Why Propensity Scores Should Not Be Used For Matching¹

Gary King²

Institute for Quantitative Social Science Harvard University

(Talk at the U.S. Food and Drug Administration [CBER/OBE], 8/25/2015)

¹Based on joint work with Rich Nielsen

²GaryKing.org

• The most commonly used matching method

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- ~ This paper is about: propensity score matching,

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- — This paper is about: propensity score matching, as used in practice.

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:

- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g.,

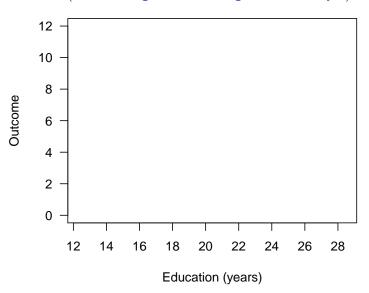
- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g., regression adjustment,

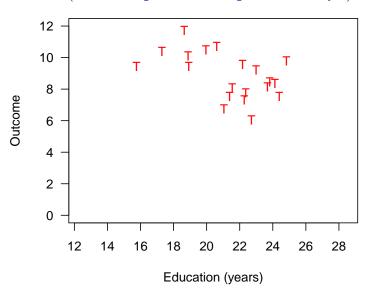
- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g., regression adjustment, inverse weighting,

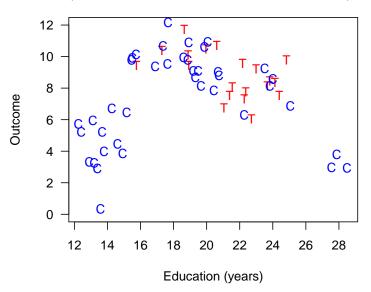
- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g., regression adjustment, inverse weighting, stratification,

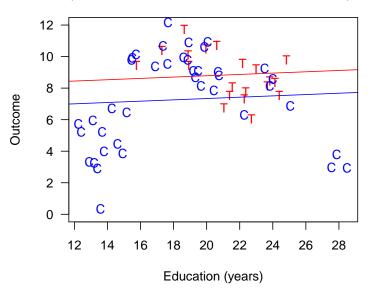
- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g., regression adjustment, inverse weighting, stratification, pscores used in other methods

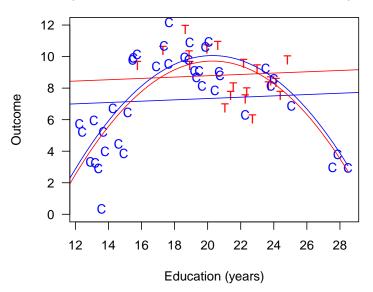
- The most commonly used matching method
- In 49,600 articles! (according to Google Scholar)
- Maybe even "the most developed and popular strategy for causal analysis in observational studies" (Pearl, 2010)
- This paper is about: propensity score matching, as used in practice. Not implicated by our results:
 - Other uses of propensity scores: E.g., regression adjustment, inverse weighting, stratification, pscores used in other methods
 - The mathematical theorems about propensity scores

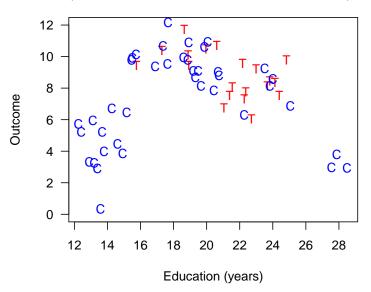


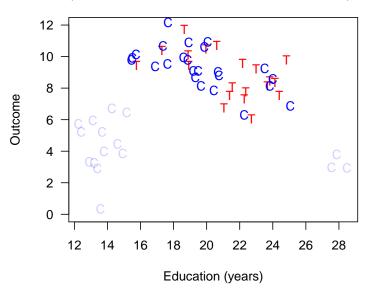


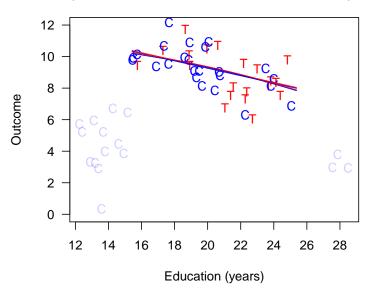












Without Matching:

