

Advanced Quantitative Research Methodology, Lecture Notes: Matching Methods for Causal Inference¹

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- $\rightsquigarrow$ Lots of insights revealed in the process

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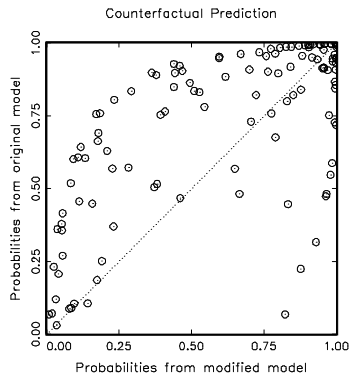
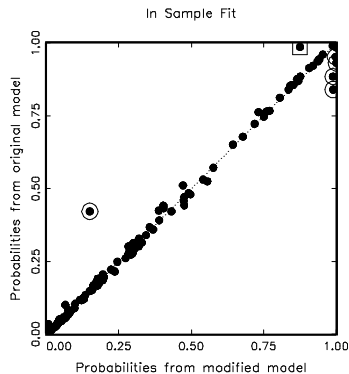
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- **Data analysis:** Logit model
- **The question:** How *model dependent* are the results?

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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 - If each treated unit **exactly matches** a control unit w.r.t. X , then: (1) treated and control groups are identical, (2) X is no longer a confounder, (3) no need to worry about the functional form ($\bar{X}_T - \bar{X}_C$ is good enough).

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 - If treated and control groups are **better balanced** than when you started, due to pruning, model dependence is reduced

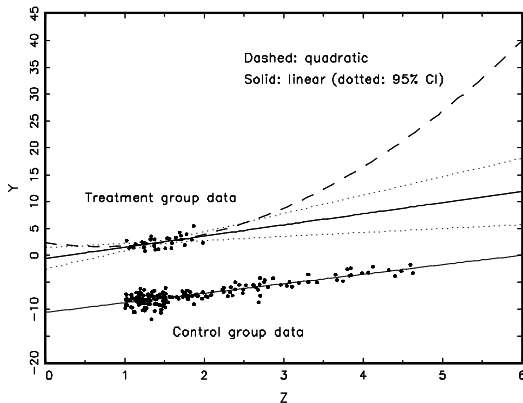
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(King and Zeng, 2006: fig.4 *Political Analysis*)

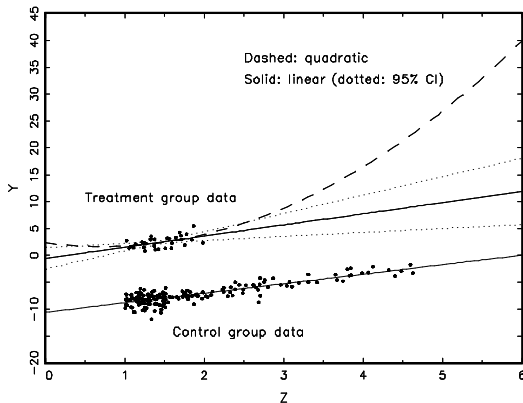
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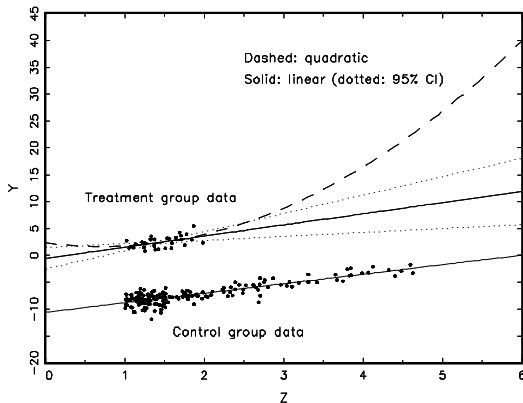
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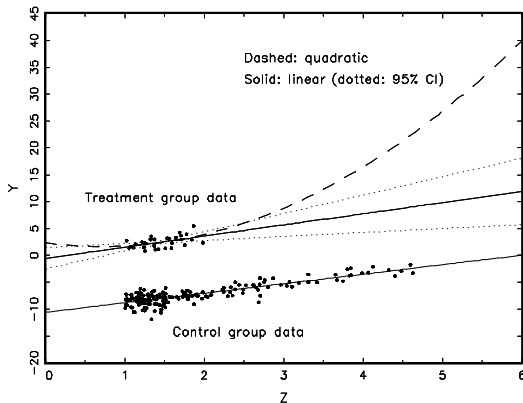


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- Preprocess I: Eliminate extrapolation region

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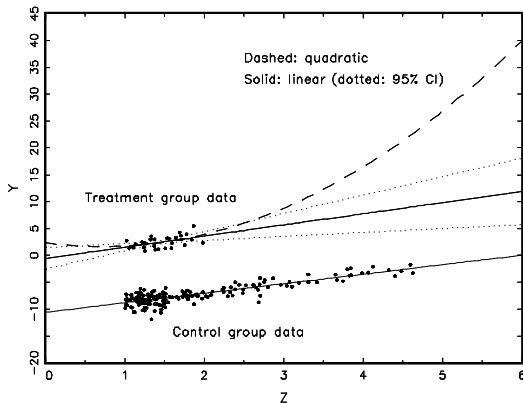


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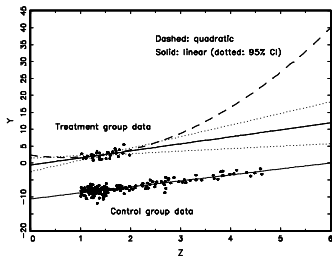


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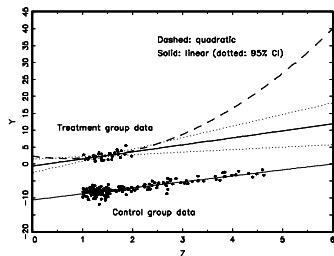
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- Model remaining imbalance

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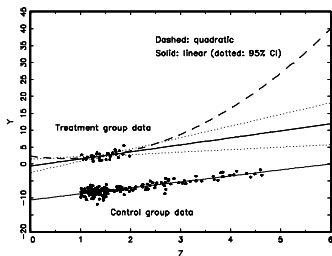


