

Simplifying Matching Methods for Causal Inference

Gary King¹

Institute for Quantitative Social Science
Harvard University

University of Minho, 10/22/2019

¹GaryKing.org

3 Problems, 3 Solutions

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:
 - ~→ “Why Propensity Scores Should Not Be Used for Matching” (*PA*, 2019. Gary King, Richard Nielsen)

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:
 - ~→ “Why Propensity Scores Should Not Be Used for Matching” (*PA*, 2019. Gary King, Richard Nielsen)
2. Do powerful methods have to be complicated?

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:
 - ~> “Why Propensity Scores Should Not Be Used for Matching” (*PA*, 2019. Gary King, Richard Nielsen)
2. Do powerful methods have to be complicated?
 - ~> “Causal Inference Without Balance Checking: Coarsened Exact Matching” (*PA*, 2011. Stefano Iacus, Gary King, and Giuseppe Porro)

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:
 - ↪ “Why Propensity Scores Should Not Be Used for Matching” (*PA*, 2019. Gary King, Richard Nielsen)
2. Do powerful methods have to be complicated?
 - ↪ “Causal Inference Without Balance Checking: Coarsened Exact Matching” (*PA*, 2011. Stefano Iacus, Gary King, and Giuseppe Porro)
3. Matching methods optimize either imbalance (\approx bias) or # units pruned (\approx variance); users need both simultaneously:

3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 179,000 articles!) sounds magical:
 - ↪ “Why Propensity Scores Should Not Be Used for Matching” (*PA*, 2019. Gary King, Richard Nielsen)
2. Do powerful methods have to be complicated?
 - ↪ “Causal Inference Without Balance Checking: Coarsened Exact Matching” (*PA*, 2011. Stefano Iacus, Gary King, and Giuseppe Porro)
3. Matching methods optimize either imbalance (\approx bias) or # units pruned (\approx variance); users need both simultaneously:
 - ↪ “The Balance-Sample Size Frontier in Matching Methods for Causal Inference” (In press, *AJPS*; Gary King, Christopher Lucas and Richard Nielsen)

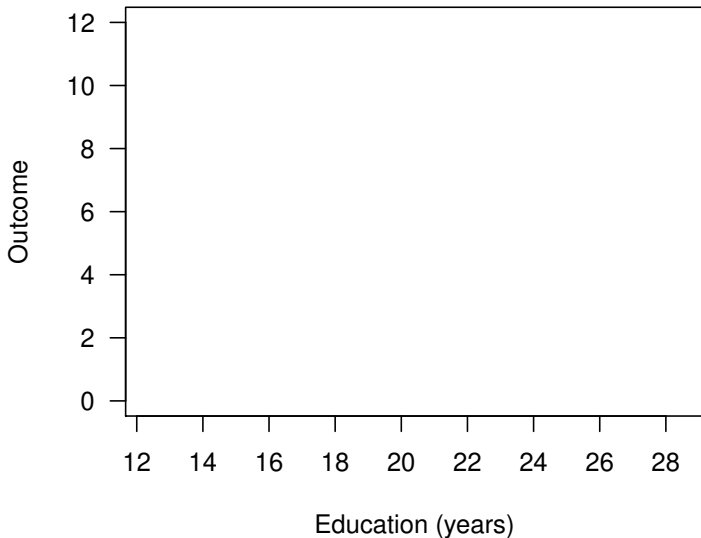
Matching to Reduce Model Dependence

Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)

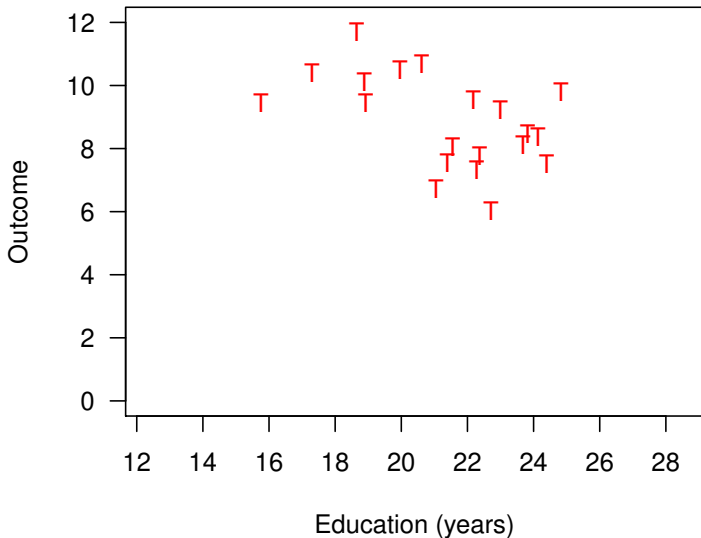
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



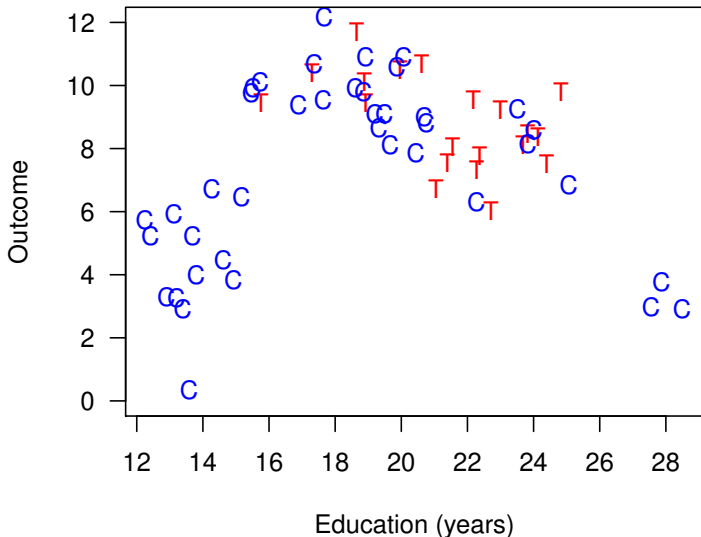
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



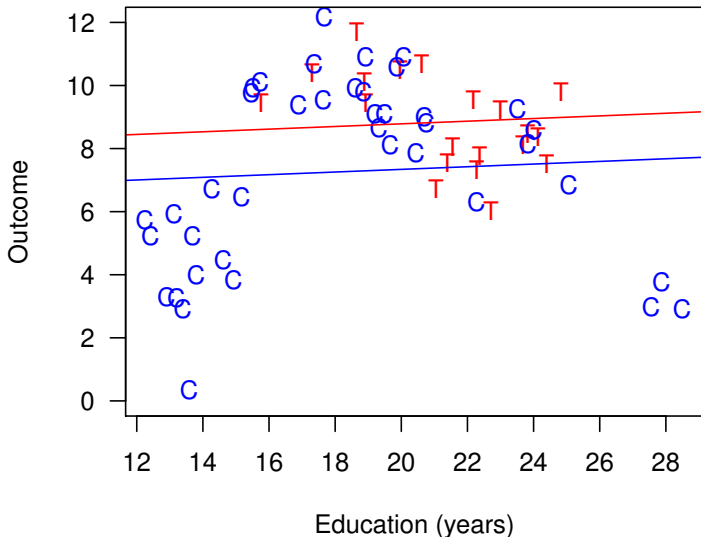
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



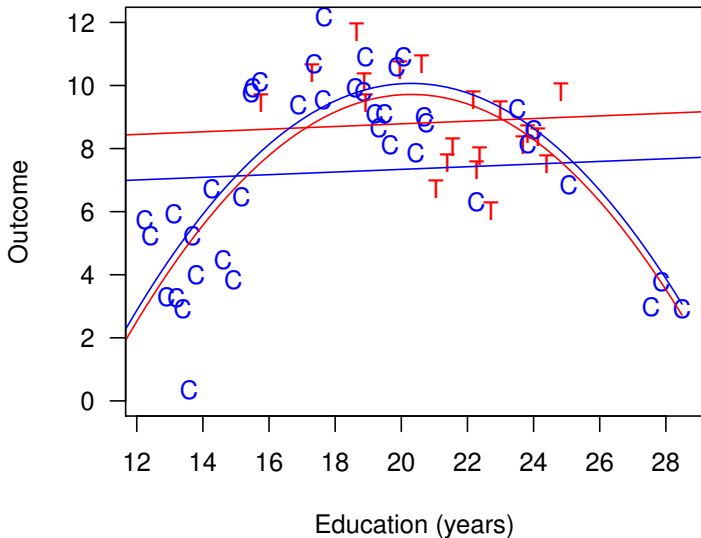
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



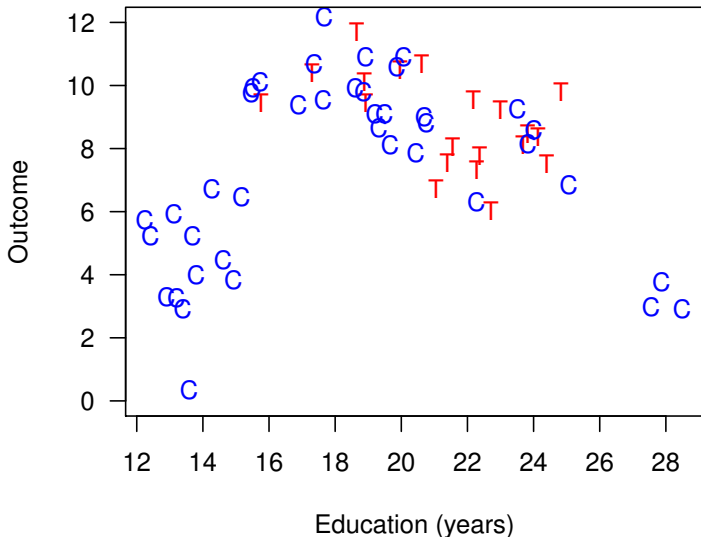
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



