

Matching Methods for Causal Inference

Gary King

Institute for Quantitative Social Science
Harvard University

(Talk at University of Rochester, 11/4/2011)

- Problem: Model dependence (review)

Overview

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)

Overview

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications

Overview

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications
- Solution: The Space Graph helps us choose

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications
- Solution: The Space Graph helps us choose
- Problem: The most commonly used method can increase imbalance!

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications
- Solution: The Space Graph helps us choose
- Problem: The most commonly used method can increase imbalance!
- Solution: Other methods do not share this problem

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications
- Solution: The Space Graph helps us choose
- Problem: The most commonly used method can increase imbalance!
- Solution: Other methods do not share this problem
- (Coarsened Exact Matching is simple, easy, and powerful)

- Problem: Model dependence (review)
- Solution: Matching to preprocess data (review)
- Problem: Many matching methods & specifications
- Solution: The Space Graph helps us choose
- Problem: The most commonly used method can increase imbalance!
- Solution: Other methods do not share this problem
- (Coarsened Exact Matching is simple, easy, and powerful)
- \rightsquigarrow Lots of insights revealed in the process

Model Dependence Example

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

Replication: Doyle and Sambanis, APSR 2000

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

Model Dependence Example

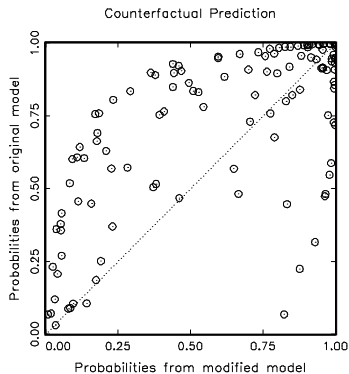
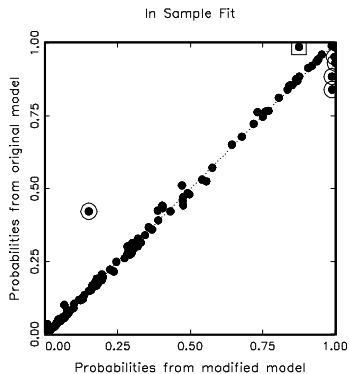
Replication: Doyle and Sambanis, APSR 2000

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



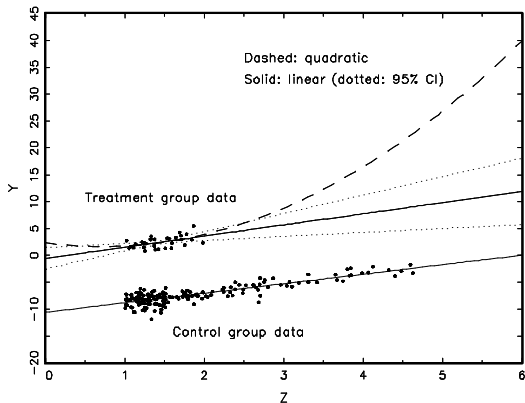
Model Dependence: A Simpler Example

Model Dependence: A Simpler Example

(King and Zeng, 2006: fig.4 *Political Analysis*)

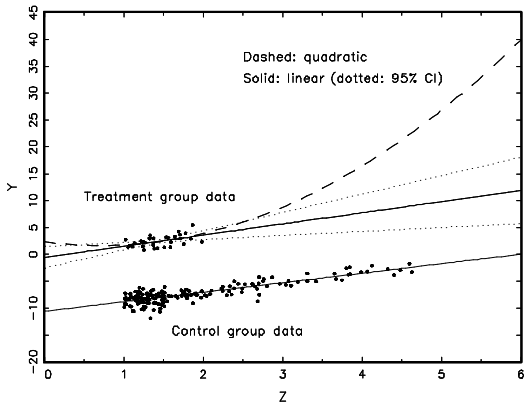
Model Dependence: A Simpler Example

(King and Zeng, 2006: fig.4 *Political Analysis*)



Model Dependence: A Simpler Example

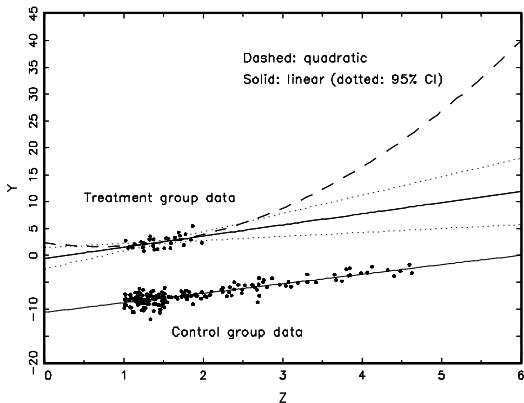
(King and Zeng, 2006: fig.4 *Political Analysis*)



What to do?

Model Dependence: A Simpler Example

(King and Zeng, 2006: fig.4 *Political Analysis*)

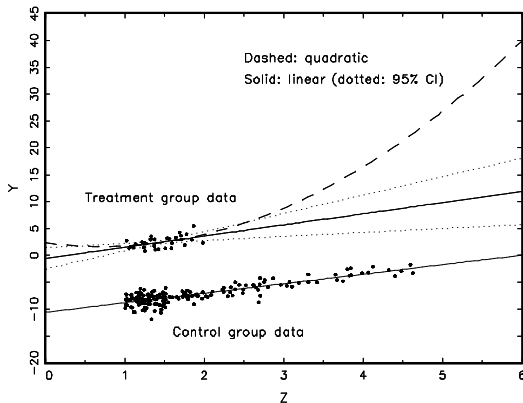


What to do?

- Preprocess I: Eliminate extrapolation region

Model Dependence: A Simpler Example

(King and Zeng, 2006: fig.4 *Political Analysis*)

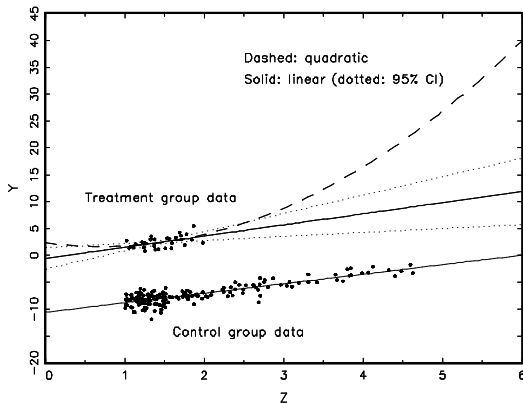


What to do?

- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region

Model Dependence: A Simpler Example

(King and Zeng, 2006: fig.4 *Political Analysis*)

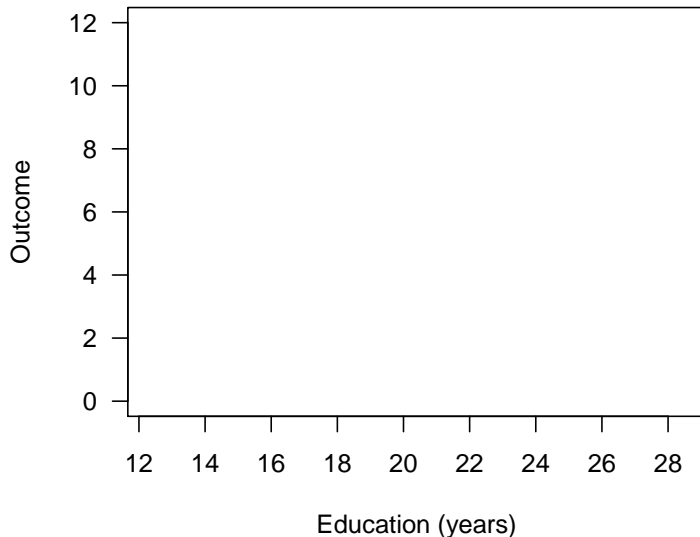


What to do?

- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

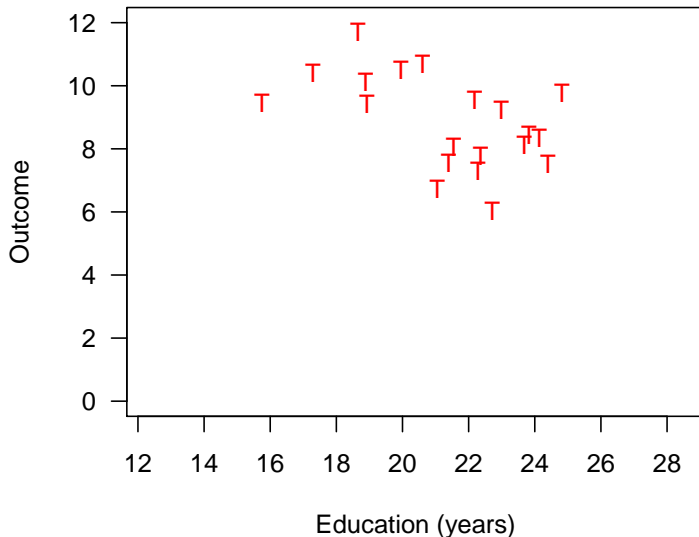
Matching within the Interpolation Region

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



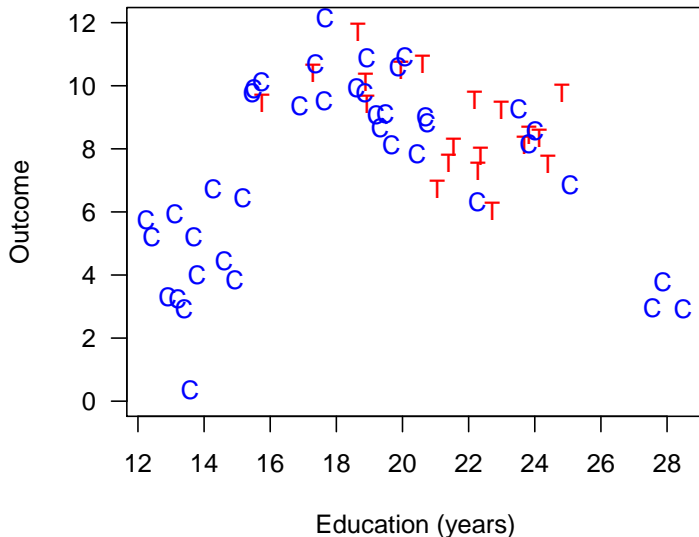
Matching within the Interpolation Region

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



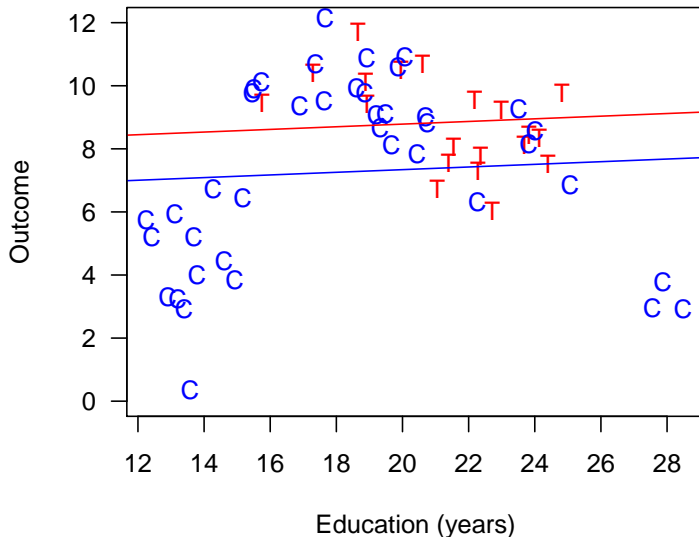
Matching within the Interpolation Region

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



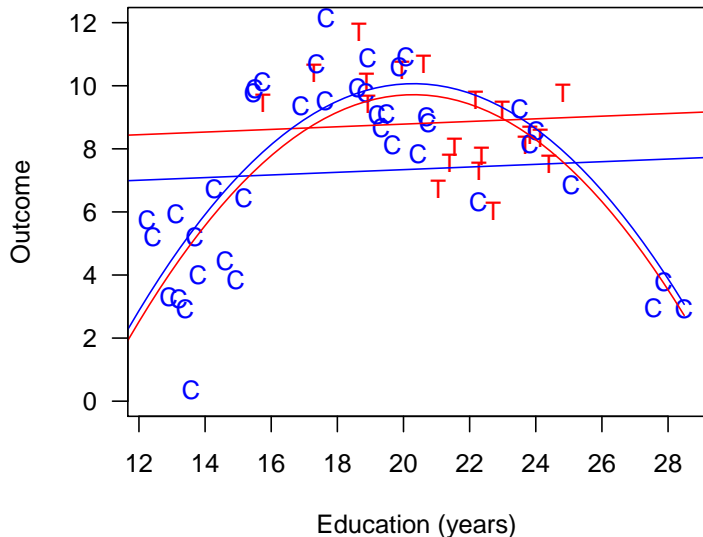
Matching within the Interpolation Region

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



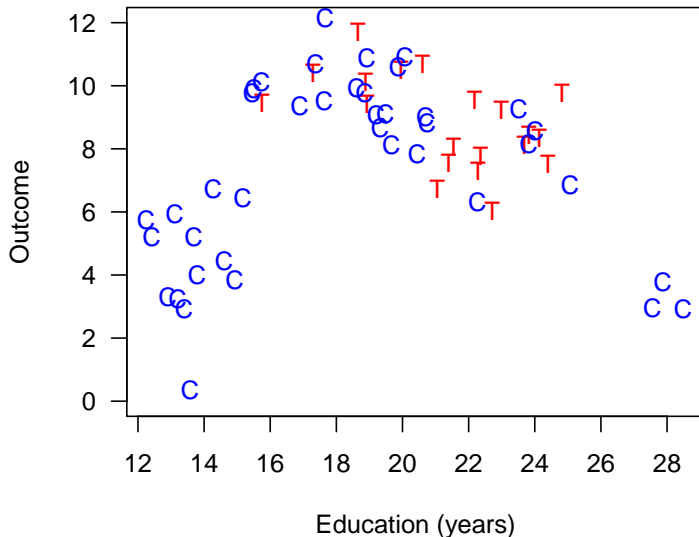
Matching within the Interpolation Region

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



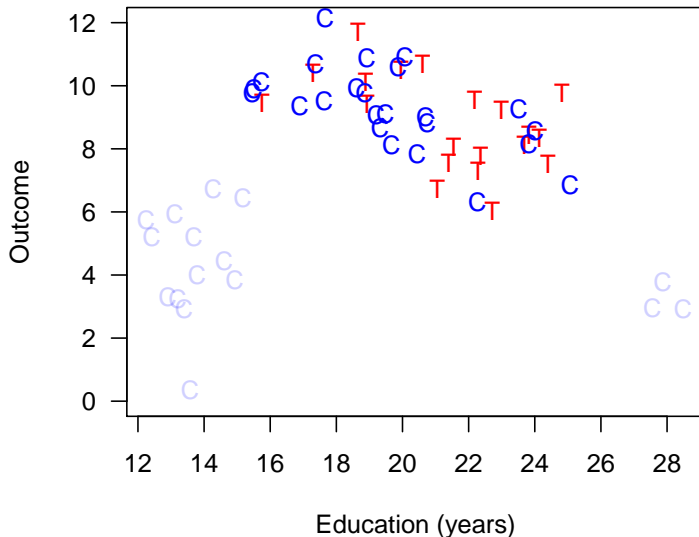
Matching within the Interpolation Region

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



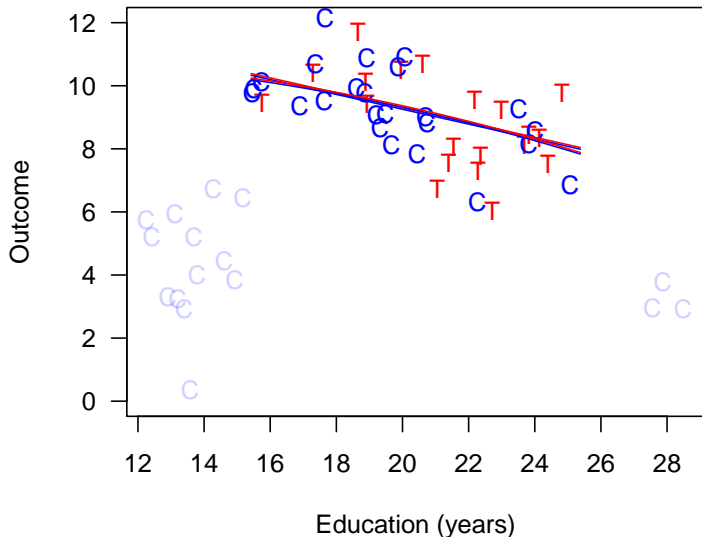
Matching within the Interpolation Region

(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

What Matching Does

What Matching Does

- Notation:

What Matching Does

- Notation:
 Y_i Dependent variable

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

What Matching Does

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

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

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

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

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

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

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

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

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

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

- Estimate $Y_i(0)$ with Y_j from matched ($X_i \approx X_j$) controls

$$\hat{Y}_i(0) = Y_j(0) \text{ or a model } \hat{Y}_i(0) = \hat{g}_0(X_j)$$

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

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

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

- Estimate $Y_i(0)$ with Y_j from matched ($X_i \approx X_j$) controls

$$\hat{Y}_i(0) = Y_j(0) \text{ or a model } \hat{Y}_i(0) = \hat{g}_0(X_j)$$

- Prune unmatched units to improve **balance** (so X is unimportant)

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

- 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 $Y_i(0)$ with Y_j from matched ($X_i \approx X_j$) controls

$$\hat{Y}_i(0) = Y_j(0) \text{ or a model } \hat{Y}_i(0) = \hat{g}_0(X_j)$$

- Prune unmatched units to improve **balance** (so X is unimportant)

- Qol: Sample Average Treatment effect on the Treated:

$$\text{SATT} = \frac{1}{n_T} \sum_{i \in \{T_i=1\}} \text{TE}_i$$

What Matching Does

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

- 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 $Y_i(0)$ with Y_j from matched ($X_i \approx X_j$) controls

$$\hat{Y}_i(0) = Y_j(0) \text{ or a model } \hat{Y}_i(0) = \hat{g}_0(X_j)$$

- Prune unmatched units to improve **balance** (so X is unimportant)

- Qol: Sample Average Treatment effect on the Treated:

$$\text{SATT} = \frac{1}{n_T} \sum_{i \in \{T_i=1\}} \text{TE}_i$$

- or Feasible Average Treatment effect on the Treated: FSATT

Method 1: Mahalanobis Distance Matching

Method 1: Mahalanobis Distance Matching

- 1 **Preprocess** (Matching)
- 2 **Estimation** Difference in means or a model

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

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

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

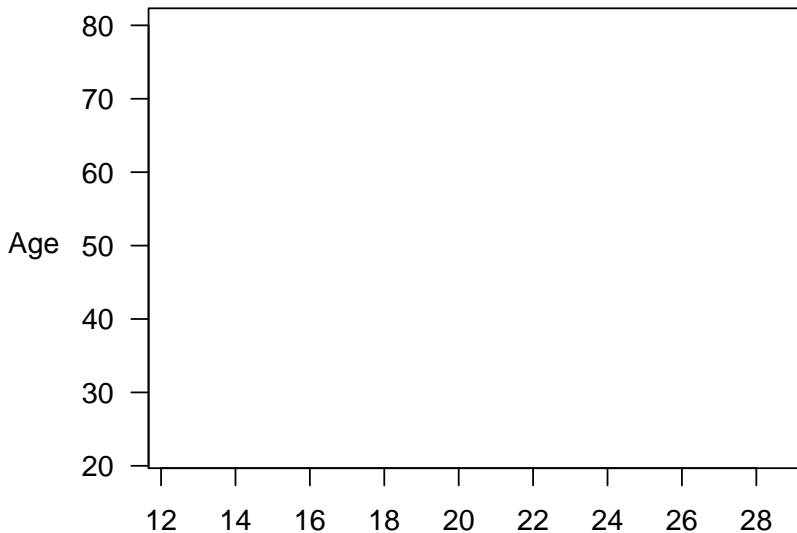
Method 1: Mahalanobis Distance Matching

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

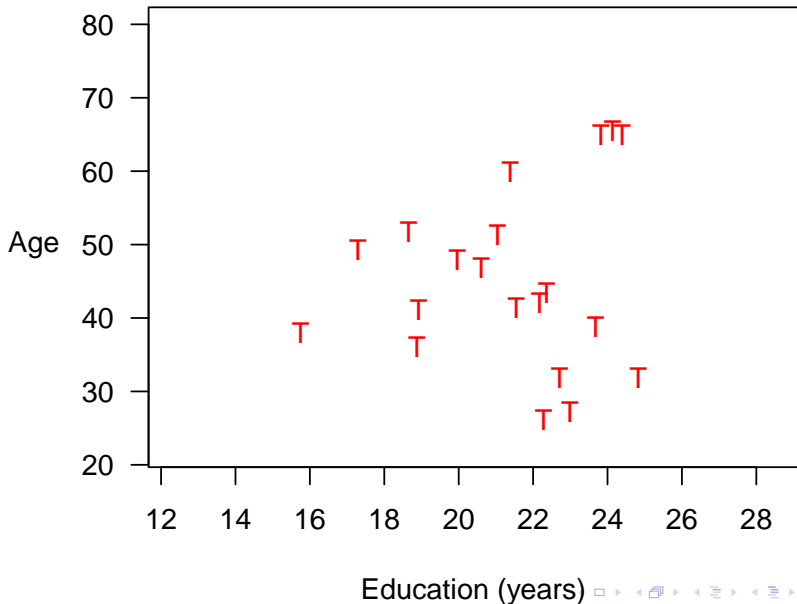
Mahalanobis Distance Matching



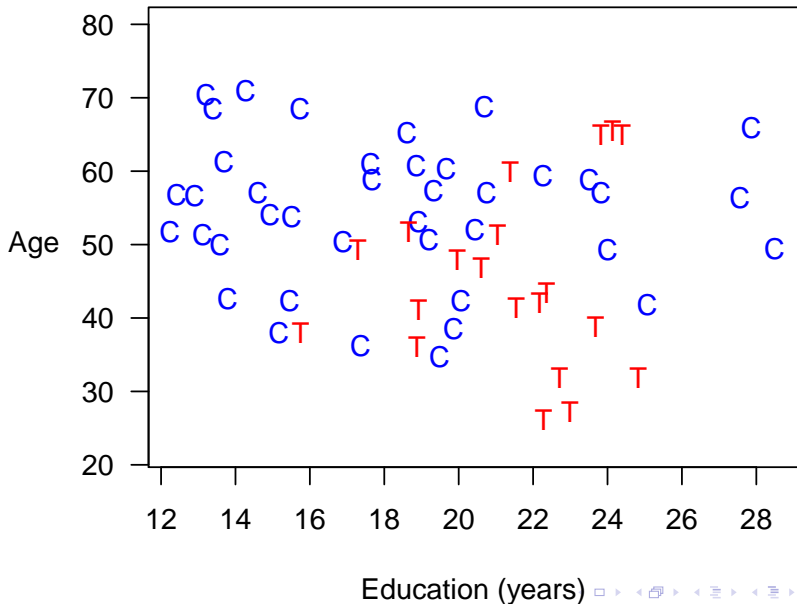
Education (years)



