Statistical Methods of Causal Inference
Lecture 2: RCTs and Matching Analysis

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(largely adapted from Dr. David Hendry)

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Outline

1. Housekeeping & General Information
2. Part 1 – Basics of Matching: Sub-classification, Background, Logic of Matching
3. Part 2 – Advanced Topics in Matching: Exact and Distance Matching, Variance-Bias Trade-offs, Propensity Score, Sensitivity Analysis, Practical Steps

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Course Roadmap:

1. 17 July: Potential Outcomes Framework
2. 18 July: RCTs and Matching $\rightarrow$ We are here!
3. 19 July: Panel Data Models
4. 20 July: Difference in Differences
5. 21 July: Instrumental Variable Regression
6. 24 July: Regression Discontinuity Design
7. 25 July: Power Analysis and Advanced Experimental Design
8. 26 July: Practical Issues in Experiments
9. 27 July: Exam Review (afternoon)
10. 28 July: Final Matters (exam in am; Causal inference socials in pm)

Mantra: People who look comparable are not really comparable. They differ in ways we have not observed.

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1 Subclassification

2 Selection On Observables: Background

3 Logic of Matching Methods

Observational Studies

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- Cannot always randomize (e.g., effect of smoking)
- Main problem in observational studies is selection bias
- Goal is to design observational study to approximate an experiment

Smoking and Mortality (Cochran 1968)

Table 1: Death Rates per 1,000 Person-Years

Smoking group	Canada	U.K.	U.S.
Non-smokers	20.2	11.3	13.5
Cigarettes	20.5	14.1	13.5
Cigars/pipes	35.5	20.7	17.4

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Table 2: Mean Ages, Years

Smoking group	Canada	U.K.	U.S.
Non-smokers	54.9	49.1	57.0
Cigarettes	50.5	49.8	53.2
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Subclassification

To control for differences in age, we would like to compare different smoking-habit groups with the same age distribution

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One possibility is to use subclassification:

- for each country, divide each group into different age subgroups
- calculate death rates within age subgroups
- average within age subgroup death rates using fixed weights (e.g., number of cigarette smokers)

Subclassification: Example

	Death Rates for Pipe Smokers	# Pipe Smokers	# Non-Smokers
Age 20 - 50	15	11	29
Age 50 - 70	35	13	9
Age + 70	50	16	2
Total		40	40

Question

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$15 \cdot (11/40) + 35 \cdot (13/40) + 50 \cdot (16/40) = 35.5$

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Table 3: Adjusted Death Rates using 3 Age groups

Smoking group	Canada	U.K.	U.S.
Non-smokers	20.2	11.3	13.5
Cigarettes	28.3	12.8	17.7
Cigars/pipes	21.2	12.0	14.2

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Selection On Observables: The Familiar Case

Subclassification, matching, and propensity-score weighting, when used to make causal inferences, are all examples of causal identification via "selection on observables"

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- Omitted variable bias

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Multivariate linear regression estimates the impact of a treatment, D on an outcome, Y, overcoming omitted variable bias, as follows

$$Y_i = \alpha + \delta D_i + \beta_1 X_{1i} + \beta_2 X_{2i} + \cdots + \beta_k X_{ki} + e_i$$

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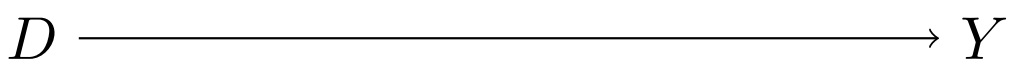

