

# Simplifying Causal Inference

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(Talk at the Centre on Population Dynamics, McGill University, 3/1/2013)

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- (Coarsened Exact Matching is simple, easy, and powerful)
- $\rightsquigarrow$  Lots of insights revealed in the process

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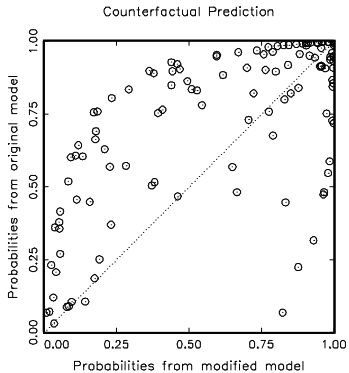
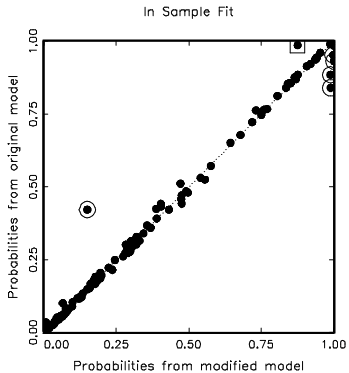
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- **Data analysis:** Logit model
- **The question:** How *model dependent* are the results?

## 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



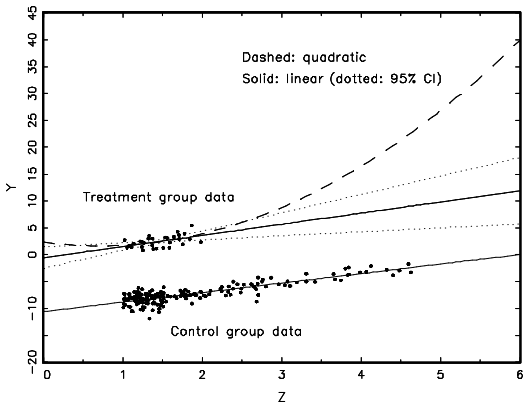
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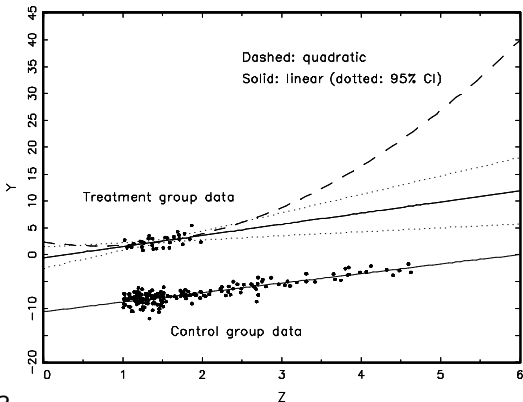
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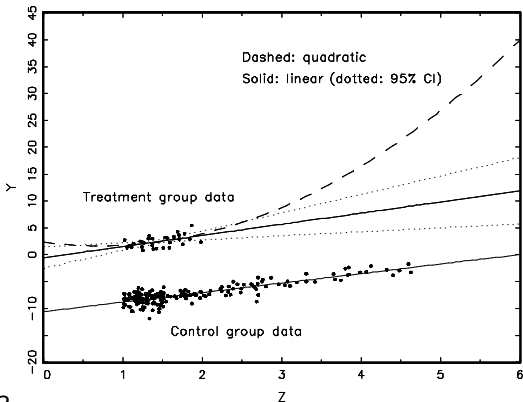
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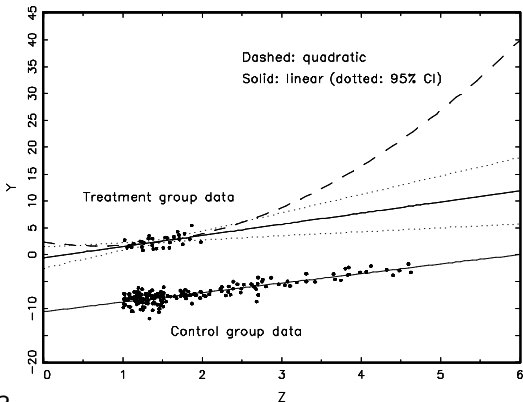


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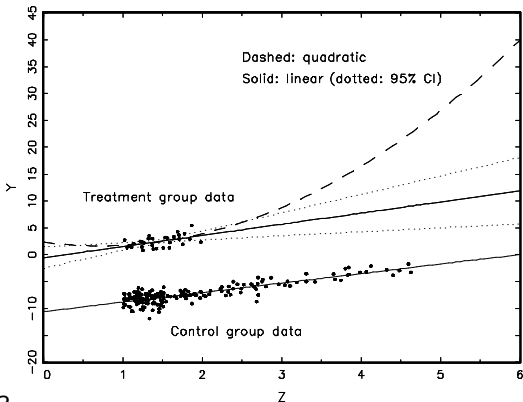


What to do?

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

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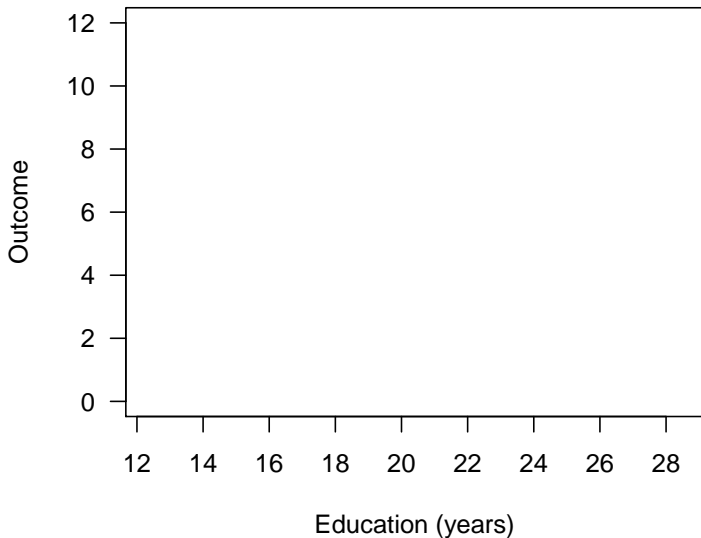


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- Preprocess I: Eliminate extrapolation region
- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