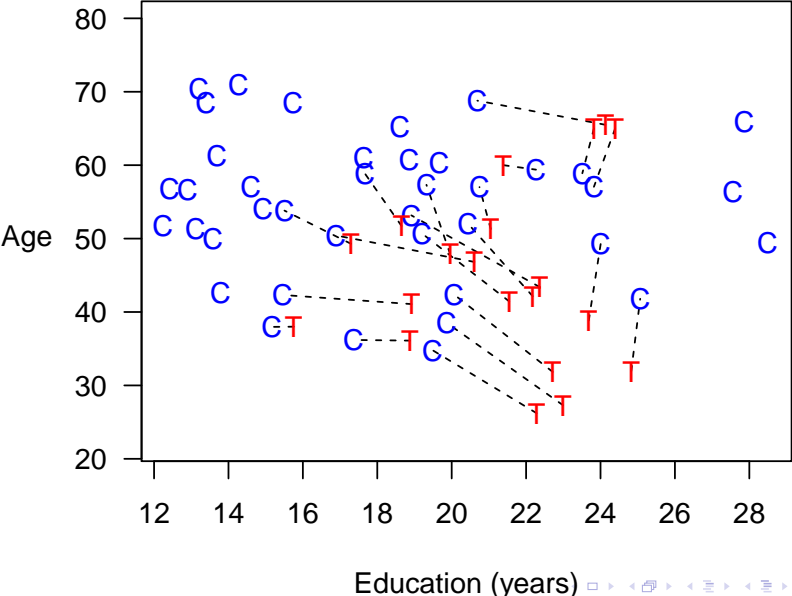
Mahalanobis Distance Matching



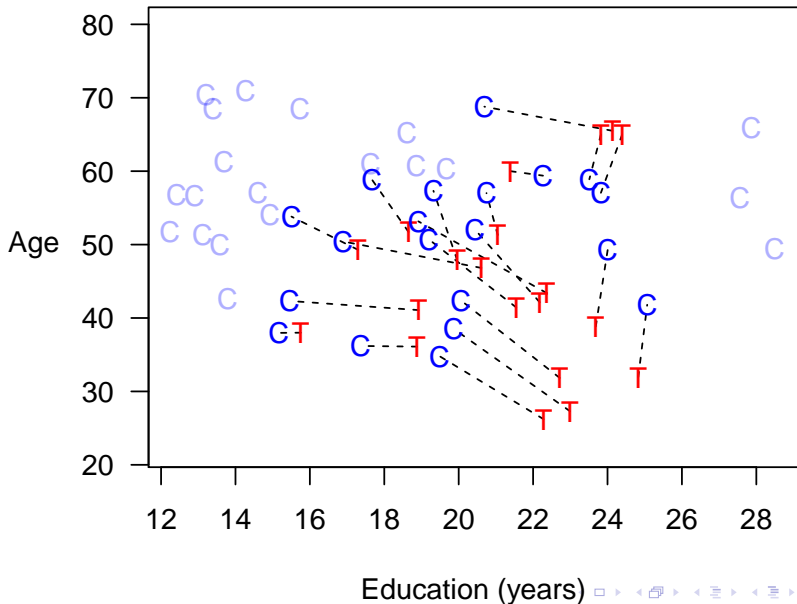
Mahalanobis Distance Matching



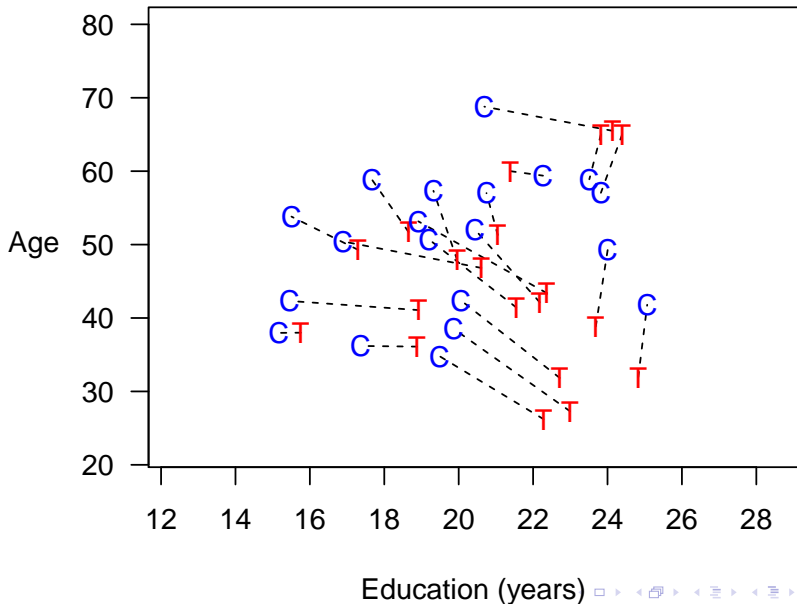
Mahalanobis Distance Matching



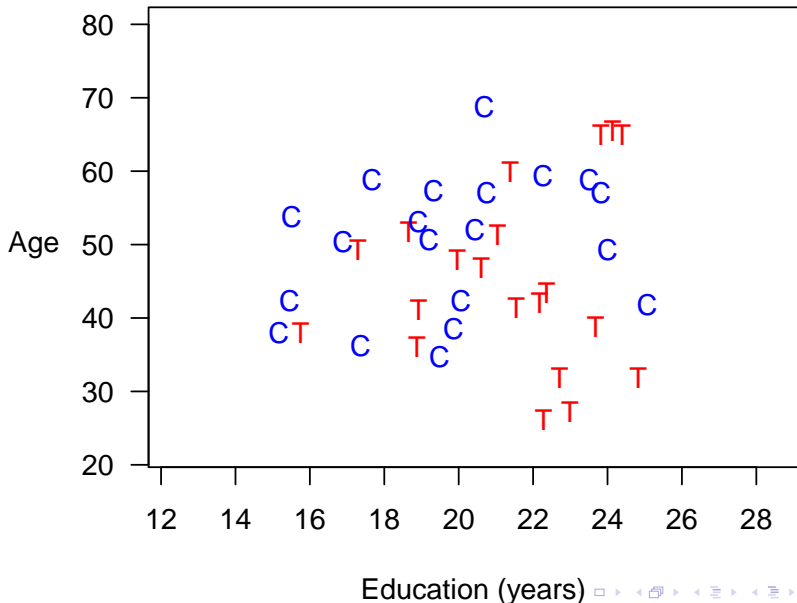
Mahalanobis Distance Matching



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

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

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

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

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

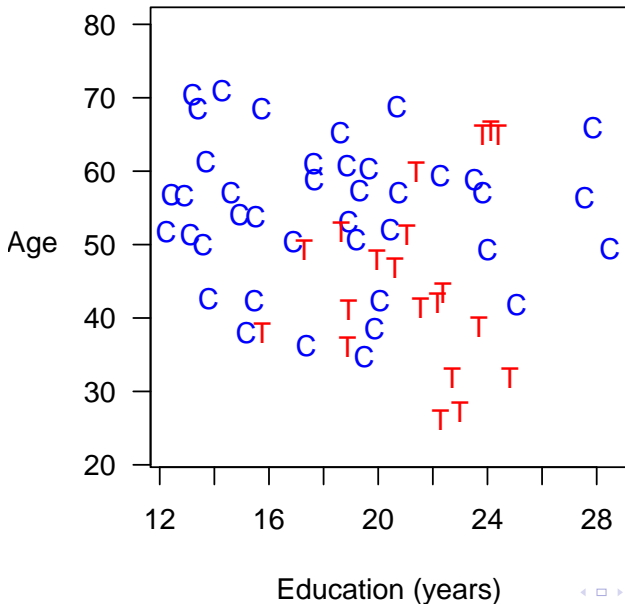
Method 2: Propensity Score Matching

1 Preprocess (Matching)

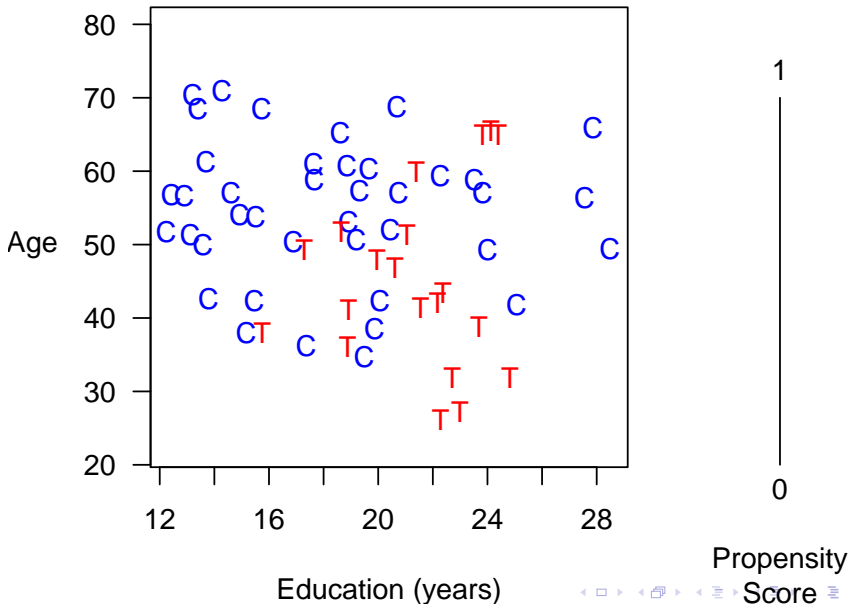
- Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$
- $\text{Distance}(X_i, X_j) = |\pi_i - \pi_j|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$

