

Optimizing Balance and Sample Size in Matching Methods for Causal Inference¹

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¹Joint work with Christopher Lucas and Richard Nielsen

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 - Solution: Other methods & our approach do not share this problem

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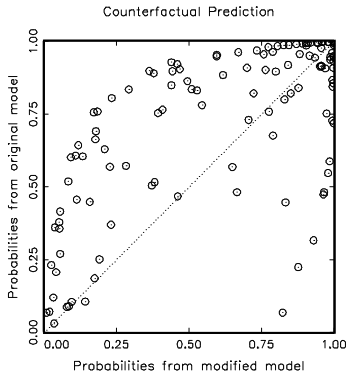
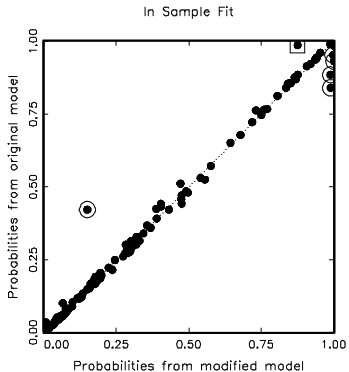
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- **The question:** How *model dependent* are the results?

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



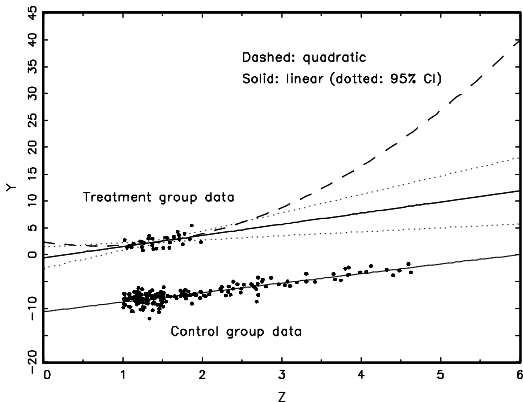
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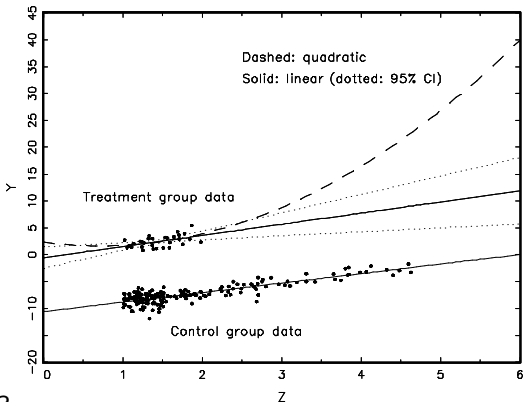
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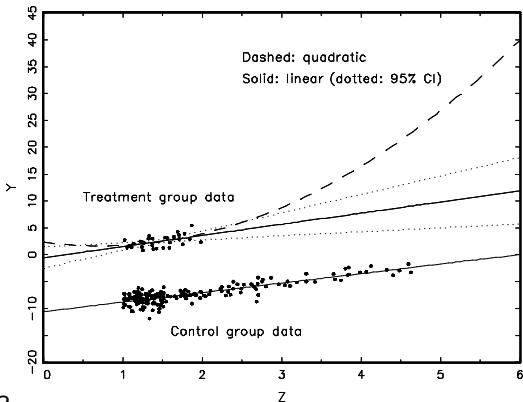
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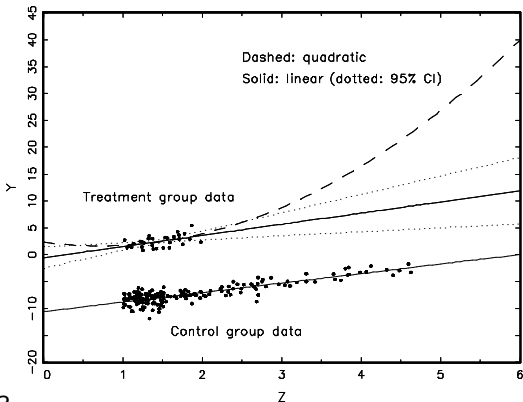


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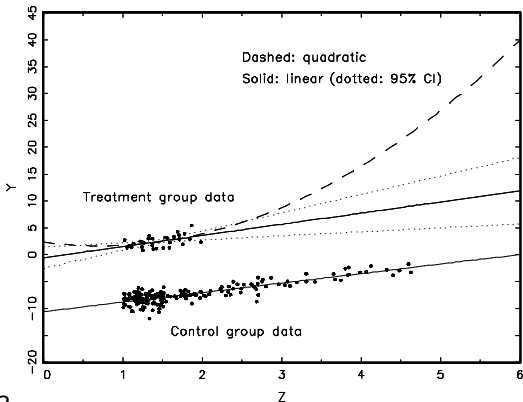


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- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

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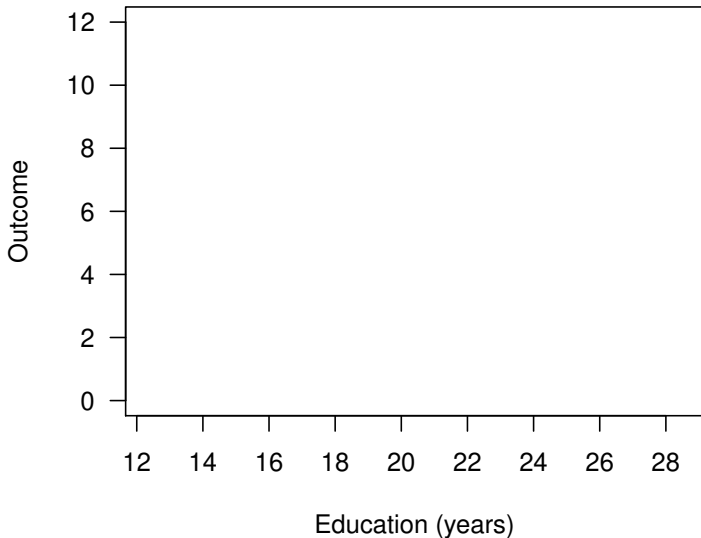
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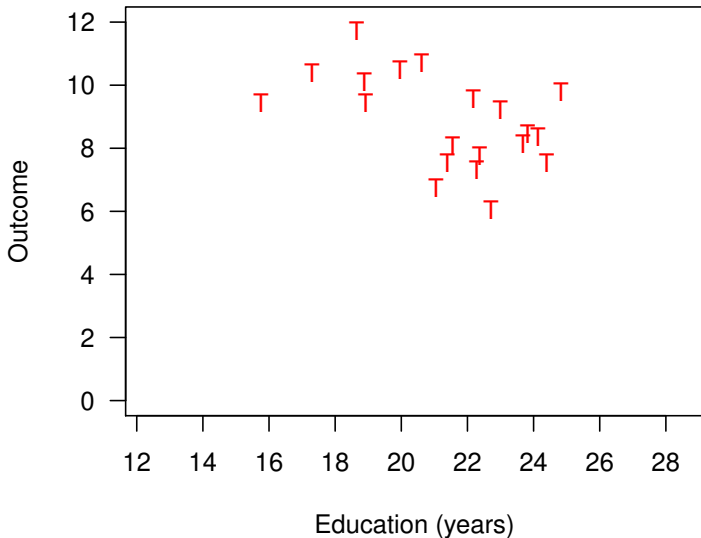
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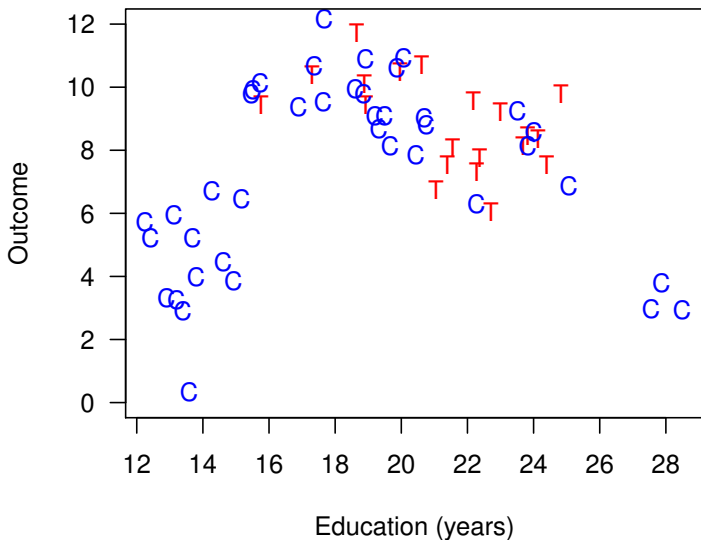
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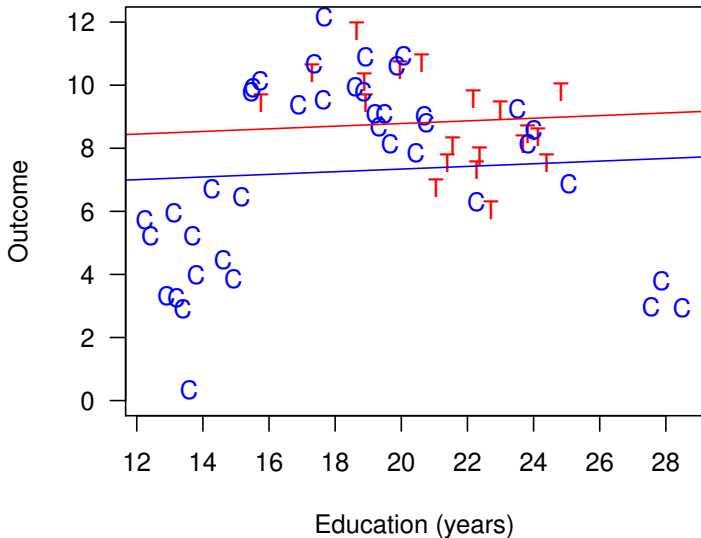
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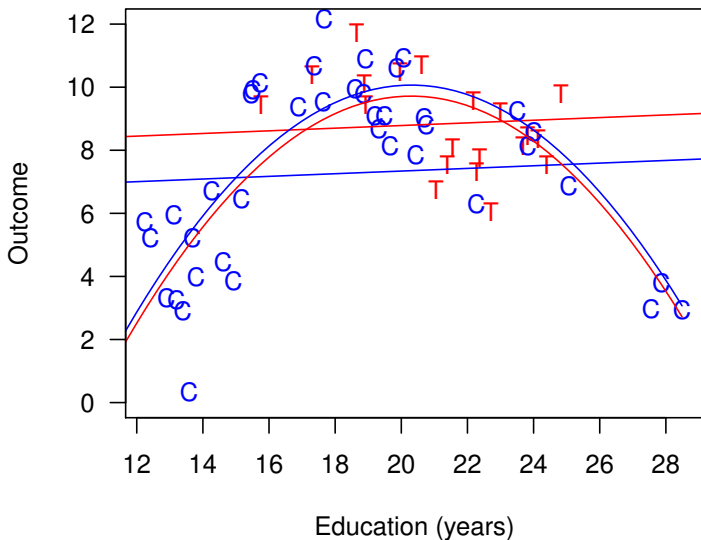
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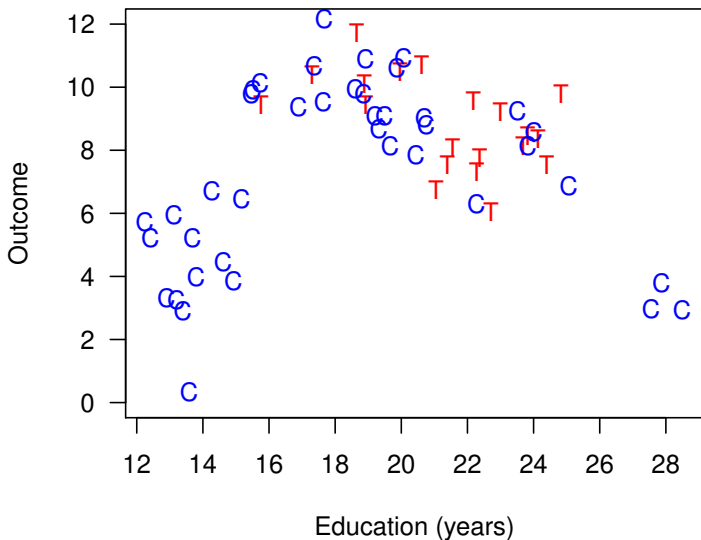
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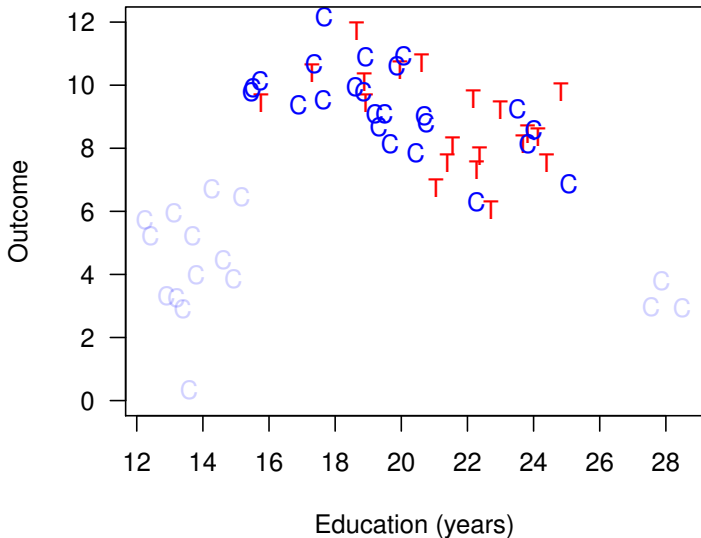
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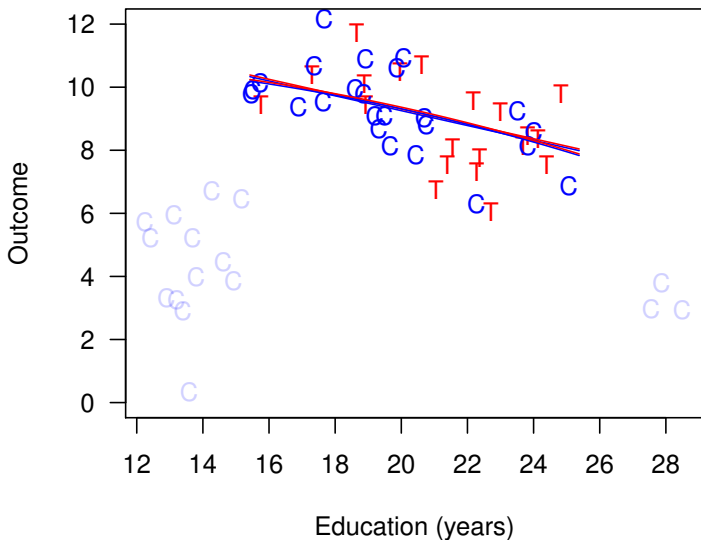
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Matching reduces model dependence, bias, and variance

