Optimizing Balance and Sample Size in Matching Methods for Causal Inference[1]

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(Talk at the Institute for Health Metrics and Evaluation, 6/10/2013)

[1] Joint work with Christopher Lucas and Richard Nielsen
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  - Solution: Not an issue with Other methods or our approach

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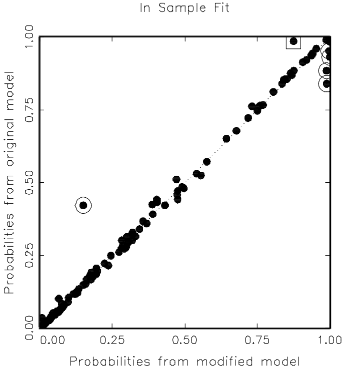
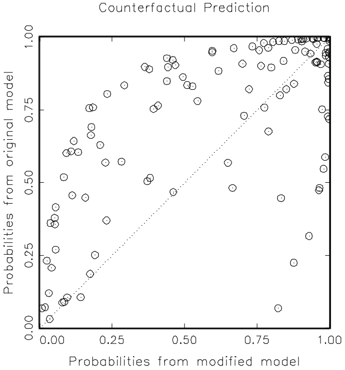
- Data analysis: Logit model
- The question: How *model dependent* are the results?

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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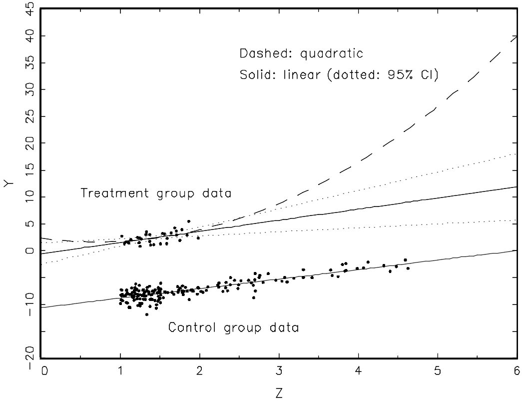

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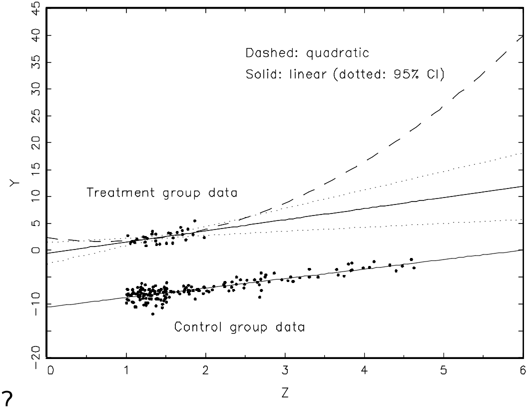

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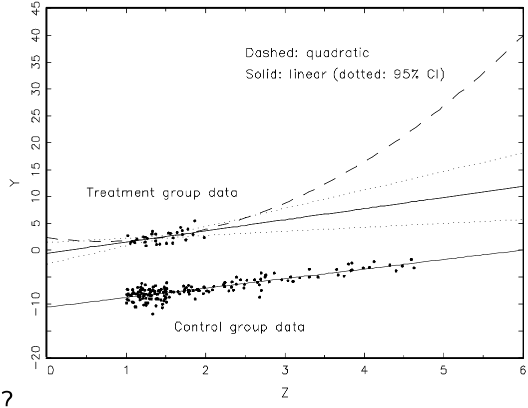

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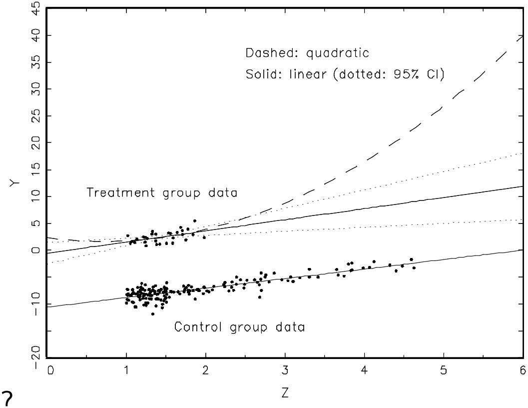

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- Preprocess II: Match (prune bad matches) within interpolation region

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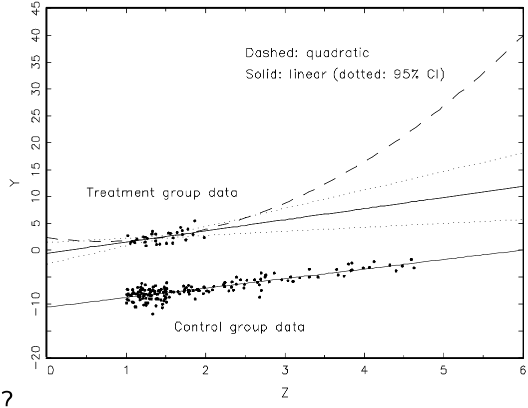

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- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

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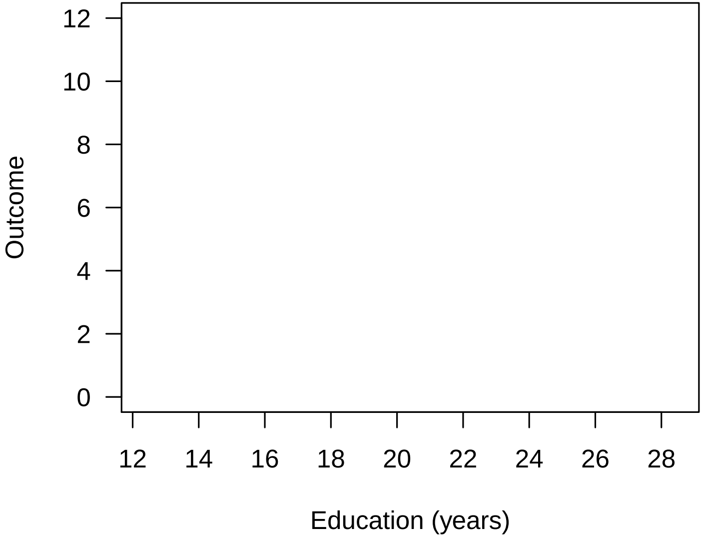

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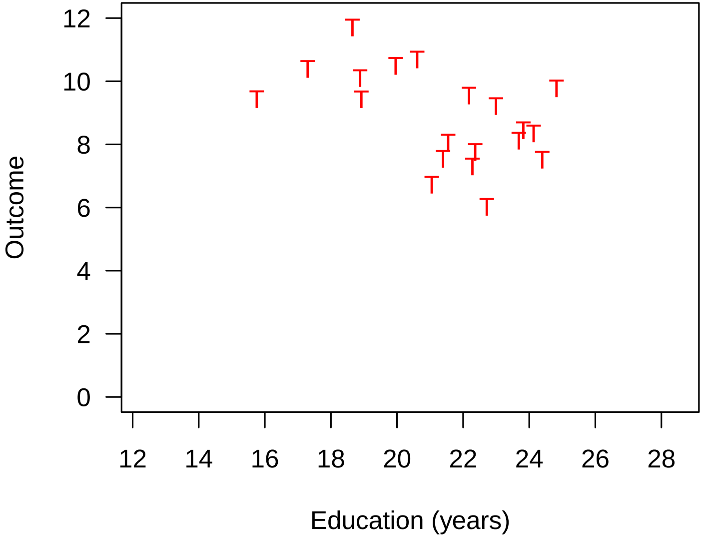

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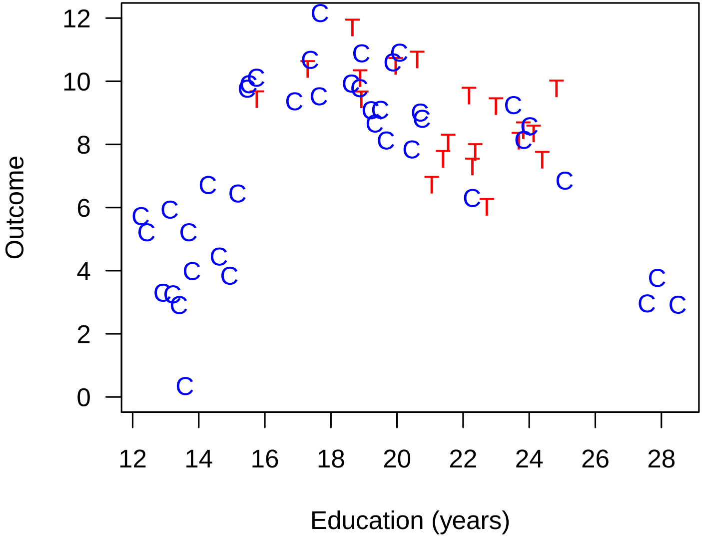

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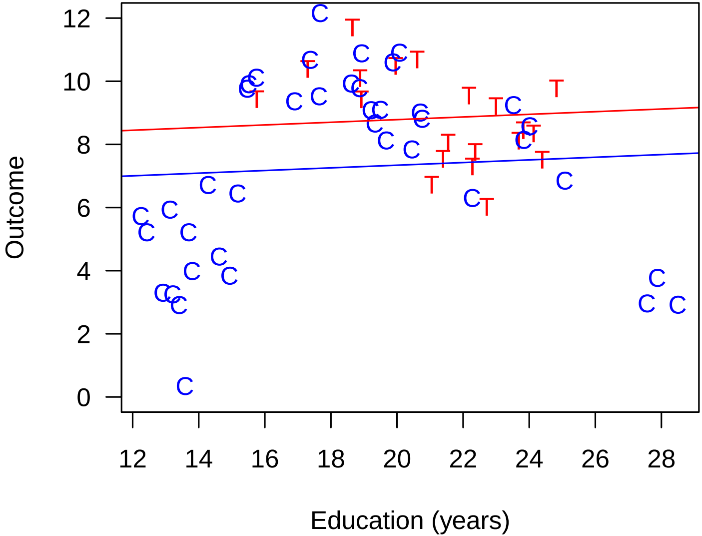

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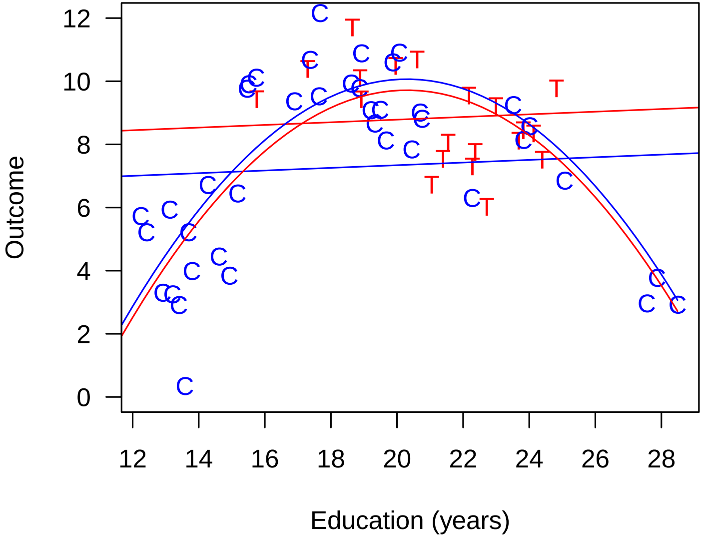