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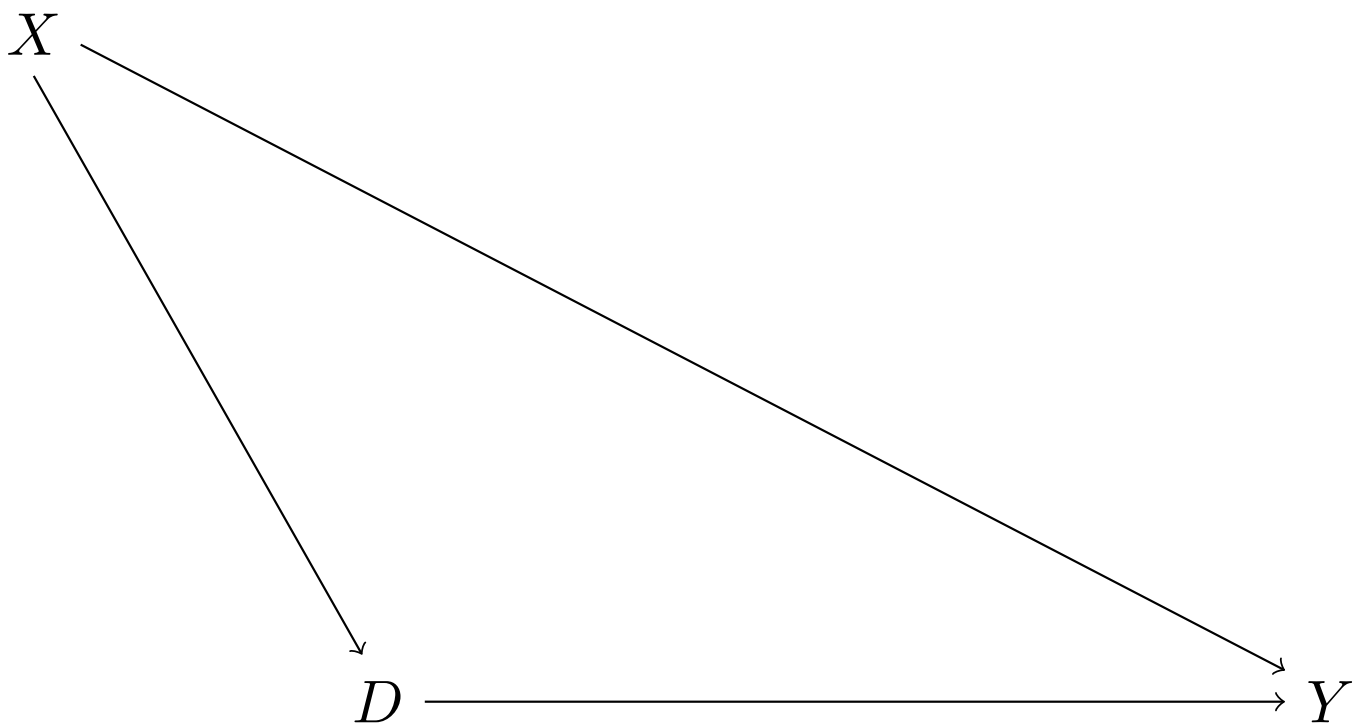

Covariates, Outcomes, and Post-Treatment Bias

Definition (Predetermined Covariates)

Variable X is predetermined with respect to the treatment D if for each individual i, $X_{0i} = X_{1i}$, i.e., the value of X_i does not depend on the value of D_i. Such characteristics are called *covariates*.

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In general, one should not condition on outcomes, because this may induce post-treatment bias

