Lecture 4: When Complete Randomization is Infeasible

Matching and Weighting

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Outline

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Complete randomization can be inefficient

Imagine you can only "afford" 20 consumers in your study.
You know beforehand **gender** is an important factor for the study outcomes.

If you were leave it to chance to assign the 20 consumers:

Randomly assign 20 consumers

```
people <- rep(c("female","male"),10)
unlist(rerun(10,
sum(sample(people,10,replace = F)=="female"))
[1] 6 4 4 4 5 6 5 7 5 3
```

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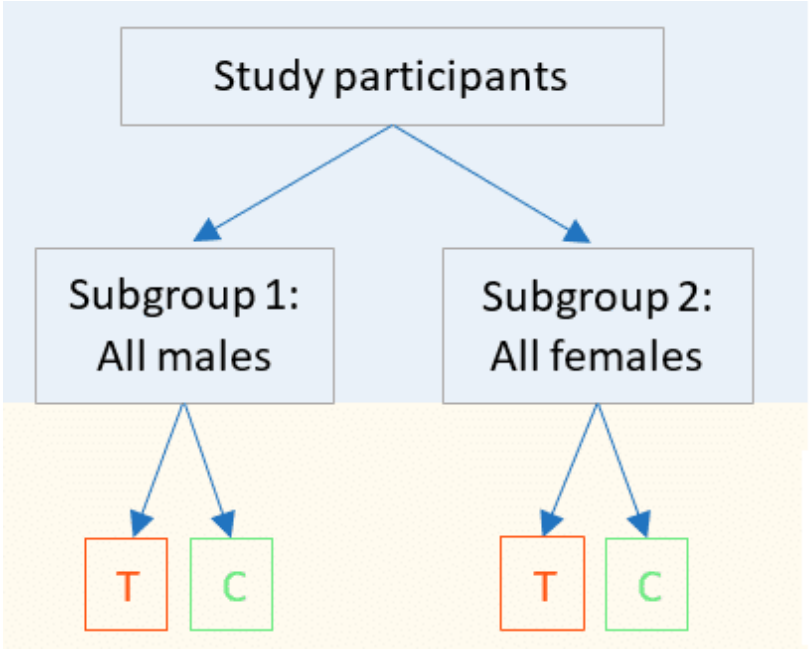
Blocking to increase efficiency

Instead, **we stratify the sample to females and males**, and **then randomize within each subgroup**.

1. Reduces sampling uncertainty and improves precision;
2. Ensures that certain subgroups are available for analysis (heterogeneity).



The treatment and control groups are forced to be equivalent regarding gender

Blocking is efficient: An example

store	block	All Stores Y_1	All Stores Y_0	Block A Y_1	Block A Y_0	Block B Y_1	Block B Y_0
1	A	4	1	4	1		
2	A	5	3	5	3		
3	A	6	2	6	2		
4	A	4	1	4	1		
5	A	3	2	3	2		
6	A	2	1	2	1		
7	B	10	8			10	8
8	B	13	10			13	10
9	B	11	9			11	9
10	B	10	8			10	8
11	B	12	10			12	10
12	B	11	11			11	11
Mean		7.6	5.5	4.0	1.7	11.2	9.3
Variance		14.2	15.6	1.7	0.6	1.1	1.2

Under complete randomization:

$$\begin{cases} \text{ATE}_{\text{CR}} & = 7.6 - 5.5 = 2.1 \\ \text{SE}_{\text{CR}}^{\text{Neyman}} & = \sqrt{\frac{14.2}{12} + \frac{15.6}{12}} = \mathbf{1.57} \end{cases}$$

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Blocking is efficient: An example

store	block	All Stores Y_1	All Stores Y_0	Block A Y_1	Block A Y_0	Block B Y_1	Block B Y_0
1	A	4	1	4	1		
2	A	5	3	5	3		
3	A	6	2	6	2		
4	A	4	1	4	1		
5	A	3	2	3	2		
6	A	2	1	2	1		
7	B	10	8			10	8
8	B	13	10			13	10
9	B	11	9			11	9
10	B	10	8			10	8
11	B	12	10			12	10
12	B	11	11			11	11
Mean		7.6	5.5	4.0	1.7	11.2	9.3
Variance		14.2	15.6	1.7	0.6	1.1	1.2

Under block randomization:

$$\begin{cases} \text{ATE}_{\text{BR}} = \sum_{b=1}^{B} \frac{N_b}{N} \text{ATE}_b & = \frac{6}{12} \cdot 2.3 + \frac{6}{12} \cdot 1.9 = 2.1 \\ \text{SE}_{\text{BR}}^{\text{Neyman}} = \sqrt{\sum_{b=1}^{B} \left(\frac{N_b}{N} \text{SE}_{\text{b}}^{\text{Neyman}} \right)^2} & = \mathbf{0.62} \end{cases}$$

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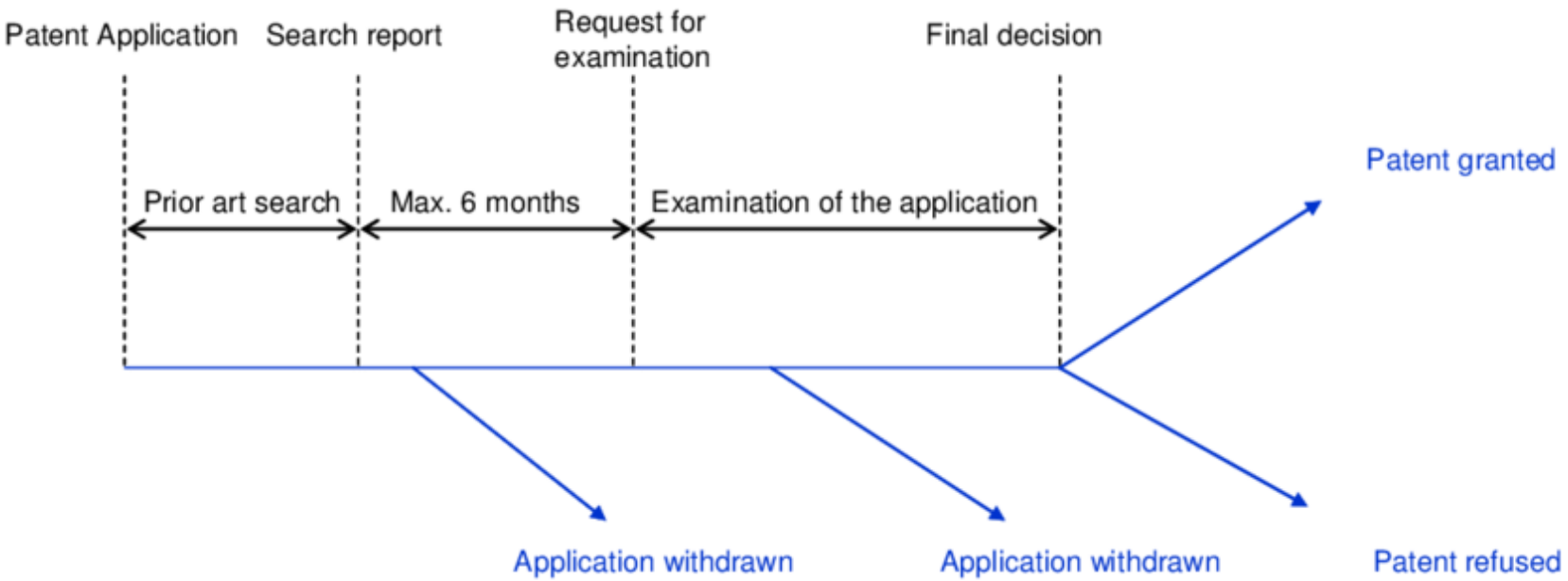
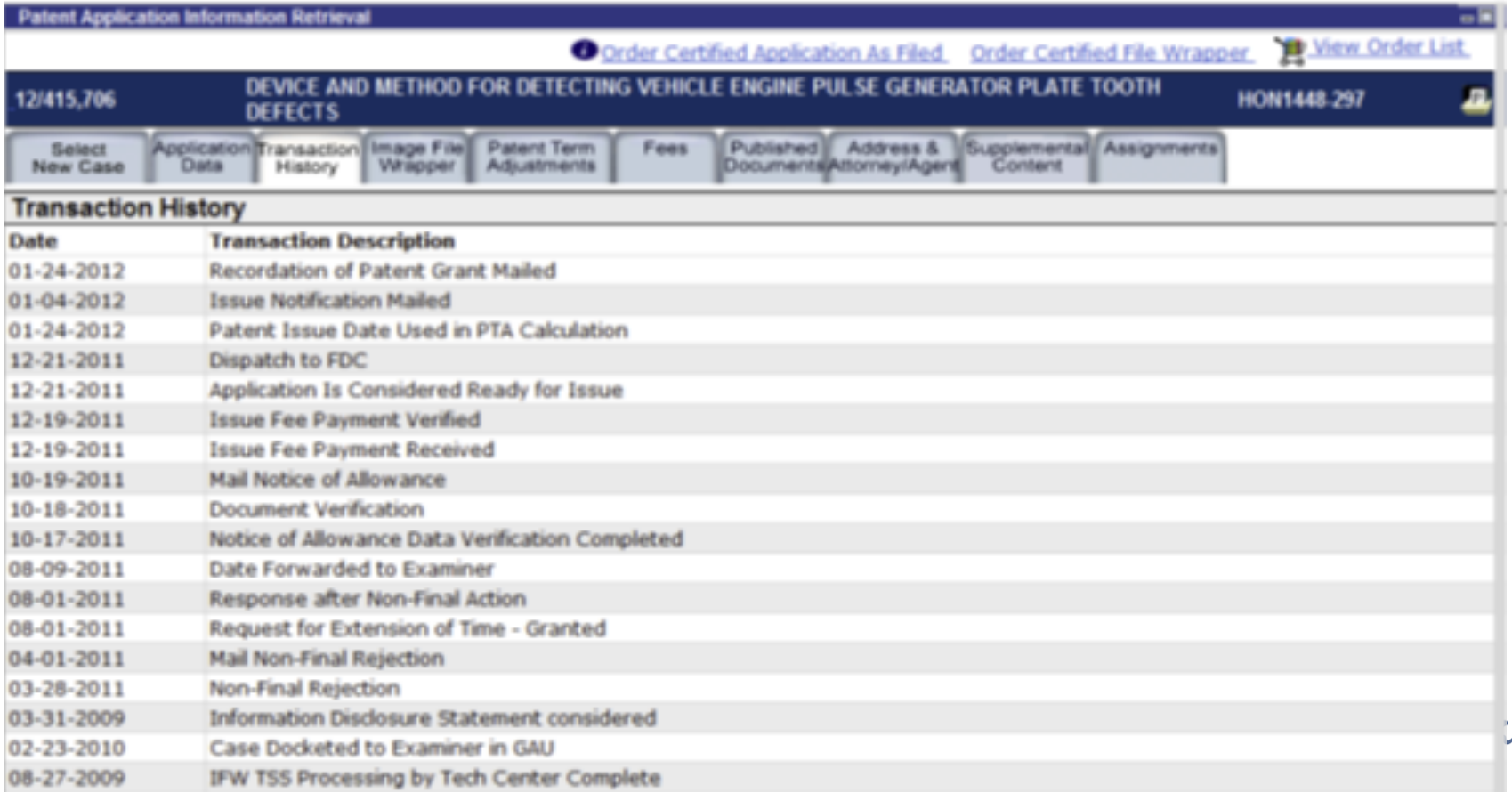
Patent examination



Patent examination

- **Treatment**: Patent granted.
- **Assignment**: Patent examination.



Patent Application Information Retrieval

Order Certified Application As Filed | Order Certified File Wrapper | View Order List

12/415,706 — DEVICE AND METHOD FOR DETECTING VEHICLE ENGINE PULSE GENERATOR PLATE TOOTH DEFECTS — HON1448-297

Select New Case | Application Data | Transaction History | Image File Wrapper | Patent Term Adjustments | Fees | Published Documents | Address & Attorney/Agent | Supplemental Content | Assignments

Transaction History

Date	Transaction Description
01-24-2012	Recordation of Patent Grant Mailed
01-04-2012	Issue Notification Mailed
01-24-2012	Patent Issue Date Used in PTA Calculation
12-21-2011	Dispatch to FDC
12-21-2011	Application Is Considered Ready for Issue
12-19-2011	Issue Fee Payment Verified
12-19-2011	Issue Fee Payment Received
10-19-2011	Mail Notice of Allowance
10-18-2011	Document Verification
10-17-2011	Notice of Allowance Data Verification Completed
08-09-2011	Date Forwarded to Examiner
08-01-2011	Response after Non-Final Action
08-01-2011	Request for Extension of Time - Granted
04-01-2011	Mail Non-Final Rejection
03-28-2011	Non-Final Rejection
03-31-2009	Information Disclosure Statement considered
02-23-2010	Case Docketed to Examiner in GAU
08-27-2009	IFW TSS Processing by Tech Center Complete

Yelp Elite

yelp elite

The 2014 Yelp Providence Elite Squad

Hey there, Phil R.!

Elite badges are so hot right now... and let's be honest, so is your writing! We received a nomination and agree that you embody the spirit of Yelp with your enthusiasm, positivity, constructive honesty and useful funny coolness. So you can consider this your official invite to be on the Providence Elite Squad!

