

Why Propensity Scores Should Not Be Used For Matching

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 - The mathematical theorems about propensity scores

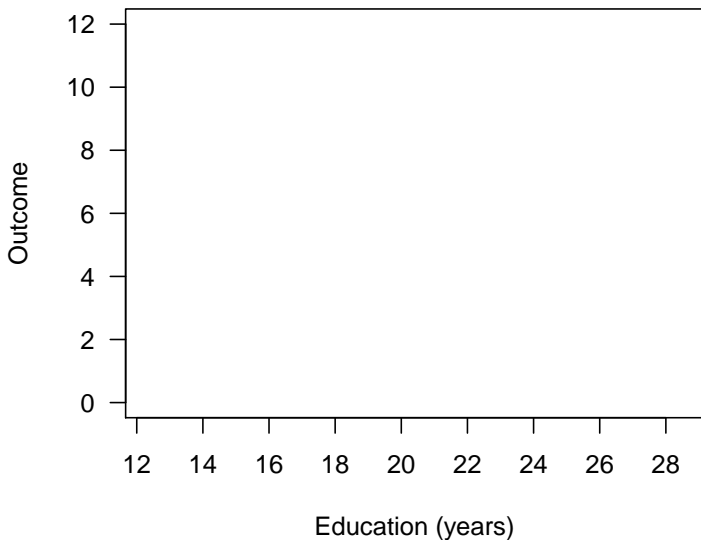
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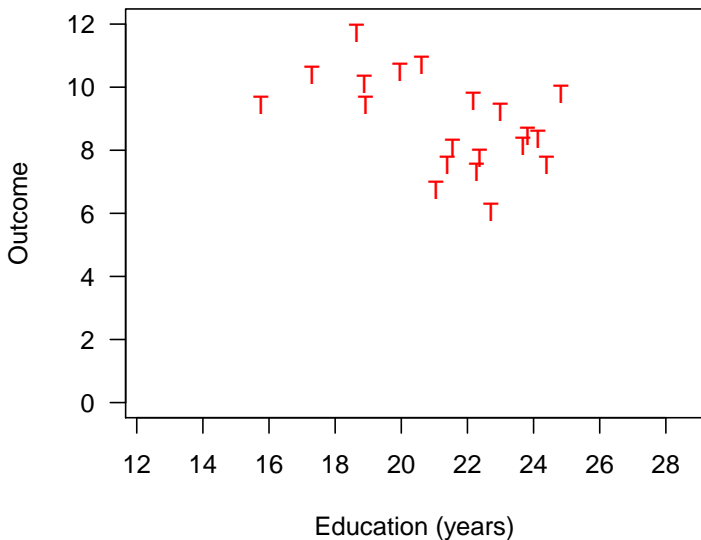
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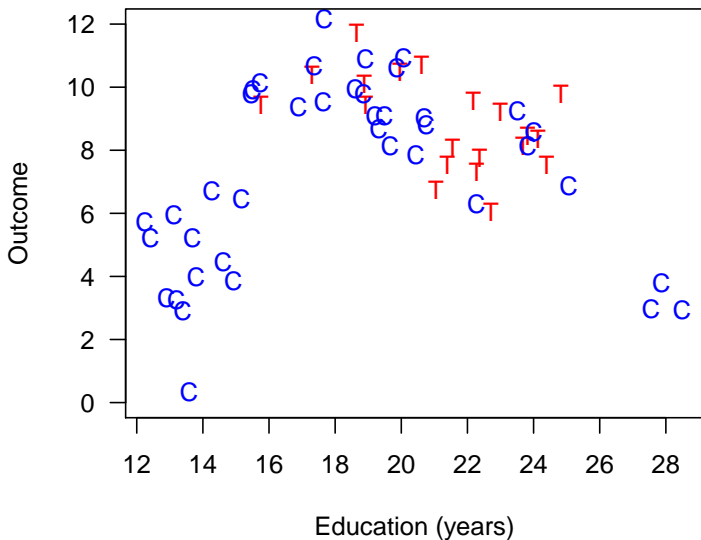
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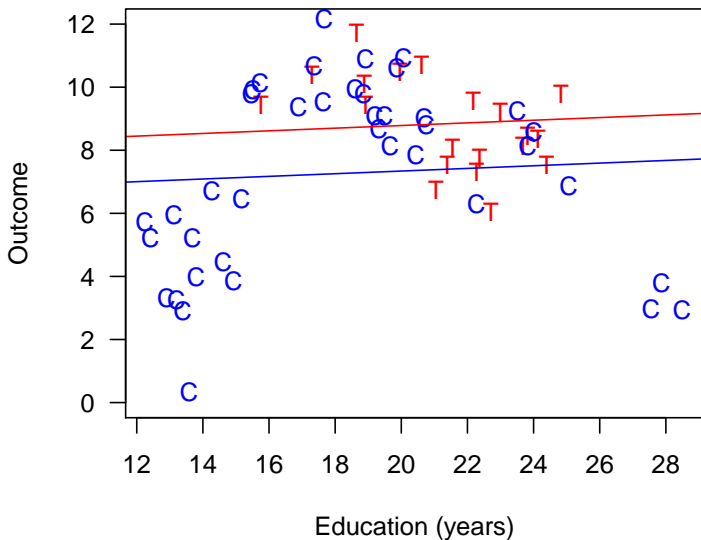
