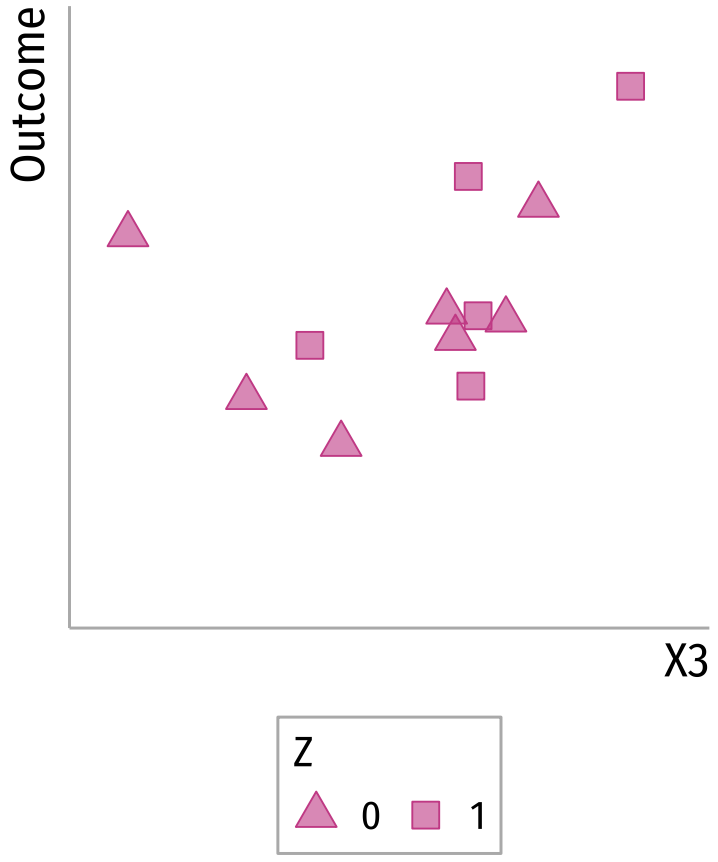

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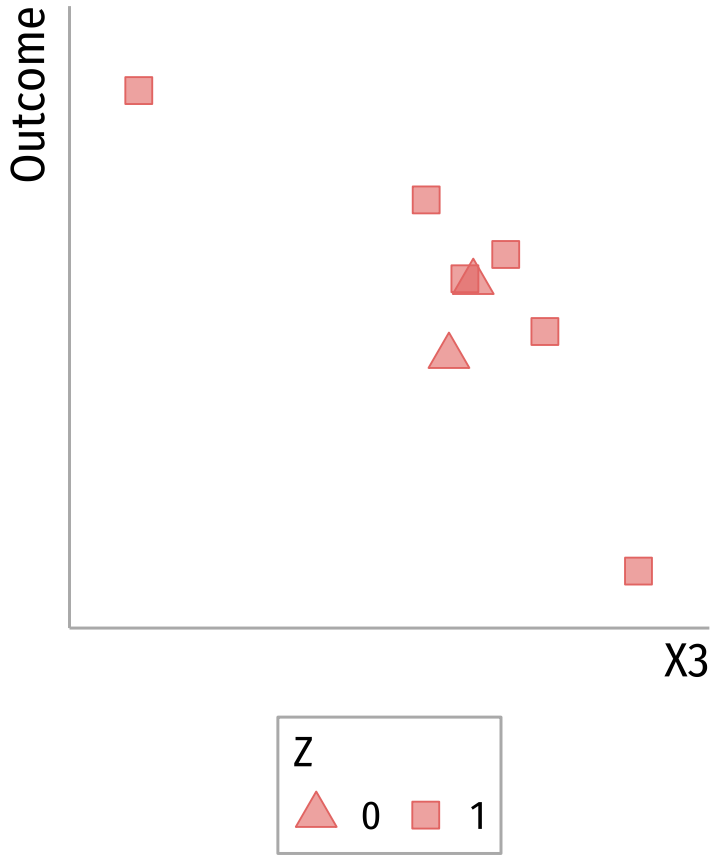

