# Simplifying Matching Methods for Causal Inference

Gary King<sup>1</sup>

Institute for Quantitative Social Science Harvard University

University of Pennsylvania, APPC, 4/1/2016

<sup>&</sup>lt;sup>1</sup>GaryKing.org

1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:

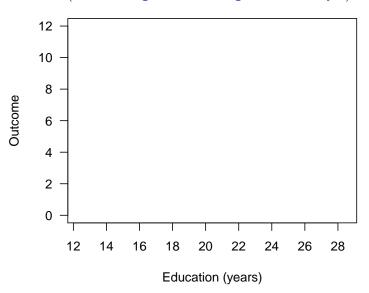
- 1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:
  - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)

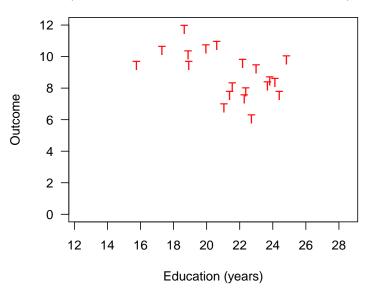
- 1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:
  - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?

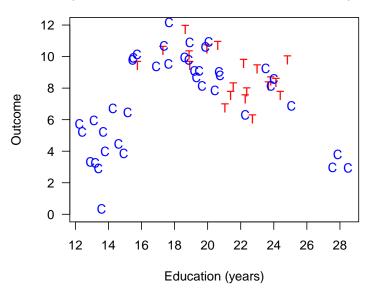
- 1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:
  - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?
  - "Causal Inference Without Balance Checking: Coarsened Exact Matching" (PA, 2011. Stefano M lacus, Gary King, and Giuseppe Porro)

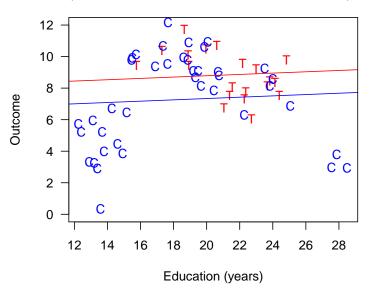
- 1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:
  - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?
- 3. Matching methods optimize either imbalance ( $\approx$  bias) or # units pruned ( $\approx$  variance); users need both simultaneously':

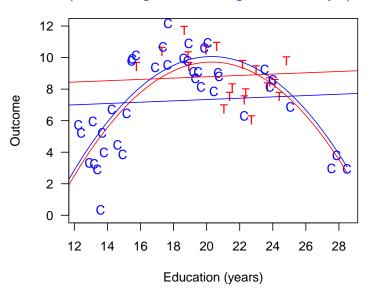
- 1. The most popular method (propensity score matching, used in 53,200 articles!) sounds magical:
  - "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
- 2. Do powerful methods have to be complicated?
  - "Causal Inference Without Balance Checking: Coarsened Exact Matching" (PA, 2011. Stefano M lacus, 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)

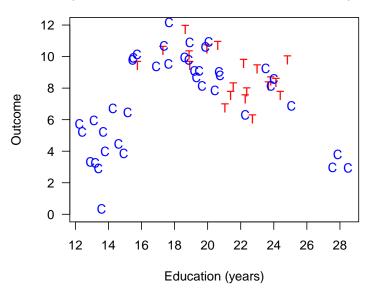


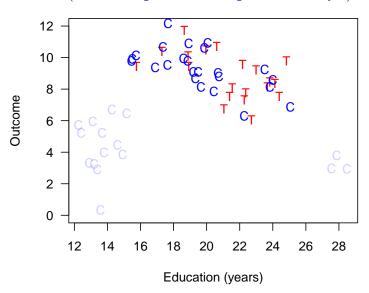


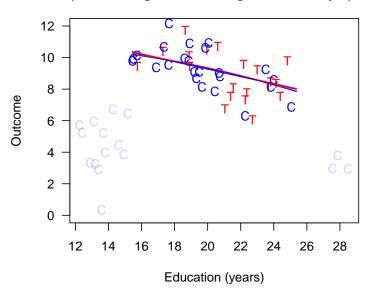












Without Matching:

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[eff]

#### 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 [eff]
- 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 [eff]
- 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 [eff]
- 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]

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

#### Without Matching:

#### Without Matching:

Model Dependence → Researcher discretion → Bias

#### 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:

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

- $Y_i$  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 <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:

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

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

- $Y_i$  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  $Y_j$  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)

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

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

- 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 treated 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

