Matching Methods for Causal Inference

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(Talk at University of Kansas, 12/2/2011)

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- Problem: Model dependence (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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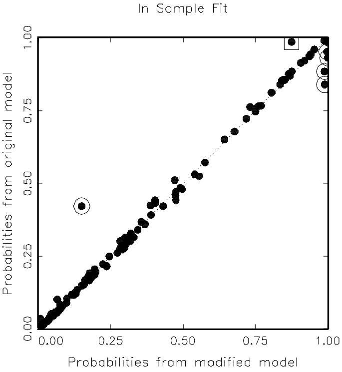
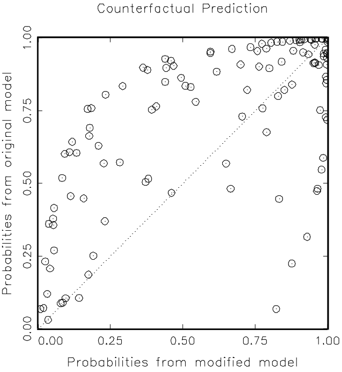
- Data analysis: Logit model
- The question: How *model dependent* are the results?

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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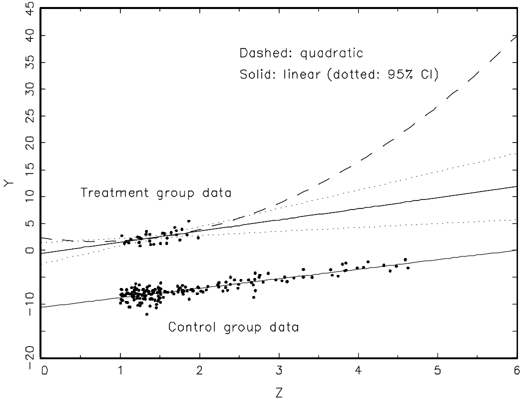

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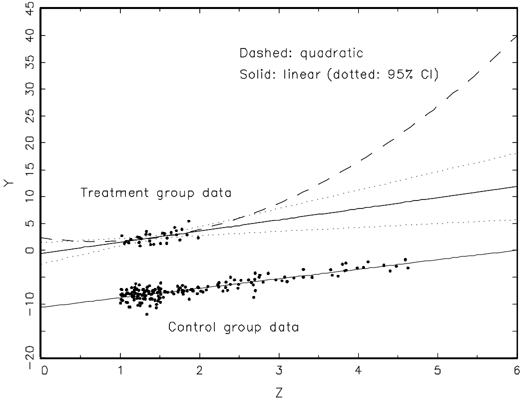

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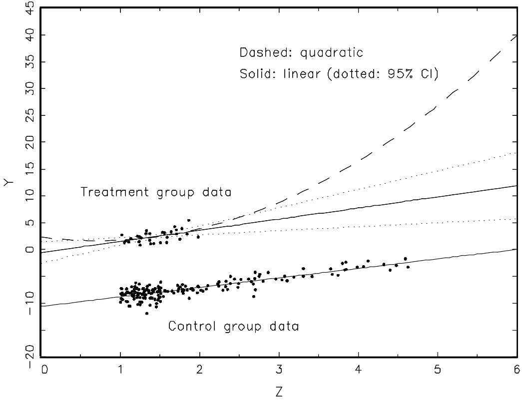

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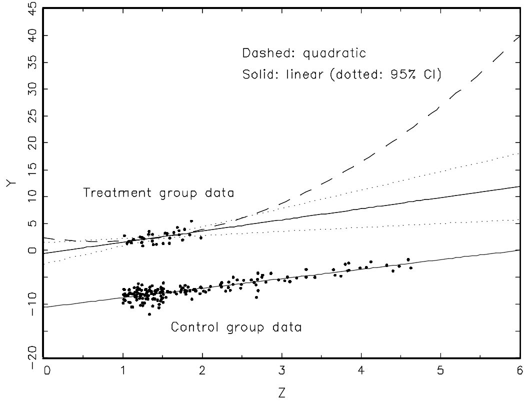

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- Preprocess II: Match (prune bad matches) within interpolation region

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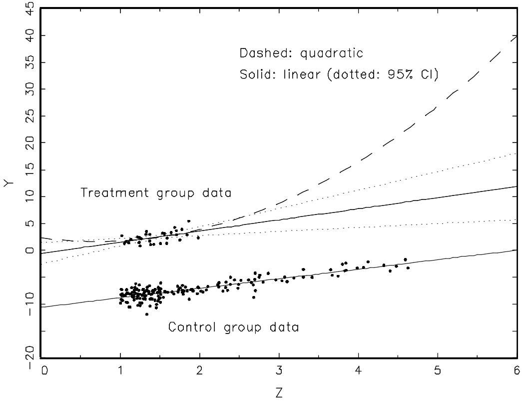

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- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

Matching within the Interpolation Region

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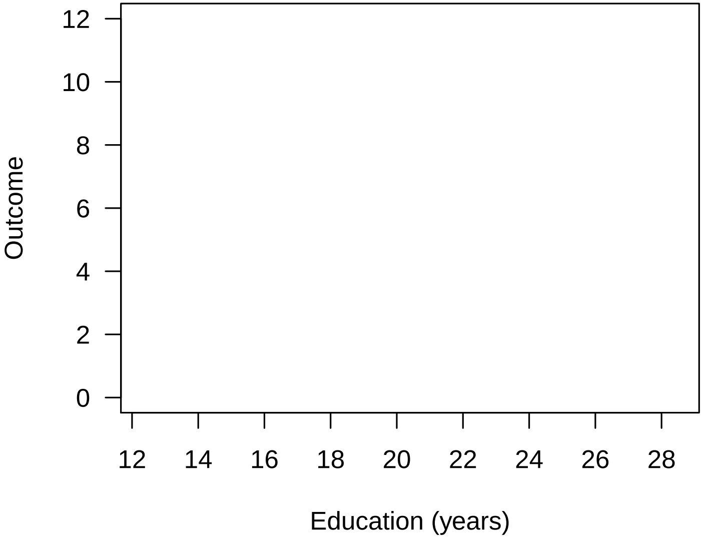

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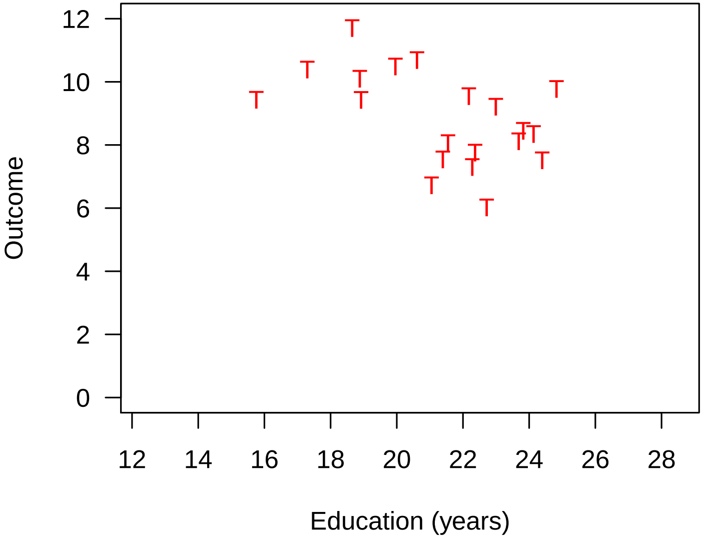