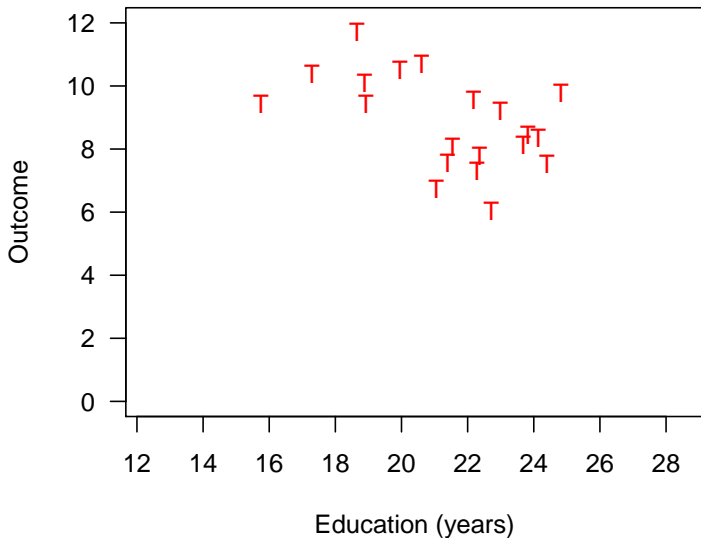
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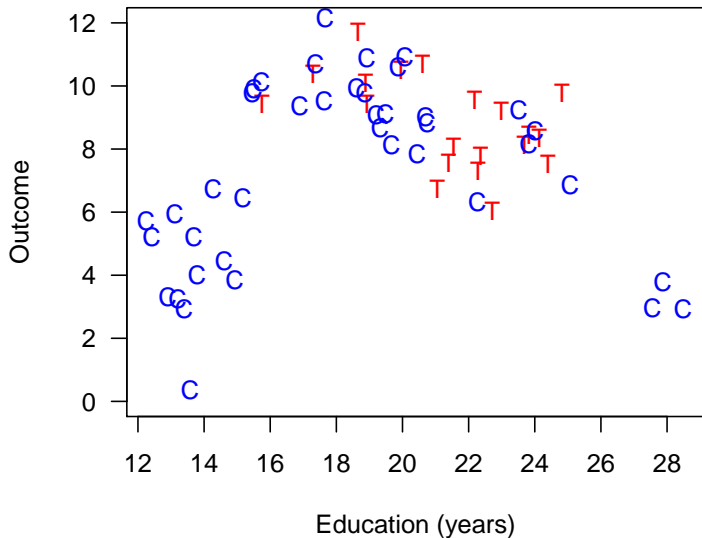
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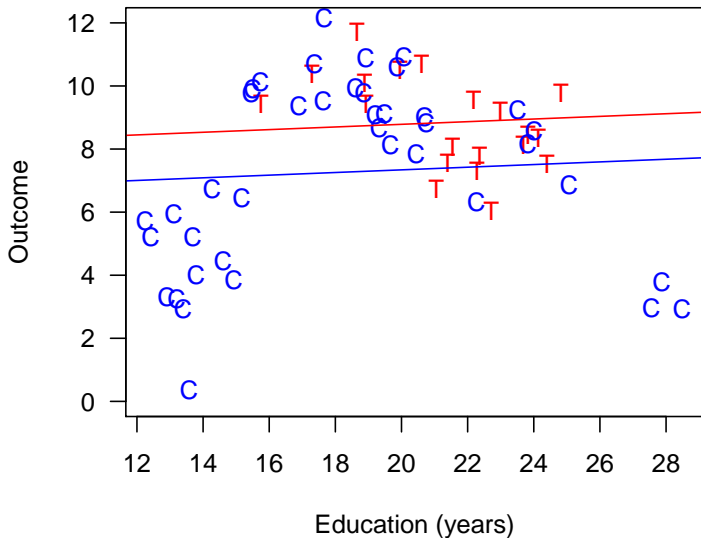
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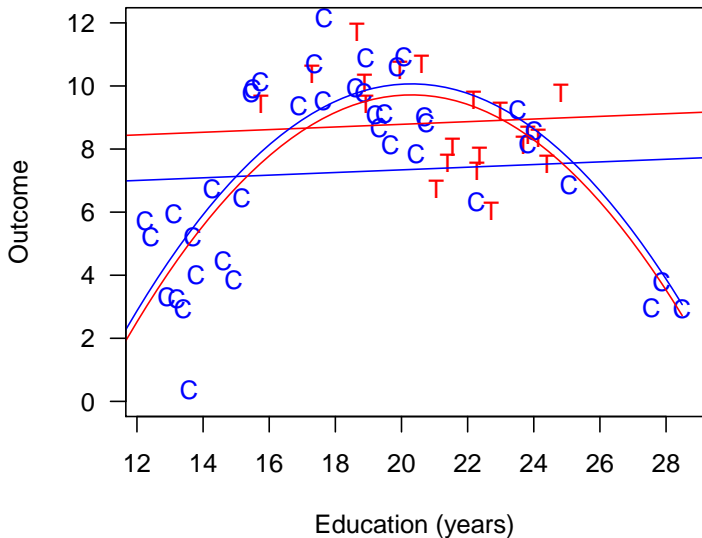
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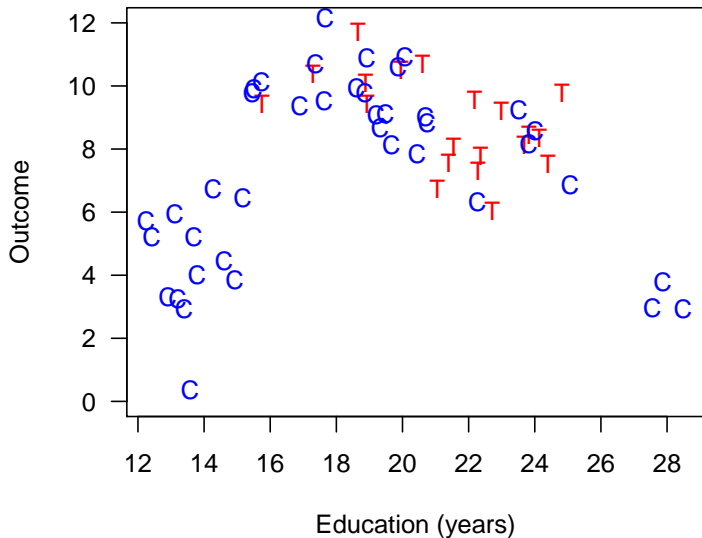
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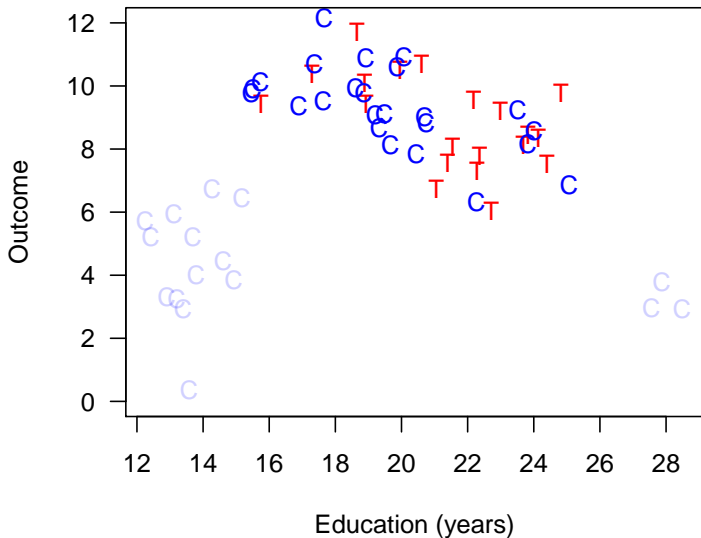
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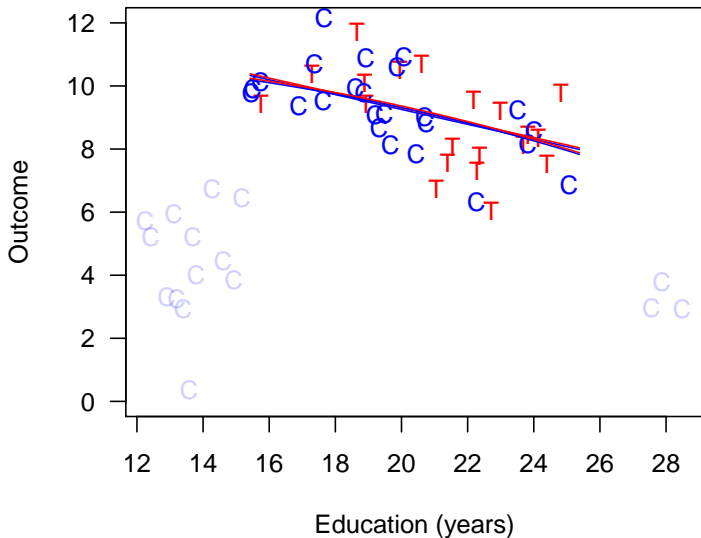
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Matching reduces model dependence, bias, and variance

