

Simplifying Causal Inference¹

Gary King²

Institute for Quantitative Social Science
Harvard University

(Talk at the University of South Carolina, 2/28/2014)

¹Joint work with Christopher Lucas and Richard Nielsen

²GaryKing.org.

Overview

Overview

- Problem: Model dependence (review)

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful
 - Estimate the (n -imbalance) “matching frontier”

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful
 - Estimate the (n -imbalance) “matching frontier”
 - Imbalance metric choice defines the frontier

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful
 - Estimate the (n -imbalance) “matching frontier”
 - Imbalance metric choice defines the frontier
- Side point:

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful
 - Estimate the (n -imbalance) “matching frontier”
 - Imbalance metric choice defines the frontier
- Side point:
 - Problem: Propensity score matching increases imbalance!

Overview

- Problem: Model dependence (review)
- Solution: Matching to reduce model dependence (review)
- Problem: Matching prunes n to improve imbalance, but
 - Some: set n and don't guarantee imbalance
 - Others: set imbalance and don't guarantee n
 - Plus: Matching methods optimize a different “imbalance” than recommended post-hoc checks
- Solution: easier & more powerful
 - Estimate the (n -imbalance) “matching frontier”
 - Imbalance metric choice defines the frontier
- Side point:
 - Problem: Propensity score matching increases imbalance!
 - Solution: Not an issue with other methods or our approach

Model Dependence Example

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success
- **Treatment:** multilateral UN peacekeeping intervention (0/1)

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success
- **Treatment:** multilateral UN peacekeeping intervention (0/1)
- **Control vars:** war type, severity, duration; development status, . . .

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success
- **Treatment:** multilateral UN peacekeeping intervention (0/1)
- **Control vars:** war type, severity, duration; development status, . . .
- **Counterfactual question:** Switch UN intervention for each war

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success
- **Treatment:** multilateral UN peacekeeping intervention (0/1)
- **Control vars:** war type, severity, duration; development status, . . .
- **Counterfactual question:** Switch UN intervention for each war
- **Data analysis:** Logit model

Model Dependence Example

Replication of Doyle and Sambanis, APSR 2000

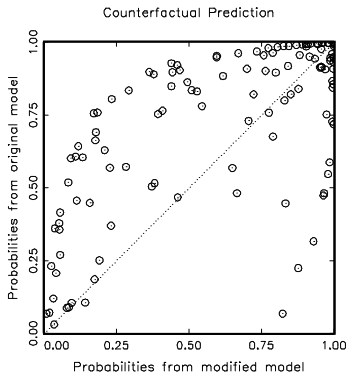
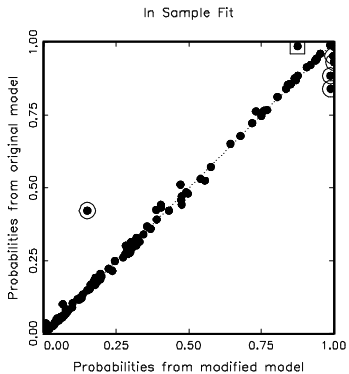
(From: King and Zeng, 2007)

- **Data:** 124 Post-World War II civil wars
- **Dependent var:** peacebuilding success
- **Treatment:** multilateral UN peacekeeping intervention (0/1)
- **Control vars:** war type, severity, duration; development status, . . .
- **Counterfactual question:** Switch UN intervention for each war
- **Data analysis:** Logit model
- **The question:** How *model dependent* are the results?

Two Logit Models, Apparently Similar Results

Variables	Original "Interactive" Model			Modified Model		
	Coeff	SE	P-val	Coeff	SE	P-val
Wartype	-1.742	.609	.004	-1.666	.606	.006
Logdead	-.445	.126	.000	-.437	.125	.000
Wardur	.006	.006	.258	.006	.006	.342
Factnum	-1.259	.703	.073	-1.045	.899	.245
Factnum2	.062	.065	.346	.032	.104	.756
Trnsfcap	.004	.002	.010	.004	.002	.017
Develop	.001	.000	.065	.001	.000	.068
Exp	-6.016	3.071	.050	-6.215	3.065	.043
Decade	-.299	.169	.077	-0.284	.169	.093
Treaty	2.124	.821	.010	2.126	.802	.008
UNOP4	3.135	1.091	.004	.262	1.392	.851
Wardur*UNOP4	—	—	—	.037	.011	.001
Constant	8.609	2.157	0.000	7.978	2.350	.000
N	122			122		
Log-likelihood	-45.649			-44.902		
Pseudo R^2	.423			.433		

Doyle and Sambanis: Model Dependence



Matching within the Interpolation Region

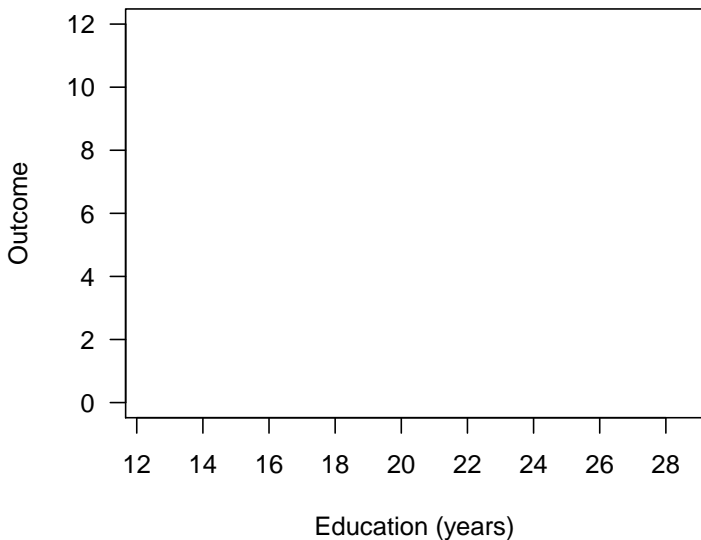
(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)

Matching within the Interpolation Region

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

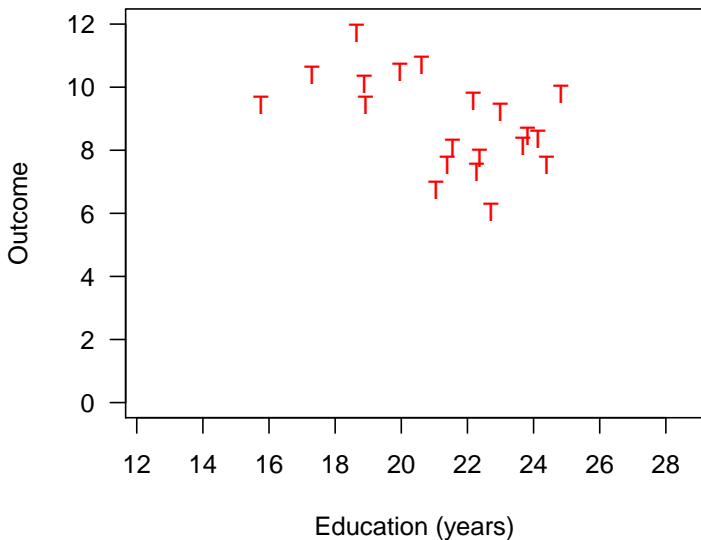
Matching within the Interpolation Region

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



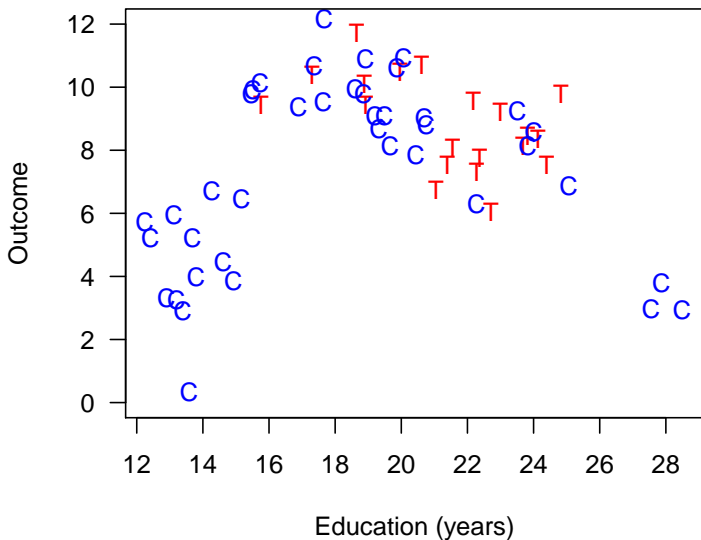
Matching within the Interpolation Region

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



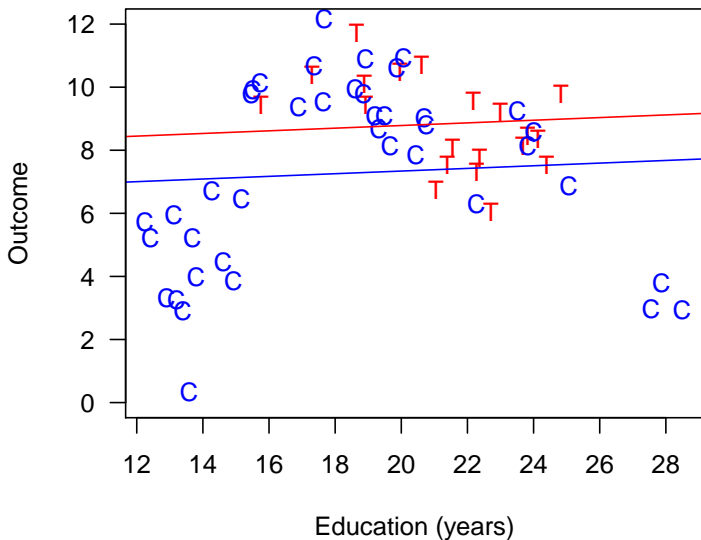
Matching within the Interpolation Region

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



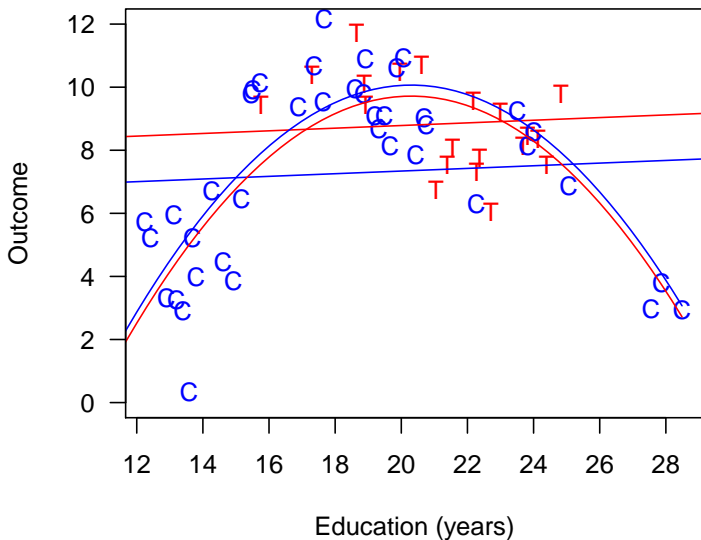
Matching within the Interpolation Region

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



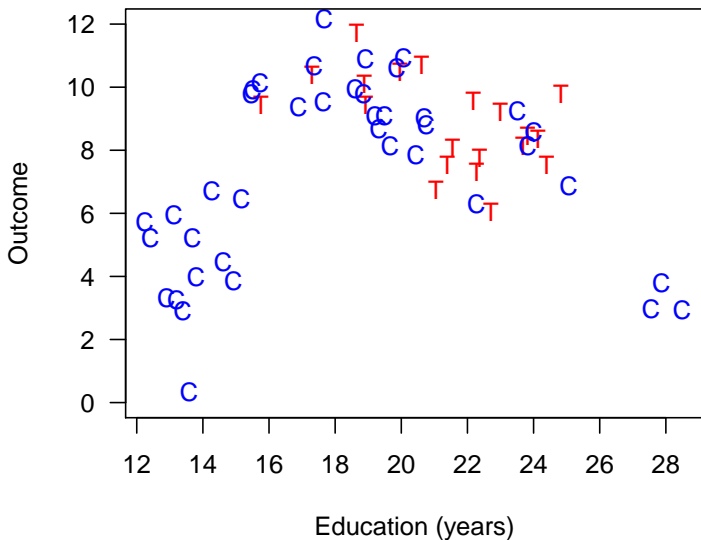
Matching within the Interpolation Region

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



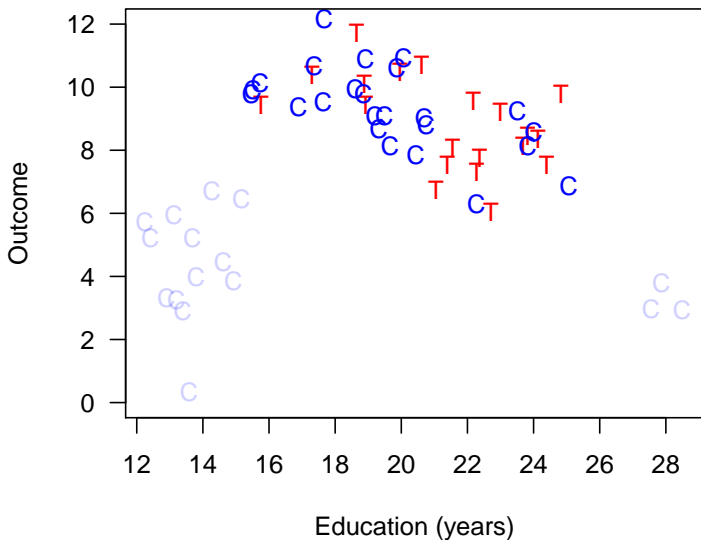
Matching within the Interpolation Region