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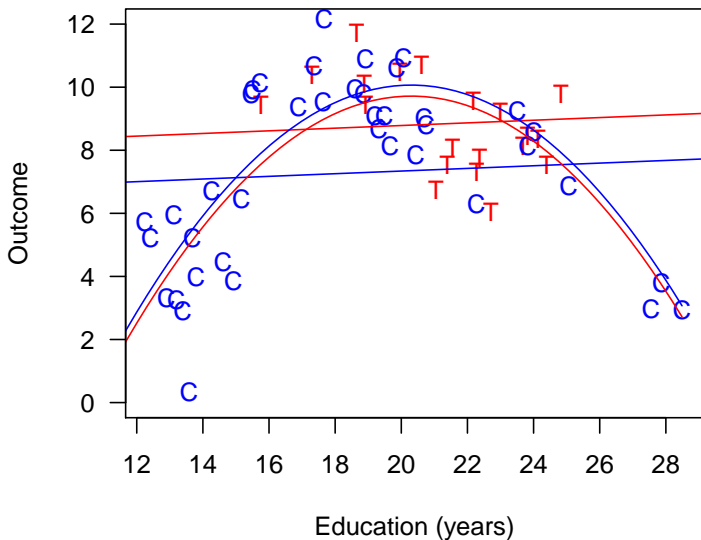
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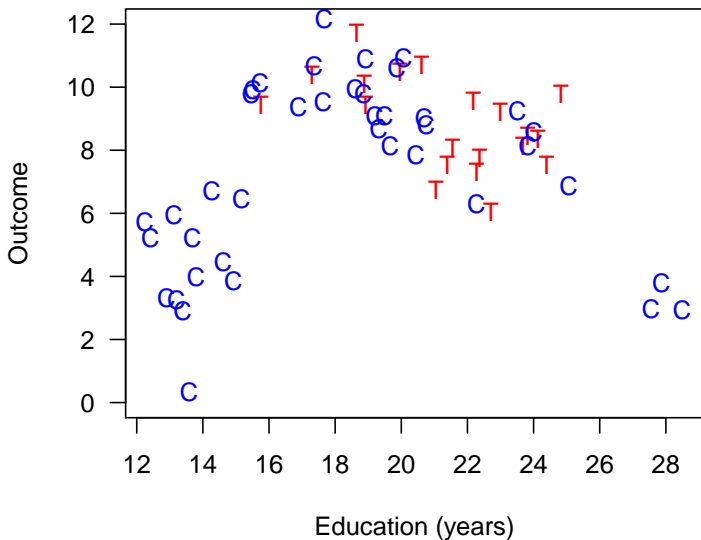
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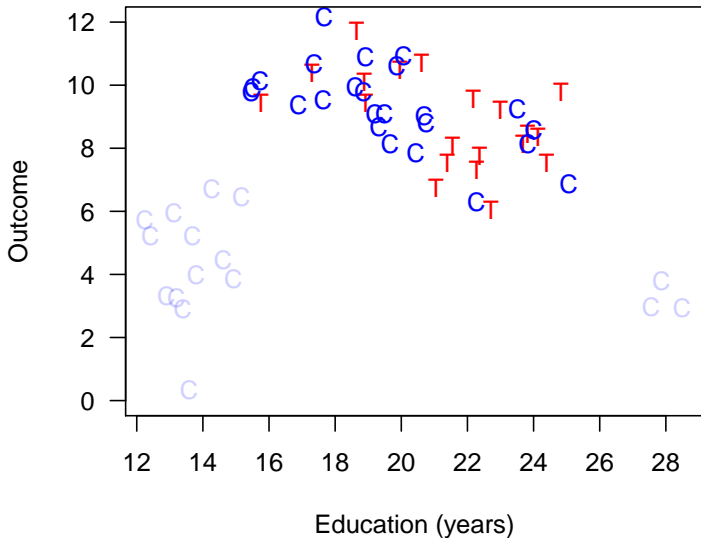
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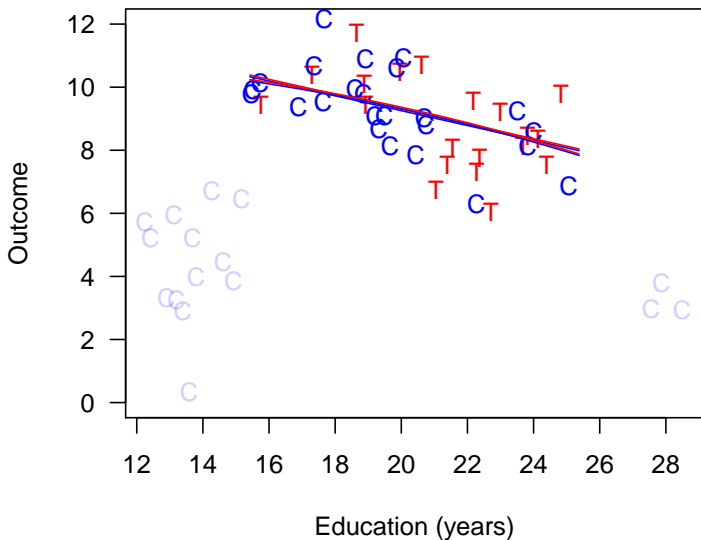
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- “Teaching psychology is mostly a waste of time” (Kahneman 2011)