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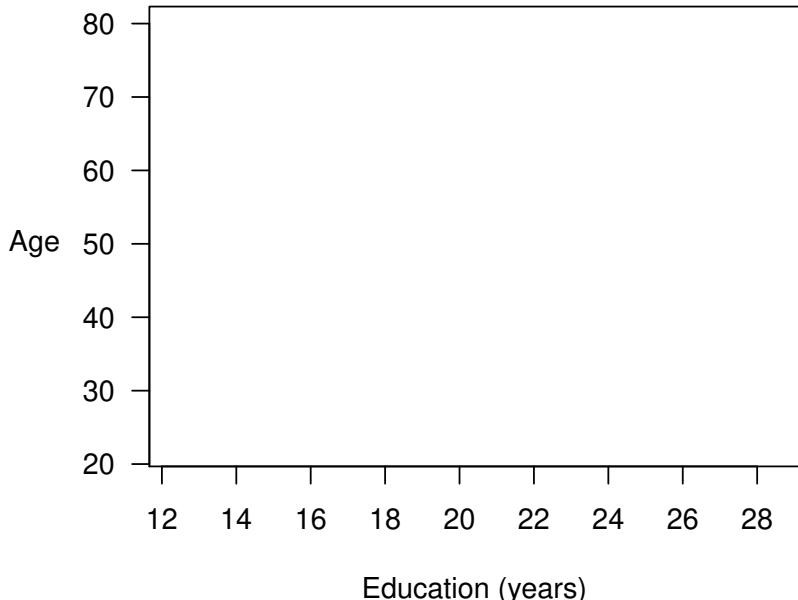
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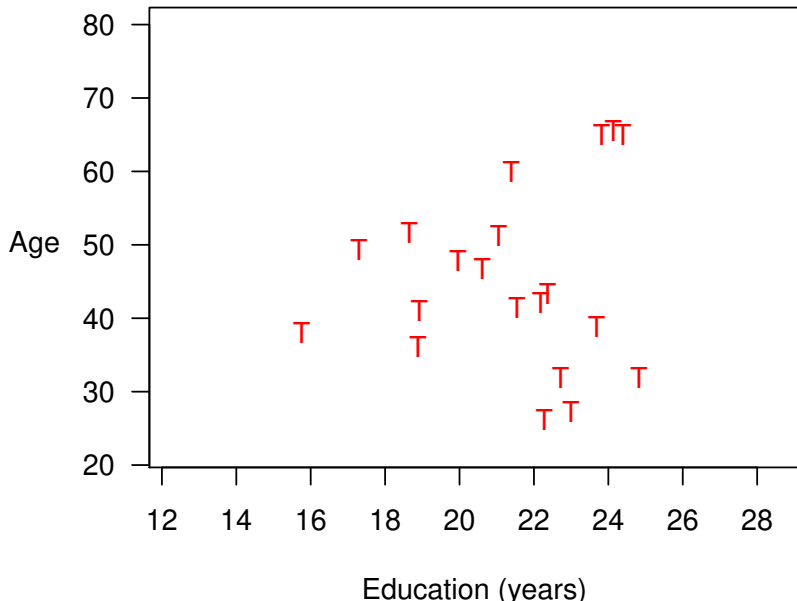
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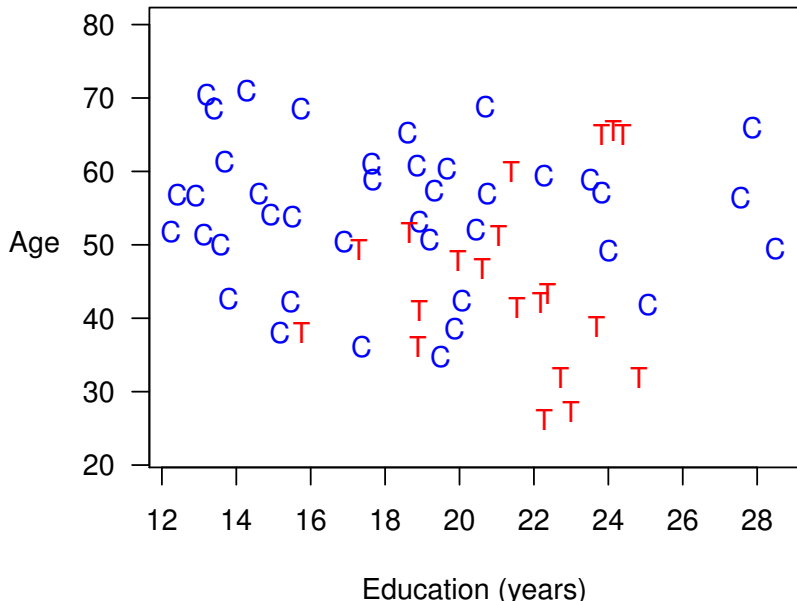
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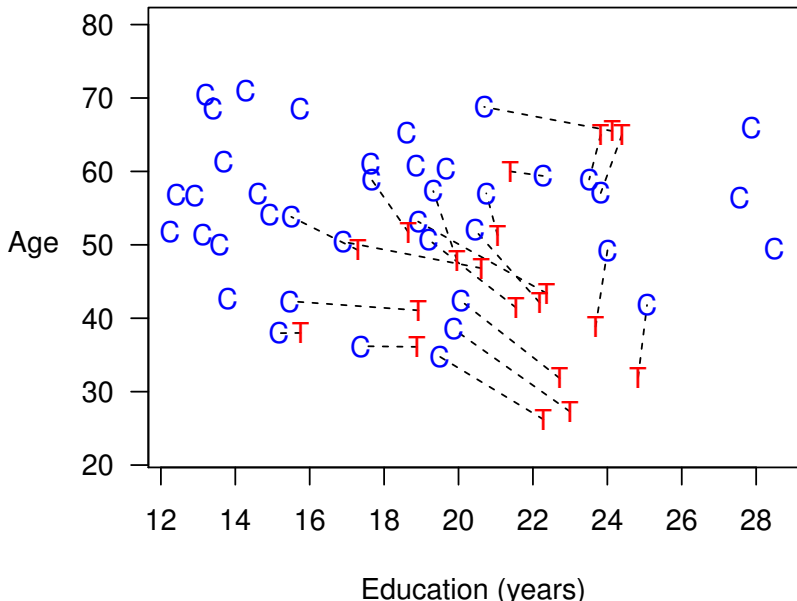
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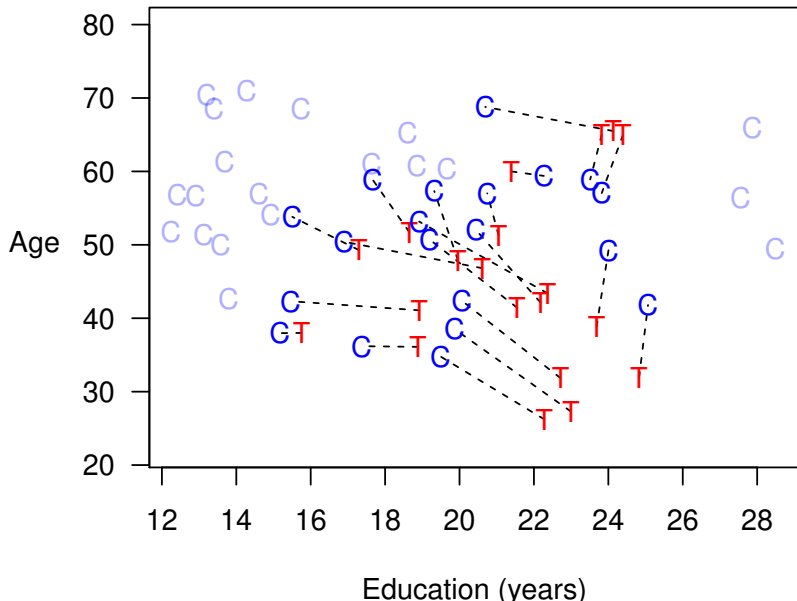
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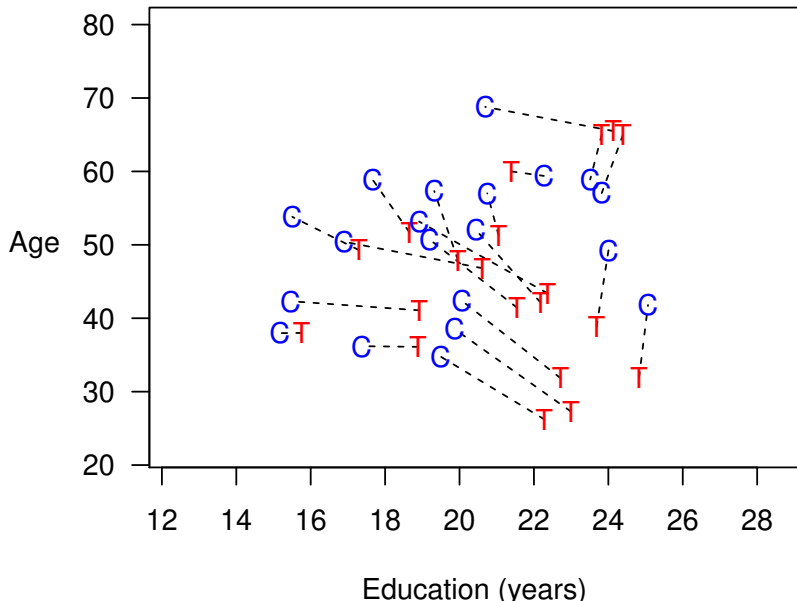
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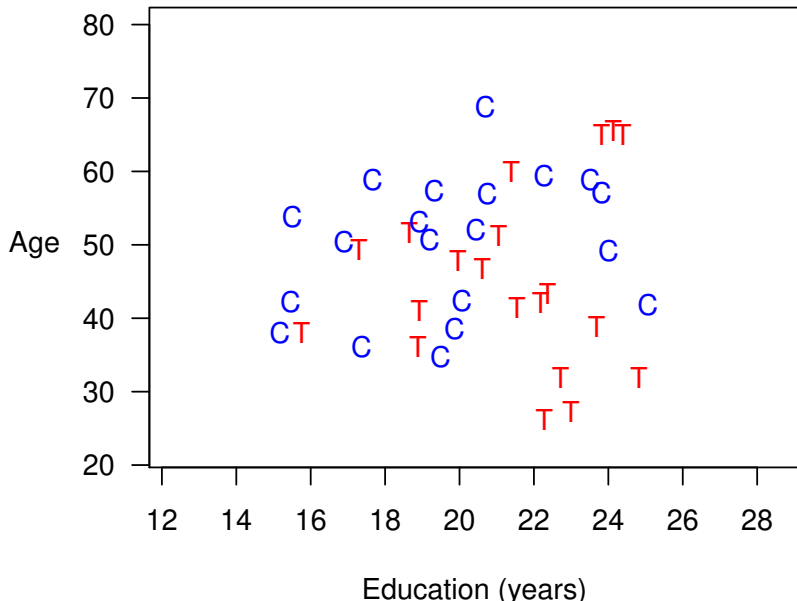
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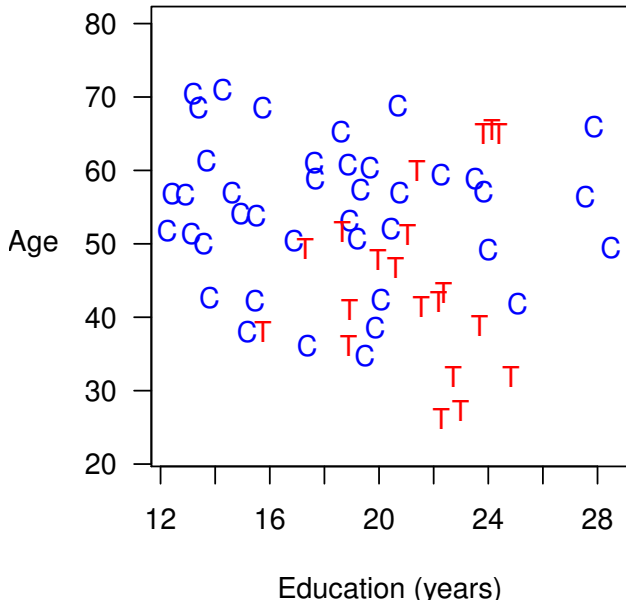
