Simplifying Causal Inference

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(Talk at the Center for Population and Development Studies, Harvard University, 11/8/2012)

Overview

- Problem: Model dependence (review)

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- Solution: Matching to preprocess data (review)

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- Solution: Other methods do not share this problem
- (Coarsened Exact Matching is simple, easy, and powerful)
- $\rightsquigarrow$ Lots of insights revealed in the process

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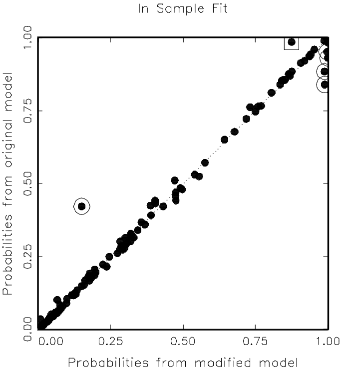
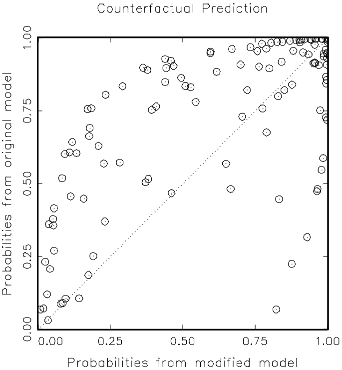
- Data analysis: Logit model
- The question: How *model dependent* are the results?

Two Logit Models, Apparently Similar Results

	Original "Interactive" Model			Modified Model		
Variables	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





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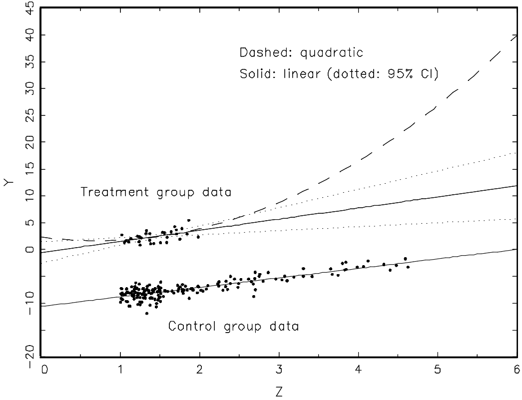

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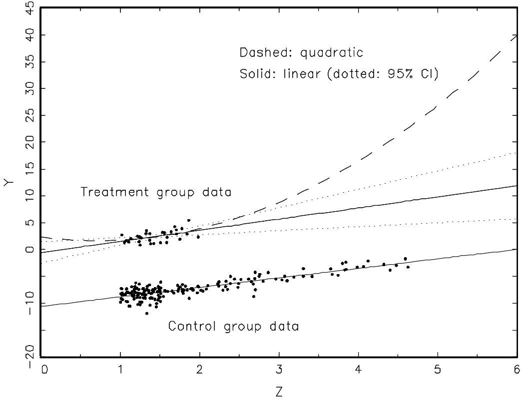

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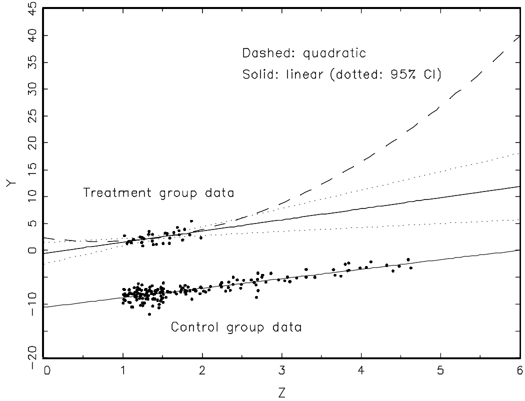

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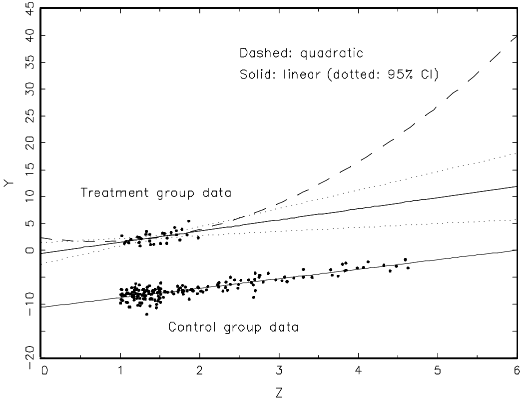

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- Preprocess II: Match (prune bad matches) within interpolation region

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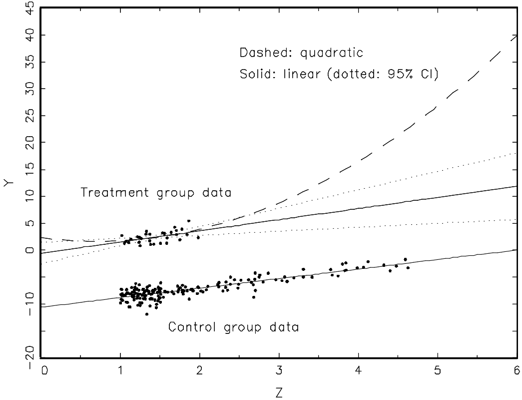

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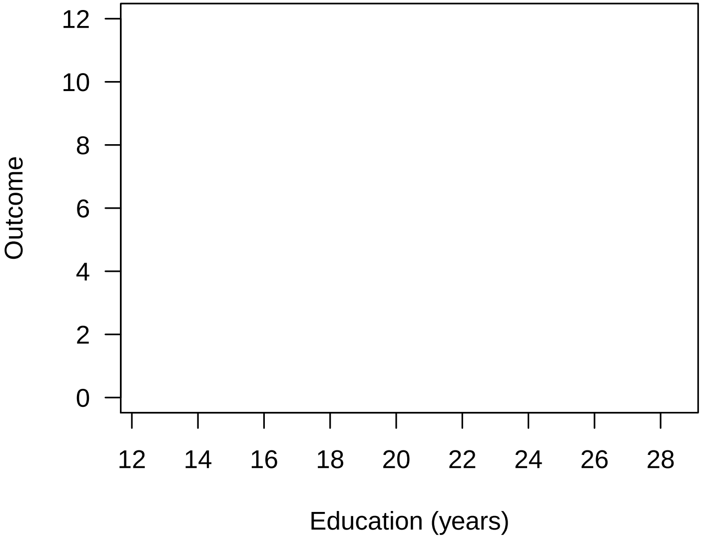
- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

Matching within the Interpolation Region

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



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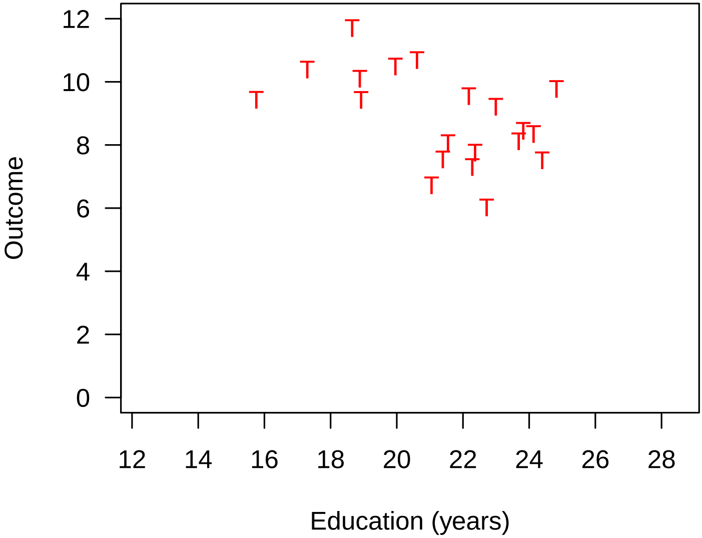