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:

Imbalance → Model Dependence → Researcher discretion → Bias

- 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:

Imbalance → Model Dependence → Researcher discretion → Bias

Without Matching:

Without Matching:

Without Matching:

Without Matching:

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_j from a matched $(X_i \approx X_j)$ 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_j from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")

- 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 from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")
- 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 from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")
- 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 treated observation i:

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

= observed – unobserved

- Estimate $Y_i(0)$ with Y_j from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")
- 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 <u>treated</u> observation i:

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

= observed – unobserved

- Estimate $Y_i(0)$ with Y_j from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")
- 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 treated observation i:

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

= observed – unobserved

- Estimate $Y_i(0)$ with Y_j from a matched $(X_i \approx X_j)$ control \rightsquigarrow Must have the right X's! (aka "ignorability")
- 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

Types of 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

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

→ 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

~ 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

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

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)

(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)

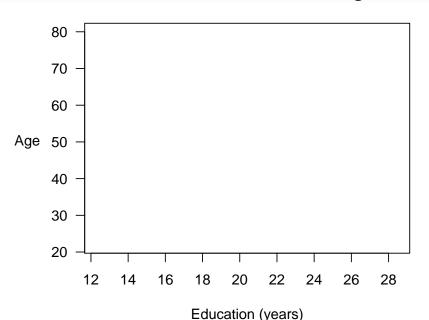
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - Control units: not reused; pruned if unused

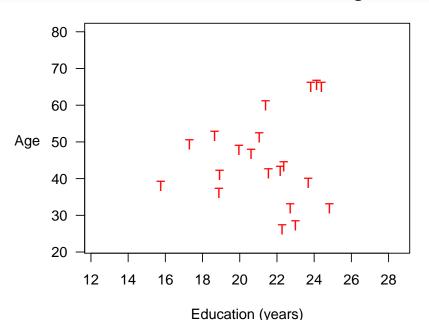
(Approximates Fully Blocked Experiment)

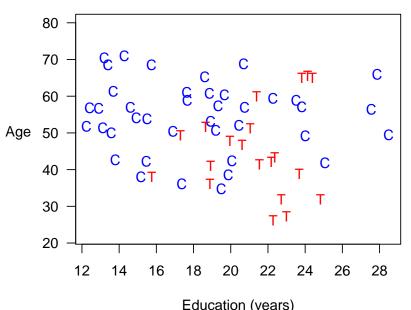
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper
-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

(Approximates Fully Blocked Experiment)

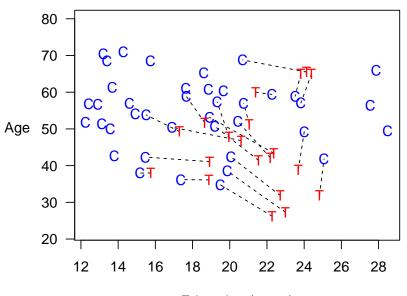
- 1. Preprocess (Matching)
 - Distance $(X_c, X_t) = \sqrt{(X_c X_t)' S^{-1} (X_c X_t)}$
 - (Mahalanobis is for methodologists; in applications, use Euclidean!)
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper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