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

### **Types of Experiments**

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

→ Fully blocked dominates complete randomization

### **Types of Experiments**

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

<sup>→</sup> Fully blocked dominates complete randomization for:

#### **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,

#### **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,

#### **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,

### **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,

### **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,

#### **Types of Experiments**

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

 $\leadsto$  Fully blocked dominates complete randomization for: imbalance, model dependence, power, efficiency, bias, research costs,

#### **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.

### **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!

#### **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)

#### **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

#### **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

## 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)

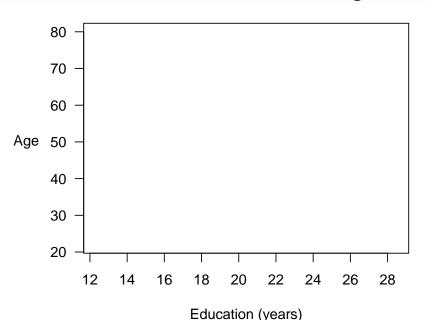
- 1. Preprocess (Matching)
  - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
  - (Mahalanobis is for methodologists; in applications, use Euclidean!)
  - Match each treated unit to the nearest control unit

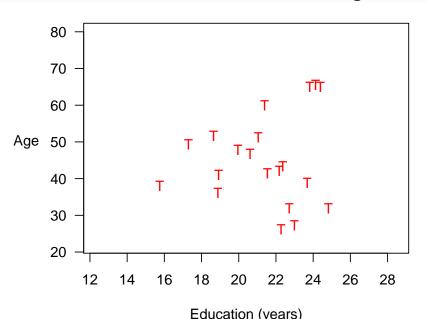
(Approximates Fully Blocked Experiment)

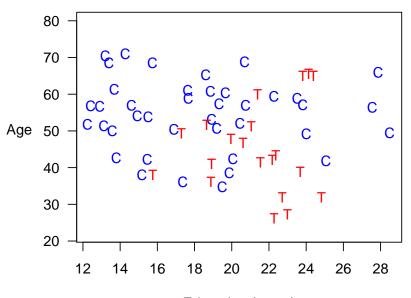
- 1. Preprocess (Matching)
  - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
  - (Mahalanobis is for methodologists; in applications, use Euclidean!)
  - Match each treated unit to the nearest control unit
  - · Control units: not reused; pruned if unused

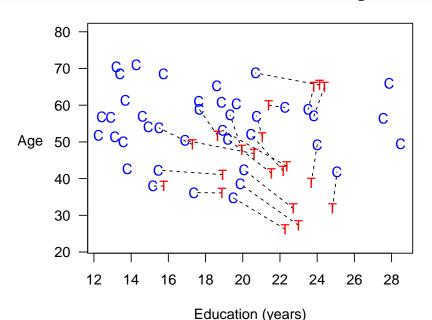
- 1. Preprocess (Matching)
  - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
  - (Mahalanobis is for methodologists; in applications, use Euclidean!)
  - Match each treated unit to the nearest control unit
  - · Control units: not reused; pruned if unused
  - Prune matches if Distance>caliper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

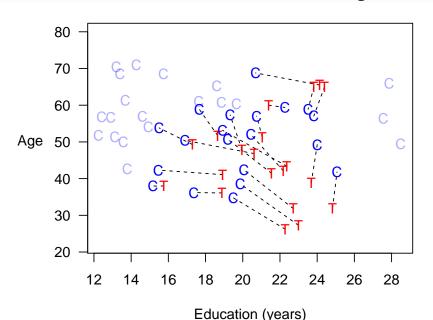
- 1. Preprocess (Matching)
  - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
  - (Mahalanobis is for methodologists; in applications, use Euclidean!)
  - Match each treated unit to the nearest control unit
  - · Control units: not reused; pruned if unused
  - Prune matches if Distance>caliper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

