Matching Methods for Causal Inference

Gary King¹

Institute for Quantitative Social Science Harvard University

National Taiwan University, 5/30/2018

¹GaryKing.org

1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:

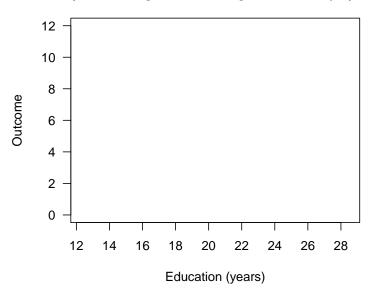
- 1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:
 - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)

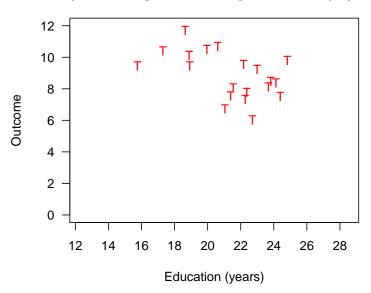
- 1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:
 - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?

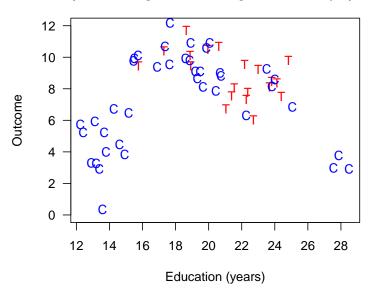
- 1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:
 - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?

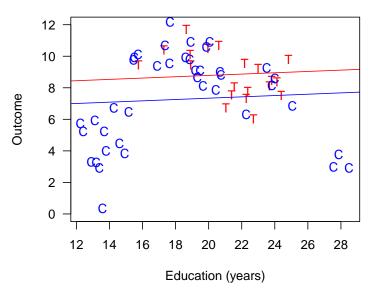
- 1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:
 - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?
- 3. Matching methods optimize either imbalance (\approx bias) or # units pruned (\approx variance); users need both simultaneously:

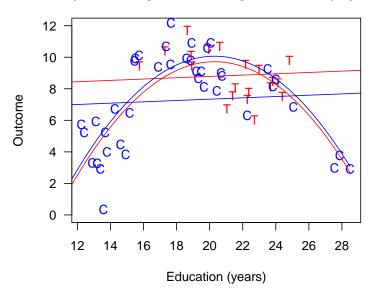
- 1. The most popular method (propensity score matching, used in 103,000 articles!) sounds magical:
 - → "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?
- 3. Matching methods optimize either imbalance (\approx bias) 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)

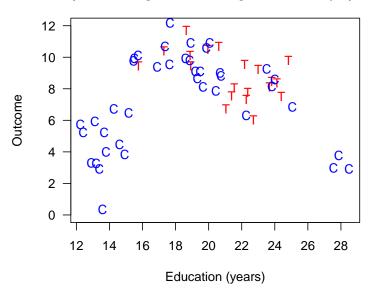


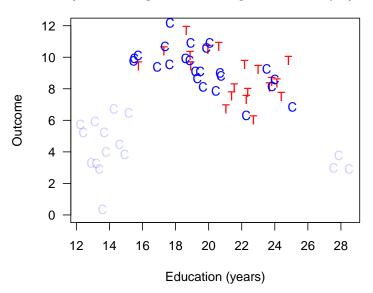


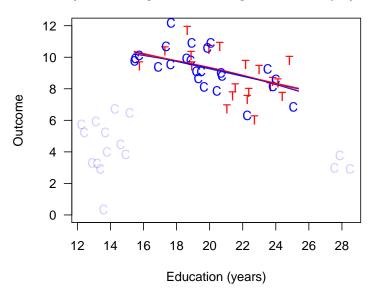












Without Matching:

Without Matching:

Imbalance

Without Matching:

Imbalance → Model Dependence

Without Matching:

Without Matching:

Without Matching:

Imbalance → Model Dependence → Researcher discretion → Bias

• Qualitative choice from unbiased estimates = biased estimator

Without Matching:

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

Without Matching:

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

Without Matching:

- 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]

Without Matching:

- 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]

Without Matching:

- 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)[reh]

Without Matching:

- 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)[reh]
- "Teaching psychology is mostly a waste of time" (Kahneman 2011)

Without Matching:

Without Matching:

Without Matching:

Model Dependence → Researcher discretion → Bias

Without Matching:

Model Dependence → Researcher discretion → Bias

Without Matching:

Model Dependence → Researcher discretion → Bias

The Problems Matching Solves

Without Matching:

```
Model Dependence → Researcher discretion → Bias
```

A central project of statistics: Automating away human discretion

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

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

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

$$\mathsf{TE}_i = Y_i(1) - \underline{Y_i(0)}$$

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

$$TE_i = Y_i(1) - Y_i(0)$$
= observed – unobserved

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

$$TE_i = Y_i - Y_i(0)$$
= observed – unobserved

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

$$TE_i = Y_i - Y_i(0)$$
= observed – unobserved

• Estimate $Y_i(0)$ with Y_i with a matched $(X_i \approx X_i)$ control

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

$$TE_i = Y_i - Y_i(0)$$
= observed – unobserved

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

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

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

= observed – unobserved

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

$$\mathsf{SATT} = \underset{i \in \{T_i = 1\}}{\mathsf{Mean}} \left(\mathsf{TE}_i \right)$$

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

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

= observed – unobserved

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

$$\mathsf{SATT} = \underset{i \in \{T_i = 1\}}{\mathsf{Mean}} \left(\mathsf{TE}_i \right)$$

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

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

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

= observed – unobserved

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

$$\mathsf{SATT} = \underset{i \in \{T_i = 1\}}{\mathsf{Mean}} (\mathsf{TE}_i)$$

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

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

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

= observed – unobserved

- 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:

$$\mathsf{SATT} = \underset{i \in \{T_i = 1\}}{\mathsf{Mean}} (\mathsf{TE}_i)$$

- 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

Complete Randomization

Complete Fully Randomization Blocked

Balance	Complete	Fully	
Covariates:	Randomization	Blocked	
Observed			
Unobserved			

Balance	Complete	Fully	
Covariates:	Randomization	Blocked	
Observed	On average		
Unobserved			

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	
Unobserved	On average	

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

[→] Fully blocked dominates complete randomization

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

[→] Fully blocked dominates complete randomization for:

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

→ Fully blocked dominates complete randomization for: imbalance,

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

→ Fully blocked dominates complete randomization for: imbalance, model dependence,

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	On average	On average

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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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!

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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)

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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

Balance	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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	Complete	Fully
Covariates:	Randomization	Blocked
Observed	On average	Exact
Unobserved	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)

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

(Approximates Fully Blocked Experiment)

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

(Approximates Fully Blocked Experiment)

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

(Approximates Fully Blocked Experiment)

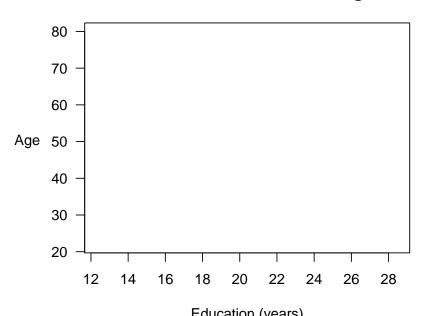
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit

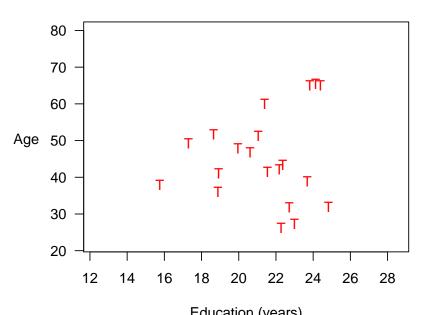
(Approximates Fully Blocked Experiment)