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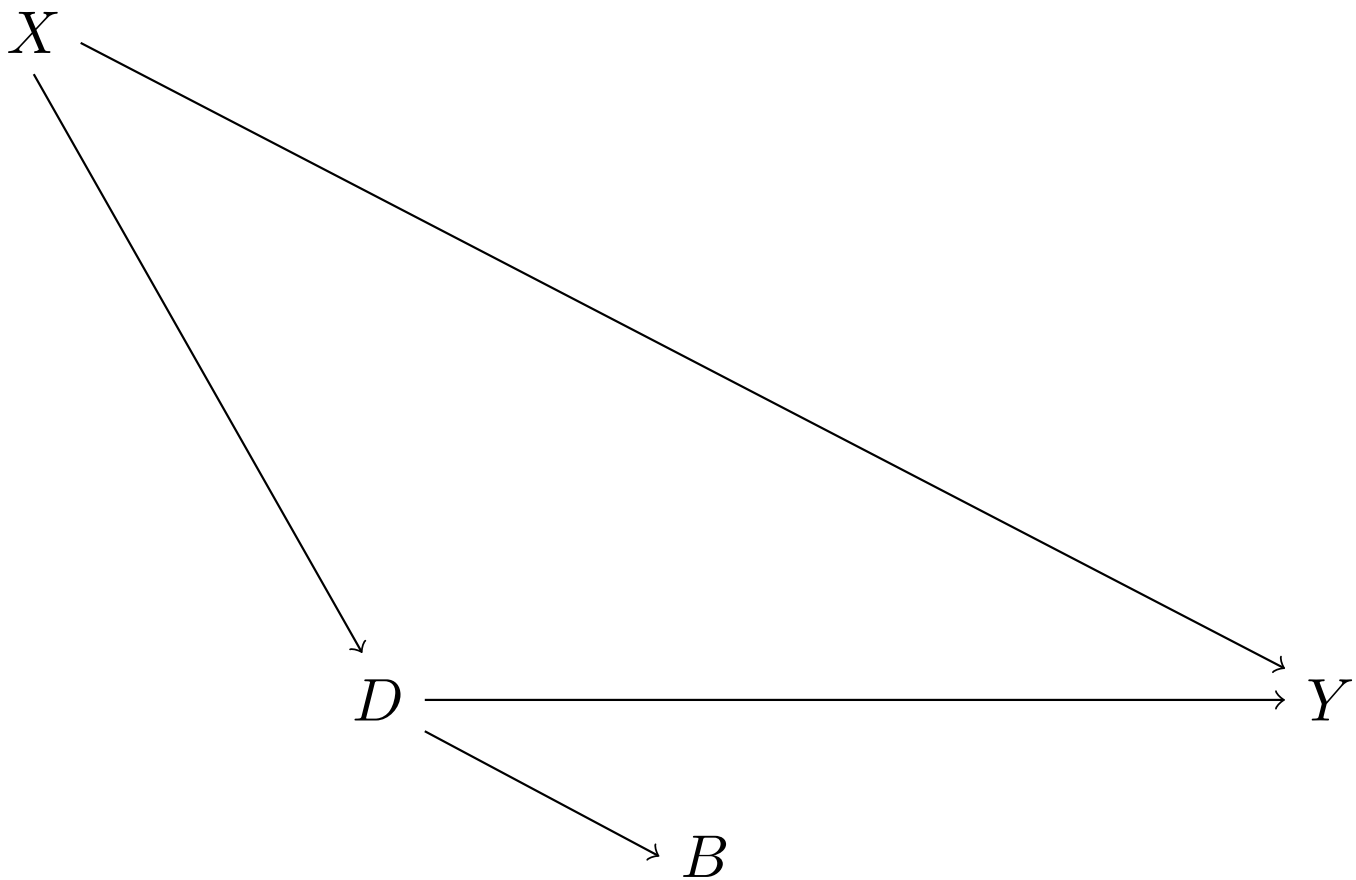
In multivariate linear regression, post-treatment bias would be induced by controlling for variables like B

$$Y_i = \alpha + \delta D_i + \beta_1 X_{1i} + \beta_2 X_{2i} + \cdots + \beta_k X_{ki} + e_i$$