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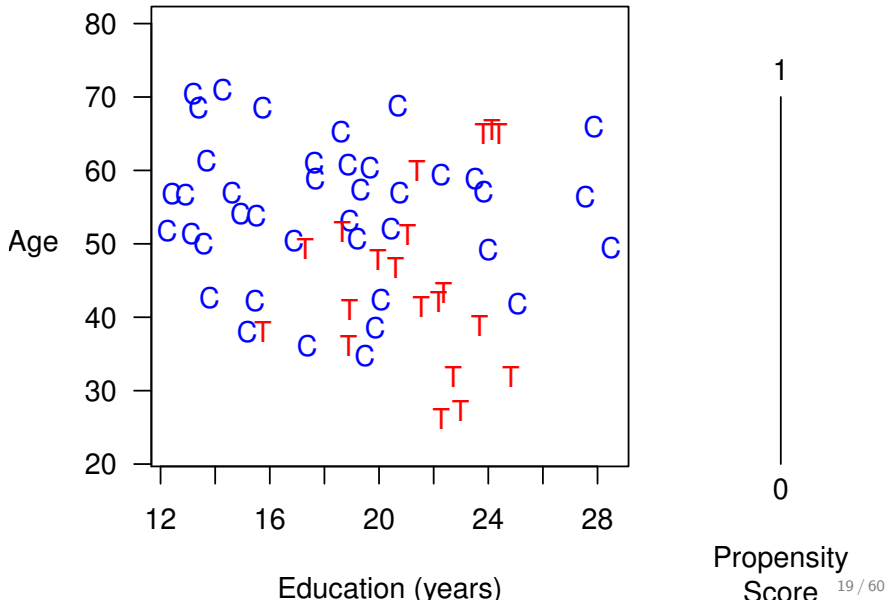
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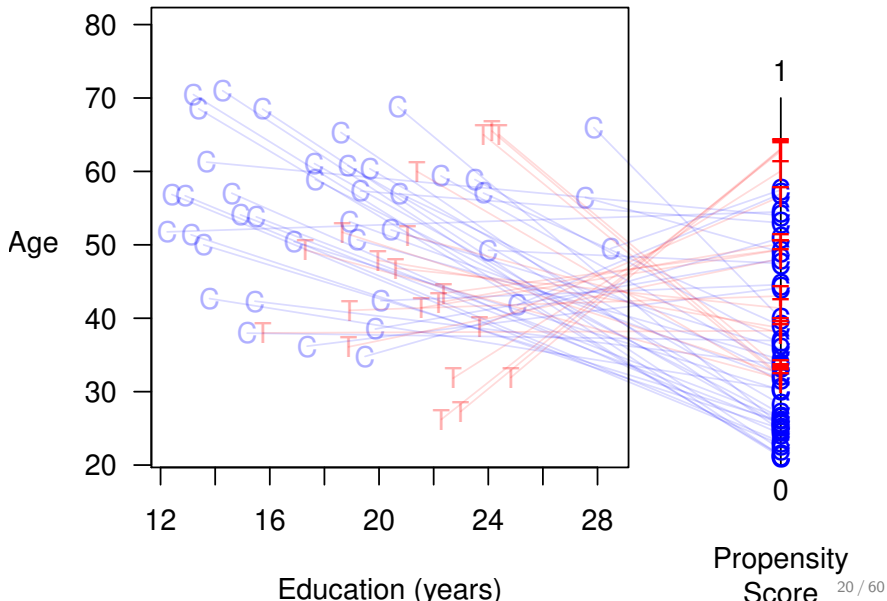
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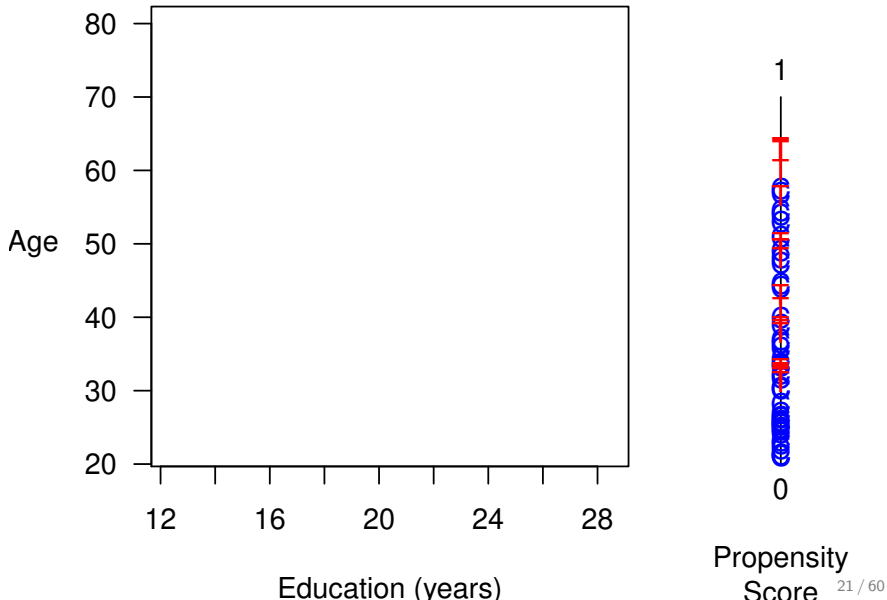
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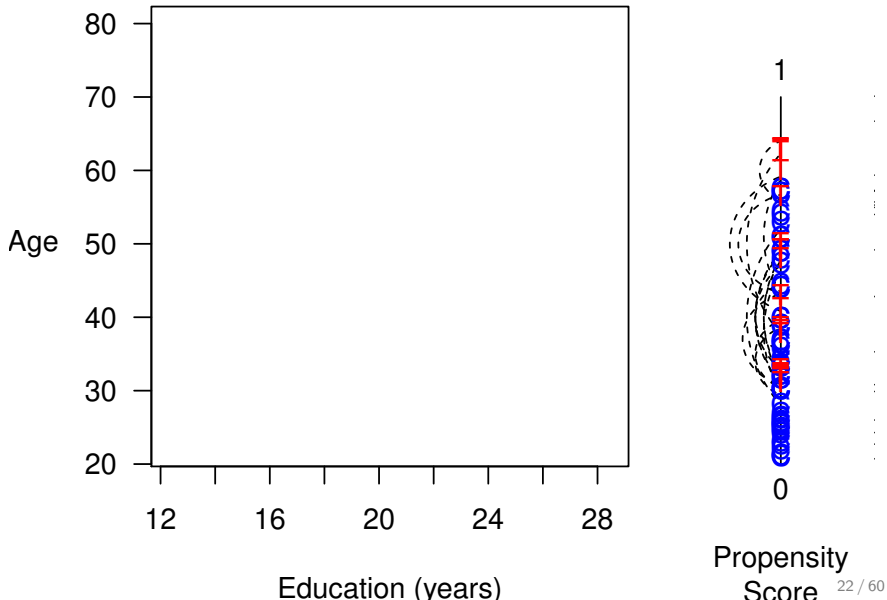
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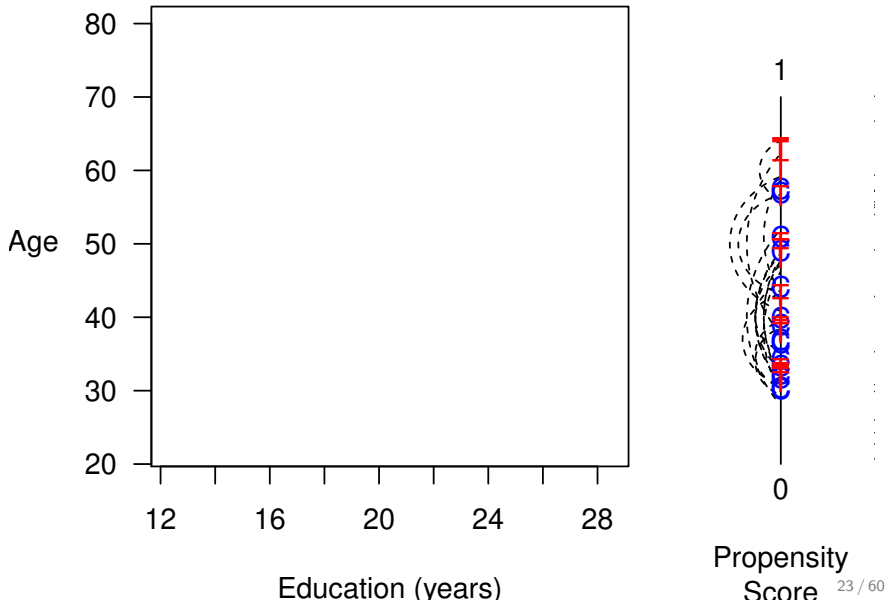
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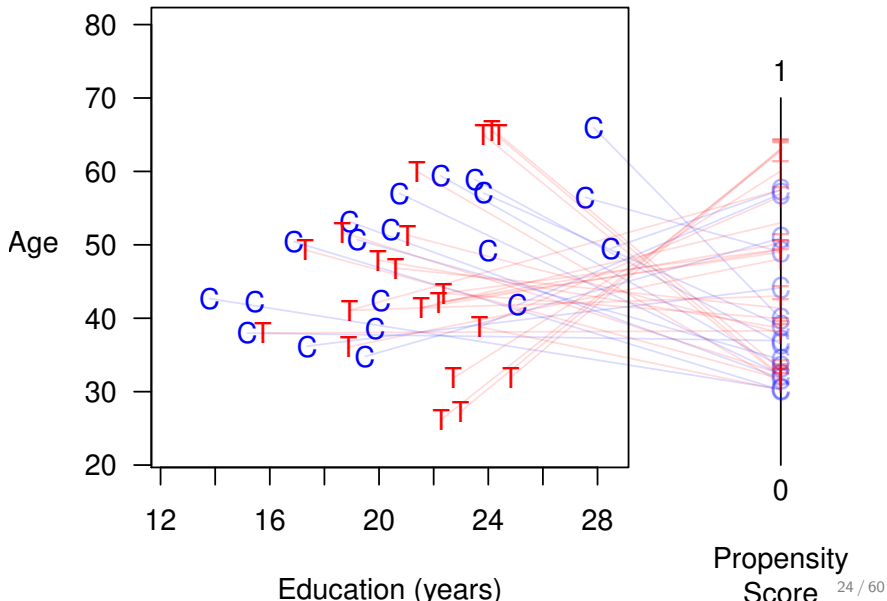
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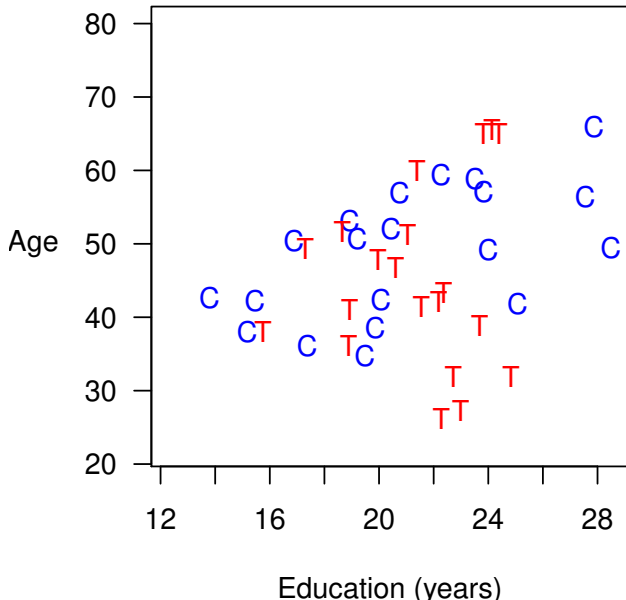
Propensity Score Matching