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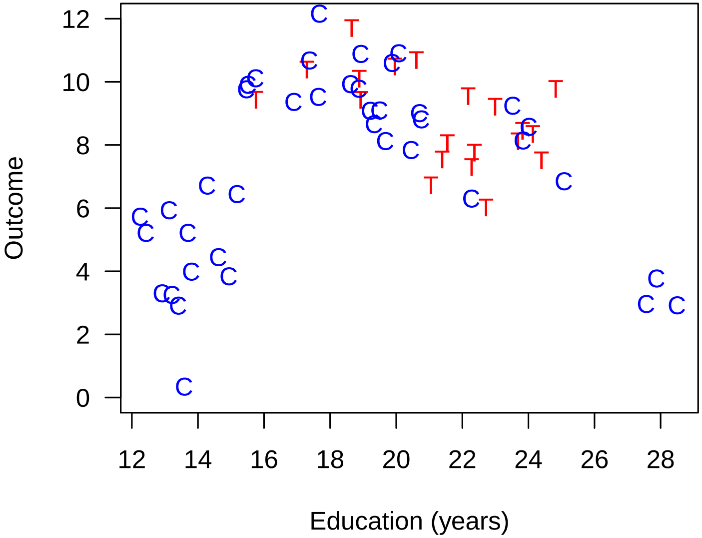

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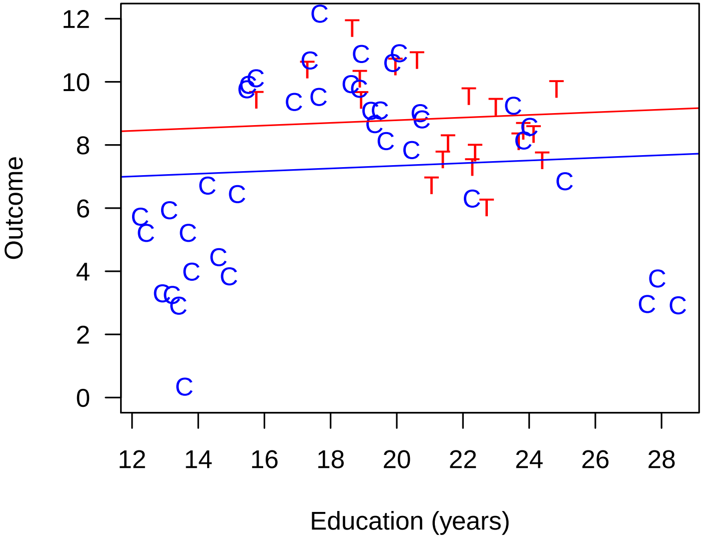

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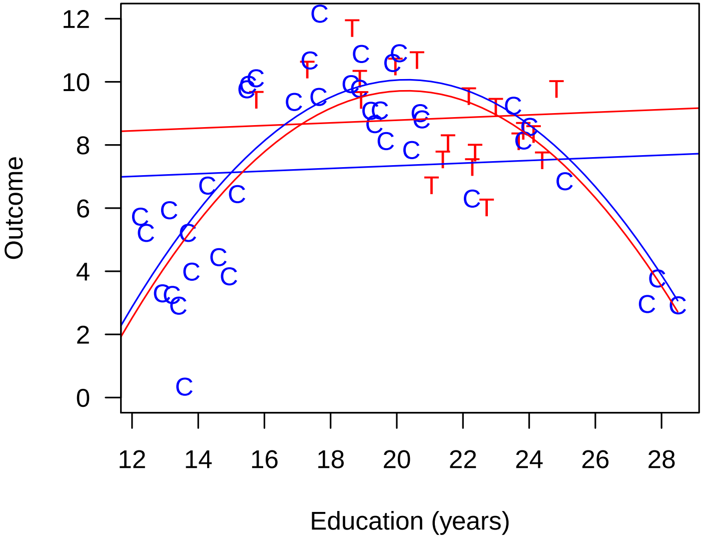

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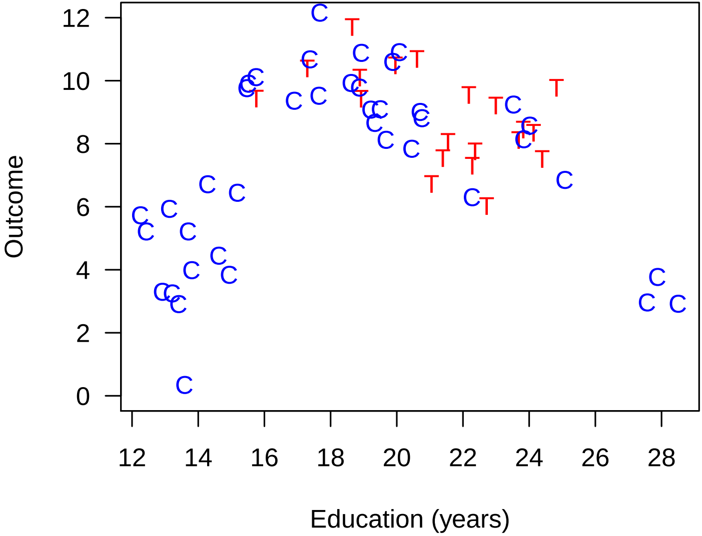

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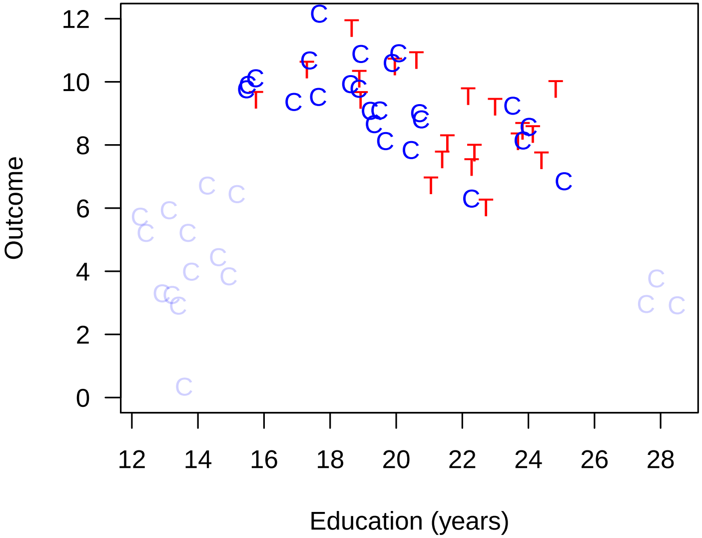

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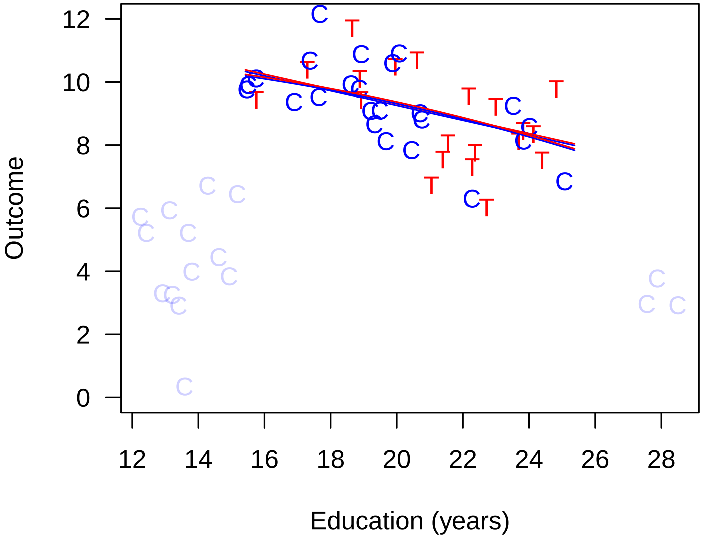