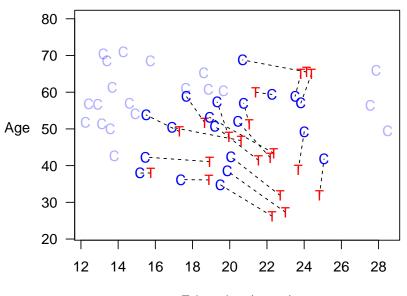


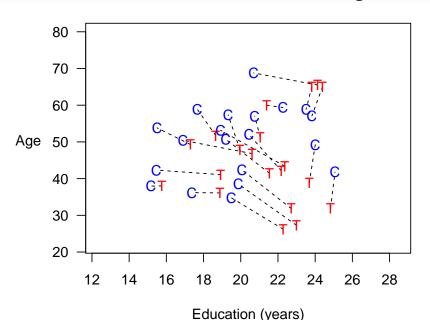


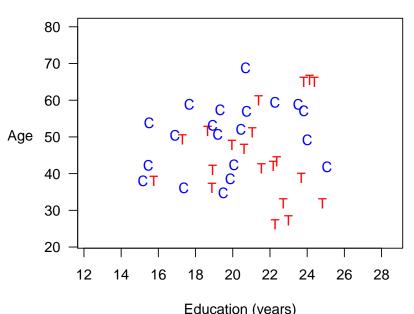


8/23





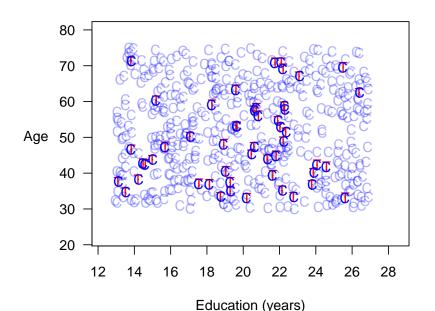




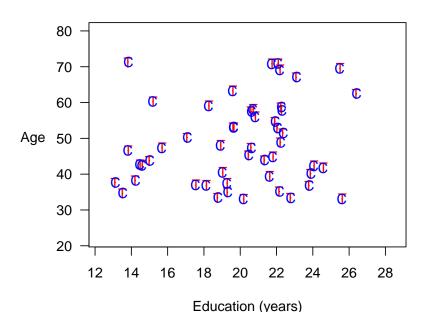
8/23

Best Case: Mahalanobis Distance Matching

Best Case: Mahalanobis Distance Matching



Best Case: Mahalanobis Distance Matching



(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)

(Approximates Fully Blocked Experiment)

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

Method 2: Coarsened Exact Matching

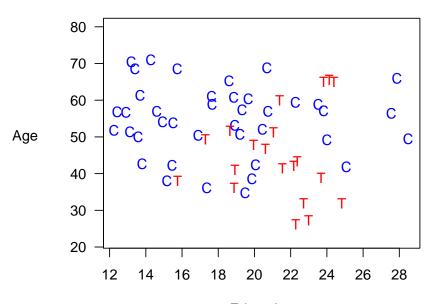
(Approximates Fully Blocked Experiment)

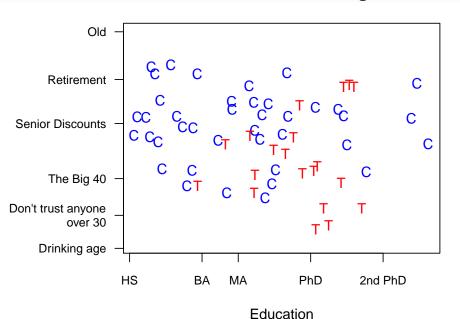
- 1. Preprocess (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Apply exact matching to the coarsened X, C(X)
 - Sort observations into strata, each with unique values of C(X)
 - Prune any stratum with 0 treated or 0 control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

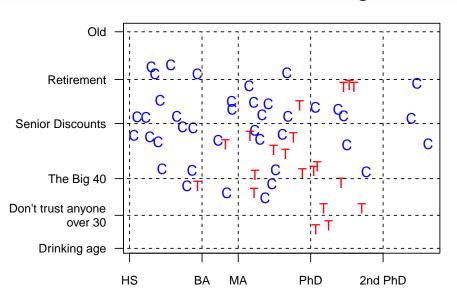
Method 2: Coarsened Exact Matching

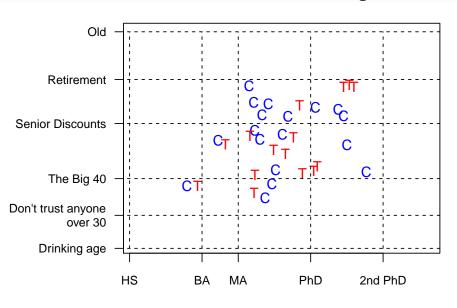
(Approximates Fully Blocked Experiment)