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A central project of statistics: Automating away human discretion

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 - **Pruning nonmatches makes control vars matter less:** reduces imbalance, model dependence, researcher discretion, & bias

Matching: Finding Hidden Randomized Experiments

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Types of Experiments



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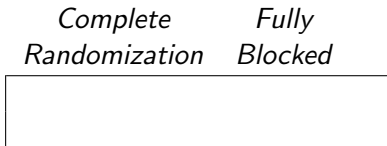
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- **Other matching methods dominate PSM** (wait, it gets worse)

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2. Estimation Difference in means or a model

Method 1: Mahalanobis Distance Matching

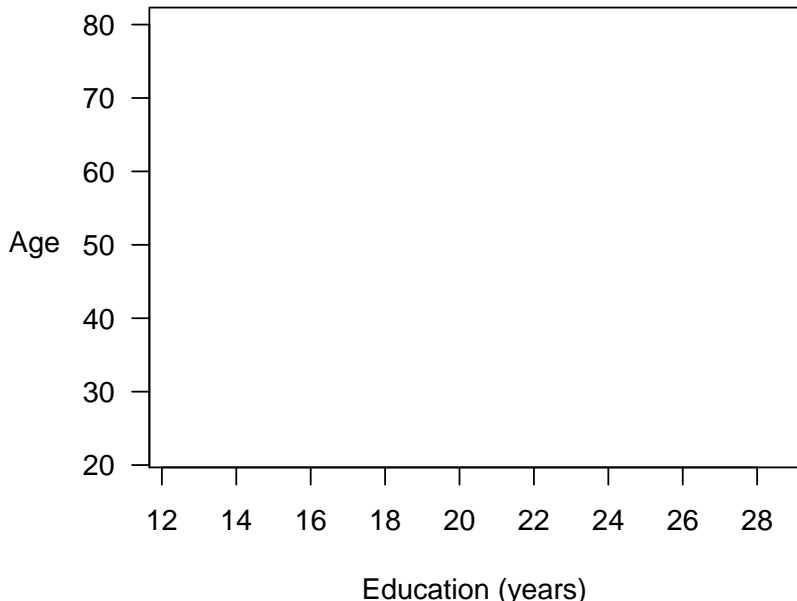
(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