Thunderous applause

As an Elite, you'll be an ambassador both on and offline. We do ask that you keep on being a stellar yelper with rich and consistently contributed reviews. A great elite also compliments other folks, votes on reviews, participates respectfully in Talk and welcomes new members to the site. As an elite, you'll be invited to attend exclusive parties and events that we throw around town and be privy to hot giveaways.

What is Yelp Elite?

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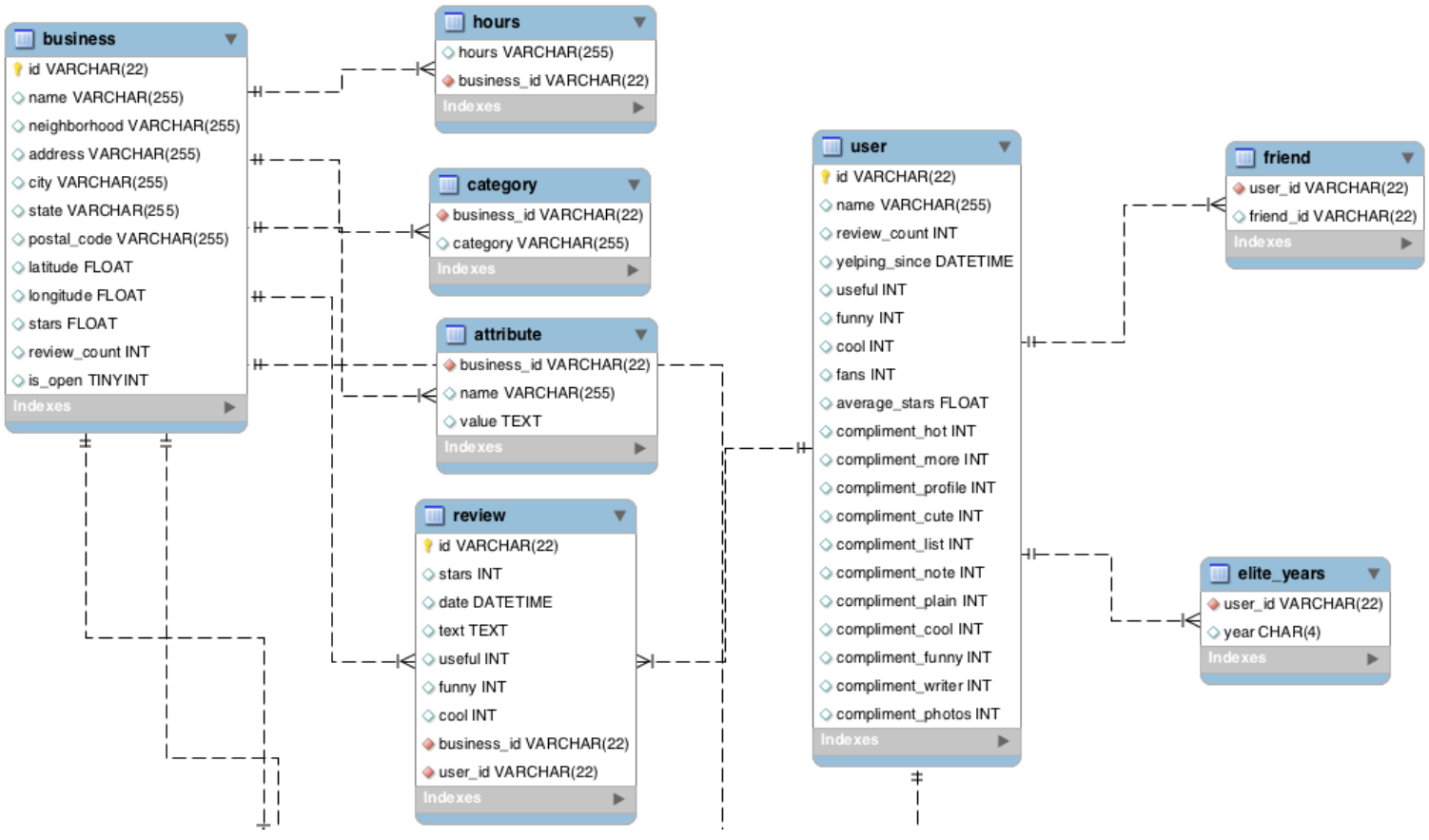
Yelp Elite



Almost all information is know, but not how Yelp selects Elites.

Outline

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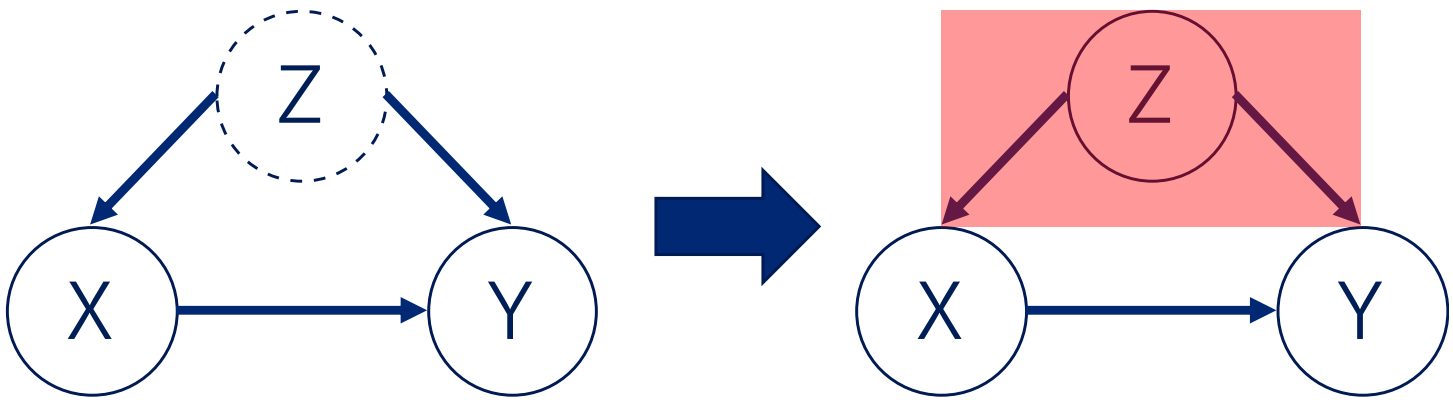
Assumptions

Identification Assumptions

1. $(Y_i^1, Y_i^0) \perp D_i \mid X_i$ (conditional unconfoundedness)
2. $p_i(D_i = 1 \mid X_i) \in (0, 1)$ (common support)



It's essentially a "conditioning" identification strategy

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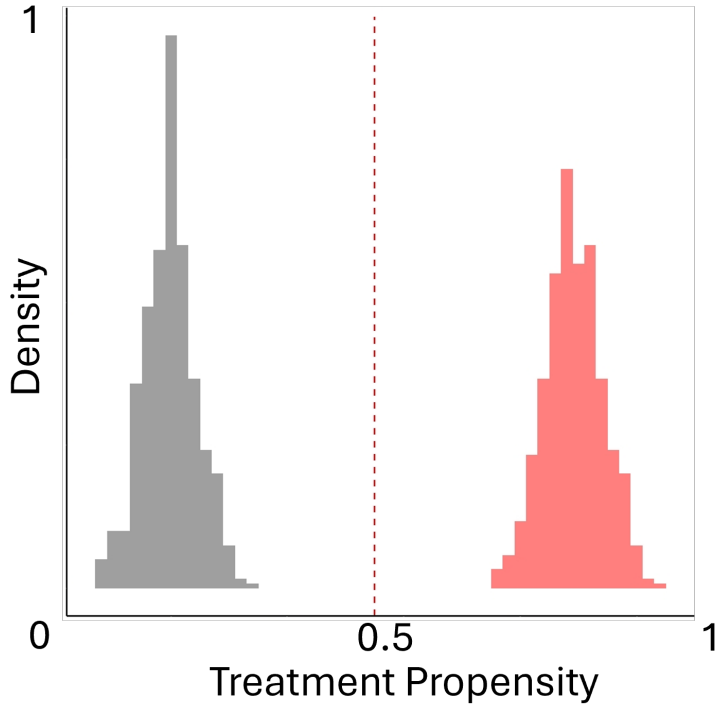
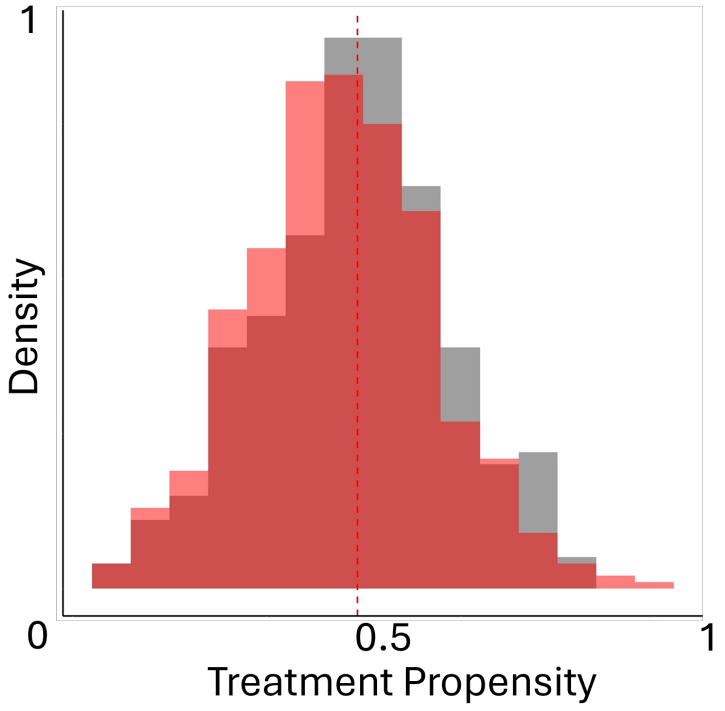
Understanding common support

The treatment propensity of the treated vs. control group must be overlapped.



(a) Non-overlapped



(b) Overlapped

Identification results: ATE

Under the conditional unconfoundedness:

$$E\left[Y_i^1 \mid X_i, D_i = 1\right] = E\left[Y_i^1 \mid X_i\right]$$
$$E\left[Y_i^0 \mid X_i, D_i = 0\right] = E\left[Y_i^0 \mid X_i\right]$$

With common support assumption:

$$\tau_{\text{ATE}} = \int \left(E\left[Y_i^1 \mid X_i\right] - E\left[Y_i^0 \mid X_i\right]\right) dP\left(X_i\right)$$

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Identification results: ATT

Under milder assumptions, in practices, also identify **ATT** (average treatment effects on the treated units).

$$\text{ATT} = E\left[Y_i^1 - Y_i^0 \mid D_i = 1\right]$$

If we assume a milder version of unconfoundedness: $Y_i^0 \perp D_i \mid X_i$ and common support $p_i\left(D_i = 1 \mid X_i\right) < 1$, ATT is identified.

$$E\left[Y_i^0 \mid X_i, D_i = 1\right] = E\left[Y_i^0 \mid X_i\right]$$

$E\left[Y_i^1 \mid X_i, D_i = 1\right]$, directly from data

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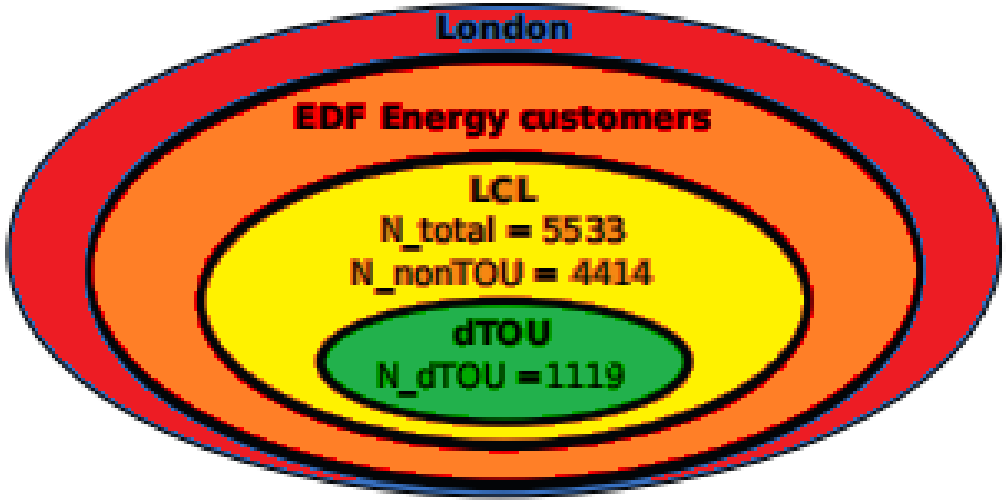
An example of ATT: "Low Carbon London" trial

Figure: Venn diagram illustrating the sample selection in LCL trial



The control group is randomly drawn and therefore ATT is identified.