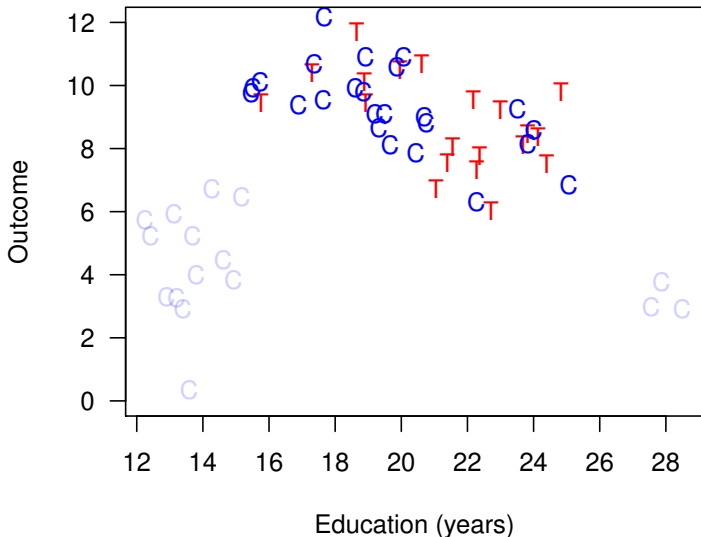
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



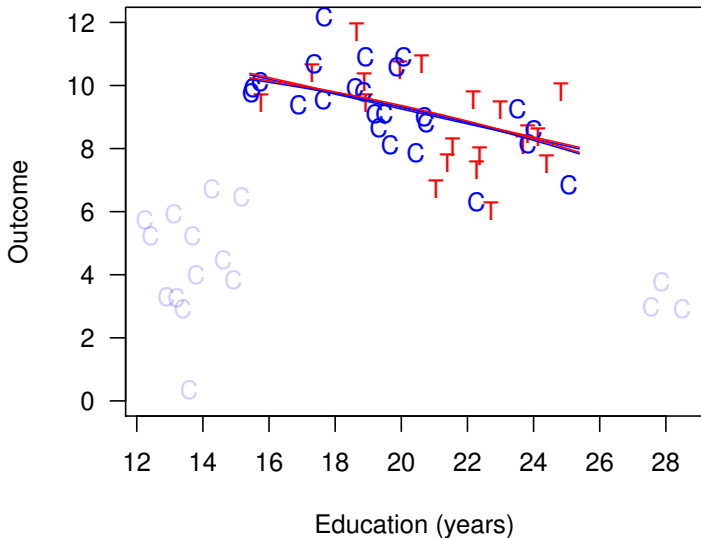
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



The Problems Matching Solves

The Problems Matching Solves

Without Matching:

The Problems Matching Solves

Without Matching:

Imbalance

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments
 - Choosing based on “plausibility” is probably worse_[effrt]

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments
 - Choosing based on “plausibility” is probably worse_[effrt]
- conscientious effort doesn't avoid biases (Banaji 2013)_[acc]

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments
 - Choosing based on “plausibility” is probably worse^[effrt]
- conscientious effort doesn't avoid biases (Banaji 2013)^[acc]
- People do not have easy access to their own mental processes or feedback to avoid the problem (Wilson and Brekke 1994)^[exprt]

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments
 - Choosing based on “plausibility” is probably worse^[effrt]
- conscientious effort doesn't avoid biases (Banaji 2013)^[acc]
- People do not have easy access to their own mental processes or feedback to avoid the problem (Wilson and Brekke 1994)^[exprt]
- Experts overestimate their ability to control personal biases more than nonexperts, and more prominent experts are the most overconfident (Tetlock 2005)^[tch]

The Problems Matching Solves

Without Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

- Qualitative choice from unbiased estimates = biased estimator
 - e.g., Choosing from *results* of 50 randomized experiments
 - Choosing based on “plausibility” is probably worse_[effrt]
- conscientious effort doesn't avoid biases (Banaji 2013)_[acc]
- People do not have easy access to their own mental processes or feedback to avoid the problem (Wilson and Brekke 1994)_[exprt]
- Experts overestimate their ability to control personal biases more than nonexperts, and more prominent experts are the most overconfident (Tetlock 2005)_[tch]
- “Teaching psychology is mostly a waste of time” (Kahneman 2011)

The Problems Matching Solves

~~Without~~ Matching:

Imbalance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

The Problems Matching Solves

~~Without~~ Matching:

~~Im~~balance \rightsquigarrow Model Dependence \rightsquigarrow Researcher discretion \rightsquigarrow Bias

The Problems Matching Solves

Without Matching:

~~Imbalance~~ \rightsquigarrow ~~Model Dependence~~ \rightsquigarrow Researcher discretion \rightsquigarrow Bias

The Problems Matching Solves

Without Matching:

~~Imbalance~~ \rightsquigarrow ~~Model Dependence~~ \rightsquigarrow ~~Researcher discretion~~ \rightsquigarrow Bias

The Problems Matching Solves

Without Matching:

~~Imbalance~~ \rightsquigarrow ~~Model Dependence~~ \rightsquigarrow ~~Researcher discretion~~ \rightsquigarrow ~~Bias~~

The Problems Matching Solves

Without Matching:

~~Imbalance~~ \rightsquigarrow ~~Model Dependence~~ \rightsquigarrow ~~Researcher discretion~~ \rightsquigarrow ~~Bias~~

A central project of statistics: Automating away human discretion

What's Matching?

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$TE_i = Y_i(1) - Y_i(0)$$

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i(1) - Y_i(0) \\ &= \text{observed} - \textit{unobserved} \end{aligned}$$

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i - Y_i(0) \\ &= \text{observed} - \textit{unobserved} \end{aligned}$$

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:
 1. SATT: Sample Average Treatment effect on the Treated:

$$SATT = \text{Mean}_{i \in \{T_i=1\}} (TE_i)$$

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} TE_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:
 1. SATT: Sample Average Treatment effect on the Treated:

$$SATT = \text{Mean}_{i \in \{T_i=1\}} (TE_i)$$

2. FSATT: Feasible SATT (prune badly matched treateds too)

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} \text{TE}_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:
 1. SATT: Sample Average Treatment effect on the Treated:

$$\text{SATT} = \text{Mean}_{i \in \{T_i=1\}} (\text{TE}_i)$$

2. FSATT: Feasible SATT (prune badly matched treateds too)
- **Big convenience:** Follow preprocessing with whatever statistical method you'd have used without matching

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i :

$$\begin{aligned} \text{TE}_i &= Y_i - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:
 1. SATT: Sample Average Treatment effect on the Treated:

$$\text{SATT} = \text{Mean}_{i \in \{T_i=1\}} (\text{TE}_i)$$

2. FSATT: Feasible SATT (prune badly matched treateds too)
- **Big convenience:** Follow preprocessing with whatever statistical method you'd have used without matching
 - **Pruning nonmatches makes control vars matter less:** reduces imbalance, model dependence, researcher discretion, & bias

Matching: Finding Hidden Randomized Experiments

Matching: Finding Hidden Randomized Experiments

Matching: Finding Hidden Randomized Experiments


Types of Experiments



Matching: Finding Hidden Randomized Experiments

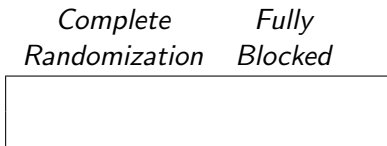
Types of Experiments

*Complete
Randomization*



Matching: Finding Hidden Randomized Experiments

Types of Experiments



Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	_____	
<i>Unobserved</i>	_____	

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	
<i>Unobserved</i>		

Matching: Finding Hidden Randomized Experiments

Types of Experiments

	<i>Complete</i>	<i>Fully</i>
Balance		
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	
<i>Unobserved</i>	On average	

Matching: Finding Hidden Randomized Experiments

Types of Experiments

	<i>Complete</i>	<i>Fully</i>
Balance		
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

↪ *Fully blocked dominates complete randomization*

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power, efficiency,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power, efficiency, bias,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power, efficiency, bias, research costs,

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power, efficiency, bias, research costs, robustness.