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Method 3: Coarsened Exact Matching

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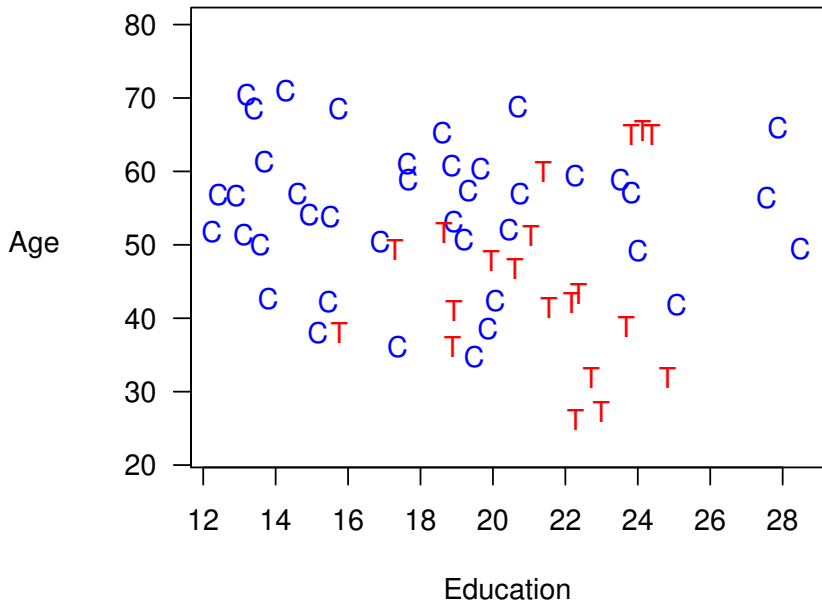
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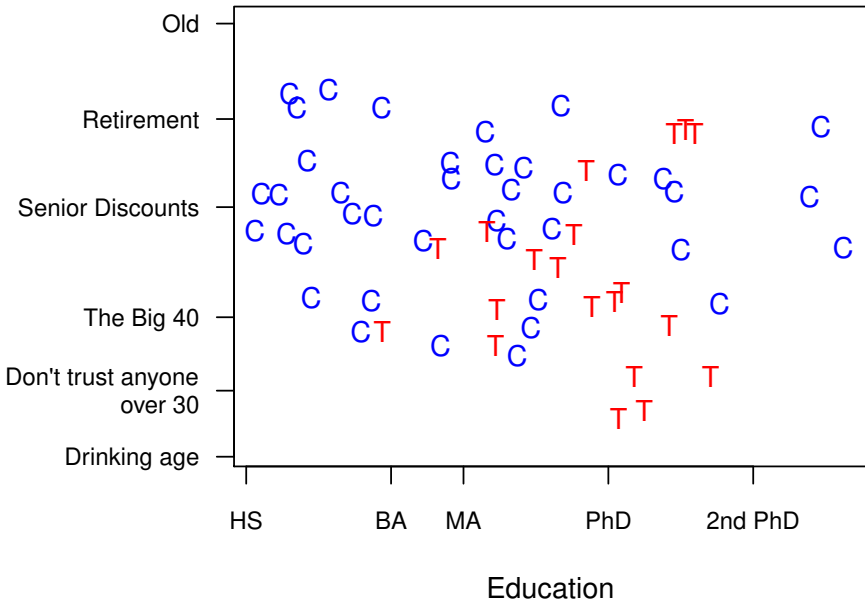
- Easier, but still iterative