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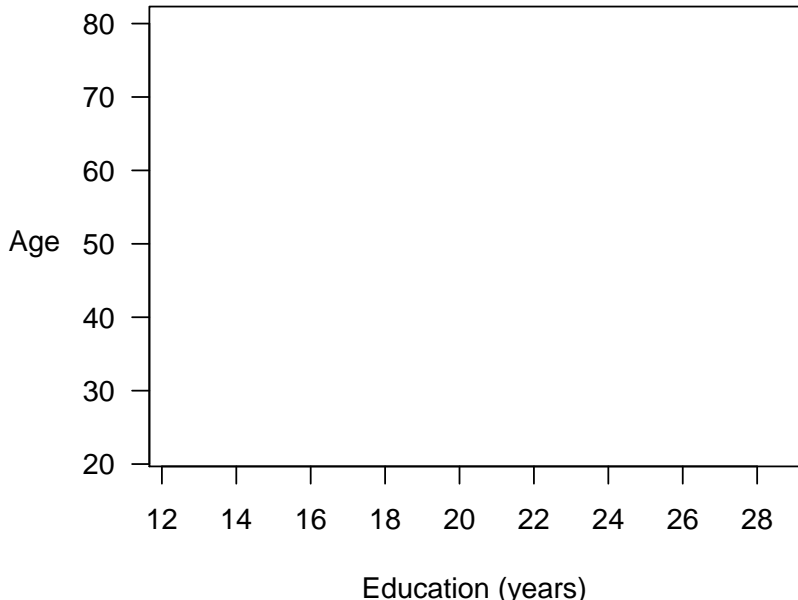
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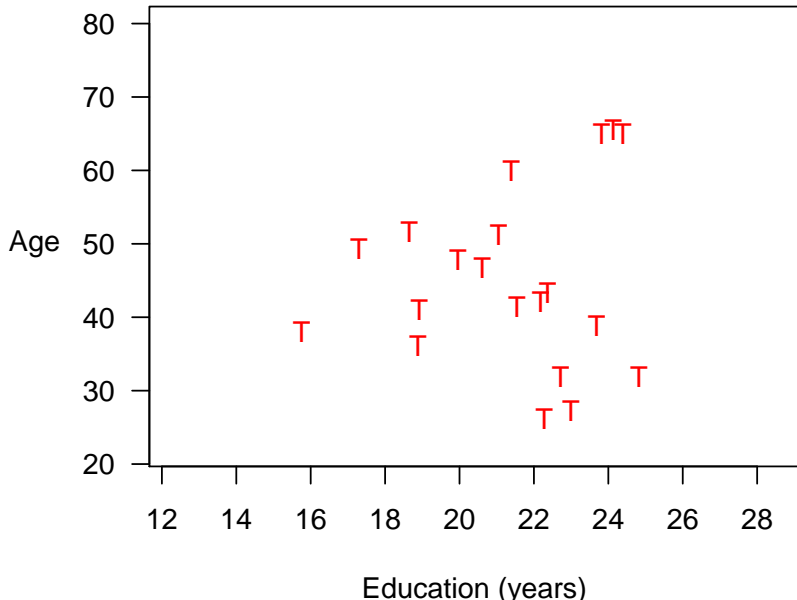
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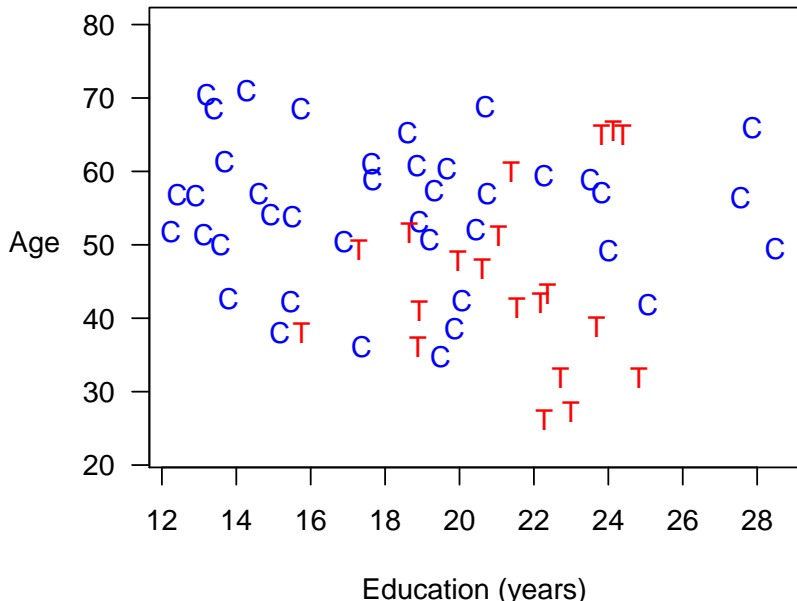