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for:
imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

↪ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

Matching: Finding Hidden Randomized Experiments

Types of Experiments

	<i>Complete</i>	<i>Fully</i>
Balance		
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

⇒ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

- PSM: *complete randomization*

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

↪ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

- PSM: *complete randomization*
- Other methods: *fully blocked*

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

↪ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

- PSM: *complete randomization*
- Other methods: *fully blocked*
- **Other matching methods dominate PSM**

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance	<i>Complete</i>	<i>Fully</i>
Covariates:	<i>Randomization</i>	<i>Blocked</i>
<i>Observed</i>	On average	Exact
<i>Unobserved</i>	On average	On average

↪ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

- PSM: *complete randomization*
- Other methods: *fully blocked*
- **Other matching methods dominate PSM** (wait, it gets worse)

Method 1: Mahalanobis Distance Matching

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)' S^{-1} (X_c - X_t)}$

2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)' S^{-1} (X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)

2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)
- Match each treated unit to the nearest control unit

2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused

2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \textit{caliper}$

2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

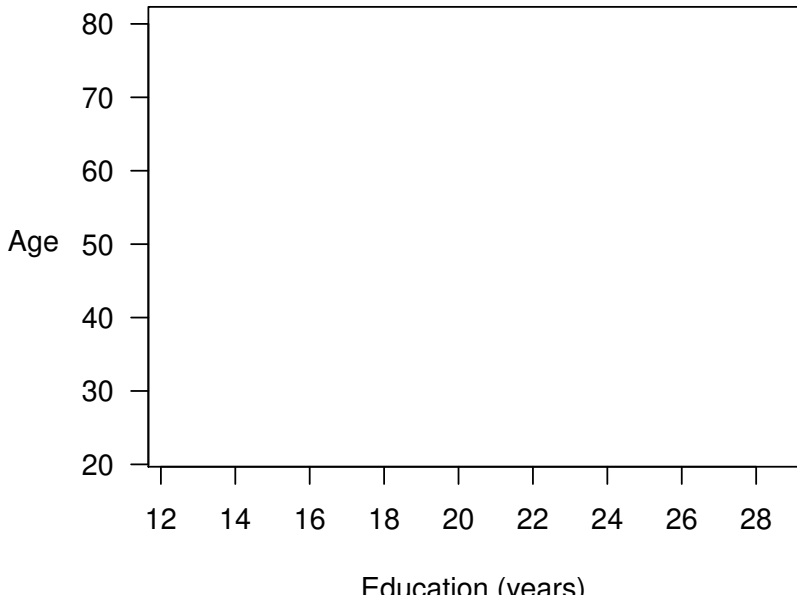
(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

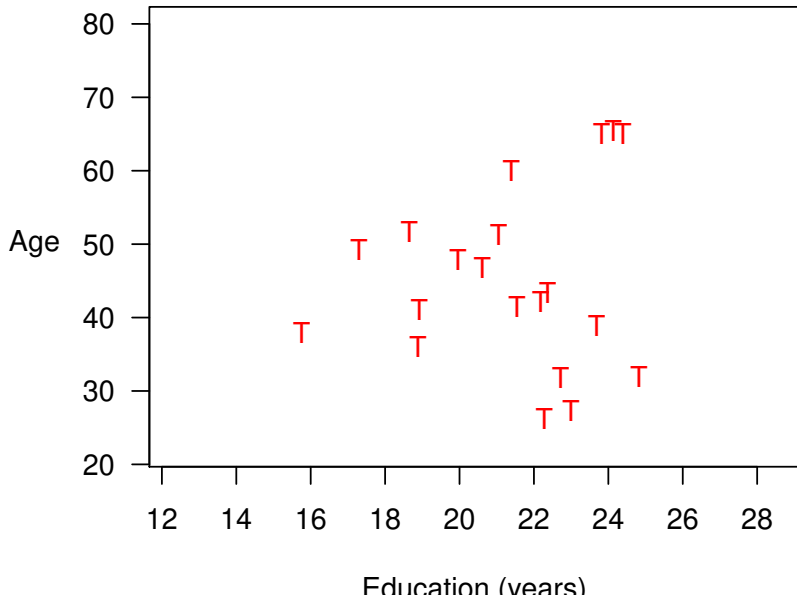
- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$
- (Many adjustments available to this basic method)