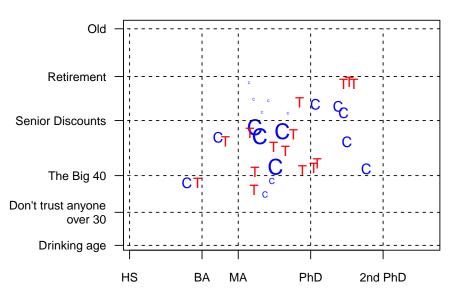
- 1. Preprocess (Matching)
 - ullet Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Apply exact matching to the coarsened X, C(X)
 - Sort observations into strata, each with unique values of C(X)
 - Prune any stratum with 0 treated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

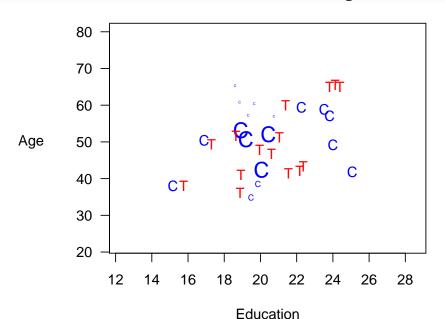


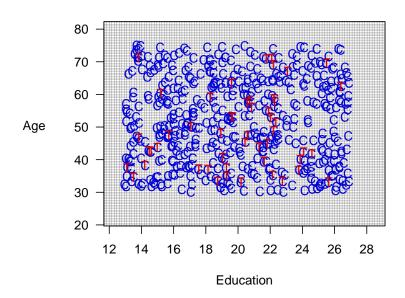


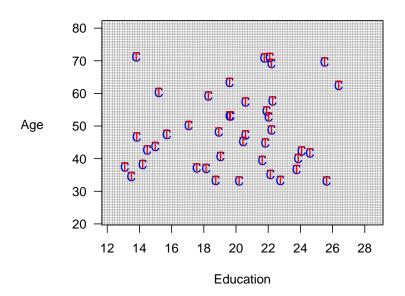


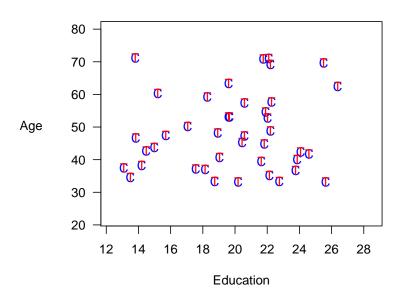












(Approximates Completely Randomized Experiment)

(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)

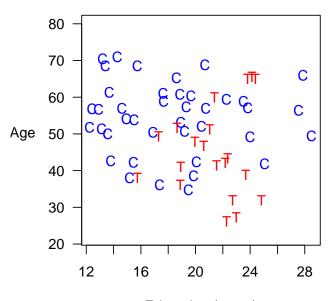
- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$
 - Distance $(X_c, X_t) = |\pi_c \pi_t|$
 - Match each treated unit to the nearest control unit
 - Control units: not reused; pruned if unused

(Approximates Completely Randomized Experiment)

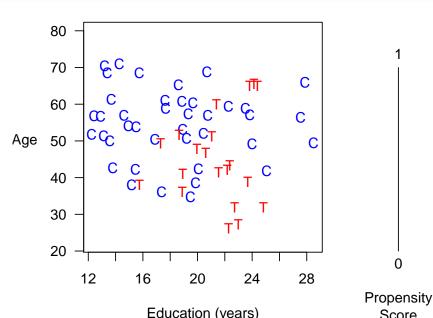
- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1 | X) = \frac{1}{1 + e^{-X_i \beta}}$
 - Distance $(X_c, X_t) = |\pi_c \pi_t|$
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper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