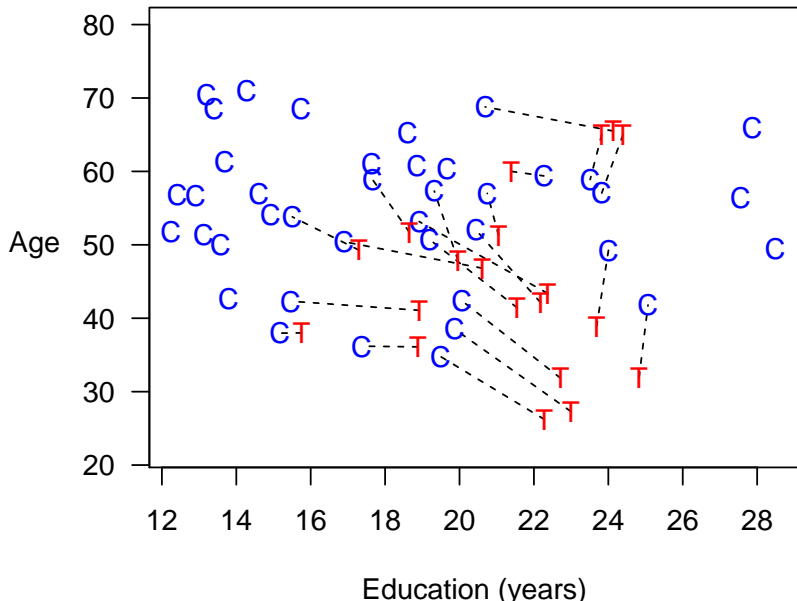
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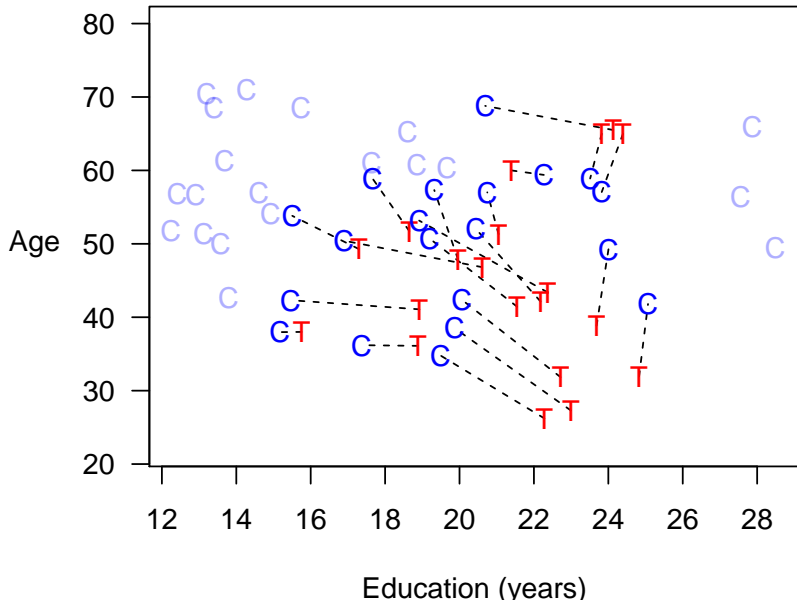
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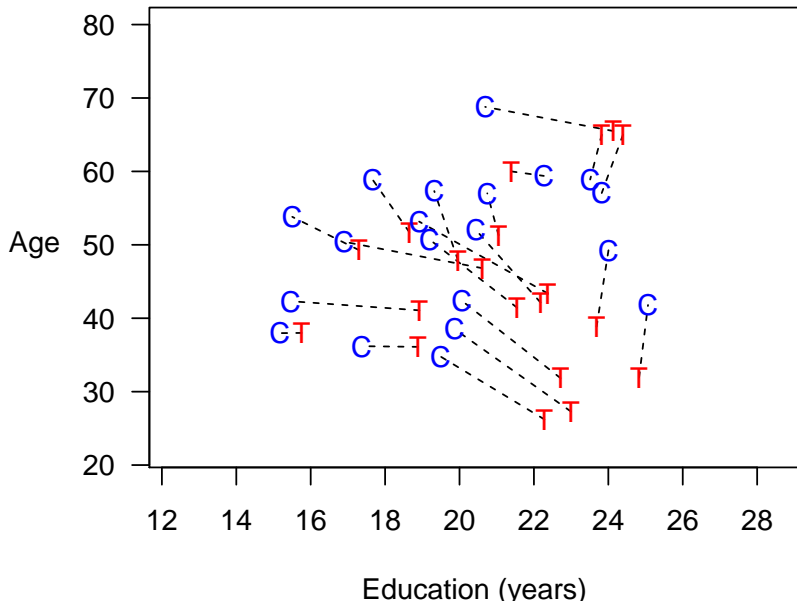
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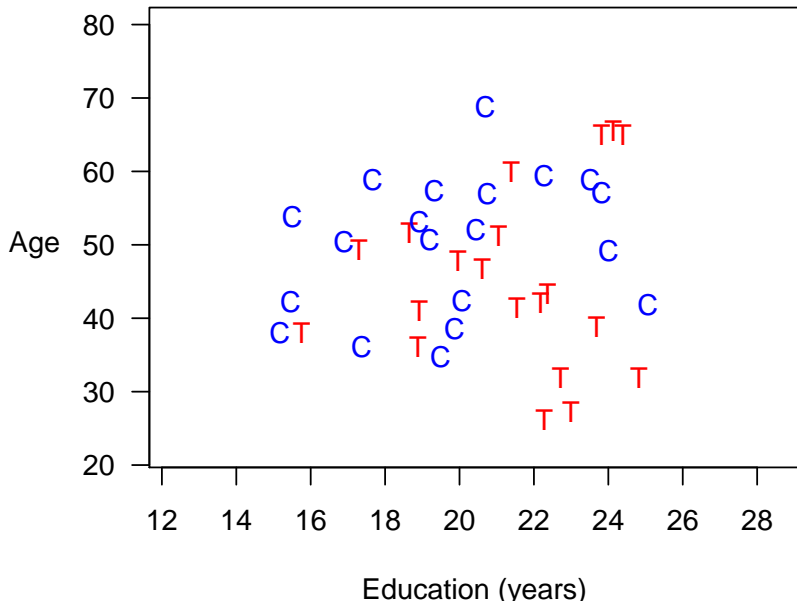
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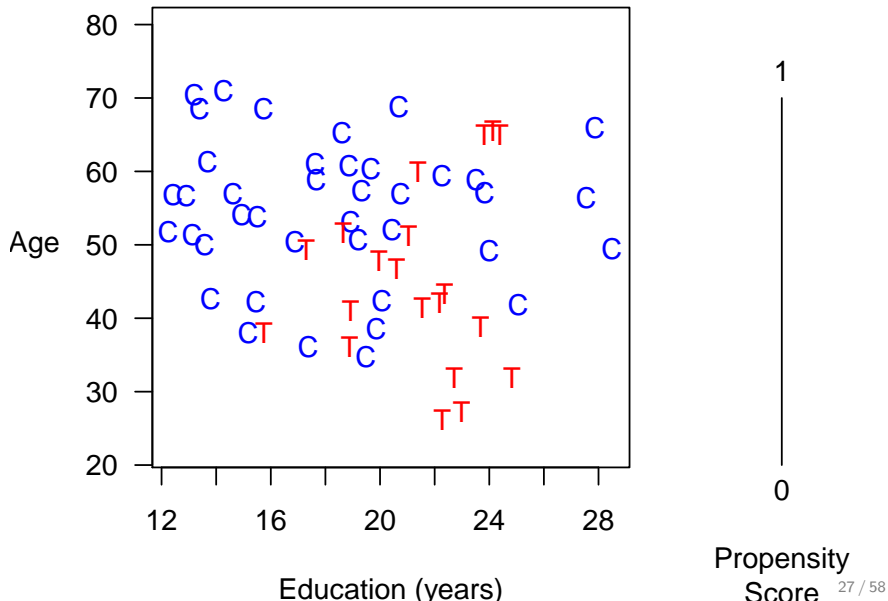
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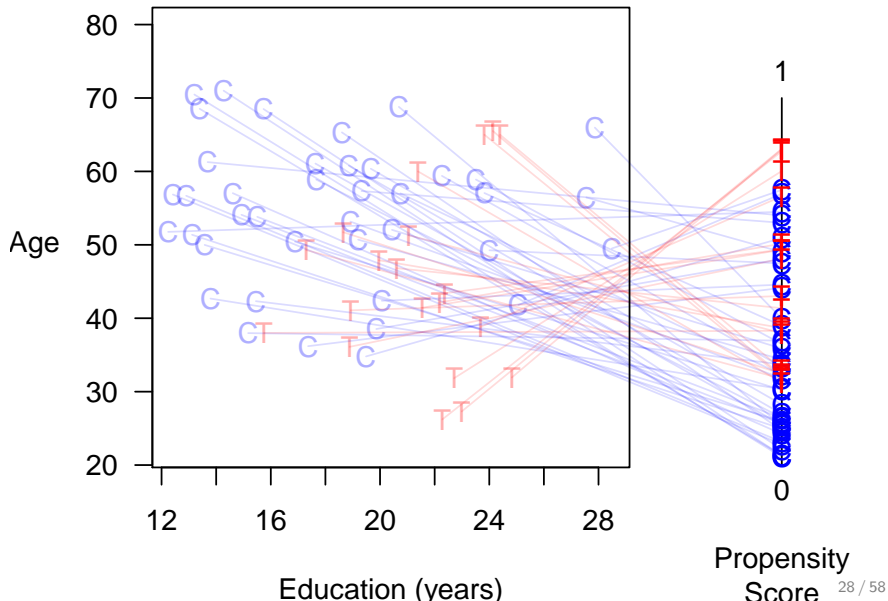
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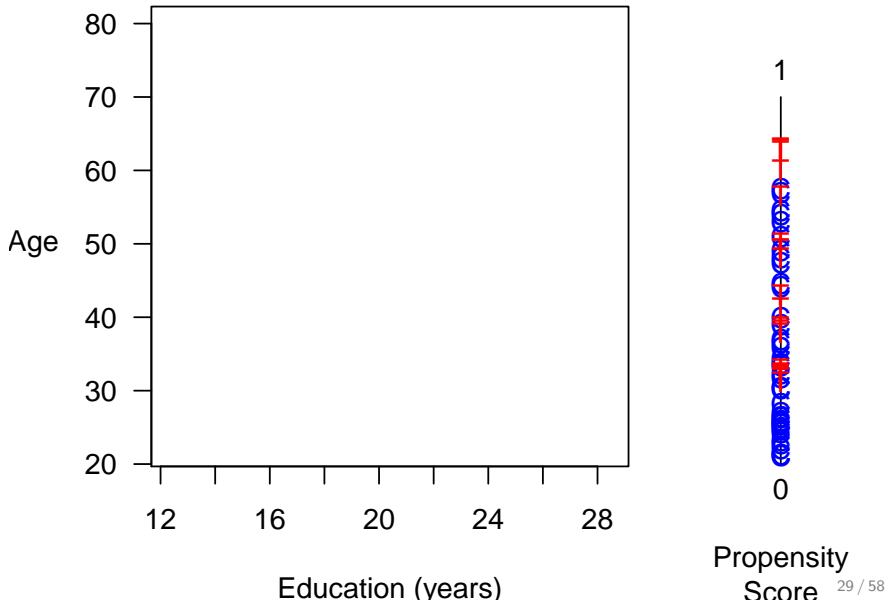