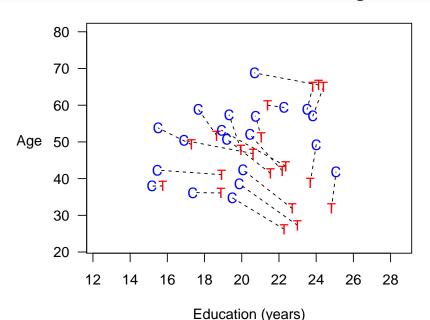


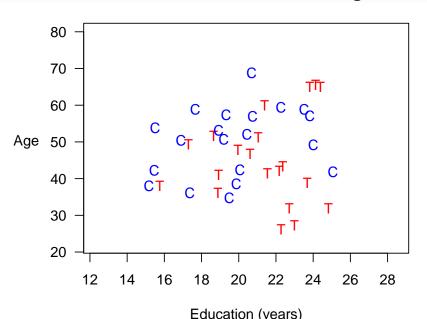






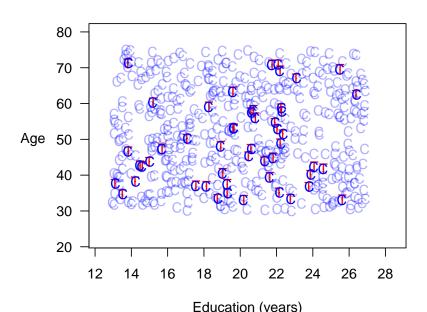




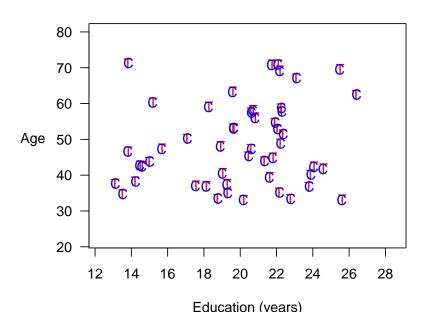


# Best Case: Mahalanobis Distance Matching

## Best Case: Mahalanobis Distance Matching



## Best Case: Mahalanobis Distance Matching



(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)

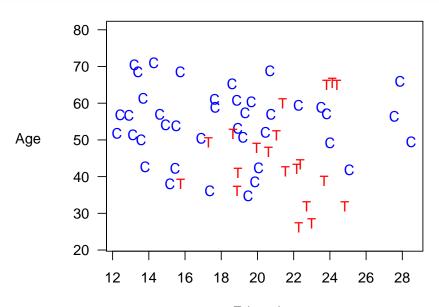
(Approximates Fully Blocked Experiment)

- 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)

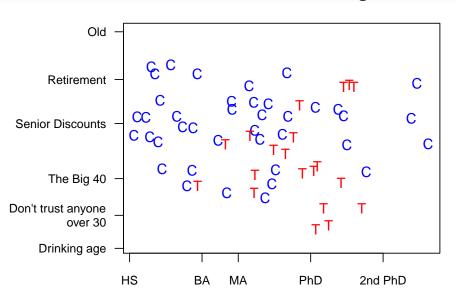
- 1. Preprocess (Matching)
  - Temporarily coarsen X as much as you're willing
    - e.g., Education (grade school, high school, college, graduate)
  - Apply exact matching to the coarsened X, C(X)
    - Sort observations into strata, each with unique values of C(X)
    - Prune any stratum with 0 treated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

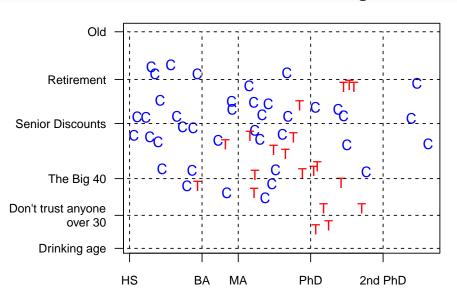
- 1. Preprocess (Matching)
  - Temporarily coarsen X as much as you're willing
    - e.g., Education (grade school, high school, college, graduate)
  - Apply exact matching to the coarsened X, C(X)
    - Sort observations into strata, each with unique values of C(X)
    - Prune any stratum with 0 treated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

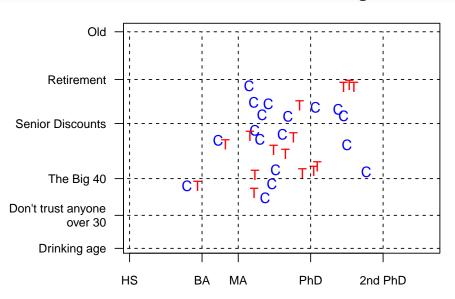
- 1. Preprocess (Matching)
  - Temporarily coarsen X as much as you're willing
    - e.g., Education (grade school, high school, college, graduate)
  - Apply exact matching to the coarsened X, C(X)
    - Sort observations into strata, each with unique values of C(X)
    - Prune any stratum with 0 treated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