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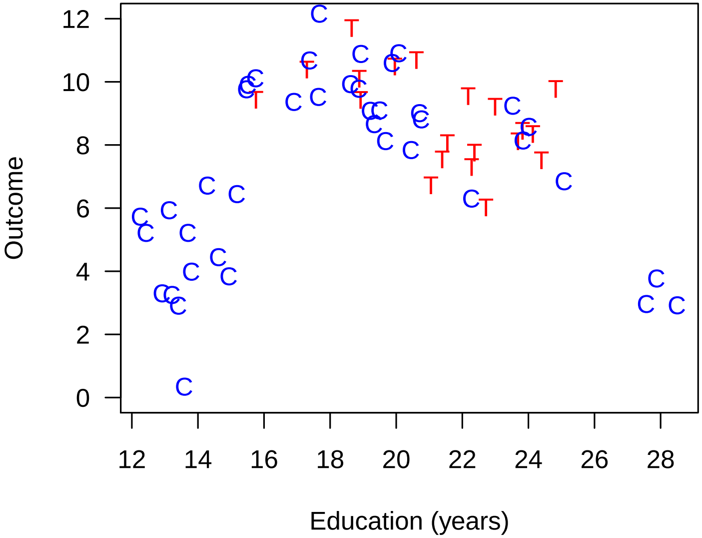

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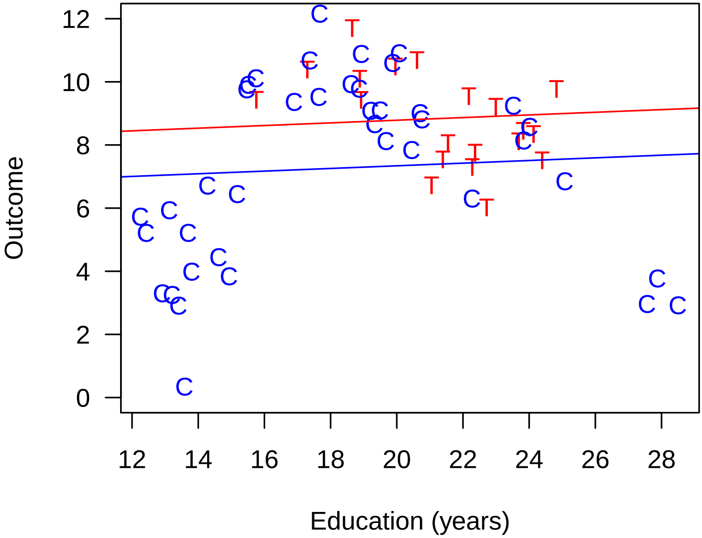

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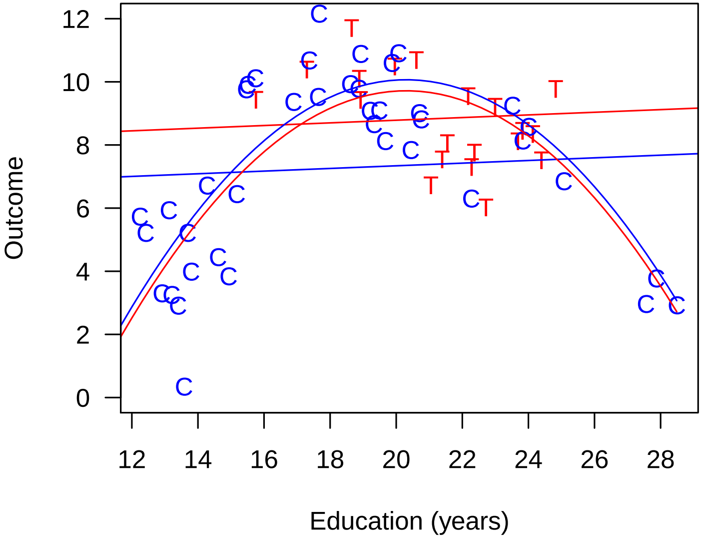

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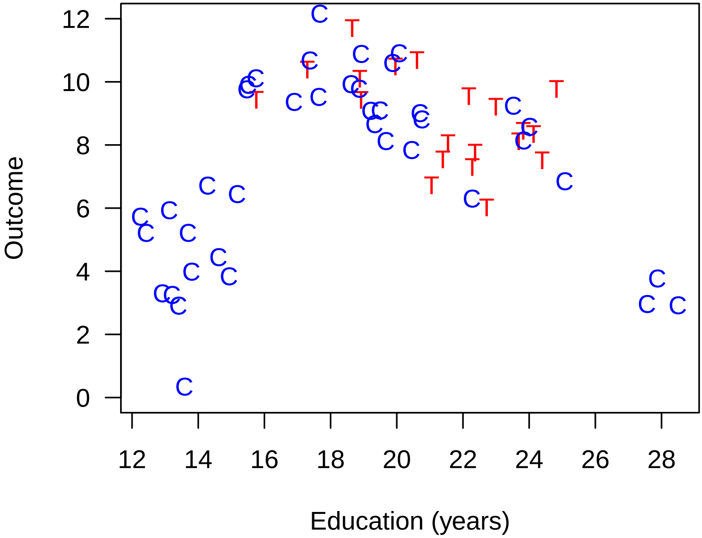

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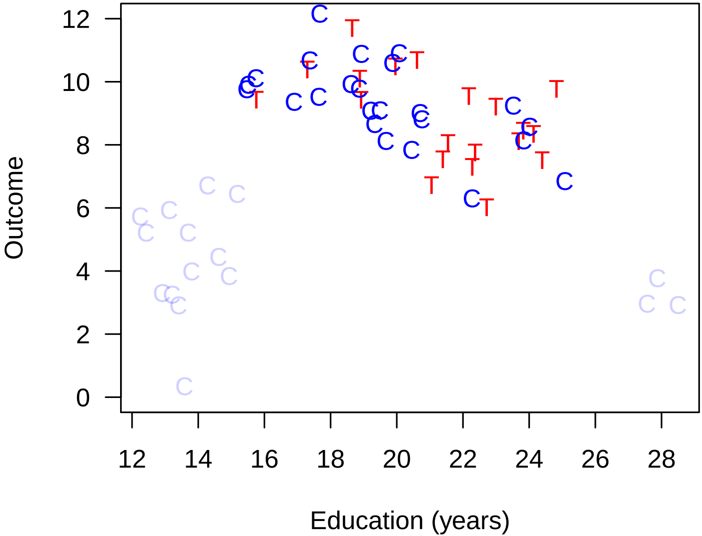

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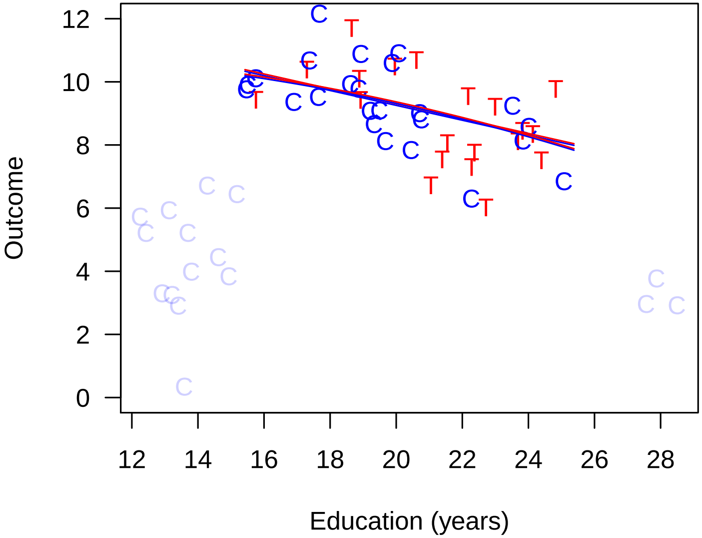

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Matching reduces model dependence, bias, and variance