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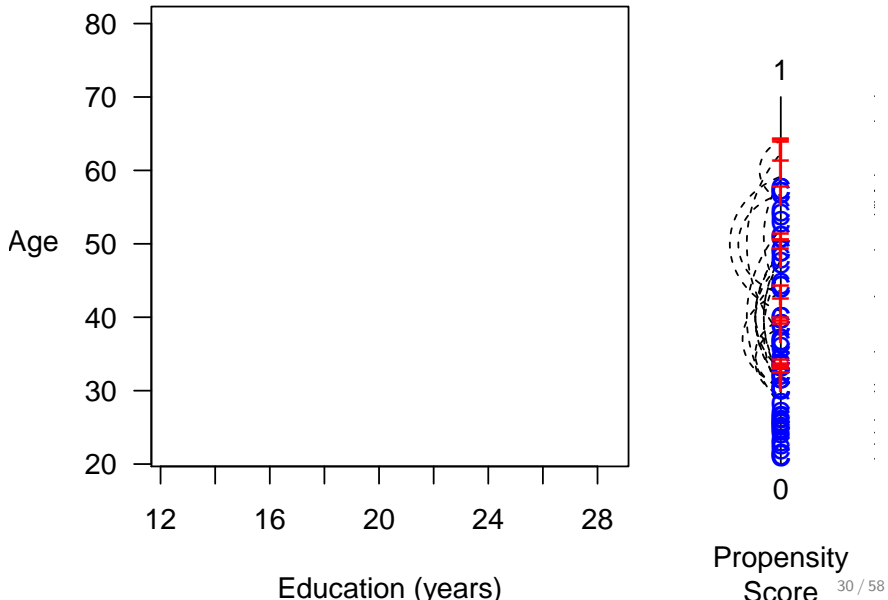