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Matching reduces model dependence, bias, and variance

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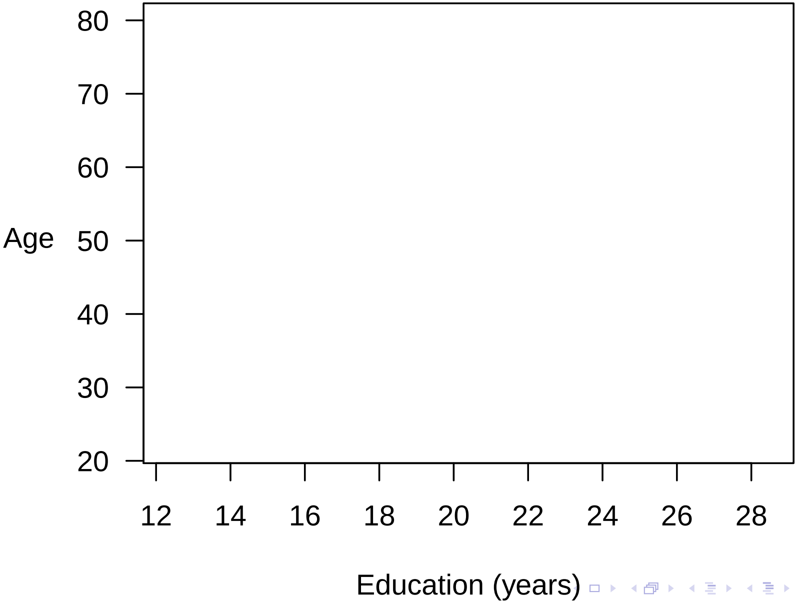

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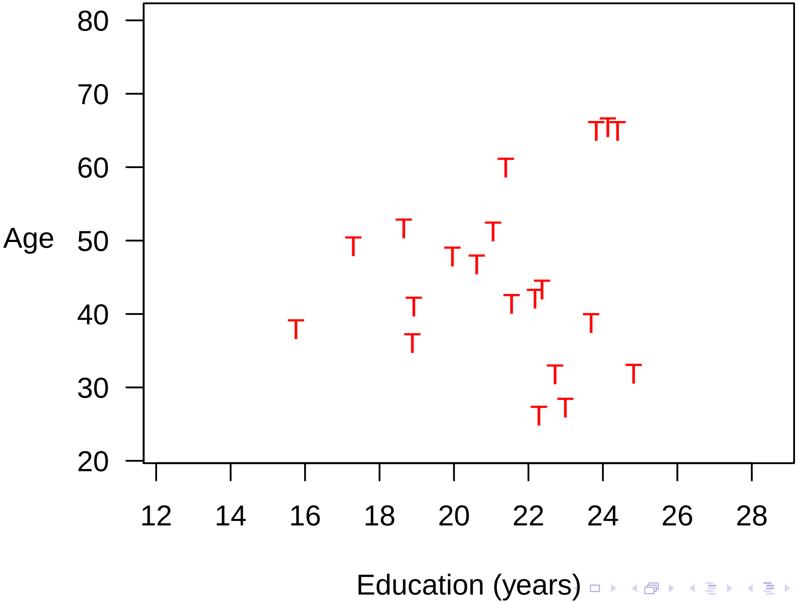

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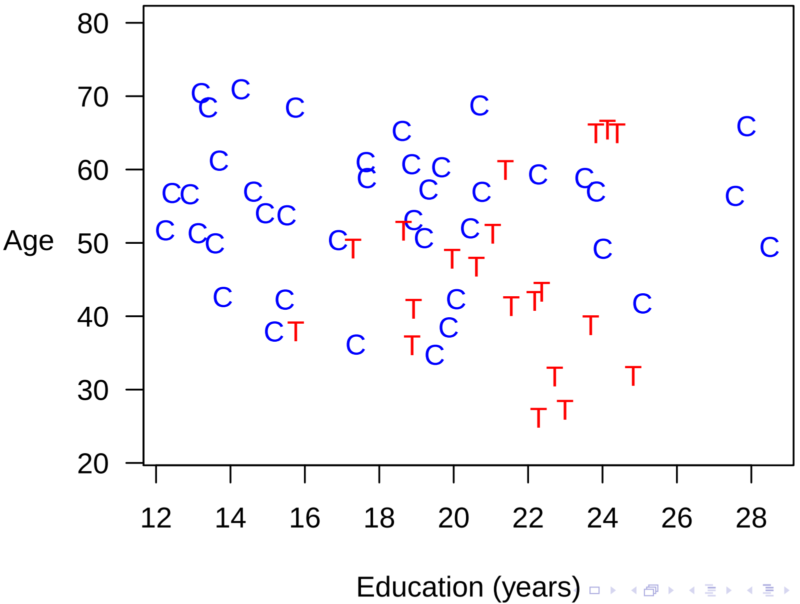

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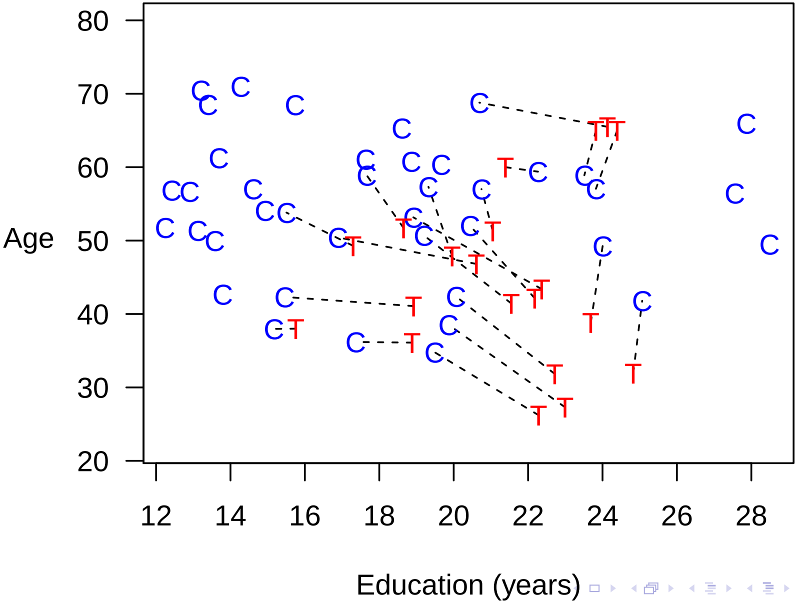