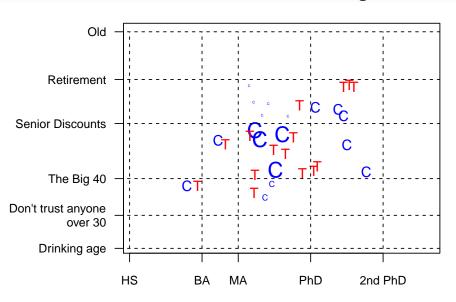
Education



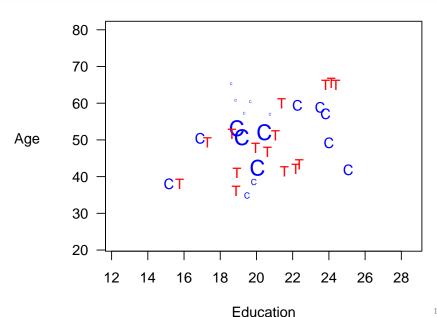


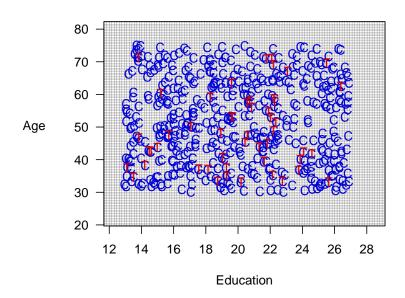


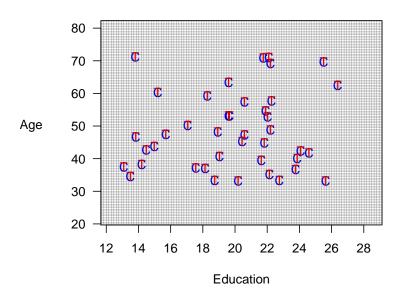
### **Coarsened Exact Matching**

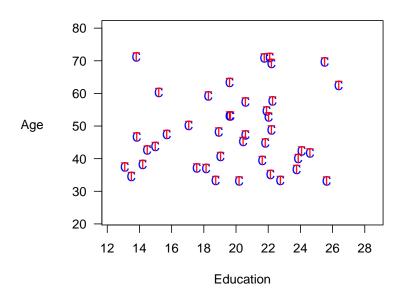


#### **Coarsened Exact Matching**









(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)

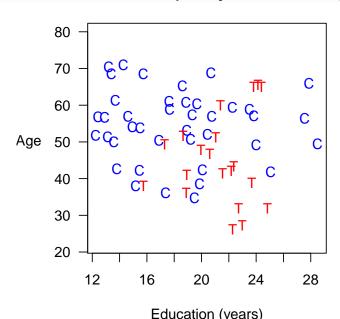
- 1. Preprocess (Matching)
  - Reduce k elements of X to scalar  $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$
  - Distance $(X_c, X_t) = |\pi_c \pi_t|$
  - Match each treated unit to the nearest control unit
  - · Control units: not reused; pruned if unused

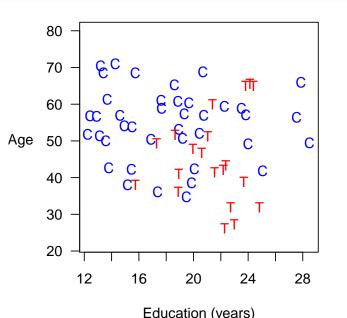
(Approximates Completely Randomized Experiment)