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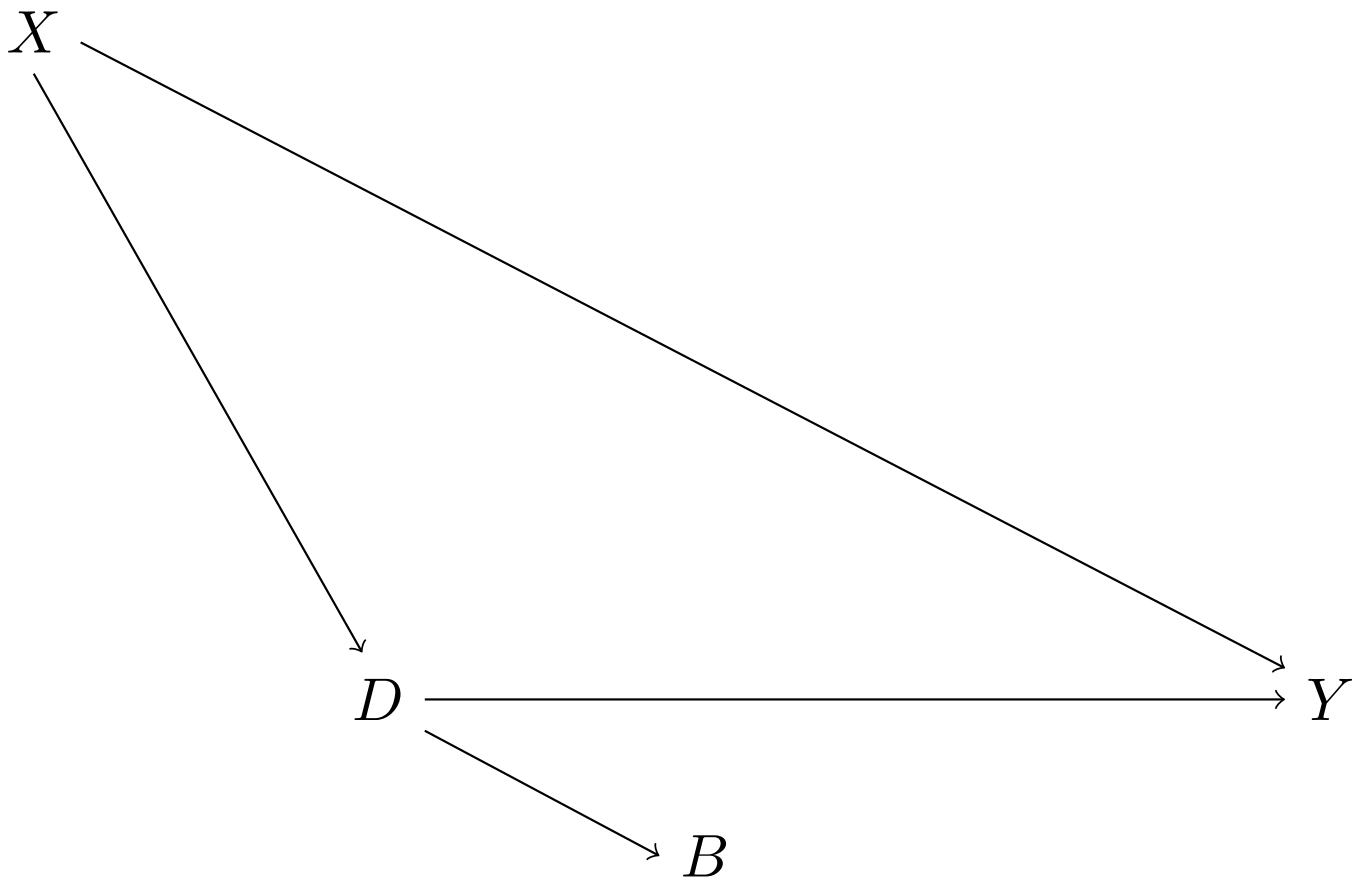

If we control for variables like B, some of the real explained variance from D to Y will be accounted for by the coefficient estimate for B, which is not what we want

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Regression vs. Matching and Weighting

A note of caution:

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- Both regression and matching/weighting achieve causal identification via the selection-on-observables assumption
  - Implies no unmeasured confounders
  - Equally (im)plausible irrespective of the estimation method

The Logic of Matching Methods

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So if multivariate regression and matching/weighting are relying on the same underlying assumption to reach a causal interpretation of their estimates, then why do we not just use regression?

- Matching and weighting have the additional benefit of reducing so-called "model dependence"
- That is, we rid ourselves of the functional-form assumptions necessary for multivariate regression to work

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2. Calculate a simple difference of means (with some corrections to the point estimates and standard errors) to estimate a causal effect

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- Suggests we will often be interested in the *average treatment effect on the treated* rather than the *average treatment effect*
  - Take the treated units as given and worry about constructing their counterfactuals
- Often, but not always, all of the hard work of achieving a plausible case for causal inference will happen through sample construction

Identification under Selection on Observables

Identification Assumptions

1. $(Y_1, Y_0) \perp\!\!\!\perp D|X$ *(selection on observables)*

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   - *Implies that we need to observe all factors that are correlated with both the outcome,* Y*, and treatment assignment,* D *(i.e., confounders)*
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2. $0 < \Pr(D = 1|X = x) < 1 \ \forall \ X$ *(common support)*
   - *For any given realized value of* $X = x$*, there is at least one unit in each of the experimental groups (in this case,* $D = 1$ *and* $D = 0$*)*
   - *If we do not have this, we are unable to estimate counterfactual expected outcomes conditional on* $X = x$
   - *Note: In least squares estimation, we ignore common support and simply use linearity to project conditional expectations onto regions of the distribution of* X *where there is no data*