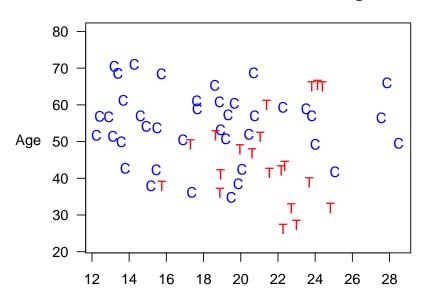
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused

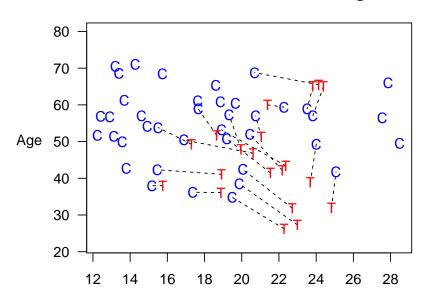
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper
- 2. Estimation Difference in means or a model

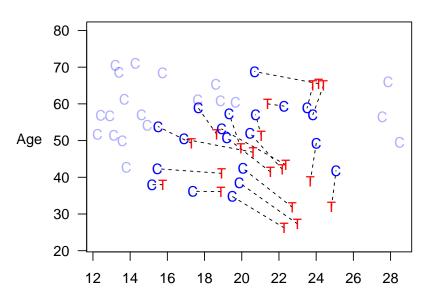
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper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

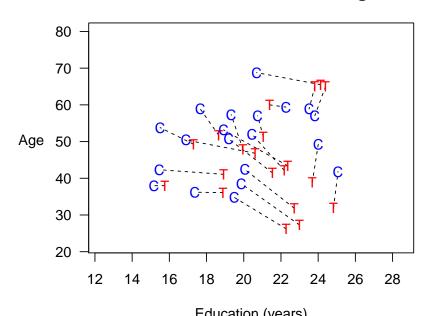


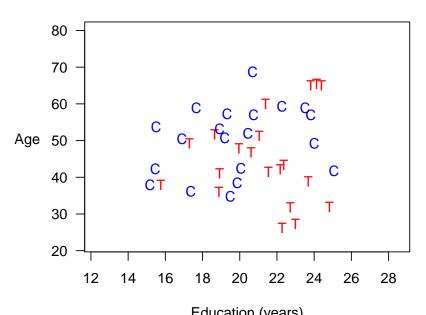






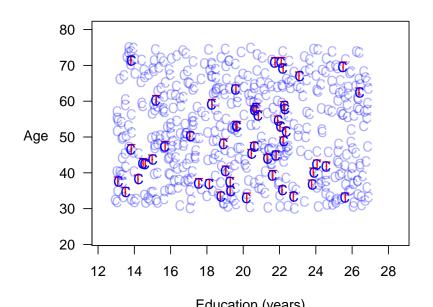




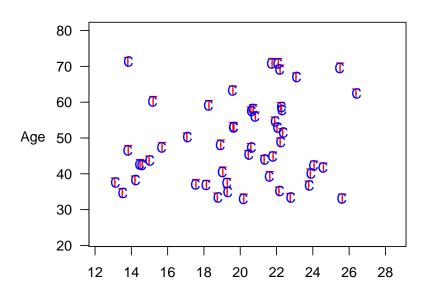


Best Case: Mahalanobis Distance Matching

Best Case: Mahalanobis Distance Matching



Best Case: Mahalanobis Distance Matching



Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach) (Approximates Fully Blocked Experiment)

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

(Approximates Fully Blocked Experiment)

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

(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)

(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)

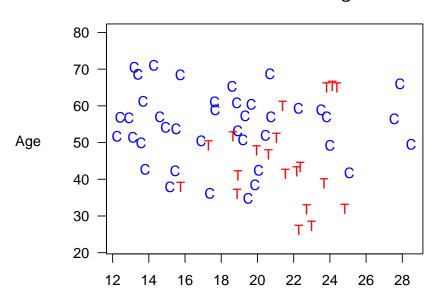
(Approximates Fully Blocked Experiment)