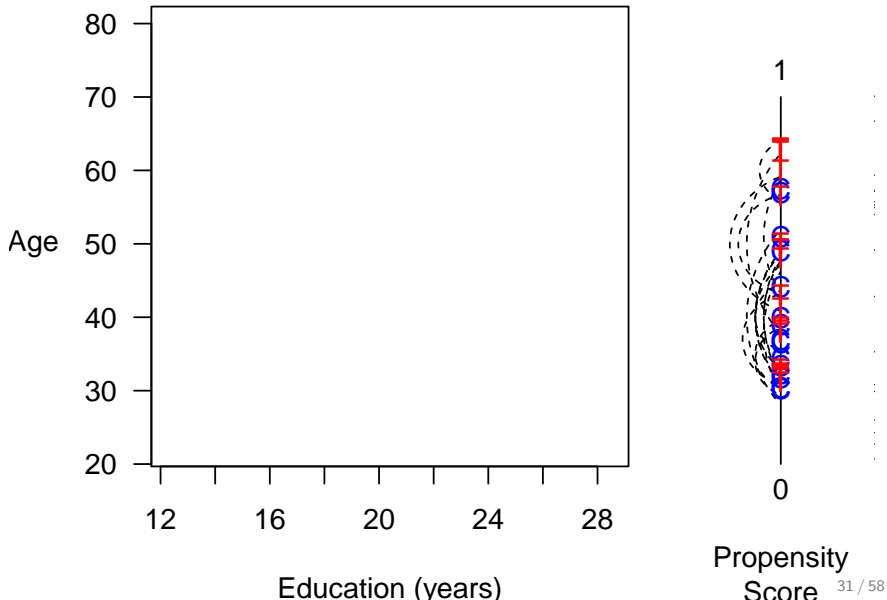
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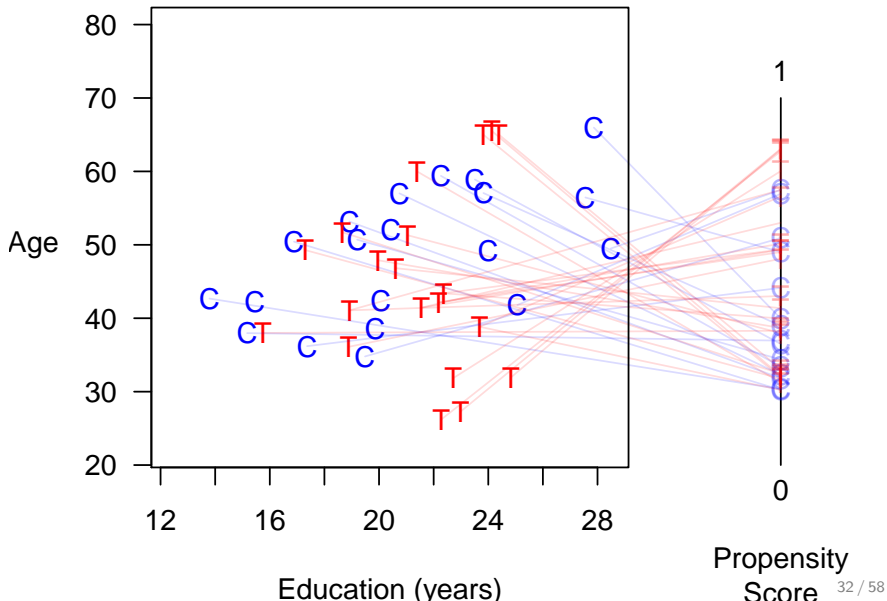
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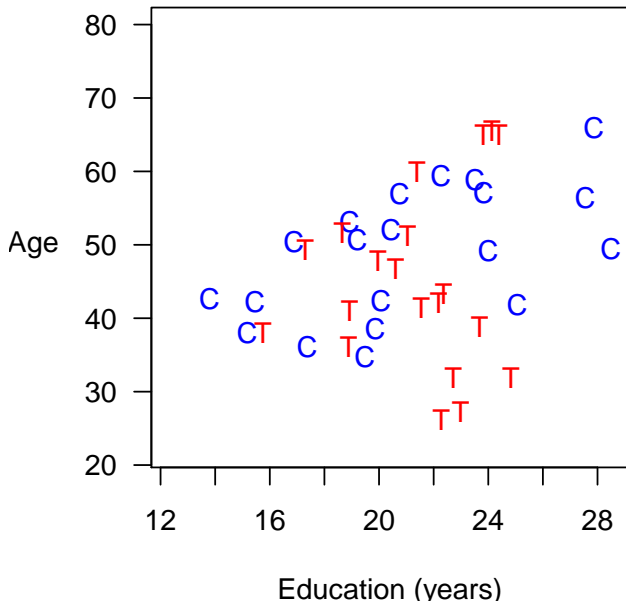
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  - Temporarily coarsen  $X$  as much as you're willing
  
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- Apply exact matching to the coarsened  $X$ ,  $C(X)$ 
  - Sort observations into strata, each with unique values of  $C(X)$
  - Prune any stratum with 0 treated or 0 control units

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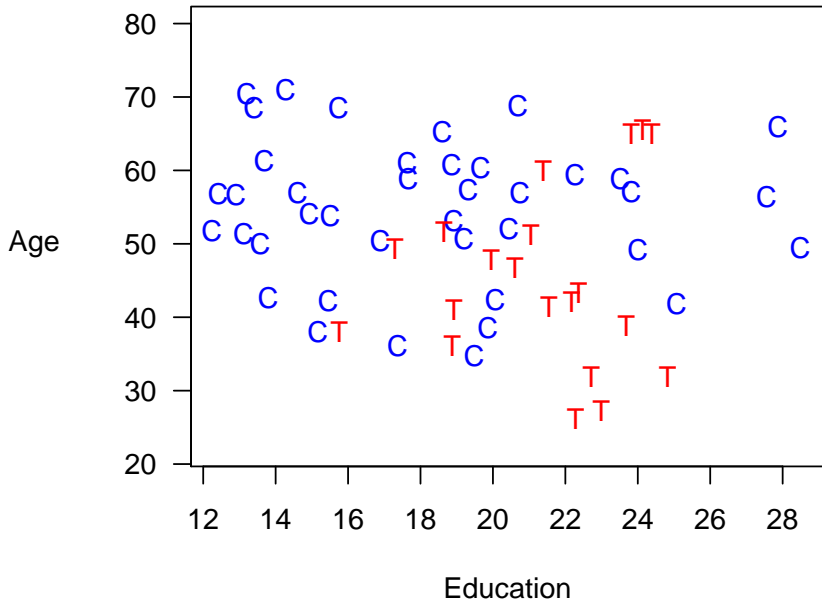
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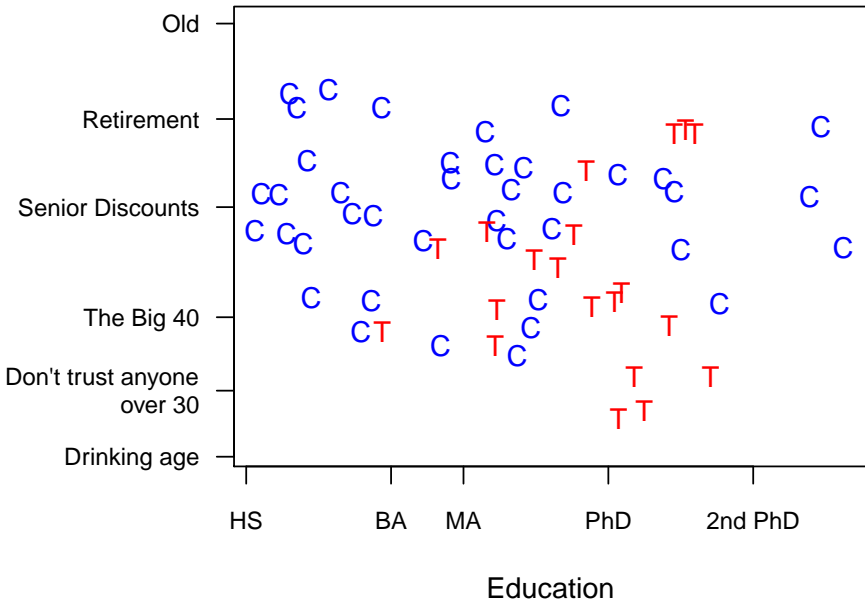