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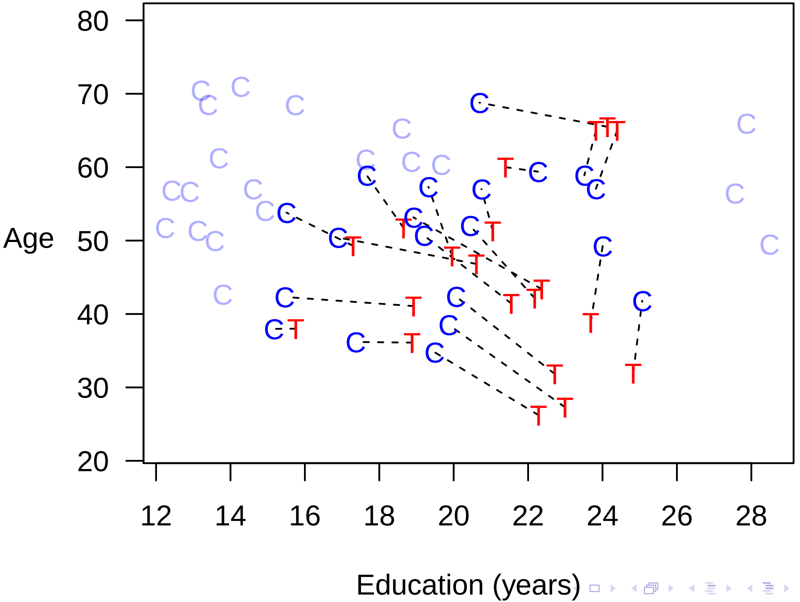

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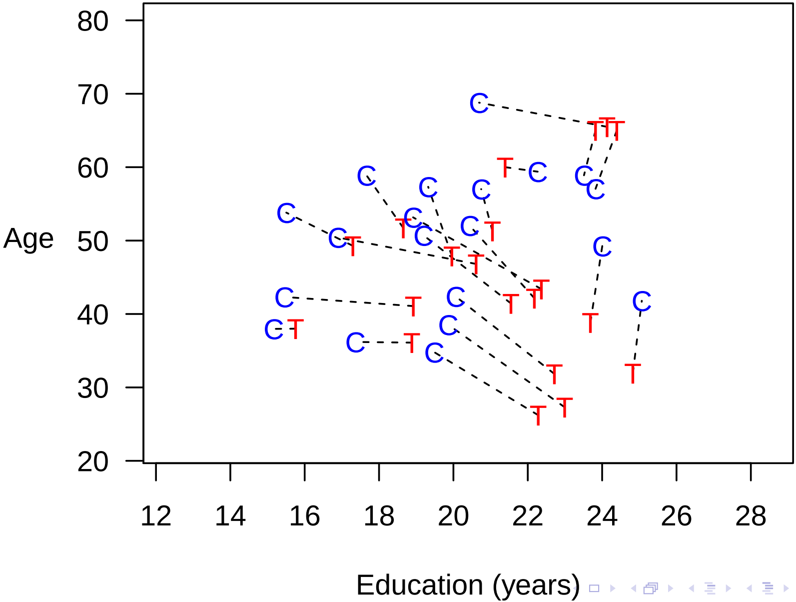

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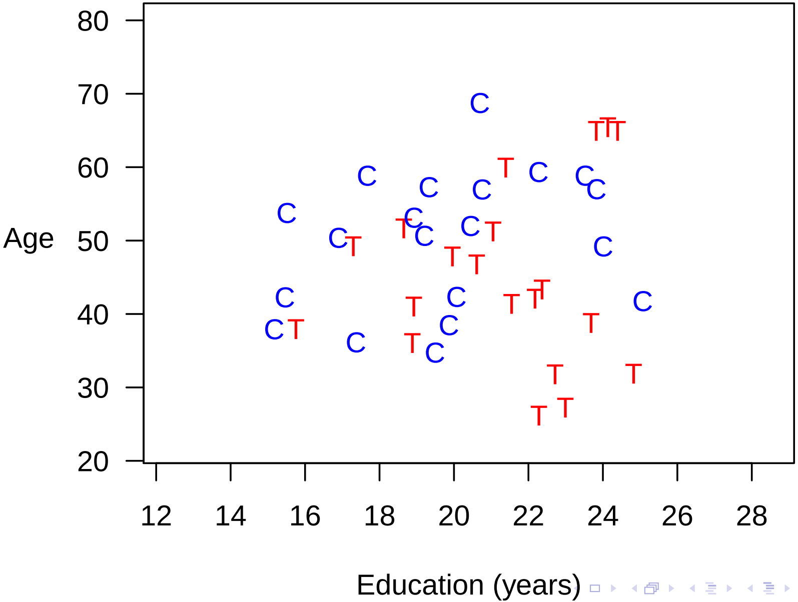

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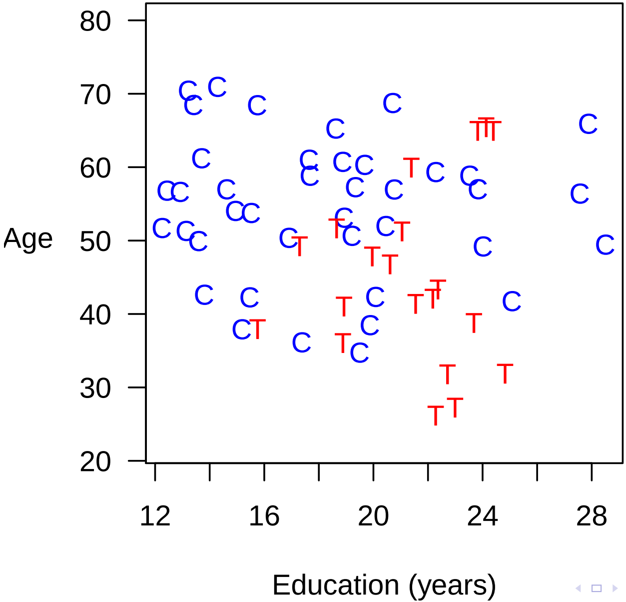

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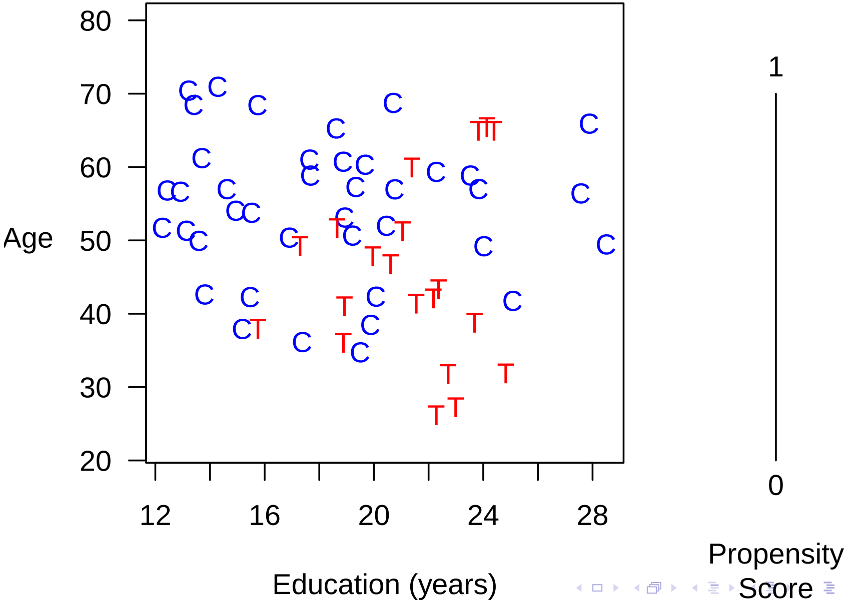