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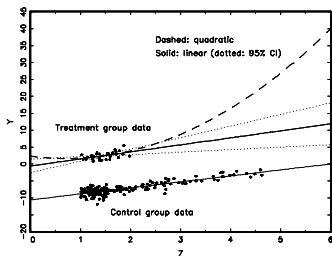
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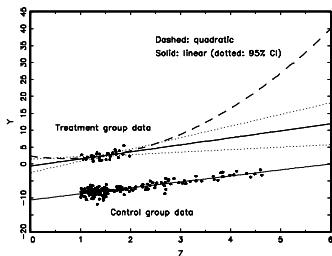
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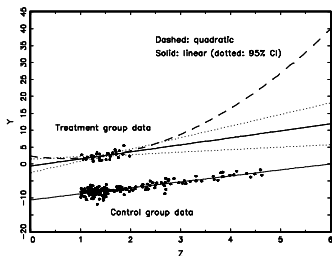
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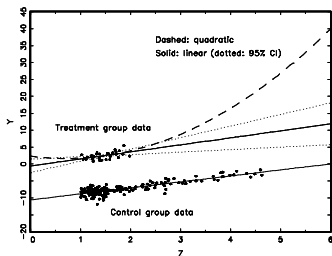
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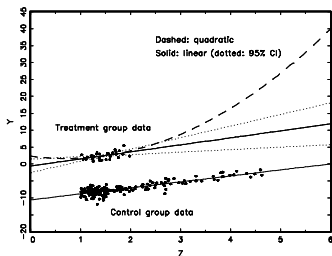
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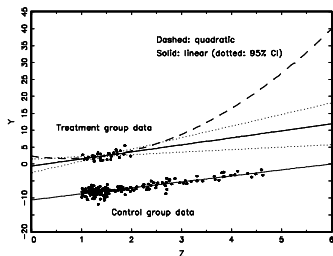
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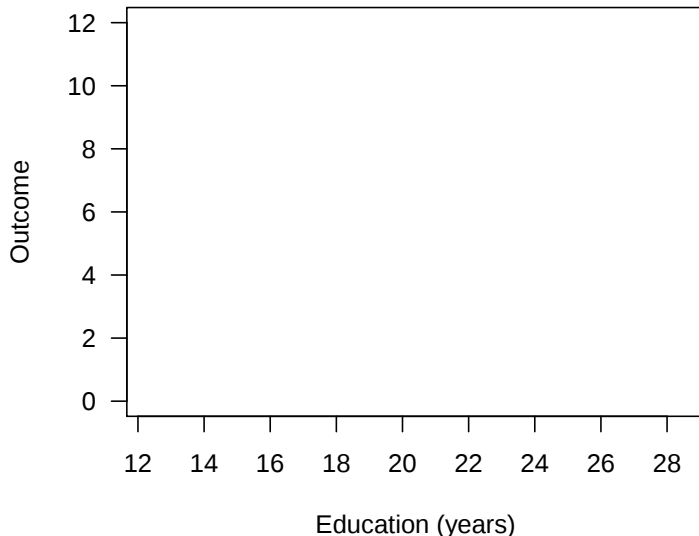
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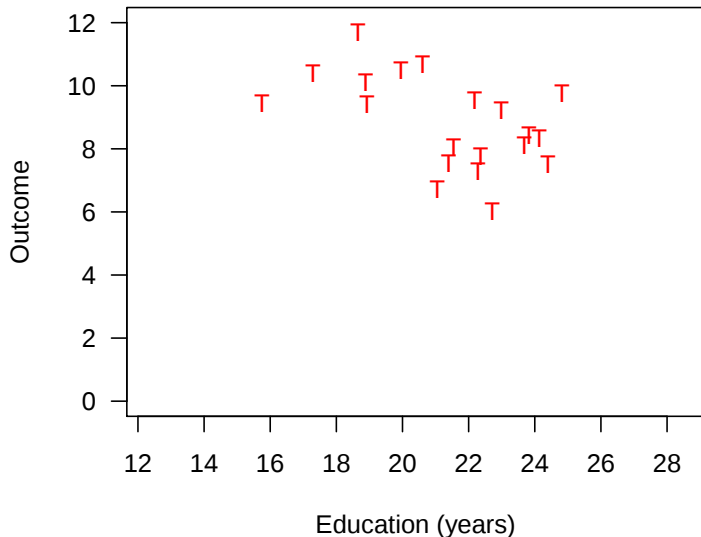
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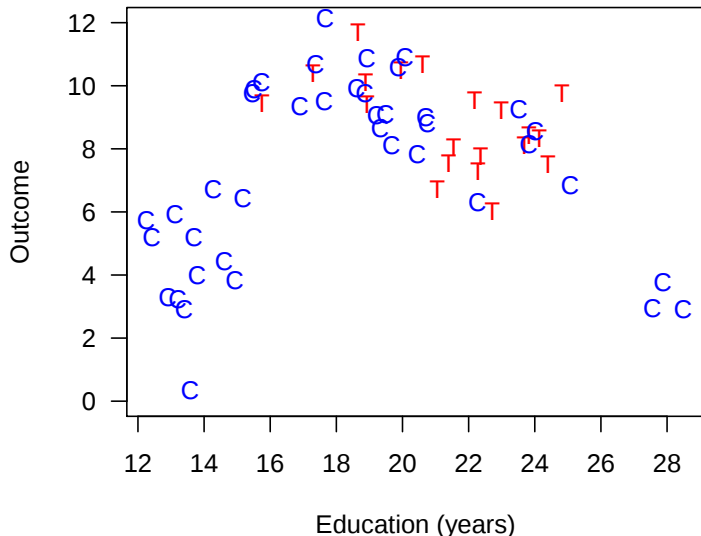
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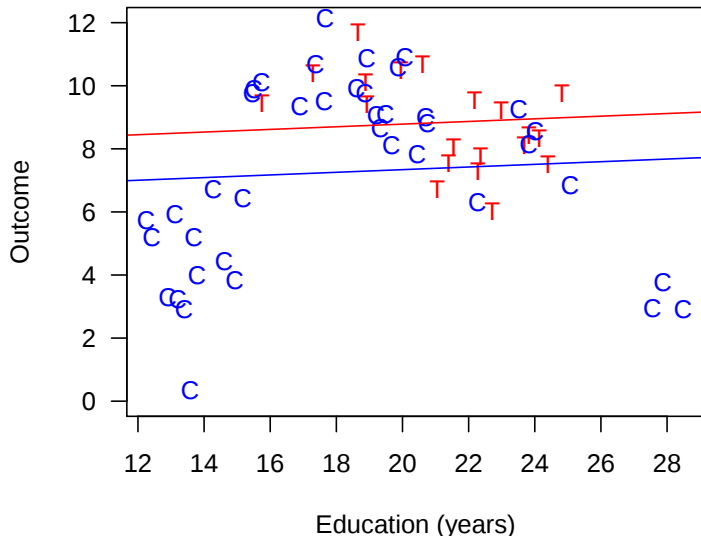
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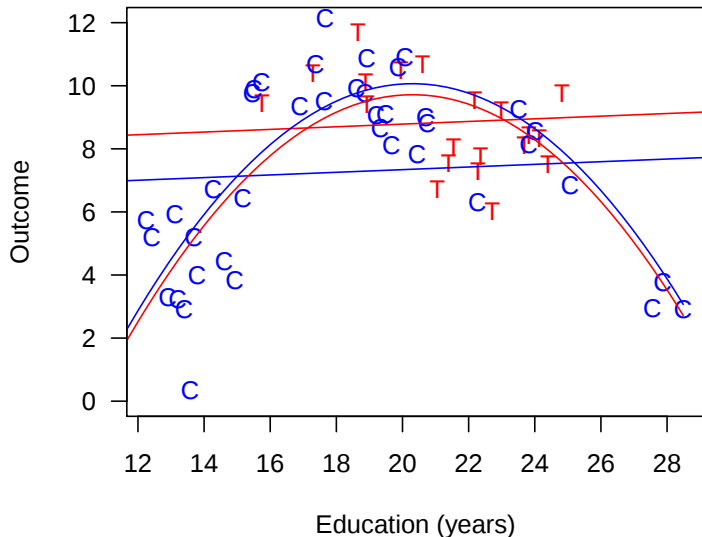
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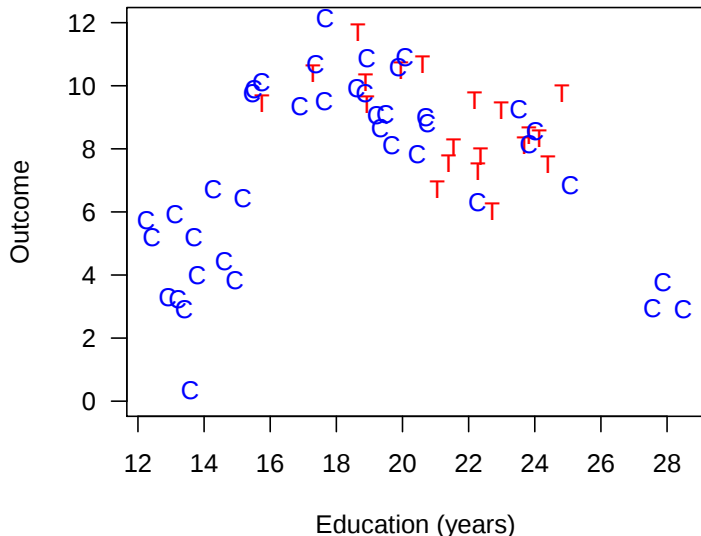
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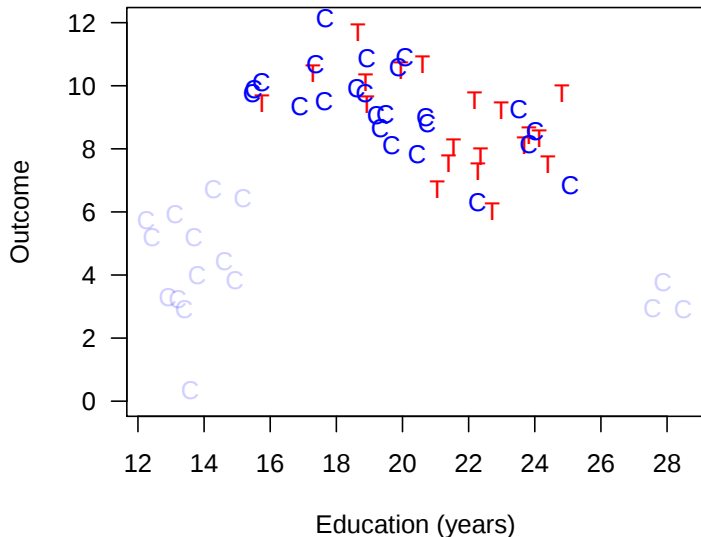
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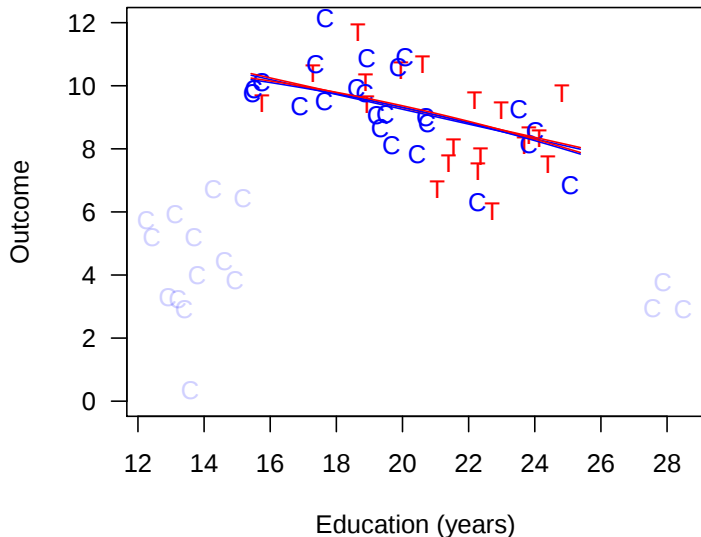
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Matching reduces model dependence, bias, and variance