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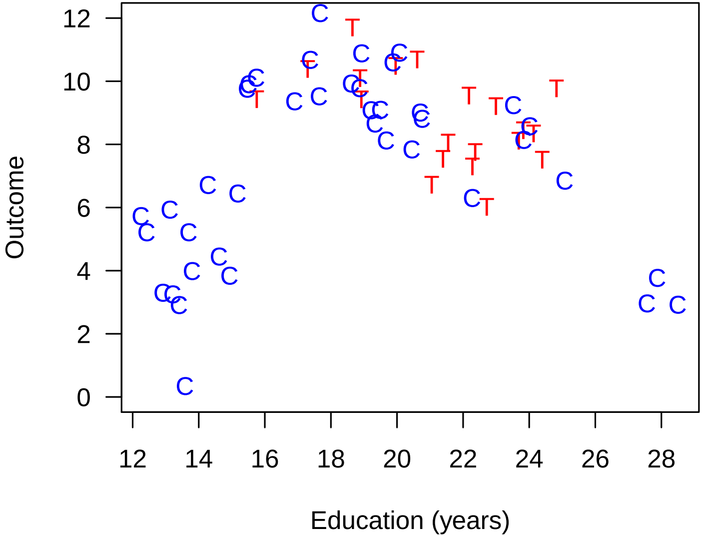

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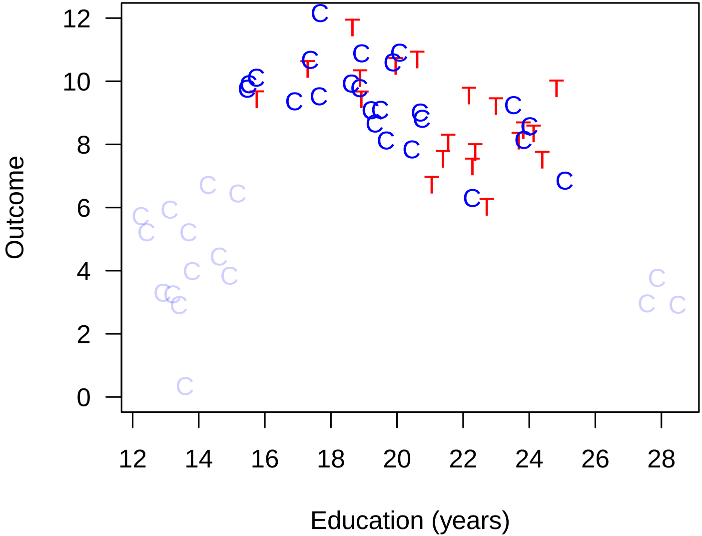

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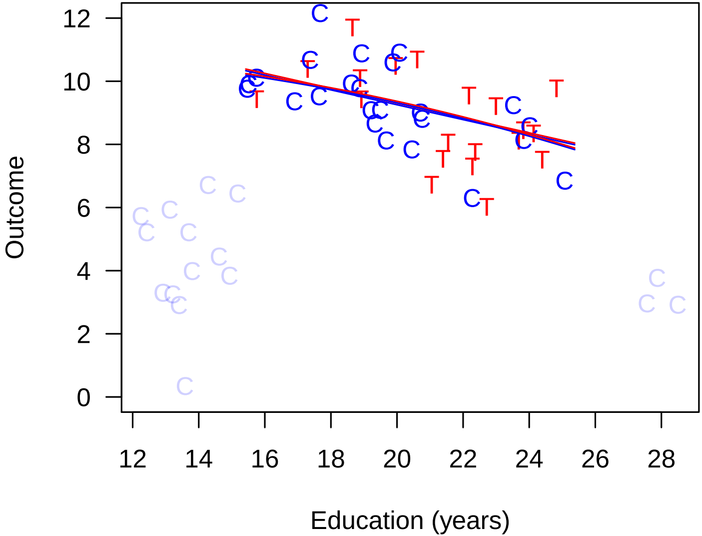

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Matching reduces model dependence, bias, and variance

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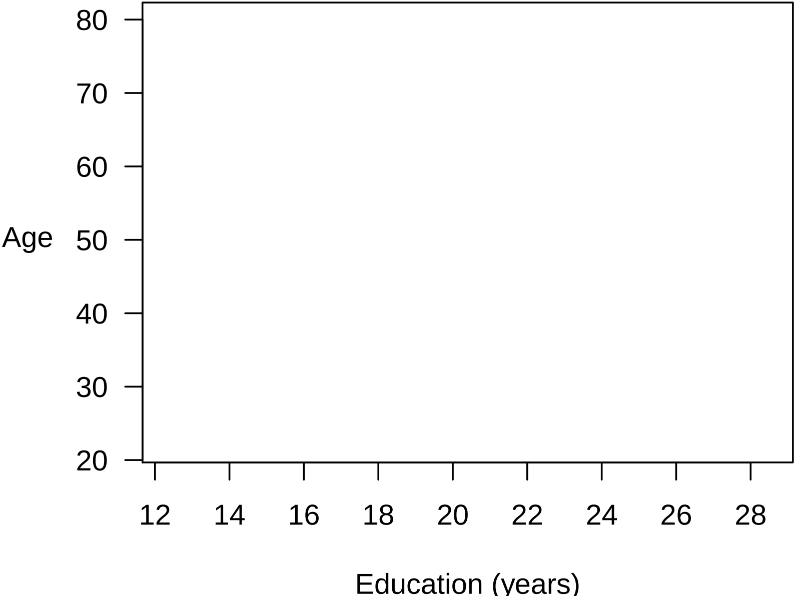

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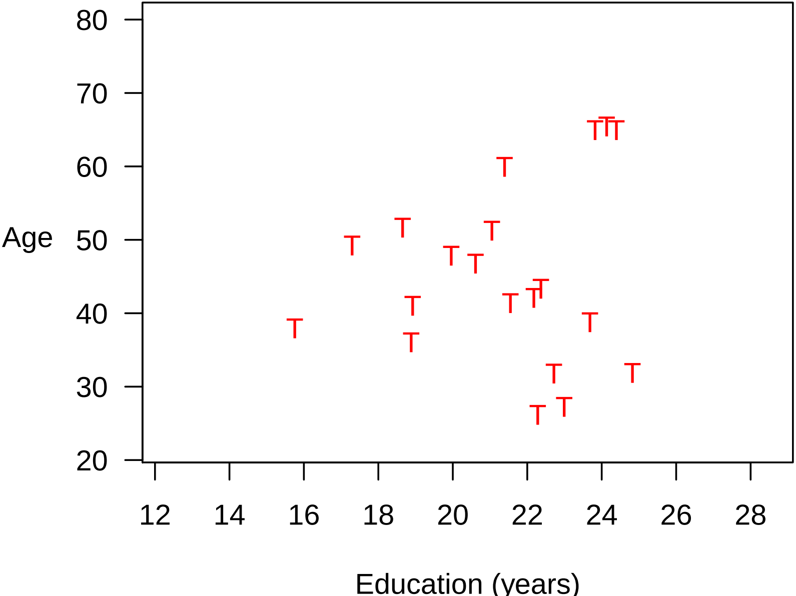

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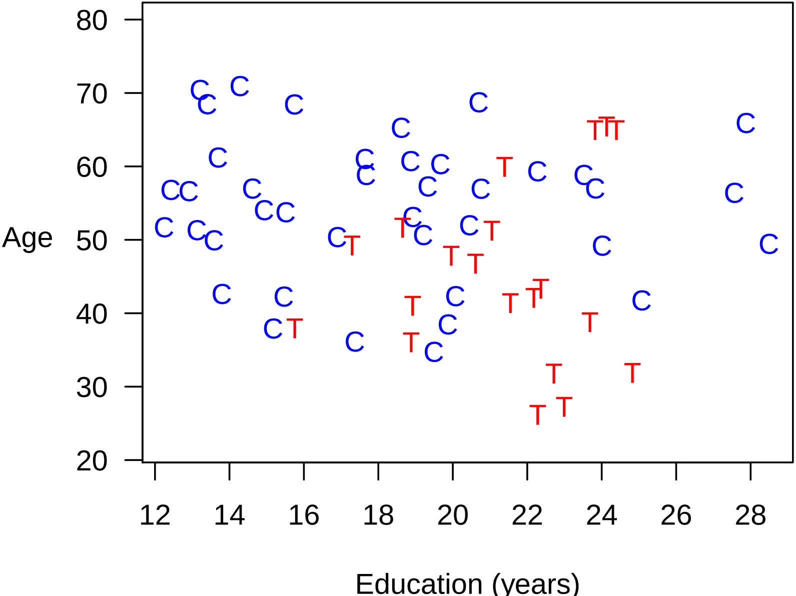

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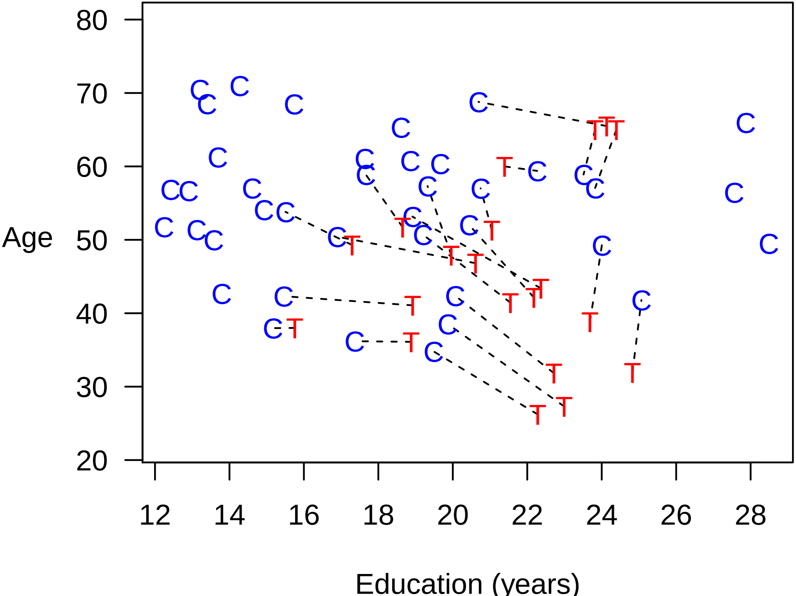