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



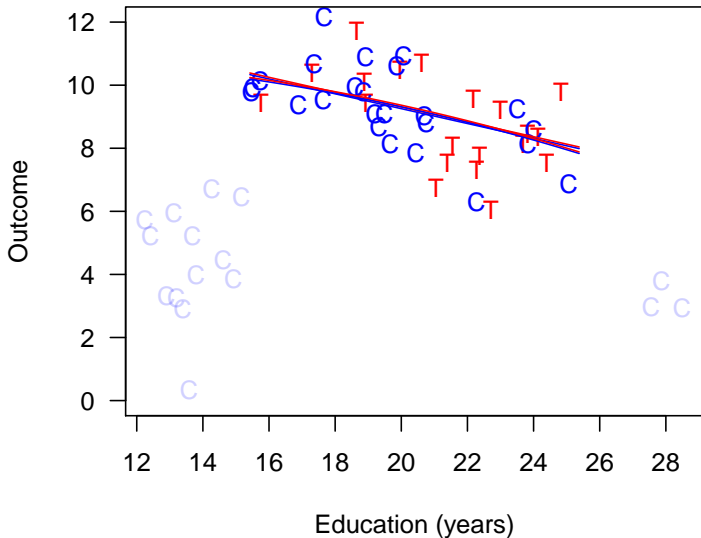
Matching within the Interpolation Region

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



Matching within the Interpolation Region

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



Matching within the Interpolation Region

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

Matching reduces model dependence, bias, and variance

How Matching Works

How Matching Works

- Notation:

How Matching Works

- Notation:
 Y_i Dependent variable

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

How Matching Works

- Notation:
 - Y_i Dependent variable
 - T_i Treatment variable (0/1, or more general)
 - X_i Pre-treatment covariates
- Estimation

How Matching Works

- Notation:
 - Y_i Dependent variable
 - T_i Treatment variable (0/1, or more general)
 - X_i Pre-treatment covariates
- Estimation
 - **Treatment Effect** for treated ($T_i = 1$) observation i :

How Matching Works

- Notation:

- Y_i Dependent variable

- T_i Treatment variable (0/1, or more general)

- X_i Pre-treatment covariates

- Estimation

- Treatment Effect for treated ($T_i = 1$) observation i :

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

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned} \text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned} \text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(T_i = 0)$ with Y_j from matched ($X_i \approx X_j$) controls
 $\hat{Y}_i(T_i = 0) = Y_j(T_i = 0)$ (or a model)

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned} \text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(T_i = 0)$ with Y_j from matched ($X_i \approx X_j$) controls
 $\hat{Y}_i(T_i = 0) = Y_j(T_i = 0)$ (or a model)
- Prune unmatched units to improve **balance** (so X is unimportant)

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned} \text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

- Estimate $Y_i(T_i = 0)$ with Y_j from matched ($X_i \approx X_j$) controls
 $\hat{Y}_i(T_i = 0) = Y_j(T_i = 0)$ (or a model)
- Prune unmatched units to improve **balance** (so X is unimportant)
- Quantities of Interest:

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned}\text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved}\end{aligned}$$

- Estimate $Y_i(T_i = 0)$ with Y_j from matched ($X_i \approx X_j$) controls
 $\hat{Y}_i(T_i = 0) = Y_j(T_i = 0)$ (or a model)
 - Prune unmatched units to improve **balance** (so X is unimportant)
- Quantities of Interest:
 1. SATT: Sample Average Treatment effect on the Treated:

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

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1, or more general)

X_i Pre-treatment covariates

- Estimation

- **Treatment Effect** for treated ($T_i = 1$) observation i :

$$\begin{aligned}\text{TE}_i &= Y_i(T_i = 1) - Y_i(T_i = 0) \\ &= \text{observed} - \text{unobserved}\end{aligned}$$

- Estimate $Y_i(T_i = 0)$ with Y_j from matched ($X_i \approx X_j$) controls
 $\hat{Y}_i(T_i = 0) = Y_j(T_i = 0)$ (or a model)
 - Prune unmatched units to improve **balance** (so X is unimportant)
- Quantities of Interest:

1. SATT: Sample Average Treatment effect on the Treated:

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

2. FSATT: Feasible Average Treatment effect on the Treated

Method 1: Mahalanobis Distance Matching

Method 1: Mahalanobis Distance Matching

1. **Preprocess** (Matching)
2. **Estimation** Difference in means or a model
3. **Checking** Measure imbalance, tweak, repeat, ...

Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)

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

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)

- $\text{Distance}(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)}$
- Match each treated unit to the nearest control unit

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)

- $\text{Distance}(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)}$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)

- $\text{Distance}(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)}$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)

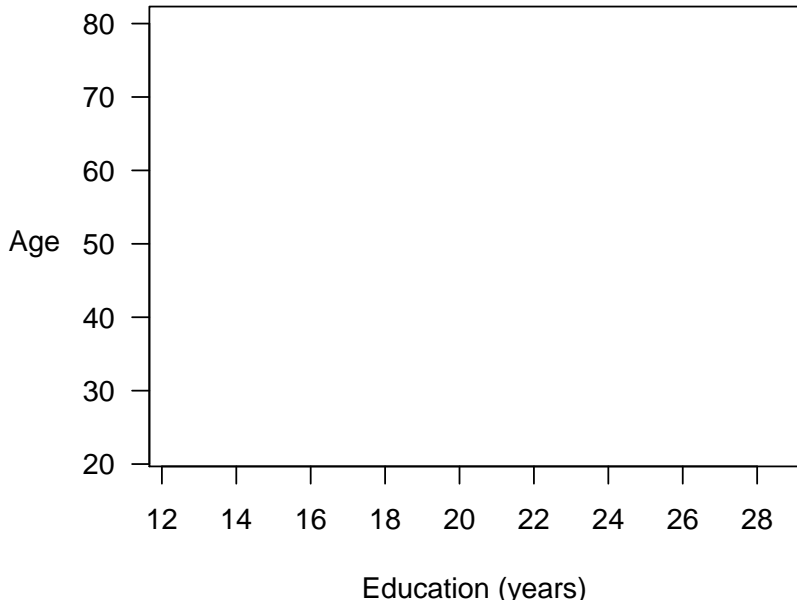
- $\text{Distance}(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)}$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$

2. Estimation Difference in means or a model

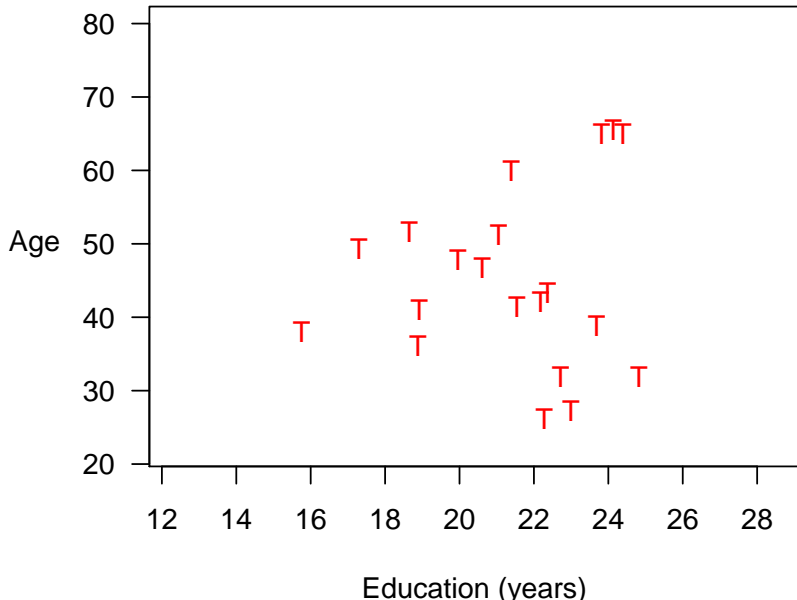
3. Checking Measure imbalance, tweak, repeat, ...