Coarsened Exact Matching

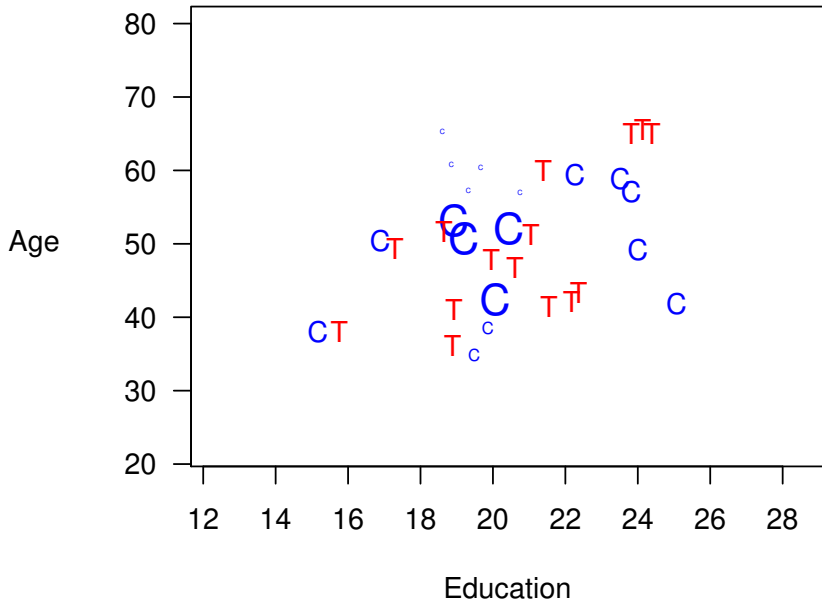
Coarsened Exact Matching



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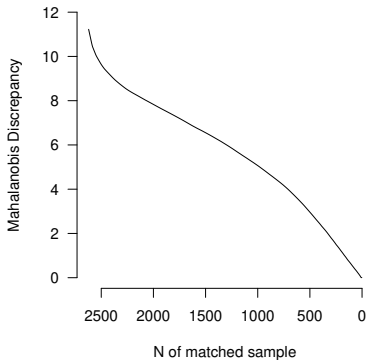
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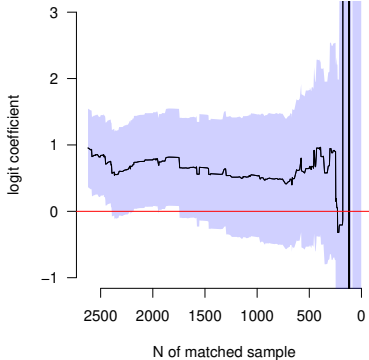
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- **Result:** Optimal. No need to iterate. Choice of solution left to researcher.