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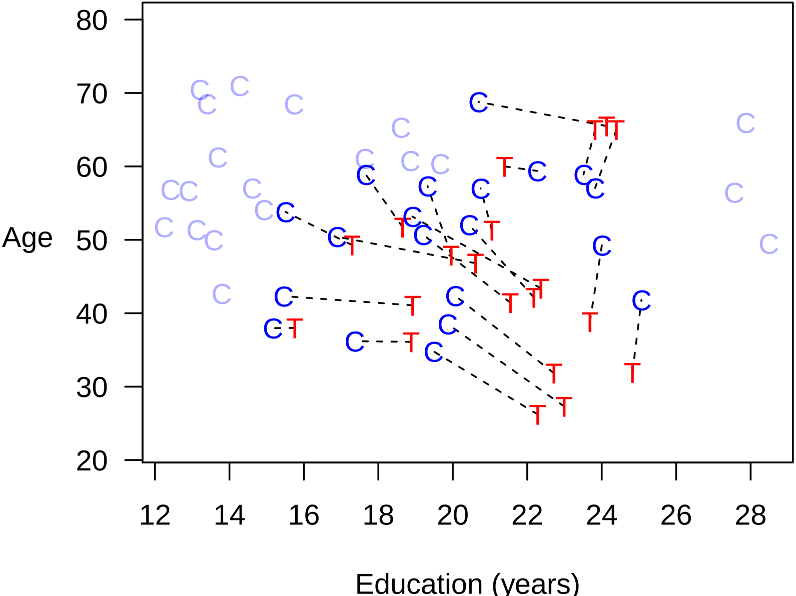

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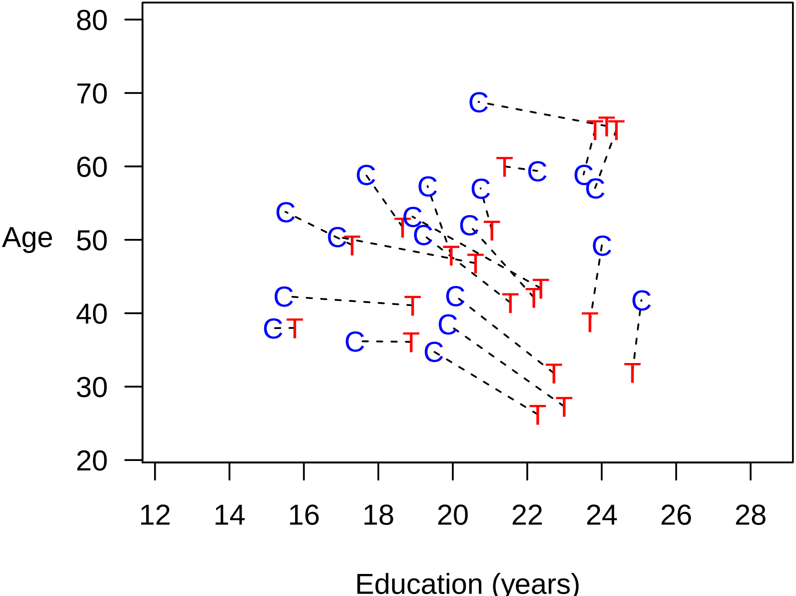

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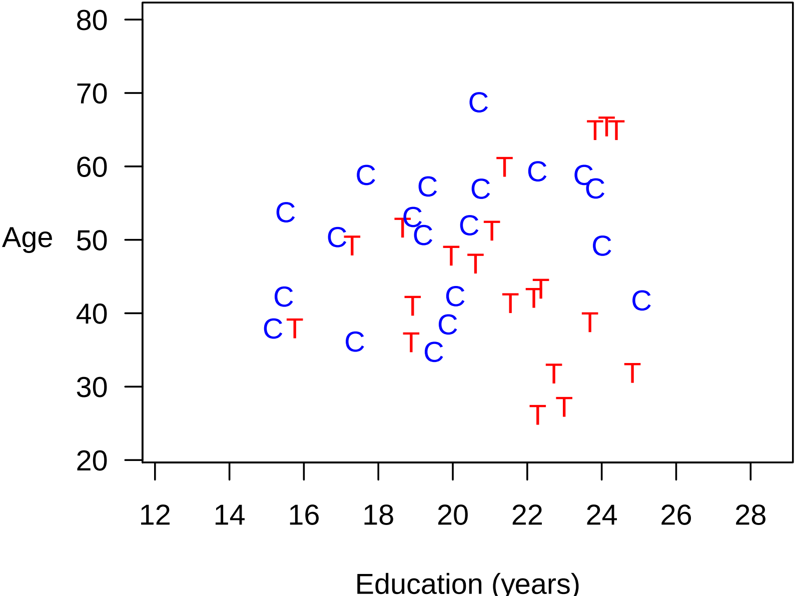

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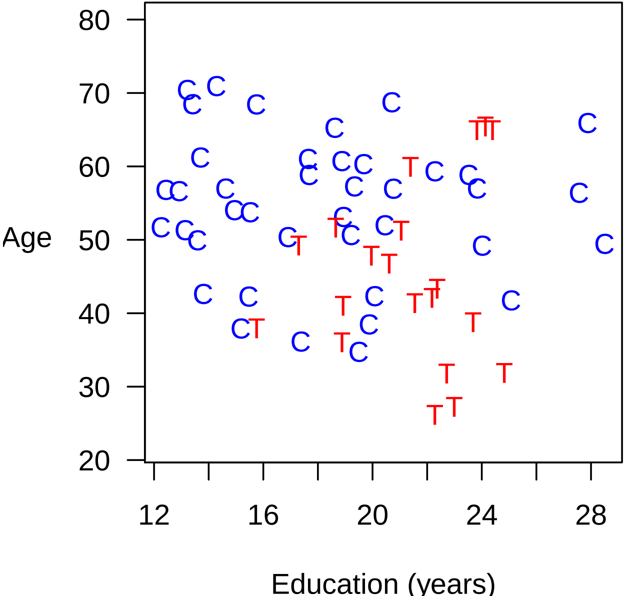

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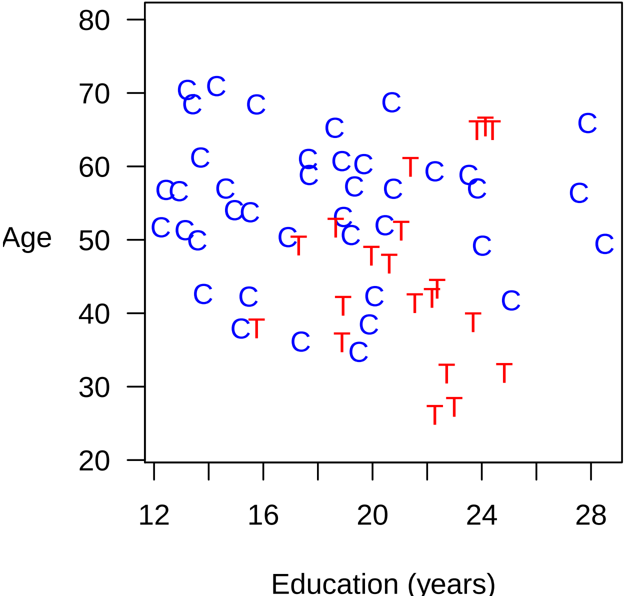

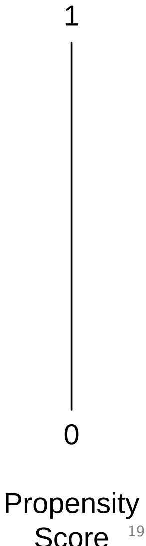

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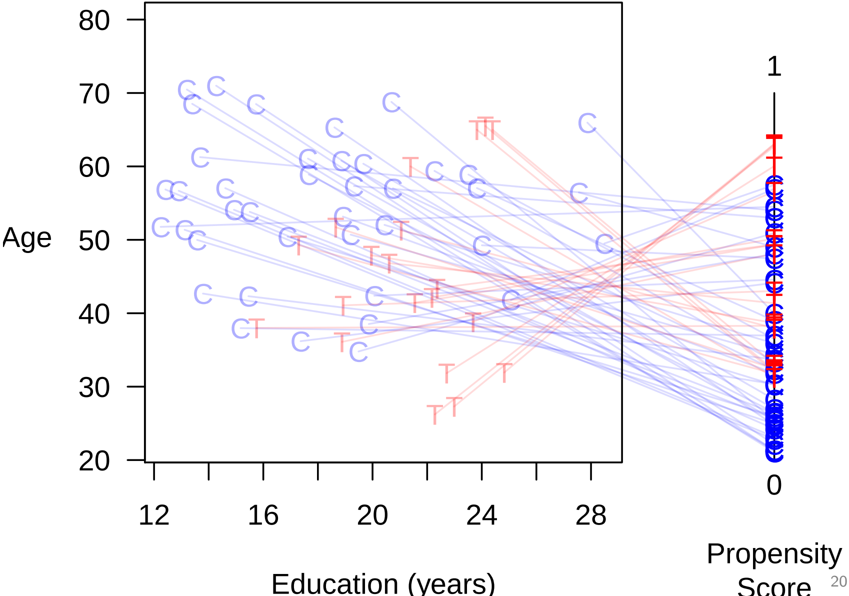

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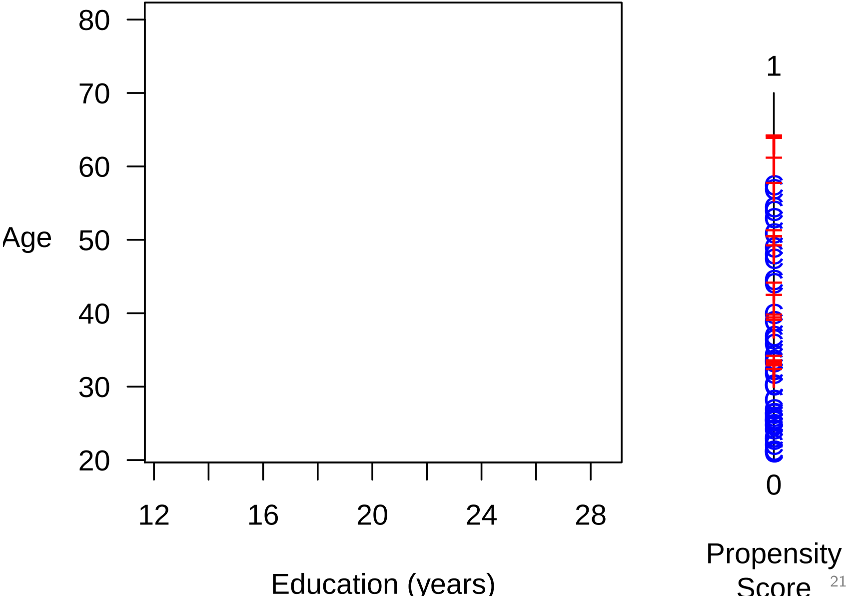