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- 18 control variables (clinical factors, firm characteristics, media variables, etc.)

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- (Normal applications would only do one or a small number of specifications.)

Reducing Model Dependence

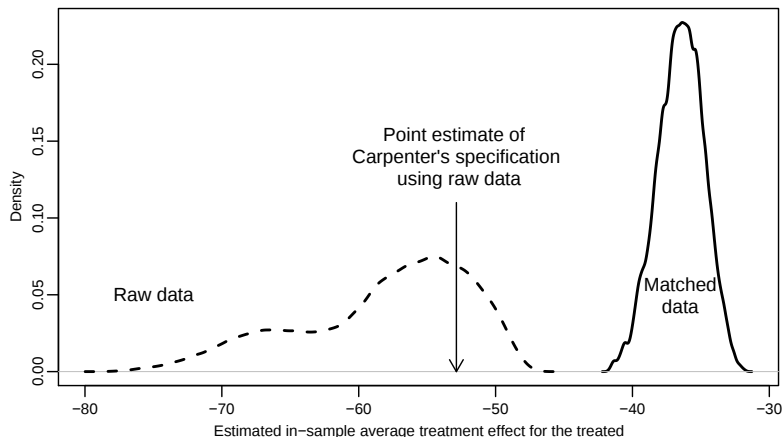


Figure: Histogram of estimated in-sample average treatment effect for the treated (ATT) of the Democratic Senate majority on FDA drug approval time across 262,143 specifications.

Another Example: Jeffrey Koch, AJPS, 2002

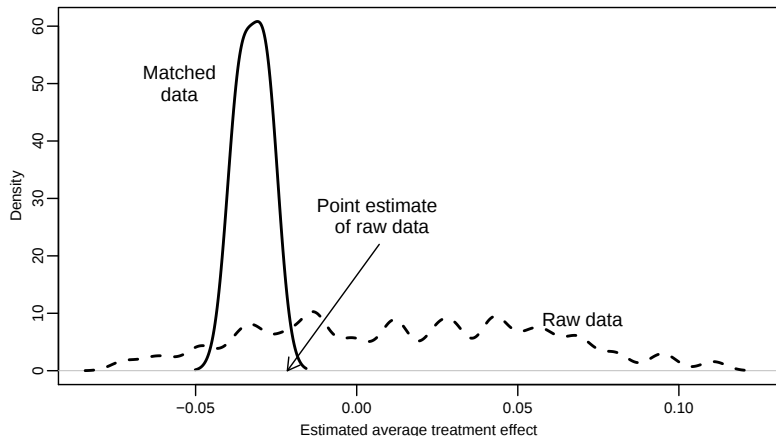


Figure: Estimated effects of being a highly visible female Republican candidate across 63 possible specifications with the Koch data.

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- Prune unmatched units to improve **balance** (so X is unimportant)

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$$\hat{Y}_i(0) = Y_j(0) \text{ or a model } \hat{Y}_i(0) = \hat{g}_0(X_j)$$

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$$\text{SATT} = \frac{1}{n_T} \sum_{i \in \{T_i=1\}} \text{TE}_i$$

How Matching Works

- Notation:

Y_i Dependent variable

T_i Treatment variable (0/1)

X_i Pre-treatment covariates

- Treatment Effect for treated ($T_i = 1$) observation i :