2 Estimation Difference in means or a model

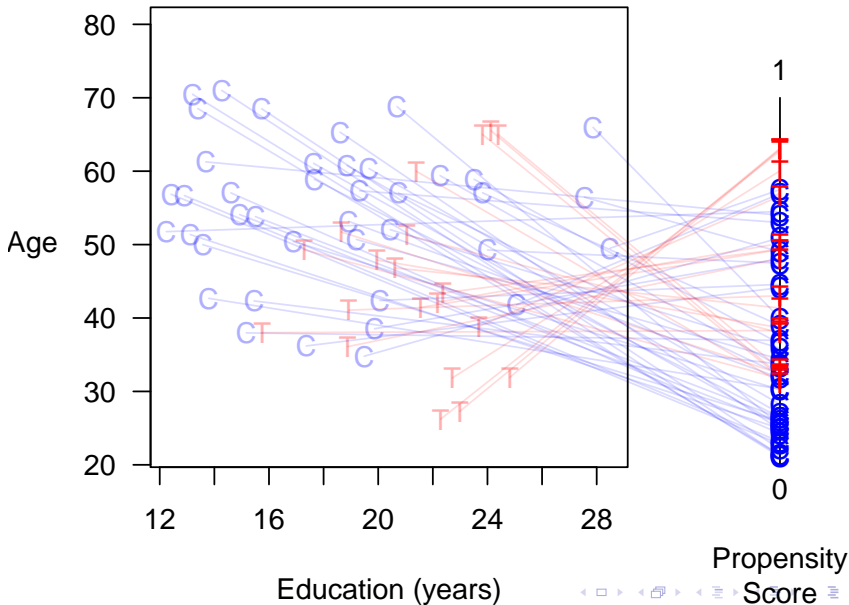
Propensity Score Matching



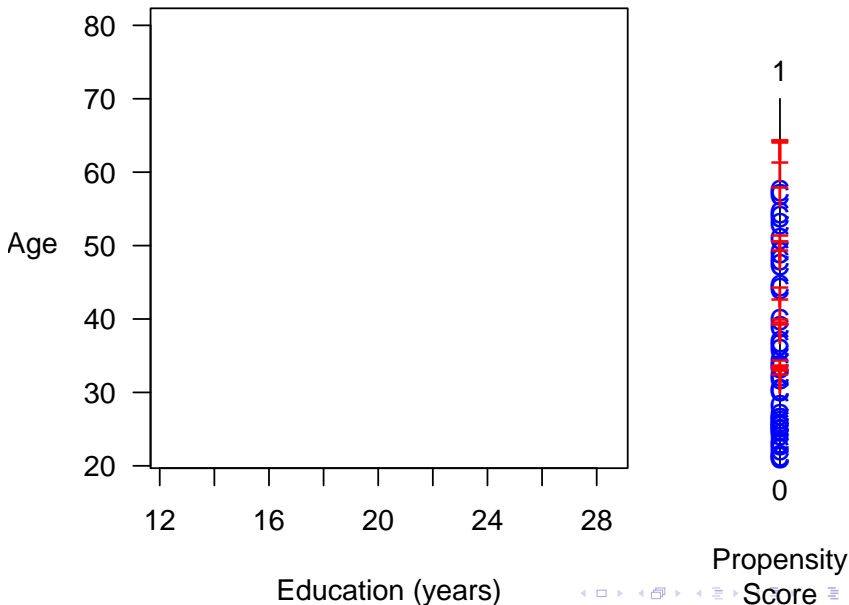
Propensity Score Matching



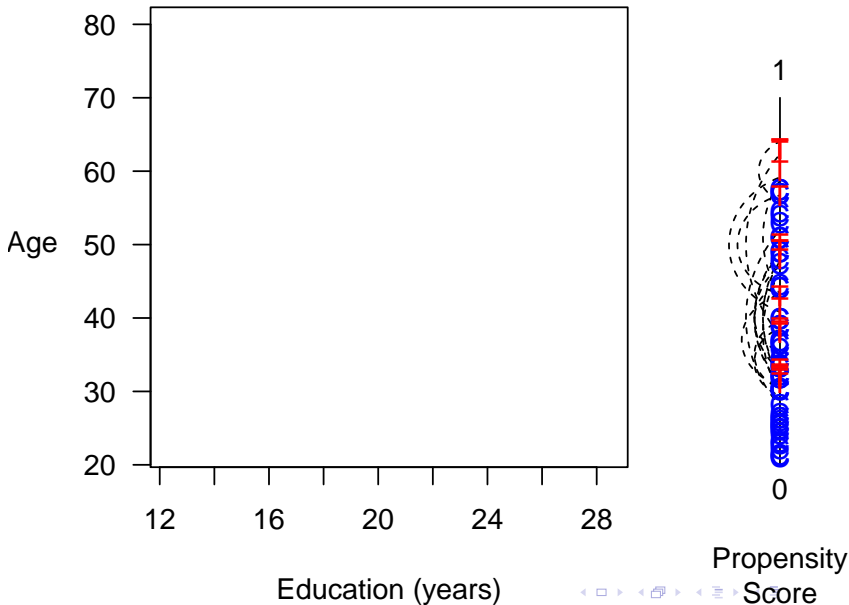
Propensity Score Matching



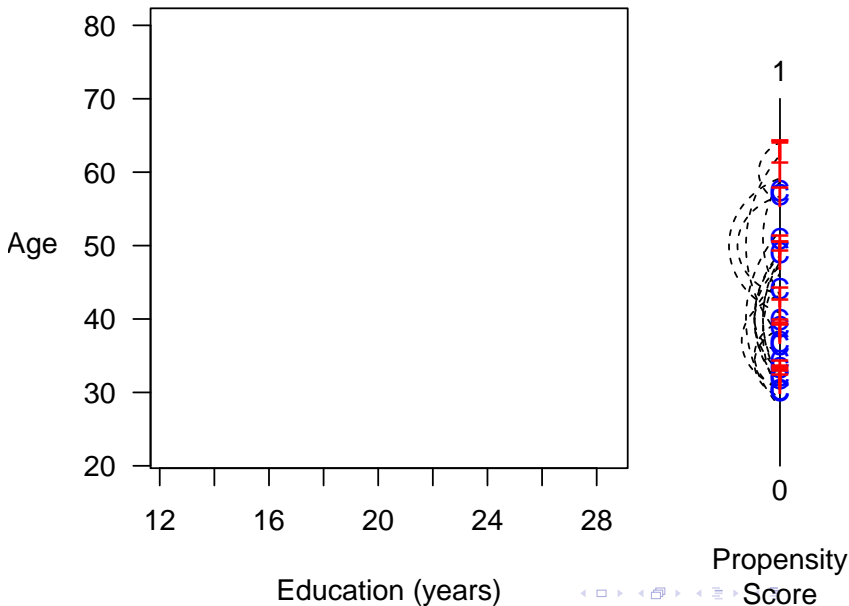
Propensity Score Matching



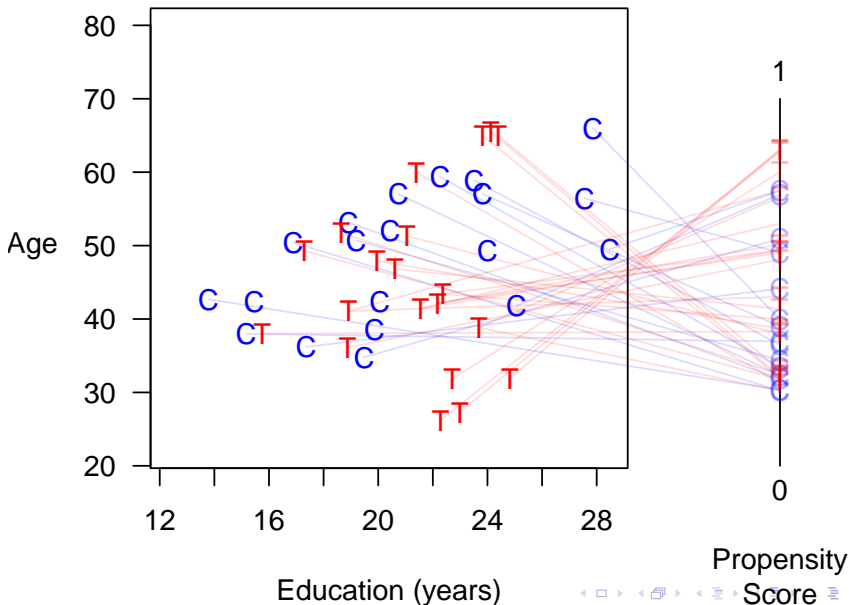
Propensity Score Matching



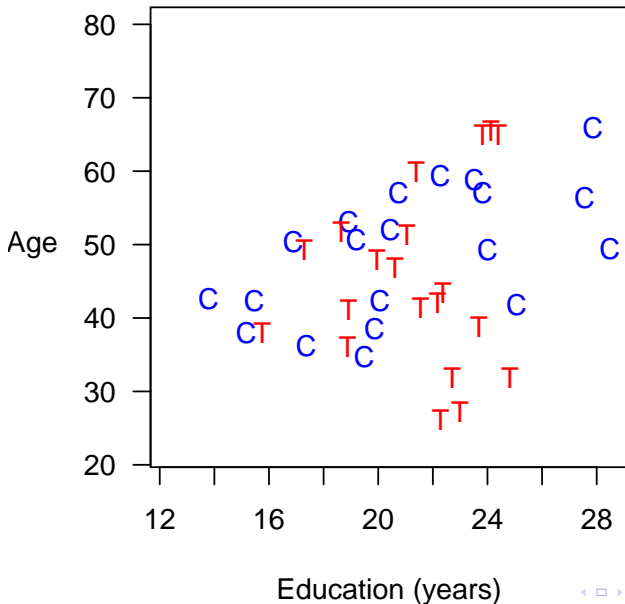
Propensity Score Matching



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

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

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

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

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

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