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- Estimate ${\color{red}Y_i(T_i = 0)}$ with Y_j from matched ($X_i \approx X_j$) controls
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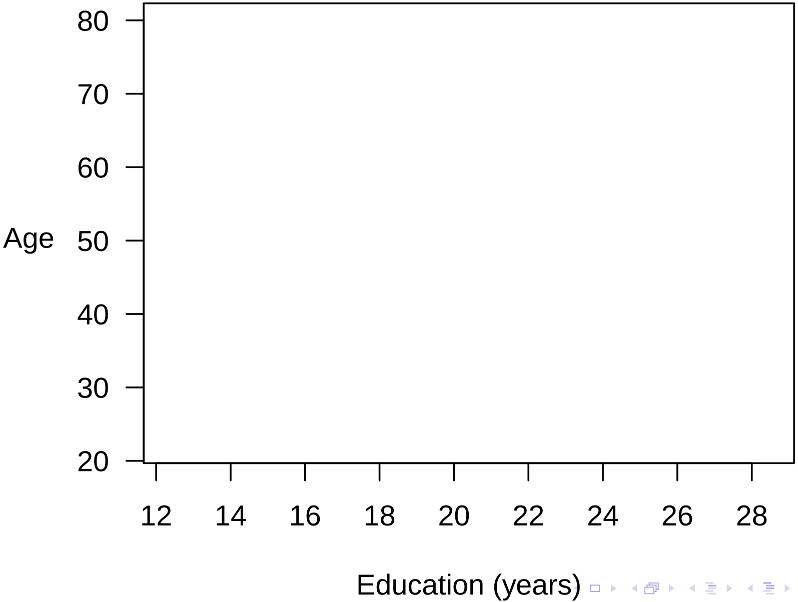

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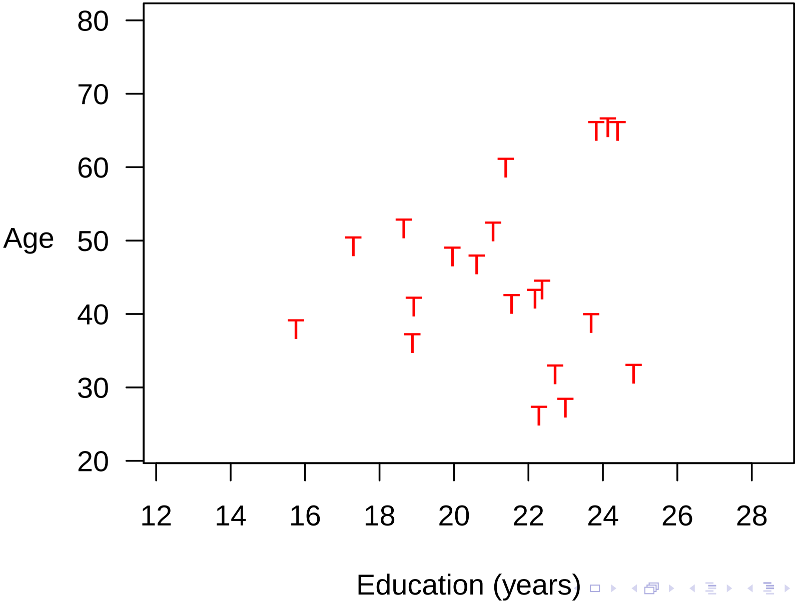

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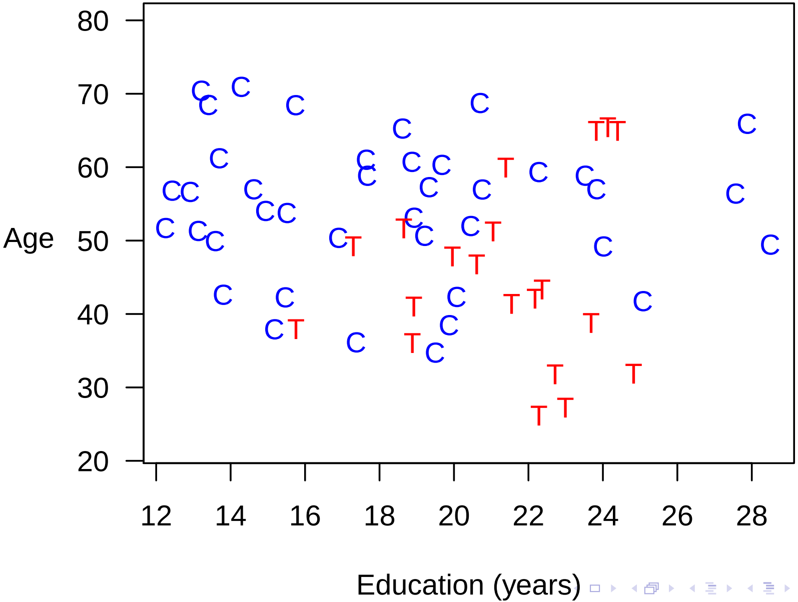

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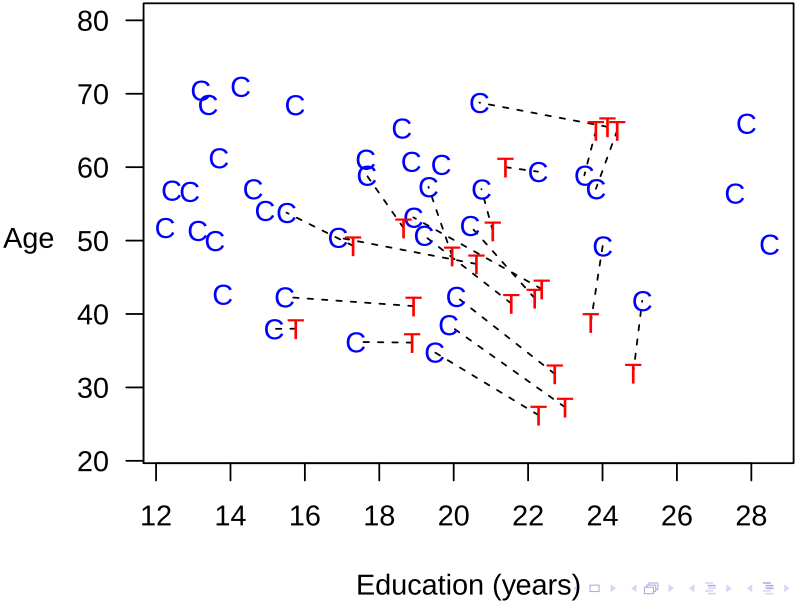

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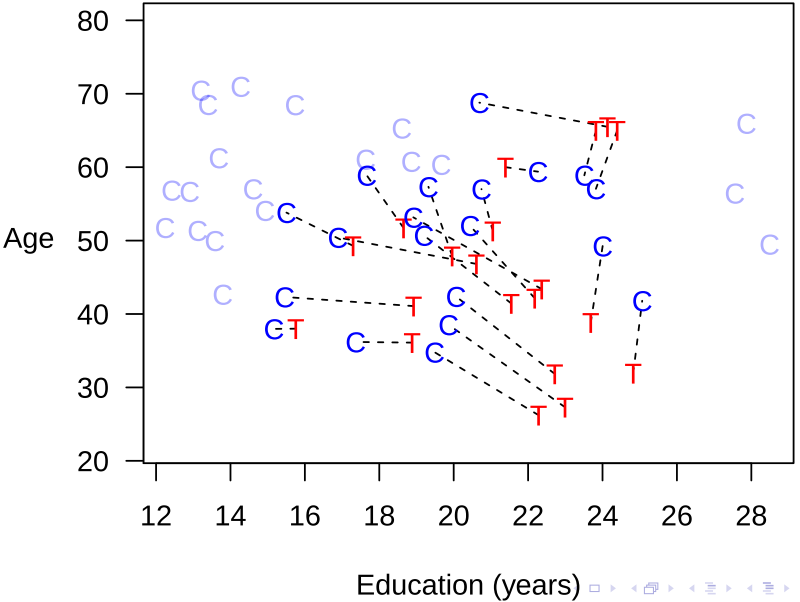