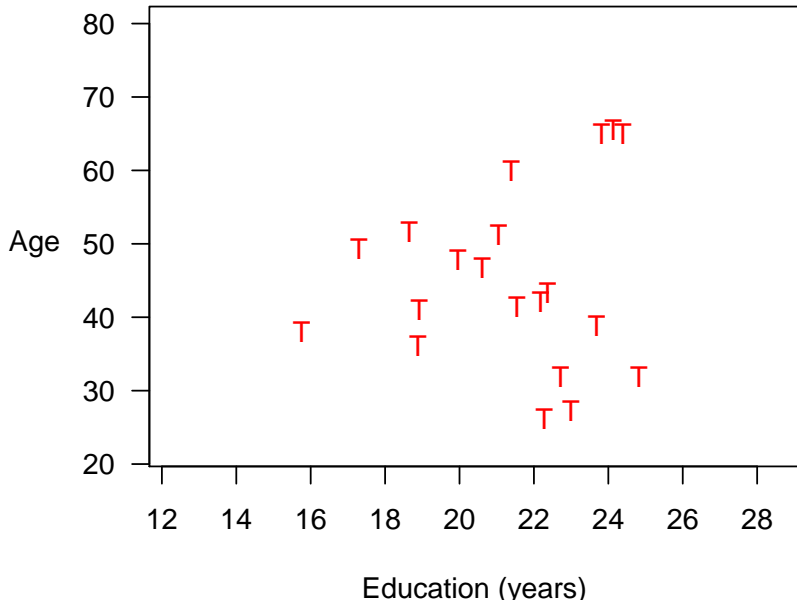
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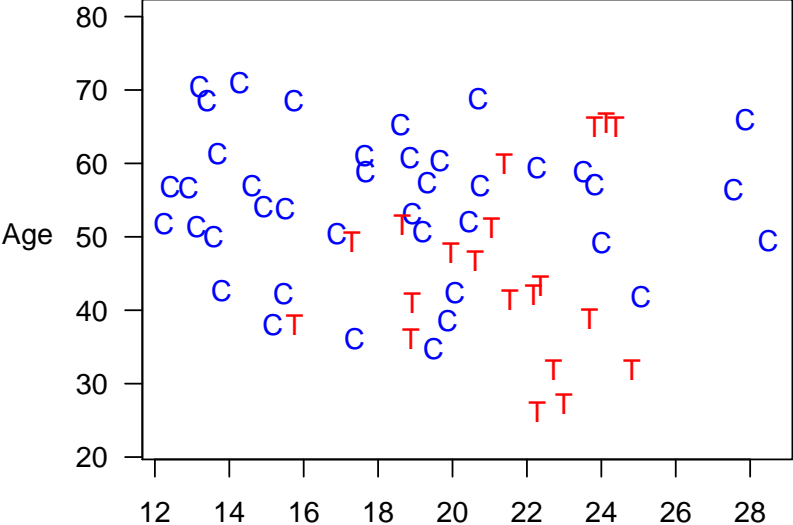
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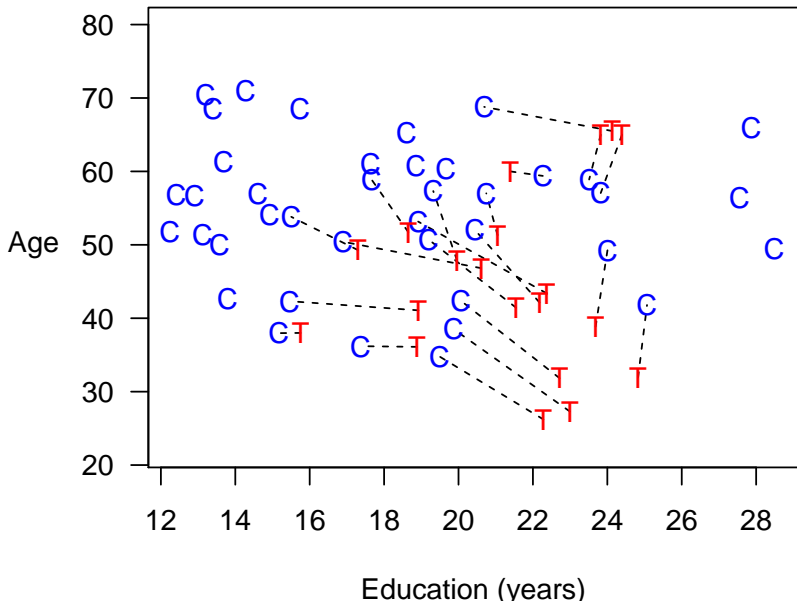
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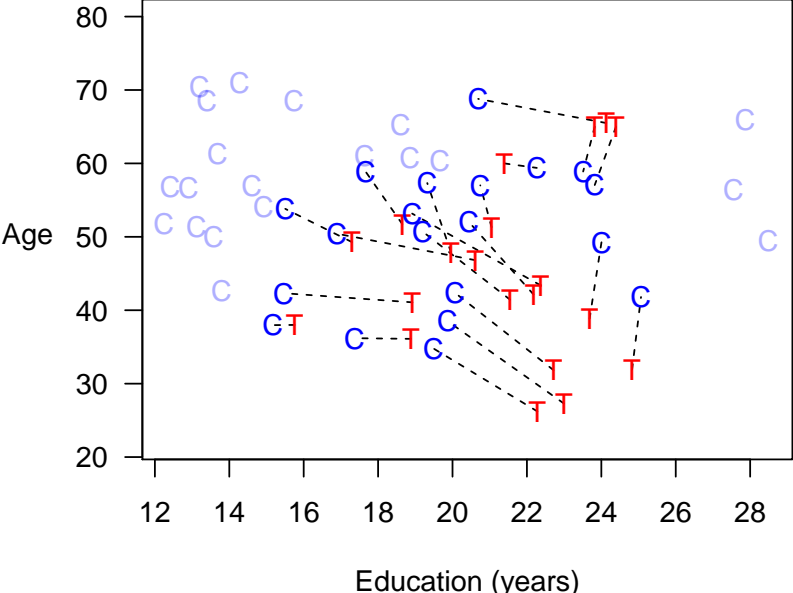