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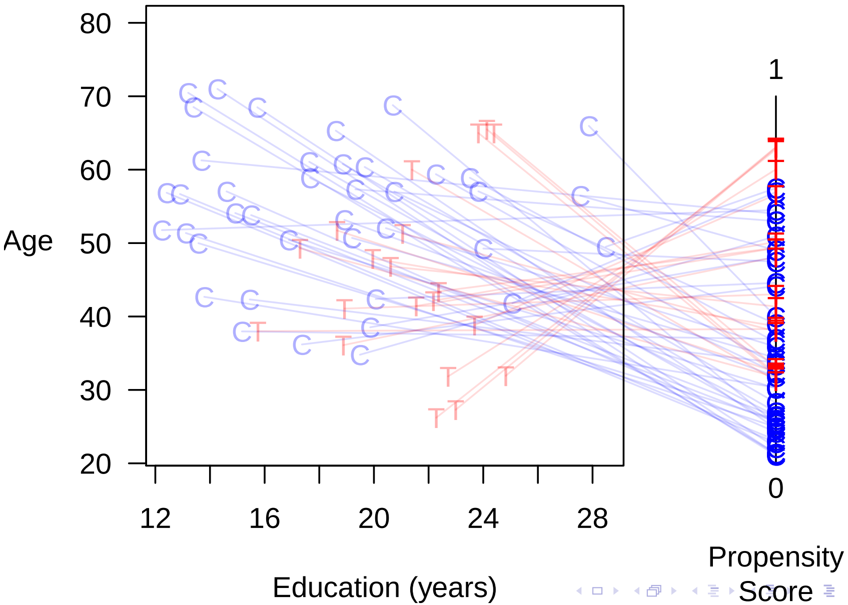

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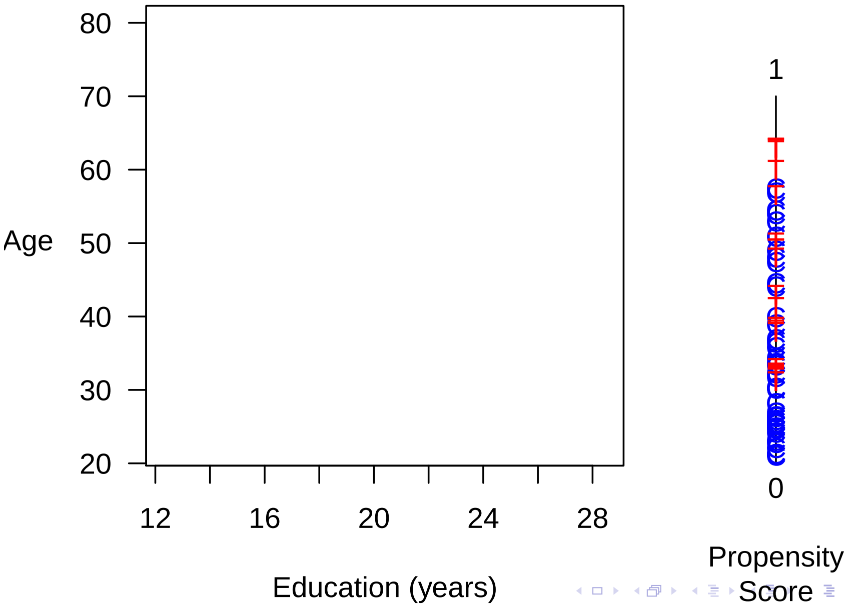

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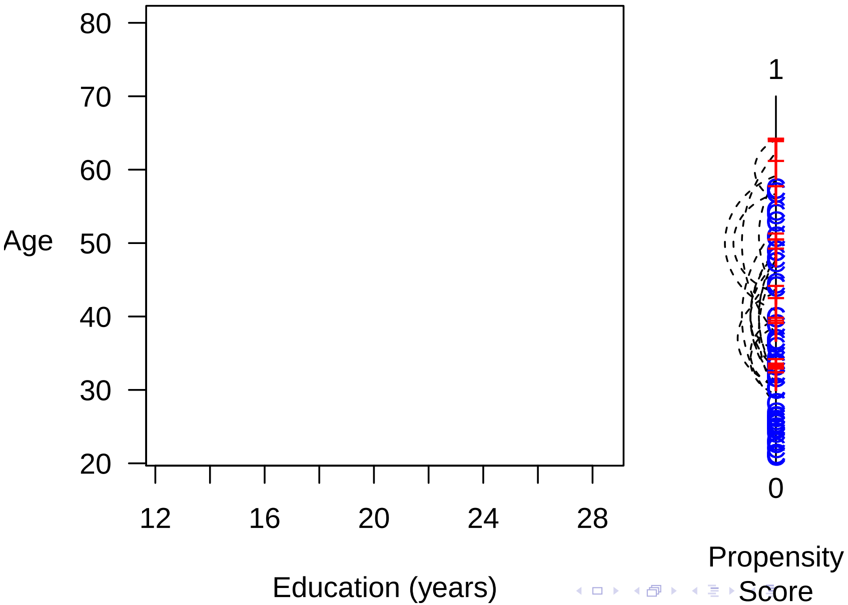

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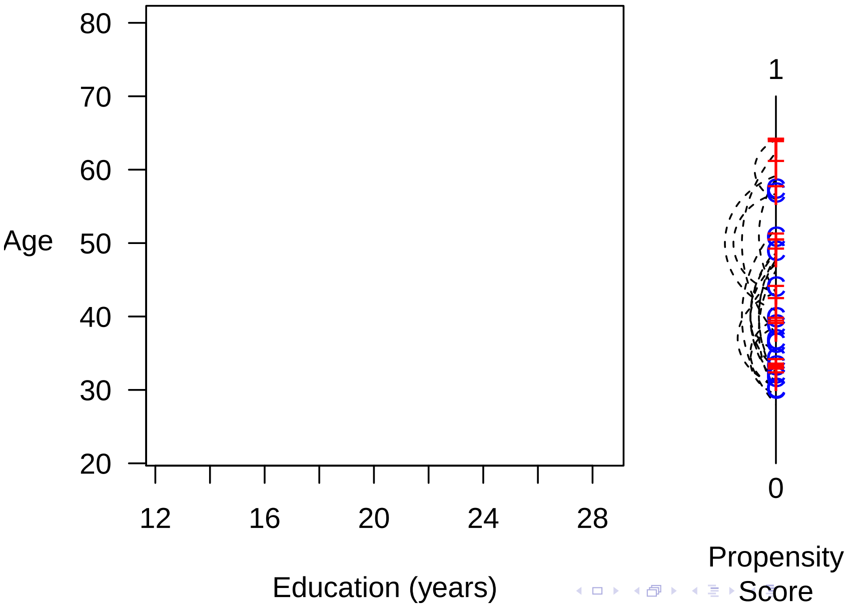

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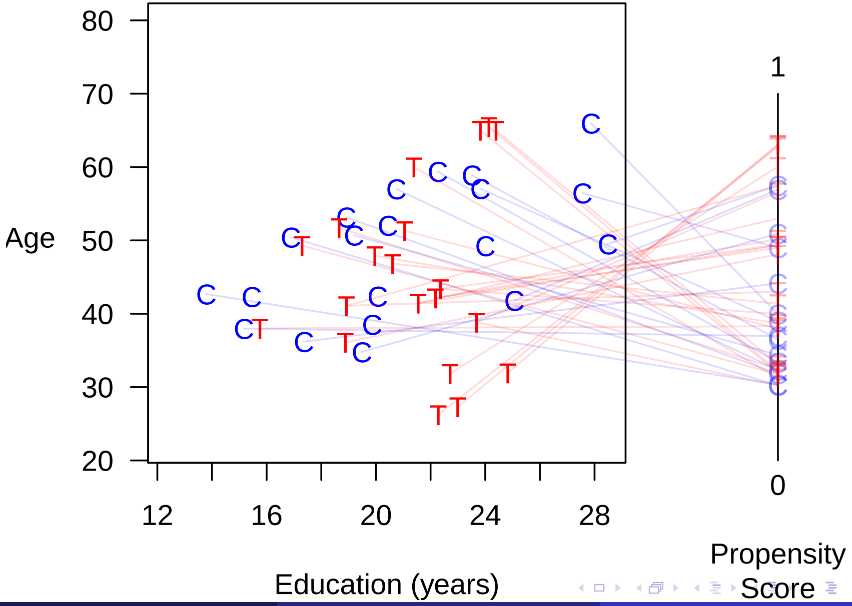