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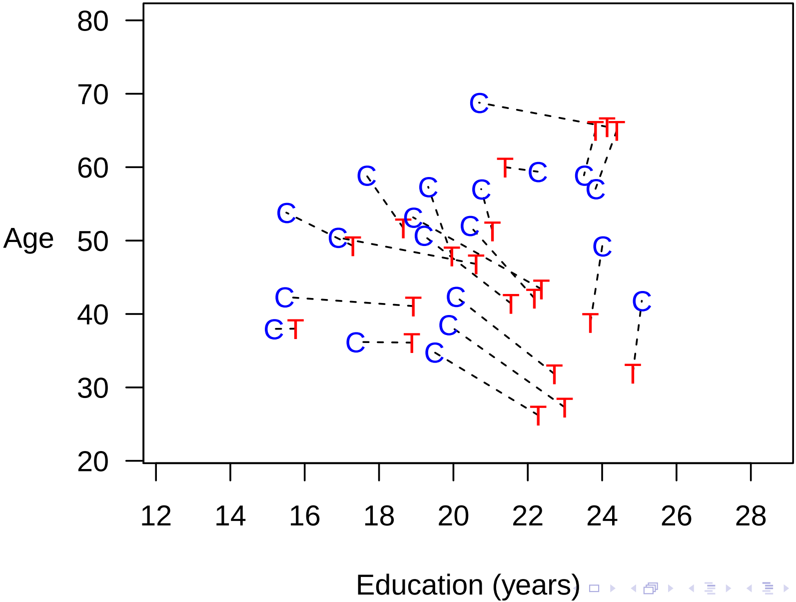

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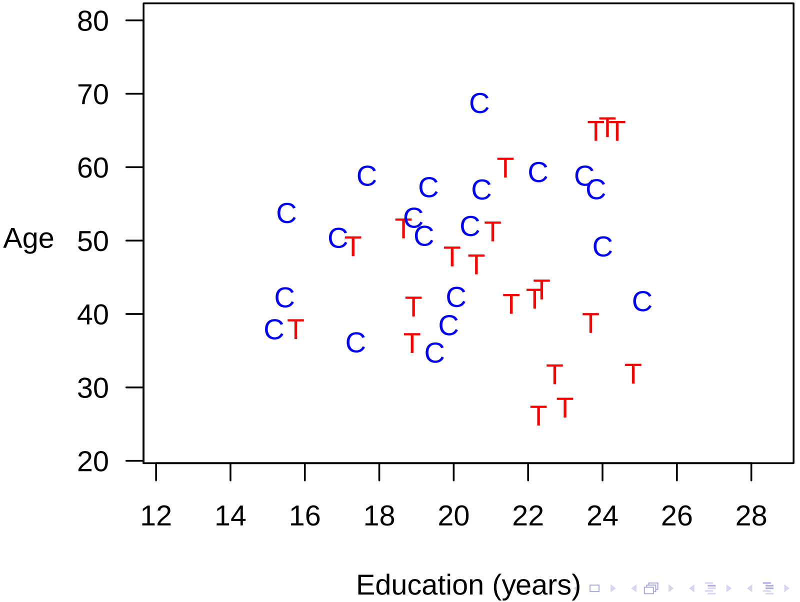

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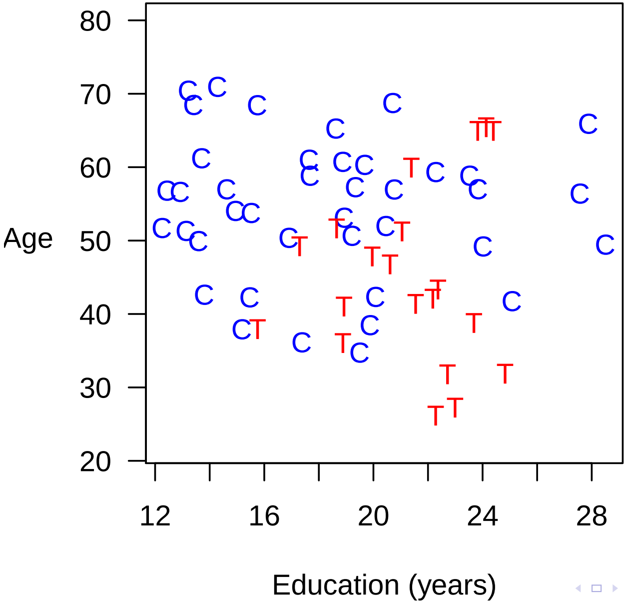

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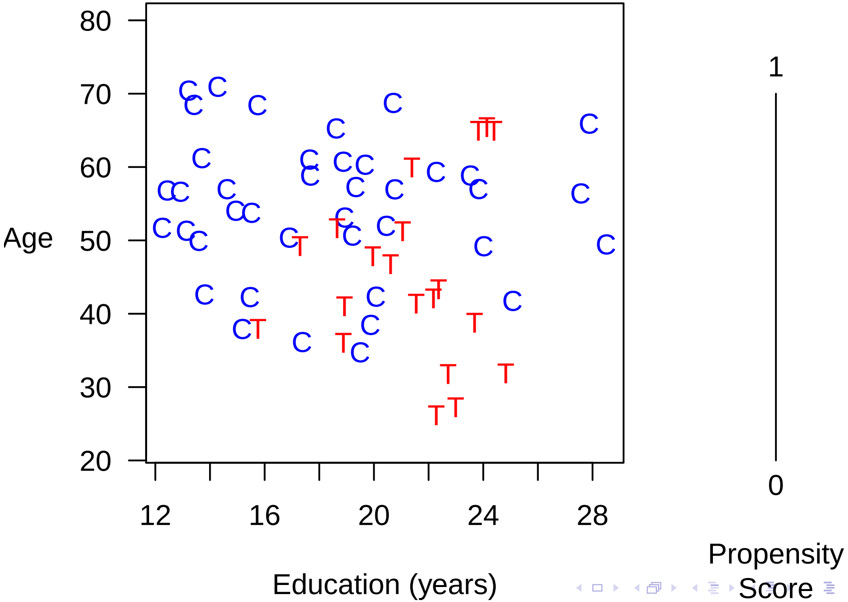

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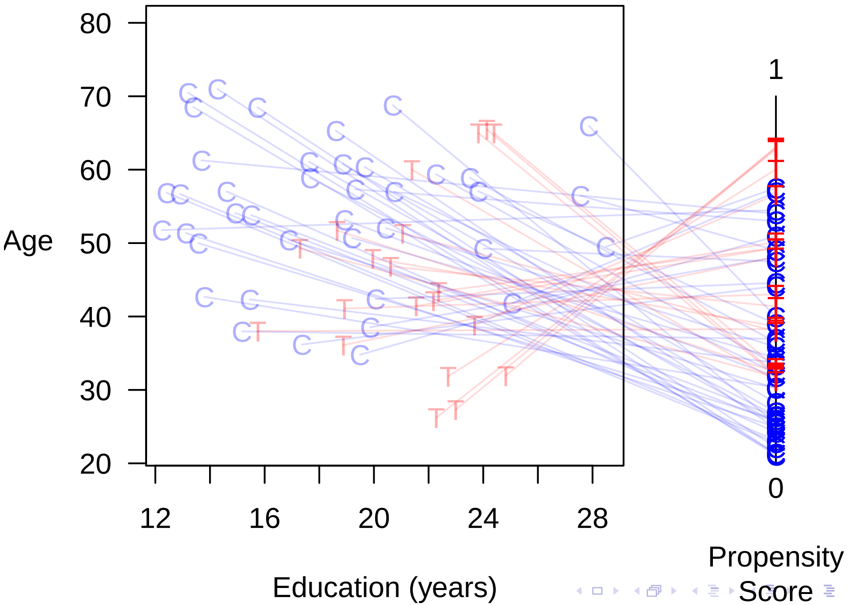