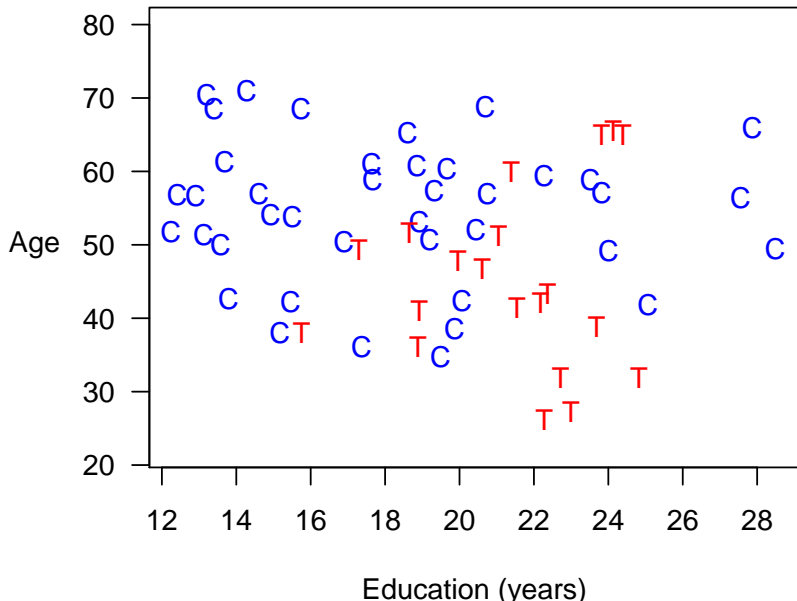
Mahalanobis Distance Matching



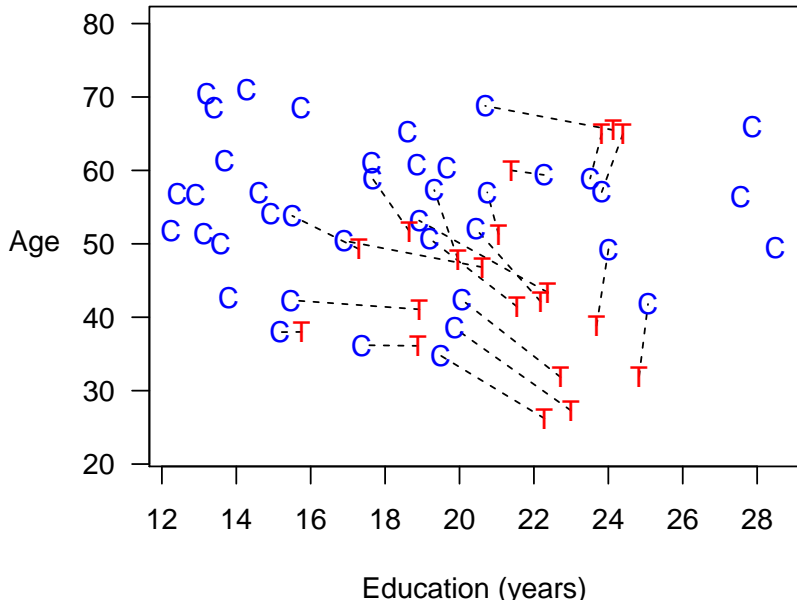
Mahalanobis Distance Matching



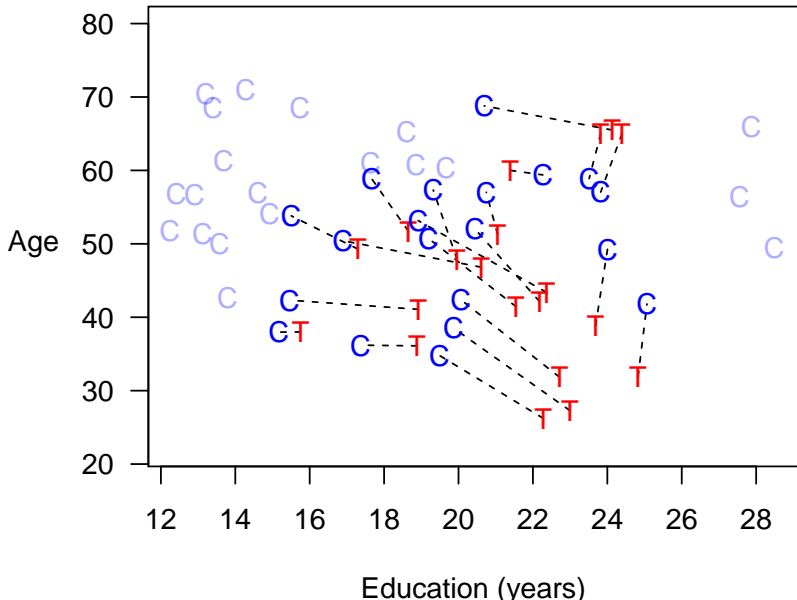
Mahalanobis Distance Matching



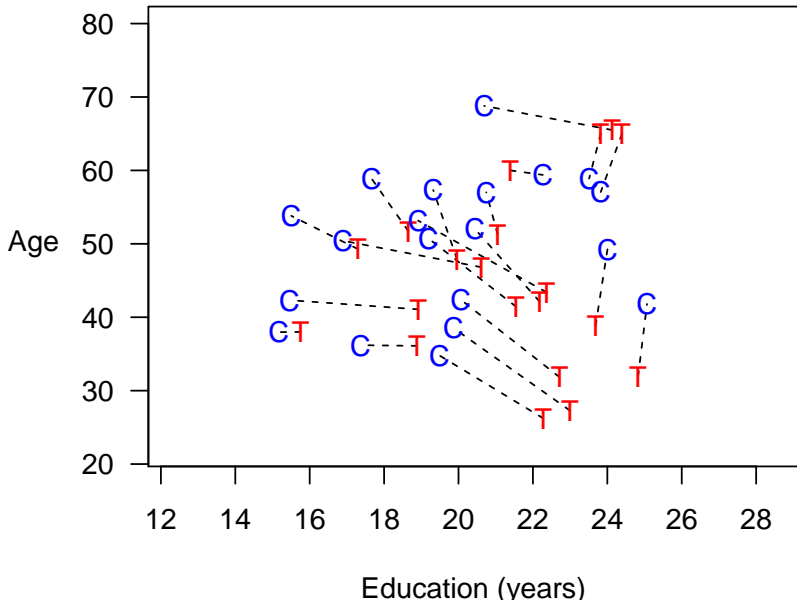
Mahalanobis Distance Matching



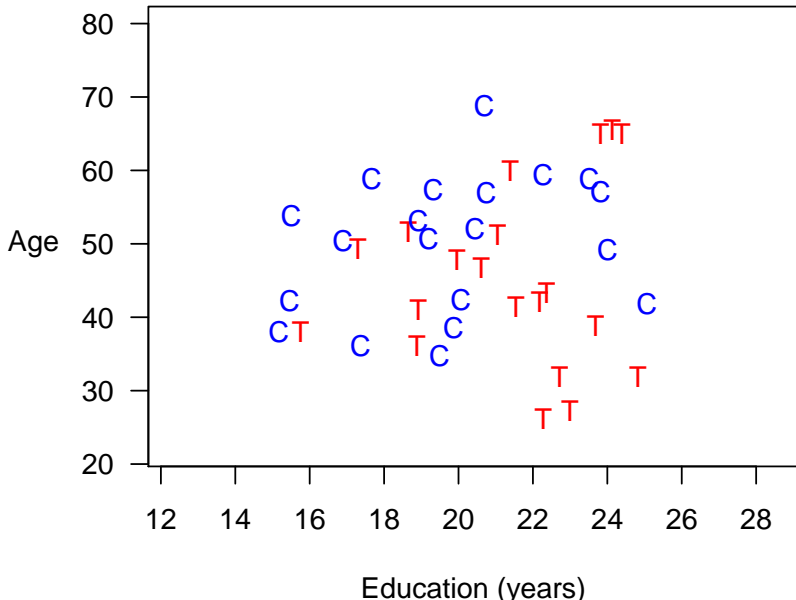
Mahalanobis Distance Matching



Mahalanobis Distance Matching



Mahalanobis Distance Matching



Method 2: Propensity Score Matching

Method 2: Propensity Score Matching

1. **Preprocess** (Matching)
2. **Estimation** Difference in means or a model
3. **Checking** Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

1. Preprocess (Matching)

- Reduce k elements of X to scalar

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

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

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_i, X_j) = $|\pi_i - \pi_j|$

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

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_i, X_j) = $|\pi_i - \pi_j|$
- Match each treated unit to the nearest control unit

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

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_i, X_j) = $|\pi_i - \pi_j|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

1. Preprocess (Matching)

- Reduce k elements of X to scalar

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

- $\text{Distance}(X_i, X_j) = |\pi_i - \pi_j|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$

2. Estimation Difference in means or a model

3. Checking Measure imbalance, tweak, repeat, ...

Method 2: Propensity Score Matching

1. Preprocess (Matching)

- Reduce k elements of X to scalar

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

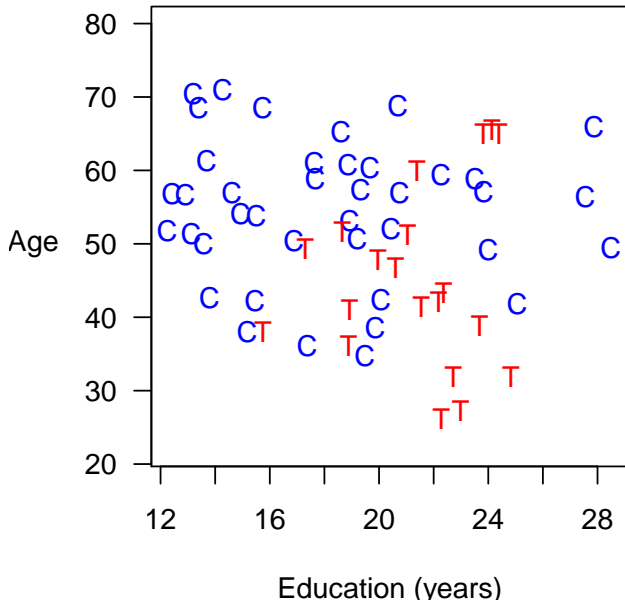
- $\text{Distance}(X_i, X_j) = |\pi_i - \pi_j|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$

2. Estimation Difference in means or a model

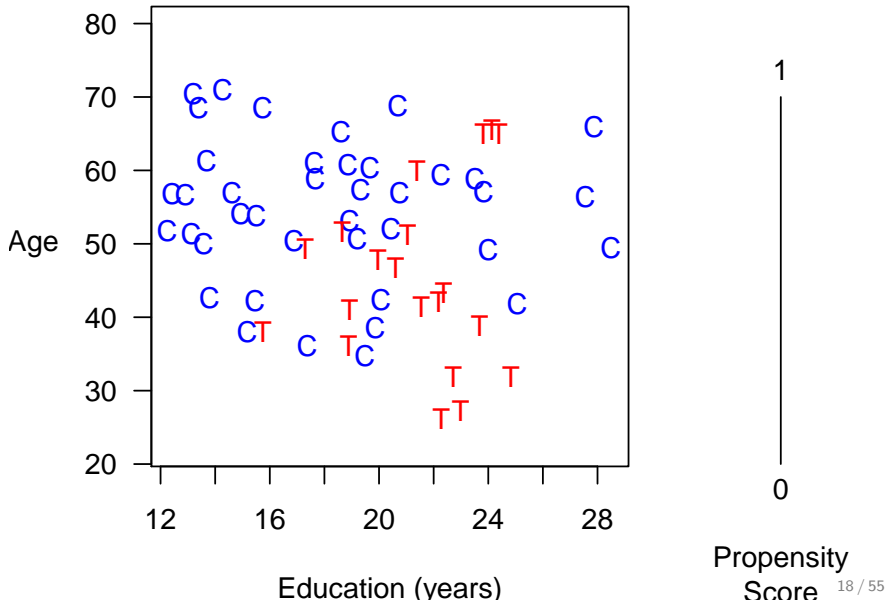
3. Checking Measure imbalance, tweak, repeat, ...