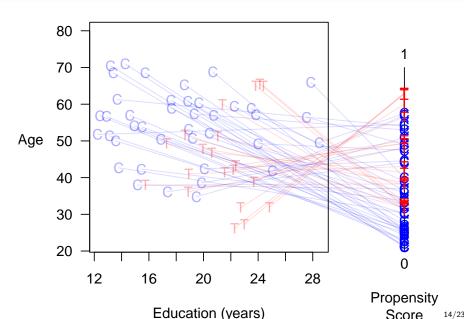
(Approximates Completely Randomized Experiment)

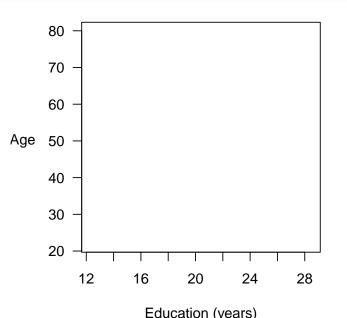
- 1. Preprocess (Matching)
 - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1 | X) = \frac{1}{1 + e^{-X_i \beta}}$
 - Distance $(X_c, X_t) = |\pi_c \pi_t|$
 - Match each treated unit to the nearest control unit
 - · Control units: not reused; pruned if unused
 - Prune matches if Distance>caliper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



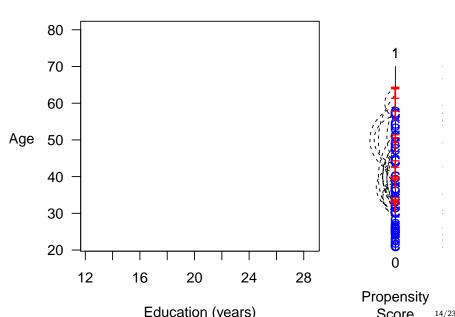
14/23

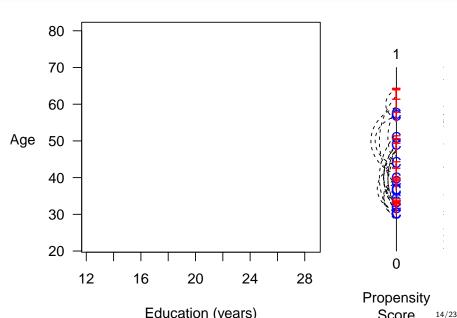


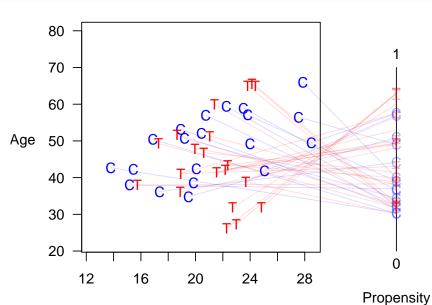








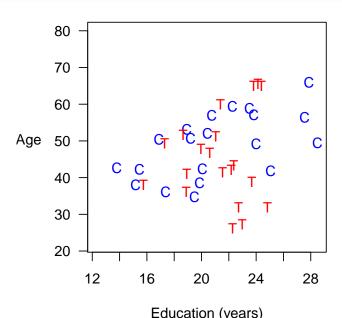


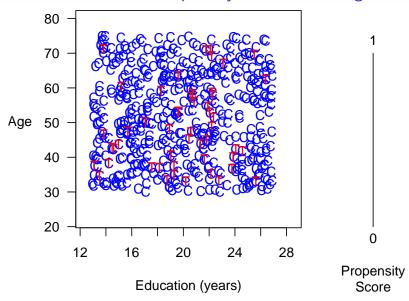


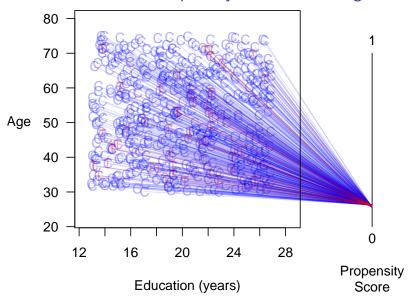
Education (vears)