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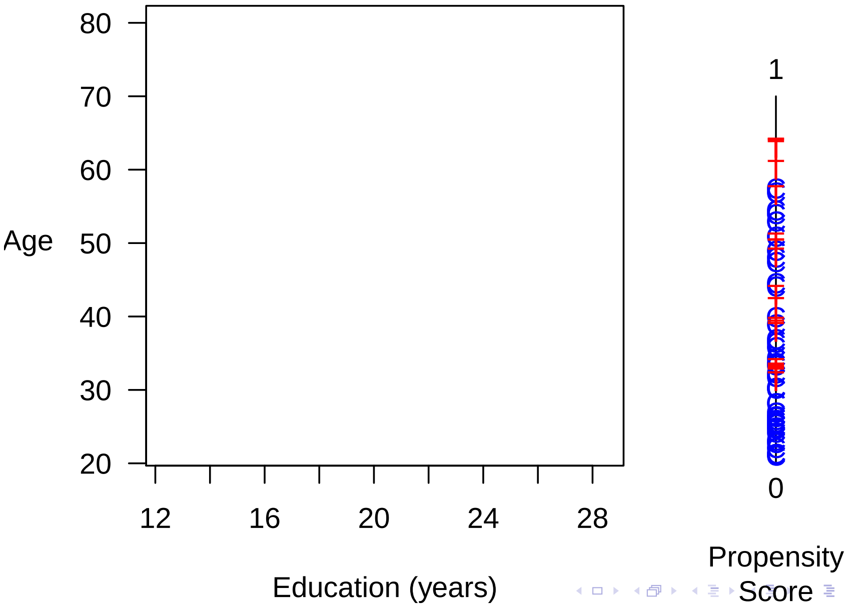

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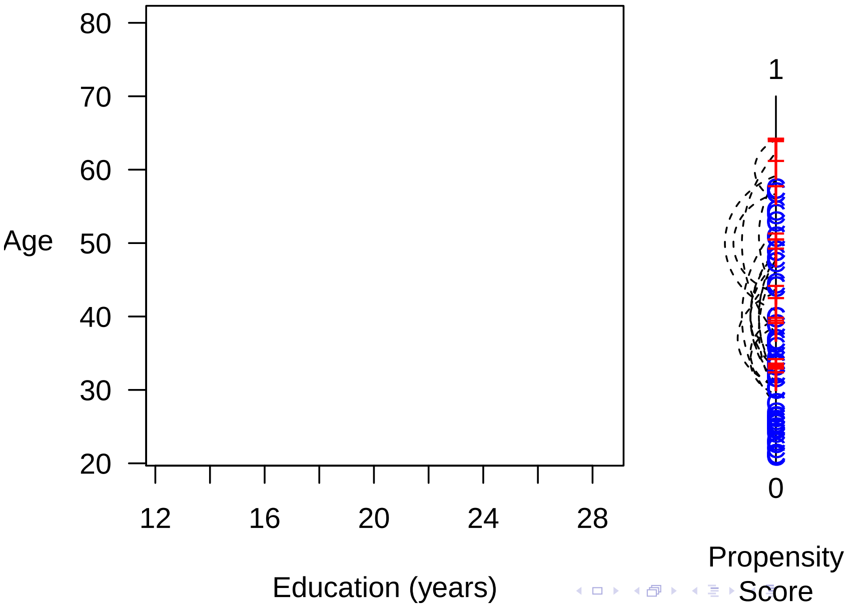

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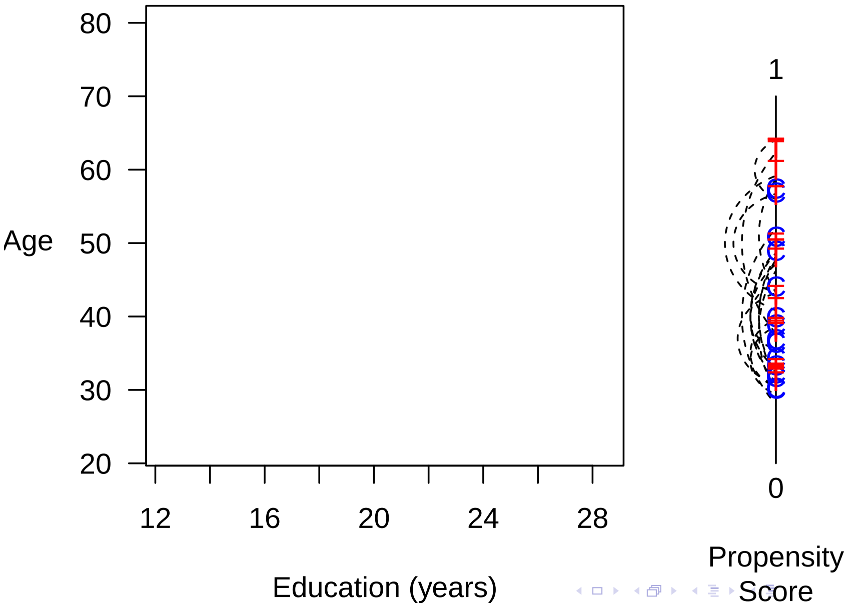

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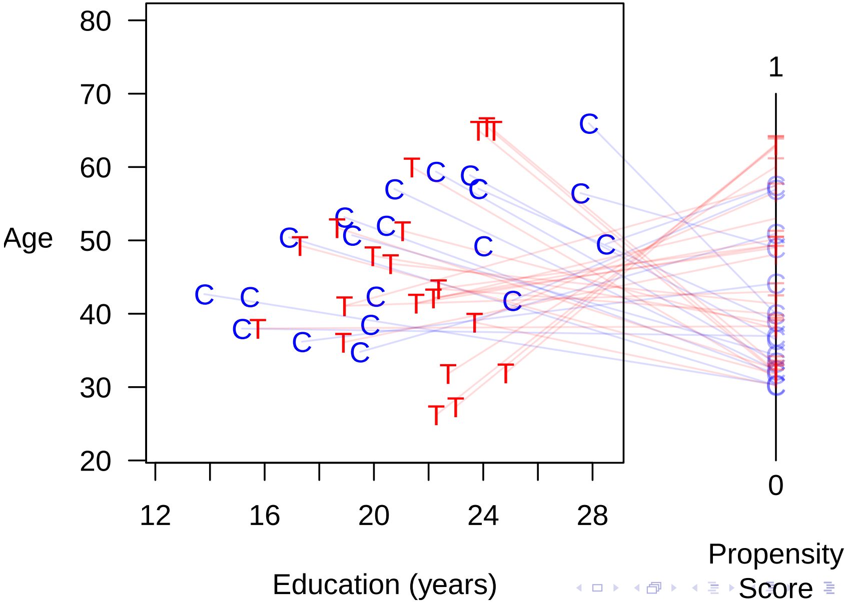

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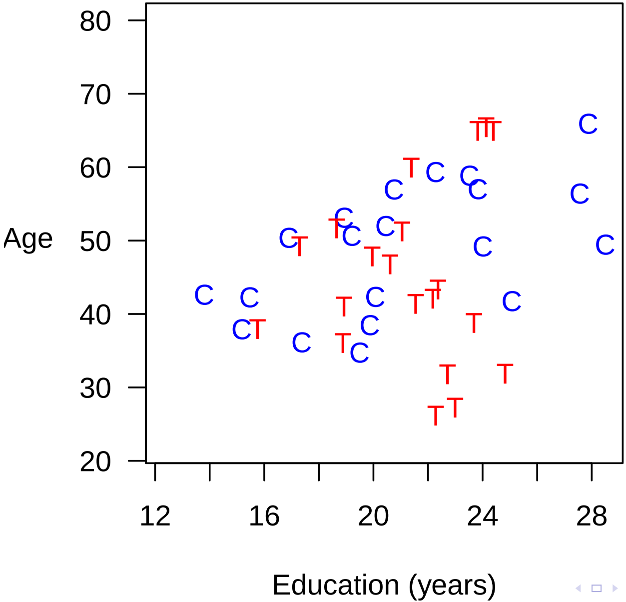