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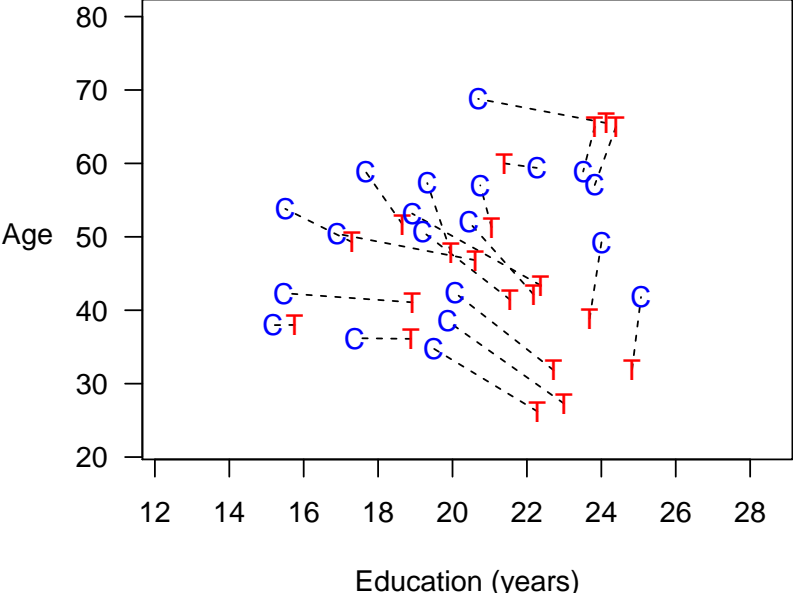
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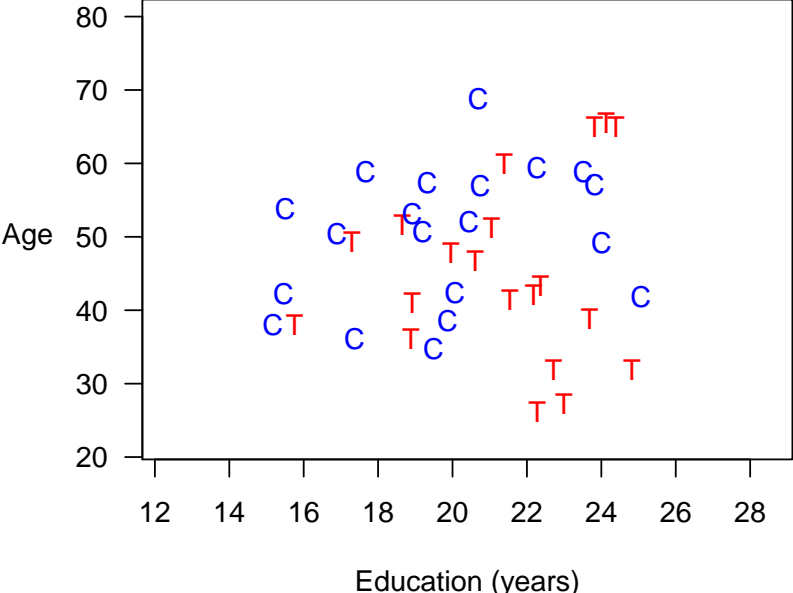
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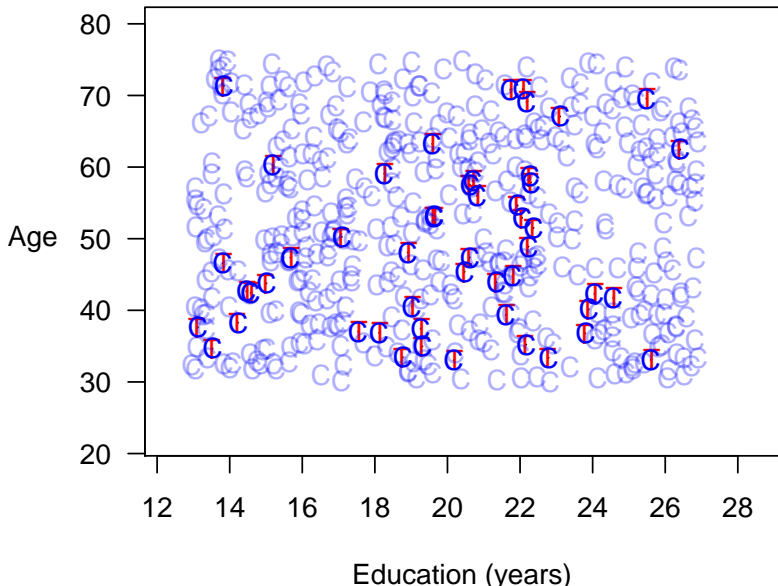