- 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

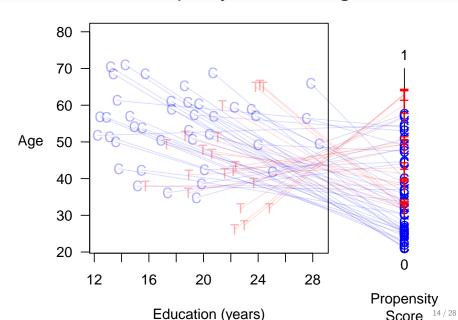


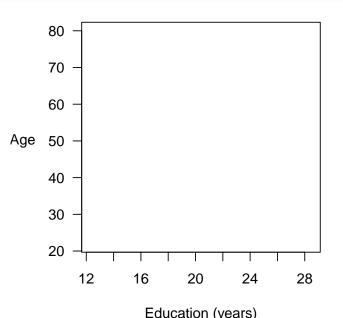




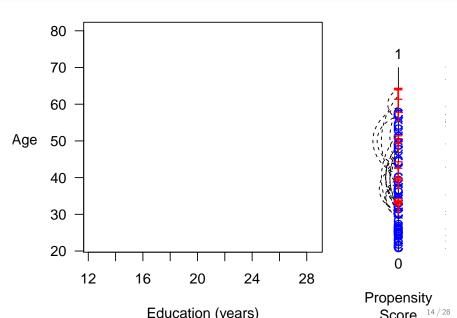
Propensity

Score

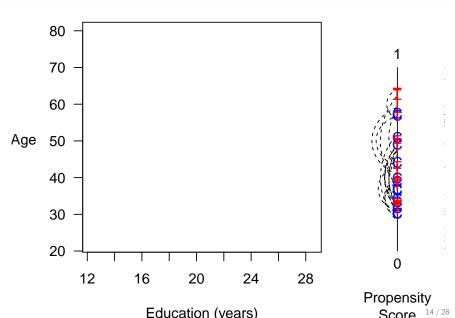




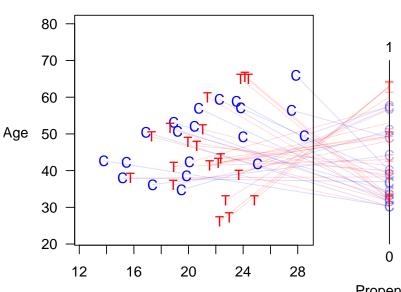
Propensity
Score 14/2



Score

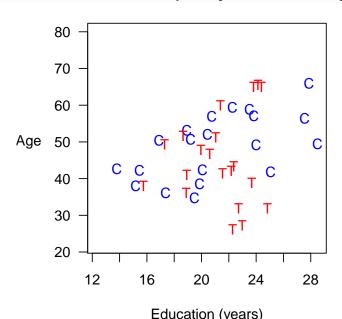


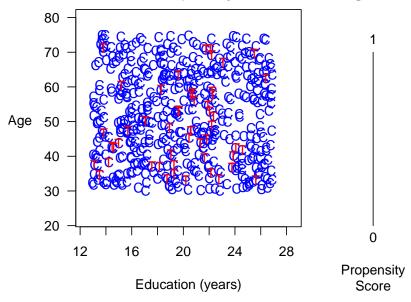
Score

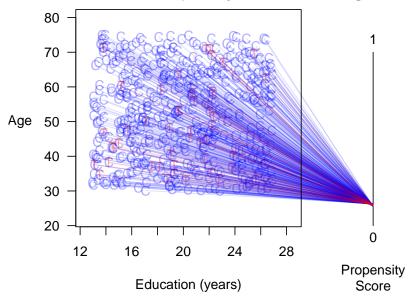


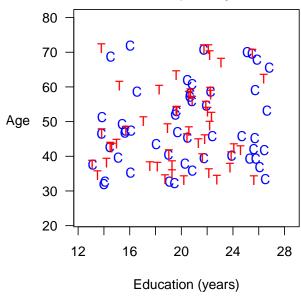
Education (vears)

Propensity
Score 14/28

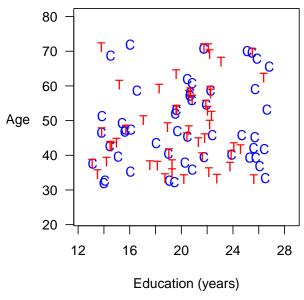








# Best Case: Propensity Score Matching is Suboptimal



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 dominate:

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

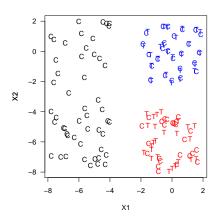
- Efficient relative to complete randomization, but
- Inefficient relative to (the more powerful) full blocking
- Other methods dominate:

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

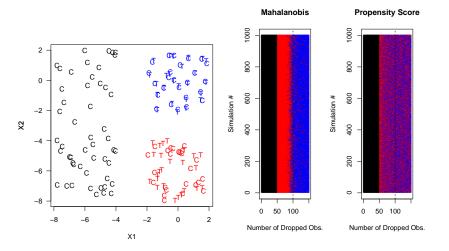
- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning)  $\leadsto$  all  $\hat{\pi} \approx 0.5$  (or constant within strata)  $\leadsto$  pruning at random  $\leadsto$  Imbalance  $\leadsto$  Inefficency  $\leadsto$  Model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



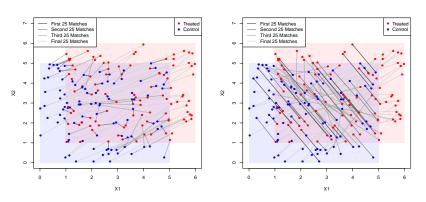
### PSM is Blind Where Other Methods Can See