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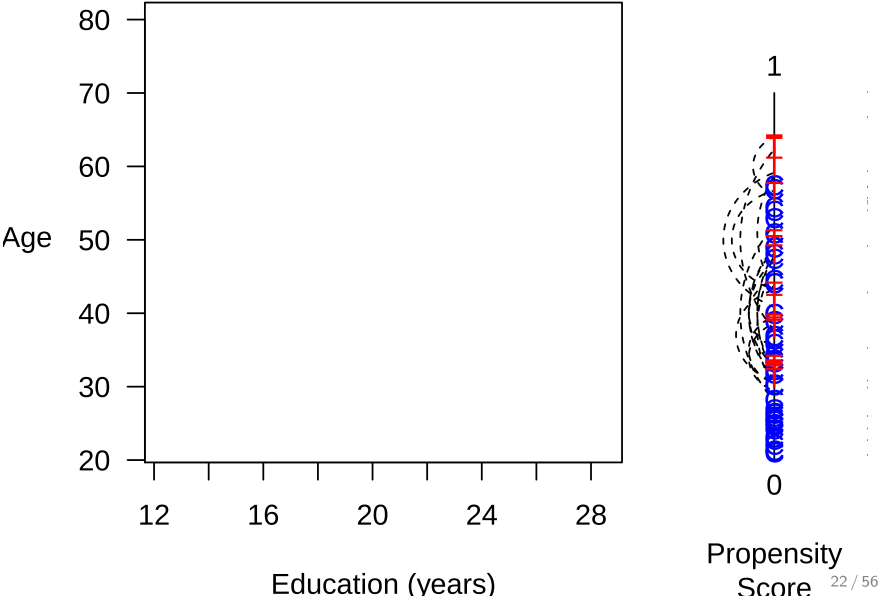

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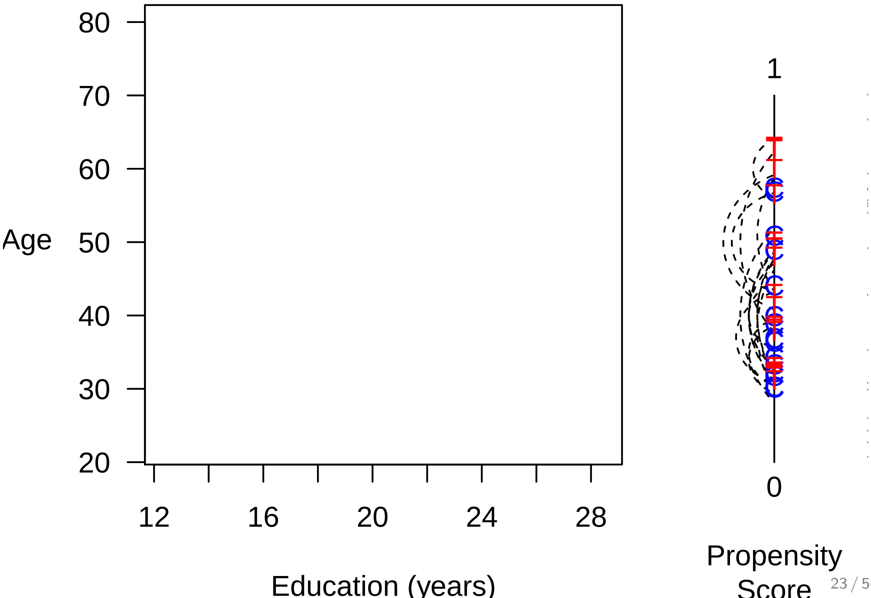

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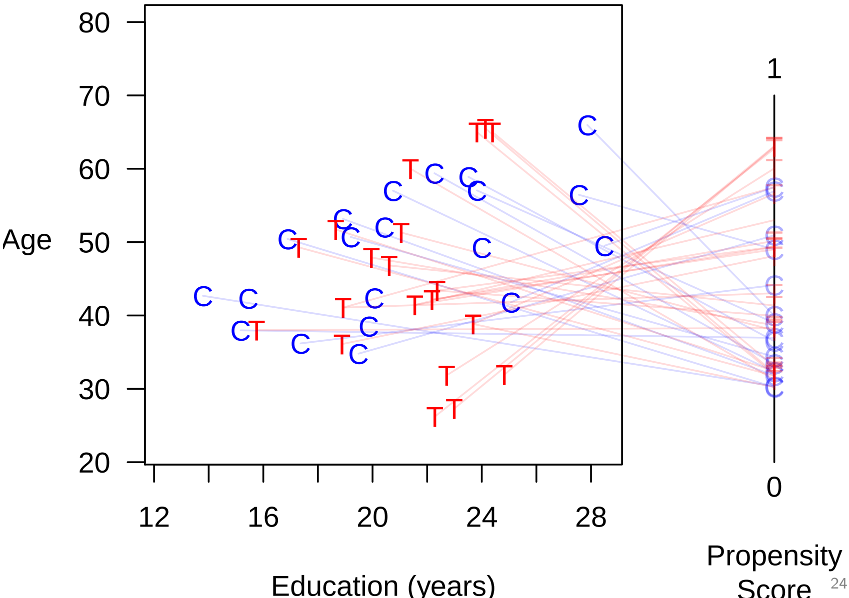

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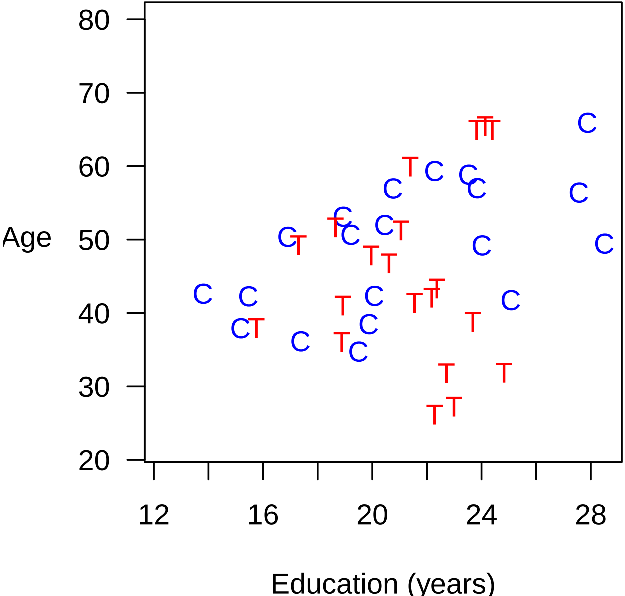

Method 3: Coarsened Exact Matching

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1. Preprocess (Matching)

2. Estimation Difference in means or a model

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

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    - Easier, but still iterative

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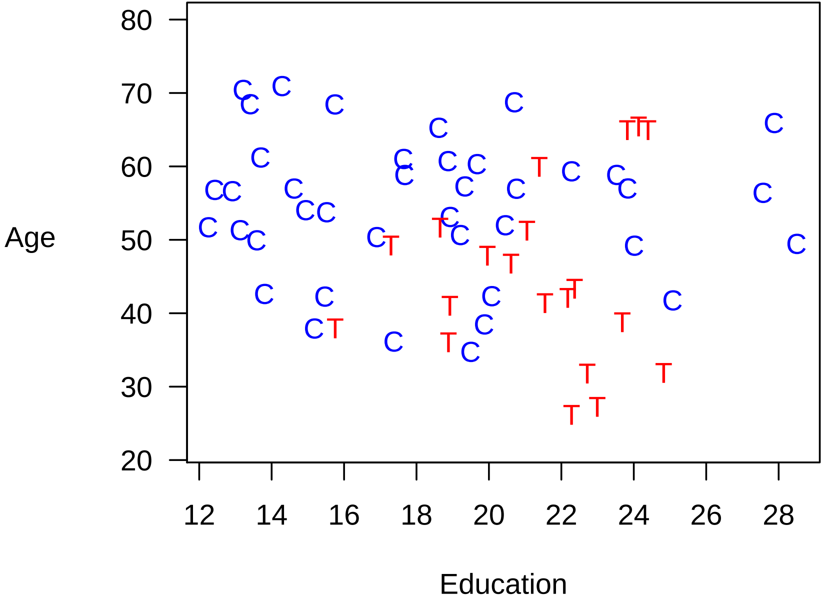

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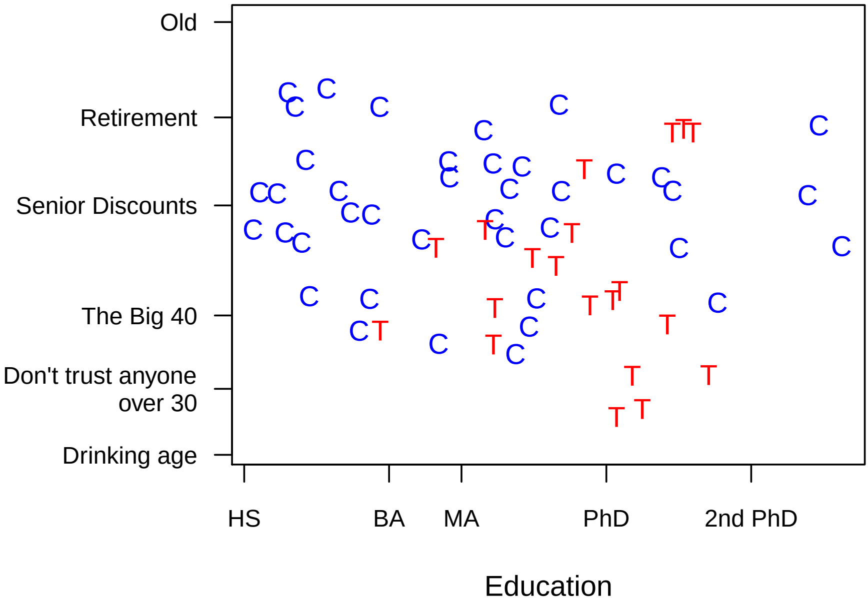

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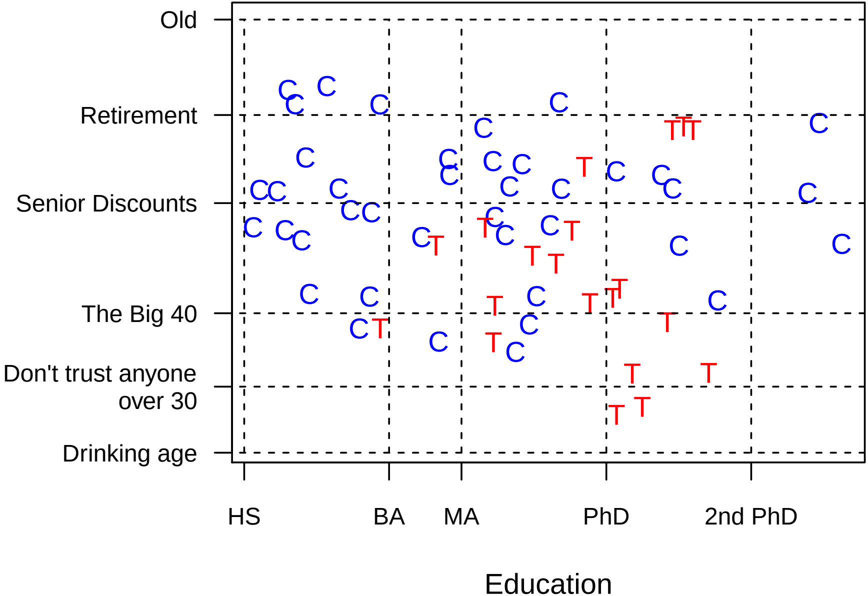