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

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

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

Method 3: Coarsened Exact Matching

1 Preprocess (Matching)

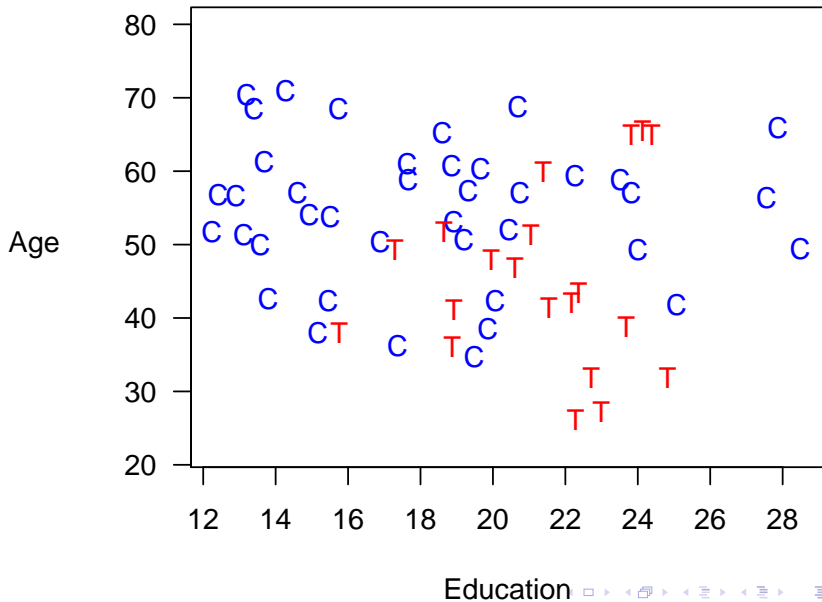
- Temporarily coarsen X as much as you're willing
 - e.g., Education (grade school, high school, college, graduate)
 - Easy to understand, or can be automated as for a histogram
- Apply exact matching to the coarsened X , $C(X)$
 - Sort observations into strata, each with unique values of $C(X)$
 - Prune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

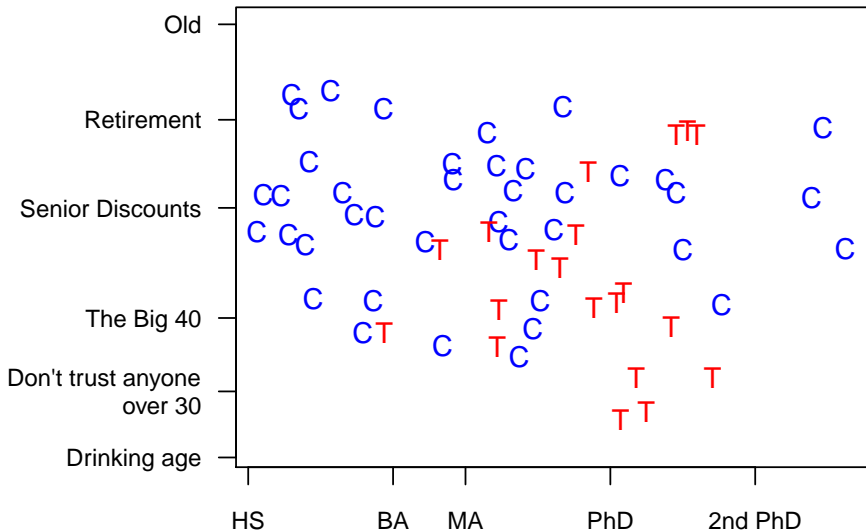
- Need to weight controls in each stratum to equal treateds
- Can apply other matching methods within CEM strata (inherit CEM's properties)