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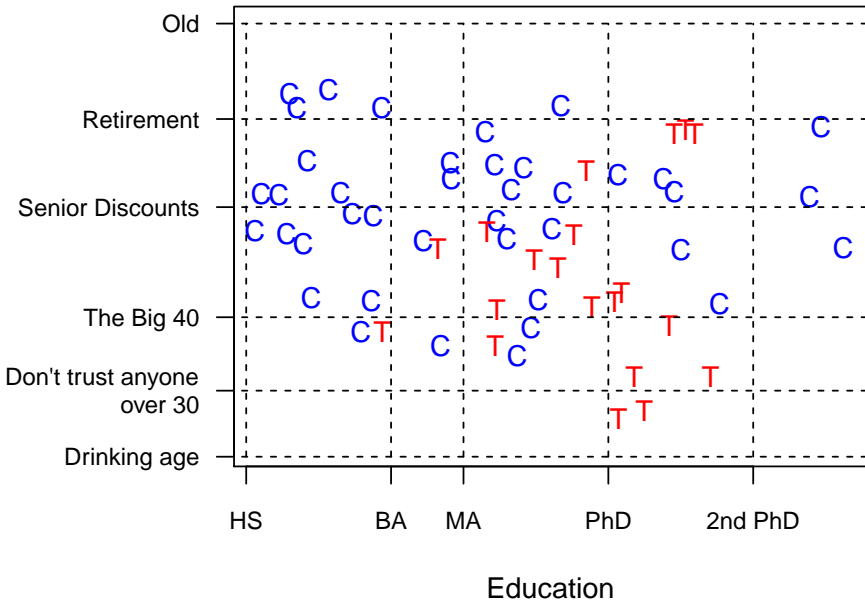
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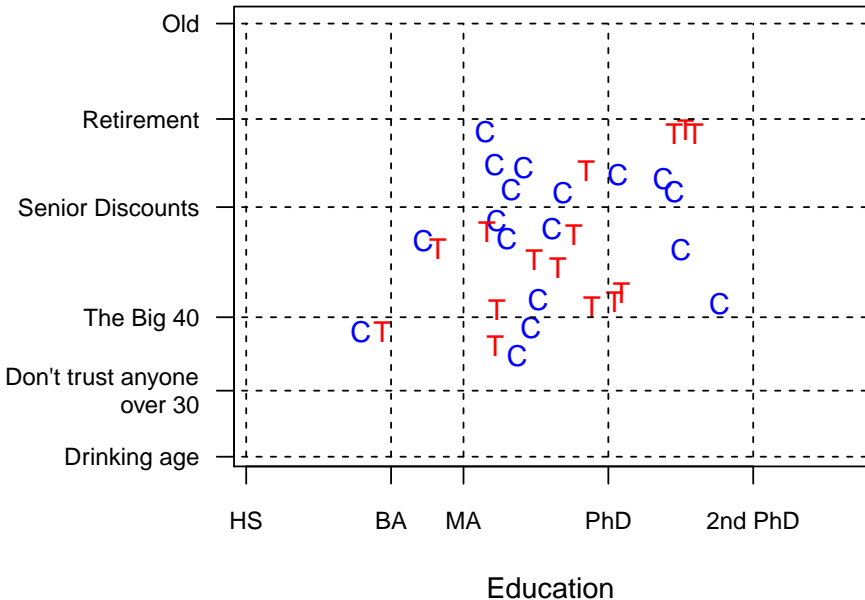
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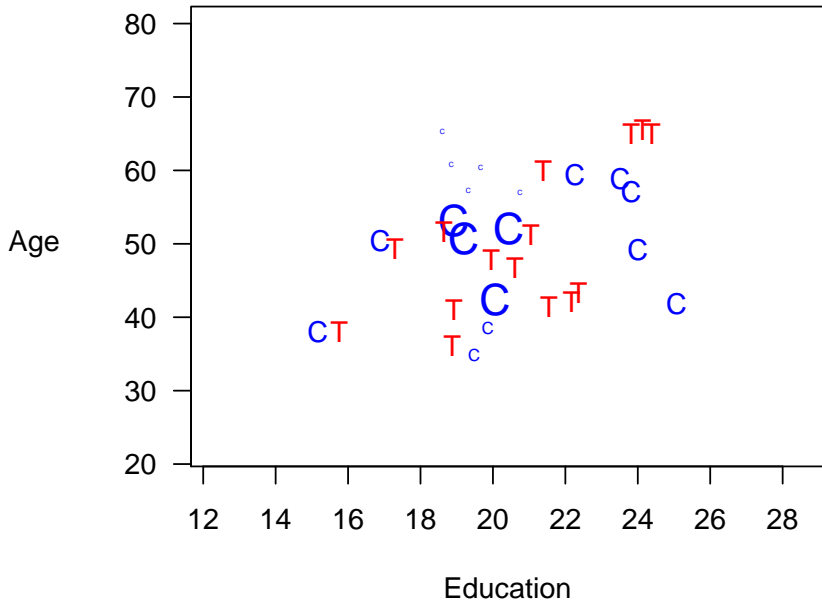


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## Coarsened Exact Matching



# The Bias-Variance Trade Off in Matching



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  - Difference of multivariate histograms (L1):

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

# Comparing Matching Methods



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- Given matched solution  $\rightsquigarrow$  matching method is irrelevant
- Our idea: Identify the *frontier*: lowest imbalance for each  $n$ ; then choose a matching solution

# A Space Graph: Foreign Aid Shocks & Conflict

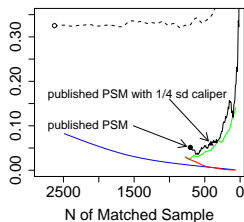
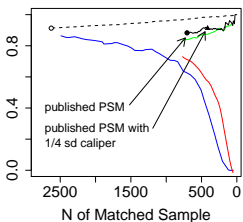
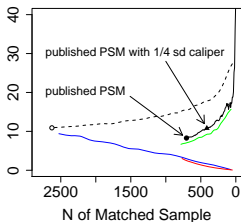
King, Nielsen, Coberley, Pope, and Wells (2012)