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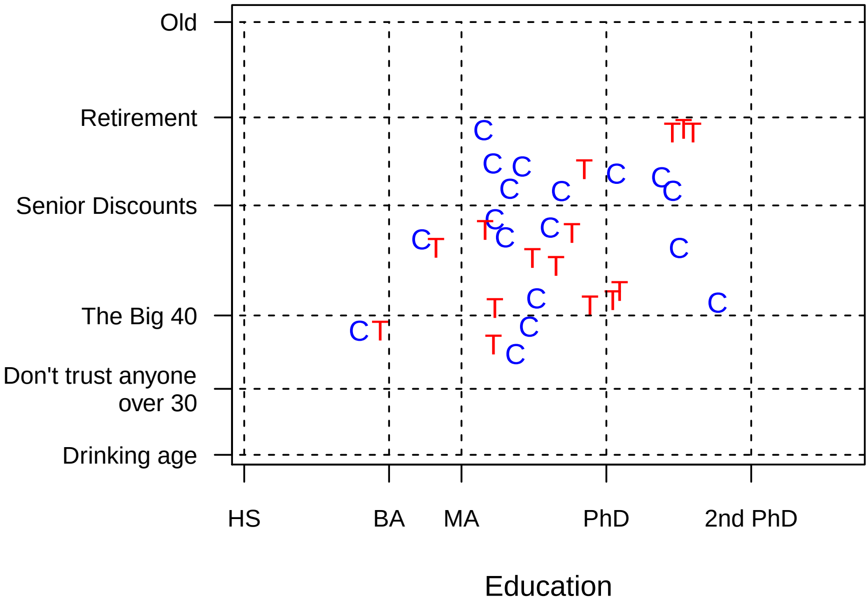

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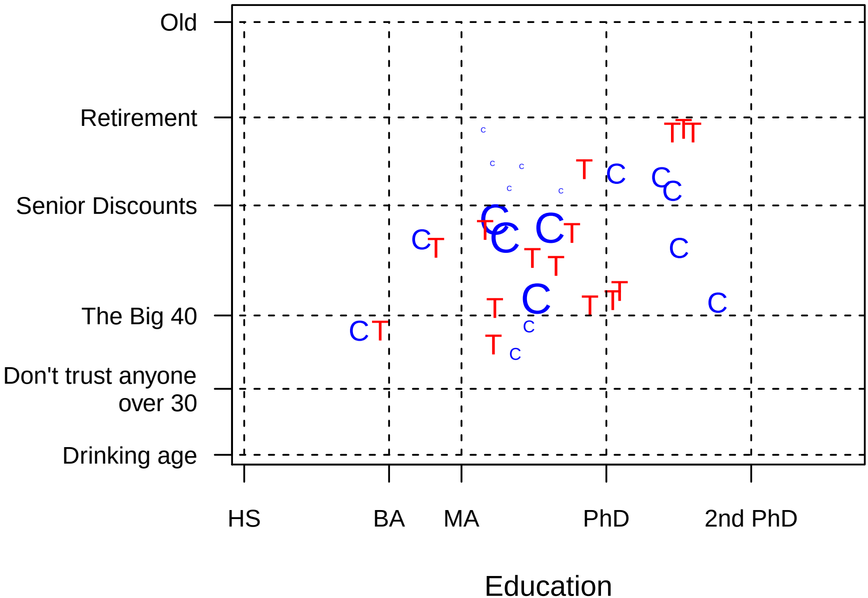

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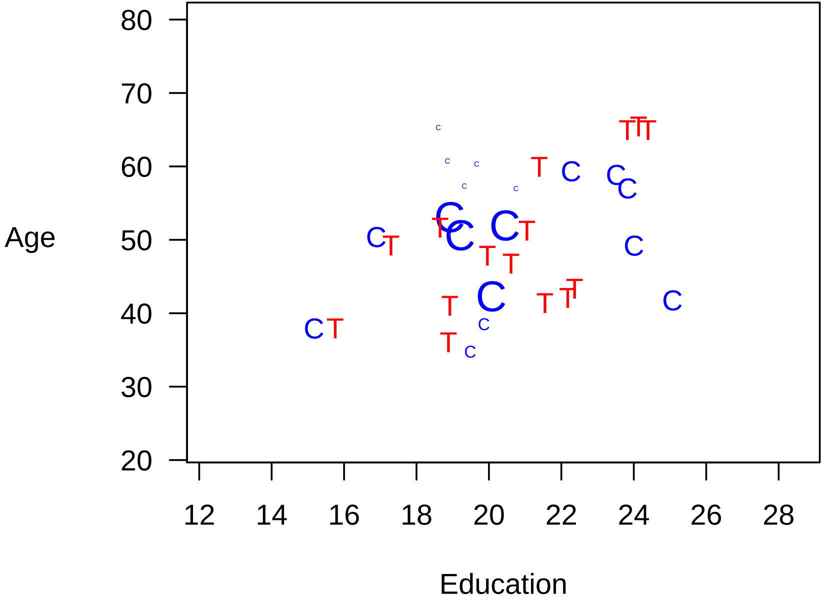

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$$\mathcal{L}_1(f, g; H) = \frac{1}{2} \sum_{\ell_1 \cdots \ell_k \in H(\mathbf{X})} |f_{\ell_1 \cdots \ell_k} - g_{\ell_1 \cdots \ell_k}|$$

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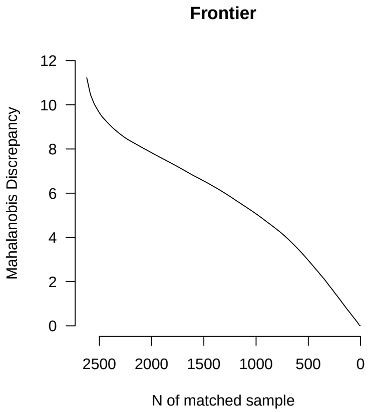
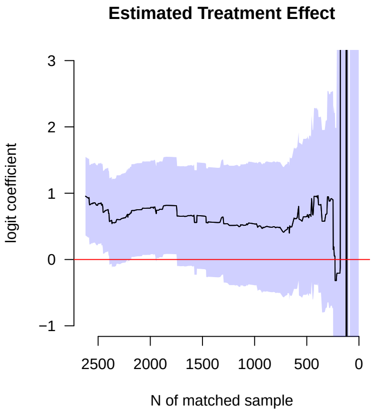
- Result: Optimal. No need to iterate. Choice of solution left to researcher.

Example Frontier, and Results





Constructing the Mahalanobis Frontier

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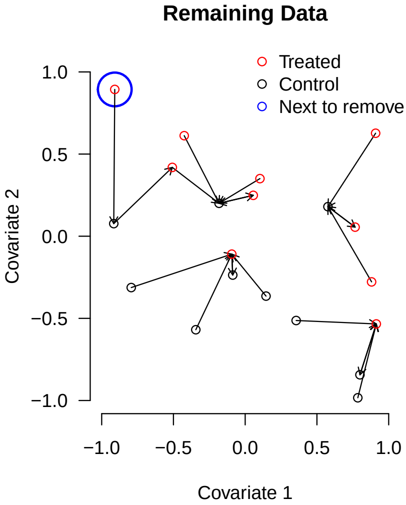

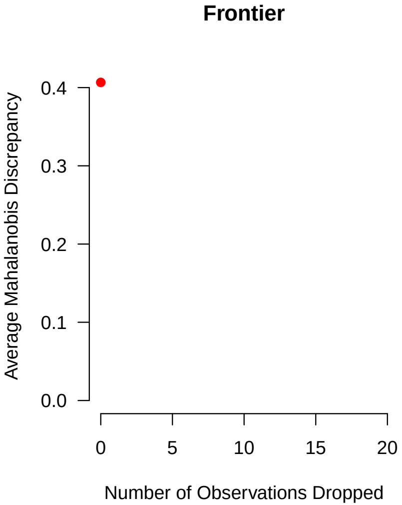

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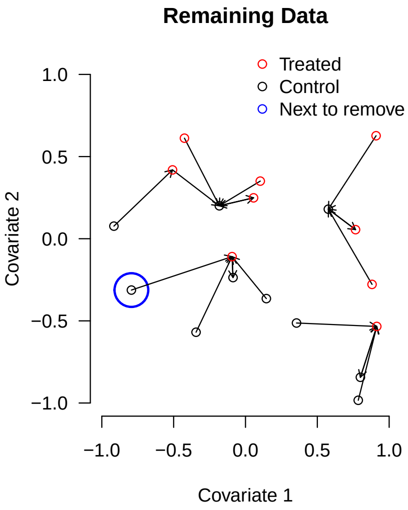

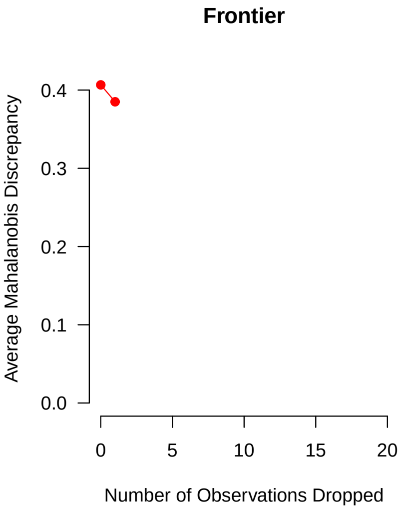

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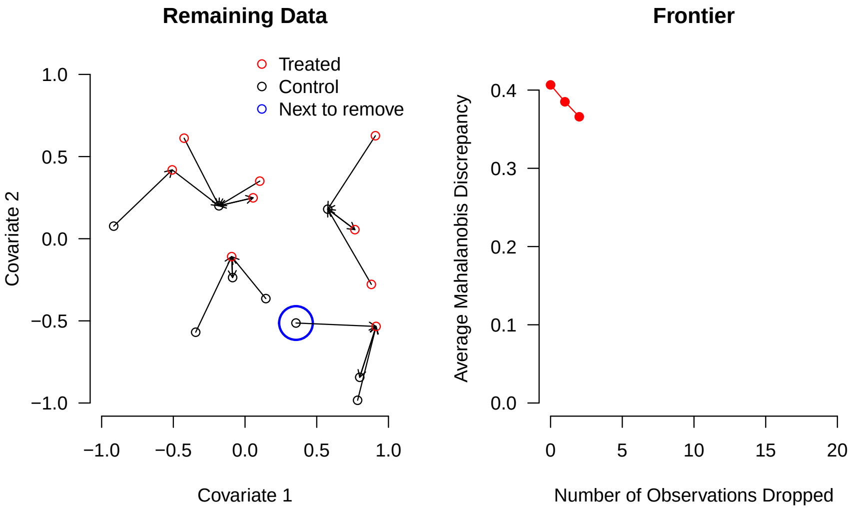