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- 1 **Preprocess** (Matching)
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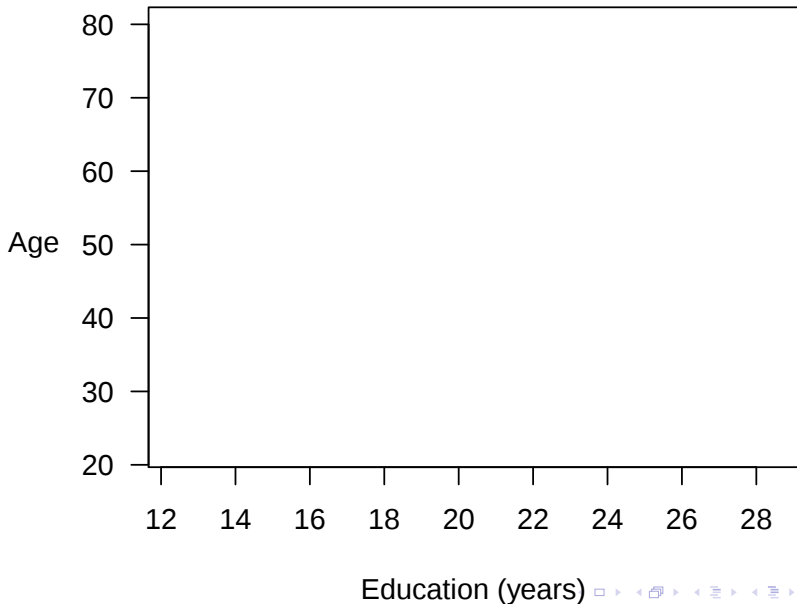
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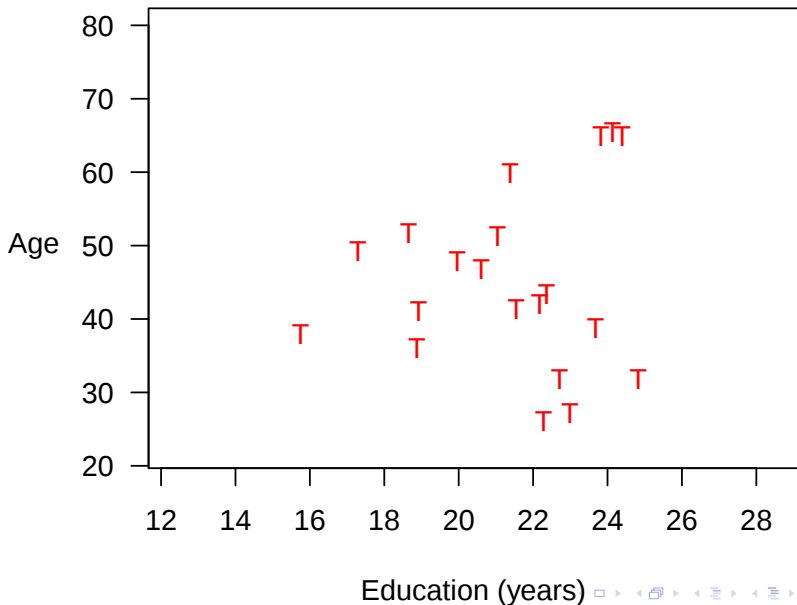
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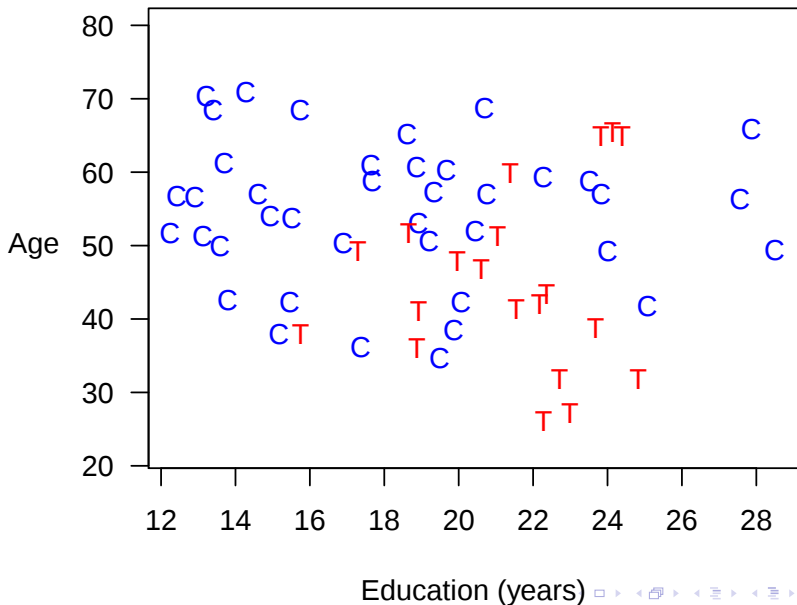
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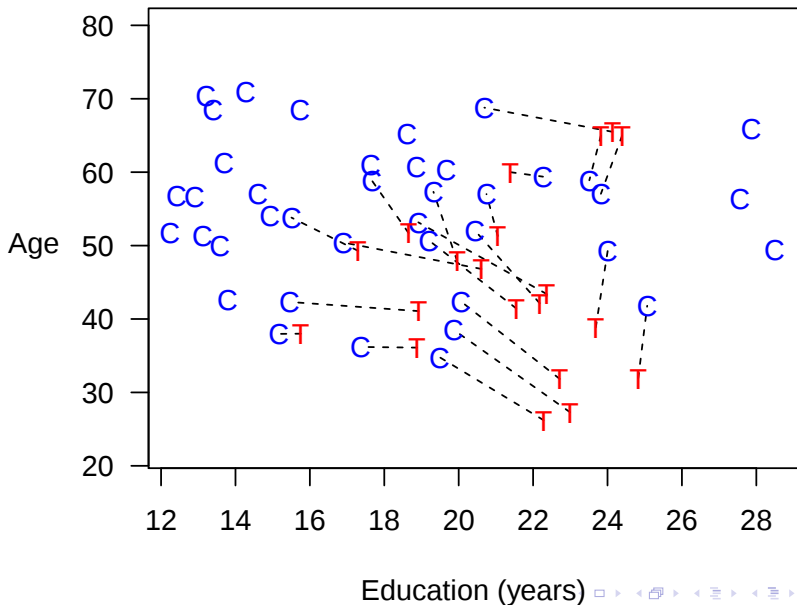
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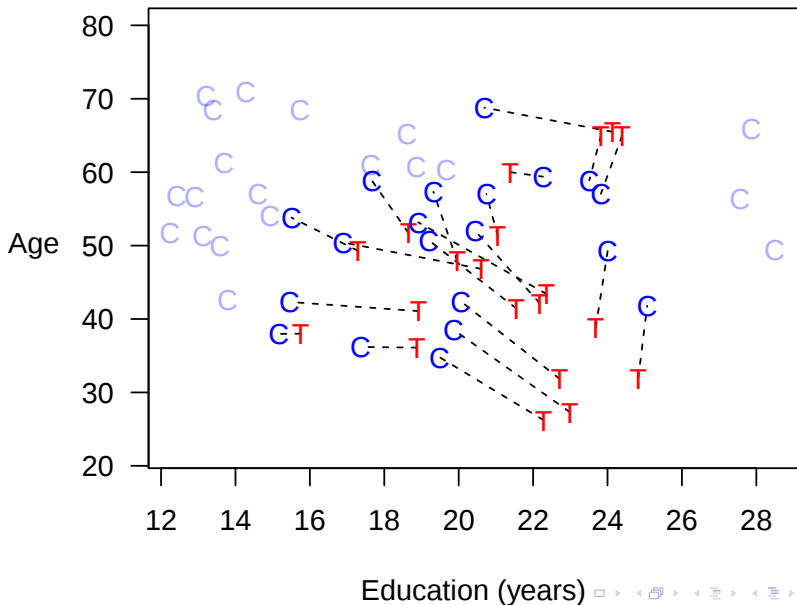
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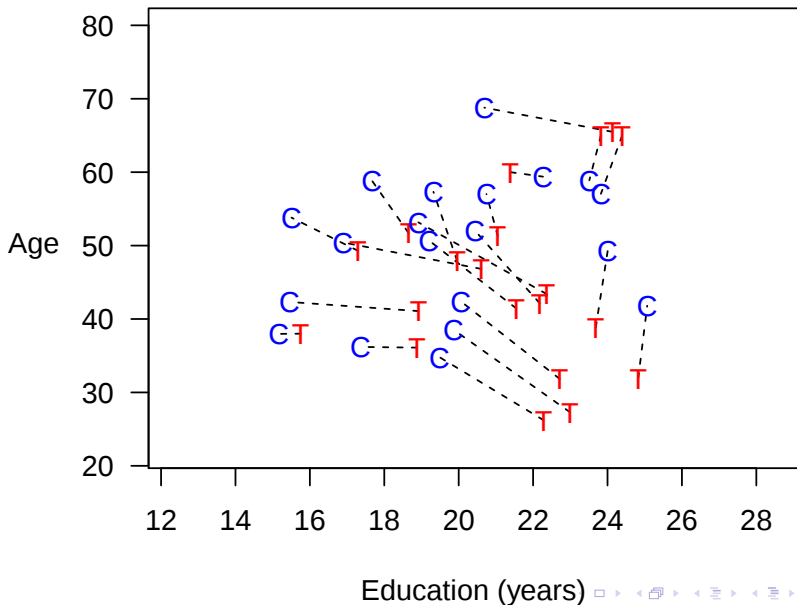
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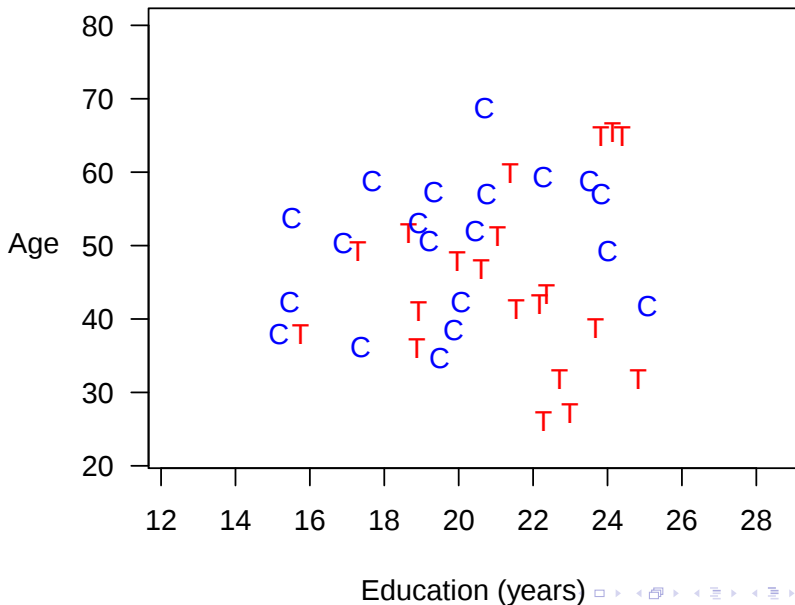
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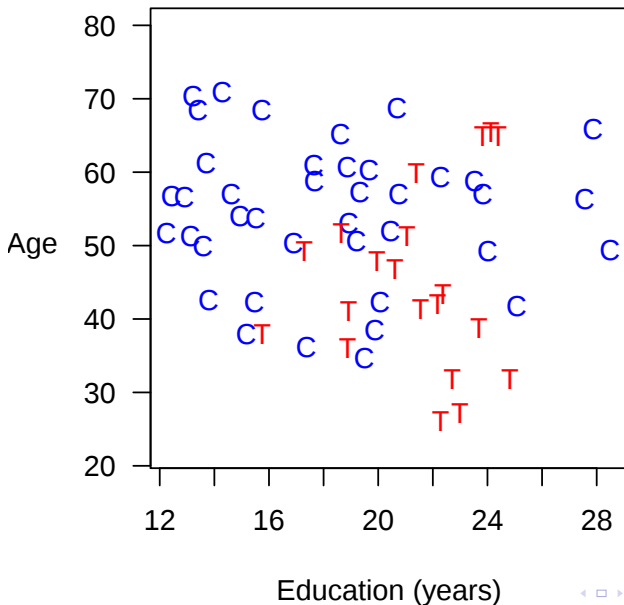