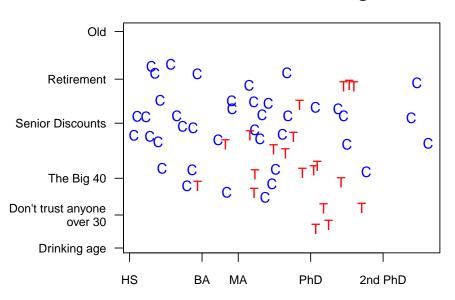
- 1. Preprocess (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Apply exact matching to the coarsened X, C(X)
 - Sort observations into strata, each with unique values of C(X)

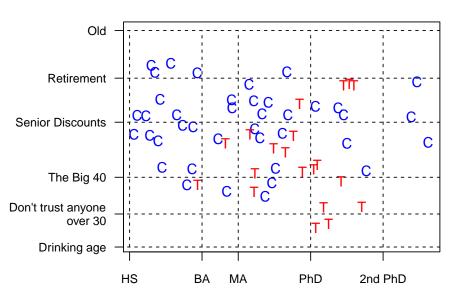
- 1. Preprocess (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Apply exact matching to the coarsened X, C(X)
 - Sort observations into strata, each with unique values of C(X)
 - Prune any stratum with 0 treated or 0 control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

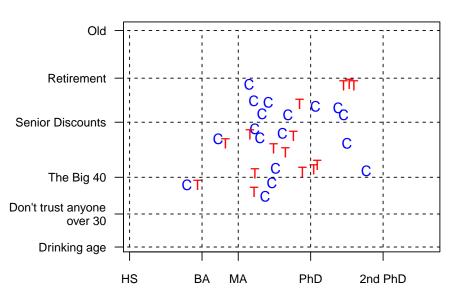
- 1. Preprocess (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Apply exact matching to the coarsened X, C(X)
 - Sort observations into strata, each with unique values of C(X)
 - Prune any stratum with 0 treated or 0 control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

- 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 treateds



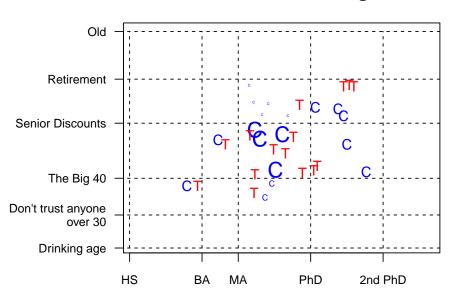






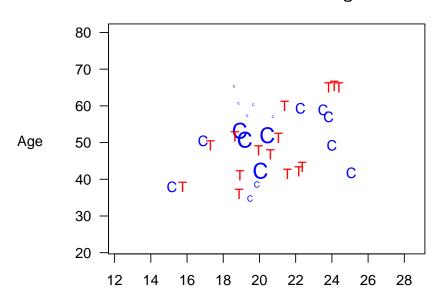
Coarsened Exact Matching

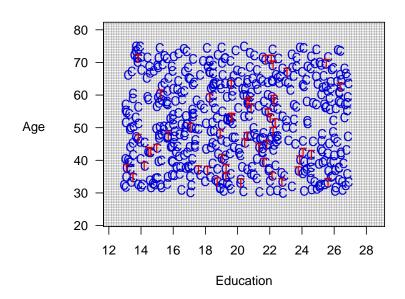
Education

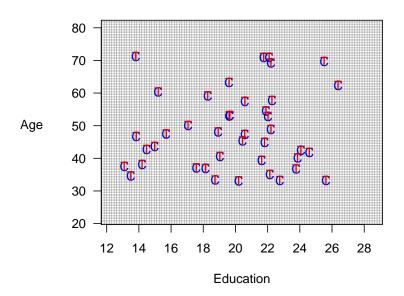


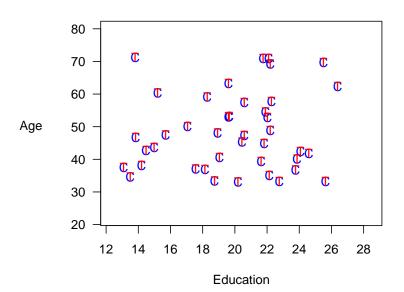
Coarsened Exact Matching

Education









(Approximates Completely Randomized Experiment)