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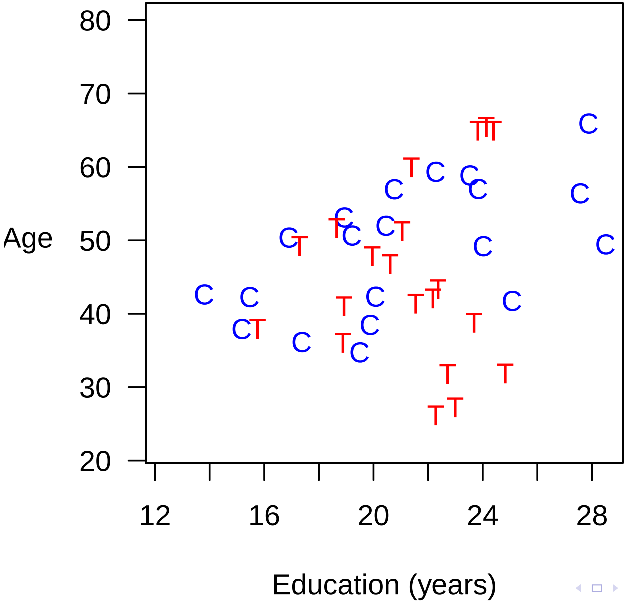

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   - Apply exact matching to the coarsened X, $C(X)$

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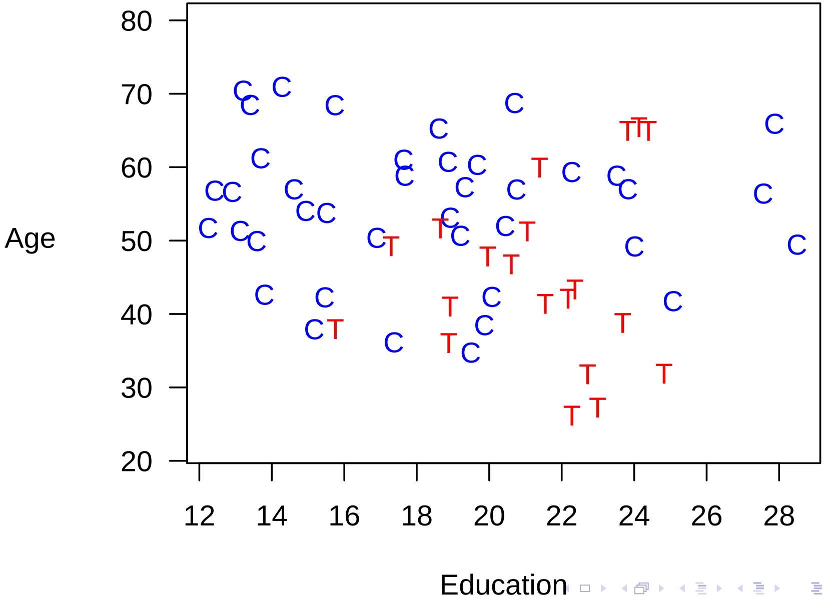

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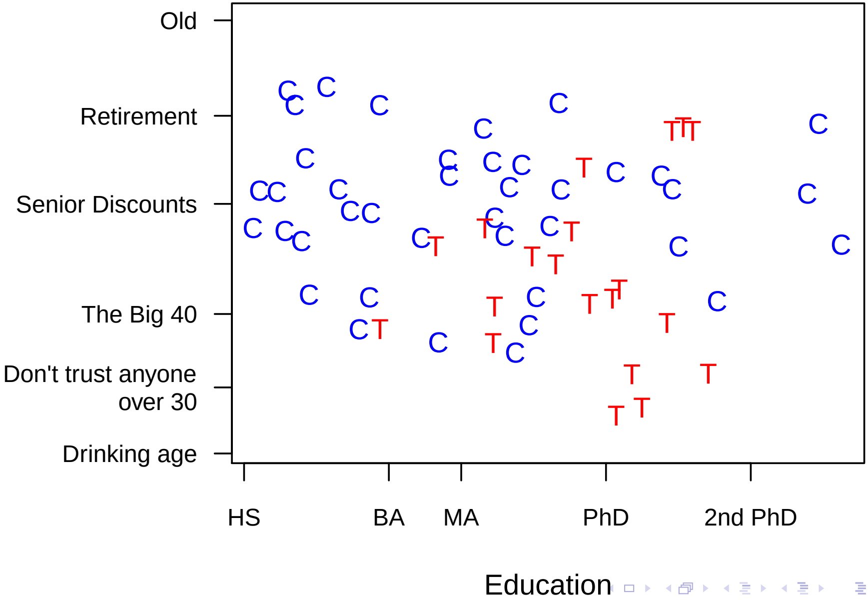

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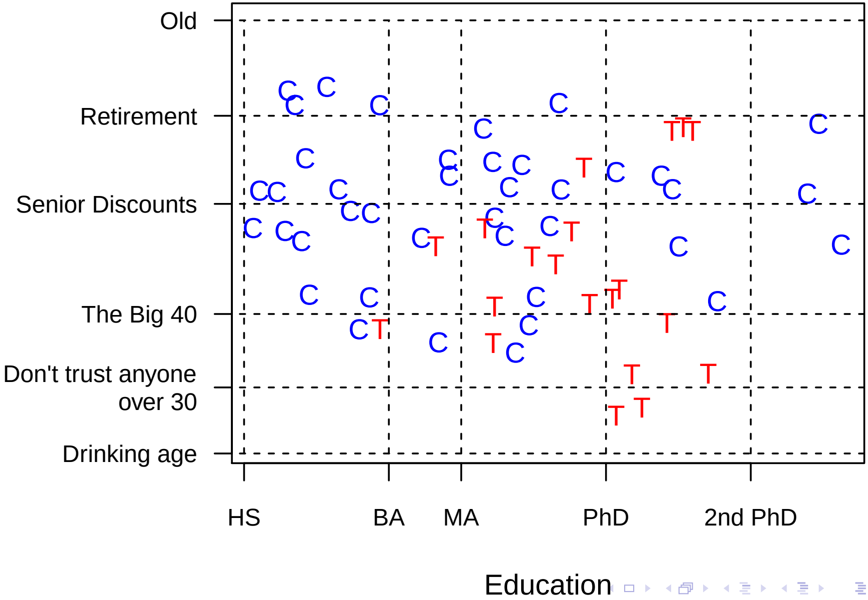