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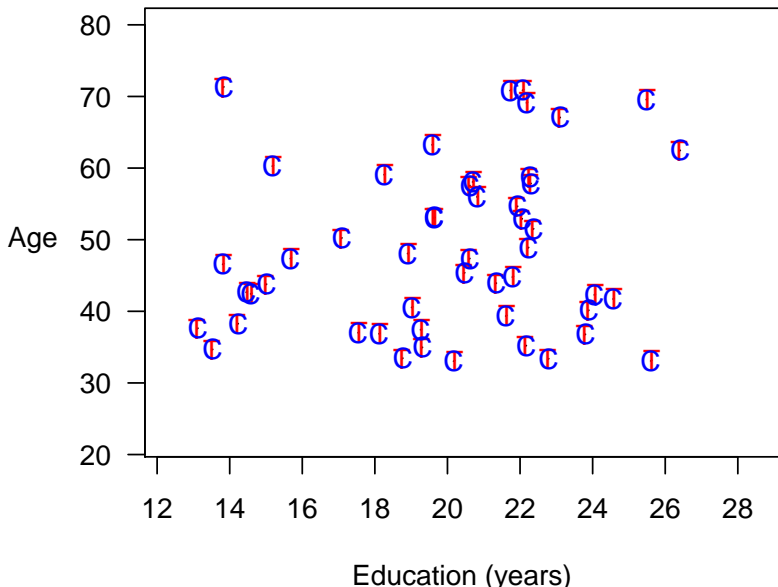