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

(Approximates Completely Randomized Experiment)

- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$

(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 $(X_c, X_t) = |\pi_c \pi_t|$

(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

(Approximates Completely Randomized Experiment)

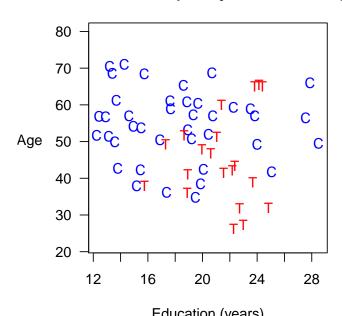
- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$
 - Distance $(X_c, X_t) = |\pi_c \pi_t|$
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused

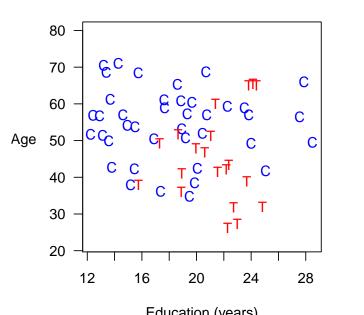
(Approximates Completely Randomized Experiment)

- 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

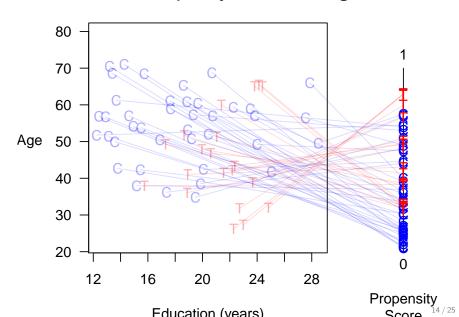
(Approximates Completely Randomized Experiment)

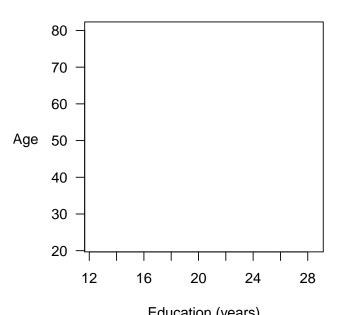
- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1 | X) = \frac{1}{1 + e^{-X_i \beta}}$
 - Distance $(X_c, X_t) = |\pi_c \pi_t|$
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper
 - (Many adjustments available to this basic method)
- 2. Estimation Difference in means or a model