Identification under Selection on Observables

Identification Assumptions

1. *Selection on Observables*
   - *ATE Version:* $(Y_1, Y_0) \perp\!\!\!\perp D|X$
     - *There exists a set of observable covariates, X, such that after controlling for X, potential outcomes are independent of treatment status*
   - *ATT Version:* $Y_0 \perp\!\!\!\perp D|X$
     - *There exists a set of observable covariates, X, such that after controlling for X, counterfactual outcomes for treated units and observed outcomes for untreated units are independent of treatment status*
2. *Common Support*
   - *ATE Version:* $0 < \Pr(D = 1|X = x) < 1$
     - *For each value of X, there is a positive probability of observing both treated and untreated units*
   - *ATT Version:* $\Pr(D = 1|X = x) < 1$, *with* $\Pr(D = 1) > 0$
     - *For each value of X observed for a treated unit, there should exist an untreated unit with the same value of X*

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Matching

When X is continuous we can estimate α_{ATT} by "imputing" the missing potential outcome of each treated unit using the observed outcome from the "closest" control unit:

$$\widehat{\alpha}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left(Y_i - Y_{j(i)} \right)$$

where $Y_{j(i)}$ is the outcome of an untreated observation such that $X_{j(i)}$ is the closest value to X_i among the untreated observations.

We can also use the average for M closest matches:

$$\widehat{\alpha}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left\{ Y_i - \left(\frac{1}{M} \sum_{m=1}^{M} Y_{j_{m(i)}}, \right) \right\}$$

Works well when we can find good matches for each treated unit.

Matching: Example with single X

unit	Potential Outcome under Treatment	Potential Outcome under Control		
i	Y_{1i}	Y_{0i}	D_i	X_i
1	6	?	1	3
2	1	?	1	1
3	0	?	1	10
4	?	0	0	2
5	?	9	0	3
6	?	1	0	-2

Question

What is $\widehat{\alpha}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left(Y_i - Y_{j(i)} \right)$*?*

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Question

What is $\widehat{\alpha}_{ATT} = \frac{1}{N_1} \sum_{D_i=1} \left(Y_i - Y_{j(i)}\right)$*?*

$$\widehat{\alpha}_{ATT} = 1/3 \cdot (6-9) + 1/3 \cdot (1-0) + 1/3 \cdot (0-9) = -3.7$$

Matching: Distance Metric

Note: Matrix multiplication and inversion are not examinable

Matching: Distance Metric

"Closeness" is often defined by a distance metric that projects the distance between the multivariate covariate vectors $X_i = (X_{i1}, X_{i2}, ..., X_{ik})'$ and $X_j = (X_{j1}, X_{j2}, ..., X_{jk})'$ onto a univariate scale

A commonly used distance is the Mahalanobis distance:

$$D_M(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)} \ ,$$

where S is the sample variance-covariance-matrix.

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2. 1:1 or 1:M nearest-neighbor matching, with $M > 1$
   - 1:1 matching means that for every treated unit, we construct a control by identifying the one closest match among the control cases
   - 1:M matching means that for every treated unit, we construct a control by identifying the M closest matches among the control cases, averaging over their X and Y values, thereby constructing a composite control

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The decisions of whether to use matching with vs. without replacement and 1:1 vs. 1:M matching both involve a decision to use more or less cases

- In 1:1 matching, we use 1 control unit per treated unit, while in 1:M matching, we use M control units per treated unit
- In matching with replacement, we use the same case(s) potentially more than once, and hence end up using fewer cases than in matching without replacement

Bias-Variance Tradeoff in Matching

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1:1 Matching with Replacement