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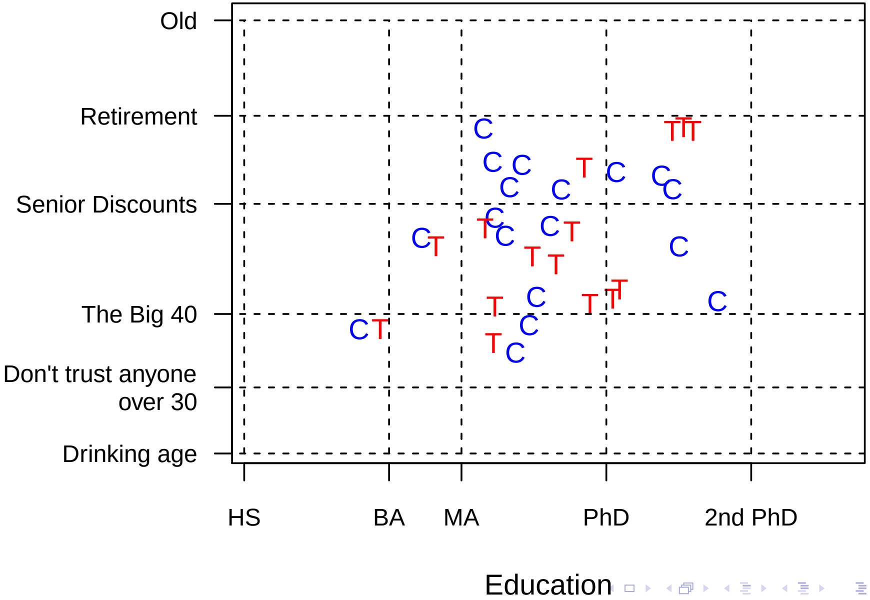

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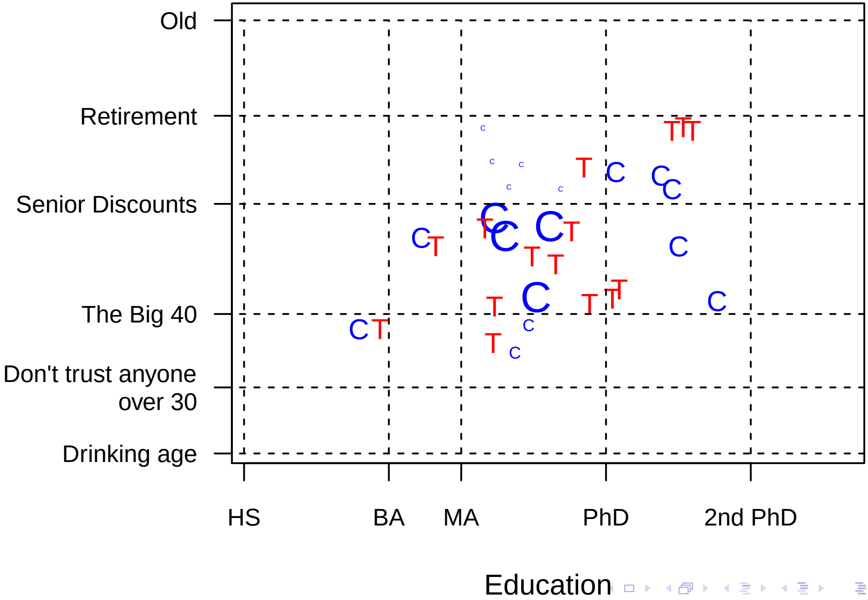

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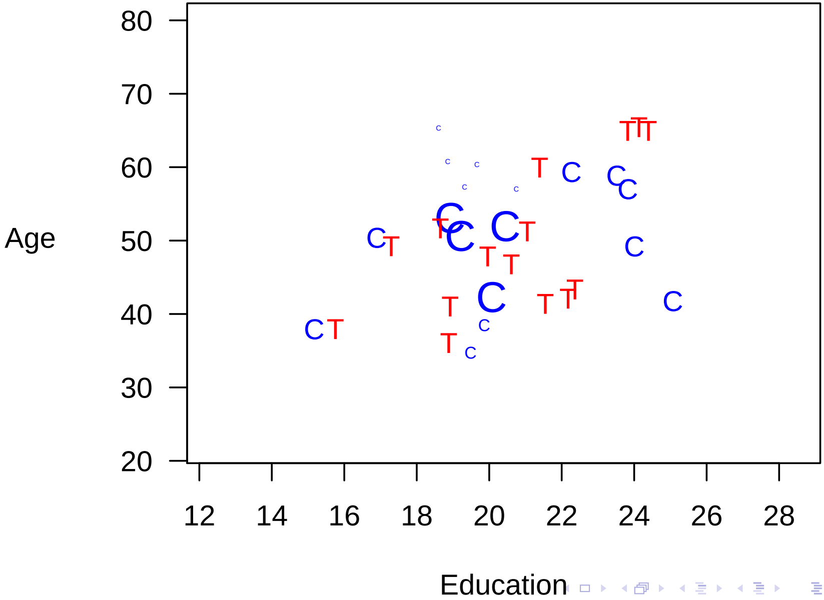

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  - Another measure: Mahalanobis distance to closest unit in other group, averaged over each unit

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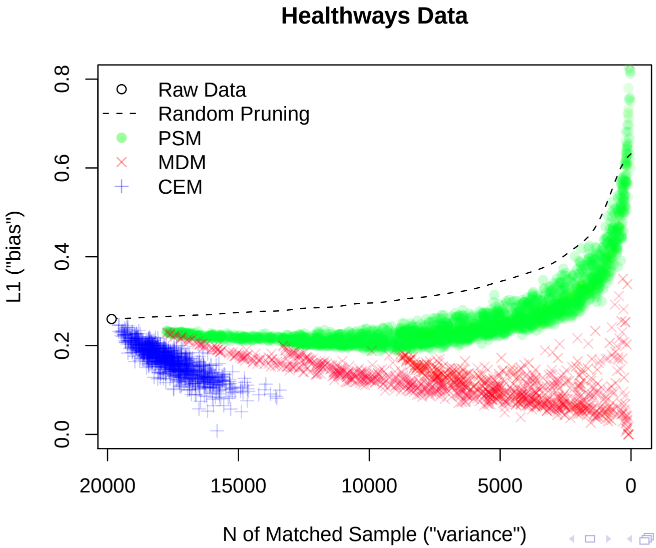
- Choose matched solution & matching method becomes irrelevant
- Our idea: Compute lots of matching solutions, identify the frontier of lowest imbalance for each given n, and choose a matching solution

A Space Graph: Real Data

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



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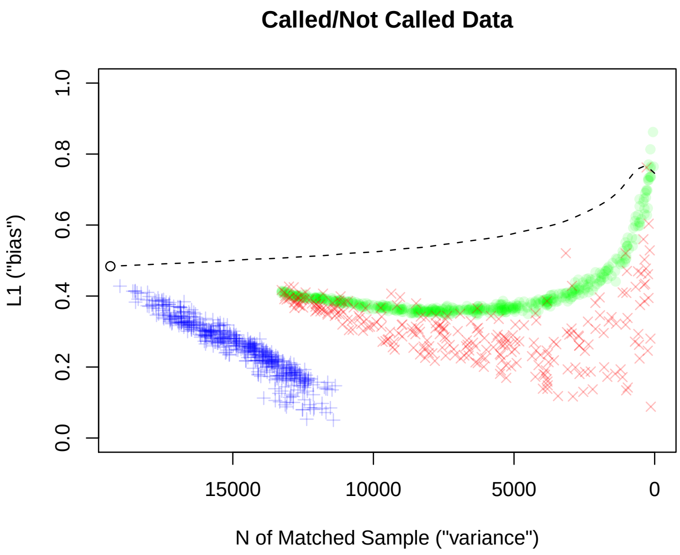