2. Estimation Difference in means or a model

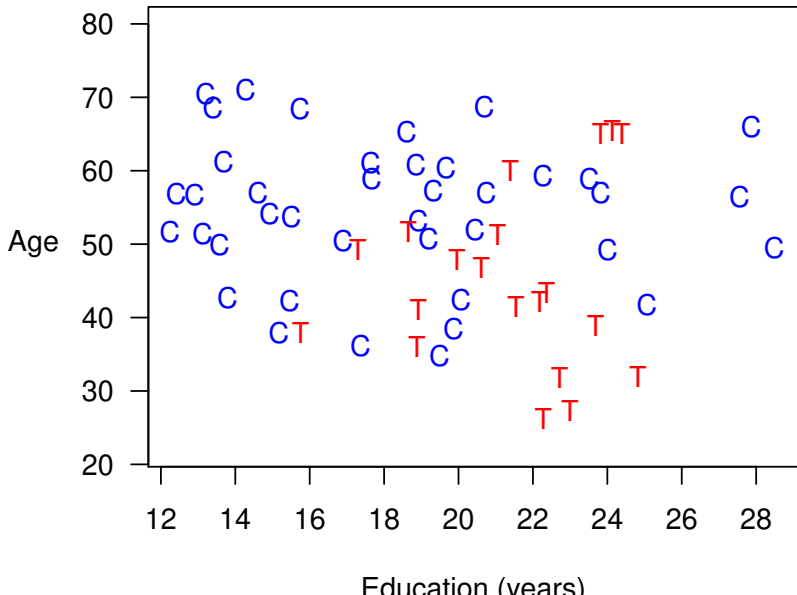
Mahalanobis Distance Matching



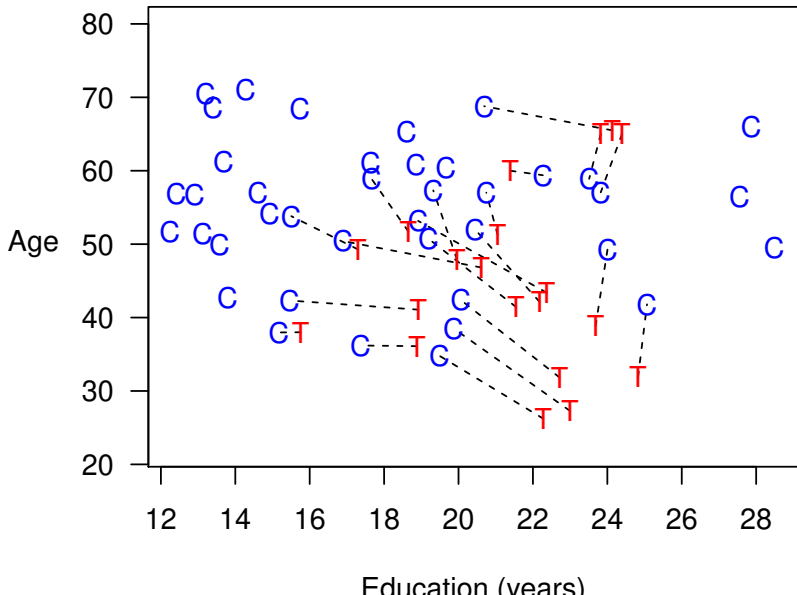
Mahalanobis Distance Matching



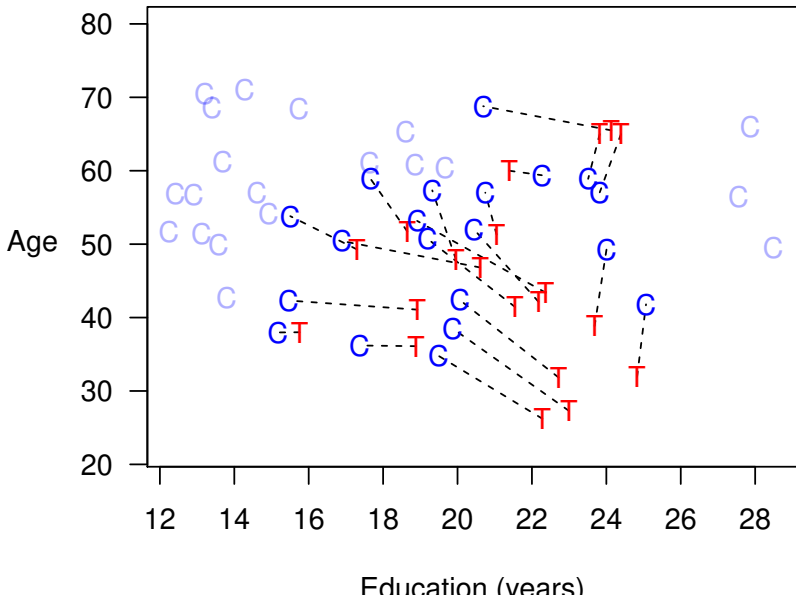
Mahalanobis Distance Matching



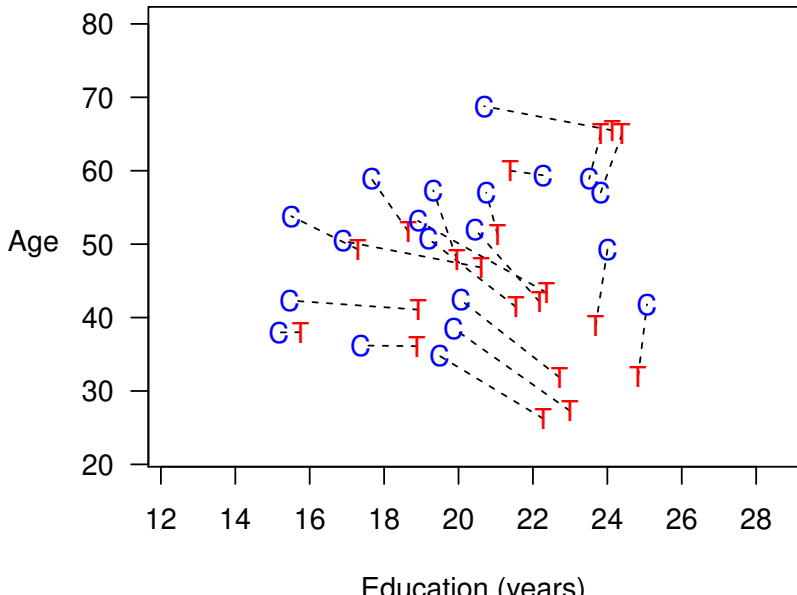
Mahalanobis Distance Matching



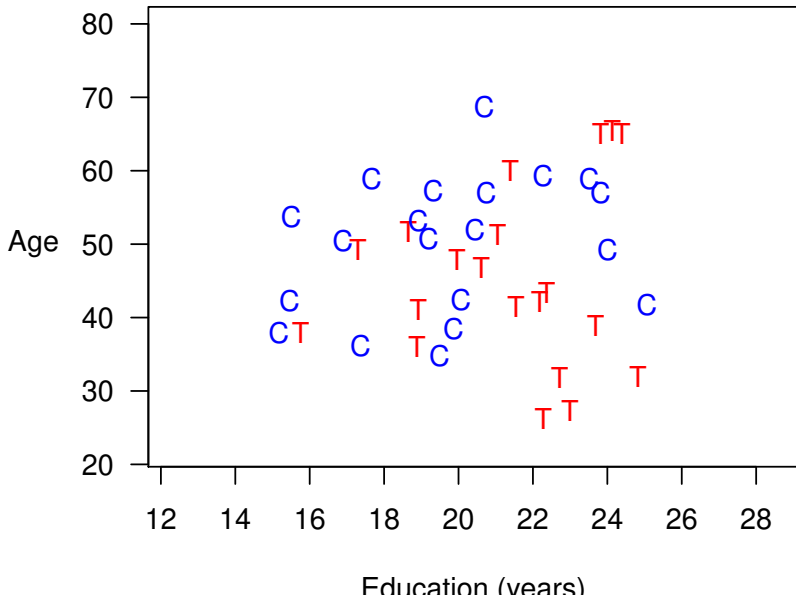
Mahalanobis Distance Matching



Mahalanobis Distance Matching

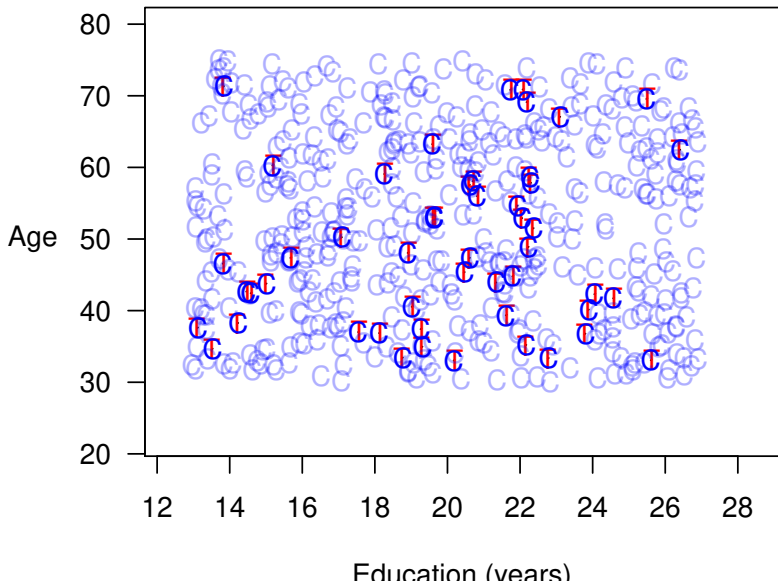


Mahalanobis Distance Matching

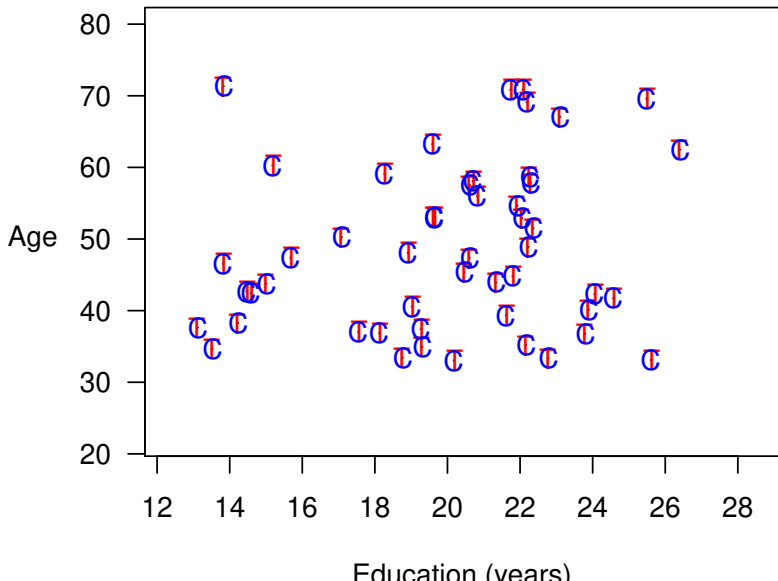


Best Case: Mahalanobis Distance Matching

Best Case: Mahalanobis Distance Matching



Best Case: Mahalanobis Distance Matching



Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)
 - Temporarily coarsen X as much as you're willing

2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)

2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
- Apply exact matching to the coarsened X , $C(X)$

2. Estimation Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
- Apply exact matching to the coarsened X , $C(X)$
 - Sort observations into strata, each with unique values of $C(X)$

2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
- Apply exact matching to the coarsened X , $C(X)$
 - Sort observations into strata, each with unique values of $C(X)$
 - Prune any stratum with 0 treated or 0 control units

2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
- Apply exact matching to the coarsened X , $C(X)$
 - Sort observations into strata, each with unique values of $C(X)$
 - Prune any stratum with 0 treated or 0 control units
- Pass on original (uncoarsened) units except those pruned

2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. **Preprocess** (Matching)

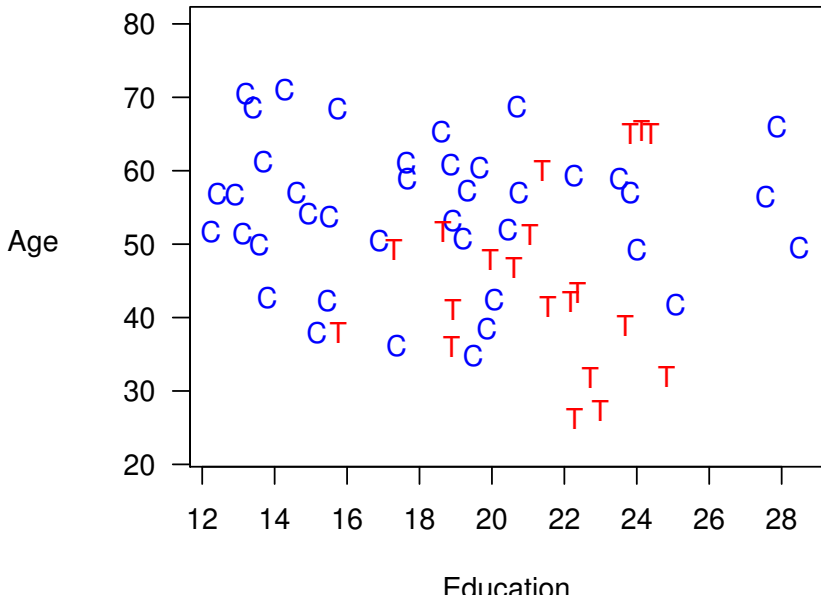
- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
- Apply exact matching to the coarsened X , $C(X)$
 - Sort observations into strata, each with unique values of $C(X)$
 - Prune any stratum with 0 treated or 0 control units
- Pass on original (uncoarsened) units except those pruned

2. **Estimation** Difference in means or a model

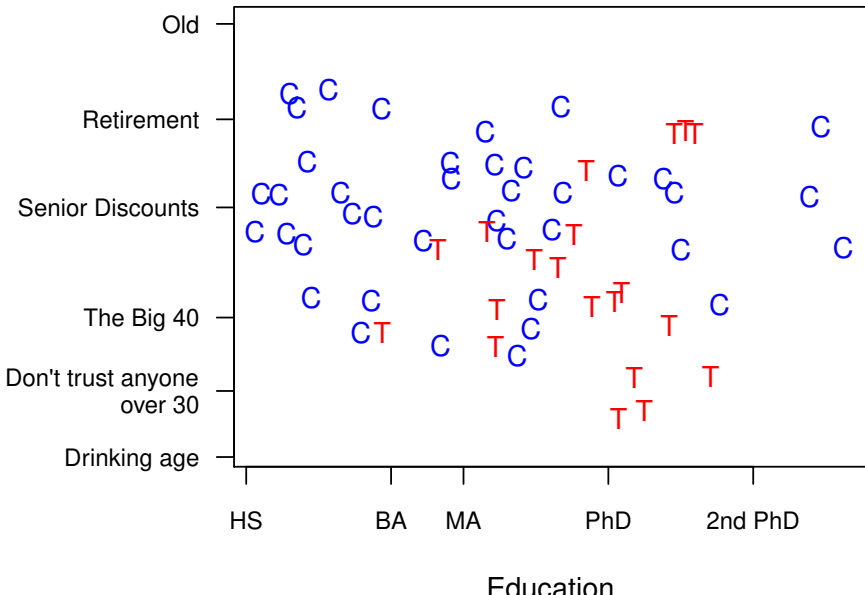
- Weight controls in each stratum to equal treated