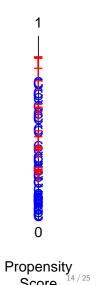


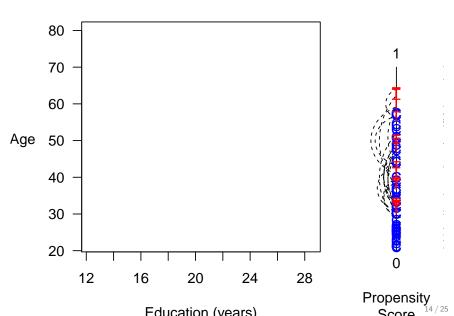


Propensity Score 14/25

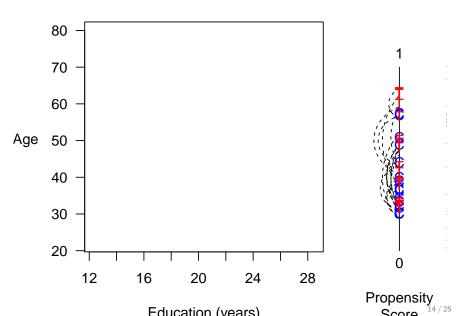




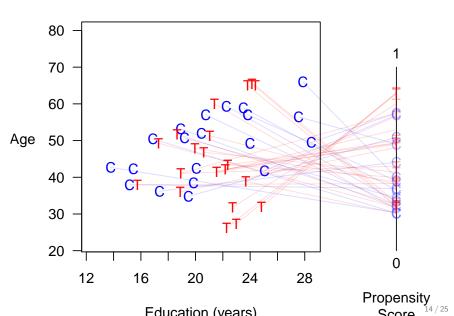


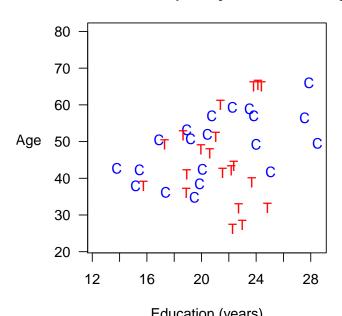


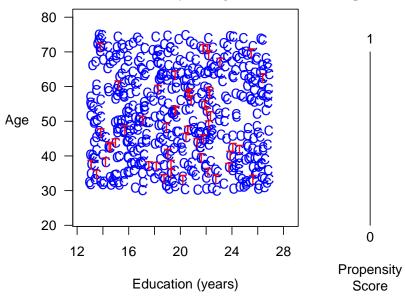
Education (years)

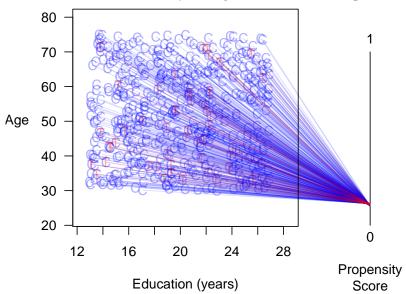


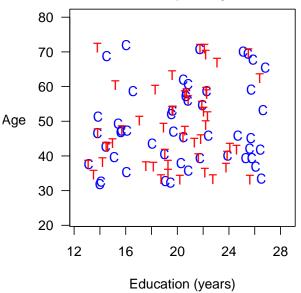
Education (years)



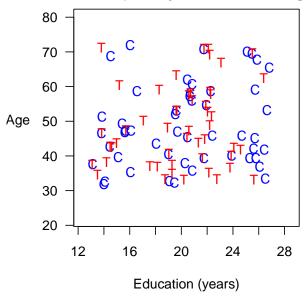








Best Case: Propensity Score Matching is Suboptimal



1. Low Standards: Sometimes helps, never optimizes

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

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

- 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:

- 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:

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

- 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:

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

- 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:

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

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

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

- 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:

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

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

- 2. The PSM Paradox: When you do "better," you do worse
 - Background: Random matching increases imbalance

- 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:

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

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

- 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)

- 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:

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

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

- 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) \leadsto all $\hat{\pi} \approx 0.5$ (or constant within strata)

- 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:

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

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

- 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) \leadsto all $\hat{\pi} \approx 0.5$ (or constant within strata) \leadsto pruning at random

- 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:

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

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

- 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) \leadsto all $\hat{\pi} \approx 0.5$ (or constant within strata) \leadsto pruning at random \leadsto Imbalance

- 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:

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

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

- 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) \leadsto all $\hat{\pi}\approx 0.5$ (or constant within strata) \leadsto pruning at random \leadsto Imbalance \leadsto Inefficency

- 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:

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

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

- 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) \leadsto all $\hat{\pi}\approx 0.5$ (or constant within strata) \leadsto pruning at random \leadsto Imbalance \leadsto Inefficency \leadsto Model dependence

- 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:

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

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

- 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) \leadsto all $\hat{\pi}\approx 0.5$ (or constant within strata) \leadsto pruning at random \leadsto Imbalance \leadsto Inefficency \leadsto Model dependence \leadsto Bias

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:

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

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

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

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:

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

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

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

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:

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

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

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

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:

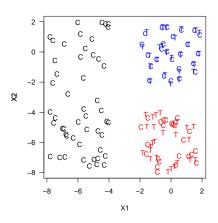
$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