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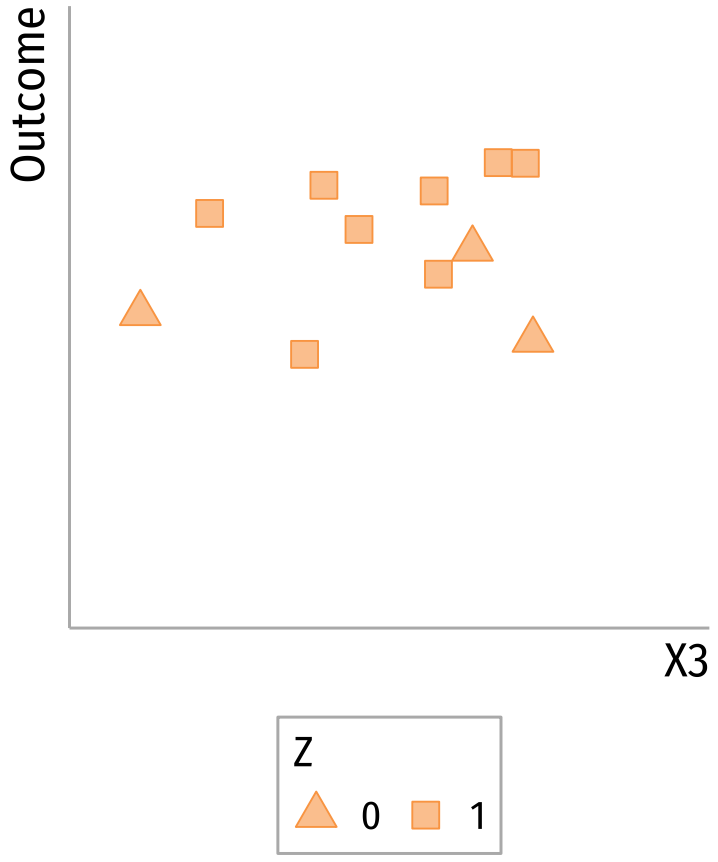

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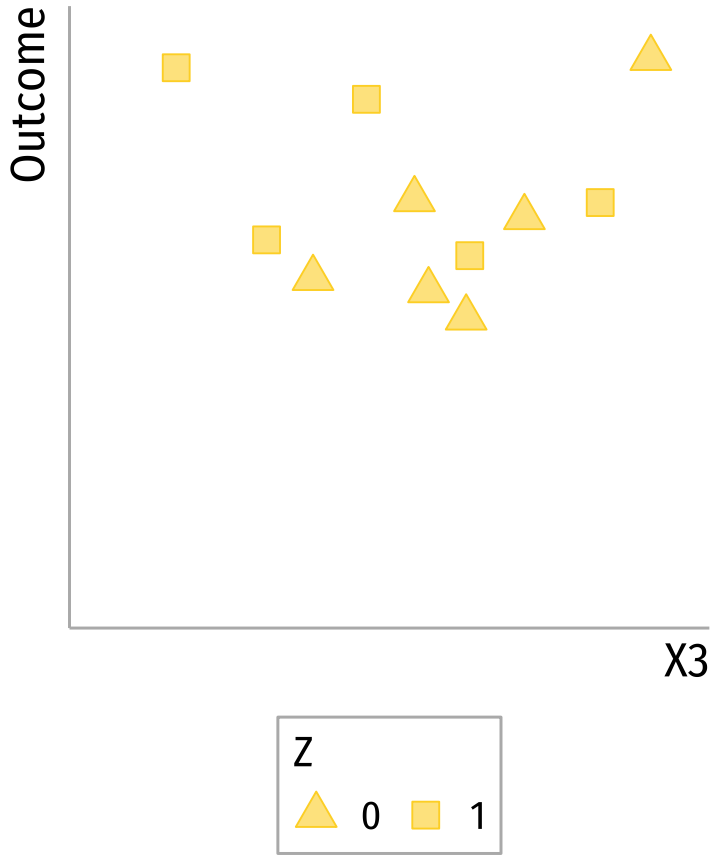

# Subclassification

- 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**!
- Very possible that a stratum only has treatment or control units.

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

**Propensity score**

- Importance of overlap region

# 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 $i$, $\mu$ 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)
```

# 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

# Propensity score matching

**Super popular method**

**There are mathy reasons why it's not great for matching *for identification purposes***

**Some researchers argue propensity scores are fine! Using them for matching isn't!**

PA

# Why Propensity Scores Should Not Be Used for Matching

**Gary King**[1] **and Richard Nielsen**[2]

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[2] *Department of Political Science, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA. Email: rnielsen@mit.edu, URL: http://www.mit.edu/~rnielsen*

## Abstract

We show that propensity score matching (PSM), an enormously popular method of preprocessing data for causal inference, often accomplishes the opposite of its intended goal—thus increasing imbalance, inefficiency, model dependence, and bias. The weakness of PSM comes from its attempts to approximate a completely randomized experiment, rather than, as with other matching methods, a more efficient fully blocked randomized experiment. PSM is thus uniquely blind to the often large portion of imbalance that can be eliminated by approximating full blocking with other matching methods. Moreover, in data balanced enough to approximate complete randomization, either to begin with or after pruning some observations, PSM approximates random matching which, we show, increases imbalance even relative to the original data. Although these results suggest researchers replace PSM with one of the other available matching methods, propensity scores have other productive uses.

*Keywords:* matching, propensity score matching, coarsened exact matching, Mahalanobis distance matching, model dependence

# 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


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- Imbens, G. and D. Rubin. (2015). "Causal Inference for Statistics, Social, and Biomedical Sciences: An Introduction". *Chapter 3*
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