Coarsened Exact Matching

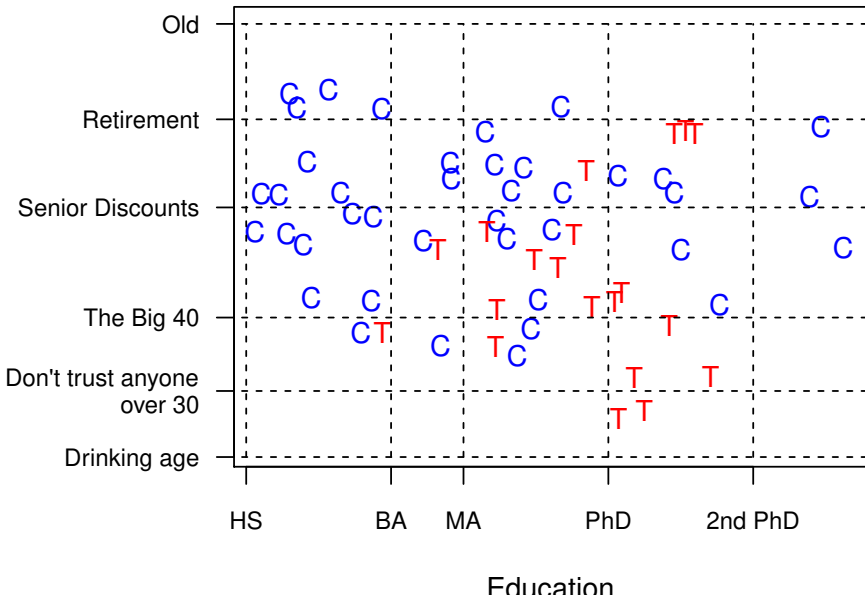
Coarsened Exact Matching



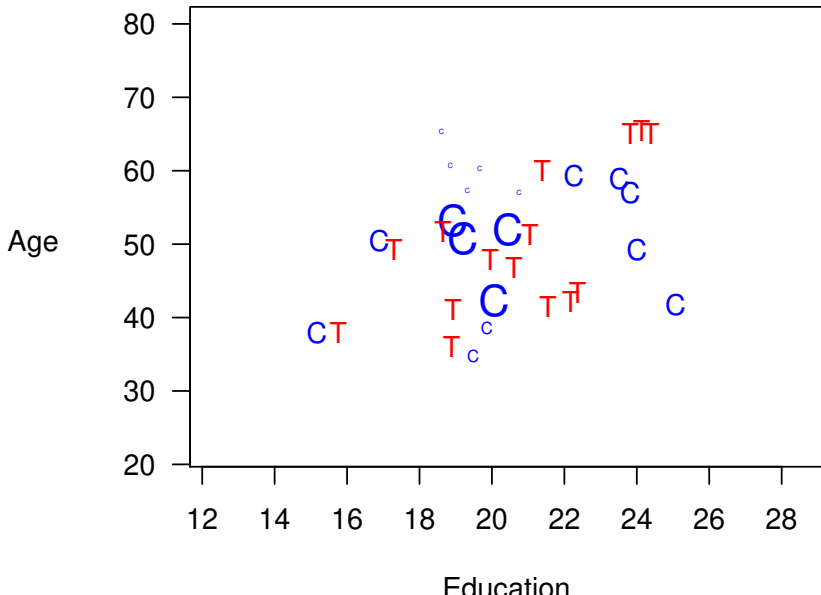
Coarsened Exact Matching



Coarsened Exact Matching

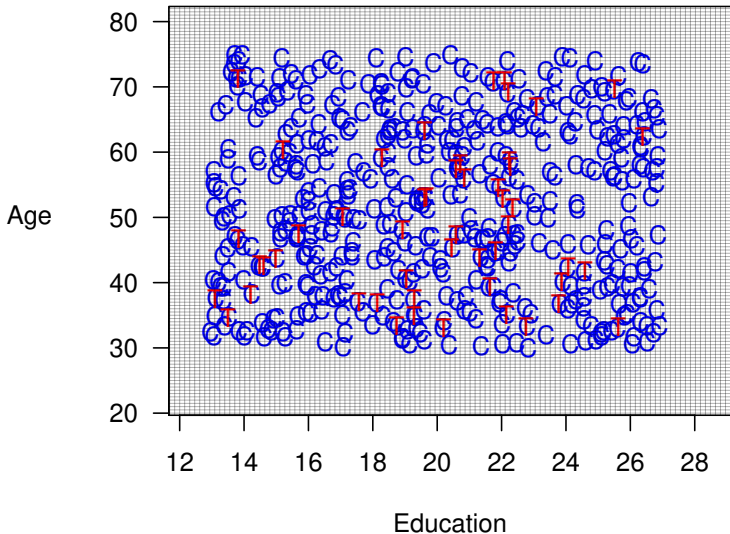


Coarsened Exact Matching

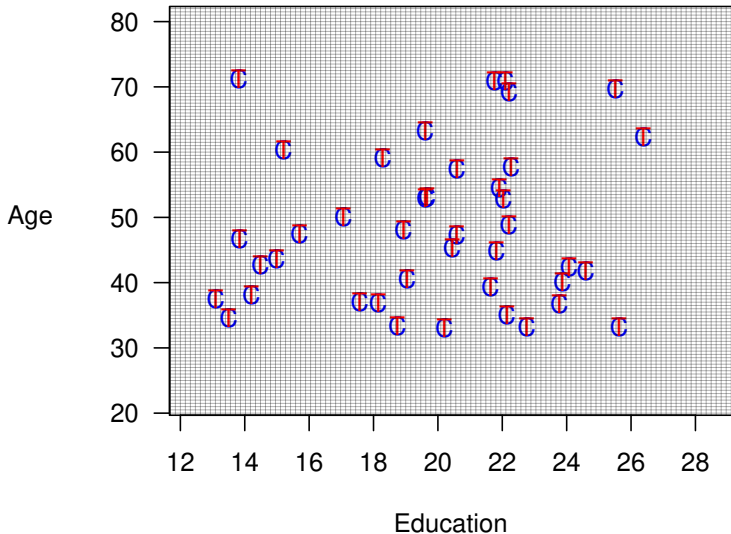


Best Case: Coarsened Exact Matching

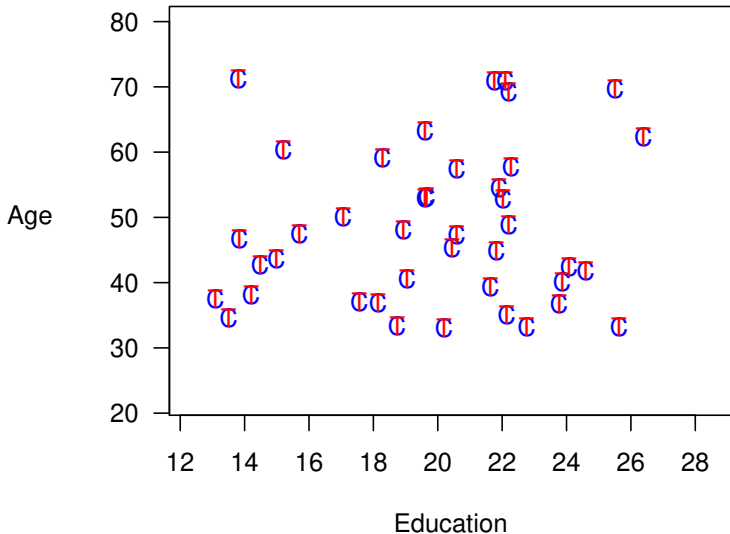
Best Case: Coarsened Exact Matching



Best Case: Coarsened Exact Matching



Best Case: Coarsened Exact Matching



Method 3: Propensity Score Matching

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

- $\text{Distance}(X_c, X_t) = |\pi_c - \pi_t|$

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

- Distance(X_c, X_t) = $|\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

- Distance(X_c, X_t) = $|\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

- Distance(X_c, X_t) = $|\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if Distance > *caliper*

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

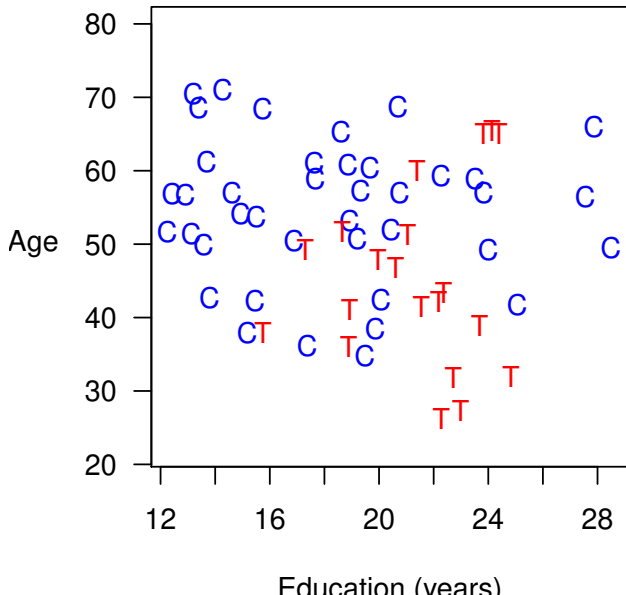
- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