Example Frontier, and Results

Frontier

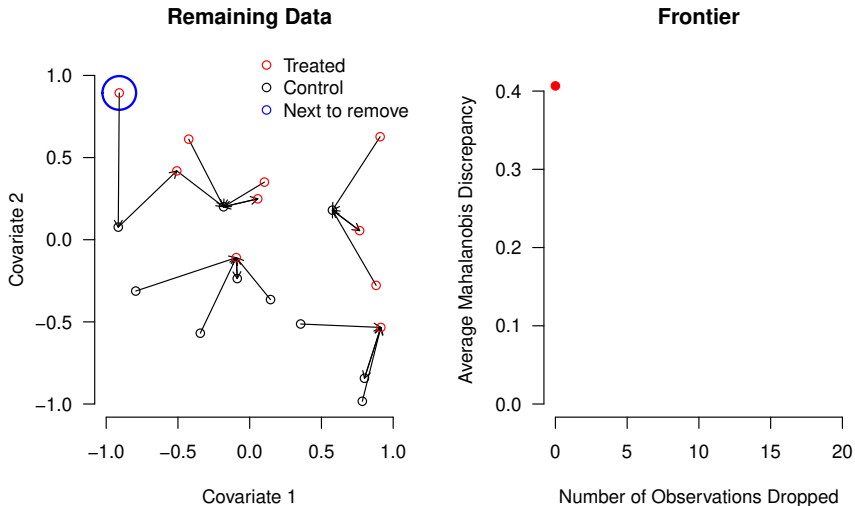


Estimated Treatment Effect

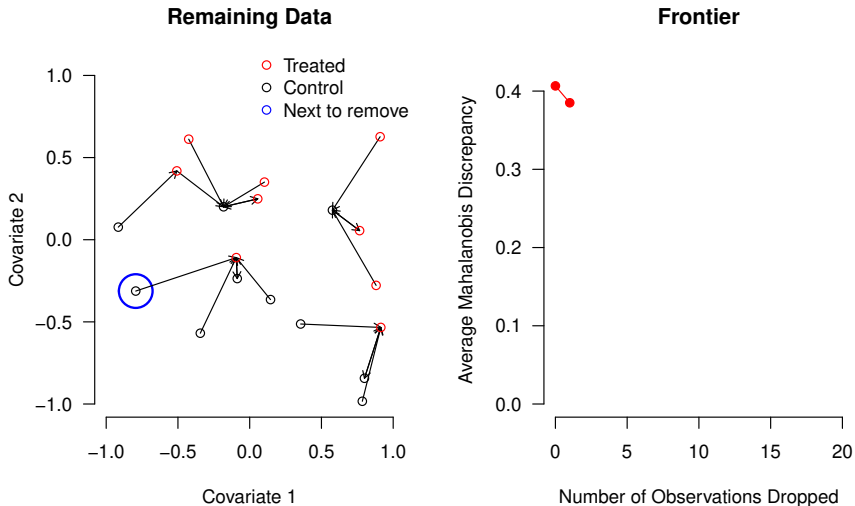


Constructing the Mahalanobis Frontier

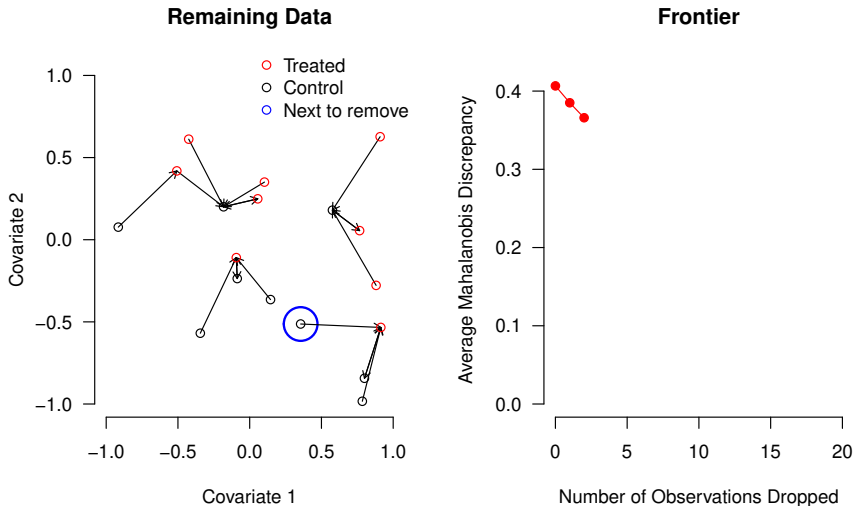
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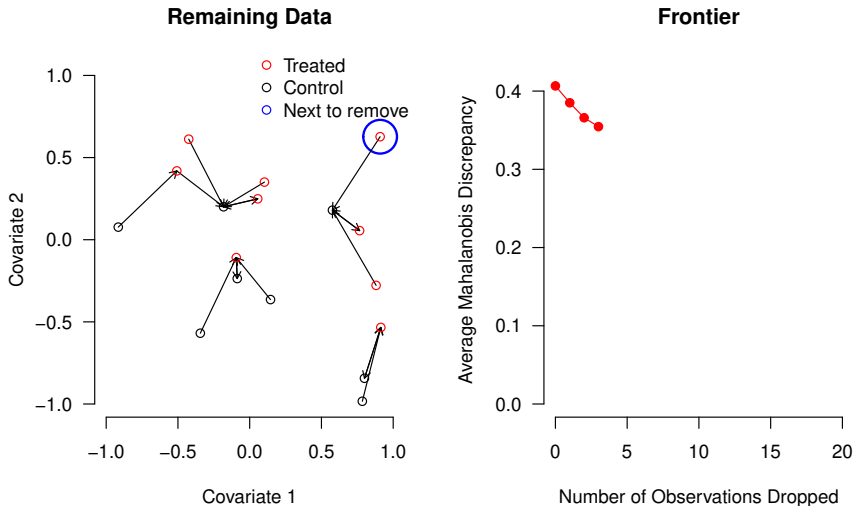
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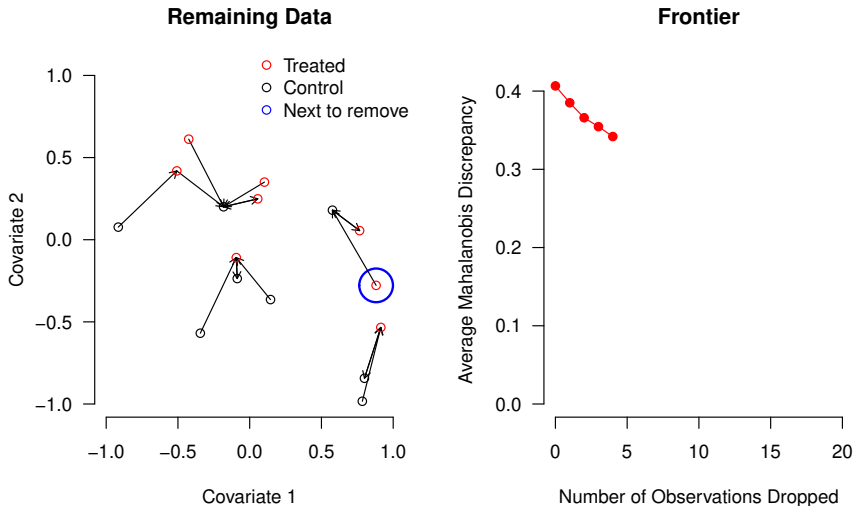
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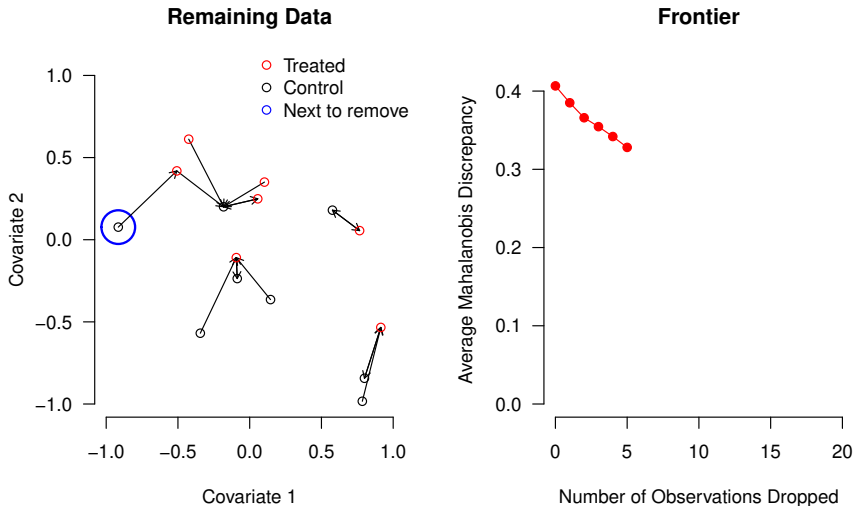
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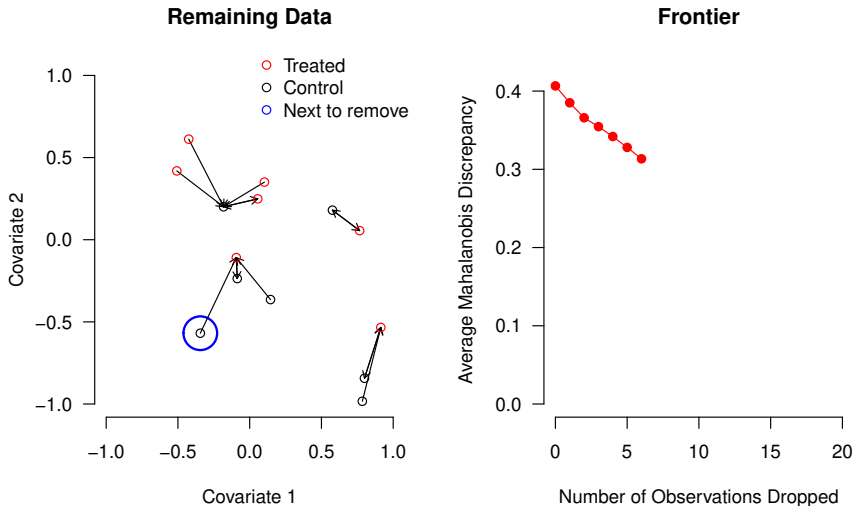
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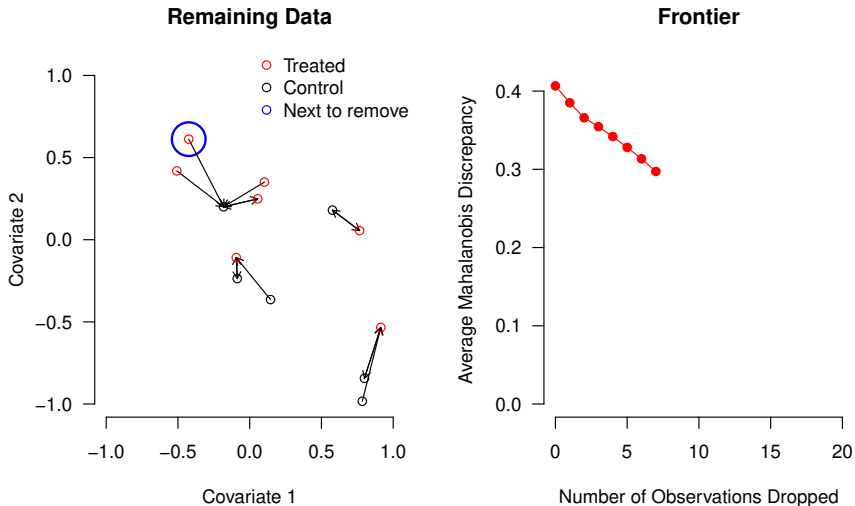
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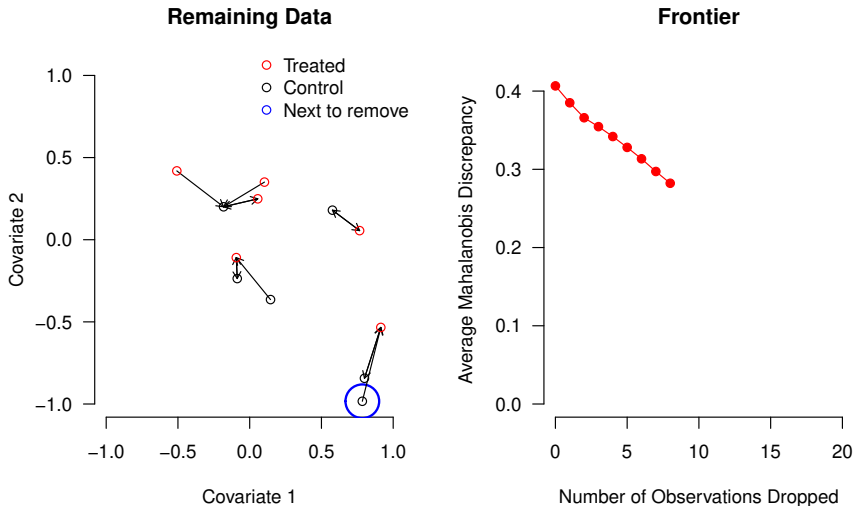
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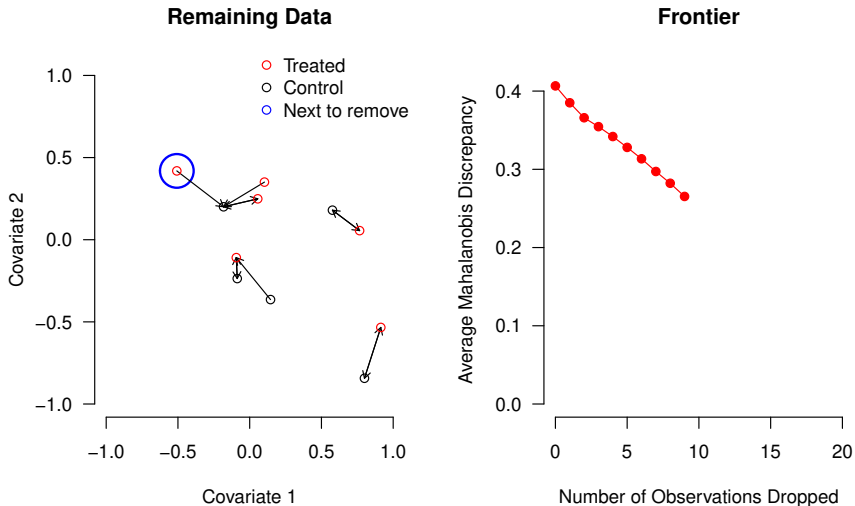
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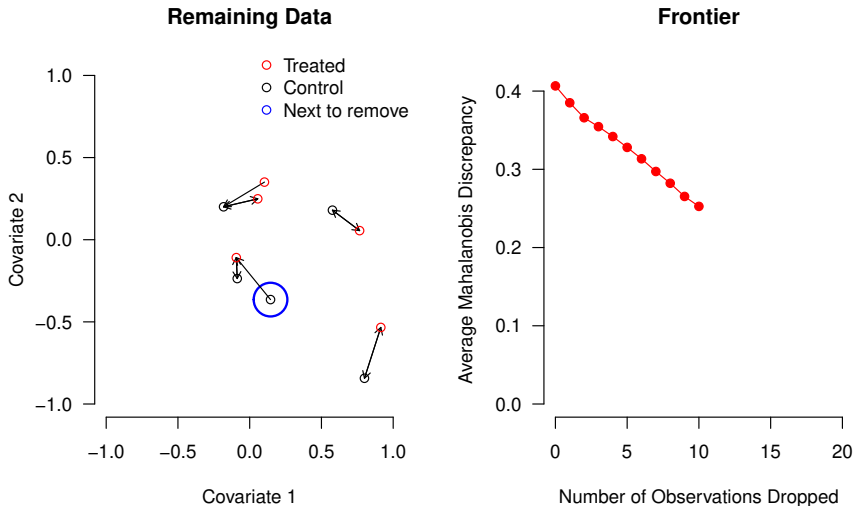
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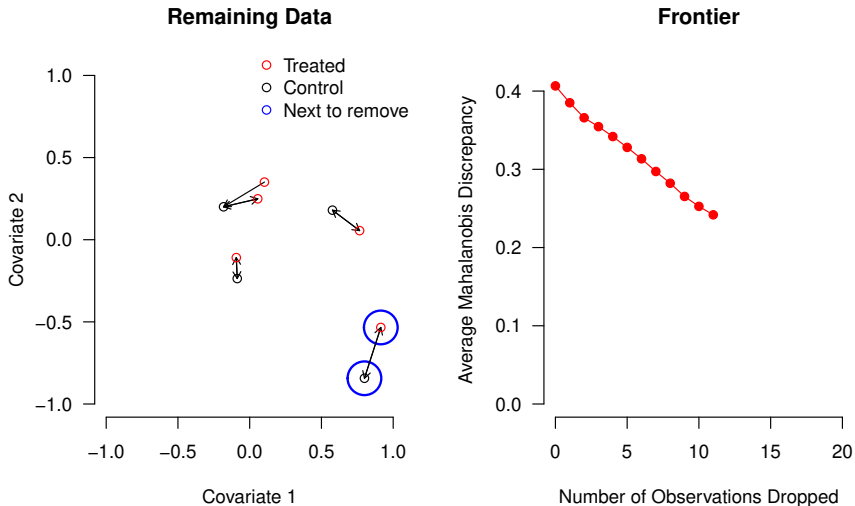
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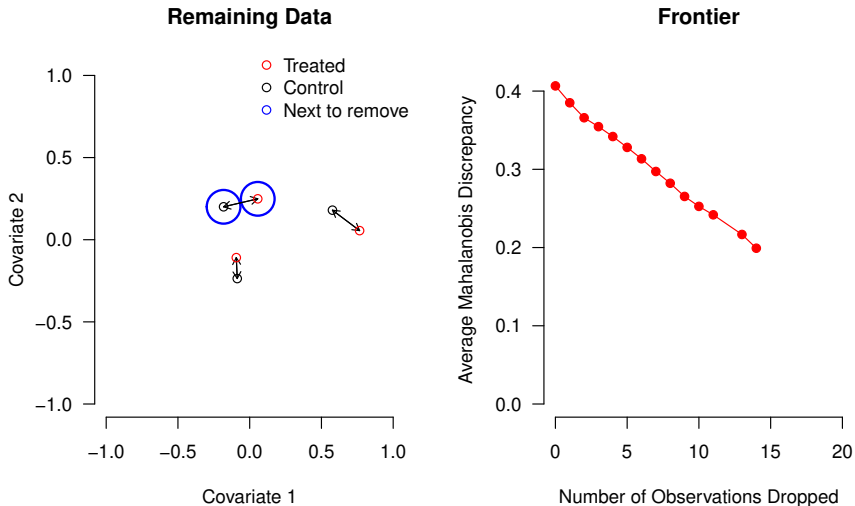
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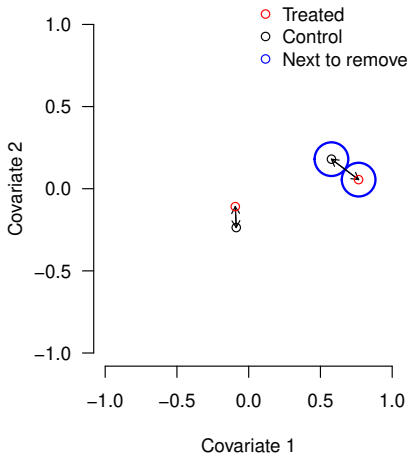