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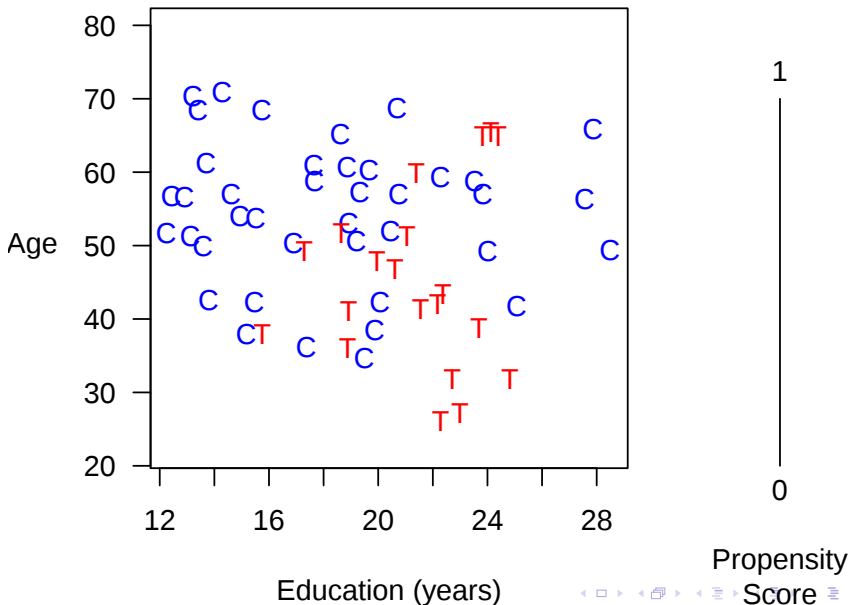
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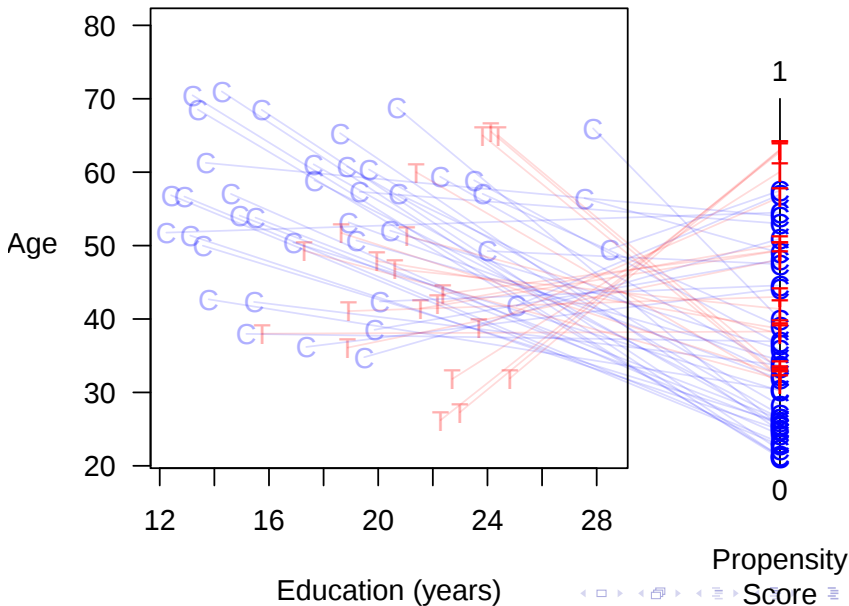
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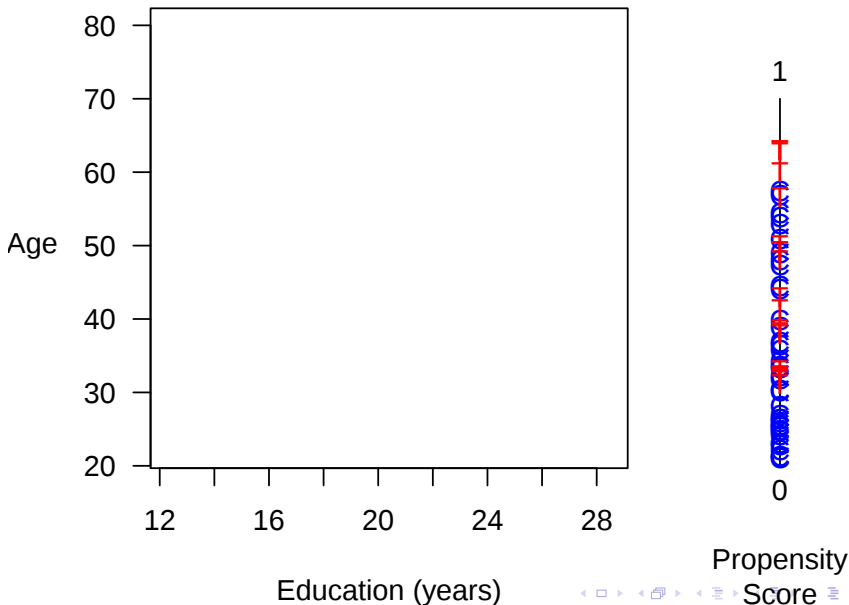
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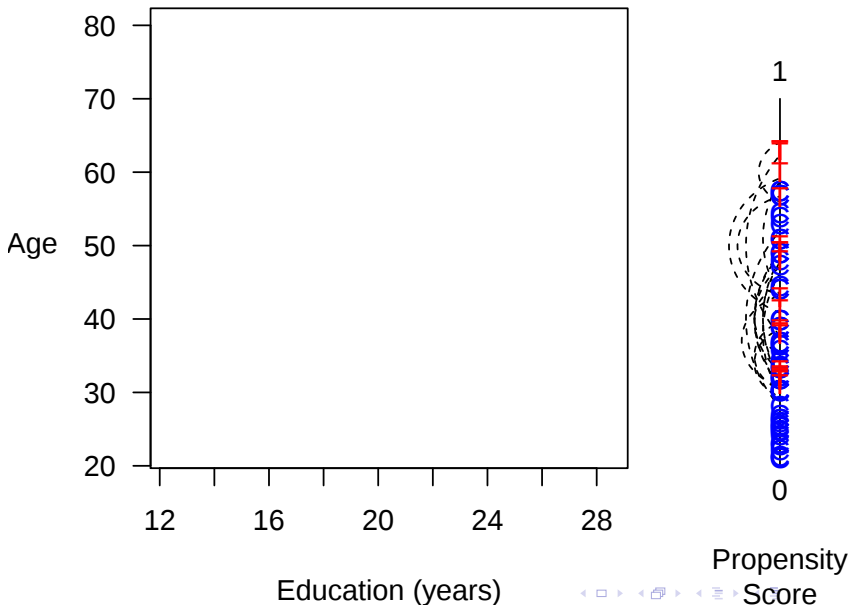
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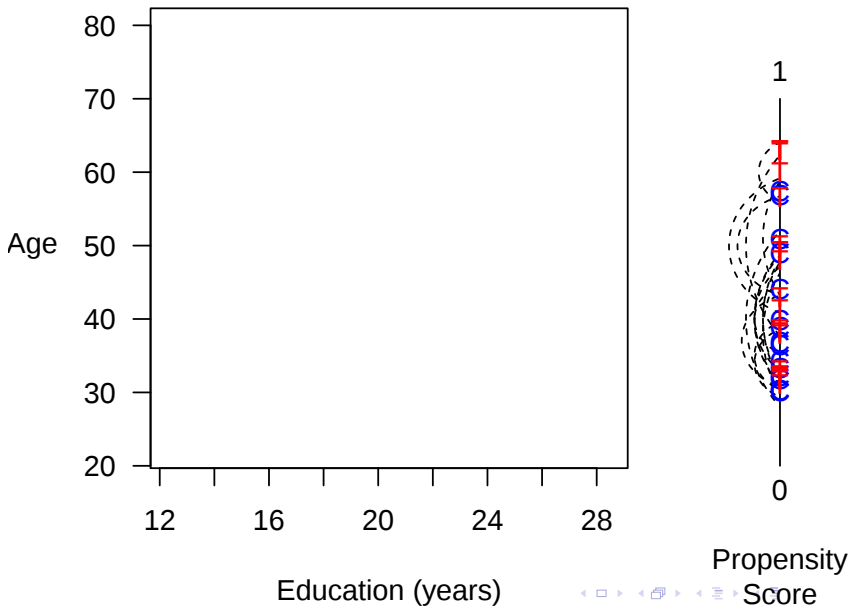
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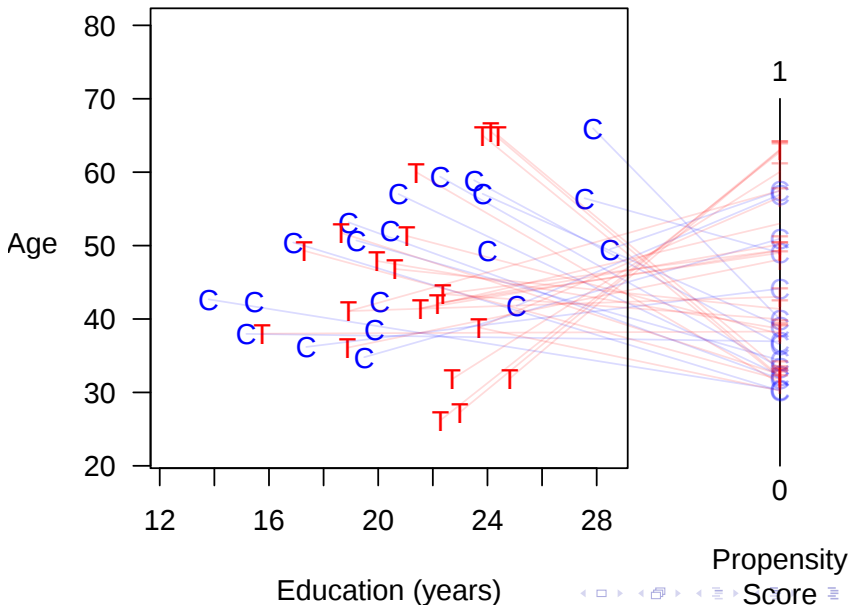
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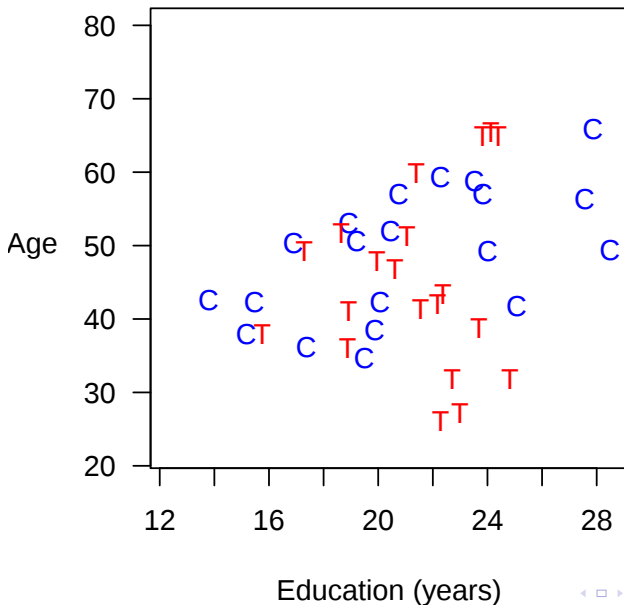
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Method 3: Coarsened Exact Matching