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

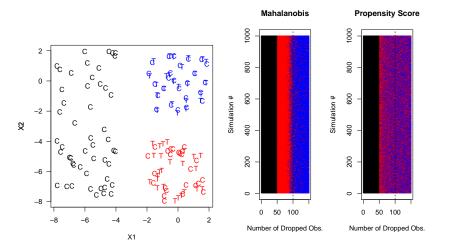
- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning) \leadsto all $\hat{\pi}\approx 0.5$ (or constant within strata) \leadsto pruning at random \leadsto Imbalance \leadsto Inefficency \leadsto Model dependence \leadsto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



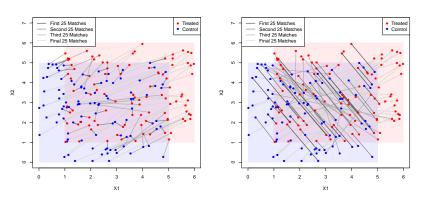
PSM is Blind Where Other Methods Can See



What Does PSM Match?

MDM Matches

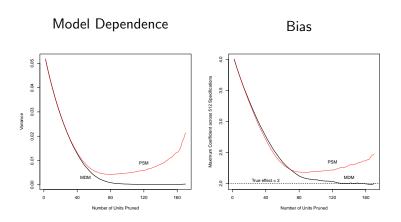
PSM Matches



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

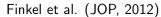


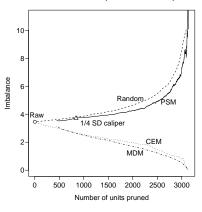
$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$

$$\epsilon_i \sim N(0, 1)$$

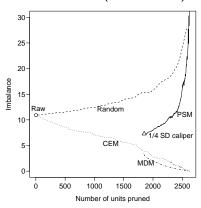
The Propensity Score Paradox in Real Data

The Propensity Score Paradox in Real Data

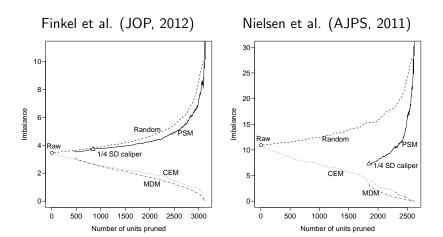




Nielsen et al. (AJPS, 2011)



The Propensity Score Paradox in Real Data



Similar pattern for > 20 other real data sets we checked

• Frontier = matched dataset with lowest imbalance for each n

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

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

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

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

- Frontier = matched dataset with lowest imbalance for each *n*
- Bias-Variance trade off → 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

- Frontier = matched dataset with lowest imbalance for each n
- Bias-Variance trade off → 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

- Frontier = matched dataset with lowest imbalance for each n
- Bias-Variance trade off → 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.

• Consider 1 point on the SATT frontier:

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

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

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

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

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

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

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

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for <u>all</u> $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for <u>each</u> 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
 - → It's hard to calculate!

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for <u>all</u> $\binom{N}{n}$ subsets of rows of X_0
 - · Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for <u>each</u> 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
 - → It's hard to calculate!
- We develop algorithms for the (optimal) frontier which:

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for <u>all</u> $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for <u>each</u> 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
 - → It's hard to calculate!
- We develop algorithms for the (optimal) frontier which:
 - runs very fast

- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for <u>all</u> $\binom{N}{n}$ subsets of rows of X_0
 - · Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for <u>each</u> 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
 - → It's hard to calculate!
- We develop algorithms for the (optimal) frontier which:
 - · runs very fast
 - operate as "greedy" but we prove are optimal

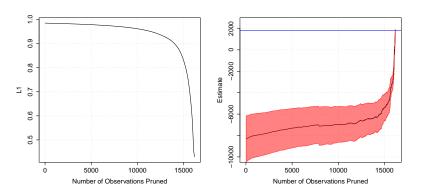
- Consider 1 point on the SATT frontier:
 - Start with matrix of N control units X_0
 - Calculate imbalance for <u>all</u> $\binom{N}{n}$ subsets of rows of X_0
 - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for <u>each</u> sample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

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

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

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

• Propensity score matching:

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

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

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

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

- 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;

- 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;

- 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;

- 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.

- 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

- 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

- 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

- 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

- 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

- 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
- Wing more information is simpler and more powerful

For more information, articles, & software

GaryKing.org