### What Does PSM Match?

#### MDM Matches

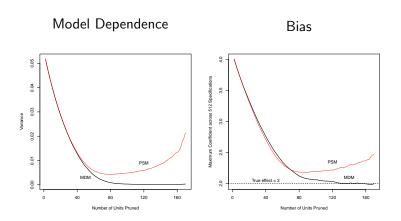
#### PSM Matches



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

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

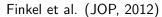
# PSM Increases Model Dependence & Bias

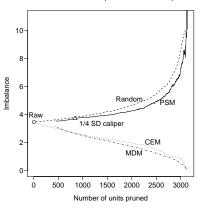


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
  
$$\epsilon_i \sim N(0, 1)$$

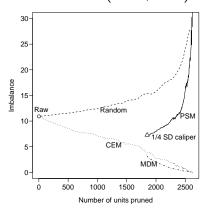
# The Propensity Score Paradox in Real Data

## The Propensity Score Paradox in Real Data

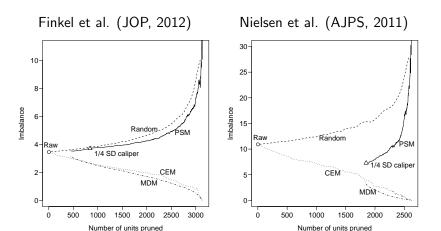




### Nielsen et al. (AJPS, 2011)



# 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 all  $\binom{N}{n}$  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

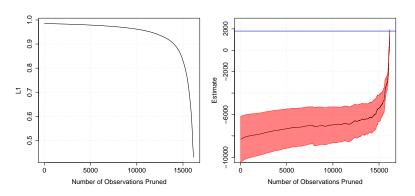
- Consider 1 point on the SATT frontier:
  - Start with matrix of N control units  $X_0$
  - Calculate imbalance for <u>all</u>  $\binom{N}{n}$  subsets of rows of  $X_0$
  - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
  - $\binom{N}{n}$  evaluations for 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

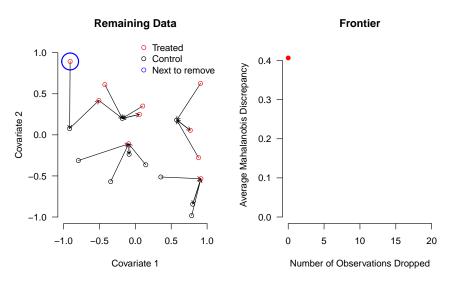
- Consider 1 point on the SATT frontier:
  - Start with matrix of N control units  $X_0$
  - Calculate imbalance for <u>all</u>  $\binom{N}{n}$  subsets of rows of  $X_0$
  - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
  - $\binom{N}{n}$  evaluations for 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

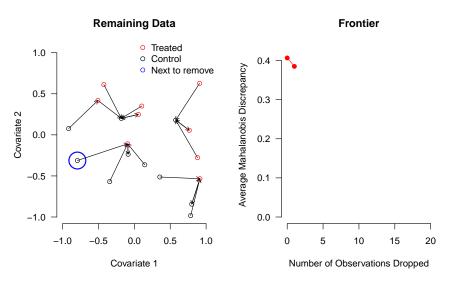
- Consider 1 point on the SATT frontier:
  - Start with matrix of N control units  $X_0$
  - Calculate imbalance for <u>all</u>  $\binom{N}{n}$  subsets of rows of  $X_0$
  - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
  - $\binom{N}{n}$  evaluations for 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

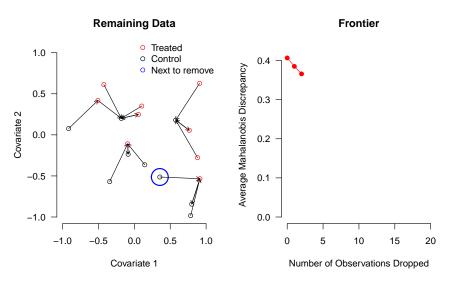
## Job Training Data: Frontier and Causal Estimates

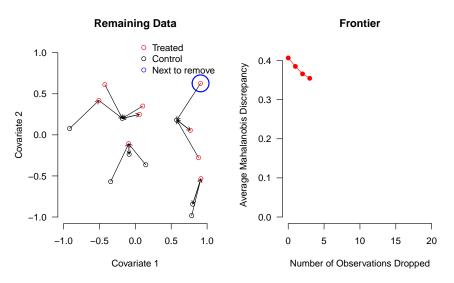


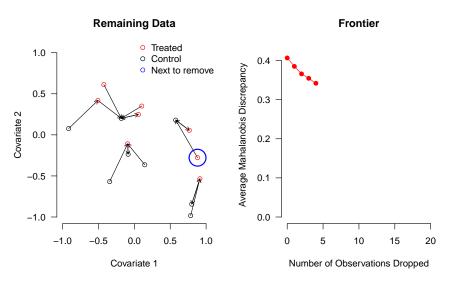
- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after pruning most Cs
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