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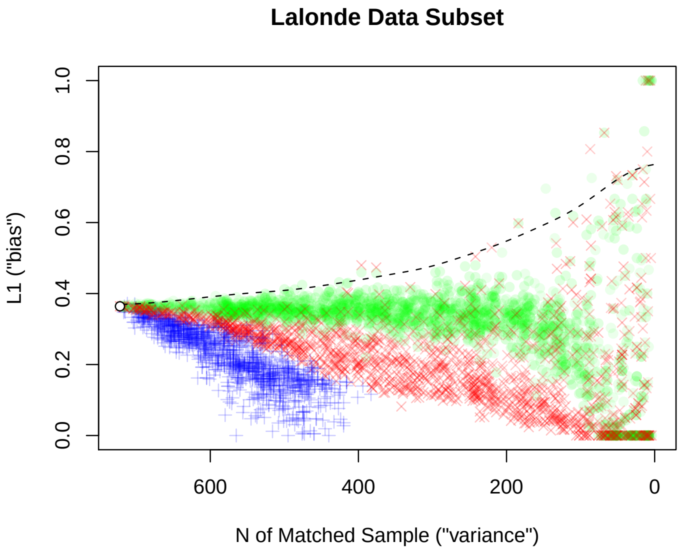
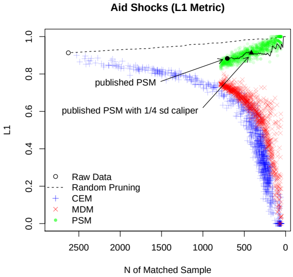
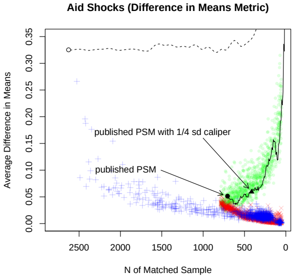
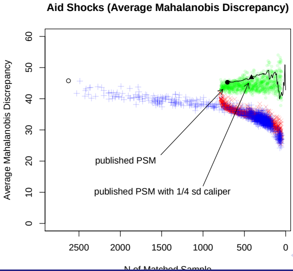


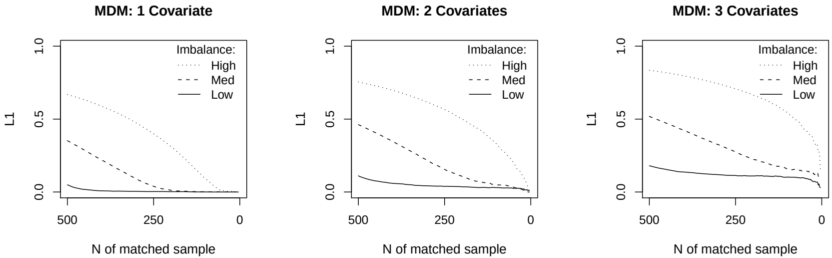
Space Graphs: Different Imbalance Metrics



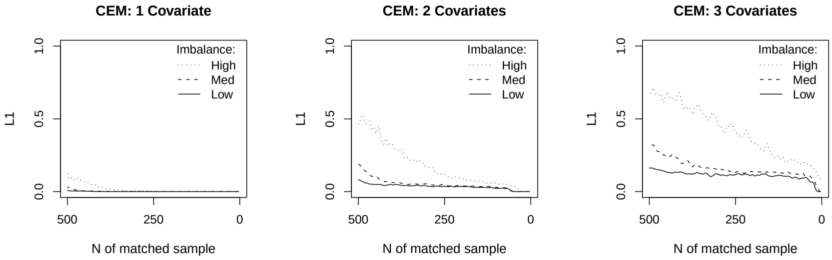




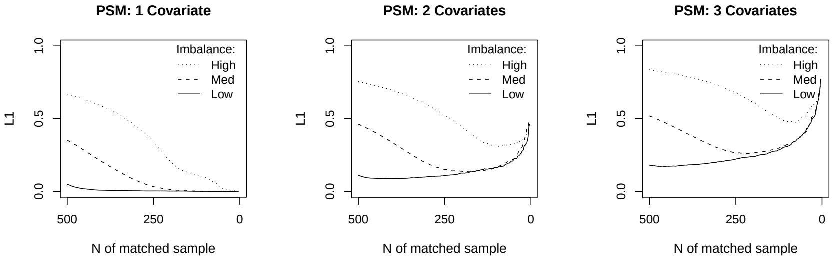
A Space Graph: Simulated Data — Mahalanobis



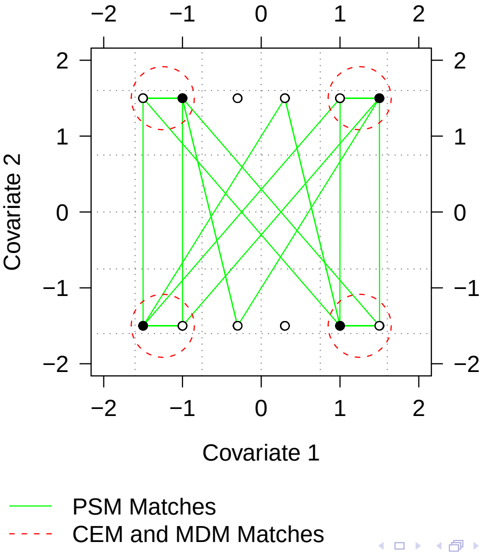
A Space Graph: Simulated Data — CEM



A Space Graph: Simulated Data — Propensity Score



PSM Approximates Random Matching in Balanced Data



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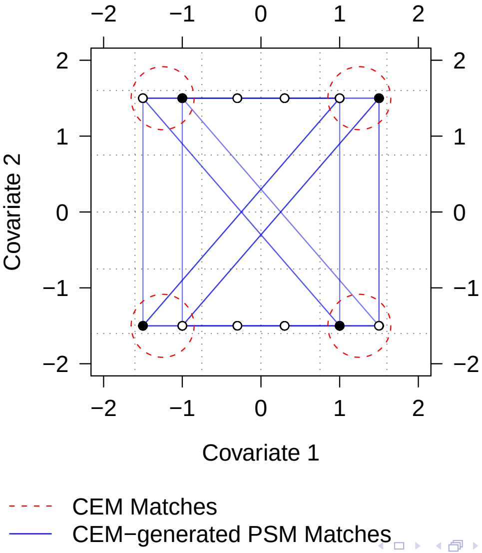
Destroying CEM with PSM's Two Step Approach



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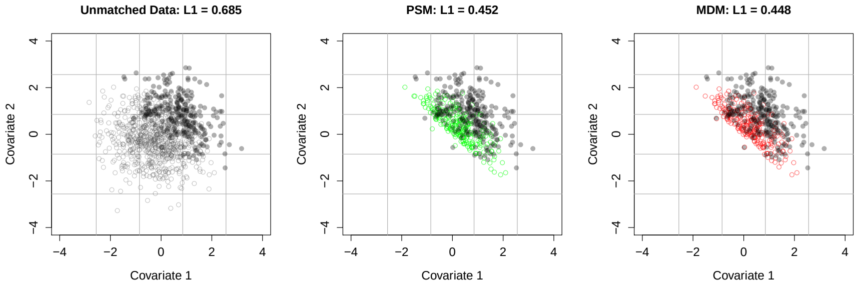
For papers, software (for R, Stata, & SPSS), tutorials, etc.

http://GKing.Harvard.edu/cem

Data where PSM Works Reasonably Well — PSM & MDM



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