T_1 T_2 T_3

C_1 C_2 C_3 C_4 C_5

1:1 Matching without Replacement

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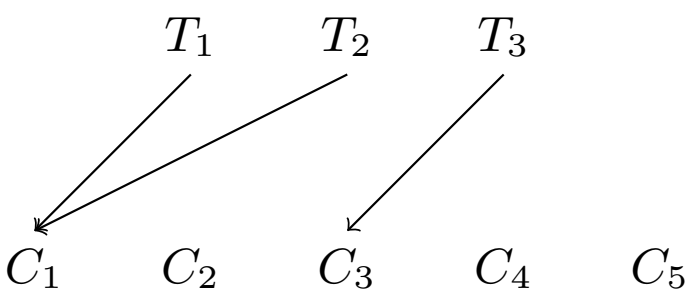

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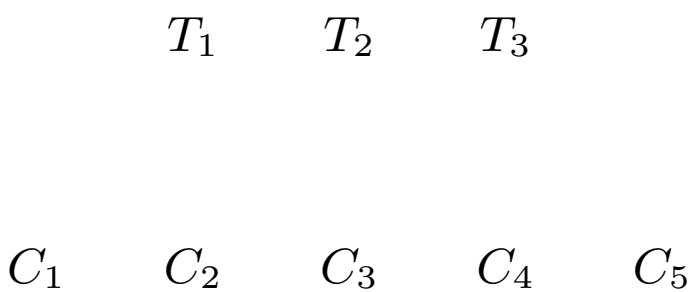

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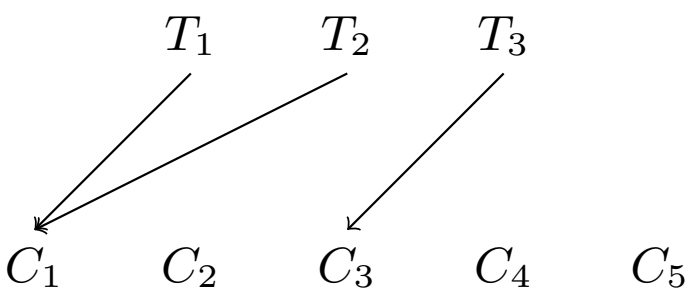

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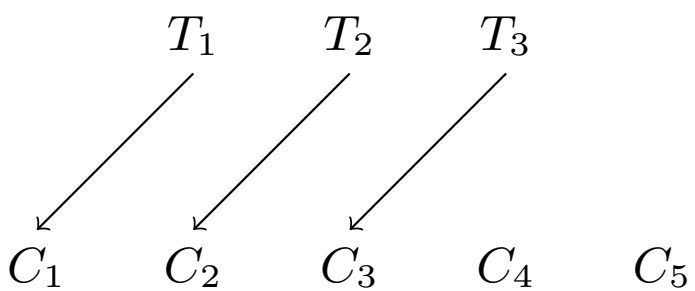

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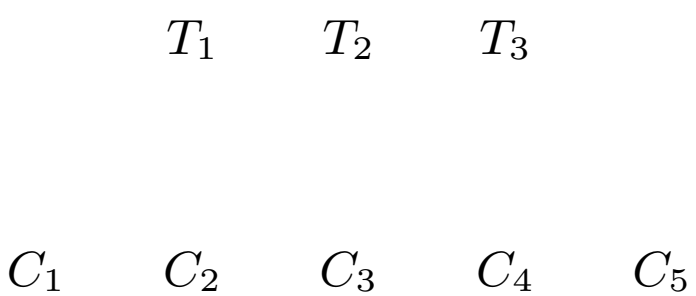
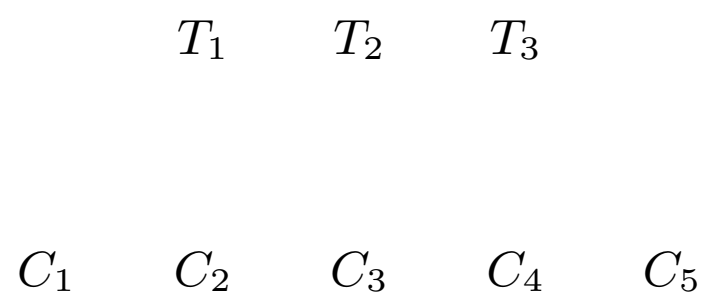