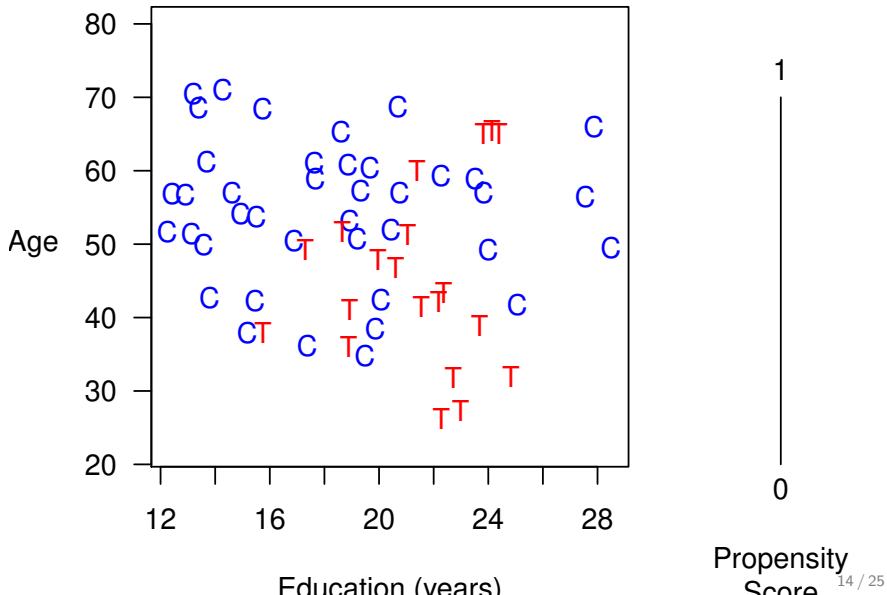
- Distance(X_c, X_t) = $|\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if Distance > *caliper*
- (Many adjustments available to this basic method)