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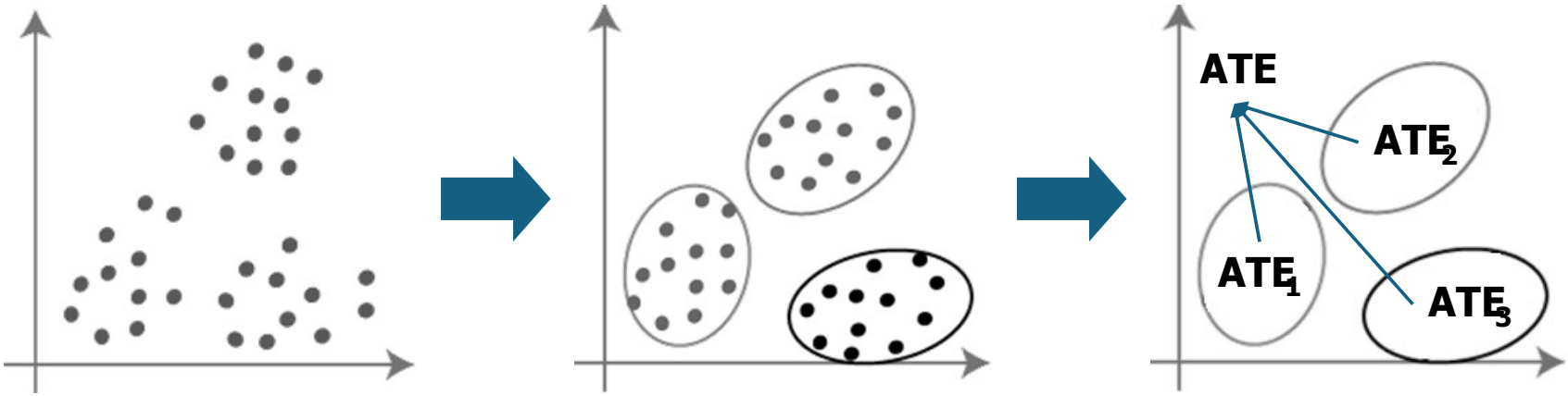
Subclassification: the process

Given $(Y_i^1, Y_i^0) \perp D_i \mid X_i$, emulate blocking by creating "blocks" based on X_i:

- Discrete variables: to use directly.
- Continuous variables: to first discretize and then use.



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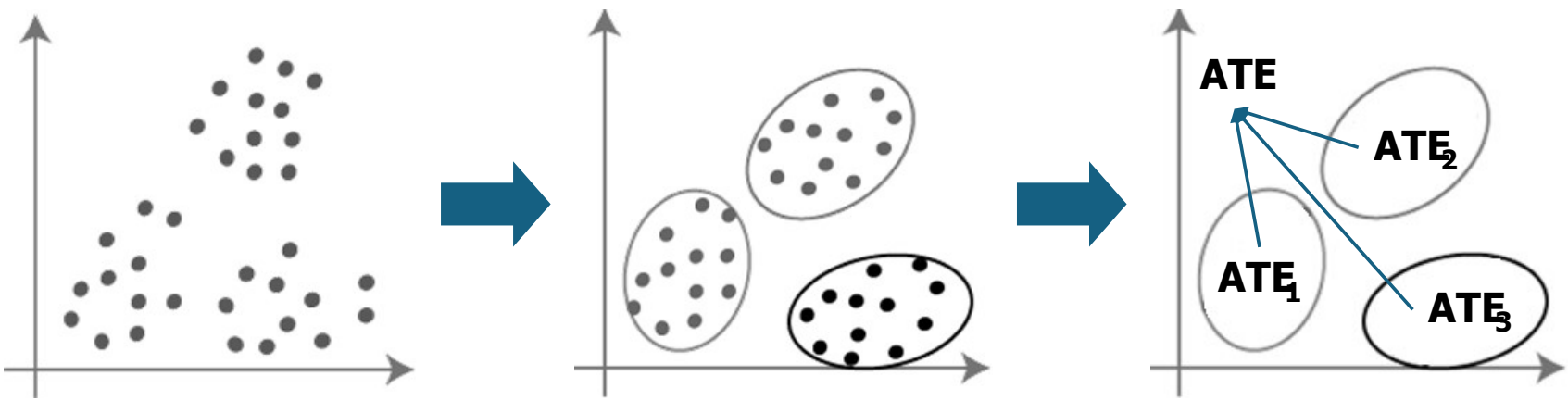
Subclassfication: the process

By creating K groups, with size N_k for a group k:

$$\begin{cases} \widehat{\tau}_{\text{ATE}} & = \sum_{k=1}^{K} \frac{N_k}{N} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \\ \widehat{\tau}_{\text{ATT}} & = \sum_{k=1}^{K} \frac{N_k^1}{N^1} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \end{cases}$$



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Subclassification: an example

Usage	**Average Purchase**		**Diff.**	**# Ad Viewers**	**# Units**
	With Ads	**No Ads**			
X_i	$\overline{Y}_1^k$	$\overline{Y}_0^k$		N_k^1	N_k
Heavy	€28	€24	€4	3	10
Light	€22	€16	€6	7	10
Total				10	20

$$\widehat{\tau}_{\text{ATE}} = \sum_{k=1}^{K} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \frac{N_k}{N} = 4 \cdot \frac{10}{20} + 6 \cdot \frac{10}{20} = €5$$

$$\widehat{\tau}_{\text{ATT}} = \sum_{k=1}^{K} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \frac{N_k^1}{N^1} = 4 \cdot \frac{3}{10} + 6 \cdot \frac{7}{10} = €5.4$$

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Subclassification: potential problems

Usage	Average Purchase		Diff.	# Ad Viewers	# Units
	With Ads	No Ads			
Heavy, Male	€28	€22	€4	3	7
Heavy, Female	??	€24	??	**0**	3
Light, Male	€21	€16	€5	3	4
Light, Female	€23	€17	€6	4	6
Total				10	20

$$\widehat{\tau}_{\text{ATE}} = \sum_{k=1}^{K} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \frac{N_k}{N} = ???$$

$$\widehat{\tau}_{\text{ATT}} = \sum_{k=1}^{K} \left(\overline{Y}_1^k - \overline{Y}_0^k \right) \frac{N_k^1}{N^1} = ???$$

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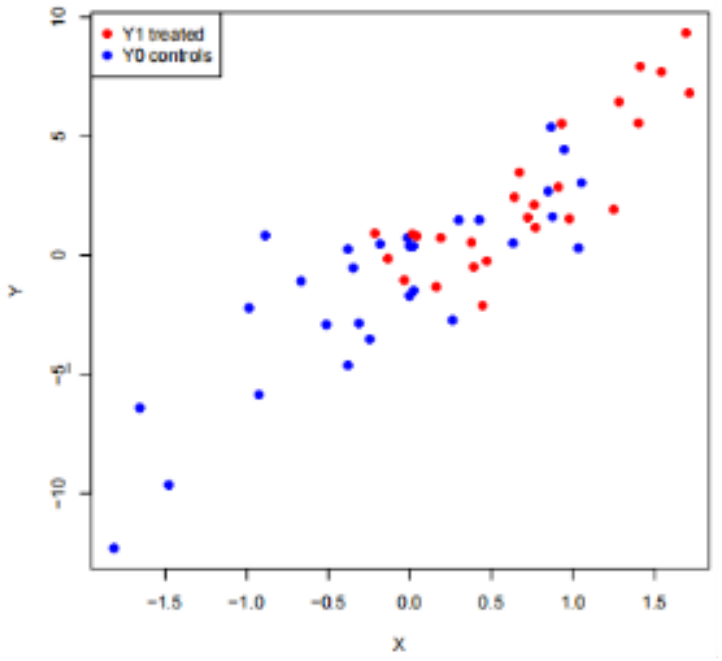
Matching: the basic idea

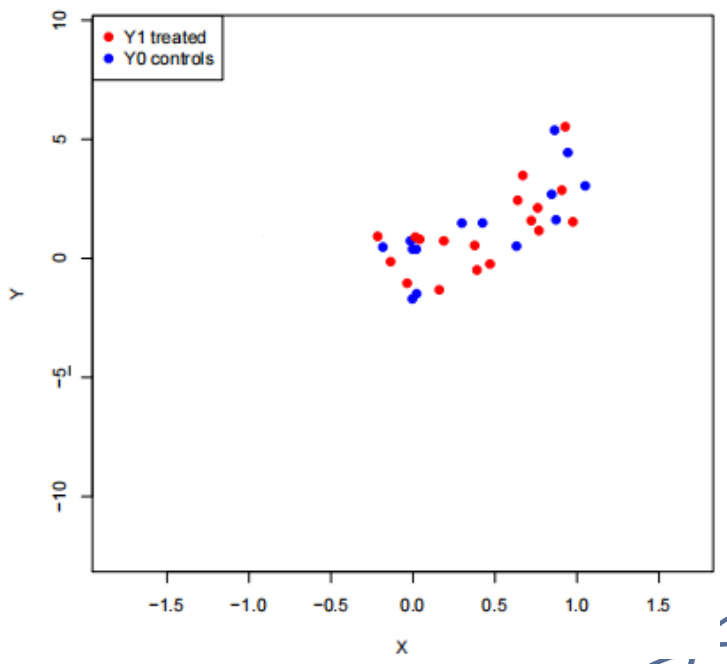
Recall the conditional uncoufoundedness:

$$E\left[Y_i^D \mid X_i, D_i\right] = E\left[Y_i^D \mid X_i\right]$$

Implication: **to equalize the distribution of X_i for the treated and control**.



(a) Before Matching



(b) After Matching

Matching: a general procedure

1. SELECT A MATCHING METHOD.

2. OBTAIN THE MATCHED SAMPLES.

3. EVALUATE THE MATCHING PERFORMANCES.

4. CALCULATE THE TREATMENT EFFECTS

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Matching: a simple example

Unit	Potential Outcome		Treatment	Variables
	Under Treatment	Under Control		
i	Y_i^1	Y_i^0	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
7		1	0	-4

What is $\widehat{\tau}_{\text{ATT}} = \frac{1}{N_1} \sum_{i:D_i=1} \left(Y_i^1 - \overline{Y_j^0} \right)$?
Match and plug in potential outcomes.

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Matching: a simple example

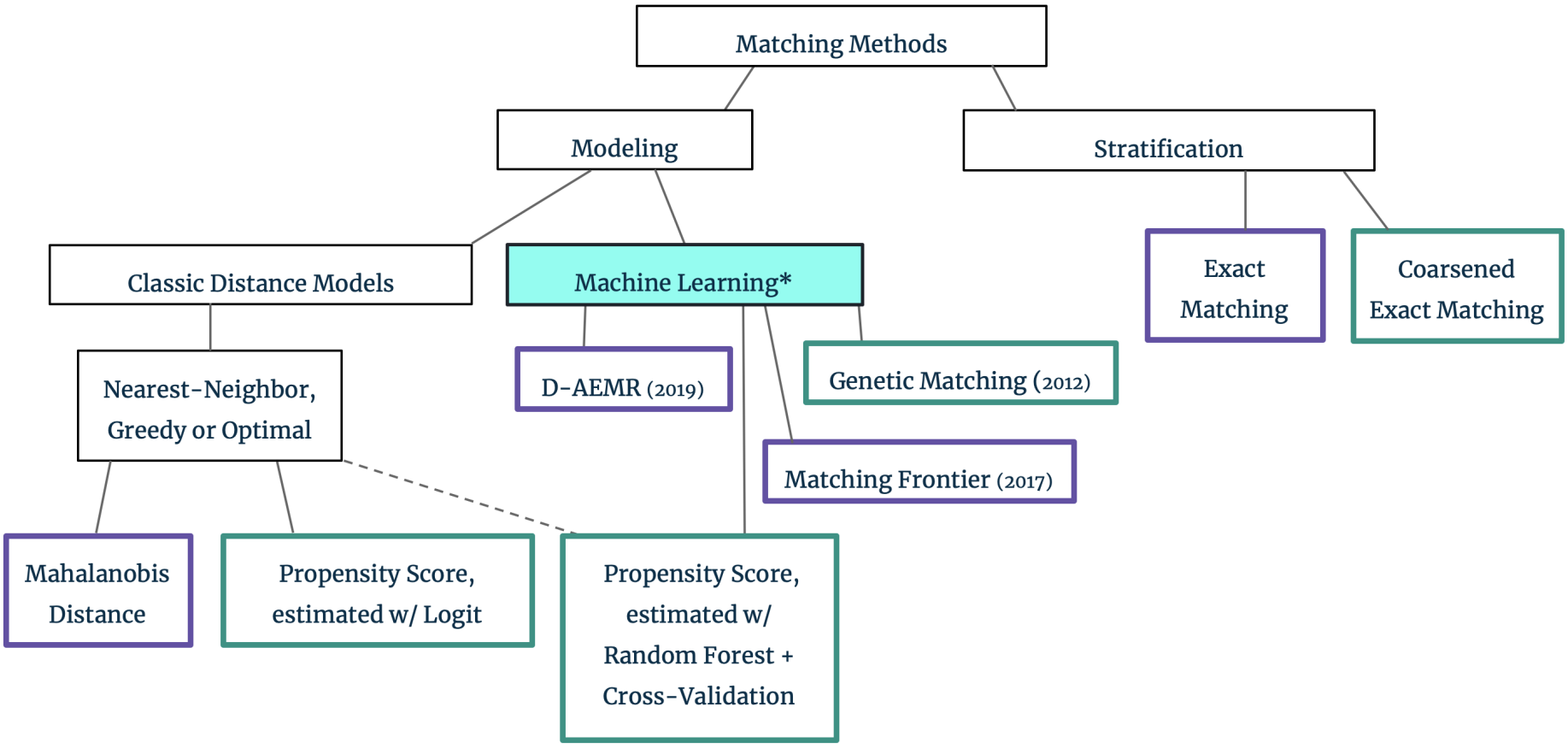
Unit	Potential Outcome		Treatment	Variables
	Under Treatment	Under Control		
i	Y_i^1	Y_i^0	D_i	X_i
1	6	9	1	3
2	1	0	1	1
3	0	9	1	10
4		0	0	2
5		9	0	3
6		1	0	-2
7		1	0	-4