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   - Can apply other matching methods within CEM strata (inherit CEM's properties)

Coarsened Exact Matching

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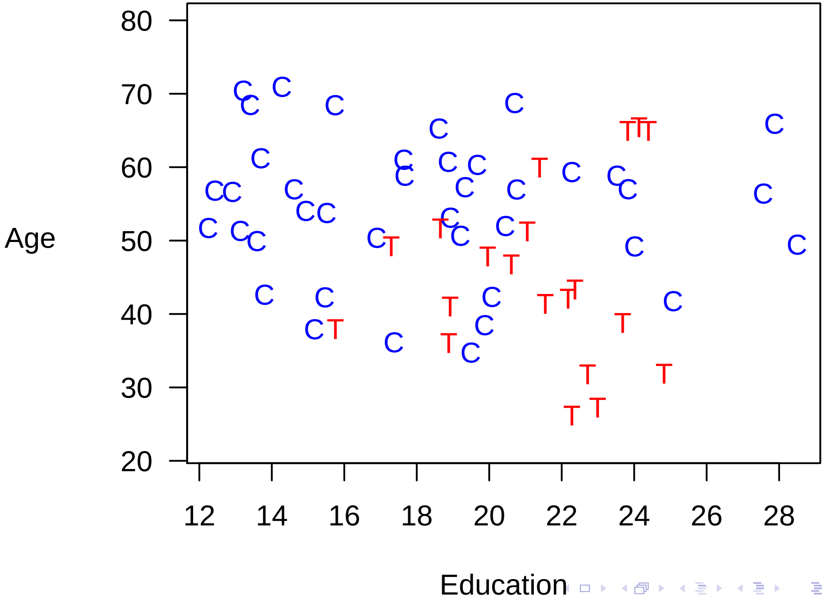

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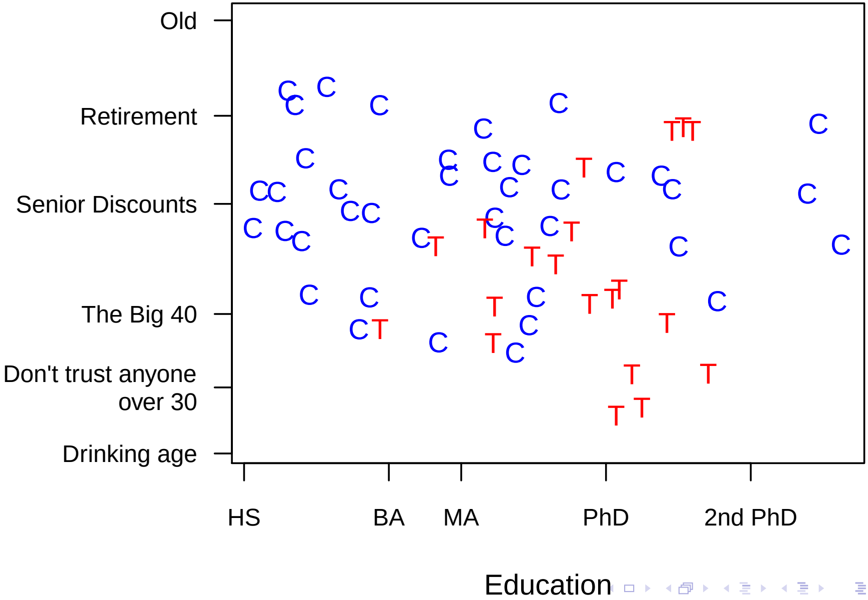

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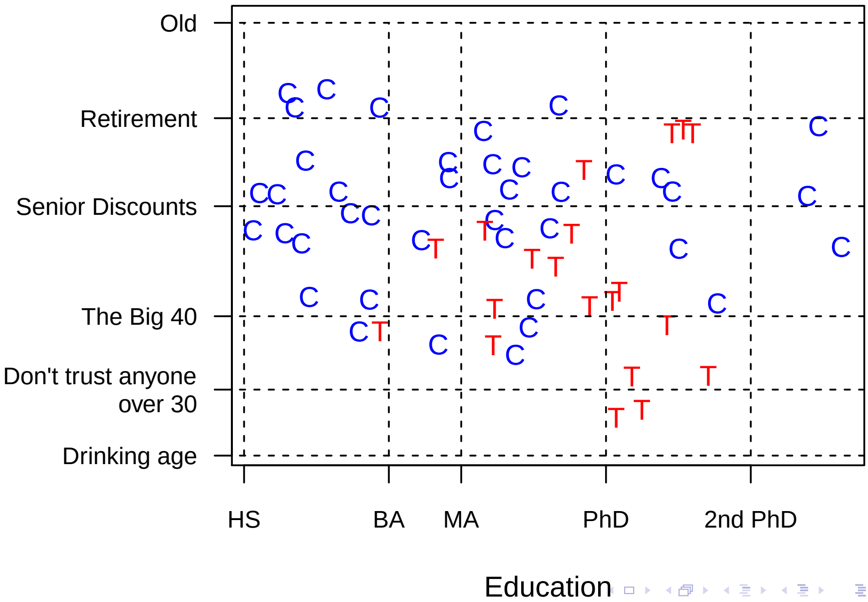

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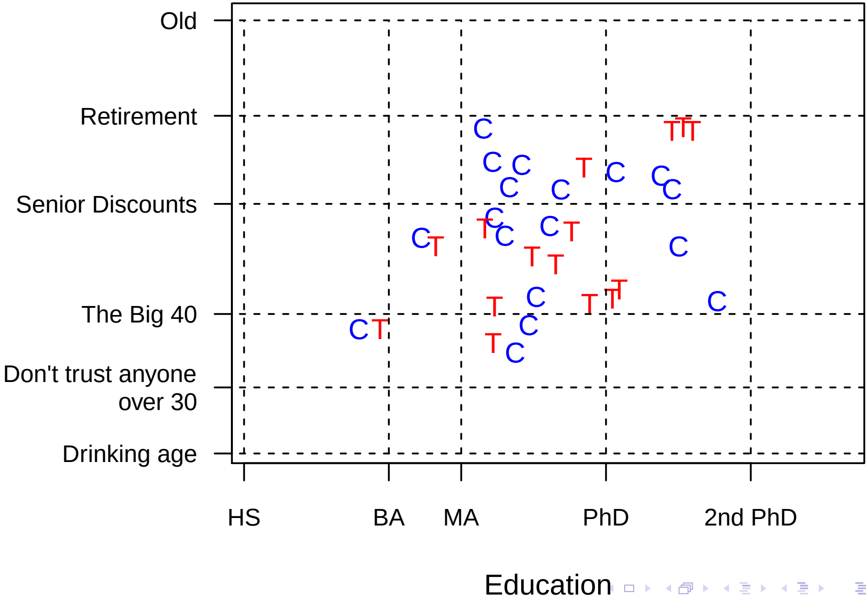