1:2 Matching with Replacement



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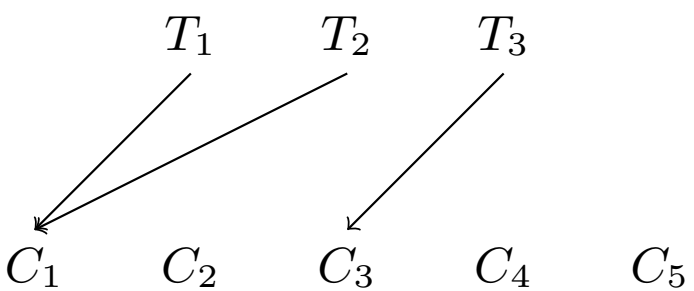

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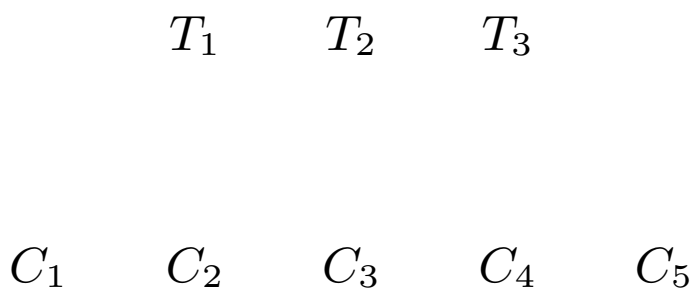

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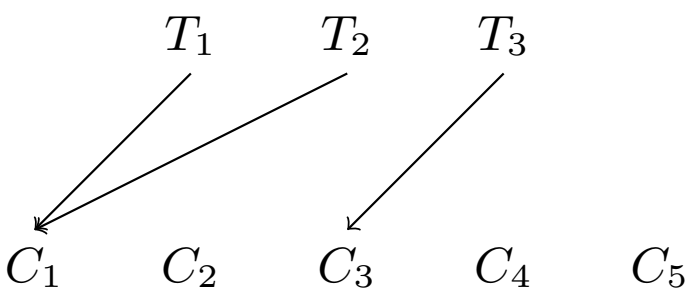

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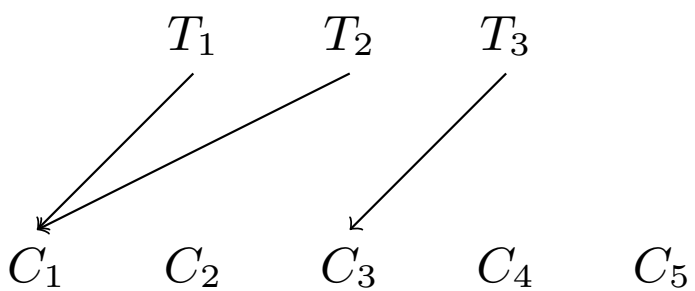

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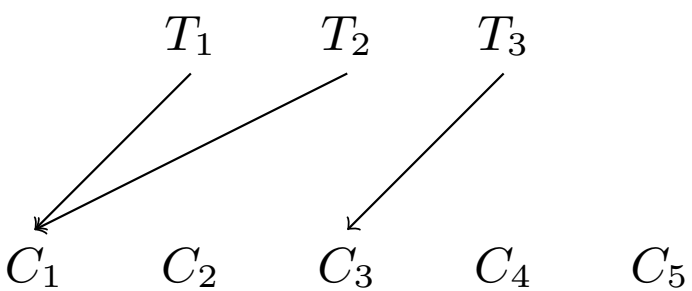

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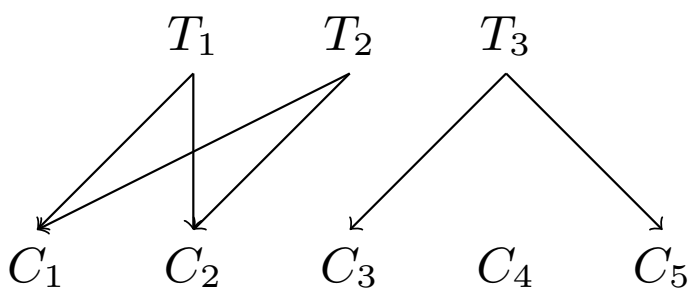