What is $\widehat{\tau}_{\text{ATT}} = \frac{1}{N_1} \sum_{i:D_i=1} \left(Y_i^1 - \overline{Y_j^0} \right)$[1]?

$$\widehat{\tau}_{\text{ATT}} = \frac{1}{3} \left((6-9) + (0-1) + (9-1) \right) = -3.7$$

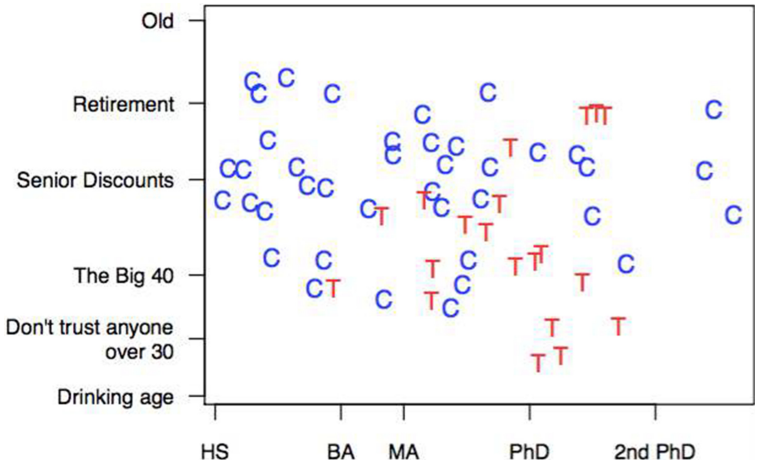
[1] Note: ATC (ATE on the control units) can be calculated similarly.

A classification of matching methods

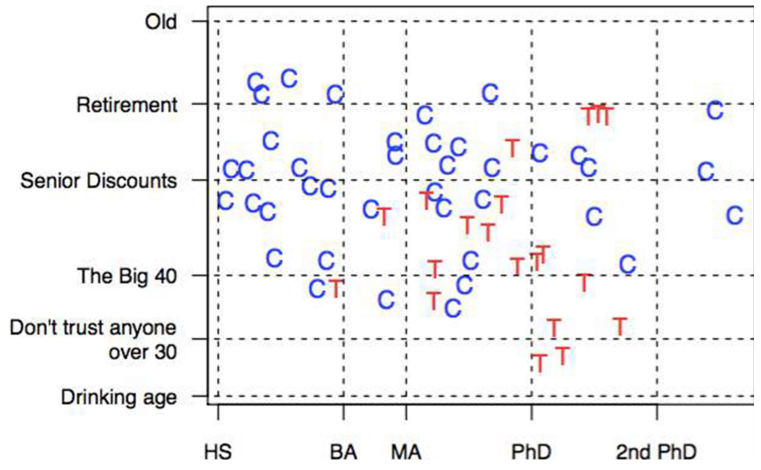


Stratification: coarsened exact matching

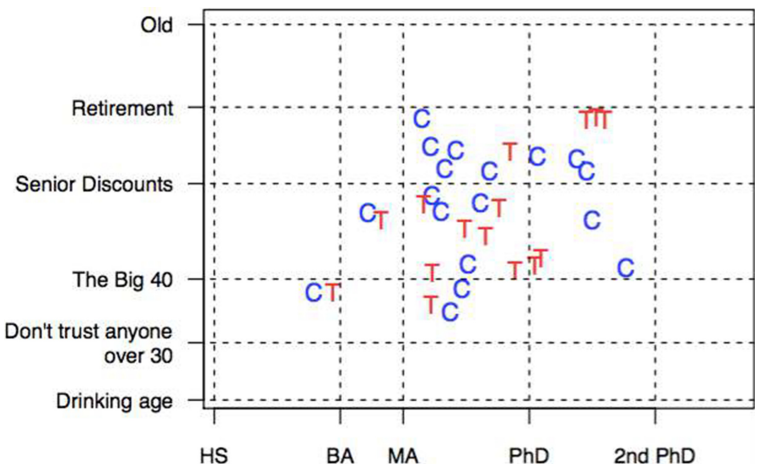
Step 1: to check overlaps



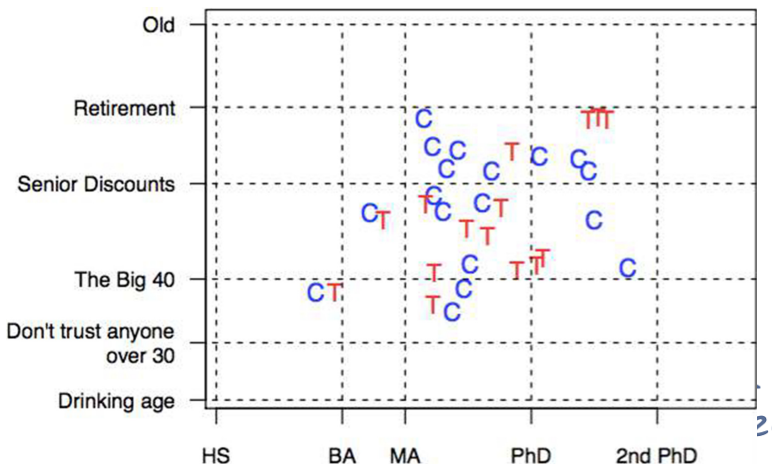
Step 2: to create bins



Step 3: to prune control samples



Step 4: to calculate treatment effects



Modeling: classic distance models

One way is to define "closeness" by a distance metric.

Classic distance metrics

Suppose we have a treated unit i and a control unit j.
A set of continuous characteristics for i and j, X_i and X_j.
Two most frequently used distance metrics:

$$\text{Mahalanobis distance:} \sqrt{(X_i - X_j)' \Sigma^{-1} (X_i - X_j)}$$

$$\text{Euclidean distance:} \sqrt{(X_i - X_j)' (X_i - X_j)}$$

For an "exact match", the distance metrics are zeros.

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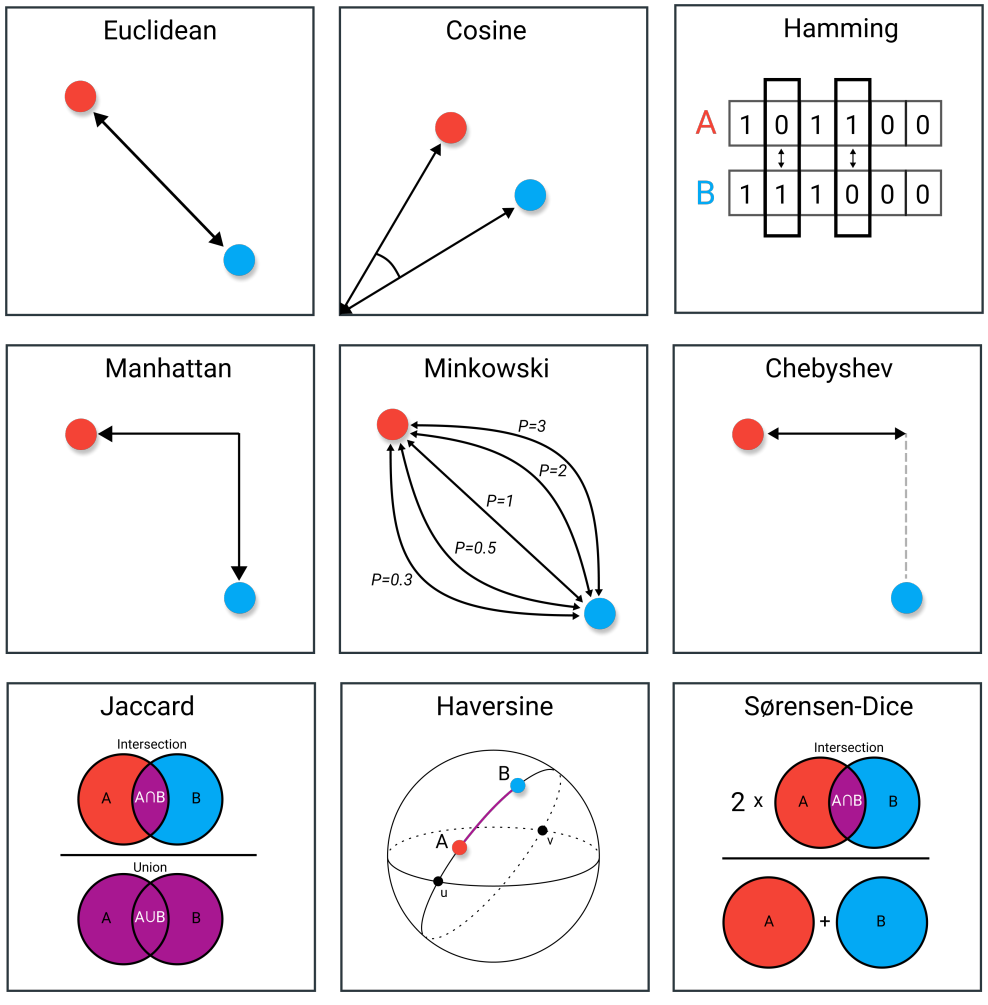
Modeling: classic distance models

A rich selection of distance metrics (probably too many...)



Examples of Distance Metrics

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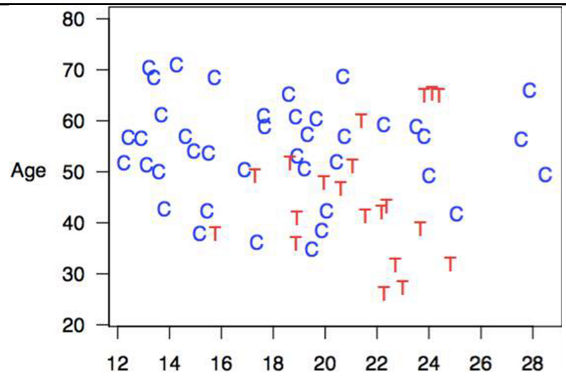
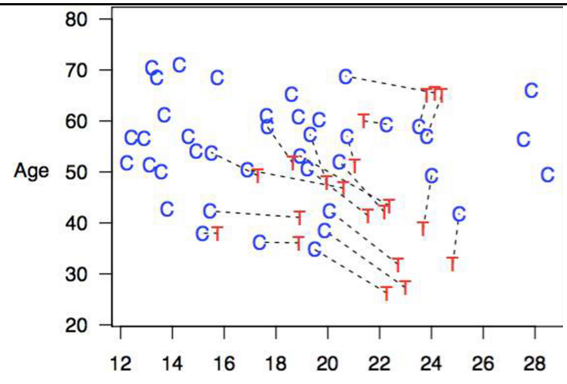
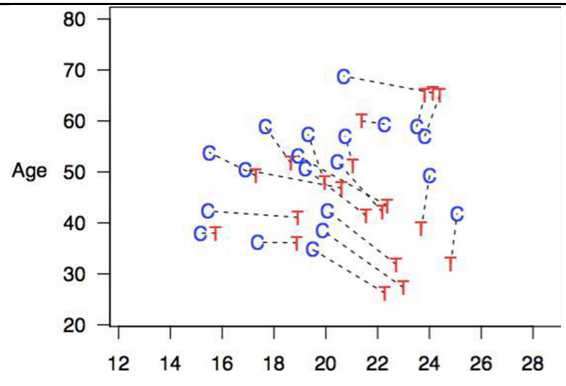
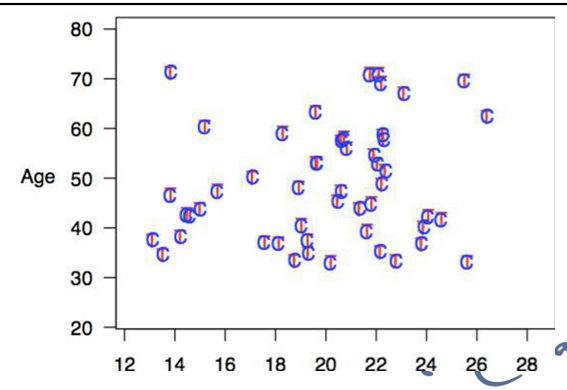
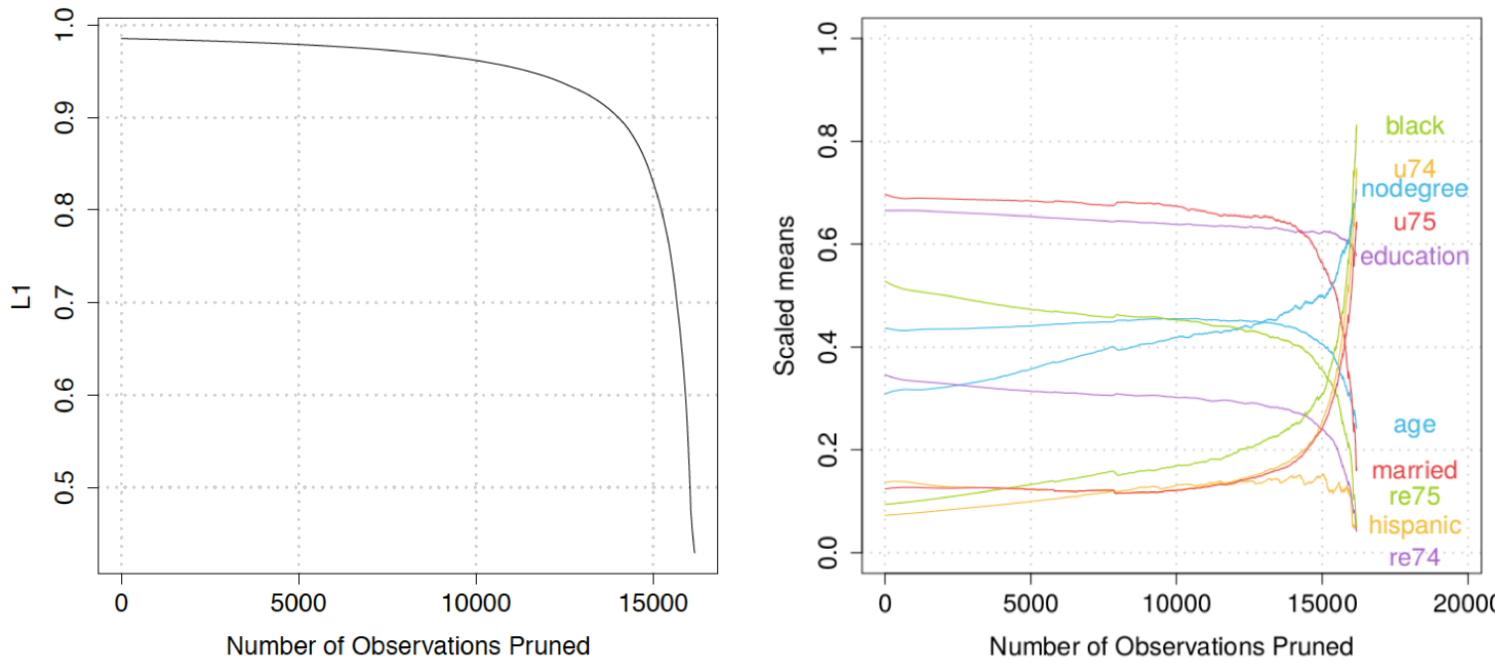
Modeling: classic distance models