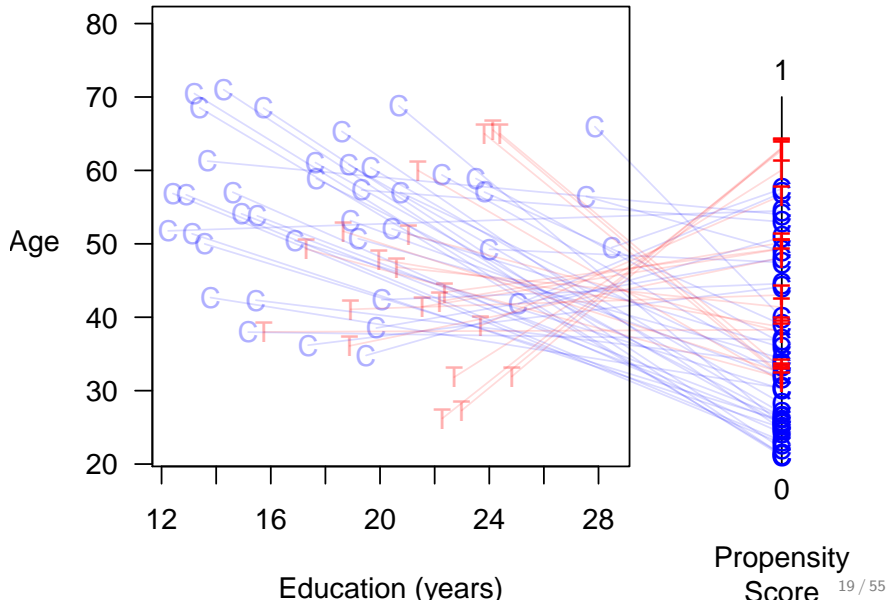
Propensity Score Matching



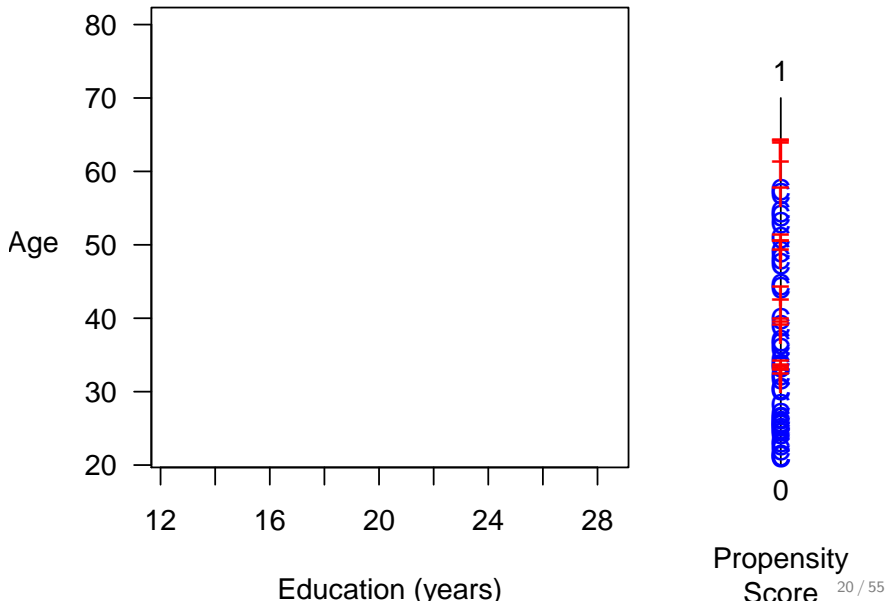
Propensity Score Matching



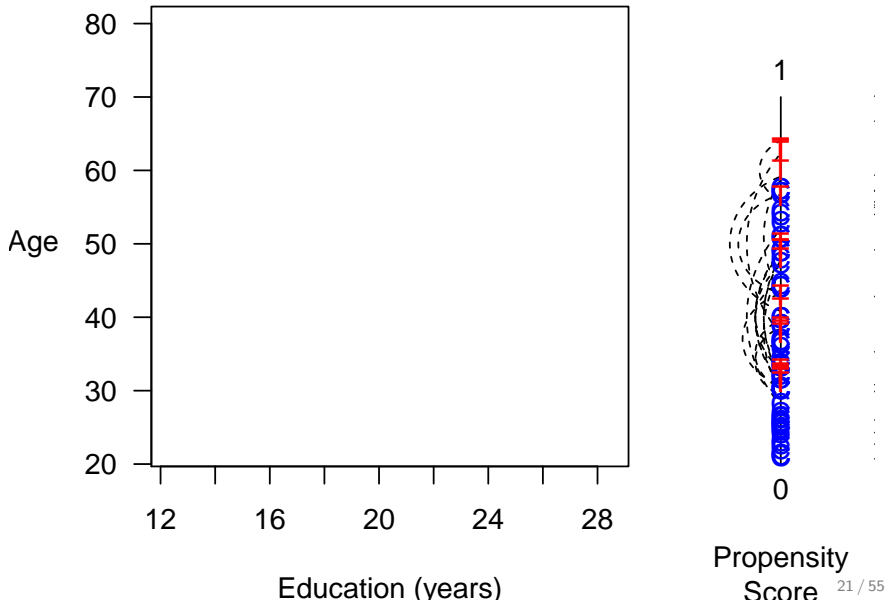
Propensity Score Matching



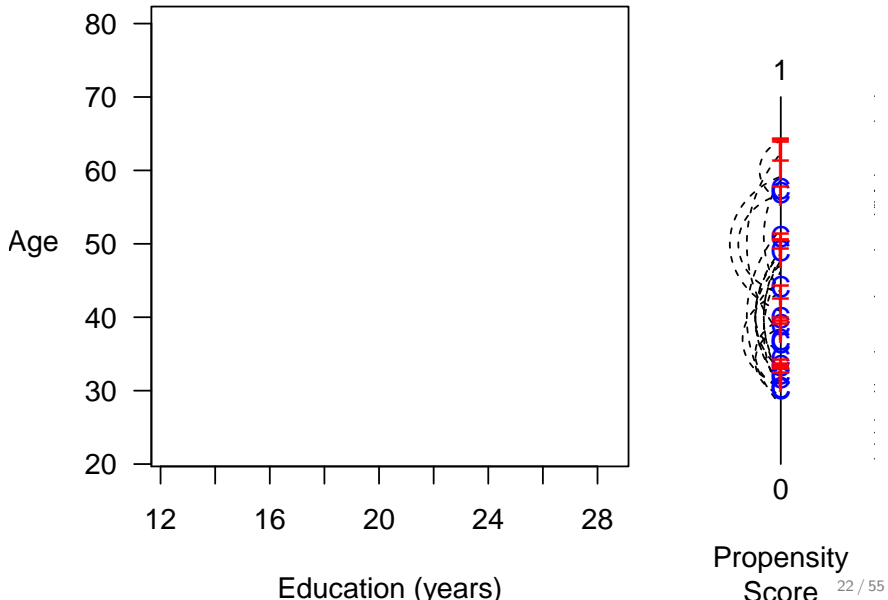
Propensity Score Matching



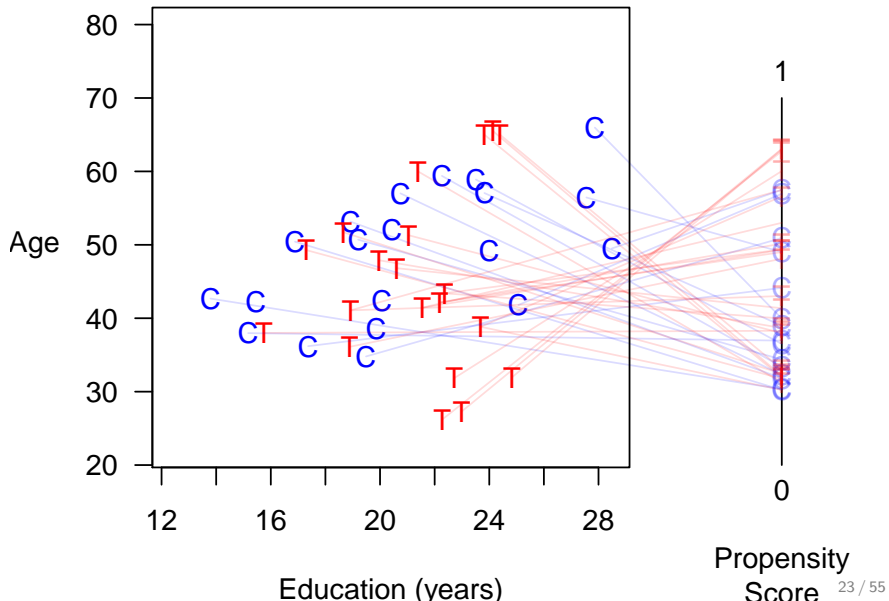
Propensity Score Matching



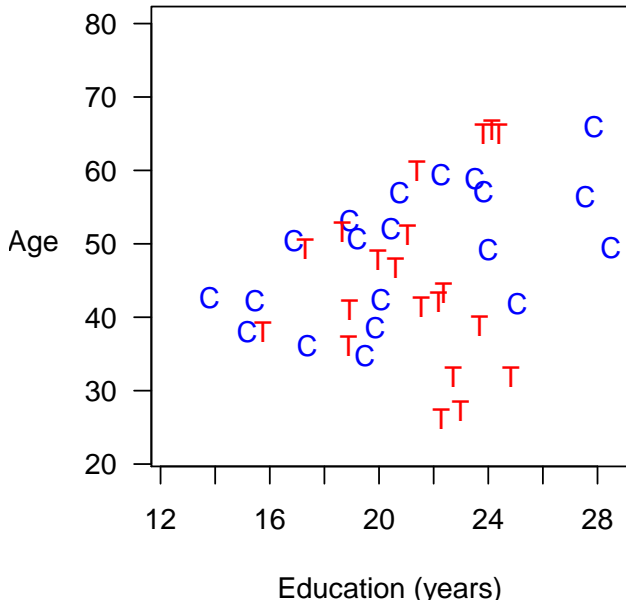
Propensity Score Matching



Propensity Score Matching



Propensity Score Matching



Method 3: Coarsened Exact Matching

Method 3: Coarsened Exact Matching

1. **Preprocess** (Matching)
2. **Estimation** Difference in means or a model
3. **Checking** Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. **Preprocess** (Matching)
 - Temporarily coarsen X as much as you're willing
2. **Estimation** Difference in means or a model
3. **Checking** Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. **Preprocess** (Matching)
 - Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
2. **Estimation** Difference in means or a model
3. **Checking** Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram

2. Estimation Difference in means or a model

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- Apply exact matching to the coarsened X , $C(X)$

2. Estimation Difference in means or a model

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. **Preprocess** (Matching)

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

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

3. **Checking** Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- 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

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- 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

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- 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

- Need to weight controls in each stratum to equal treated

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. Preprocess (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- 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

- Need to weight controls in each stratum to equal treateds
- Can apply other matching methods within CEM strata (inherit CEM's properties)

3. Checking Determine matched sample size, tweak, repeat, ...

Method 3: Coarsened Exact Matching

1. **Preprocess** (Matching)

- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- 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

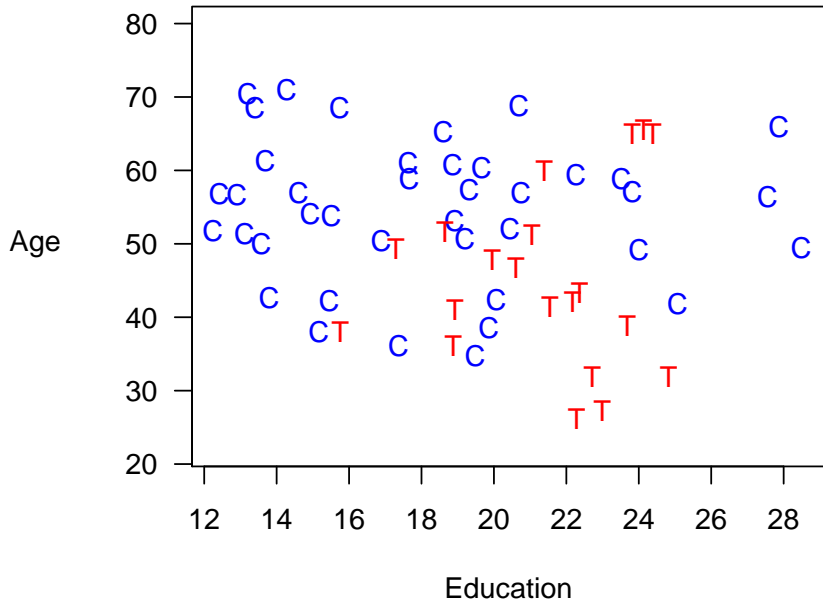
- Need to weight controls in each stratum to equal treateds
- Can apply other matching methods within CEM strata (inherit CEM's properties)

3. **Checking** Determine matched sample size, tweak, repeat, ...

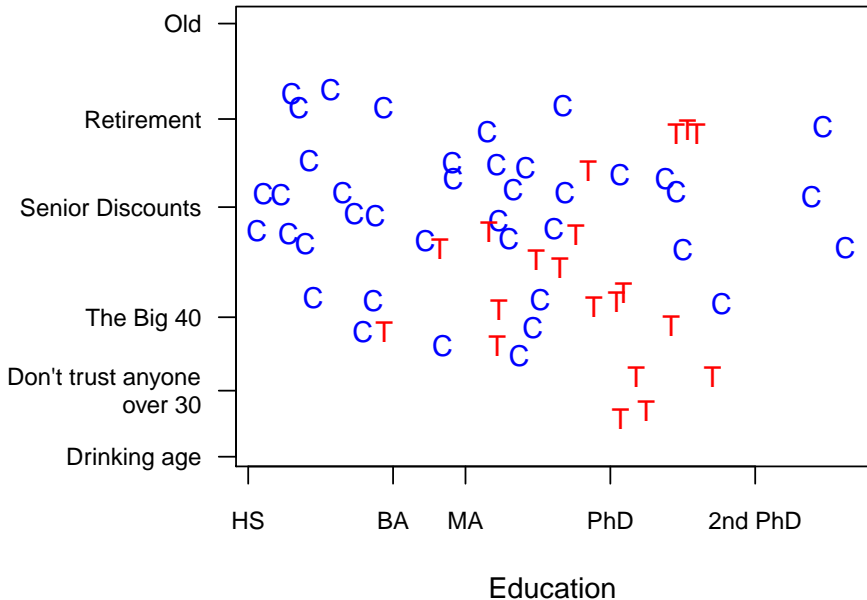
- Easier, but still iterative

Coarsened Exact Matching

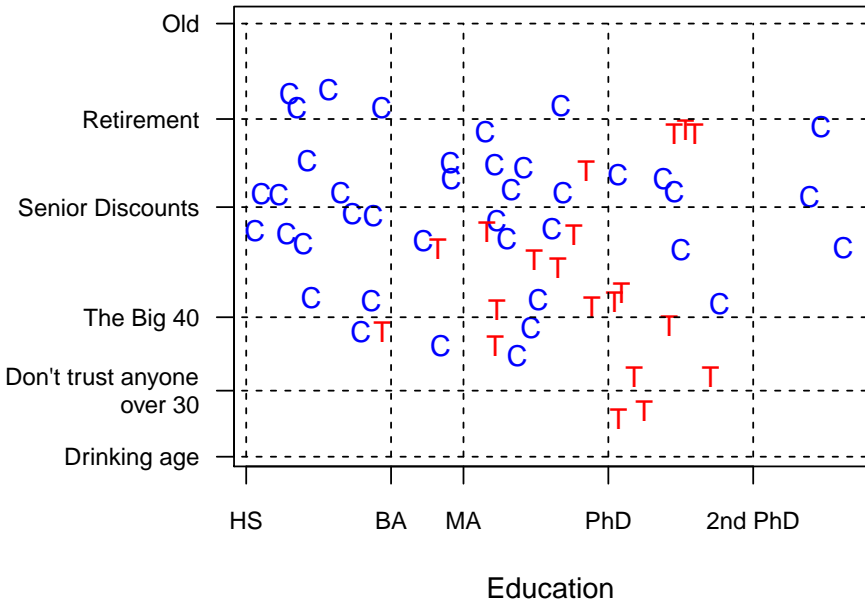
Coarsened Exact Matching



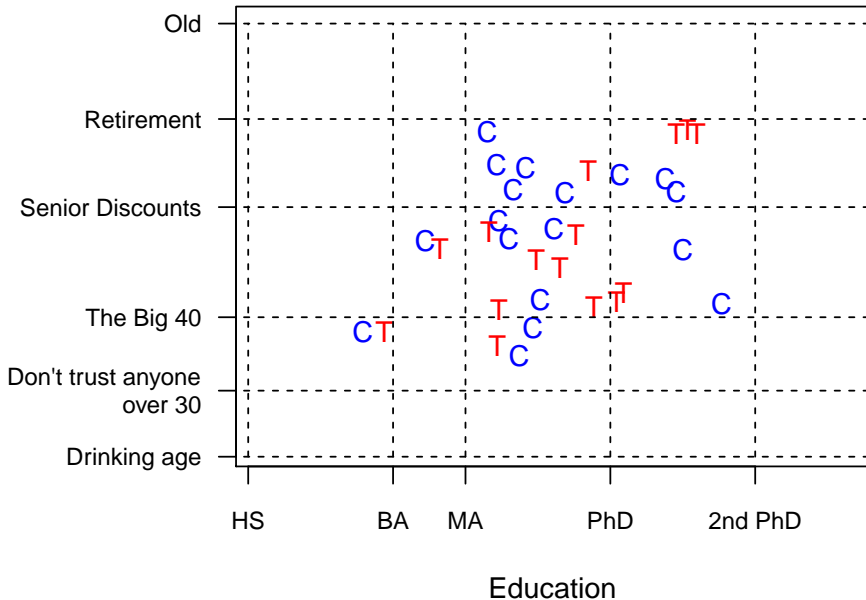
Coarsened Exact Matching



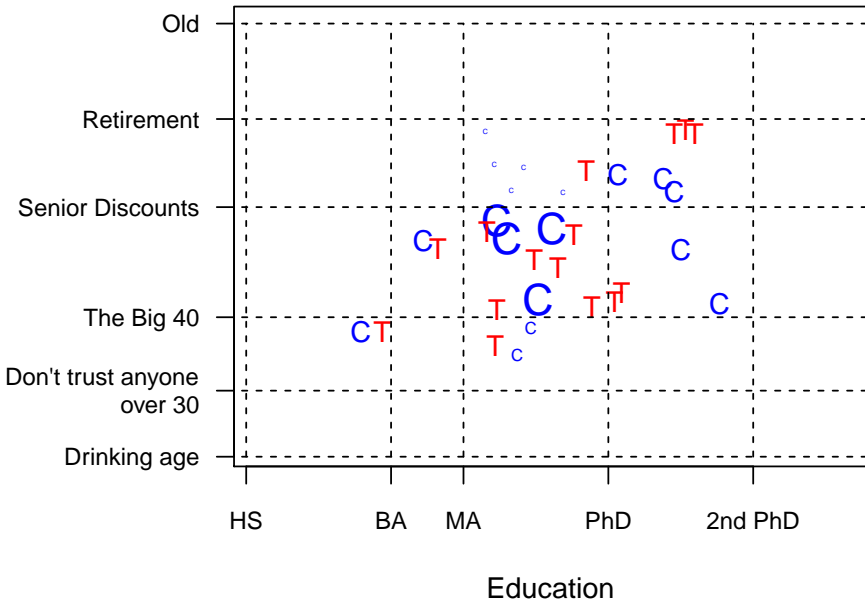
Coarsened Exact Matching



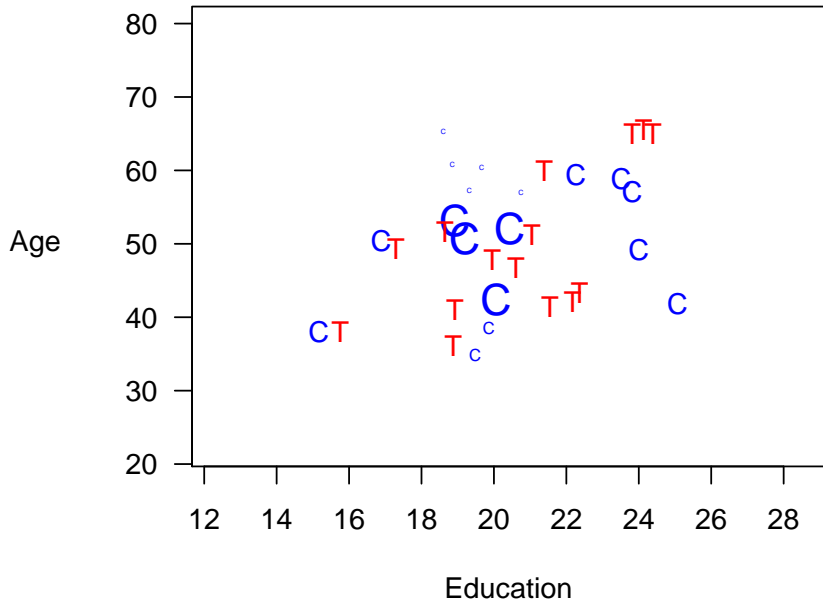
Coarsened Exact Matching



Coarsened Exact Matching



Coarsened Exact Matching



The Matching Frontier

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off
Frontier = matched dataset with lowest imbalance for each n
- To use, make 3 choices:

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:
 1. Imbalance metric, e.g.:

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

- Result:

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

- Result:

- Simple to use

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

- Result:

- Simple to use
- All solutions are optimal

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

- Result:

- Simple to use
- All solutions are optimal
- No iteration or diagnostics required

The Matching Frontier

- Bias-Variance trade off \rightsquigarrow Imbalance- n Trade Off

Frontier = matched dataset with lowest imbalance for each n

- To use, make 3 choices:

1. Imbalance metric, e.g.:

- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

2. Quantity of interest: SATT (prune Cs only) or FSATT

3. Fixed- or variable-ratio matching

- Result:

- Simple to use
- All solutions are optimal
- No iteration or diagnostics required
- No cherry picking possible

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
 - Start with $(N \times k)$ control matrix X_0

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

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

How hard is the frontier to calculate?

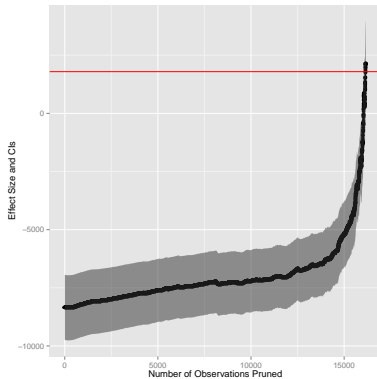
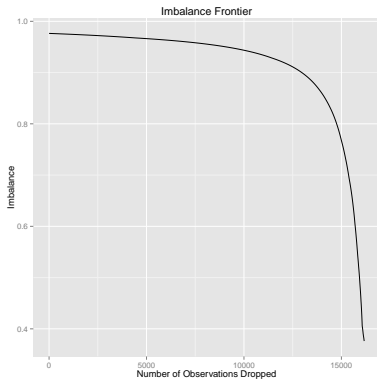
- Consider 1 point on the SATT frontier:
 - Start with $(N \times k)$ control matrix X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose the (or a) subset with the lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each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

How hard is the frontier to calculate?

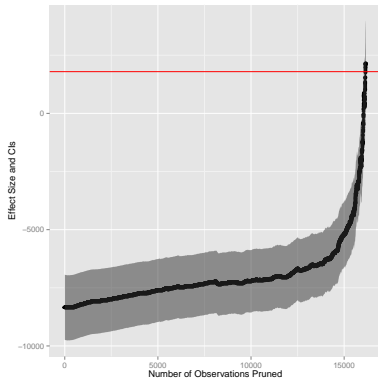
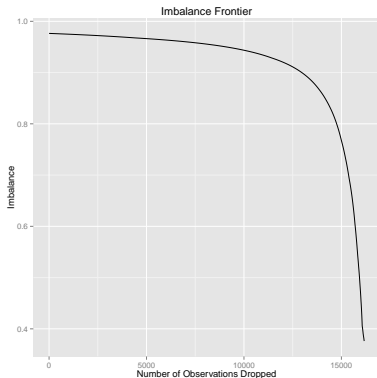
- Consider 1 point on the SATT frontier:
 - Start with $(N \times k)$ control matrix X_0
 - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
 - Choose the (or a) subset with the lowest imbalance
- Evaluations needed to compute the entire frontier:
 - $\binom{N}{n}$ evaluations for each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

Job Training Data: Frontier and Causal Estimates

Job Training Data: Frontier and Causal Estimates

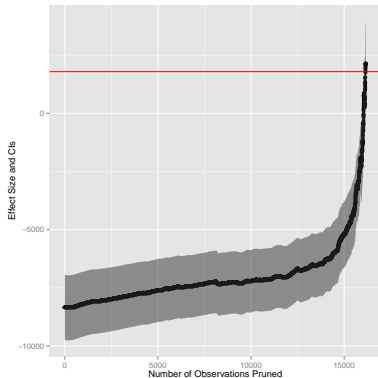
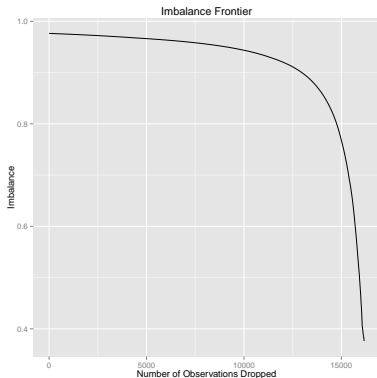


Job Training Data: Frontier and Causal Estimates



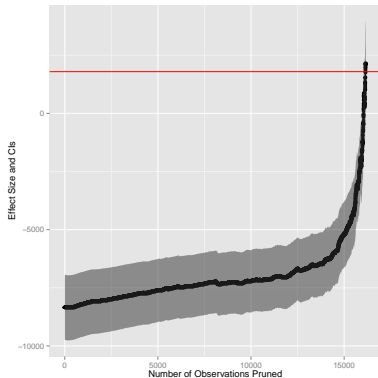
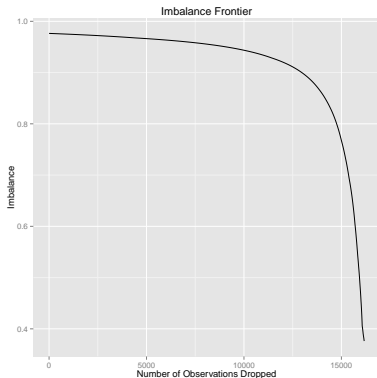
- 185 Ts; pruning most 16,252 Cs won't increase variance much

Job Training Data: Frontier and Causal Estimates



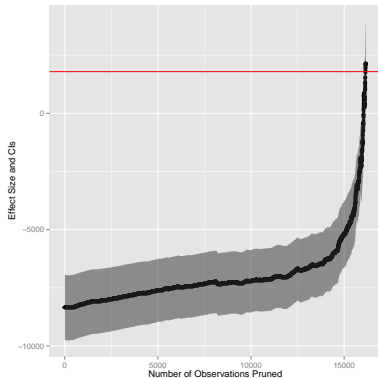
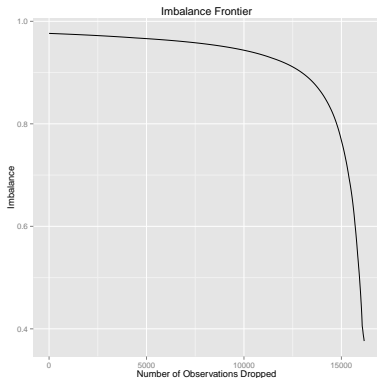
- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after most are pruned

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 most are pruned
- Estimates converge to experiment after removing bias

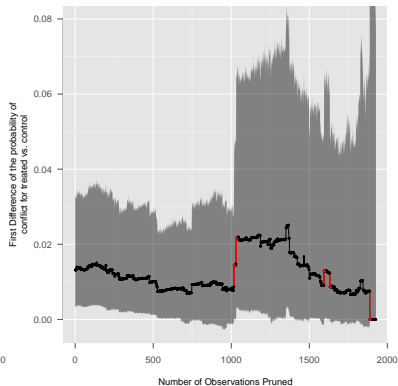
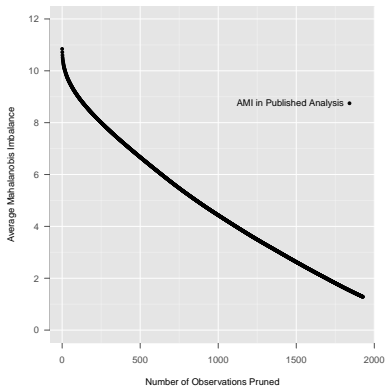
Job Training Data: Frontier and Causal Estimates



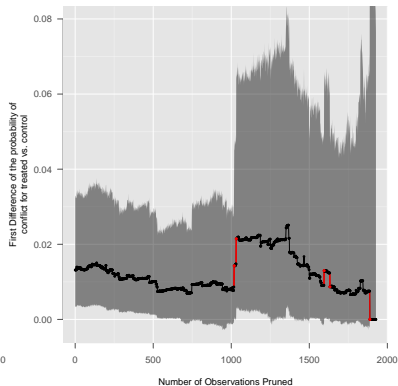
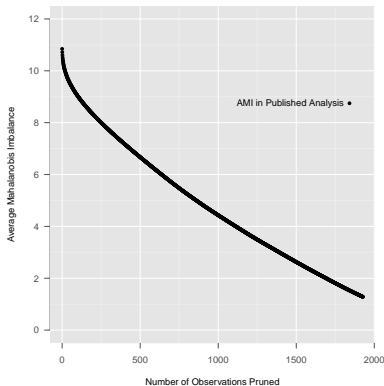
- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after most are pruned
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

Aid Shocks Data: Frontier and Causal Estimates

Aid Shocks Data: Frontier and Causal Estimates

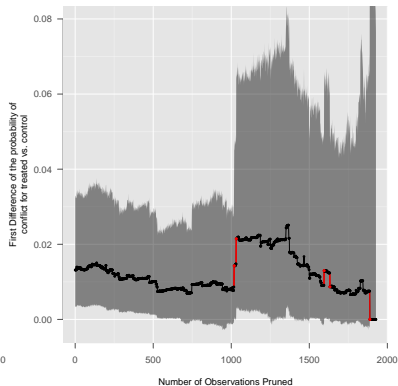
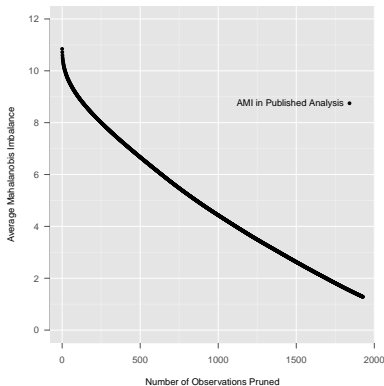


Aid Shocks Data: Frontier and Causal Estimates



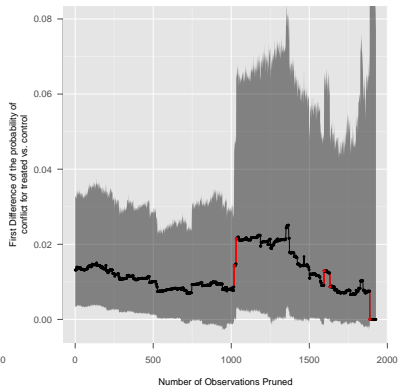
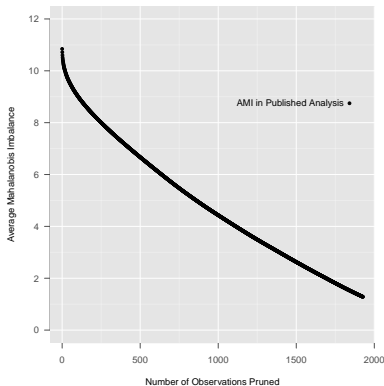
- Frontier is nearly linear (left)

Aid Shocks Data: Frontier and Causal Estimates



- Frontier is nearly linear (left)
- Causal effects have big **jumps** (right)

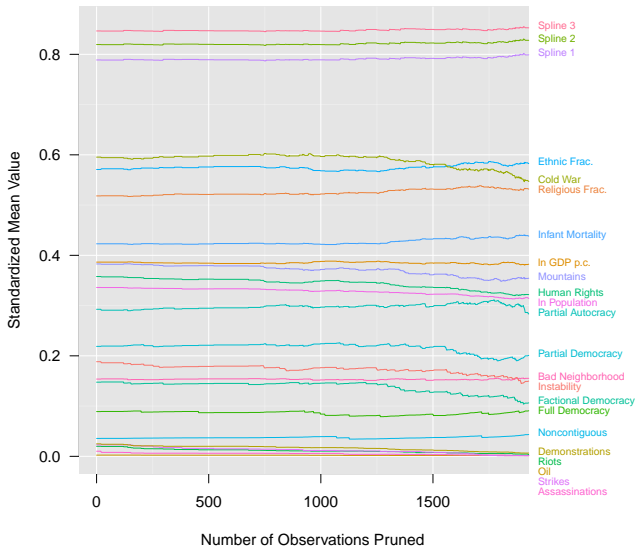
Aid Shocks Data: Frontier and Causal Estimates