2. Estimation Difference in means or a model

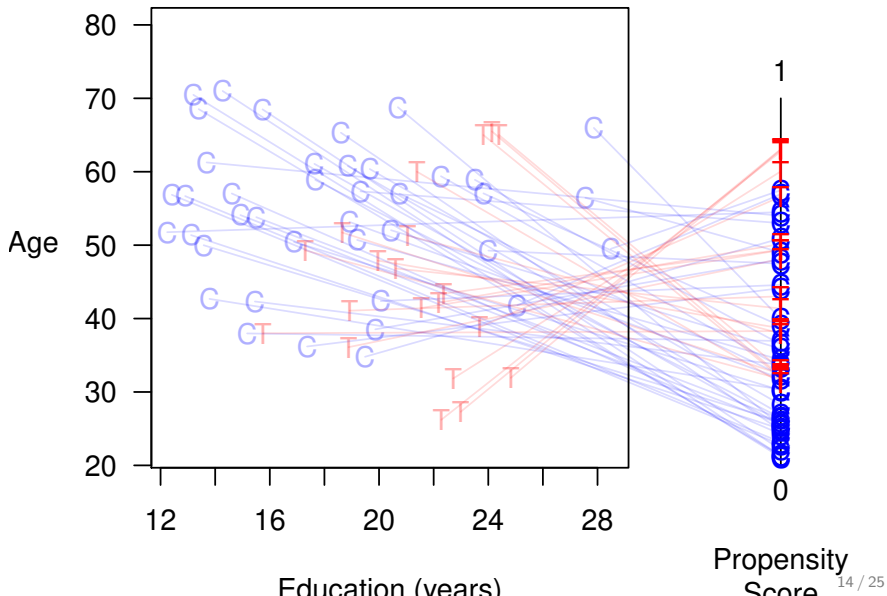
Propensity Score Matching



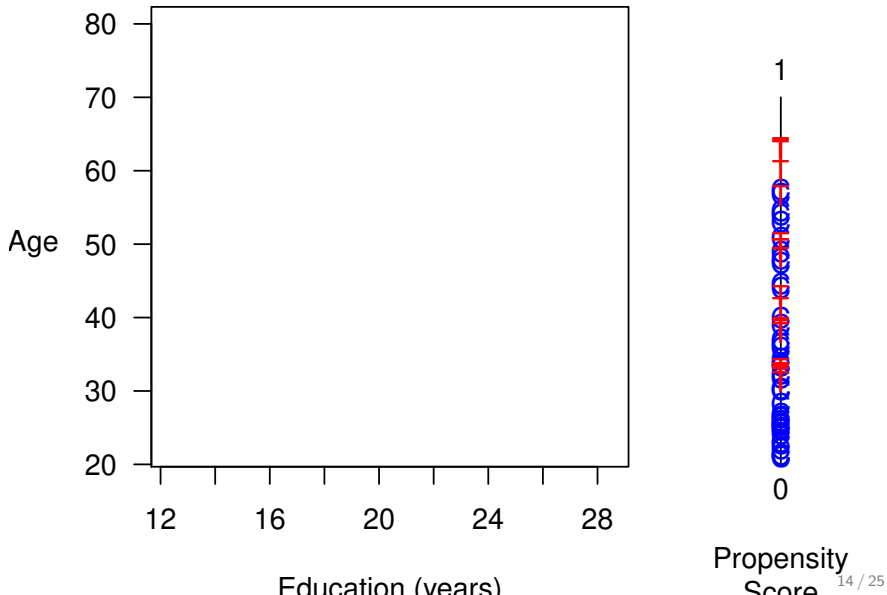
Propensity Score Matching



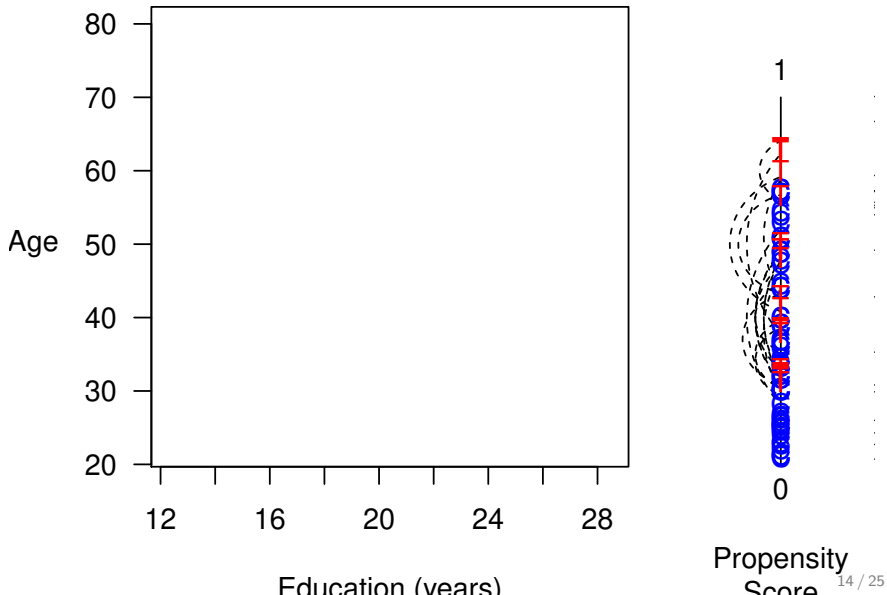
Propensity Score Matching



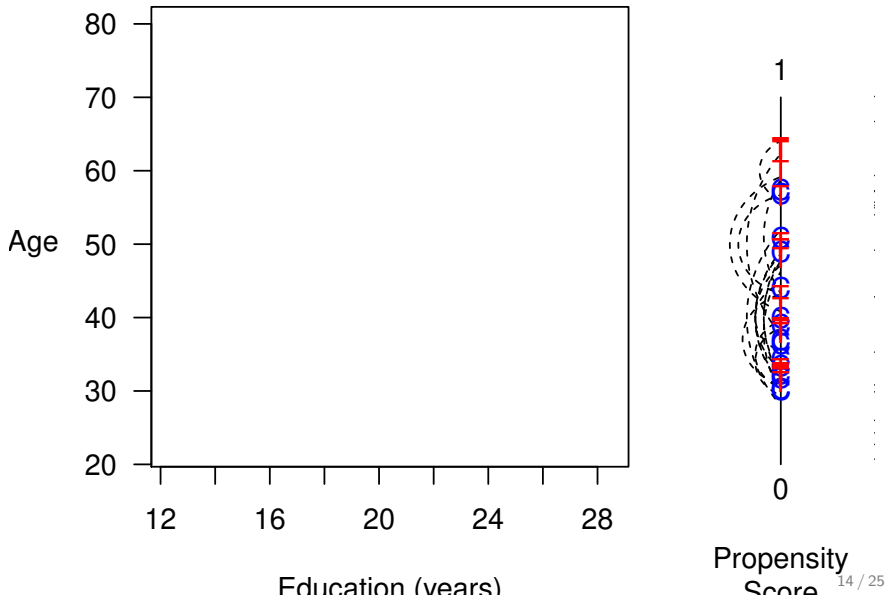
Propensity Score Matching



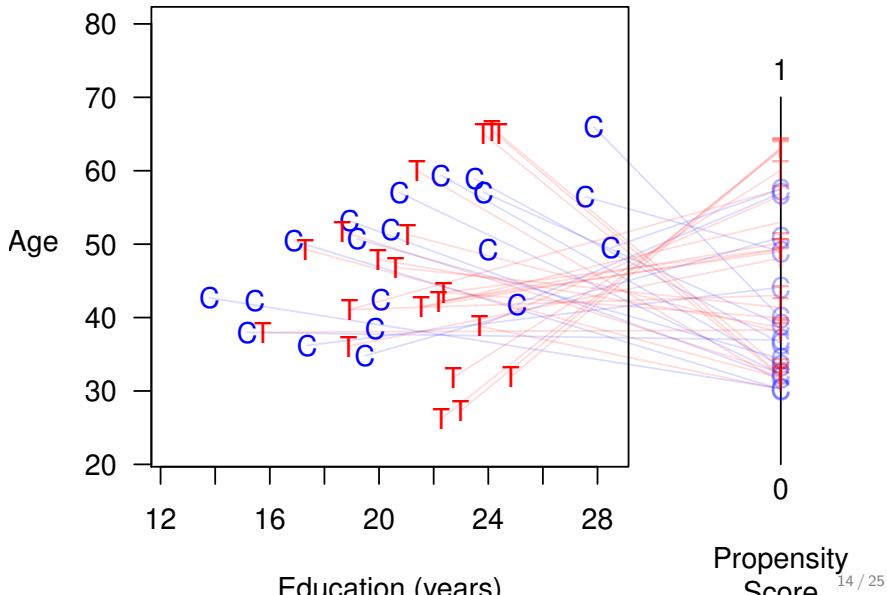
Propensity Score Matching



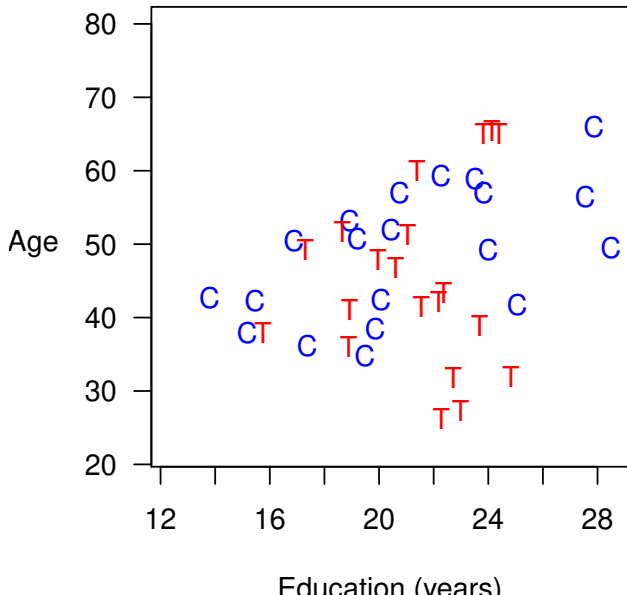
Propensity Score Matching



Propensity Score Matching

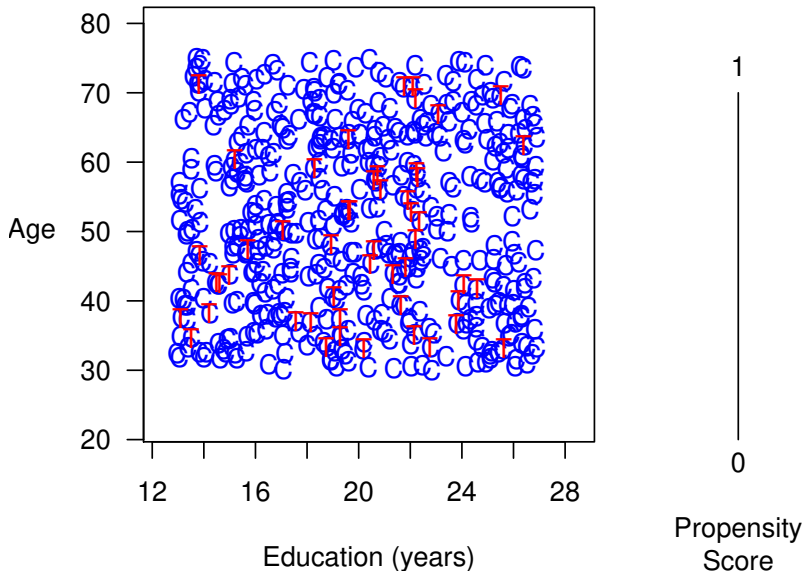


Propensity Score Matching

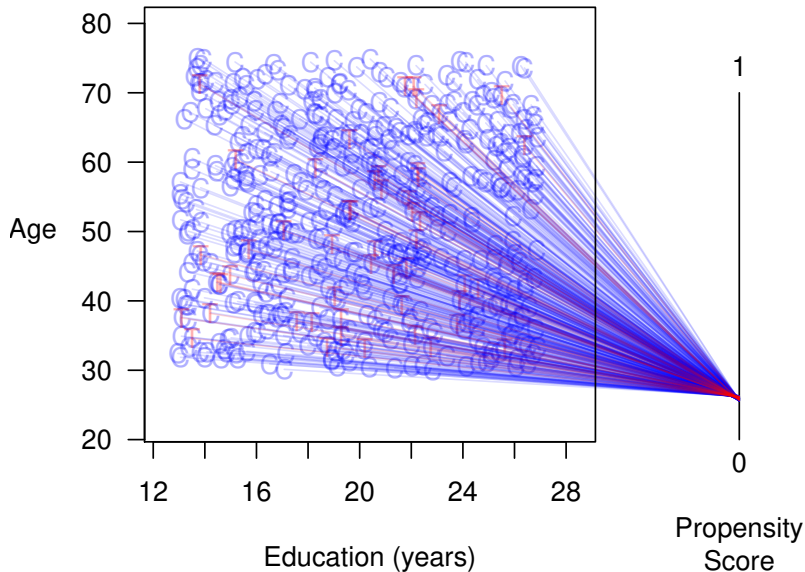


Best Case: Propensity Score Matching

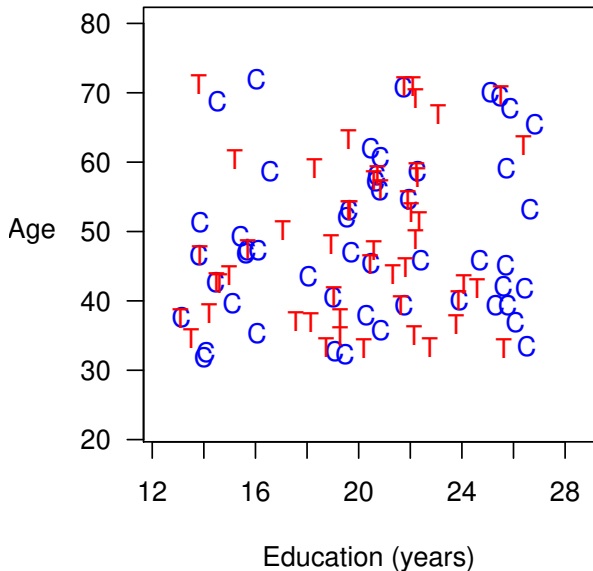
Best Case: Propensity Score Matching



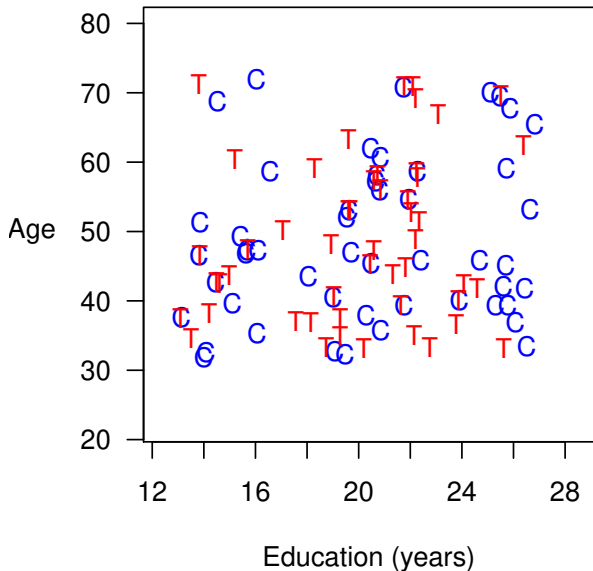
Best Case: Propensity Score Matching



Best Case: Propensity Score Matching



Best Case: Propensity Score Matching is Suboptimal



PSM's Statistical Properties

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes
 - *Efficient* relative to complete randomization, but

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes
 - *Efficient* relative to complete randomization, but
 - *Inefficient* relative to (the more powerful) full blocking

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes
 - *Efficient* relative to complete randomization, but
 - *Inefficient* relative to (the more powerful) full blocking
 - Other methods usually dominate:

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t$$

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\implies X_c = X_t$$

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning)

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata)

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\implies X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias
- If the data have no good matches, the paradox won't be a problem but you're cooked anyway.

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do "better," you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias
- If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
- Doesn't PSM solve the curse of dimensionality problem?

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

$$\pi_c = \pi_t \not\Rightarrow X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias
- If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
- Doesn't PSM solve the curse of dimensionality problem? Nope.