Step 1: to calculate the distances	Step 2: to find the matches **Methods: greedy vs. optimal**
	
Step 3: to prune the unmatched control units	**Step 4: to obtain the matched samples**
	

Modeling: matching frontier



Source: King et al. (2017)

Formalize a standard bias-variance trade-off in matching:

Poor covariate balance can lead to biased causal effect estimates but pruning too many observations can increase the variance of the estimates.

Evaluate matching: balance tests

The performance of matching depends on **the resulting balance of** X_i between matched samples[2].

How should one assess the balance of matched data?

- Ideally, compare the joint distribution of all X_i for the matched samples.
- In practice, this is impossible when X_i is high-dimensional and so check various lower-dimensional summaries.
- Statistical tests are often used; plotting is also common in practice.

[2] See the appendix for a formal proof.

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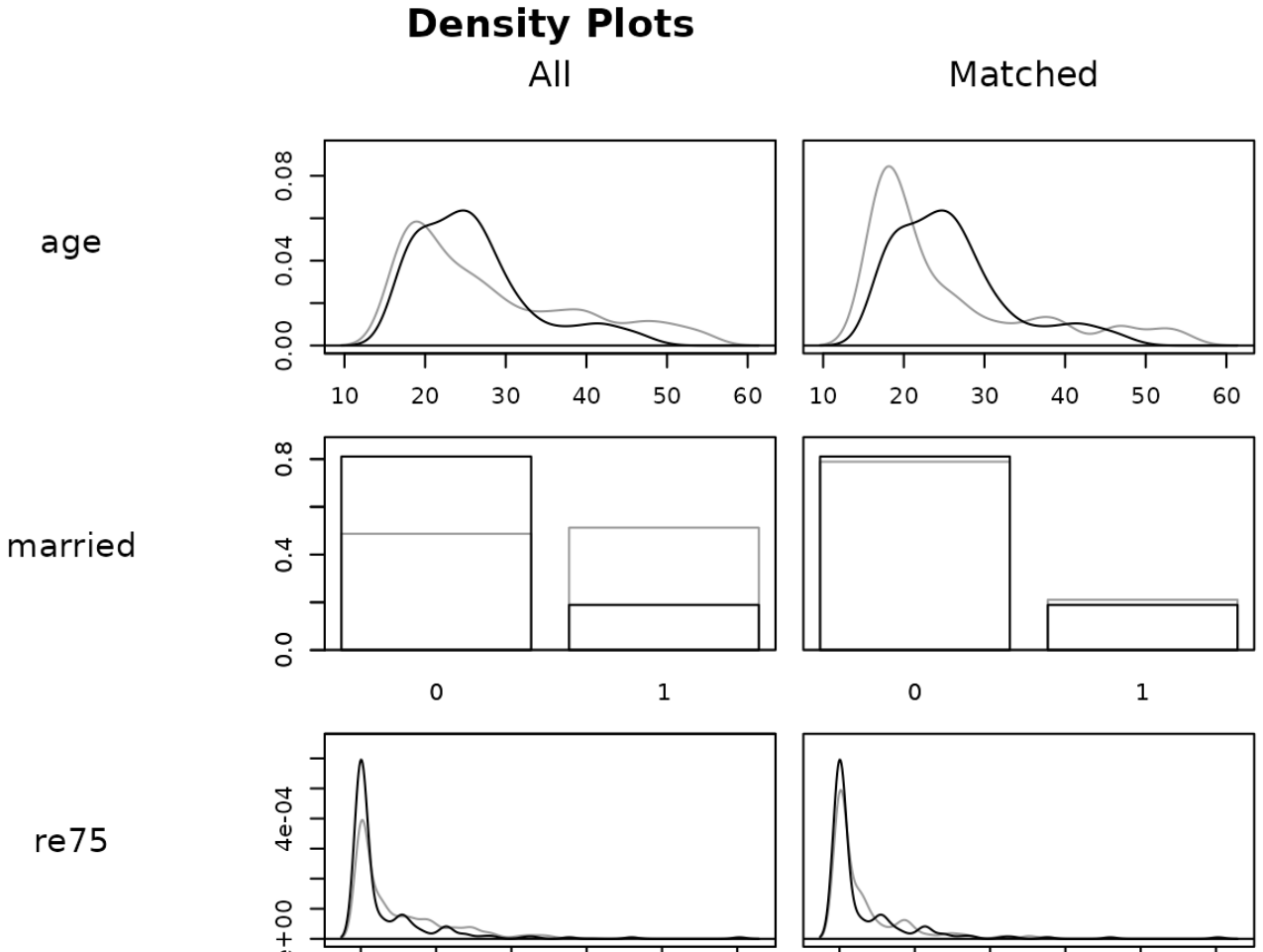
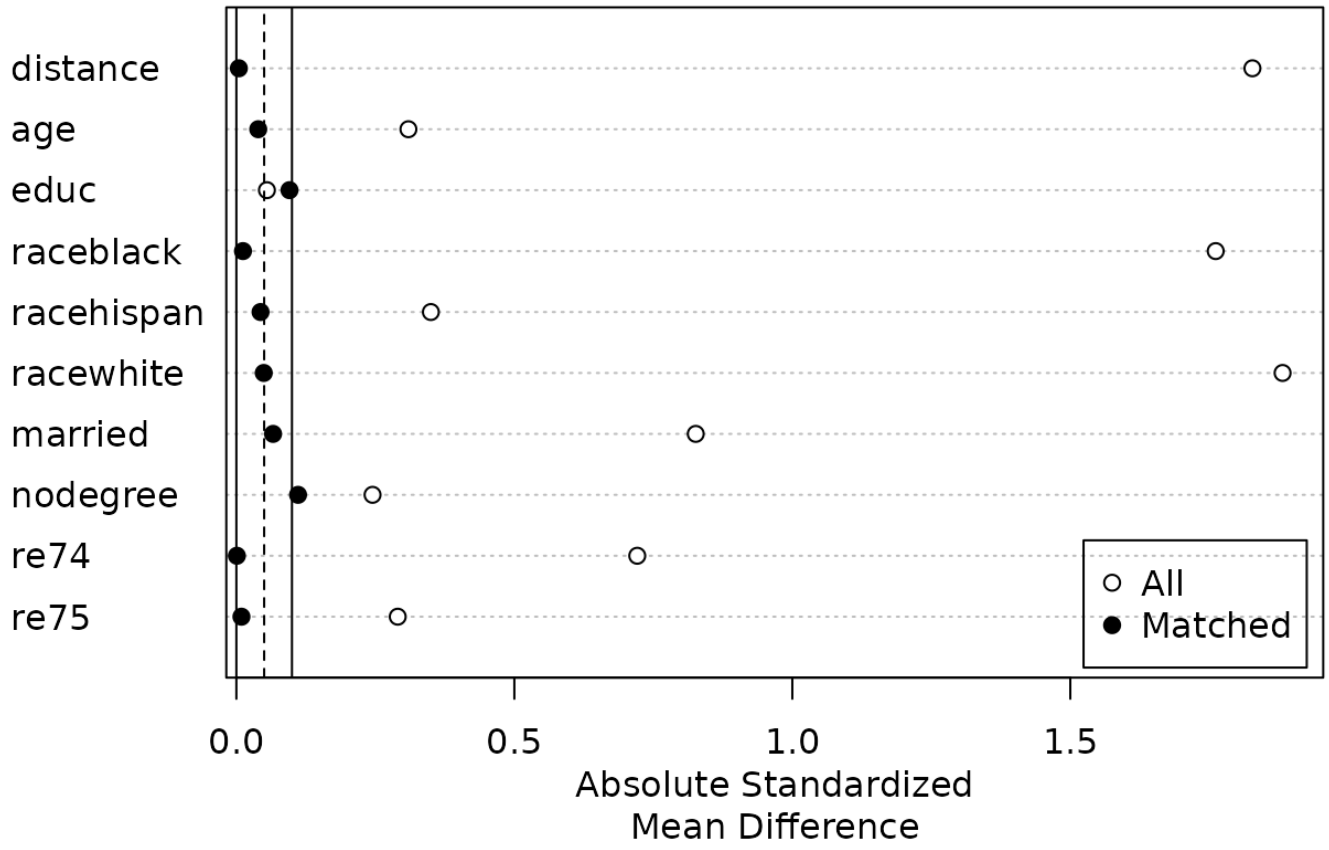
Evaluate matching: balance tests

The performance of matching depends on **the resulting balance of X_i** between matched samples[3].



Evaluate matching: balance tests

The performance of matching depends on **the resulting balance of** X_i between matched samples[4].



[4]See the appendix for a formal proof.

Balance tests fallacy

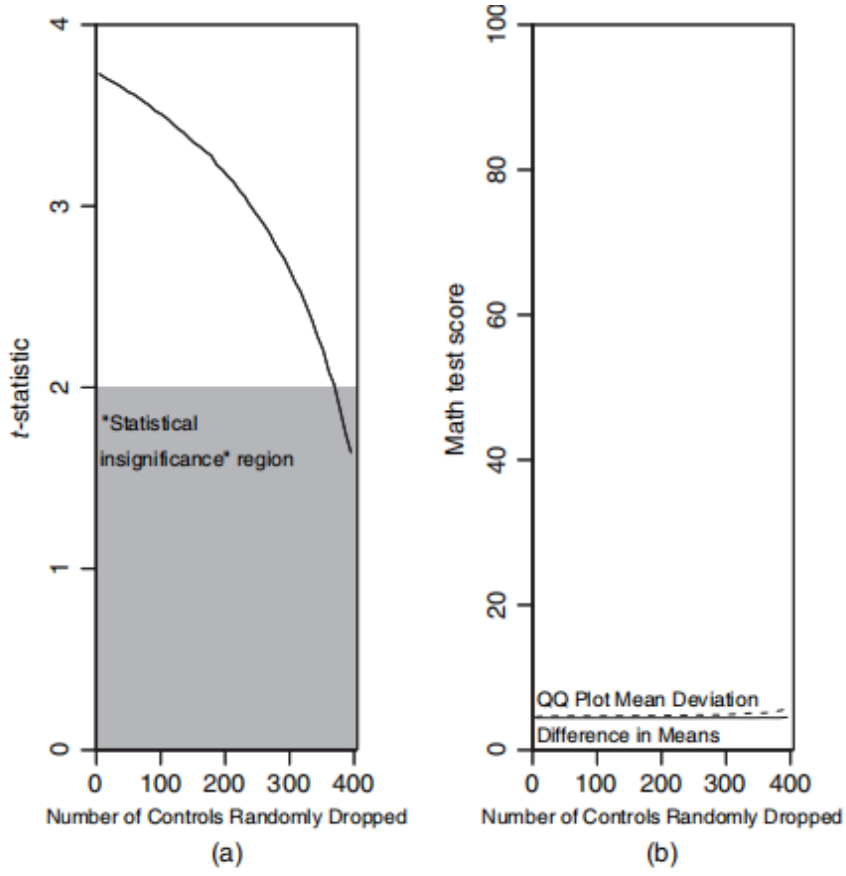


Fig. 1. Dangers in relying on *t*-statistics as a measure of balance (average value of a measure of balance when a given number of control units are randomly dropped from the data set (out of a total of 434)): with larger numbers of control units dropped (i.e. smaller numbers of control units in the resulting sample), the value of the *t*-statistic becomes closer to 0, falsely indicating improvements in balance, even though true balance does not vary systematically across the data sets (and efficiency declines); the difference in means and quantile–quantile plot mean deviation, which are given in (b), correctly indicate no change in bias as observations are randomly dropped

Source: Imai et al. (2008)

Matching: potential issues

Some difficult decisions in distance matching

1. With replacement or without replacement?
2. Which distance metrics to use?
3. A single closest control unit or multiple closer control units?