Coarsened Exact Matching

Coarsened Exact Matching



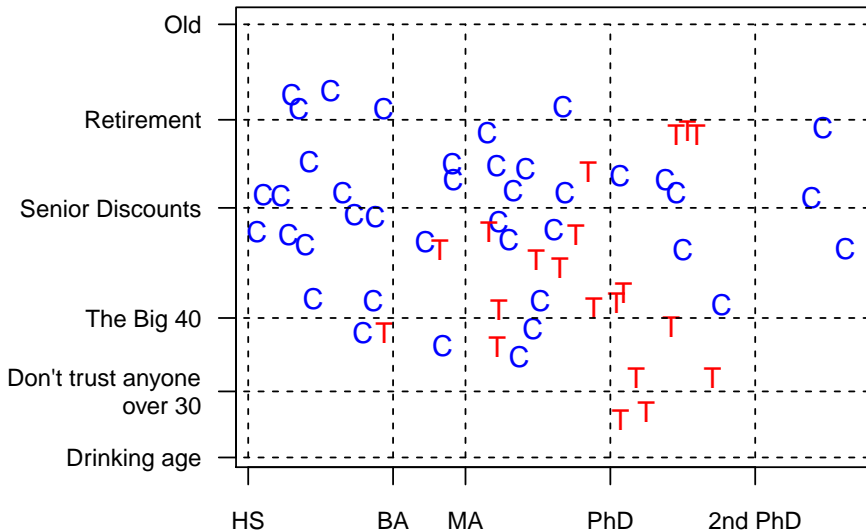
Coarsened Exact Matching



Education



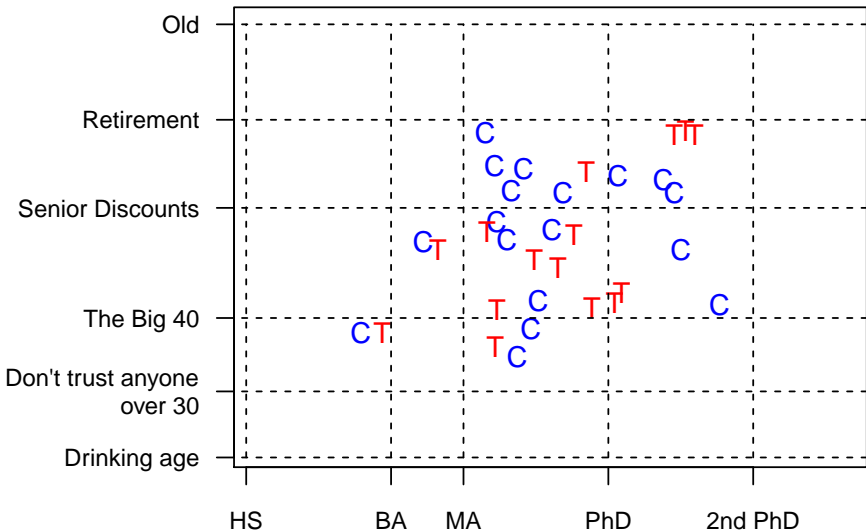
Coarsened Exact Matching



Education

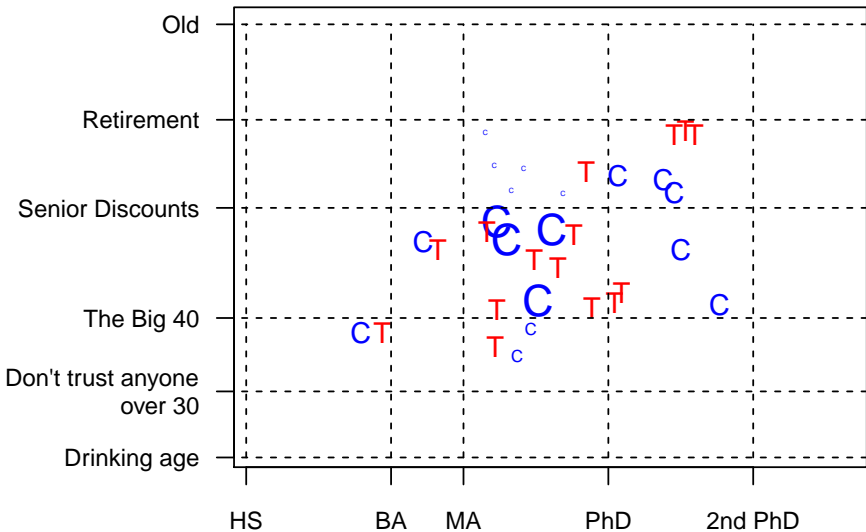


Coarsened Exact Matching



Education

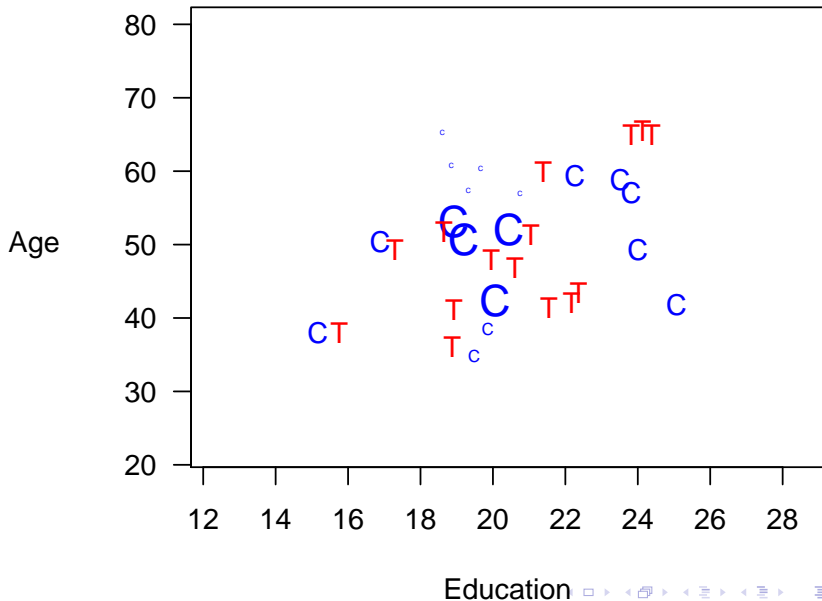
Coarsened Exact Matching



Education



Coarsened Exact Matching



The Bias-Variance Trade Off in Matching

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
 \rightsquigarrow we measure **imbalance** instead

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
↪ we measure **imbalance** instead
- **Variance** = $f(\text{matched sample size}, \text{estimator})$
↪ we measure **matched sample size** instead

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
↪ we measure **imbalance** instead
- **Variance** = $f(\text{matched sample size}, \text{estimator})$
↪ we measure **matched sample size** instead
- **Bias-Variance trade off** ↪ **Imbalance- n Trade Off**

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
↪ we measure **imbalance** instead
- **Variance** = $f(\text{matched sample size}, \text{estimator})$
↪ we measure **matched sample size** instead
- **Bias-Variance trade off** ↪ **Imbalance- n Trade Off**
- Measuring Imbalance

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
↪ we measure **imbalance** instead
- **Variance** = $f(\text{matched sample size}, \text{estimator})$
↪ we measure **matched sample size** instead
- **Bias-Variance trade off** ↪ **Imbalance- n Trade Off**
- Measuring Imbalance
 - Classic measure: Difference of means (for each variable)

The Bias-Variance Trade Off in Matching

- **Bias** (& model dependence) = $f(\text{imbalance}, \text{importance}, \text{estimator})$
 \rightsquigarrow we measure **imbalance** instead
- **Variance** = $f(\text{matched sample size}, \text{estimator})$
 \rightsquigarrow we measure **matched sample size** instead
- **Bias-Variance trade off** \rightsquigarrow **Imbalance- n Trade Off**
- Measuring Imbalance
 - Classic measure: Difference of means (for each variable)
 - Better measure (difference of multivariate histograms):

$$\mathcal{L}_1(f, g; H) = \frac{1}{2} \sum_{\ell_1 \dots \ell_k \in H(\mathbf{X})} |f_{\ell_1 \dots \ell_k} - g_{\ell_1 \dots \ell_k}|$$

Comparing Matching Methods

Comparing Matching Methods

- MDM & PSM: Choose matched n , match, check imbalance

Comparing Matching Methods

- MDM & PSM: Choose matched n , match, check imbalance
- CEM: Choose imbalance, match, check matched n

Comparing Matching Methods

- MDM & PSM: Choose matched n , match, check imbalance
- CEM: Choose imbalance, match, check matched n
- Best practice: iterate

Comparing Matching Methods

- MDM & PSM: Choose matched n , match, check imbalance
- CEM: Choose imbalance, match, check matched n
- Best practice: iterate
- Choose matched solution & matching method becomes irrelevant

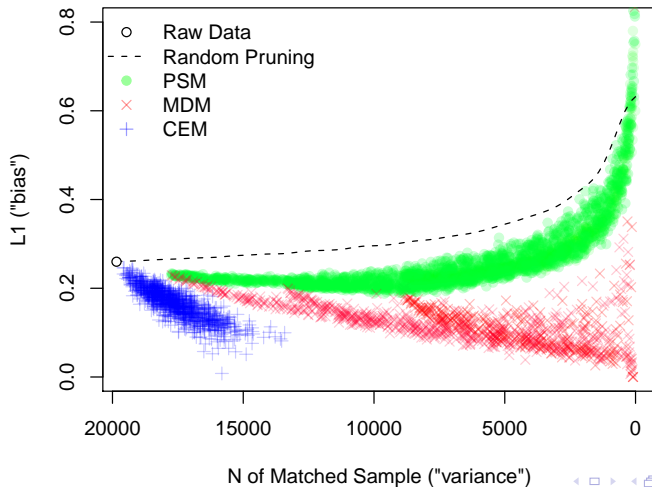
Comparing Matching Methods

- MDM & PSM: Choose matched n , match, check imbalance
- CEM: Choose imbalance, match, check matched n
- Best practice: iterate
- Choose matched solution & matching method becomes irrelevant
- Our idea: Compute lots of matching solutions, identify the frontier of lowest imbalance for each given n , and choose a matching solution

A Space Graph: Real Data

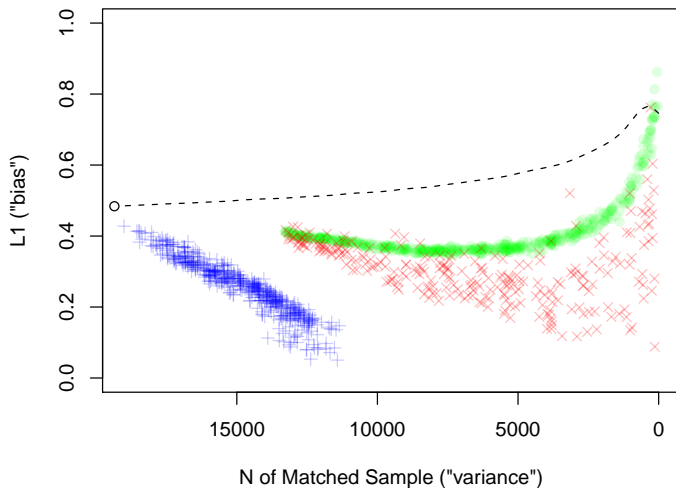
King, Nielsen, Coberley, Pope, and Wells (2011)

Healthways Data



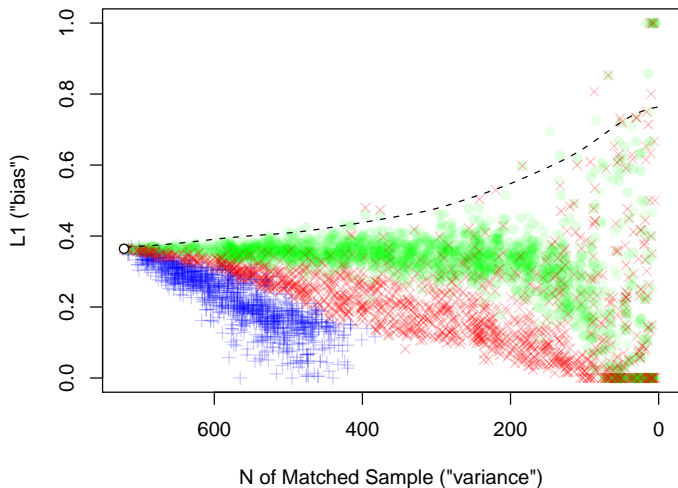
A Space Graph: Real Data

Called/Not Called Data

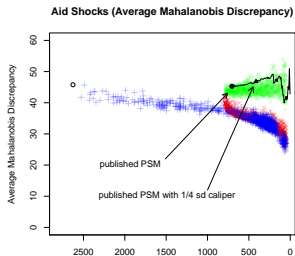
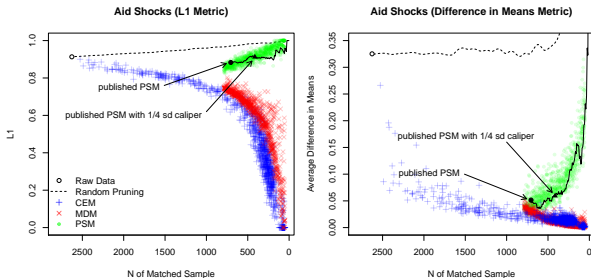