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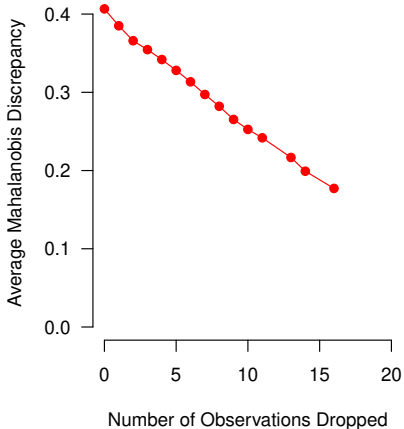


Constructing the Mahalanobis Frontier

Remaining Data

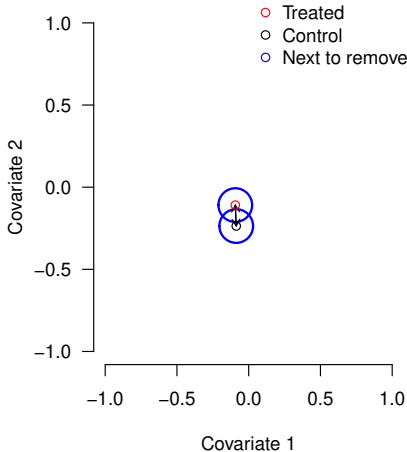


Frontier

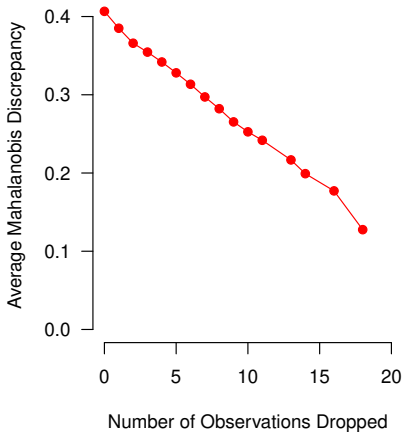


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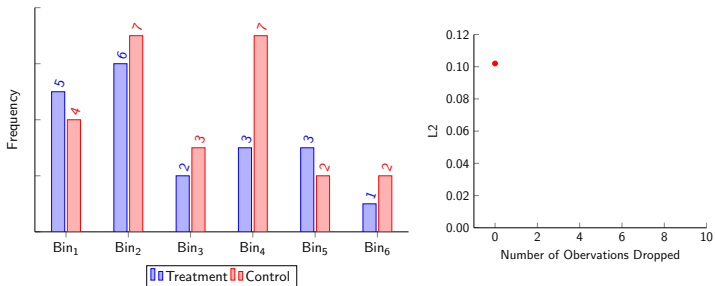
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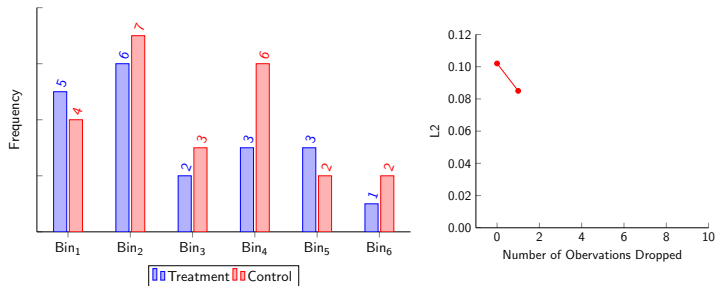
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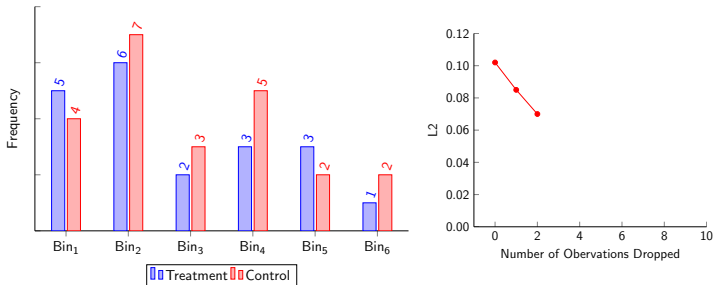
Constructing the L1/L2 Frontier