In practice, you almost always need to use multiple matching methods to show the "**robustness**".

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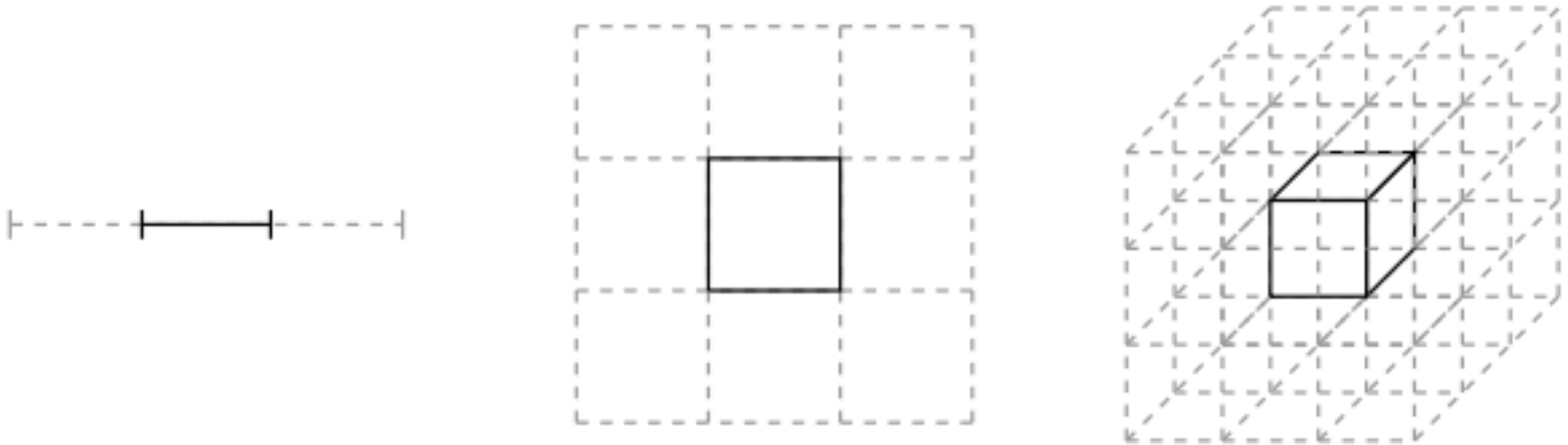
Matching: potential issues

Difficult to find "good matches" with many continuous variables or variables with large variance...



(a) (b) (c)

The probability of the "focal" region decreases exponentially:
$1/3 \to 1/9 \to 1/27$.

Source: Betancourt (2017)

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Outline

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Propensity score to the rescue

Instead of working with X_i, why not **a statistic** of X_i?

Propensity Score: $e(X_i) = P(D_i = 1 \mid X_i)$

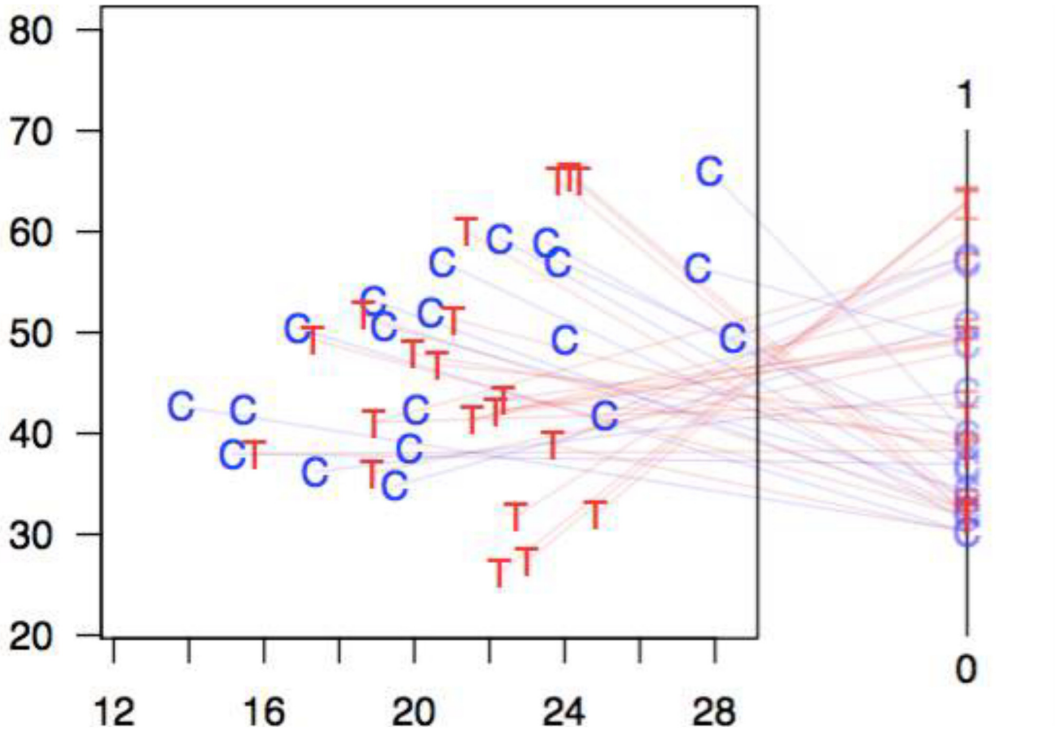
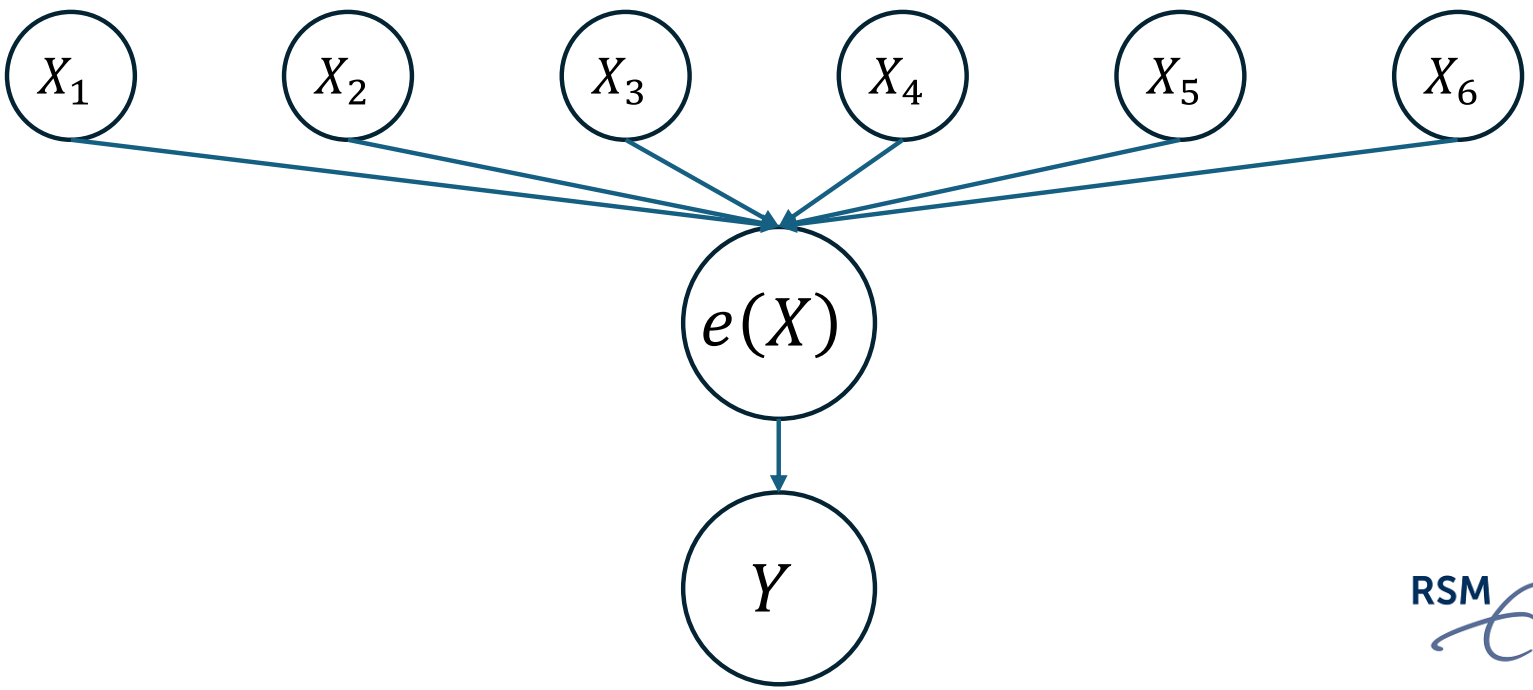


Figure: Propensity score "shrinks" X_i into a single index.

Identification results

Given **conditional unconfoundedness** and **common support**,

1. The propensity score is a sufficient statistic of X_i, such that $D_i \perp X_i \mid e(X_i)$.
2. The treatment is unconfounded given the propensity score: $D_i \perp Y_i^1, Y_i^0 \mid e(X_i)$.



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Implications of the identification results

Adjustment of the treatment-control differences in $e(X_i)$ is sufficient to remove all biases from the differences in X_i.

$$E\left[Y_i^1 - Y_i^0 \mid D_i, e(X_i)\right] \overset{\text{Unconfouded}}{=} E\left[Y_i^1 - Y_i^0 \mid e(X_i)\right]$$
$$\overset{\text{Definition}}{=} E\left[Y_i^1 - Y_i^0 \mid P(D_i = 1 \mid X_i)\right]$$

Suggests a two step procedure to estimate treatment effects:

1. **Estimate the propensity score** $\hat{e}(X_i)$.
2. **Estimate the expectations** of potential outcomes conditional on $\hat{e}(X_i)$.

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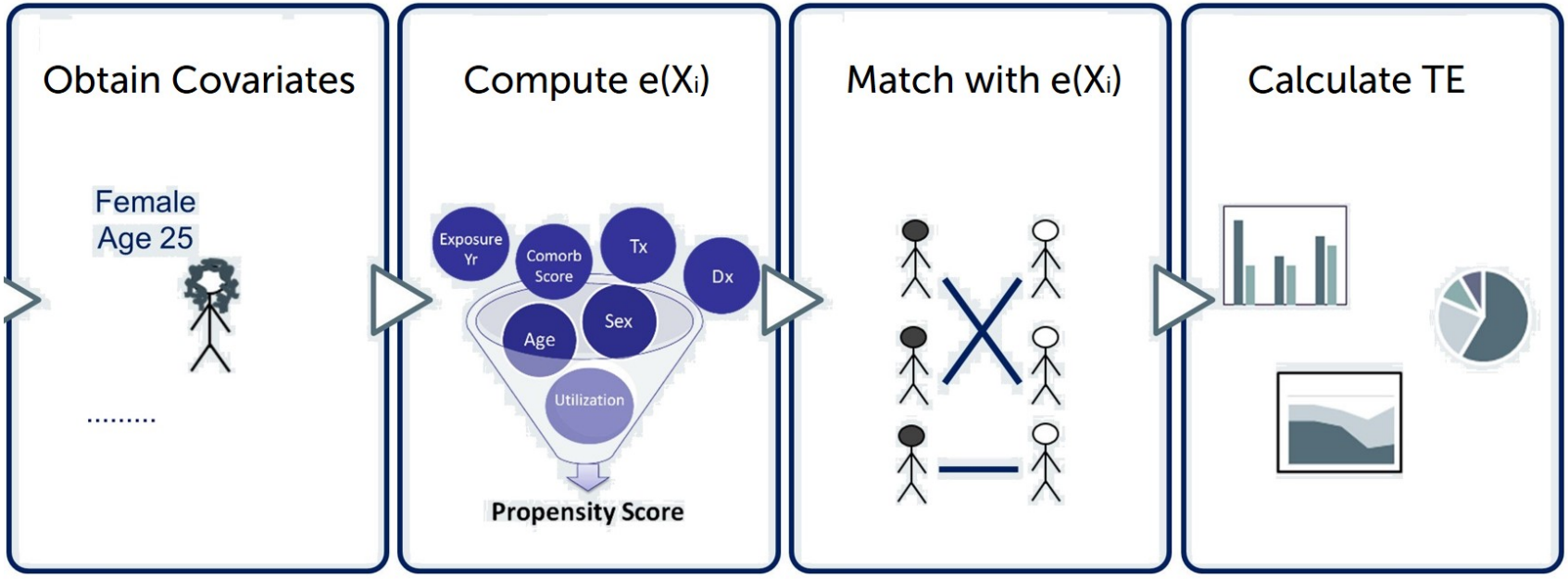
Matching with propensity score



Illustrating propensity score matching

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Weighting with propensity scores

Matching throws away samples to gain balance.
The "efficiency" is sacrificed for "precision."