PSM's Statistical Properties

1. Low Standards: Sometimes helps, never optimizes

- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods usually dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

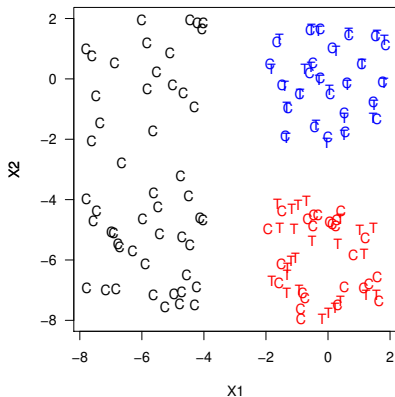
$$\pi_c = \pi_t \not\implies X_c = X_t$$

2. The PSM Paradox: When you do “better,” you do worse

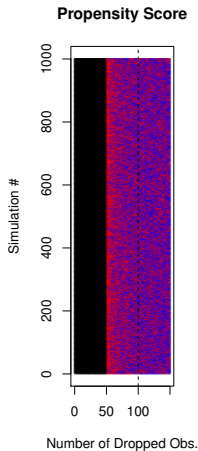
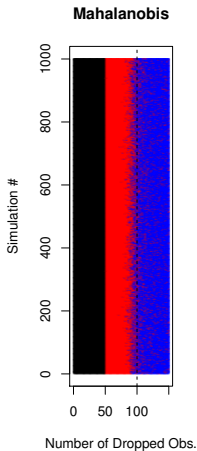
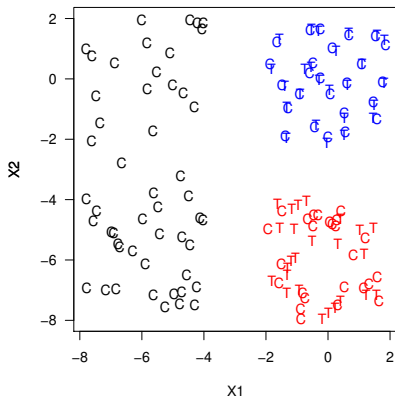
- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias
- If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
- Doesn't PSM solve the curse of dimensionality problem? Nope. The PSM Paradox gets worse with more covariates

PSM is Blind Where Other Methods Can See

PSM is Blind Where Other Methods Can See

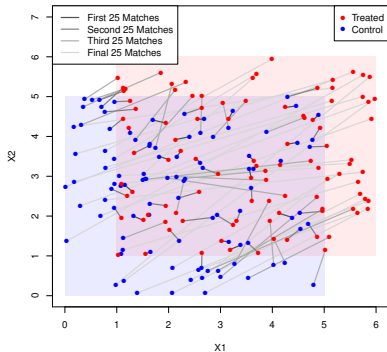


PSM is Blind Where Other Methods Can See

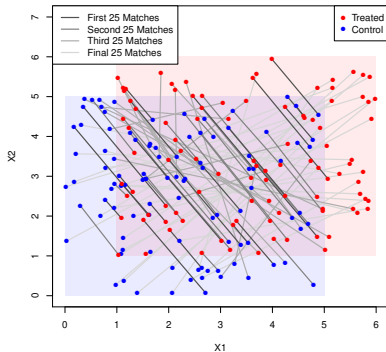


What Does PSM Match?

MDM Matches



PSM Matches

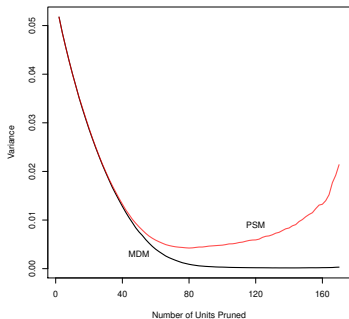


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

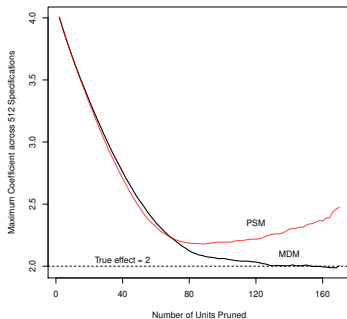
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

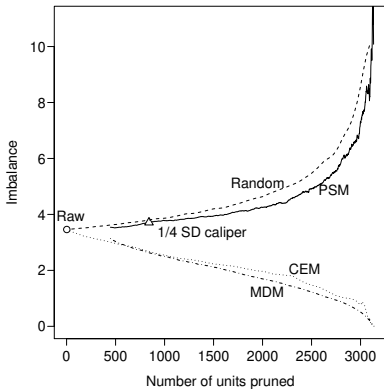


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

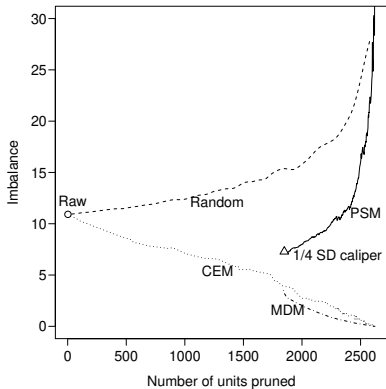
The Propensity Score Paradox in Real Data

The Propensity Score Paradox in Real Data

Finkel et al. (JOP, 2012)

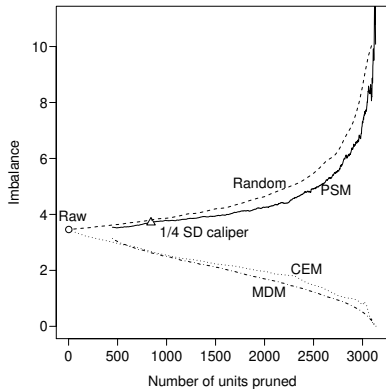


Nielsen et al. (AJPS, 2011)

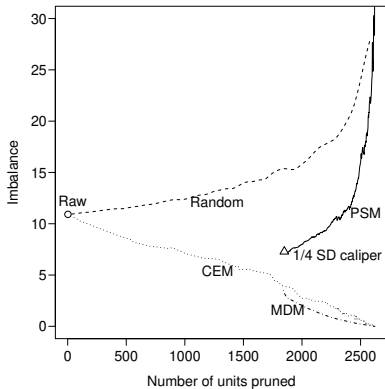


The Propensity Score Paradox in Real Data

Finkel et al. (JOP, 2012)



Nielsen et al. (AJPS, 2011)



Similar pattern for > 20 other real data sets we checked

The Matching Frontier

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use
- No need to choose or use a matching method

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use
- No need to choose or use a matching method
- All solutions are optimal

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use
- No need to choose or use a matching method
- All solutions are optimal
- No iteration or diagnostics required

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use
- No need to choose or use a matching method
- All solutions are optimal
- No iteration or diagnostics required
- No cherry picking possible; you see everything optimal

The Matching Frontier

- **Frontier** = matched dataset with lowest imbalance for each n
- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
- Simple to use
- No need to choose or use a matching method
- All solutions are optimal
- No iteration or diagnostics required
- No cherry picking possible; you see everything optimal
- Choose an imbalance metric, then run.

How hard is the frontier to calculate?

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast
 - operate as “greedy” but we prove are optimal

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast
 - operate as “greedy” but we prove are optimal
 - do not require evaluating every subset

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast
 - operate as “greedy” but we prove are optimal
 - do not require evaluating every subset
 - work with very large data sets

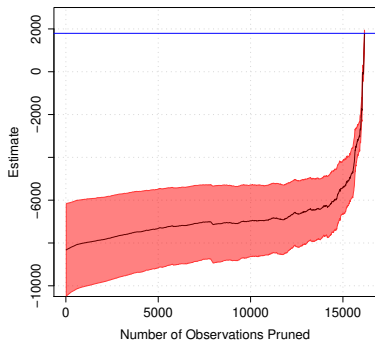
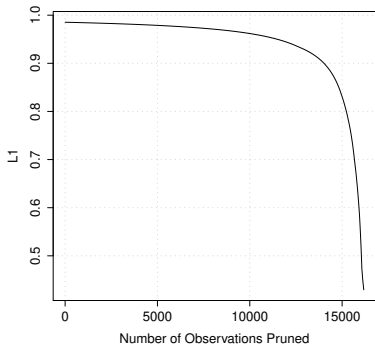
How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast
 - operate as “greedy” but we prove are optimal
 - do not require evaluating every subset
 - work with very large data sets
 - is the exact frontier (no approximation or estimation)

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each sample size $n = N, N - 1, \dots, 1$
 - The combination is the (gargantuan) “power set”
 - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
 - \rightsquigarrow It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast
 - operate as “greedy” but we prove are optimal
 - do not require evaluating every subset
 - work with very large data sets
 - is the exact frontier (no approximation or estimation)
 - \rightsquigarrow It's **easy** to calculate!

Job Training Data: Frontier and Causal Estimates



- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after pruning most Cs
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

Conclusions

Conclusions

- Propensity score matching:

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM:

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates;

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data;

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support;

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score;

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- A Simple and Powerful Method: CEM

Conclusions

- Propensity score matching:
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- A Simple and Powerful Method: CEM
- A New General Approach: The Matching Frontier

Conclusions

- **Propensity score matching:**
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- **A Simple and Powerful Method:** CEM
- **A New General Approach:** The Matching Frontier
 - Fast; easy; no iteration; Software: MatchingFrontier

Conclusions

- **Propensity score matching:**
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- **A Simple and Powerful Method:** CEM
- **A New General Approach:** The Matching Frontier
 - Fast; easy; no iteration; Software: MatchingFrontier
 - No need to choose among matching methods

Conclusions

- **Propensity score matching:**
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- **A Simple and Powerful Method:** CEM
- **A New General Approach:** The Matching Frontier
 - Fast; easy; no iteration; Software: MatchingFrontier
 - No need to choose among matching methods
 - Optimal results from your choice of imbalance metric

Conclusions

- **Propensity score matching:**
 - Approximates complete, not fully blocked, experiments
 - Ignores information; exacerbates model dependence
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- **A Simple and Powerful Method:** CEM
- **A New General Approach:** The Matching Frontier
 - Fast; easy; no iteration; Software: MatchingFrontier
 - No need to choose among matching methods
 - Optimal results from your choice of imbalance metric
- **↪ Using more information is simpler and more powerful**

For more information, articles, & software

GaryKing.org