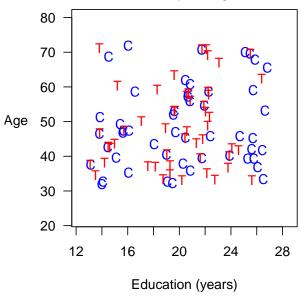
Score

14/23

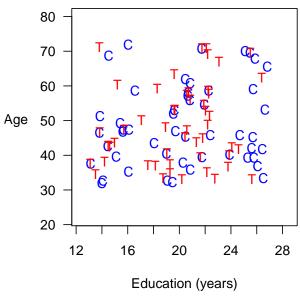








Best Case: Propensity Score Matching is Suboptimal



Random Pruning Increases Imbalance

Deleting data only helps if you're careful!

"Random pruning": pruning process is independent of X

- "Random pruning": pruning process is independent of X
- Discrete example

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control \rightsquigarrow 4 possible datasets: 2 balanced $\{M_t, M_c\}$, $\{F_t, F_c\}$
 - 2 imbalanced $\{M_t, F_c\}$, $\{F_t, M_c\}$

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example
 - Dataset: $T \in \{0,1\}$ randomly assigned; X any fixed variable; with n units

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example
 - Dataset: $T \in \{0,1\}$ randomly assigned; X any fixed variable; with n units
 - Measure of imbalance: squared difference in means d^2 , where $d=\bar{X}_t-\bar{X}_c$

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example
 - Dataset: $T \in \{0,1\}$ randomly assigned; X any fixed variable; with n units
 - Measure of imbalance: squared difference in means d^2 , where $d=\bar{X}_t-\bar{X}_c$
 - $E(d^2) = V(d) \propto 1/n$ (note: E(d) = 0)

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example
 - Dataset: $T \in \{0,1\}$ randomly assigned; X any fixed variable; with n units
 - Measure of imbalance: squared difference in means d^2 , where $d = \bar{X}_t \bar{X}_c$
 - $E(d^2) = V(d) \propto 1/n$ (note: E(d) = 0)
 - Random pruning \rightsquigarrow *n* declines \rightsquigarrow $E(d^2)$ increases

- "Random pruning": pruning process is independent of X
- Discrete example
 - Sex-balanced dataset: treateds M_t , F_t , controls M_c , F_c
 - Randomly prune 1 treated & 1 control → 4 possible datasets:
 2 balanced {M_t, M_c}, {F_t, F_c}
 2 imbalanced {M_t, F_c}, {F_t, M_c}
 - \implies random pruning increases imbalance
- Continuous example
 - Dataset: $T \in \{0,1\}$ randomly assigned; X any fixed variable; with n units
 - Measure of imbalance: squared difference in means d^2 , where $d = \bar{X}_t \bar{X}_c$
 - $E(d^2) = V(d) \propto 1/n$ (note: E(d) = 0)
 - Random pruning \rightsquigarrow *n* declines \rightsquigarrow $E(d^2)$ increases
 - \implies random pruning increases imbalance

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:

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

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

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

$$X_c = X_t \implies \pi_c = \pi_t \text{ but } \pi_c = \pi_t \not \implies X_c = X_t$$

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
 - 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:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but } \pi_c = \pi_t \not \implies X_c = X_t$$

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

$$X_c = X_t \implies \pi_c = \pi_t \text{ but } \pi_c = \pi_t \not \implies X_c = X_t$$

- 2. The PSM Paradox: When you do "better," you do worse
 - When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi}\approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random

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

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

$$X_c = X_t \implies \pi_c = \pi_t \text{ but } \pi_c = \pi_t \not \implies X_c = X_t$$

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

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

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

- 2. The PSM Paradox: When you do "better," you do worse
 - When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi}\approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficency \rightsquigarrow Model dependence \rightsquigarrow 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:

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

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

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

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

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

- 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
 - When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi}\approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficency \rightsquigarrow Model dependence \rightsquigarrow Bias
 - If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
 - Doesn't PSM solve the curse of dimensionality problem?
 Nope. The PSM Paradox gets worse with more covariates
 - What if I match on a few important covariates and then use PSM?