Question: Can we do better?
Observe two equations given propensity scores[5]:

$$\begin{cases} E\left(\frac{D_i \cdot Y_i^{\text{obs}}}{e(X_i)}\right) & = E\left[Y_i^1 \mid X_i\right] \\ E\left(\frac{(1-D_i) \cdot Y_i^{\text{obs}}}{1-e(X_i)}\right) & = E\left[Y_i^0 \mid X_i\right] \end{cases}$$

[5] The original construction is in Horvitz and Thompson (1952).

Weighting with propensity scores

Technical Proof:

$$
\begin{aligned}
E\left(\frac{D_i \cdot Y_i^{\text{obs}}}{e(X_i)}\right) &= E\left(\frac{D_i \cdot Y_i^1}{e(X_i)}\right) \\
&= E\left[E\left(\frac{(D_i = 1) \cdot Y_i^1}{e(X_i)} \middle| X_i\right)\right] \\
&= \frac{E_D\left[D_i = 1 \mid X_i\right] E\left[Y_i^1 \mid X_i\right]}{e(X_i)} \\
&= E\left[Y_i^1 \mid X_i\right]
\end{aligned}
$$

Similar proof holds for the second equality.

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The weighting estimator

Based on the equations, we can construct two estimators:

$$\widehat{E\left[Y_i^1 \mid X_i\right]} = \frac{1}{N}\sum_{i=1}^{N}\frac{D_i \cdot Y_i^{\text{obs}}}{e\left(X_i\right)}$$

$$\widehat{E\left[Y_i^0 \mid X_i\right]} = \frac{1}{N}\sum_{i=1}^{N}\frac{\left(1-D_i\right) \cdot Y_i^{\text{obs}}}{1-e\left(X_i\right)}$$

The weighting estimator of ATE is defined as,

$$\begin{aligned}\widehat{\tau} &= \widehat{E\left[Y_i^1 \mid X_i\right]} - \widehat{E\left[Y_i^0 \mid X_i\right]} \\ &= \frac{1}{N}\sum_{i=1}^{N}\left(\frac{D_i \cdot Y_i^{\text{obs}}}{e\left(X_i\right)} - \frac{\left(1-D_i\right) \cdot Y_i^{\text{obs}}}{1-e\left(X_i\right)}\right)\end{aligned}$$

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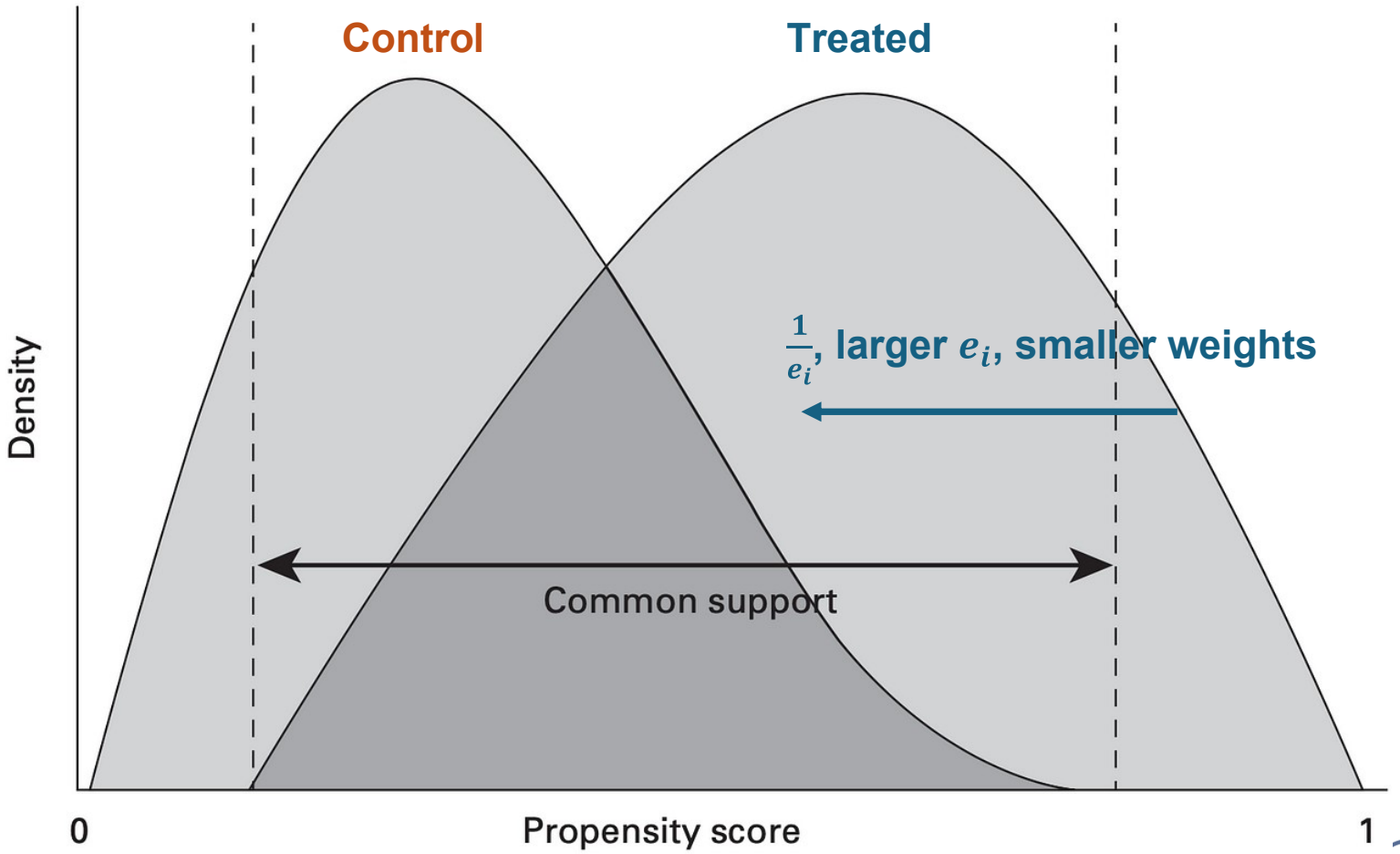
Intuitions behind weighting

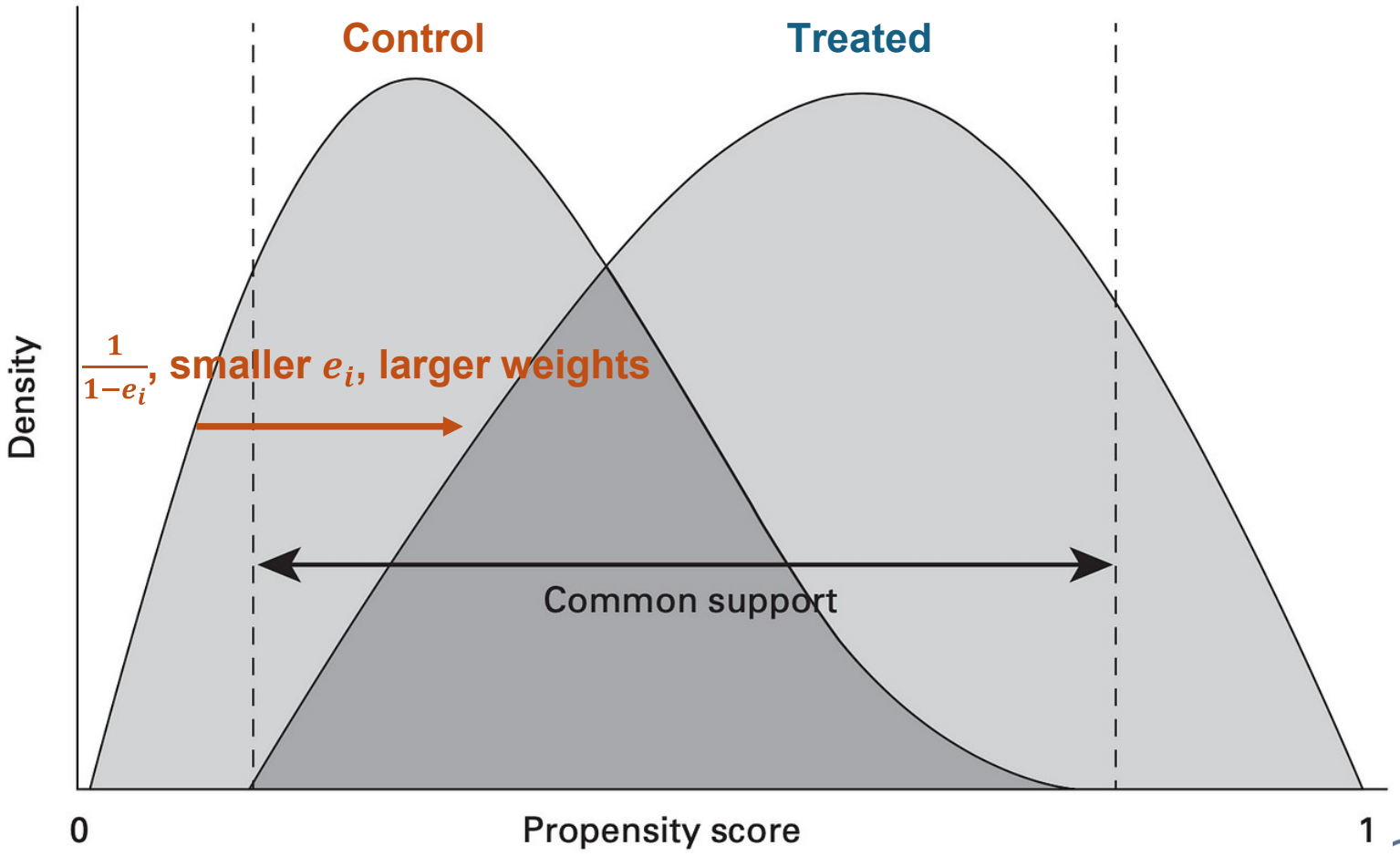
The weights w_i is $\frac{1}{e(X_i)}$ for the treated and $\frac{1}{1-e(X_i)}$ for the control.



"Expanding" the common support

Intuitions behind weighting

The weights w_i is $\frac{1}{e(X_i)}$ for the treated and $\frac{1}{1-e(X_i)}$ for the control.



"Expanding" the common support

The weighted regression estimation

The weighted regression procedure

1. Estimate the propensity scores with $P(D_i = 1 \mid X_i)$, possibly with different methods and specifications.
2. Plug in estimated propensity score $\hat{e}(X_i)$ into a weighted regression.

$$Y_i = \alpha + \tau D_i + X_i\beta + \varepsilon_i \text{ with } w_i = \begin{cases} \frac{1}{\widehat{e}(X_i)} & \text{if } D_i = 1 \\ \frac{1}{1-\widehat{e}(X_i)} & \text{if } D_i = 0 \end{cases}$$

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The weighted regression for ATT and ATC

Some procedure, but with different weights:

- The weights (odds ratio) for ATT estimation is:

$$w_i = \begin{cases} 1 & \text{if } D_i = 1 \\ \frac{\widehat{e}(X_i)}{1-\widehat{e}(X_i)} & \text{if } D_i = 0 \end{cases}$$

- The weights for ATC estimation is similar:

$$w_i = \begin{cases} \frac{1-\widehat{e}(X_i)}{\widehat{e}(X_i)} & \text{if } D_i = 1 \\ 1 & \text{if } D_i = 0 \end{cases}$$

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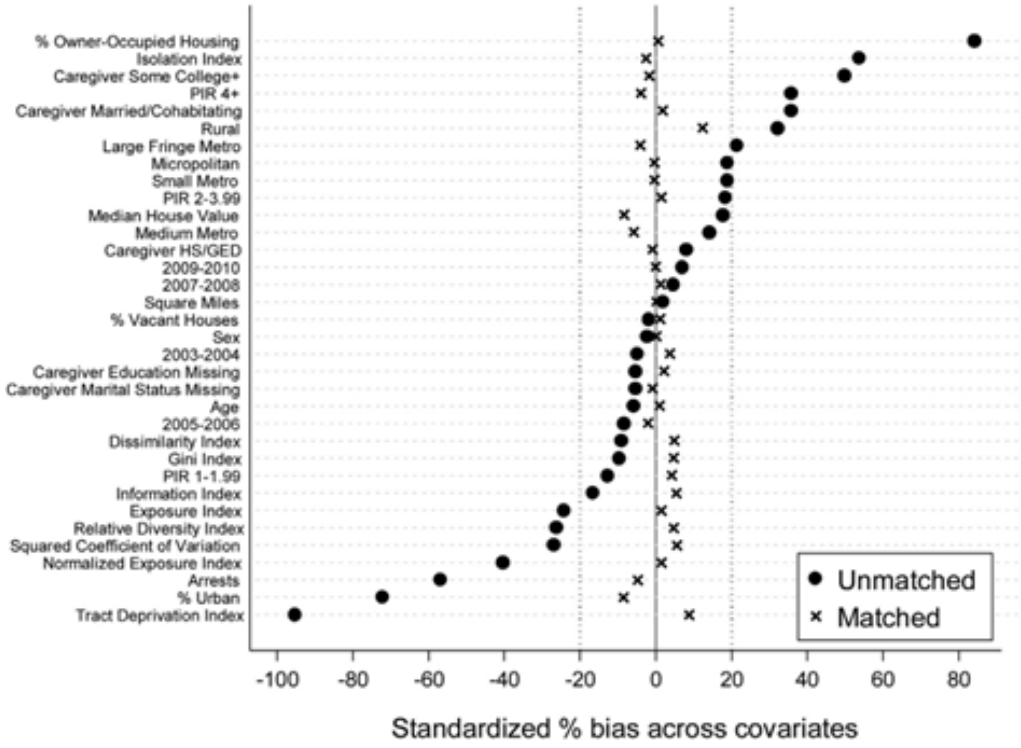
What is a good estimation of propensity score?