- Frontier is nearly linear (left)
- Causal effects have big **jumps** (right)
- More difficult inferential task

Aids Shocks: Change in Quantity of Interest

Aids Shocks: Change in Quantity of Interest



Aids Shocks: Large Unit-Level Effects

Aids Shocks: Large Unit-Level Effects

Case	T	Y	Effect change	N remaining
Gambia, 1991	1	0	0.008→0.015	1608
Niger, 1994	0	1	0.015→0.023	1595
Lesotho, 1998	1	1	0.021→0.018	1254
Cote D'Ivoire, 2002	1	1	0.011→0.008	995
Guinea, 2000	1	1	0.005→0	739

Aids Shocks: Large Unit-Level Effects

Case	T	Y	Effect change	N remaining
Gambia, 1991	1	0	0.008→0.015	1608
Niger, 1994	0	1	0.015→0.023	1595
Lesotho, 1998	1	1	0.021→0.018	1254
Cote D'Ivoire, 2002	1	1	0.011→0.008	995
Guinea, 2000	1	1	0.005→0	739

- High leverage points

Aids Shocks: Large Unit-Level Effects

Case	T	Y	Effect change	N remaining
Gambia, 1991	1	0	0.008→0.015	1608
Niger, 1994	0	1	0.015→0.023	1595
Lesotho, 1998	1	1	0.021→0.018	1254
Cote D'Ivoire, 2002	1	1	0.011→0.008	995
Guinea, 2000	1	1	0.005→0	739

- High leverage points
- Cases with few substitutes

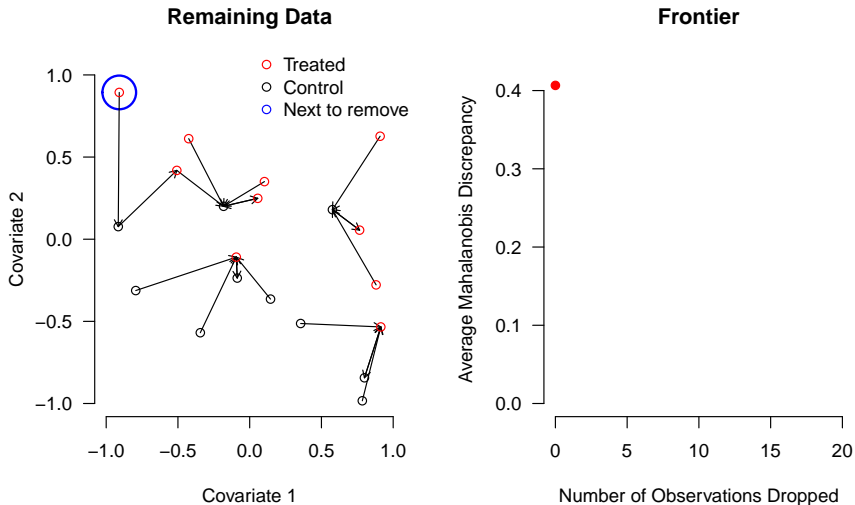
Aids Shocks: Large Unit-Level Effects

Case	T	Y	Effect change	N remaining
Gambia, 1991	1	0	0.008→0.015	1608
Niger, 1994	0	1	0.015→0.023	1595
Lesotho, 1998	1	1	0.021→0.018	1254
Cote D'Ivoire, 2002	1	1	0.011→0.008	995
Guinea, 2000	1	1	0.005→0	739

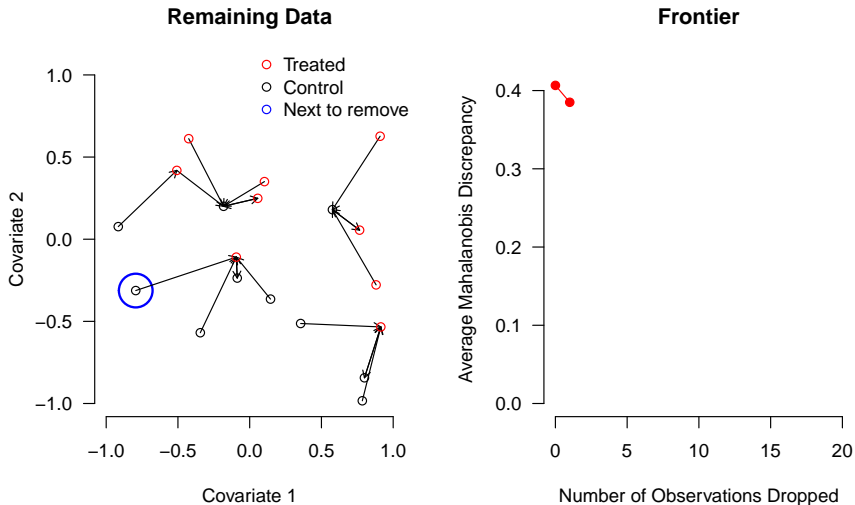
- High leverage points
- Cases with few substitutes
- Not model dependence (which matching helps with), but data dependence

Constructing the FSATT Mahalanobis Frontier

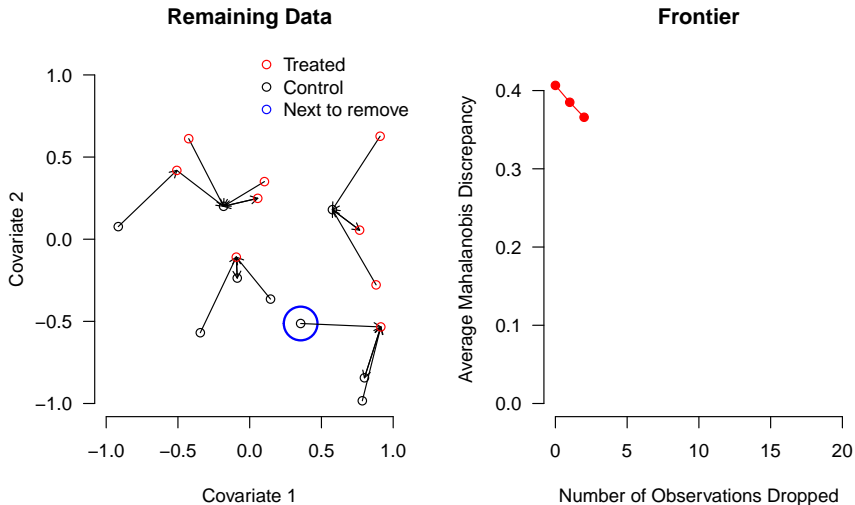
Constructing the FSATT Mahalanobis Frontier



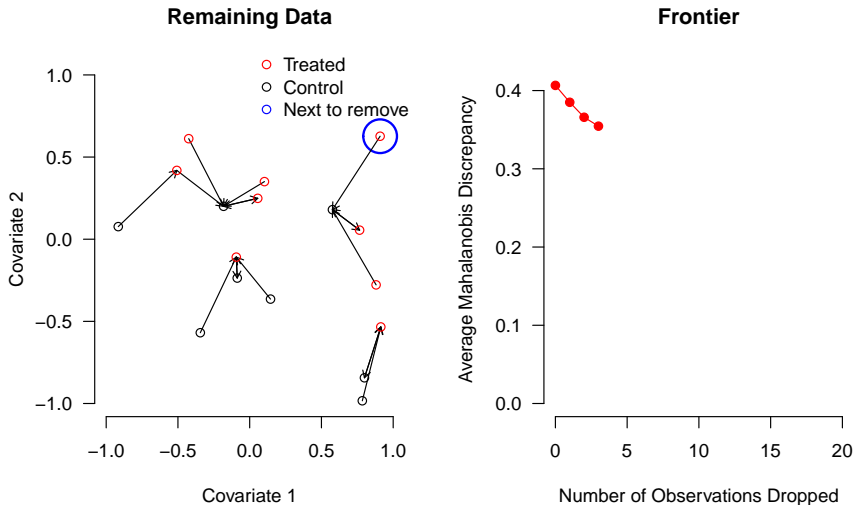
Constructing the FSATT Mahalanobis Frontier



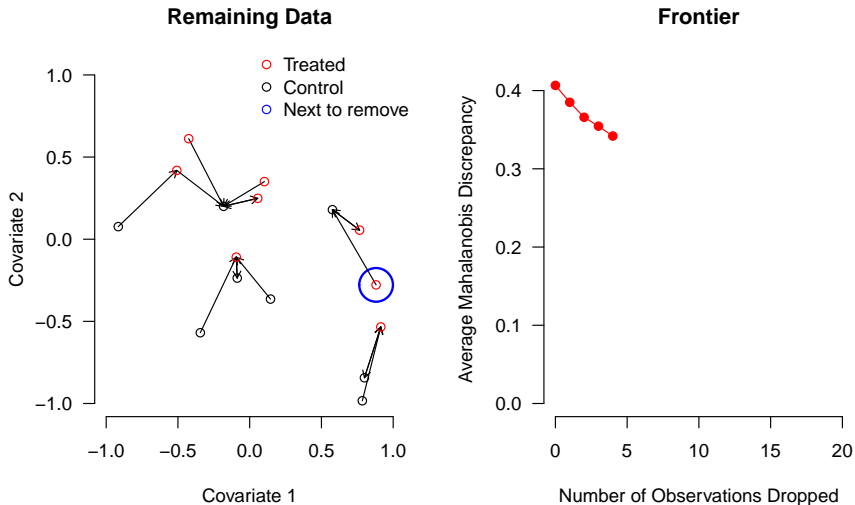
Constructing the FSATT Mahalanobis Frontier



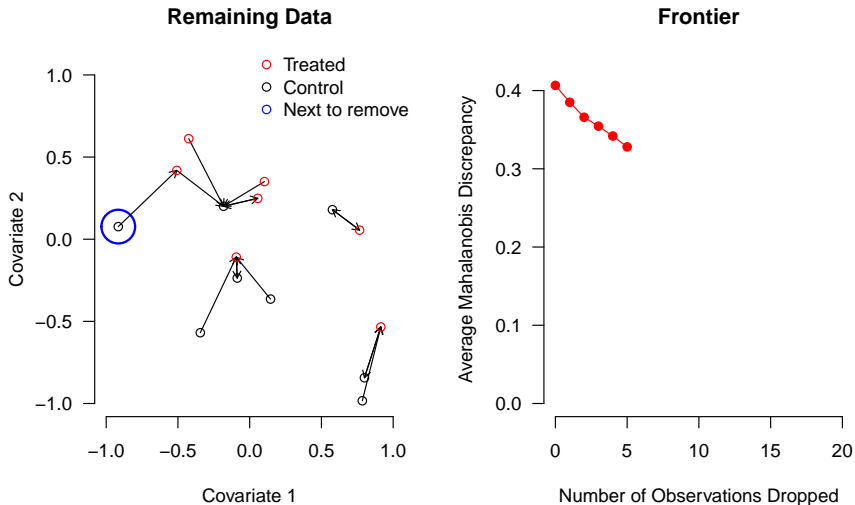
Constructing the FSATT Mahalanobis Frontier



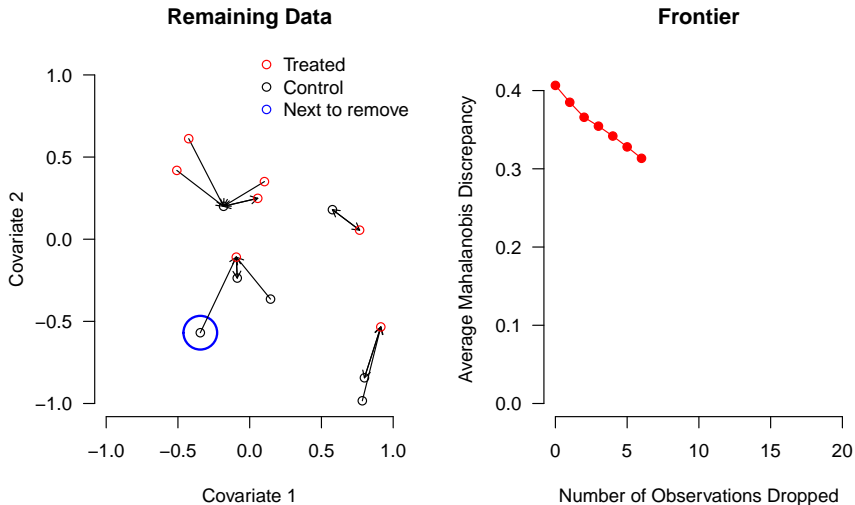
Constructing the FSATT Mahalanobis Frontier