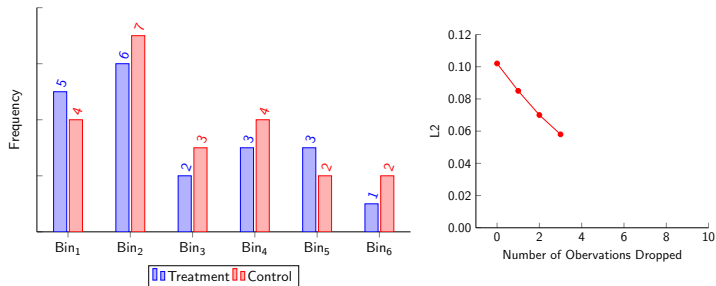
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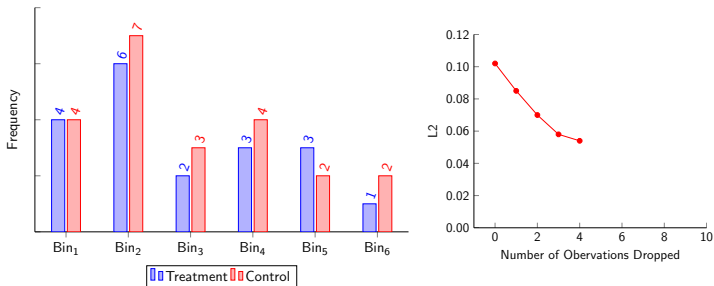
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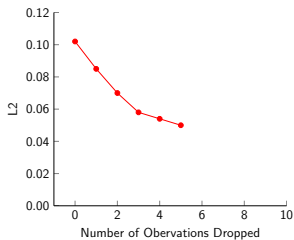
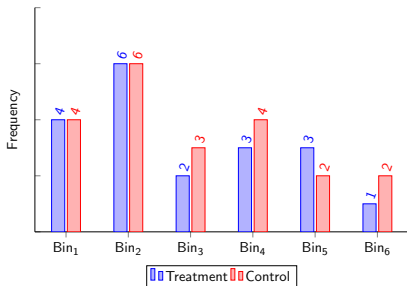
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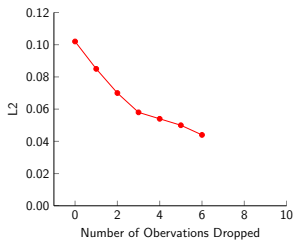
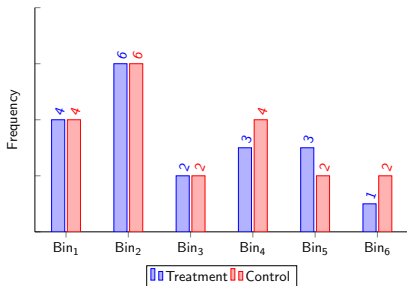
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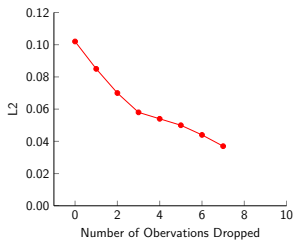
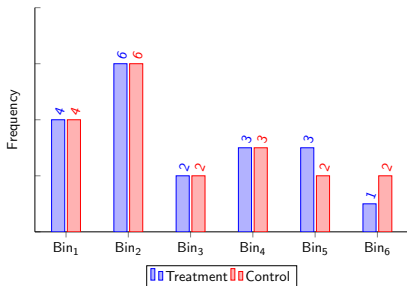
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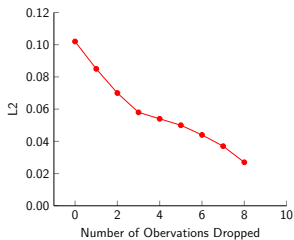
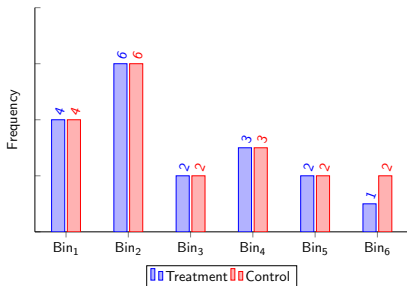
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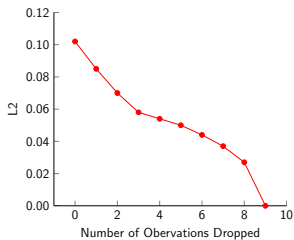
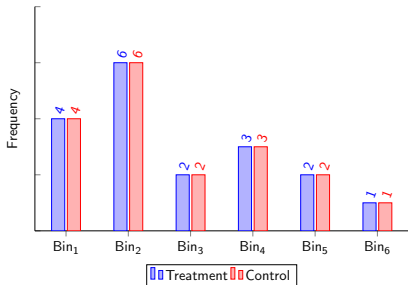
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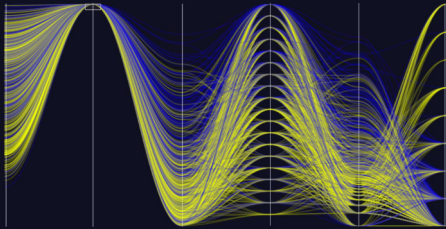
Constructing the L1/L2 Frontier



Constructing the L1/L2 Frontier



T C



L1

Matched Sample Size



Foreign Aid Shocks & Conflict

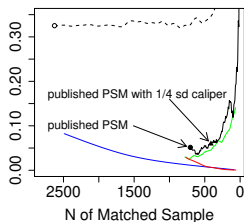
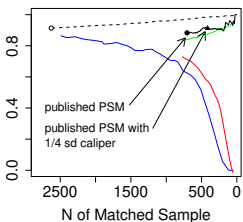
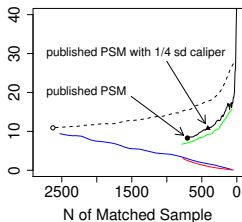
King, Nielsen, Coberley, Pope, and Wells (2012)

Imbalance Metric

Mahalanobis Discrepancy

L_1

Difference in Means



○ Raw Data
- - - Random Pruning

— "Best Practices" PSM
— PSM

— MDM
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Healthways Data

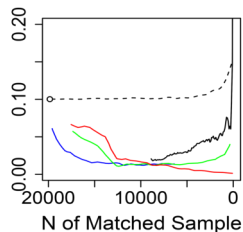
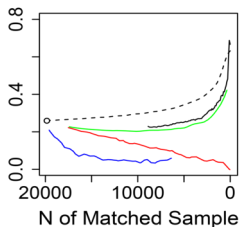
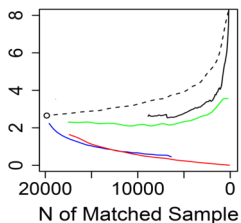
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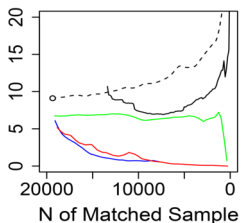
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Called/Not Called Data

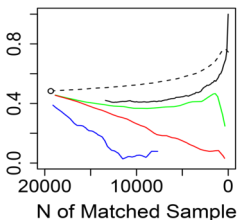
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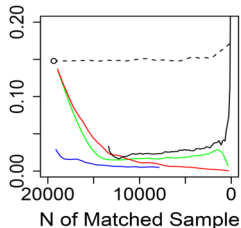
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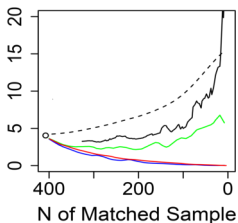
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FDA Drug Approval Times

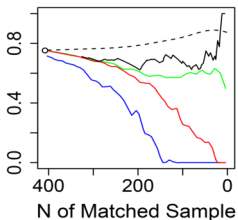
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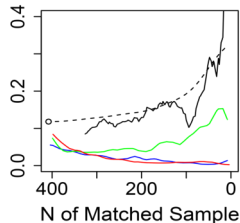
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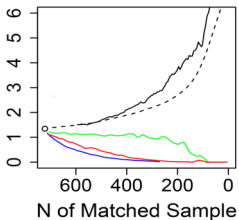
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Job Training (Lelonde Data)

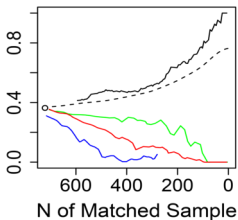
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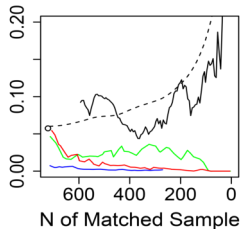
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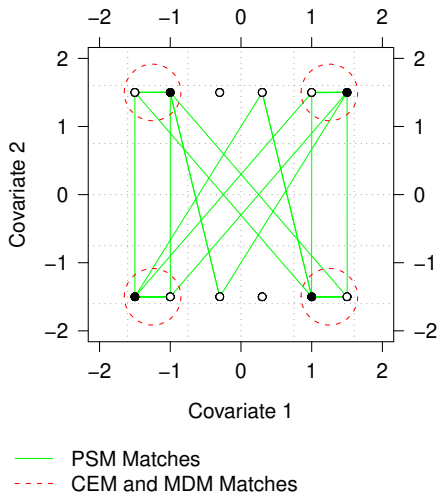


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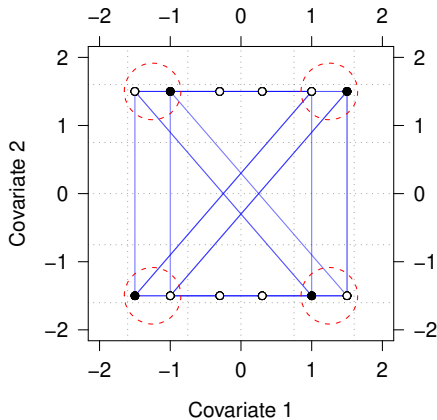
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PSM Approximates Random Matching in Balanced Data



Destroying CEM with PSM's Two Step Approach



- CEM Matches
- CEM-generated PSM Matches

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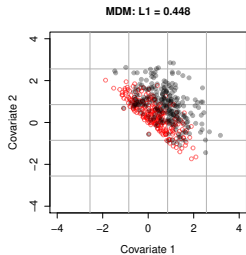
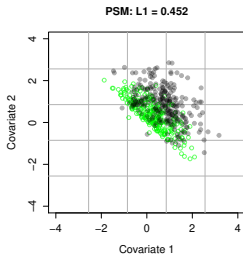
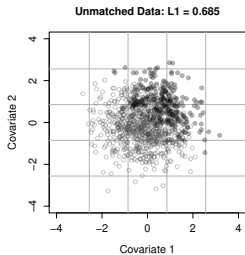
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For more information,

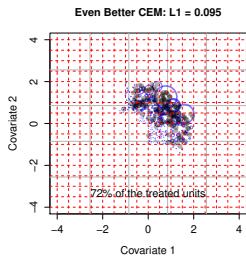
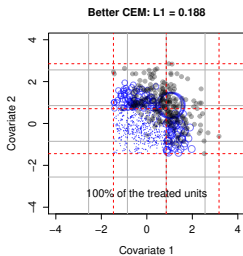
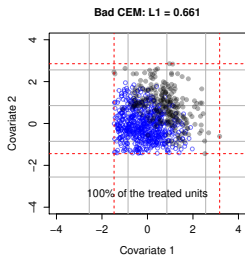


GaryKing.org/cem

Data where PSM Works Reasonably Well — PSM & MDM



Data where PSM Works Reasonably Well — CEM



CEM Weights and Nonparametric Propensity Score

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