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2 The Bias-Variance Tradeoff in Matching

3 Matching and Weighting with the Propensity Score

4 Sensitivity Analysis

5 Practical Steps in Matching

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- *I.e., conditioning on the propensity score is enough to have independence between the treatment indicator and potential outcomes if and only if selection on observables and common support hold.*
- *Implies substantial dimension reduction*

Matching on the Propensity Score

Corollary

If $(Y_1, Y_0) \perp\!\!\!\perp D|X$, *then*

$$E[Y|D=1, \pi(X)=\bar{\pi}] - E[Y|D=0, \pi(X)=\bar{\pi}] = E[Y_1 - Y_0|\pi(X)=\bar{\pi}]$$

Suggests a two step procedure to estimate causal effects under selection on covariates:

1. Estimate the propensity score $\pi(X) = \Pr(D=1|X)$
   - In practice, this is almost always done using logistic regression
2. Match units on their propensity scores rather than the multidimensional distance between their X variables

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But is there anything that we can do?

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- In matching, most sensitivity analyses ask: How badly can we violate the selection-on-observables assumption and still be confident in our estimate of the treatment effect?

Sensitivity Analysis Using Rosenbaum Bounds

The logic of the most common form of sensitivity analysis in matching is as follows:

- Suppose we have units in our data that have an exact match on their covariates, but yet have different probabilities of being assigned to treatment
  - Formally, $X_j = X_k$ but $\pi(X_j) \neq \pi(X_k)$ for units j and k
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  - Known as "hidden bias"
- Think of a factor Γ that represents how much two units with the same X values could differ in their odds of receiving treatment
  - $\Gamma = 1$ means no hidden bias
  - $\Gamma = 2$ means that two units with the same X could differ in their odds of receiving treatment by a factor of 2
  - ... and so on

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Rosenbaum shows that for units j and k with an exact match on X_j and X_k,

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In a sensitivity test using this framework, we would try out different values of Γ to show how inferences might change in the presence of hidden bias

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    - In matching exercises, prior to constructing a matched sample, this can involve...
        - Simple difference-of-means tests on the outcome variable
        - Regression-adjusted difference-of-means tests on the outcome variable using pre-treatment covariates

Practical Steps in Matching

2. Construct the matched sample
   - Whether using distance-matching or propensity scores, try multiple specifications, using different choices for covariates, numbers of control units for each treatment unit, matching with and without replacement, etc.
   - Check for balance on pre-treatment covariates (e.g., t-tests for balance on pre-treatment covariates, graphical overlays of covariate densities between treatment groups)
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    - For propensity-score matching, explore the distribution of the propensity score across treatment groups
    - Choose your method based on balance, not treatment effects!
        - For best practices, do not even look at treatment effects before the matching method is chosen

Practical Steps in Matching

3. Estimate treatment effects
    - Simple difference-of-means tests between experimental groups
    - Regression-adjusted difference of means tests using pre-treatment variables as controls
    - Same types of graphical techniques used for difference-of-means and regressions
    - Comparisons to unmatched analyses
    - If possible, comparisons to an experimental benchmark

Practical Steps in Matching

4. Evaluate the selection-on-observables assumption with sensitivity analysis
    - Rosenbaum bounds are probably the most widely used test
    - Usually will take the form of asking: How bad will our inferences be if we left out an important covariate?

Summary

The goal of matching is to generate greater balance in the distribution of pretreatment potential confounders between treatment and control groups in a non-experimental setting

- A search for a subset or transformed set of data that resembles an experiment but is contained within an observational study
- Requires some version of the selection on observables and common support assumptions

Selection on observables (along with other assumptions) gives us causal identification if we can claim that we can account for all of the variables that affect both treatment assignment and outcomes

- Very demanding assumption
- No omitted variables assumption of linear regression is one form of the assumption
- Other methods like subclassification and matching require it, but do not rely on the parametric assumptions of linear regression

Common support

- Not required in linear regression
- Required in matching because it does not rely on the functional form assumptions of linear regression
- Depending on our chosen estimand, requires us to have comparable cases with respect to X in the treatment and control groups