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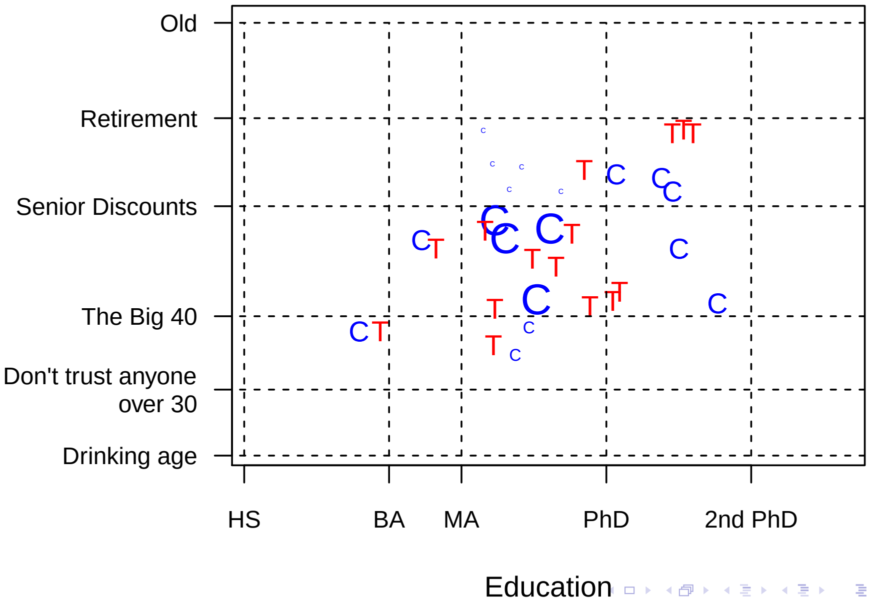

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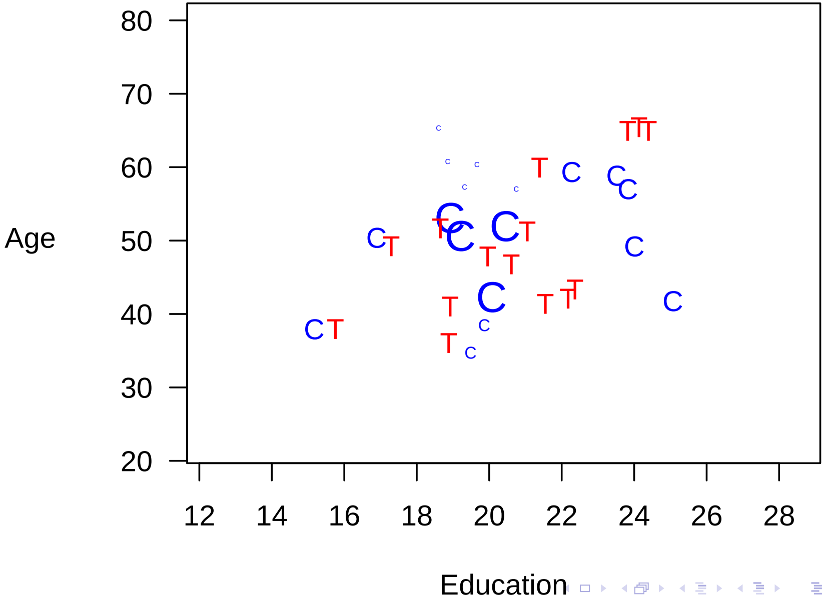

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  - Classic measure: Difference of means (for each variable)
  - Better measure (difference of multivariate histograms):

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

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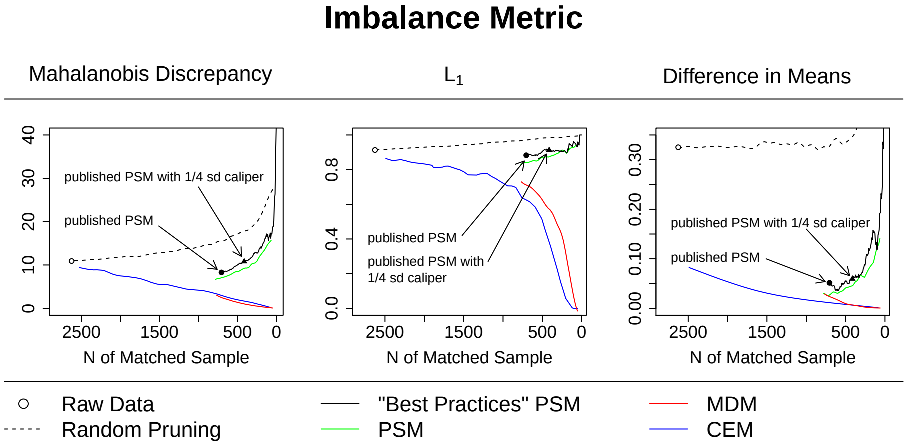
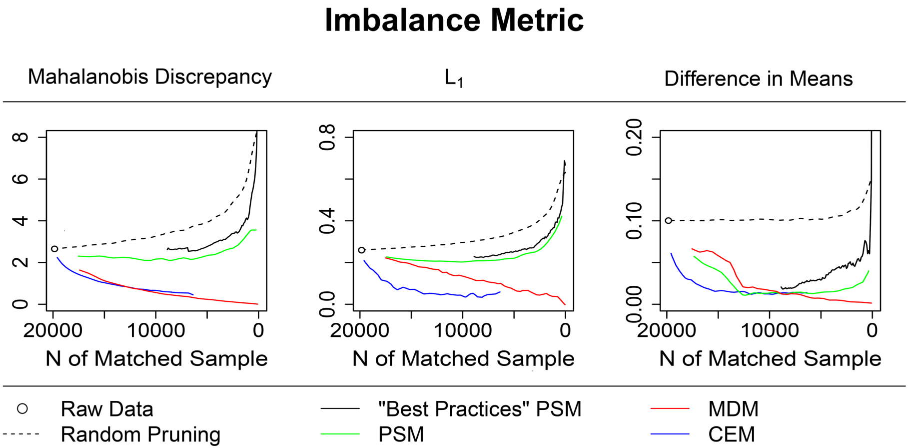
- Our idea: Identify the frontier of lowest imbalance for each given n, and choose a matching solution



Imbalance Metric
Mahalanobis Discrepancy
L1
Difference in Means
published PSM with 1/4 sd caliper
published PSM
published PSM with
1/4 sd caliper
N of Matched Sample
2500
1500
500
0
Raw Data
Random Pruning
"Best Practices" PSM
PSM
MDM
CEM