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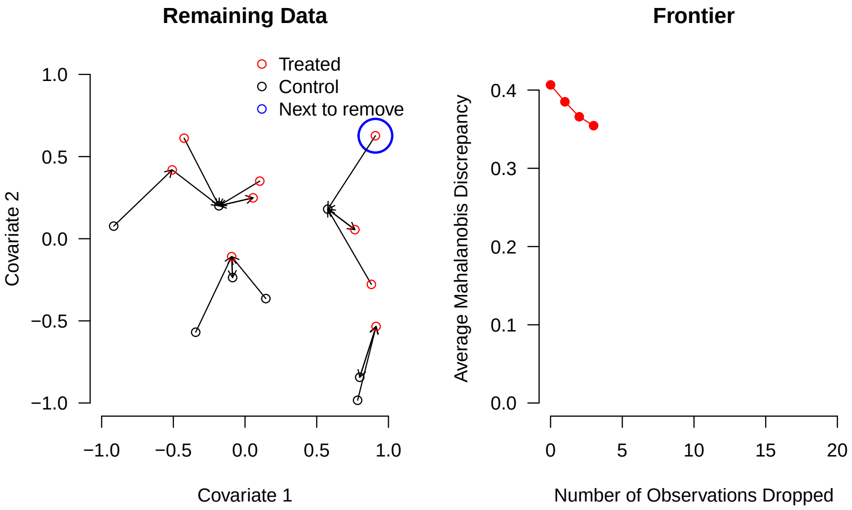

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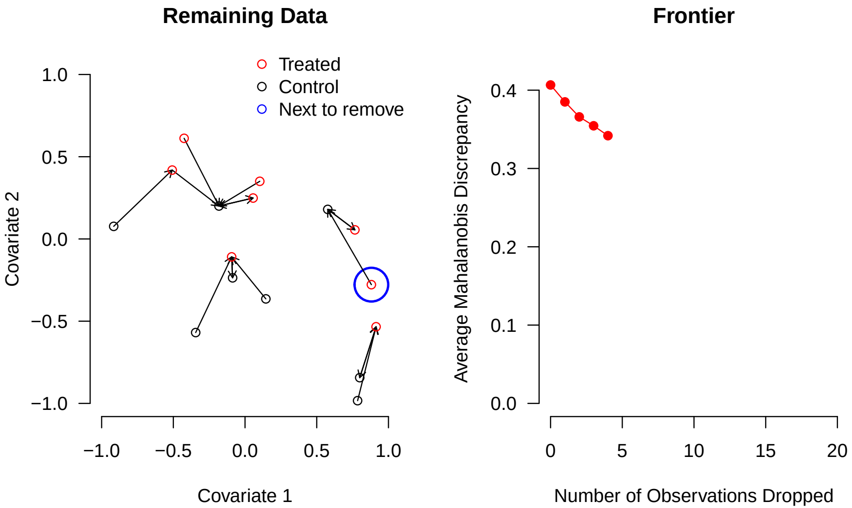

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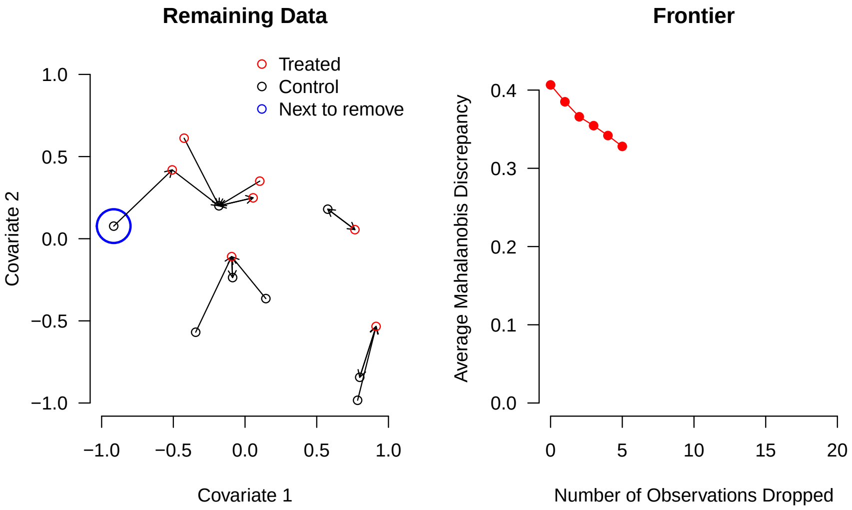

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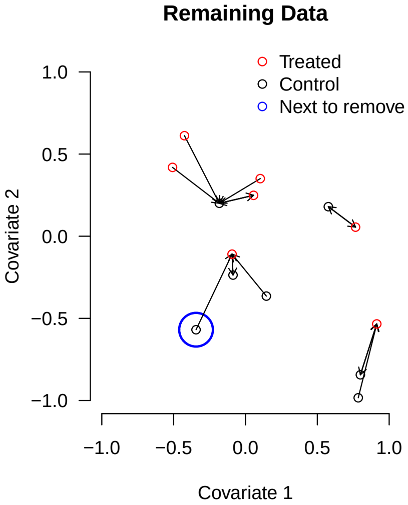

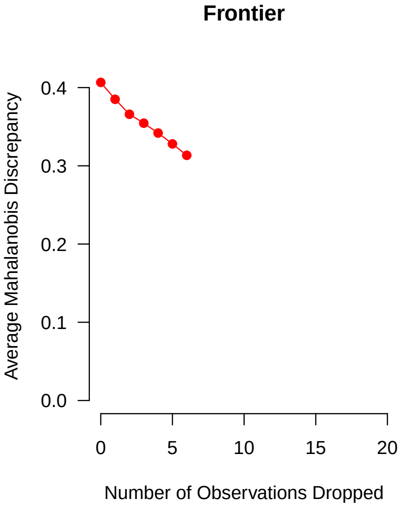

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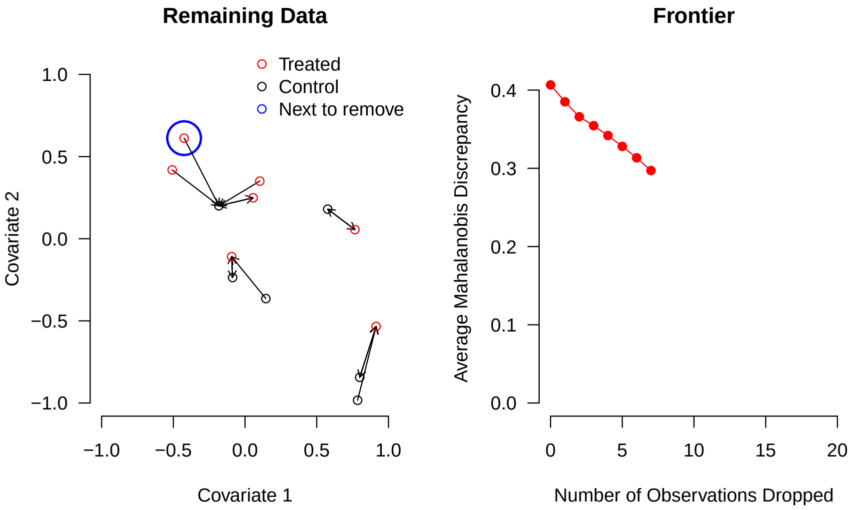

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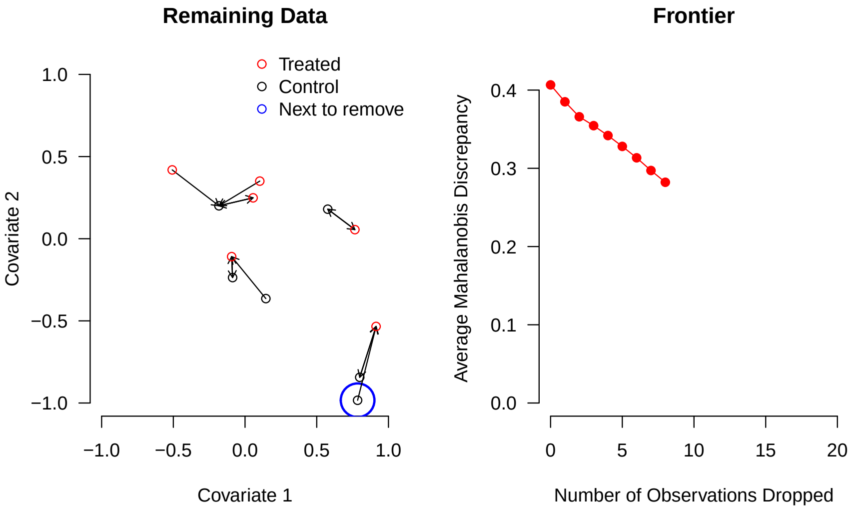

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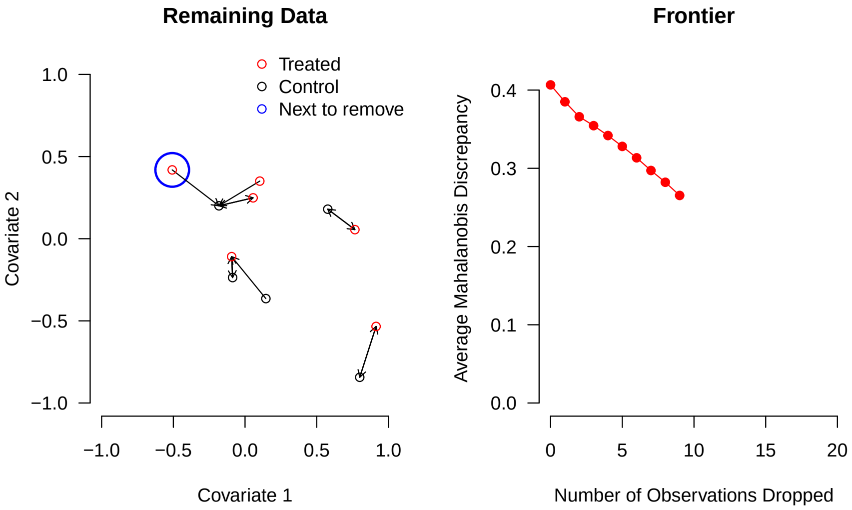

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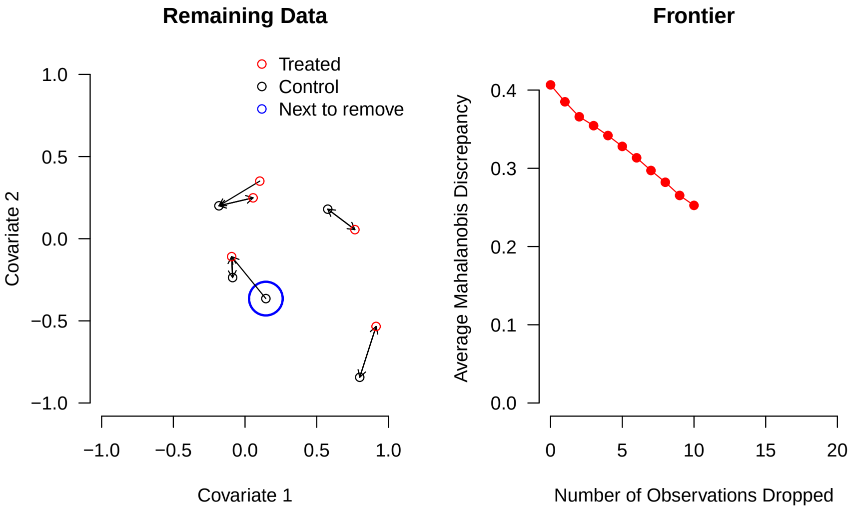