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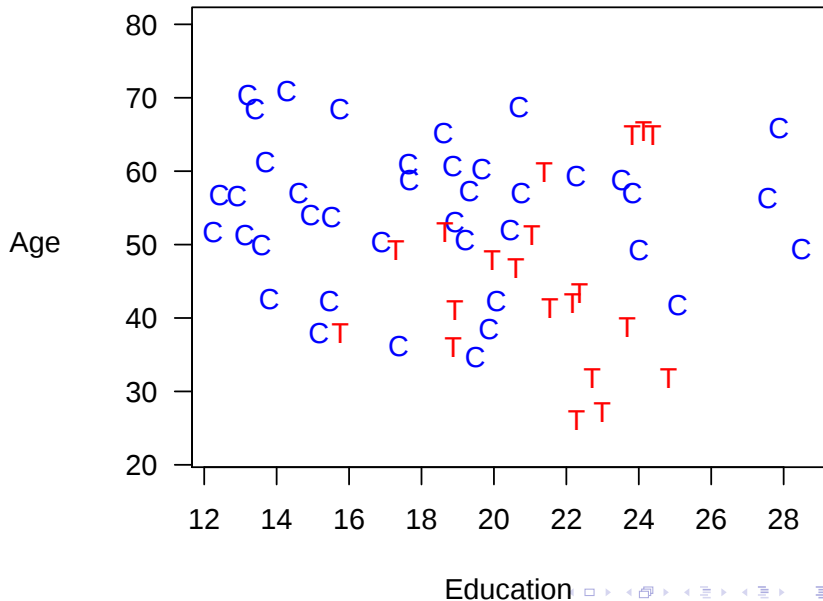
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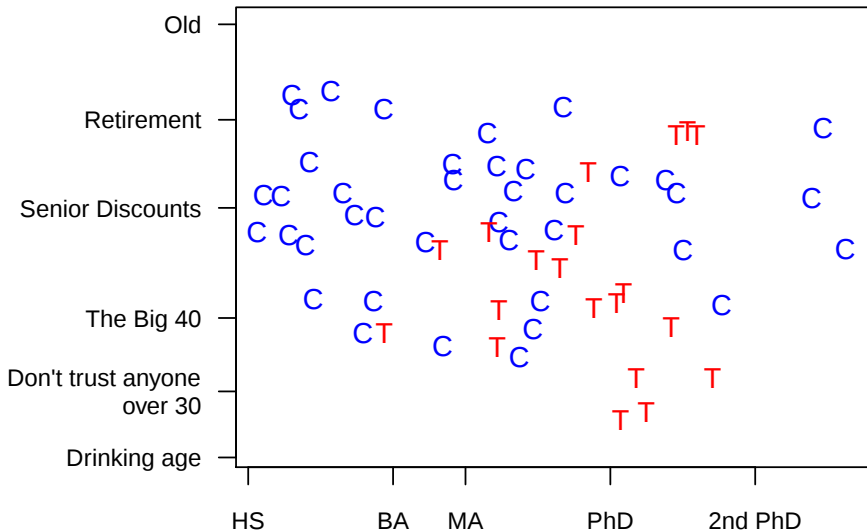
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- Can apply other matching methods within CEM strata (inherit CEM's properties)