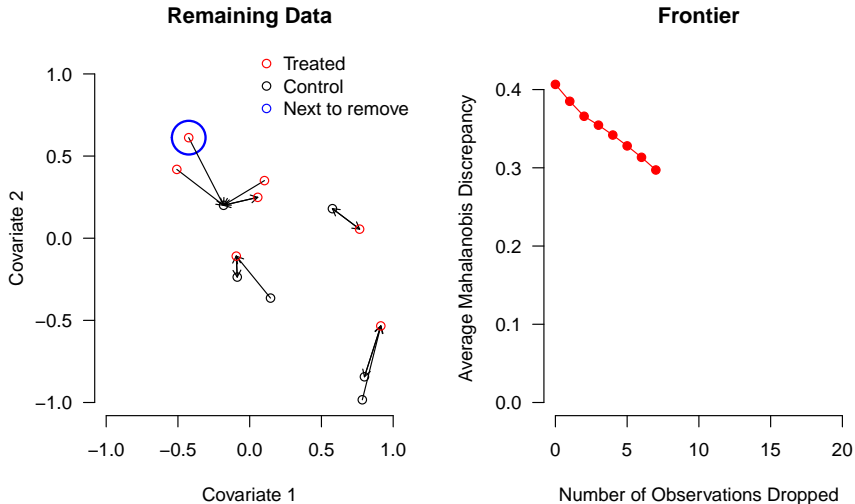
Constructing the FSATT Mahalanobis Frontier



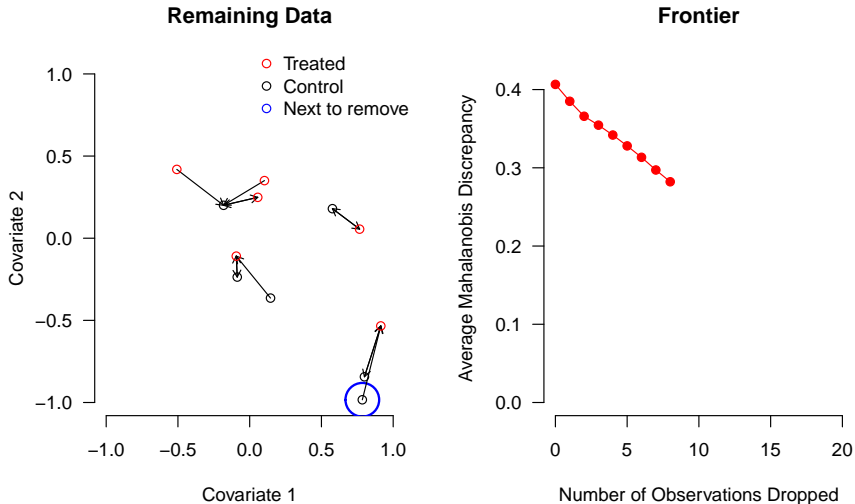
Constructing the FSATT Mahalanobis Frontier



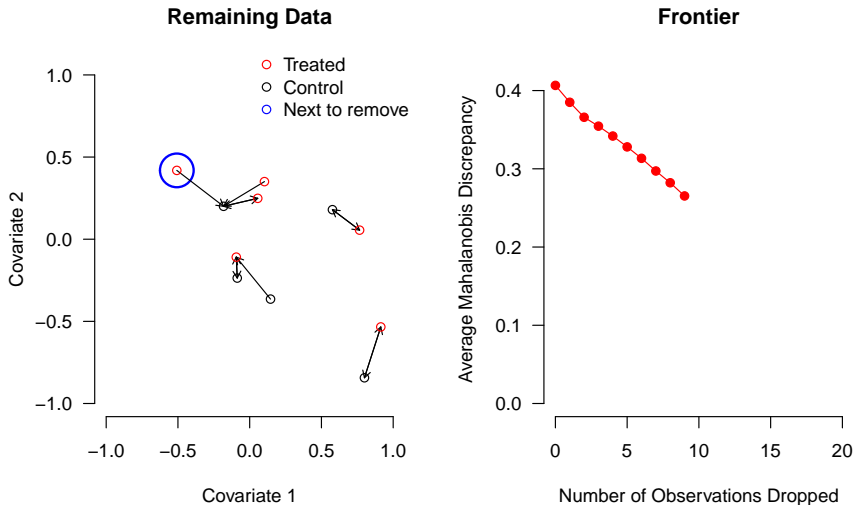
Constructing the FSATT Mahalanobis Frontier