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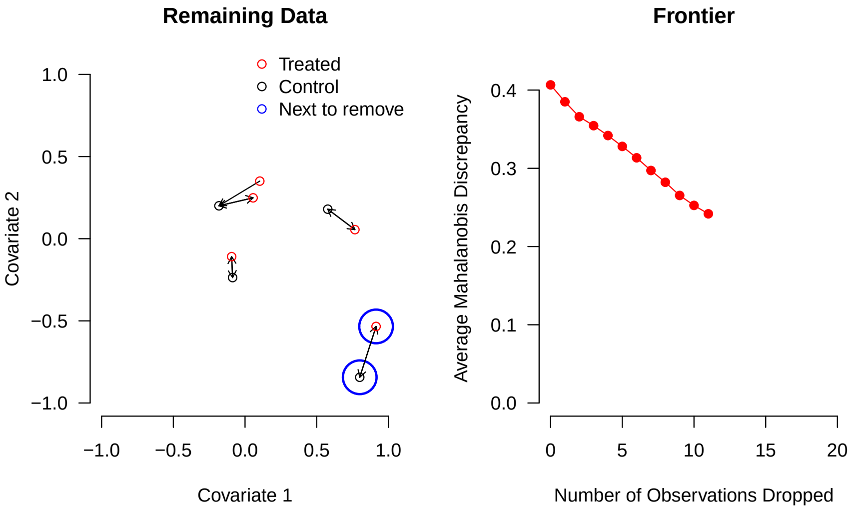

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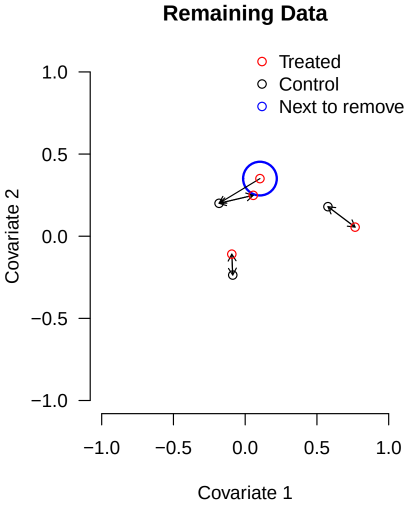

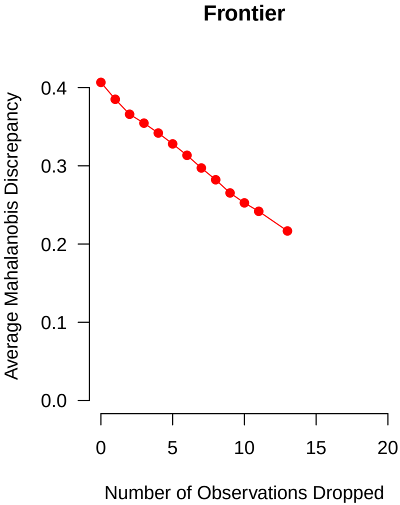

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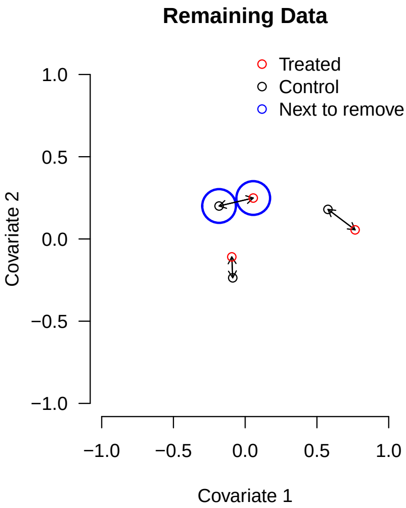

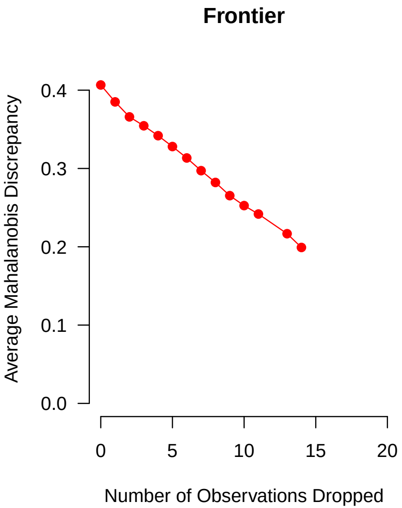

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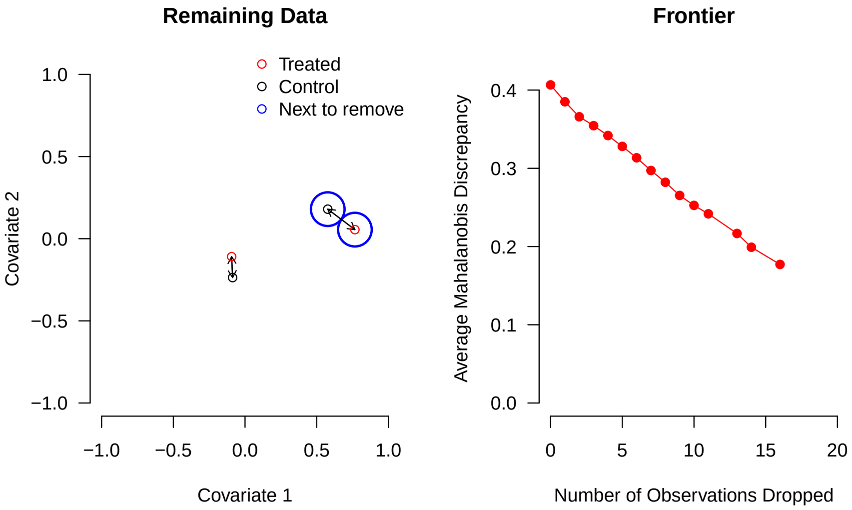

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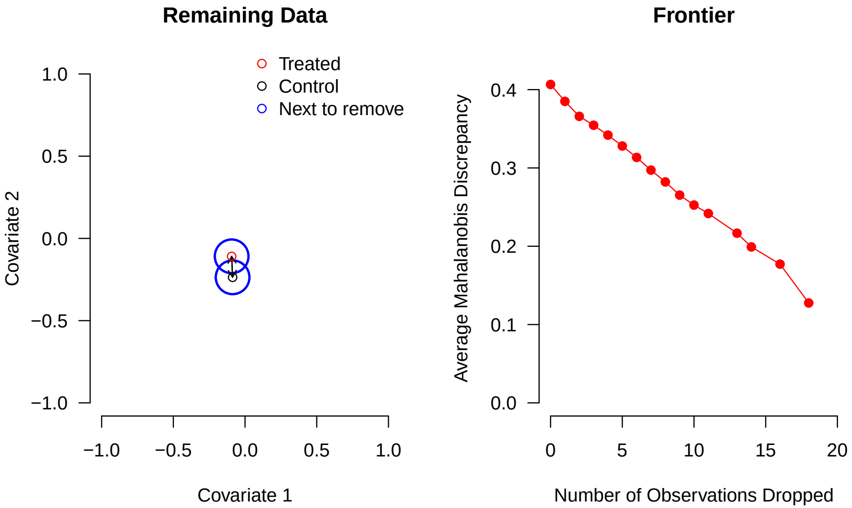
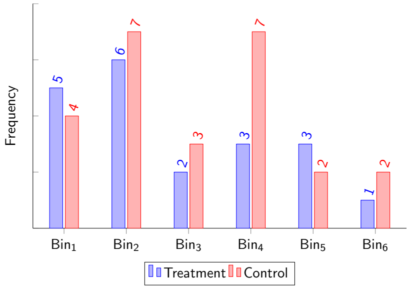
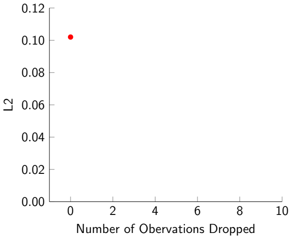


Constructing the L1/L2 Frontier





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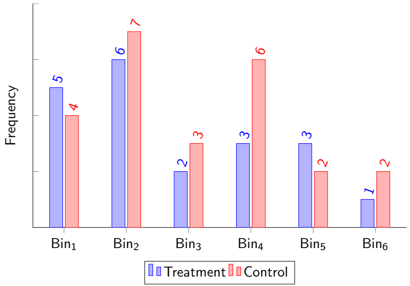

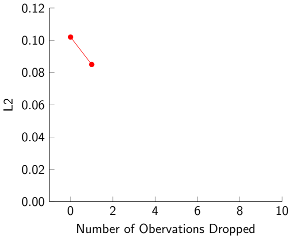

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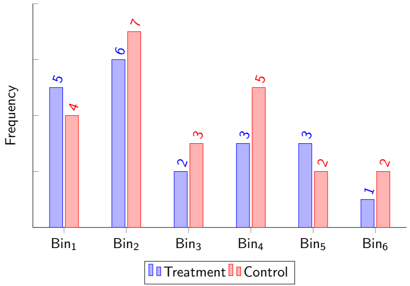

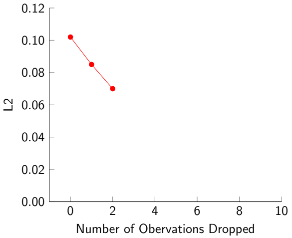

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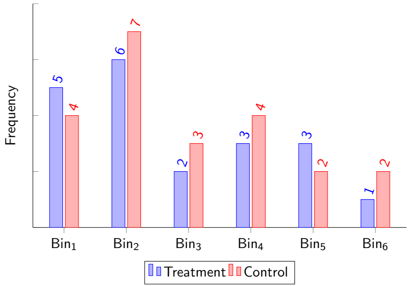

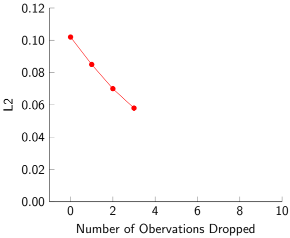

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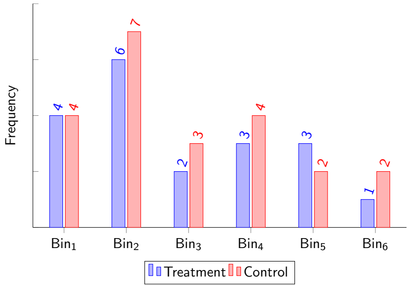

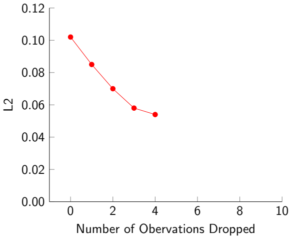

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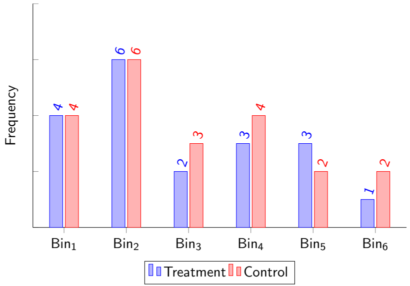