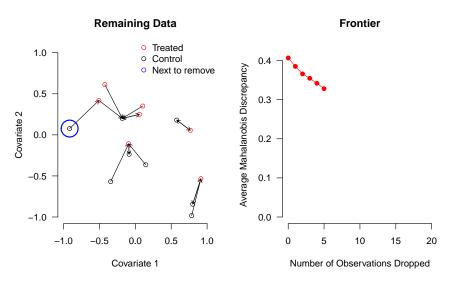


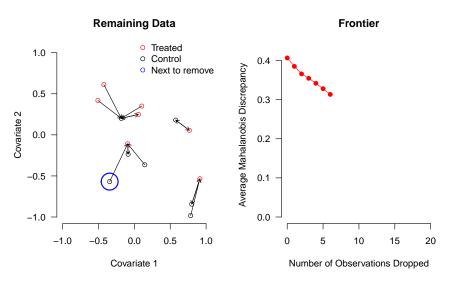


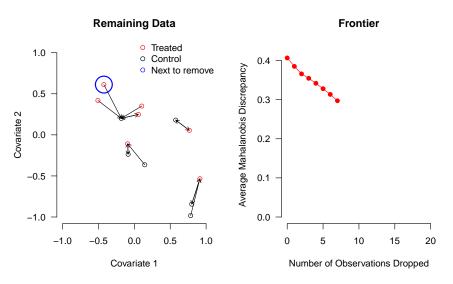


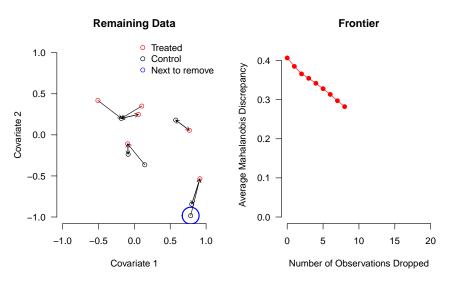


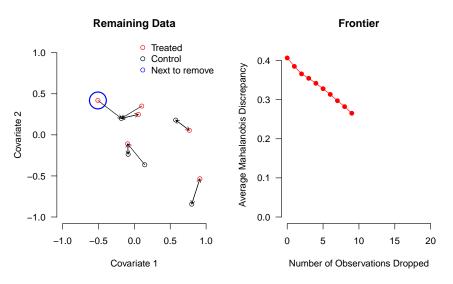


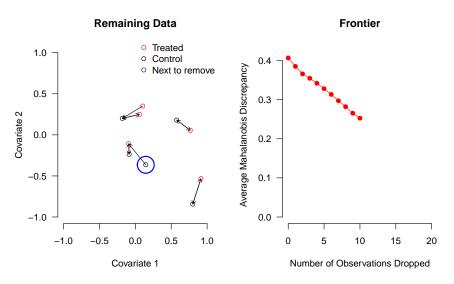


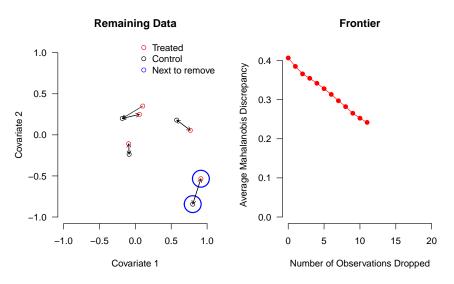


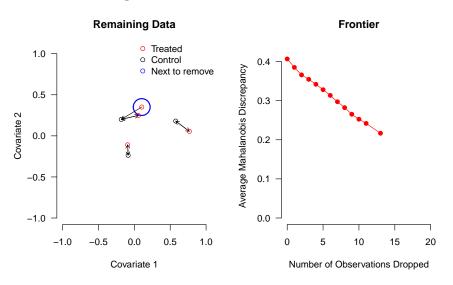


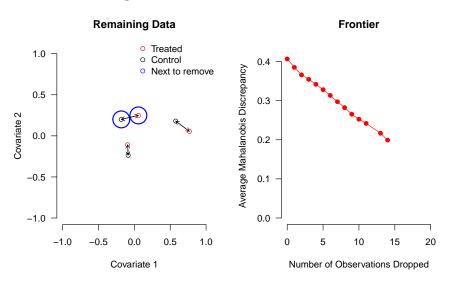


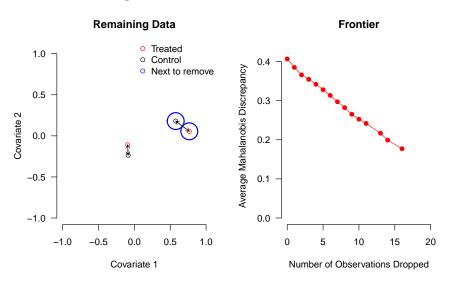


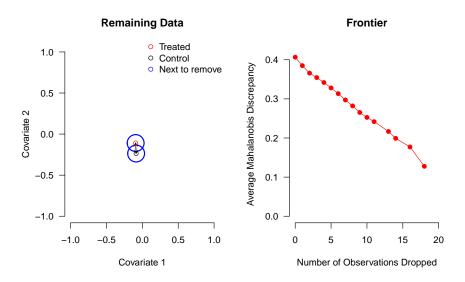


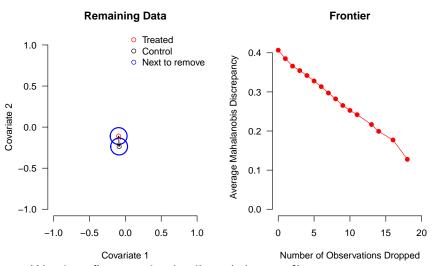




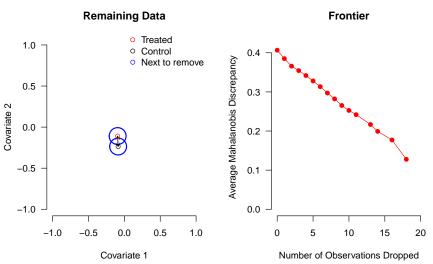




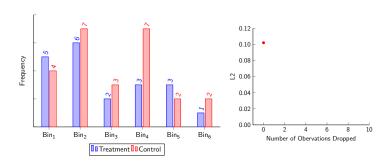


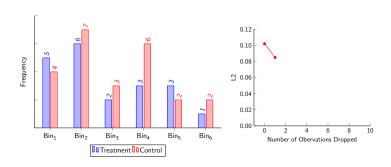


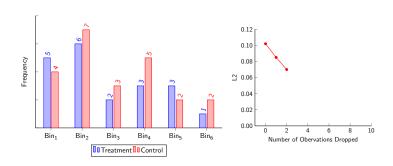
Warning: figure omits details and the proof!

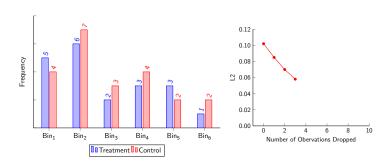


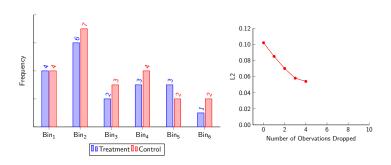
- Warning: figure omits details and the proof!
- Very fast; works with any continuous imbalance metric