Coarsened Exact Matching

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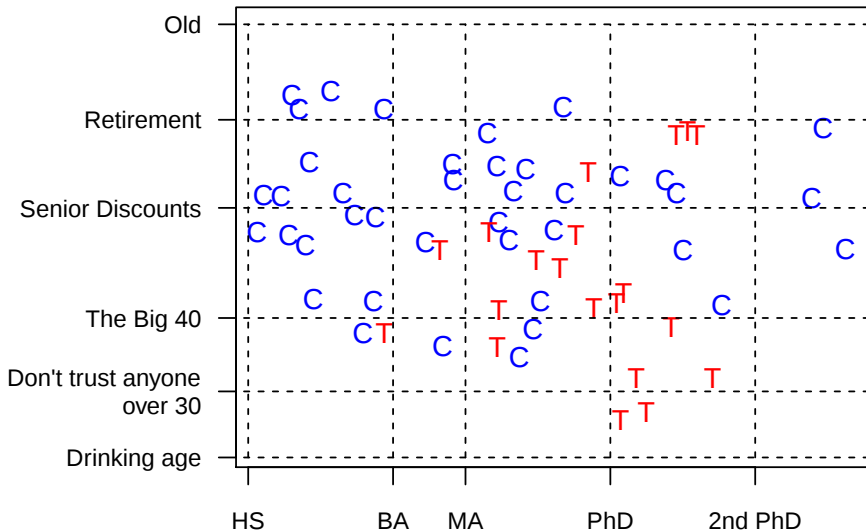


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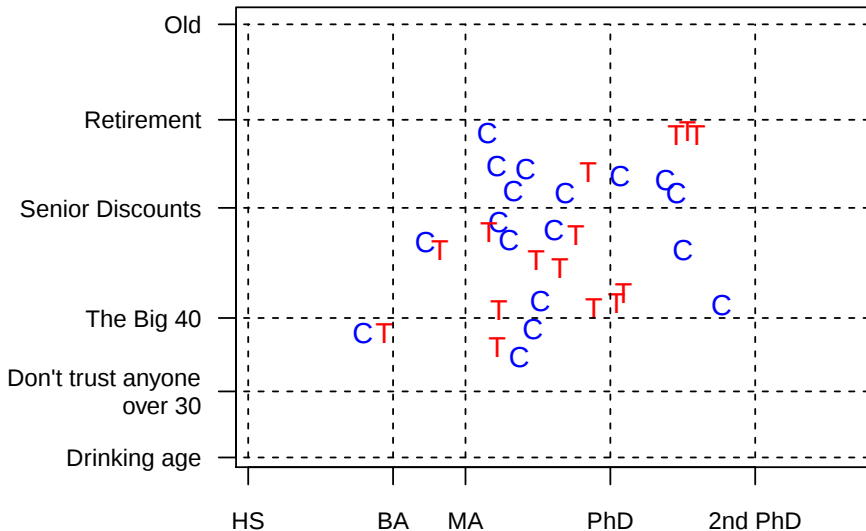


Education

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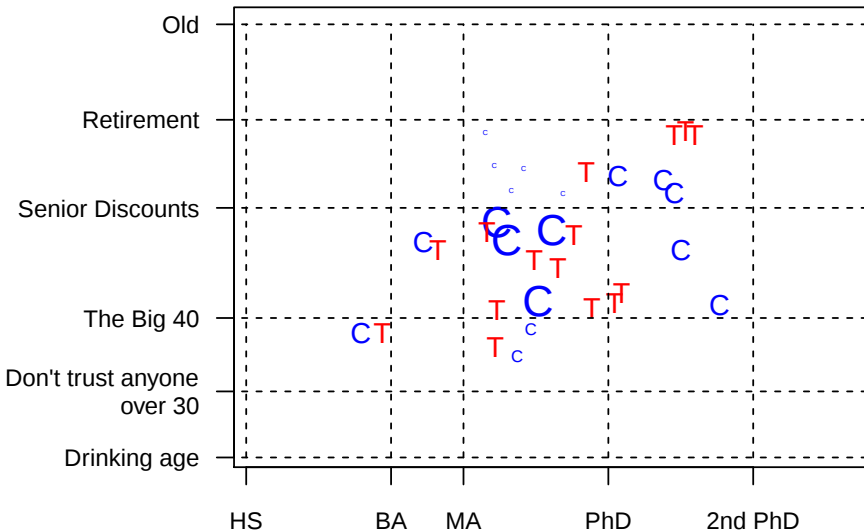


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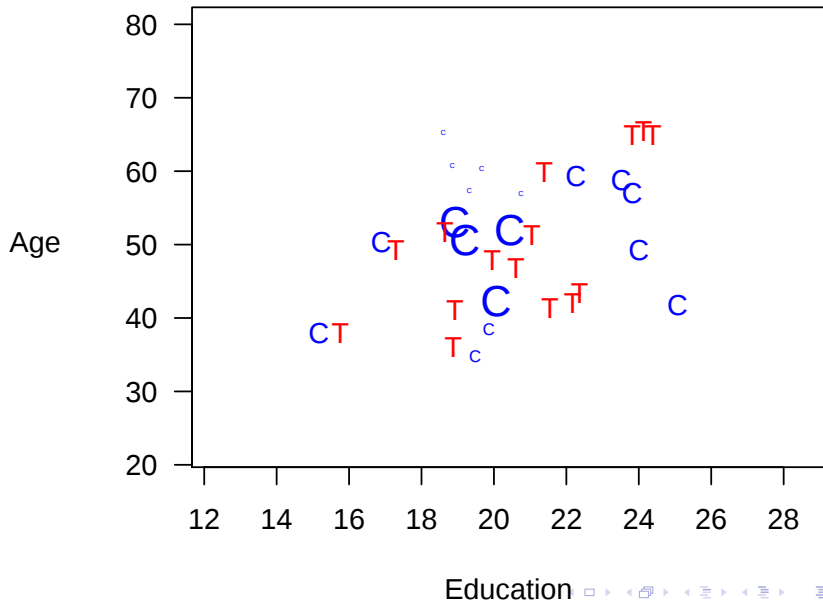


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$$\mathcal{L}_1(f, g; H) = \frac{1}{2} \sum_{\ell_1 \dots \ell_k \in H(\mathbf{X})} |f_{\ell_1 \dots \ell_k} - g_{\ell_1 \dots \ell_k}|$$

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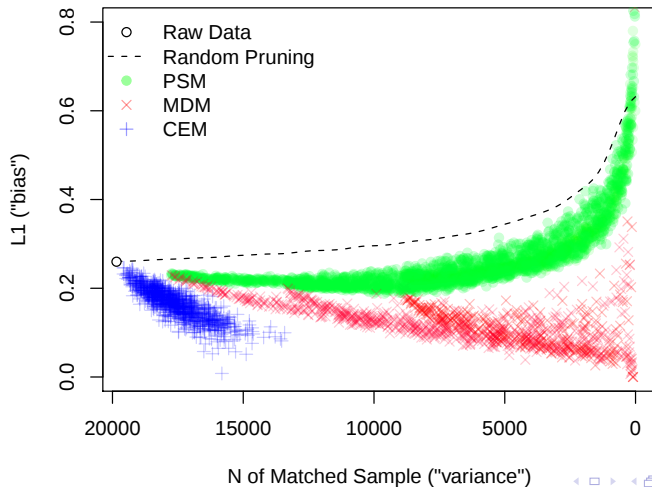
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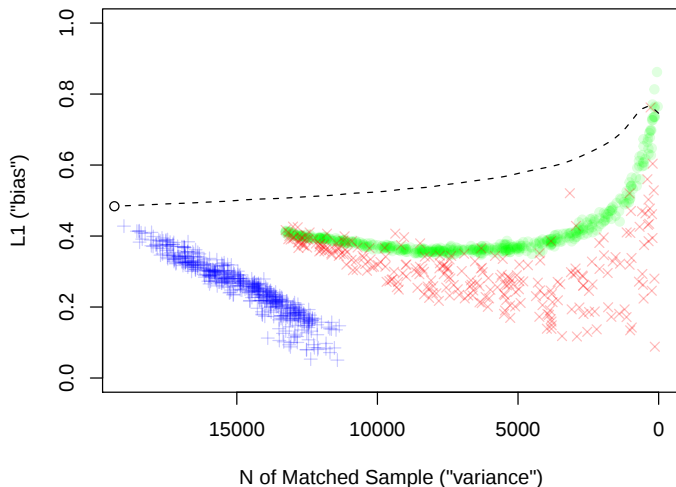
King, Nielsen, Coberley, Pope, and Wells (2011)