## Imbalance Metric

Mahalanobis Discrepancy

$L_1$

Difference in Means



○ Raw Data  
- - - Random Pruning

— "Best Practices" PSM  
— PSM

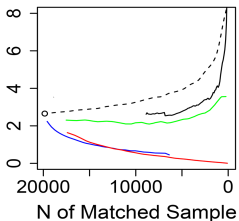
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# A Space Graph: Healthways Data

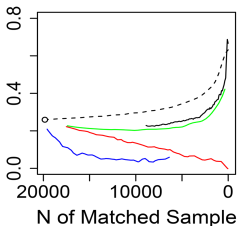
King, Nielsen, Coberley, Pope, and Wells (2012)

## Imbalance Metric

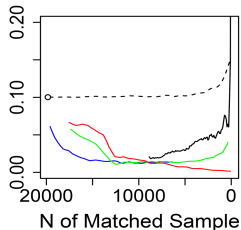
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# A Space Graph: Called/Not Called Data

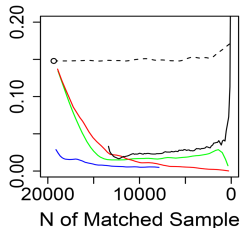
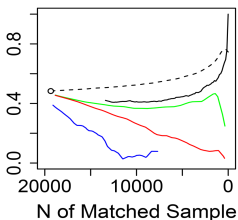
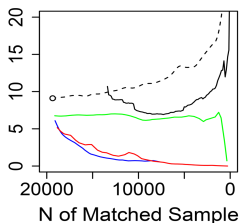
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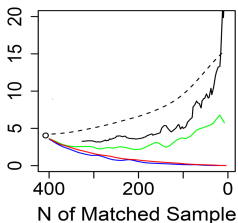


# A Space Graph: FDA Drug Approval Times

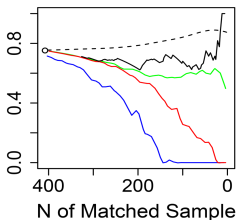
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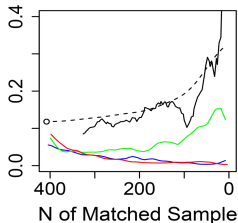
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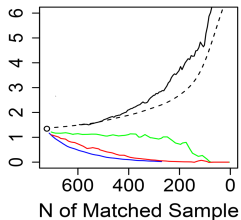
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# A Space Graph: Job Training (Lelonde Data)

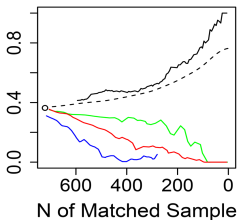
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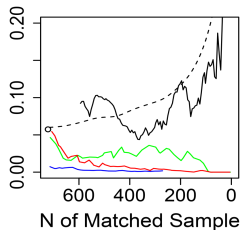
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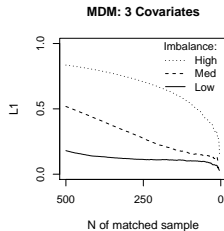
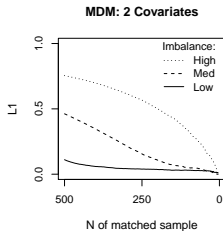
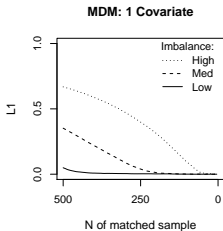


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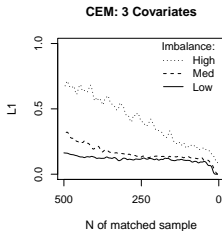
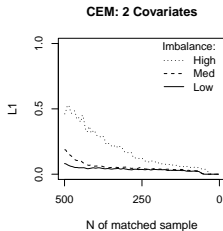
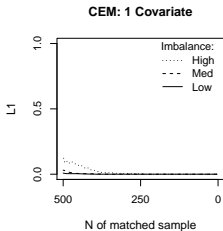
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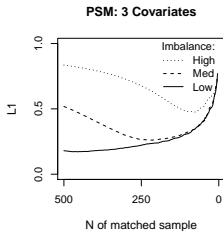
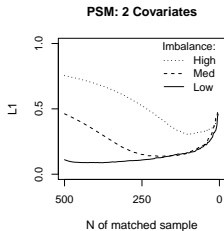
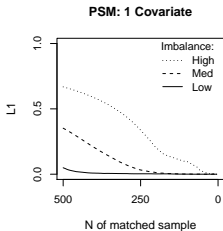
# A Space Graph: Simulated Data — Mahalanobis



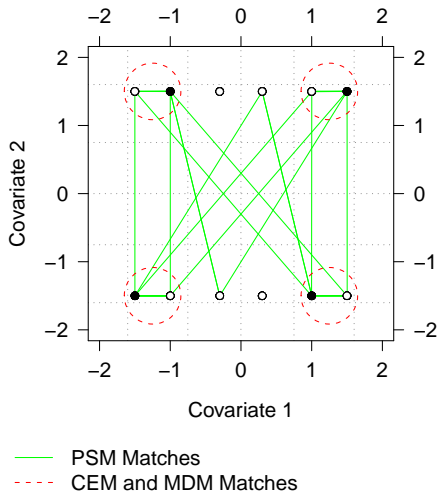
# A Space Graph: Simulated Data — CEM



# A Space Graph: Simulated Data — Propensity Score



# PSM Approximates Random Matching in Balanced Data



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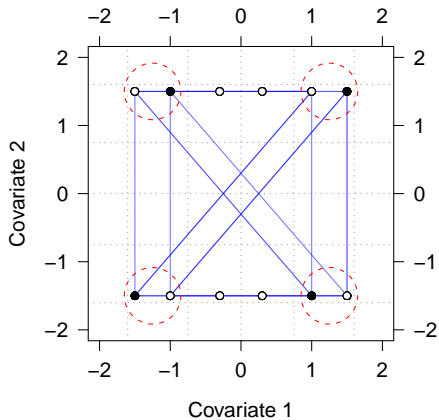
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# Destroying CEM with PSM's Two Step Approach



- - - CEM Matches
- CEM-generated PSM Matches

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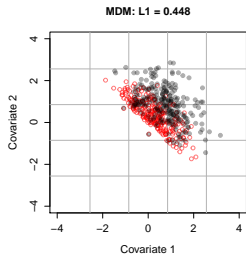
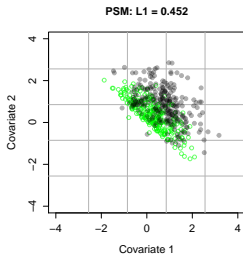
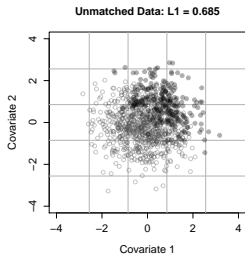
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For papers, software (for R, Stata, & SPSS), tutorials, etc.



[GaryKing.org/cem](http://GaryKing.org/cem)

# Data where PSM Works Reasonably Well — PSM & MDM



# Data where PSM Works Reasonably Well — CEM