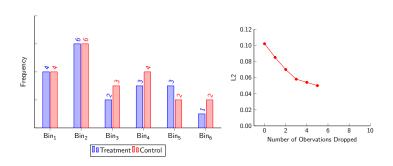


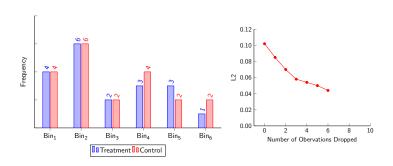


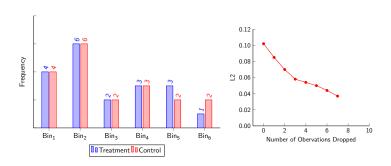


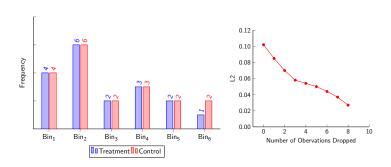


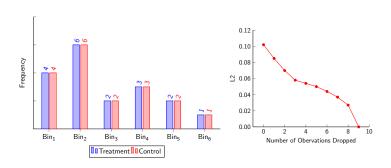












• Warning: This figure omits some technical details too!

- Warning: This figure omits some technical details too!
- Works very fast, even with very large data sets

• 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 iteratation; 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 iteratation; 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 iteratation; 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 iteratation; Software: MatchingFrontier
  - No need to choose among matching methods
  - Optimal results from your choice of imbalance metric
- Wising more information is simpler and more powerful

### For more information, articles, & software

GaryKing.org