A Space Graph: Real Data

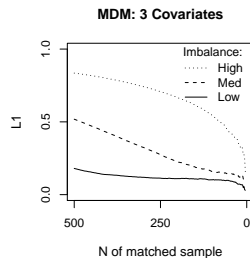
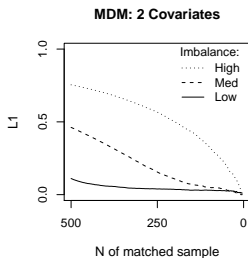
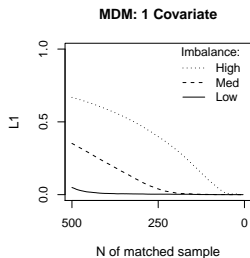
Lalonde Data Subset



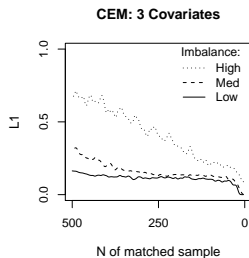
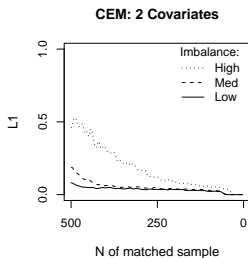
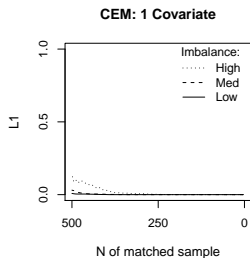
Space Graphs: Different Imbalance Metrics



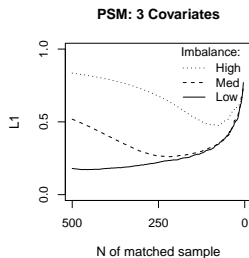
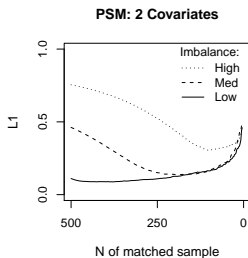
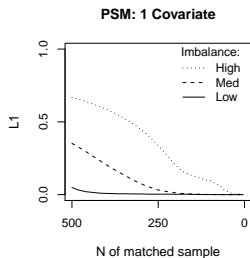
A Space Graph: Simulated Data — Mahalanobis



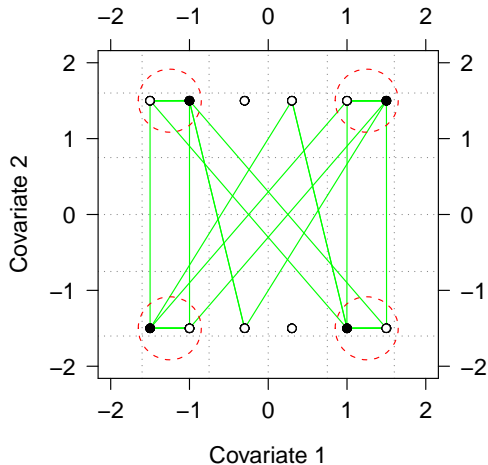
A Space Graph: Simulated Data — CEM



A Space Graph: Simulated Data — Propensity Score



PSM Approximates Random Matching in Balanced Data



- PSM Matches
- - - CEM and MDM Matches

CEM Weights and Nonparametric Propensity Score

CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (+ normalization)

CEM Weights and Nonparametric Propensity Score

CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (+ normalization)

CEM Pscore: $\hat{\Pr}(T_i = 1|X_i) = \frac{m_i^T}{m_i^T + m_i^C}$

CEM Weights and Nonparametric Propensity Score

CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (+ normalization)

CEM Pscore: $\hat{\Pr}(T_i = 1|X_i) = \frac{m_i^T}{m_i^T + m_i^C}$

⇒ CEM:

CEM Weights and Nonparametric Propensity Score

CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (+ normalization)

CEM Pscore: $\hat{\Pr}(T_i = 1|X_i) = \frac{m_i^T}{m_i^T + m_i^C}$

⇒ CEM:

- Gives a better pscore than PSM

CEM Weights and Nonparametric Propensity Score

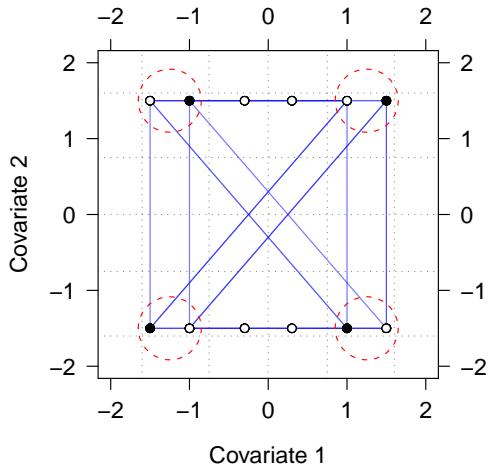
CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (+ normalization)

CEM Pscore: $\hat{\Pr}(T_i = 1|X_i) = \frac{m_i^T}{m_i^T + m_i^C}$

⇒ CEM:

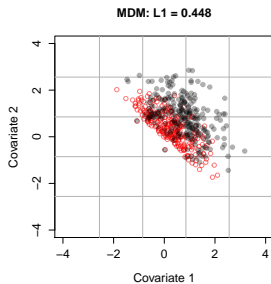
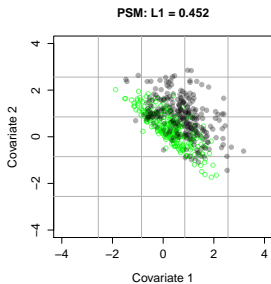
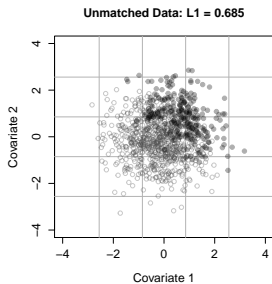
- Gives a better pscore than PSM
- Doesn't match based on crippled information

Destroying CEM with PSM's Two Step Approach

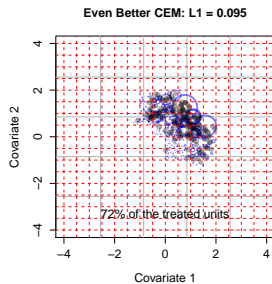
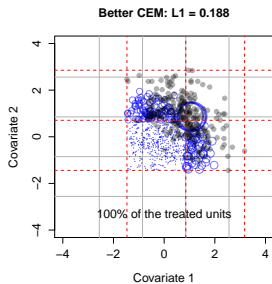
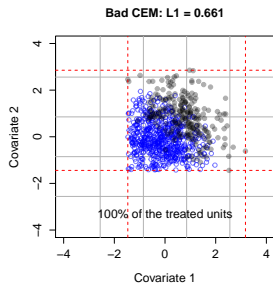


- CEM Matches
- CEM-generated PSM Matches

Data where PSM Works Reasonably Well — PSM & MDM



Data where PSM Works Reasonably Well — CEM



Conclusions

Conclusions

- Propensity score matching:

Conclusions

- Propensity score matching:
 - The problem:

Conclusions

- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data

Conclusions

- Propensity score matching:
 - The problem:
 - Imbalance can be worse than original data
 - Can increase imbalance when removing the worst matches

Conclusions

- 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

- 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)
 - The Cause: unnecessary 1st stage dimension reduction

Conclusions

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - Implications:

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - Implications:
 - Balance checking required

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - Implications:
 - Balance checking required
 - Adjusting for potentially irrelevant covariates *with PSM*: mistake
 - Adjusting experimental data *with PSM*: mistake

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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
- In four data sets and many simulations:
CEM > Mahalanobis > Propensity Score

Conclusions

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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
- In four data sets and many simulations:
CEM > Mahalanobis > Propensity Score
- (Your performance may vary)

Conclusions

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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
- In four data sets and many simulations:
CEM > Mahalanobis > Propensity Score
- (Your performance may vary)
- CEM and Mahalanobis do not have PSM's problems

Conclusions

- 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)
 - The Cause: unnecessary 1st stage dimension reduction
 - 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
- In four data sets and many simulations:
CEM > Mahalanobis > Propensity Score
- (Your performance may vary)
- CEM and Mahalanobis do not have PSM's problems
- You can easily check with the Space Graph

For papers, software (for R, Stata, & SPSS), tutorials, etc.



<http://GKing.Harvard.edu/cem>