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

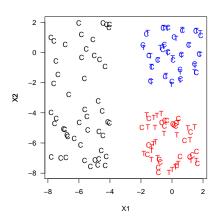
$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

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

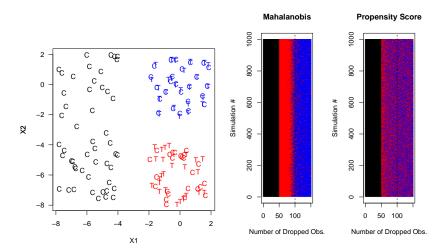
- 2. The PSM Paradox: When you do "better," you do worse
 - When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficency \rightsquigarrow Model dependence \rightsquigarrow Bias
 - If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
 - Doesn't PSM solve the curse of dimensionality problem?
 Nope. The PSM Paradox gets worse with more covariates
 - What if I match on a few important covariates and then use PSM? The low standards will be raised some, but the PSM Paradox will kick in earlier

PSM is Blind Where Other Methods Can See

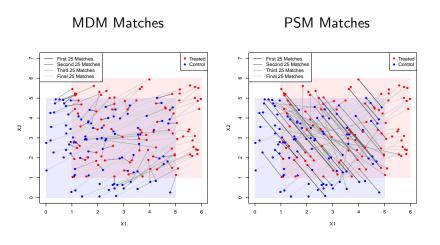
PSM is Blind Where Other Methods Can See



PSM is Blind Where Other Methods Can See

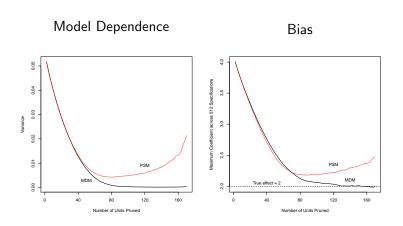


What Does PSM Match?



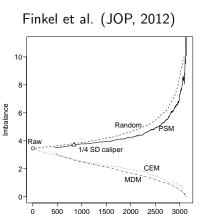
Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$ Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias



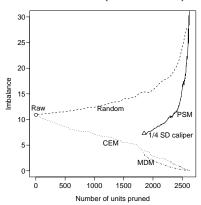
$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

The Propensity Score Paradox in Real Data



Number of units pruned

Nielsen et al. (AJPS, 2011)



• Why propensity scores should not be used for matching:

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM:

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data;

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support;

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score;

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.
 - Other methods can generate a "paradox" if you prune after approximating full blocking (rare, but possible)

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.
 - Other methods can generate a "paradox" if you prune after approximating full blocking (rare, but possible)
 - If you're not doing positive good, you may be hurting yourself

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.
 - Other methods can generate a "paradox" if you prune after approximating full blocking (rare, but possible)
 - If you're not doing positive good, you may be hurting yourself
- Matching remains a highly recommended approach to improve causal inferences

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.
 - Other methods can generate a "paradox" if you prune after approximating full blocking (rare, but possible)
 - If you're not doing positive good, you may be hurting yourself
- Matching remains a highly recommended approach to improve causal inferences
- Best to choose a matching method with higher standards

- Why propensity scores should not be used for matching:
 - Low Standards: sometimes helps, never optimizes
 - The PSM Paradox: When you do "better," you do worse
 - Some mistakes with PSM: Controlling for irrelevant covariates;
 Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 sd caliper on propensity score; Not switching to other methods.
- A warning for any matching method:
 - Pruning discards information; you must overcome this.
 - Other methods can generate a "paradox" if you prune after approximating full blocking (rare, but possible)
 - If you're not doing positive good, you may be hurting yourself
- Matching remains a highly recommended approach to improve causal inferences
- Best to choose a matching method with higher standards
 - about which more this afternoon!

For more information, papers, & software



GaryKing.org