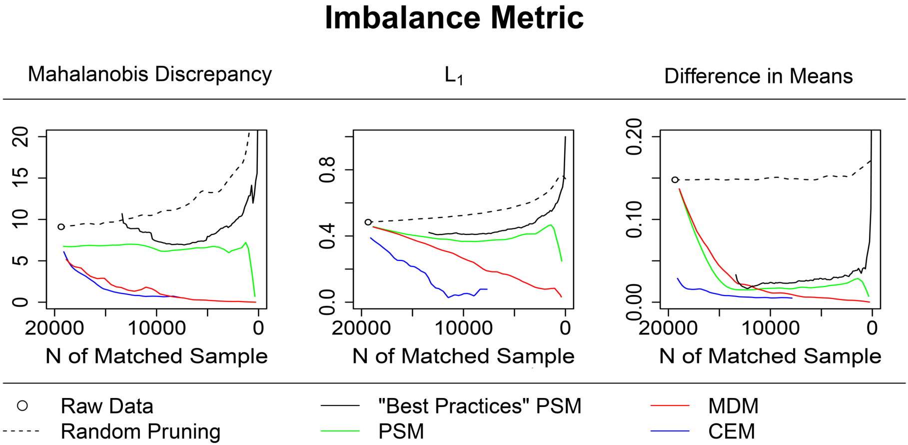
A Space Graph: Healthways Data

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



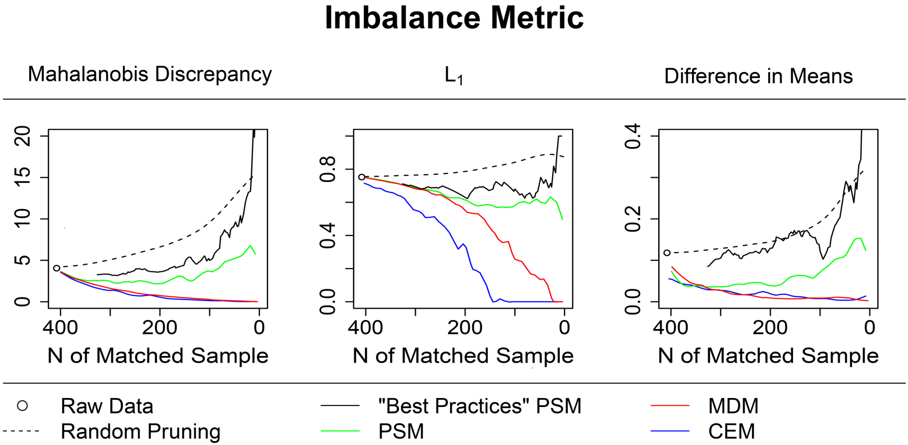
A Space Graph: Called/Not Called Data

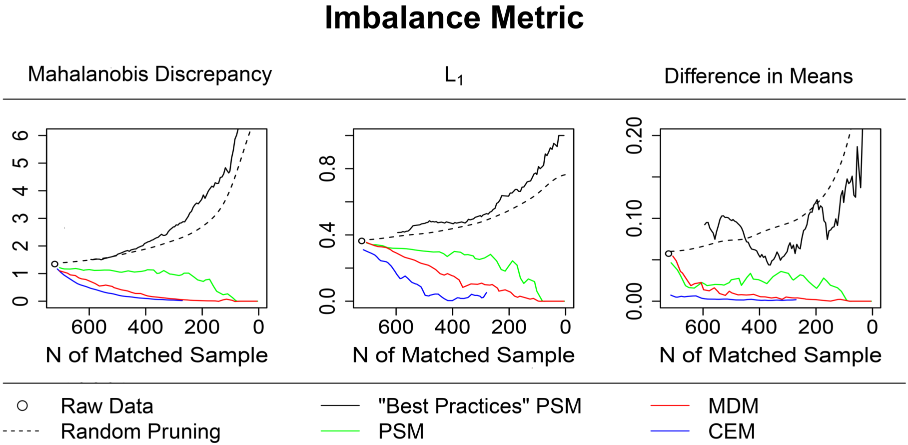
King, Nielsen, Coberley, Pope, and Wells (2012)



A Space Graph: FDA Drug Approval Times

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





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L_1
Difference in Means
0 1 2 3 4 5 6
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0.00 0.10 0.20
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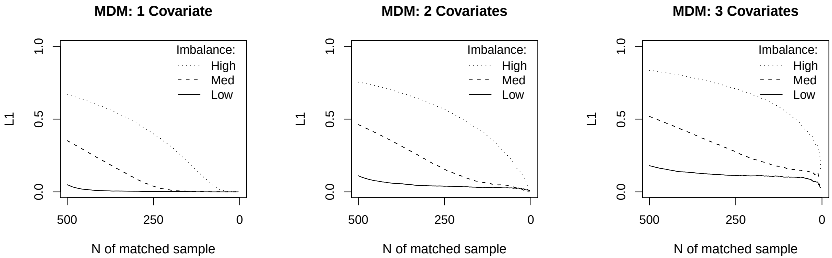
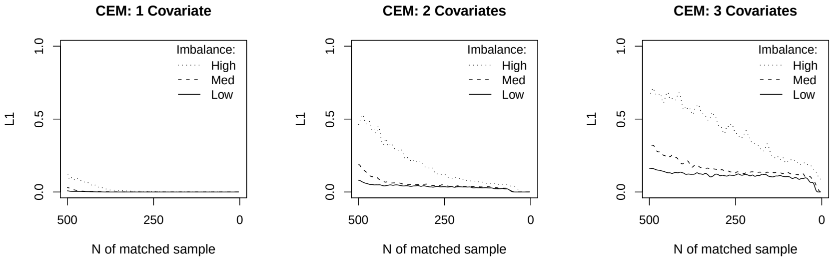
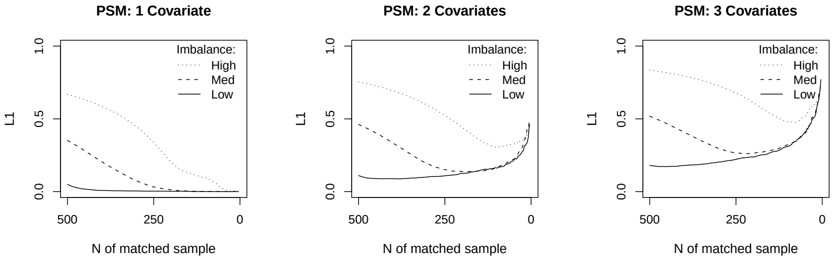
A Space Graph: Simulated Data — Mahalanobis



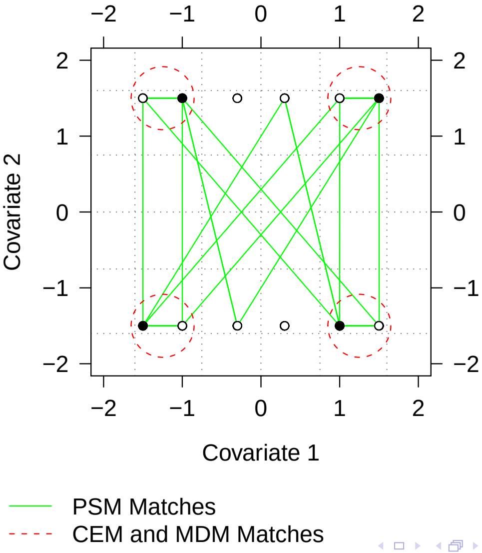
A Space Graph: Simulated Data — CEM



A Space Graph: Simulated Data — Propensity Score



PSM Approximates Random Matching in Balanced Data



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

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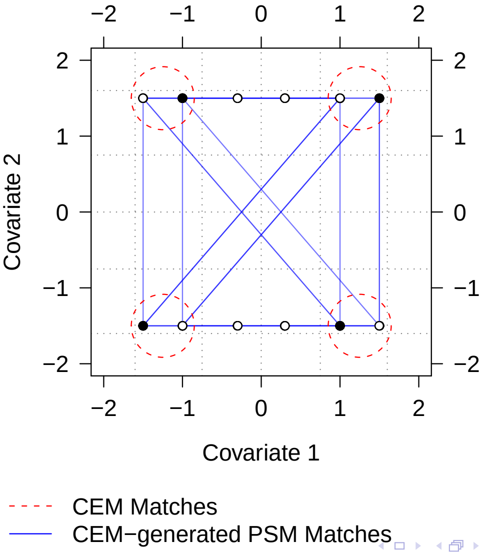
Destroying CEM with PSM's Two Step Approach



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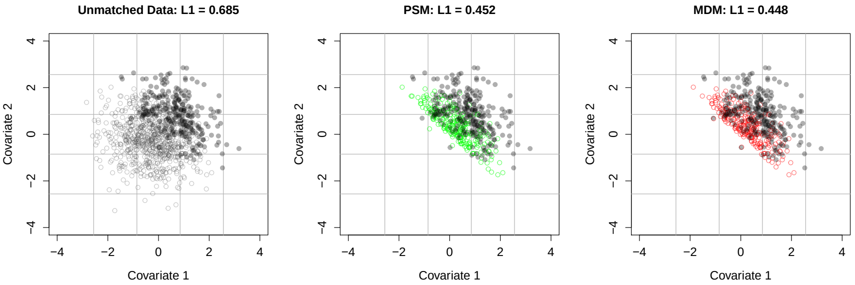
For papers, software (for R, Stata, & SPSS), tutorials, etc.

http://GKing.Harvard.edu/cem

Data where PSM Works Reasonably Well — PSM & MDM



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