Healthways Data

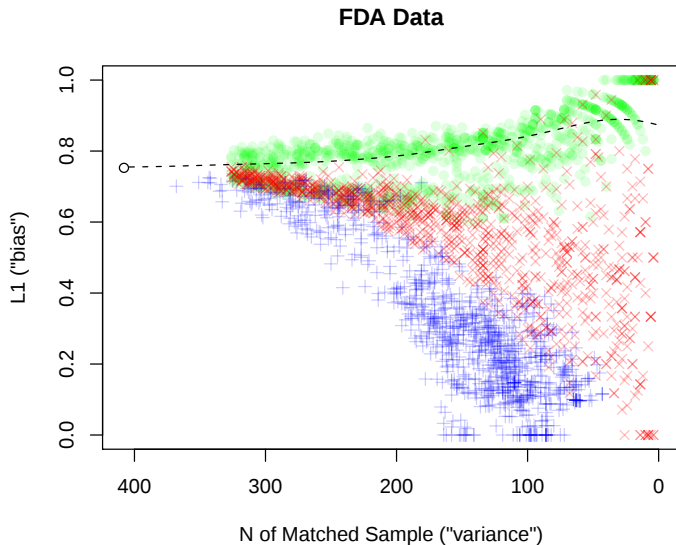


A Space Graph: Real Data

Called/Not Called Data

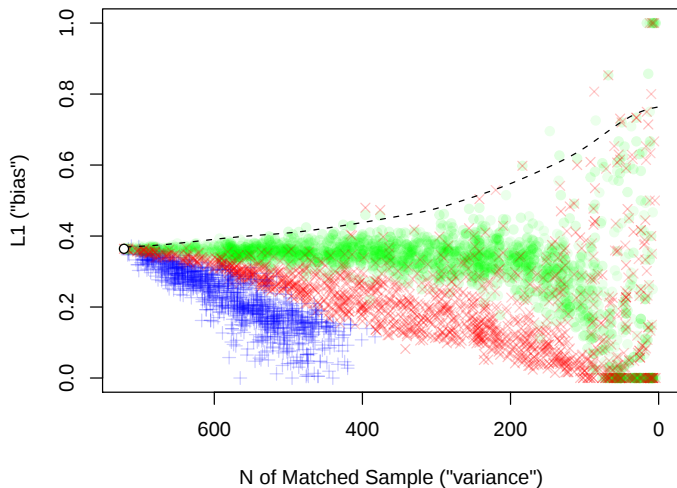


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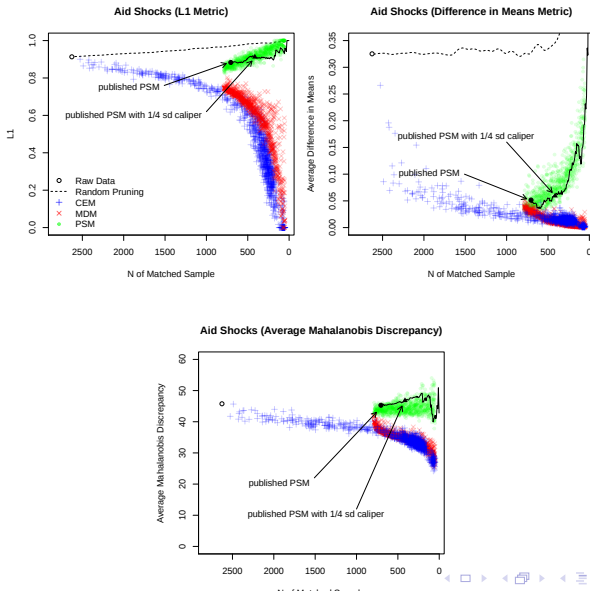


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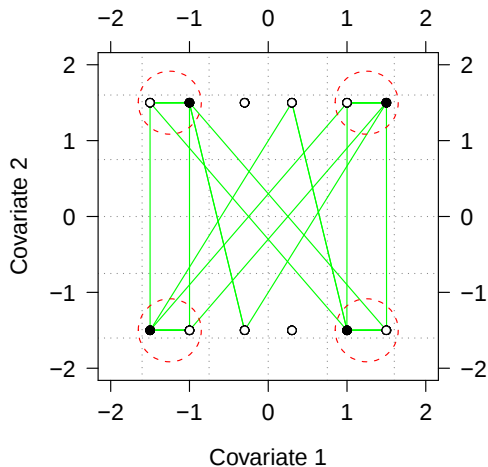
Lalonde Data Subset



Space Graphs: Different Imbalance Metrics

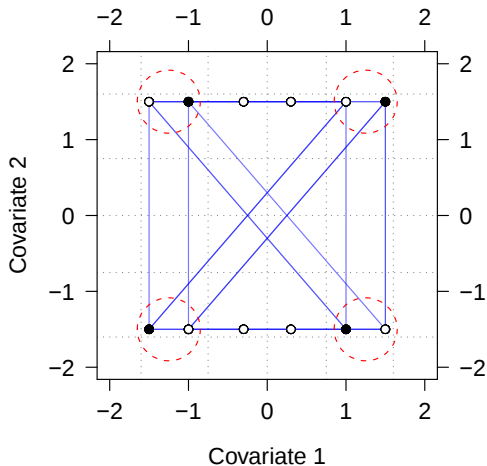


PSM Approximates Random Matching in Balanced Data



- PSM Matches
- - - CEM and MDM Matches

Destroying CEM with PSM's Two Step Approach



- CEM Matches
- CEM-generated PSM Matches

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(Is balance even improved?)

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End of planned slides for today; others follow

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- Simple to teach: coarsen, then exact match

Imbalance Measures

Variable-by-Variable Difference in Global Means

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Local Imbalance by Variable (given strata fixed by matching method)

$$I_2^{(j)} = \frac{1}{S} \sum_{s=1}^S \left| \bar{X}_{m_T^s}^{(j)} - \bar{X}_{m_C^s}^{(j)} \right|, \quad j = 1, \dots, k$$

CEM in Practice: EPBR-Compliant Data

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initial						1.24

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⇒ **CEM dominates EPBR-methods in EPBR Data**

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Monte Carlo: Exact replication of Diamond and Sekhon (2005), using data from Dehejia and Wahba (1999). CEM coarsening automated.

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⇒ CEM works well in non-EPBR data too

CEM Extensions I

- CEM and Multiple Imputation for Missing Data

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 - ① put missing observation in stratum where plurality of imputations fall

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 - 1 put missing observation in stratum where plurality of imputations fall
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 - ③ Use the usual MI combining rules to analyze

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- **Blocking in Randomized Experiments**: no modification needed; randomly assign T within CEM strata
- **Automating user choices** Histogram bin size calculations, *Estimated* SATT error bound, Progressive Coarsening

- CEM and **Multiple Imputation for Missing Data**
 - ① put missing observation in stratum where plurality of imputations fall
 - ② pass on uncoarsened imputations to analysis stage
 - ③ Use the usual MI combining rules to analyze
- **Multicategory Treatments**: No modification necessary; keep all strata with ≥ 1 unit having each value of T (L_1 is max difference across treatment groups)
- **Continuous Treatments**: Coarsen treatment and apply CEM as usual
- **Blocking in Randomized Experiments**: no modification needed; randomly assign T within CEM strata
- **Automating user choices** Histogram bin size calculations, *Estimated* SATT error bound, Progressive Coarsening
- **Detecting Extreme Counterfactuals**

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

<http://GKing.Harvard.edu/cem>