Balancing condition: samples after weights should show similar distributions of X_i

$$E\left[\frac{D_i \cdot X_i}{e(X_i)} - \frac{(1-D_i)\cdot X_i}{1-e(X_i)}\right] = 0$$



Notes on propensity scores

- The true propensity score is unknown (by definition), and estimated by a model.
- Model misspecification leads to biased treatment effects estimation.
- In practice, *ad hoc* robustness checks across different specs and models.
- In recent years, some machine learning models (non-parametric) prove to be useful.

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Outline

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Other ML methods in matching: see references

Genetic matching:

- Diamond, A., & Sekhon, J. S. (2013)

Dynamic almost exact matching with replacement:

- Dieng et al. (2019)

Propensity score matching with random forest:

- Krief and Diaz-Ordaz (2019),Ferri-Garcia and Rueda (2020)

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Proof: matching is about covariate balancing

The conditional ATE or CATE is: $\tau(X_i) = E\left[Y_i^1 - Y_i^0 \mid X_i\right]$.

Under the assumptions of conditionally unconfounded, individualistic and probabilistic assignment, the variance for CATE is[6],

$$\text{Var}(\tau(X_i)) = E\left[\frac{\sigma_c^2(X_i)}{1-e(X_i)} + \frac{\sigma_t^2(X_i)}{e(X_i)} + (\tau(X_i) - \tau)^2\right]$$

$e(X_i)$ the propensity to be treated, and τ the unconditional ATE.

The third term $(\tau(X_i) - \tau)^2$ goes to zero if the treatment effect is constant for the treated and the control.
This requires X_i has the same distributions in both groups, i.e., X_i is balanced.

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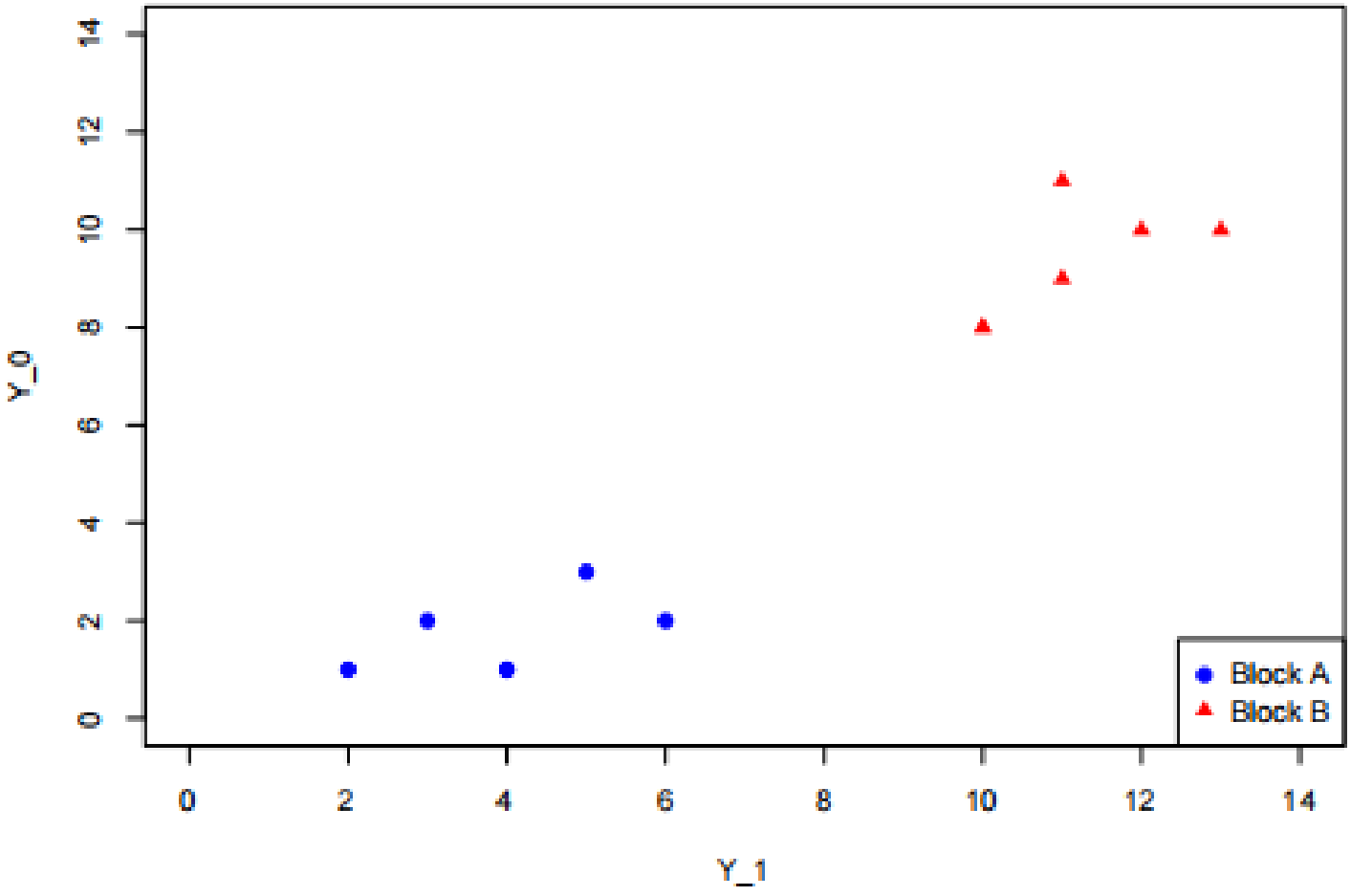
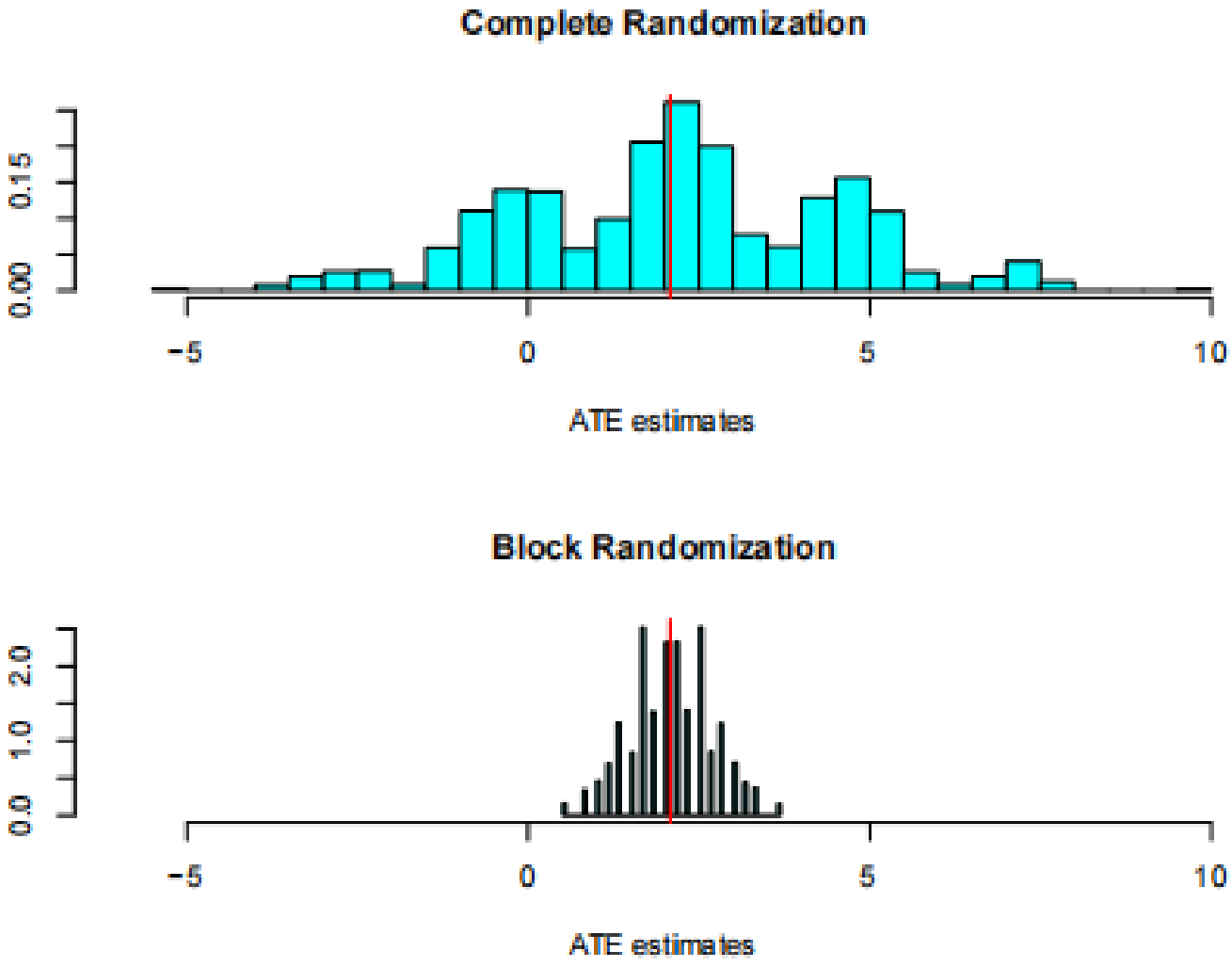
[6] Please see Imbens and Rubin (2015), p. 269 for the derivation.

Blocking is efficient: Intuition



Potential outcomes across blocks

Blocking is efficient: Intuition



Sampling distribution of ATE estimates

Blocking: summary

What to block on?

- "**Block what you can/need, randomize what you can't or don't need.**"
- Variables linked to potential outcomes.
- Variables desired for subgroup analysis.

How to block?

- Stratification
- Pairwise assignment...

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Proof: the sufficiency of propensity score

Here, we prove that the propensity score $e(X_i)$ is a sufficient statistic of X_i or:

$$D_i \perp X_i \mid e(X_i) \text{ or } P(D_i = 1 \mid X_i, e(X_i)) = P(D_i = 1 \mid e(X_i))$$

First, for the left-hand side:

$$P(D_i = 1 \mid X_i, e(X_i)) = P(D_i = 1 \mid X_i) = e(X_i)$$

Second, for the right-hand side:

$$\begin{aligned} P(D_i = 1 \mid e(X_i)) &= E[D_i \mid e(X_i)] \\ &= E[E[D_i \mid X_i, e(X_i)] \mid e(X_i)] \\ &= E[e(X_i) \mid e(X_i)] = e(X_i) \end{aligned}$$

The second equality is the iterated expectations and the third equality is proved above.

Proof: the conditional unconfoundedness of the propensity scrore

We want to prove that $D_i \perp Y_i^0, Y_i^1 \mid e(X_i)$, or

$$P\left(D_i = 1 \mid Y_i^0, Y_i^1, e(X_i)\right) = P\left(D_i = 1 \mid e(X_i)\right)$$

For the left-hand side, we have:

$$\begin{aligned} P\left(D_i = 1 \mid Y_i^0, Y_i^1, e(X_i)\right) &= E\left[D_i \mid Y_i^0, Y_i^1, e(X_i)\right] \\ &= E\left[E\left[D_i \mid Y_i^0, Y_i^1, X_i, e(X_i)\right] \mid Y_i^0, Y_i^1, e(X_i)\right] \end{aligned}$$

By conditional unconfoundedness, $E\left[D_i \mid Y_i^0, Y_i^1, X_i, e(X_i)\right] = E\left[D_i \mid X_i, e(X_i)\right]$. By the sufficiency of the propensity score, $E\left[D_i \mid X_i, e(X_i)\right] = E\left[D_i \mid e(X_i)\right]$. If we submit it to the equation above, we have:

$$E\left[E\left[D_i \mid e(X_i)\right] \mid Y_i^0, Y_i^1, e(X_i)\right] = E\left[D_i \mid e(X_i)\right] = P\left(D_i = 1 \mid e(X_i)\right)$$

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