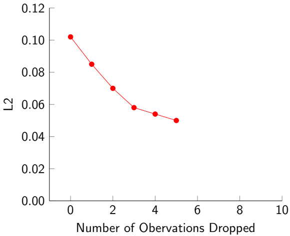

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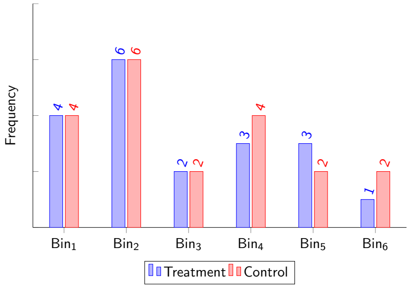

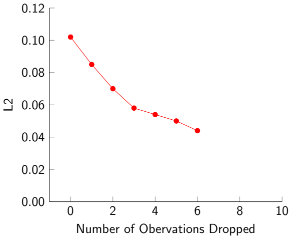

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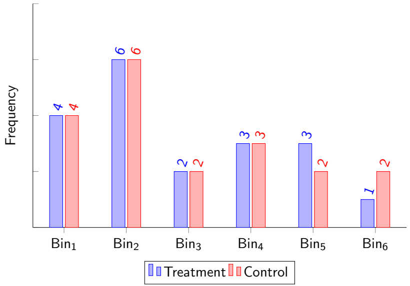

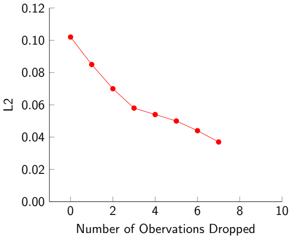

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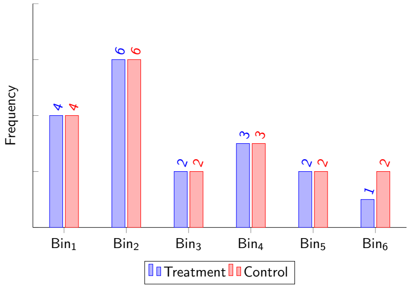

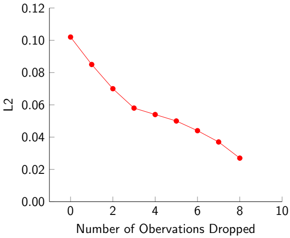

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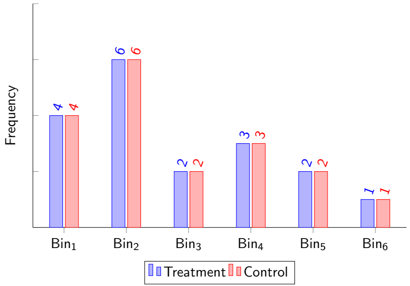
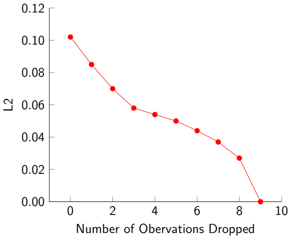
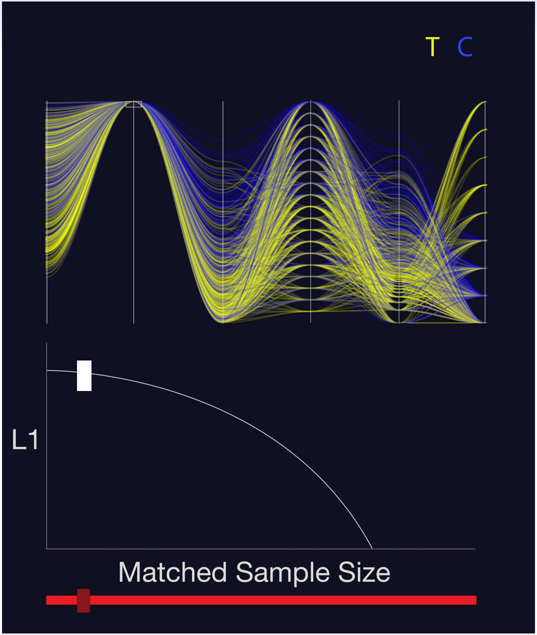
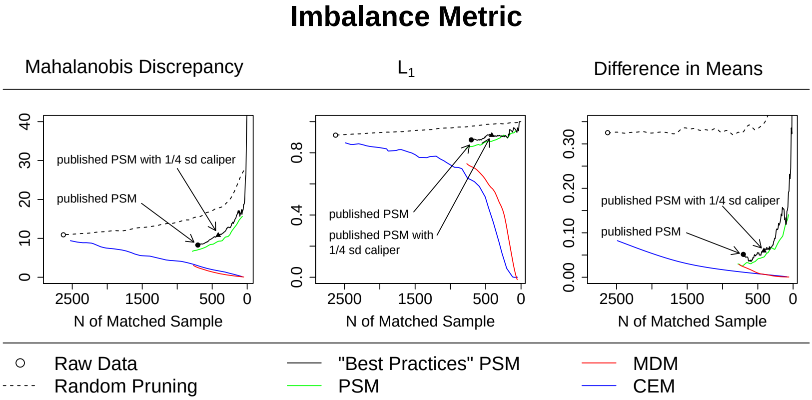





T C
L1
Matched Sample Size

Foreign Aid Shocks & Conflict

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



Healthways Data

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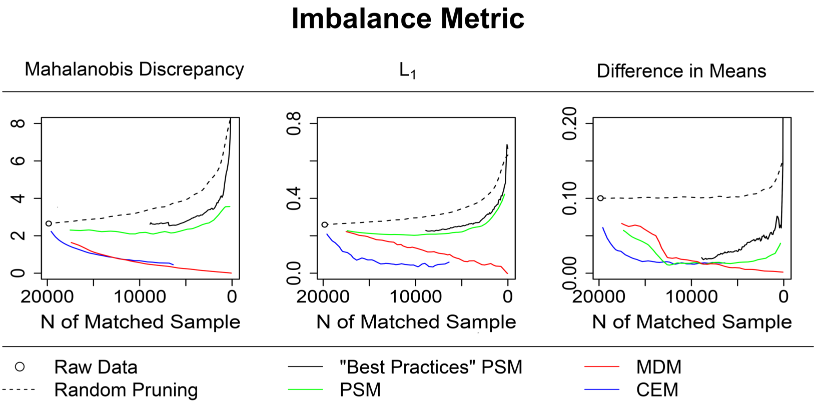

Called/Not Called Data

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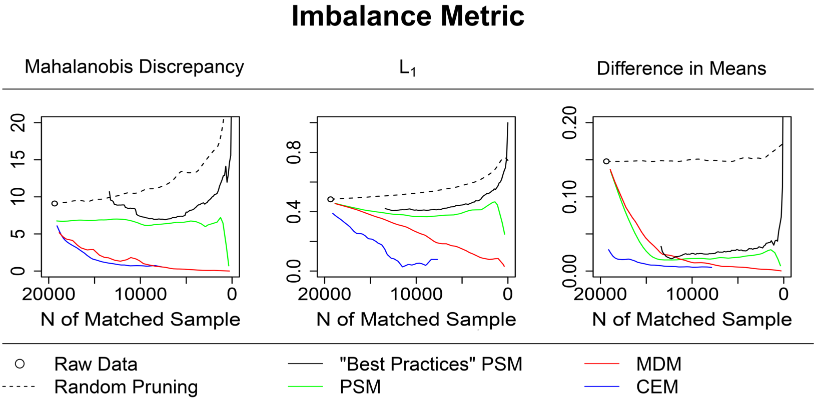
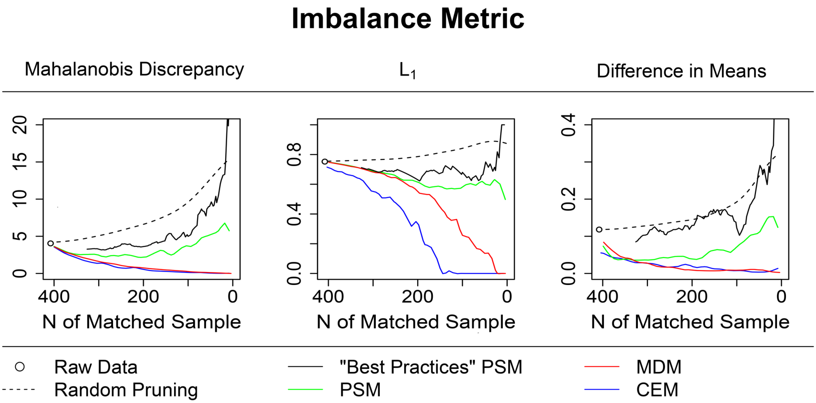


FDA Drug Approval Times

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



Job Training (Lelonde Data)

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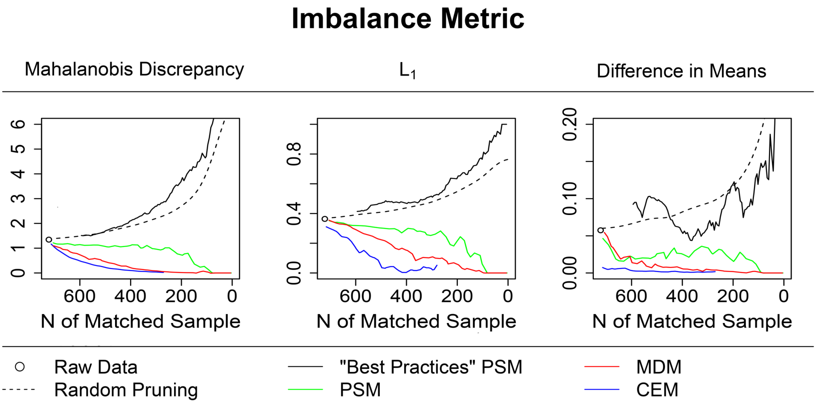
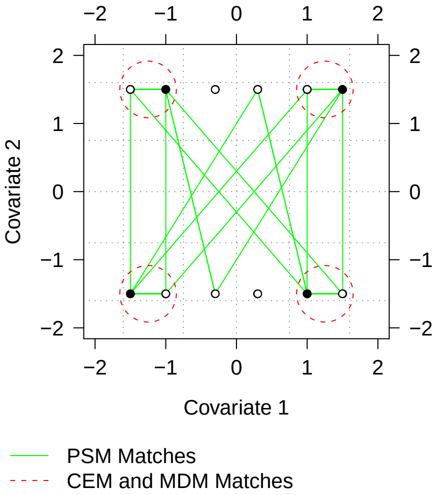
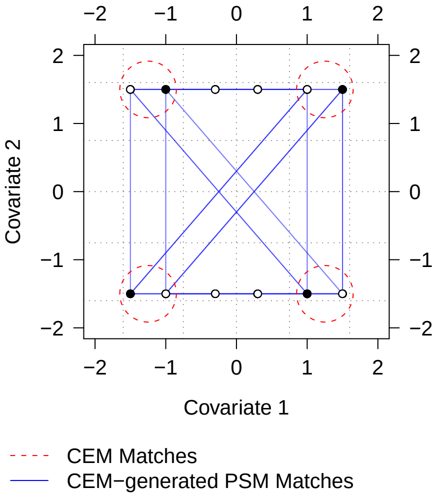


PSM Approximates Random Matching in Balanced Data



Destroying CEM with PSM's Two Step Approach



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For more information

GaryKing.org