Constructing the FSATT Mahalanobis Frontier

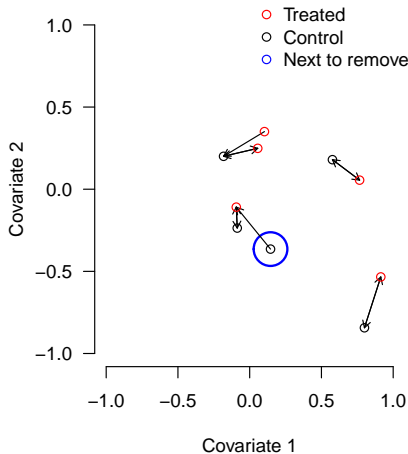


Constructing the FSATT Mahalanobis Frontier

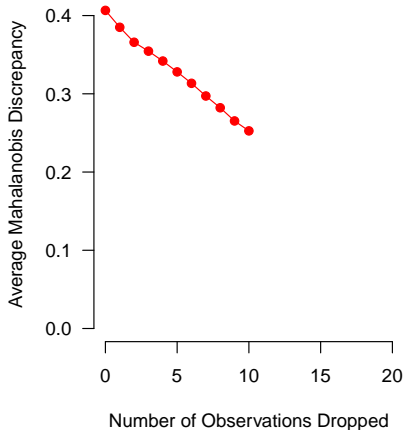


Constructing the FSATT Mahalanobis Frontier

Remaining Data

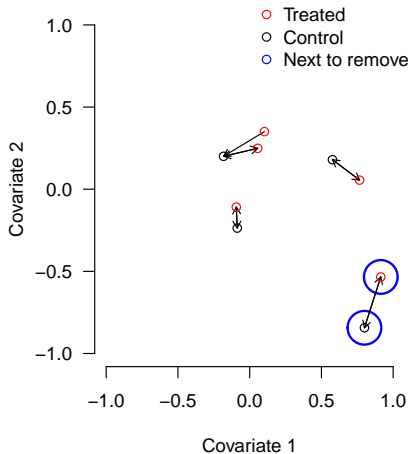


Frontier

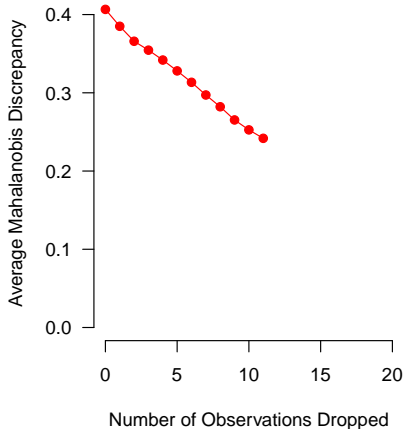


Constructing the FSATT Mahalanobis Frontier

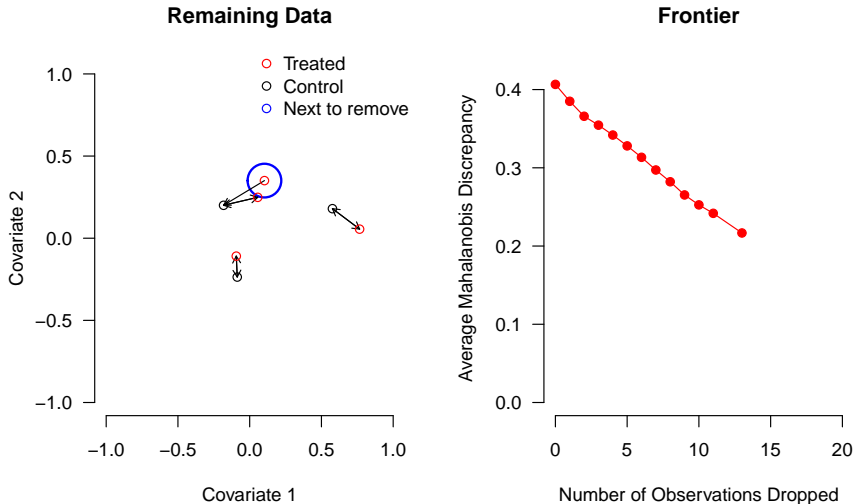
Remaining Data



Frontier

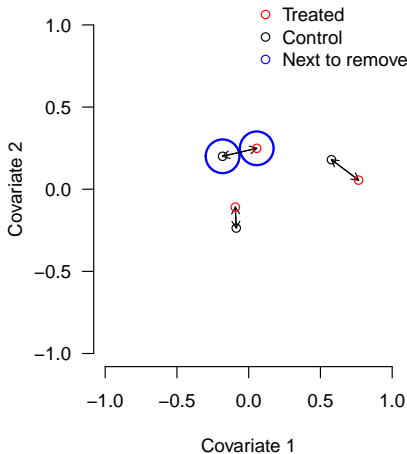


Constructing the FSATT Mahalanobis Frontier

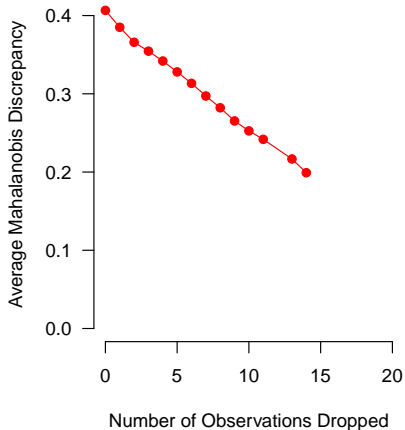


Constructing the FSATT Mahalanobis Frontier

Remaining Data

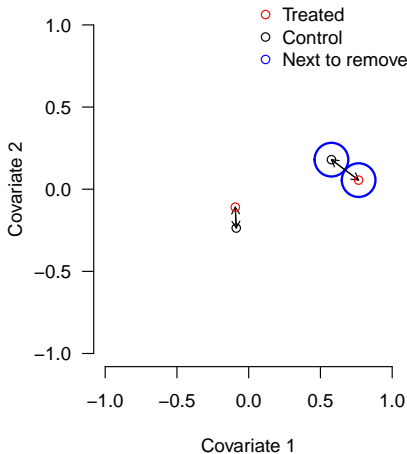


Frontier

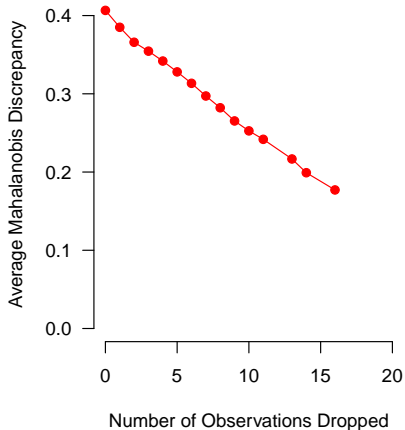


Constructing the FSATT Mahalanobis Frontier

Remaining Data

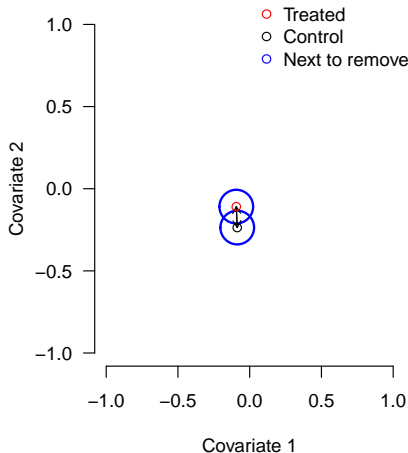


Frontier

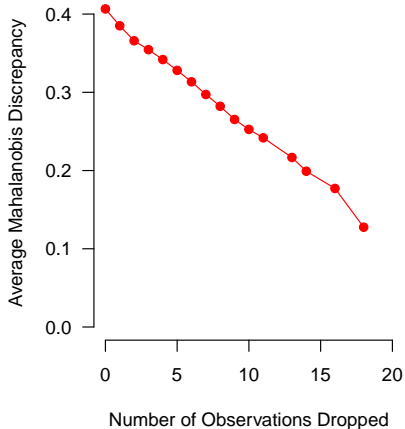


Constructing the FSATT Mahalanobis Frontier

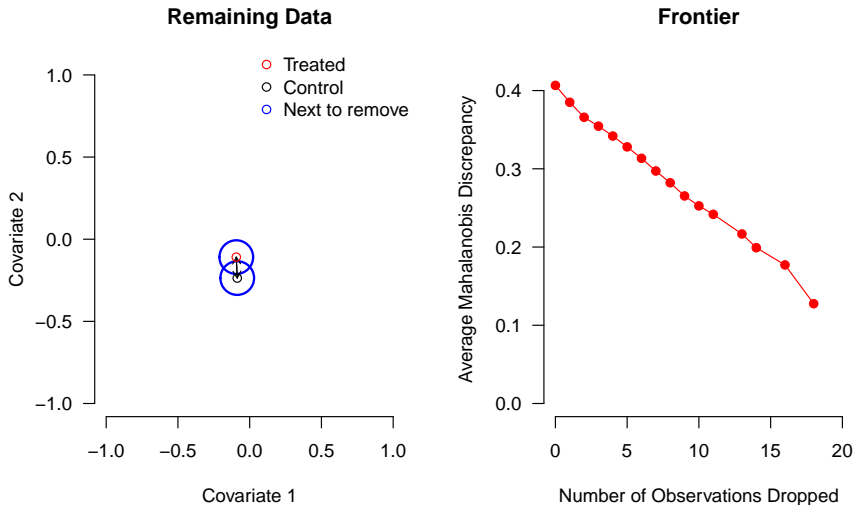
Remaining Data



Frontier

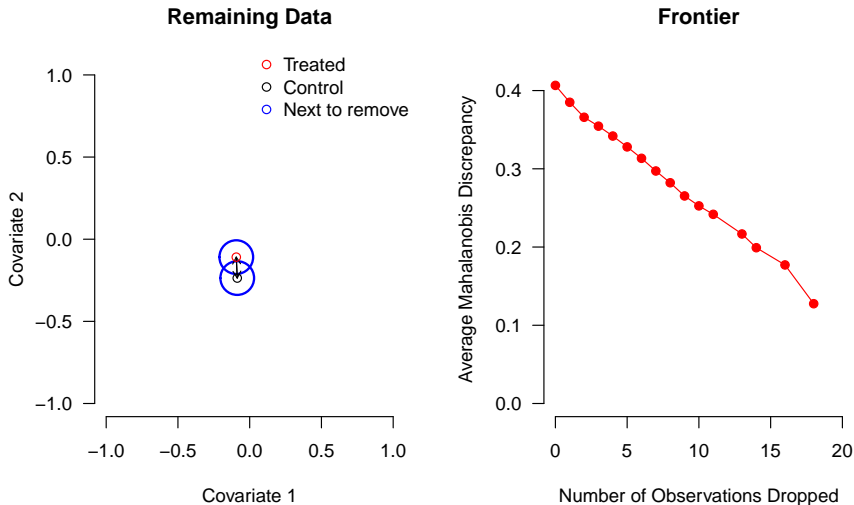


Constructing the FSATT Mahalanobis Frontier



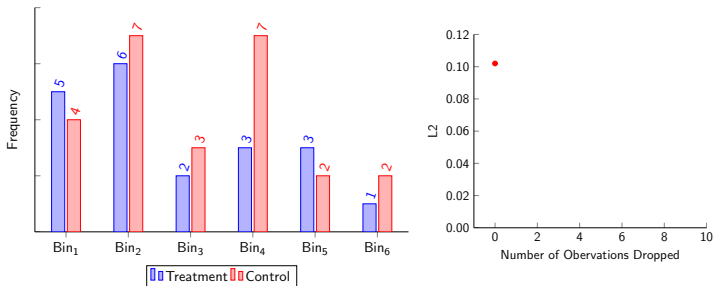
- Warning: figure omits some details!

Constructing the FSATT Mahalanobis Frontier

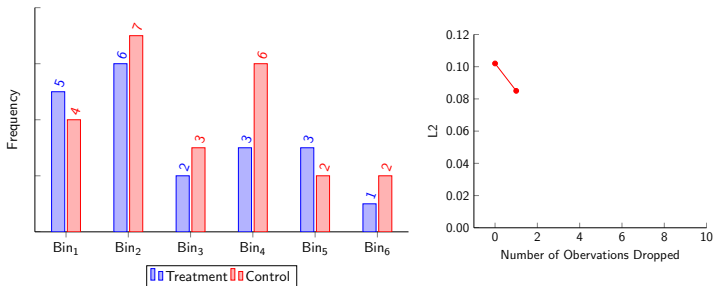


- Warning: figure omits some details!
- Very fast; works with any continuous imbalance metric

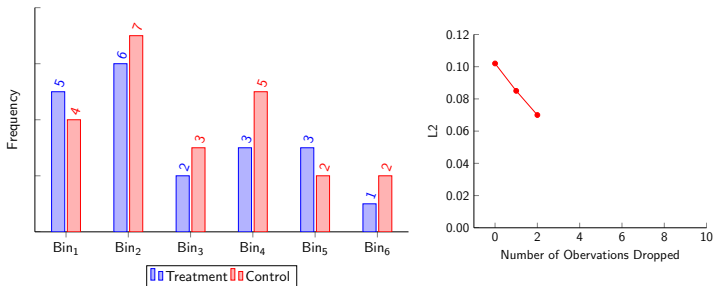
Constructing the L1/L2 SATT Frontier



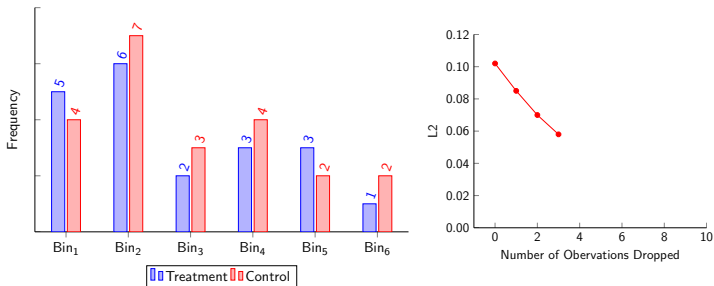
Constructing the L1/L2 SATT Frontier



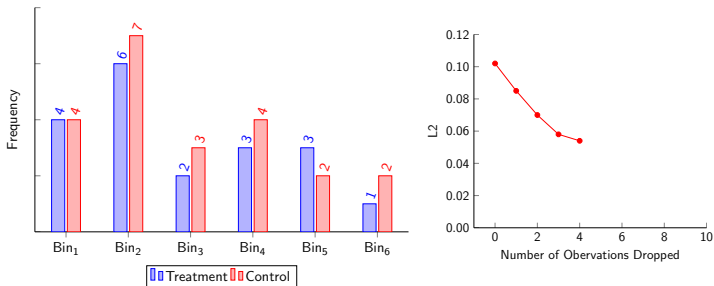
Constructing the L1/L2 SATT Frontier



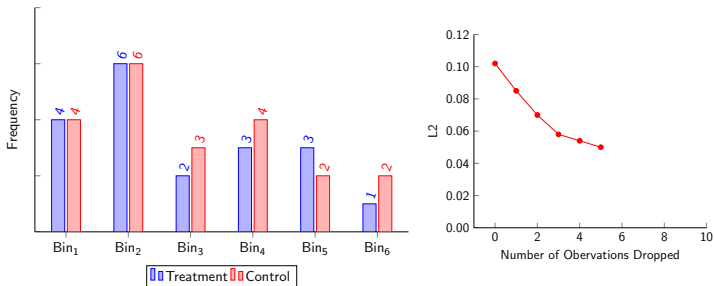
Constructing the L1/L2 SATT Frontier



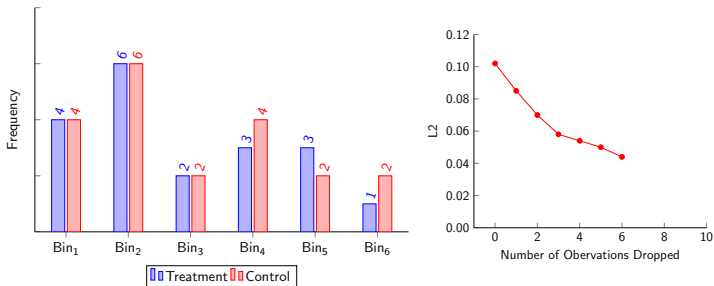
Constructing the L1/L2 SATT Frontier



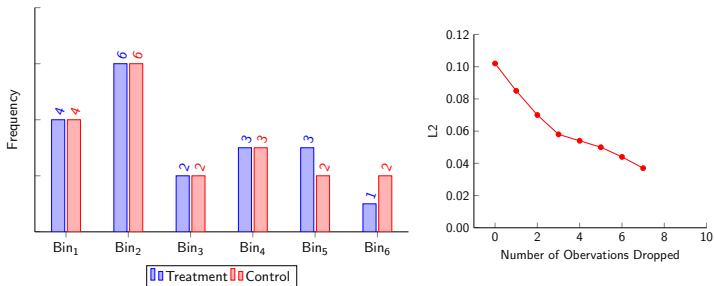
Constructing the L1/L2 SATT Frontier



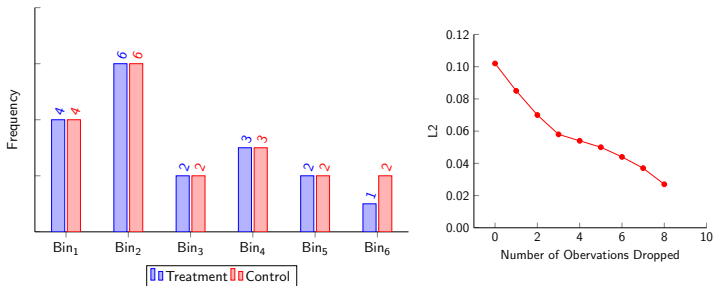
Constructing the L1/L2 SATT Frontier



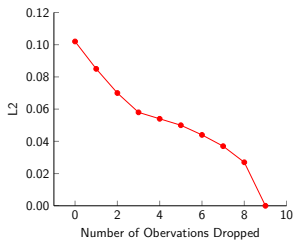
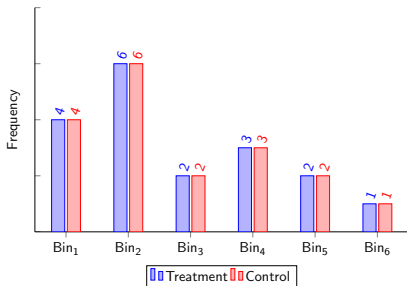
Constructing the L1/L2 SATT Frontier



Constructing the L1/L2 SATT Frontier



Constructing the L1/L2 SATT Frontier



Constructing the L1/L2 SATT Frontier

Constructing the L1/L2 SATT Frontier

- Warning: This figure omits some technical details too!

Constructing the L1/L2 SATT Frontier

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

Problems with PSM: Foreign Aid Shocks

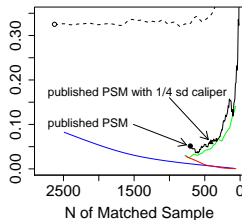
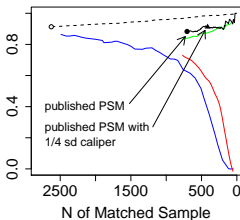
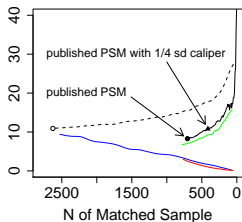
King, Nielsen, Coberley, Pope, and Wells (2012)

Imbalance Metric

Mahalanobis Discrepancy

L_1

Difference in Means



○ Raw Data
----- Random Pruning

— "Best Practices" PSM
— PSM

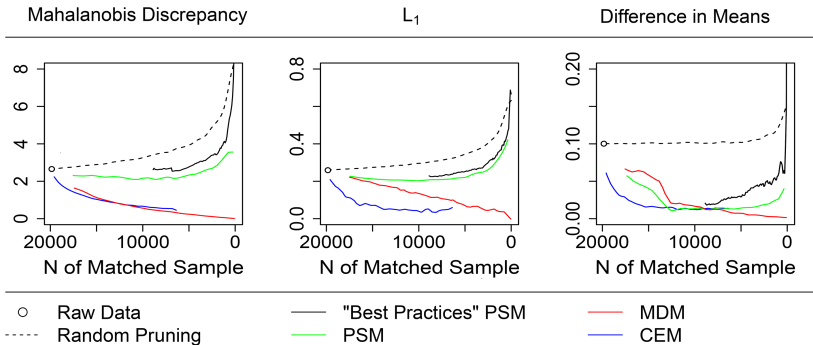
— MDM
— CEM

Methods-specific frontiers (for methodological research only)

Problems with PSM: Healthways Data

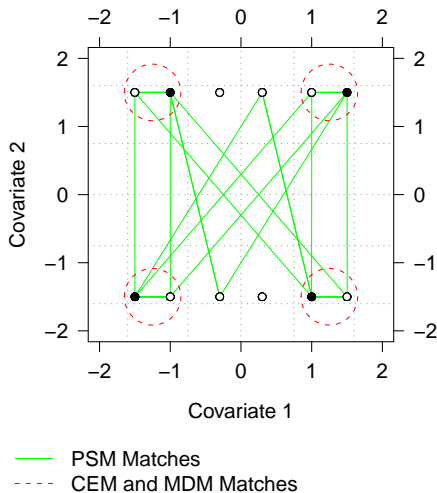
King, Nielsen, Coberley, Pope, and Wells (2012)

Imbalance Metric



Methods-specific frontiers (for methodological research only)

PSM Approximates Random Matching in Balanced Data



Conclusions

Conclusions

- The Matching Frontier

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)

Conclusions

- **The Matching Frontier**
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- **Propensity score matching:**
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data
(Random matching increases imbalance)
 - Implications:

Conclusions

- **The Matching Frontier**
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- **Propensity score matching:**
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required

Conclusions

- **The Matching Frontier**
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- **Propensity score matching:**
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake
 - Adjusting experimental data *with PSM*: mistake

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake
 - Adjusting experimental data *with PSM*: mistake
 - Reestimating the propensity score after eliminating noncommon support: mistake

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake
 - Adjusting experimental data *with PSM*: mistake
 - Reestimating the propensity score after eliminating noncommon support: mistake
 - 1/4 caliper on propensity score: mistake

Conclusions

- The Matching Frontier
 - Fast; easy to use; no need to iterate
 - No need to choose among matching methods
 - Optimal results for your choice of imbalance metric
- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches
 - Approximates random matching in well-balanced data (Random matching increases imbalance)
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake
 - Adjusting experimental data *with PSM*: mistake
 - Reestimating the propensity score after eliminating noncommon support: mistake
 - 1/4 caliper on propensity score: mistake
- Software on its way . . .

For more information



GaryKing.org