Best Case: Mahalanobis Distance Matching

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Method 2: Coarsened Exact Matching

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(Approximates Fully Blocked Experiment)

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1. **Preprocess** (Matching)
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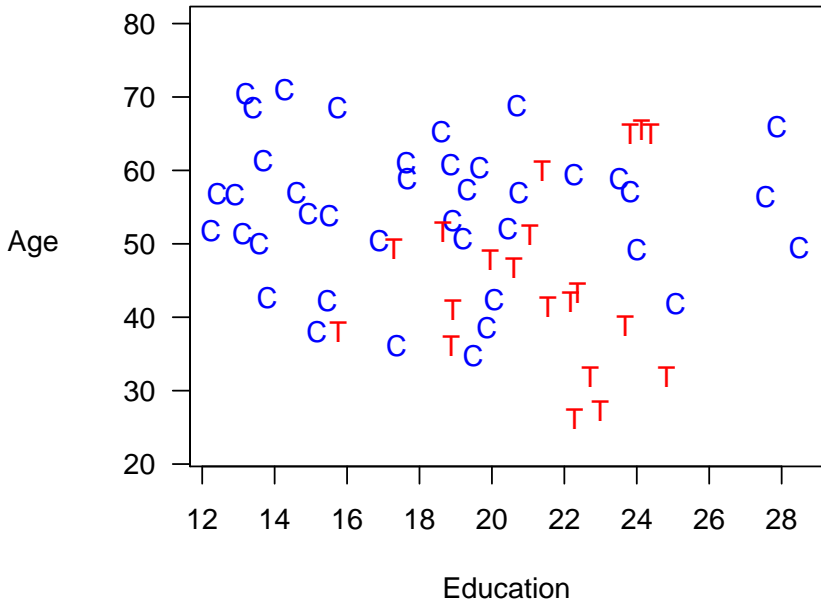
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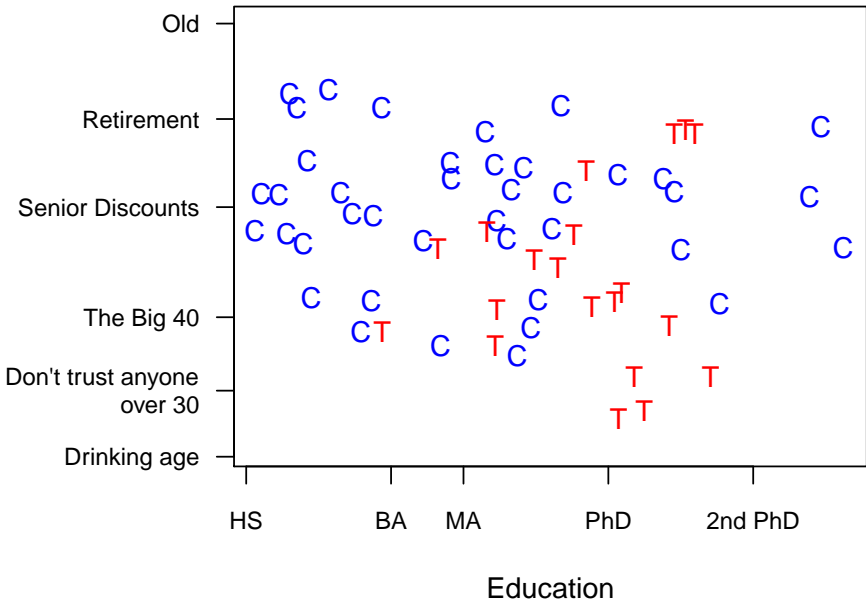
- Weight controls in each stratum to equal treateds

Coarsened Exact Matching

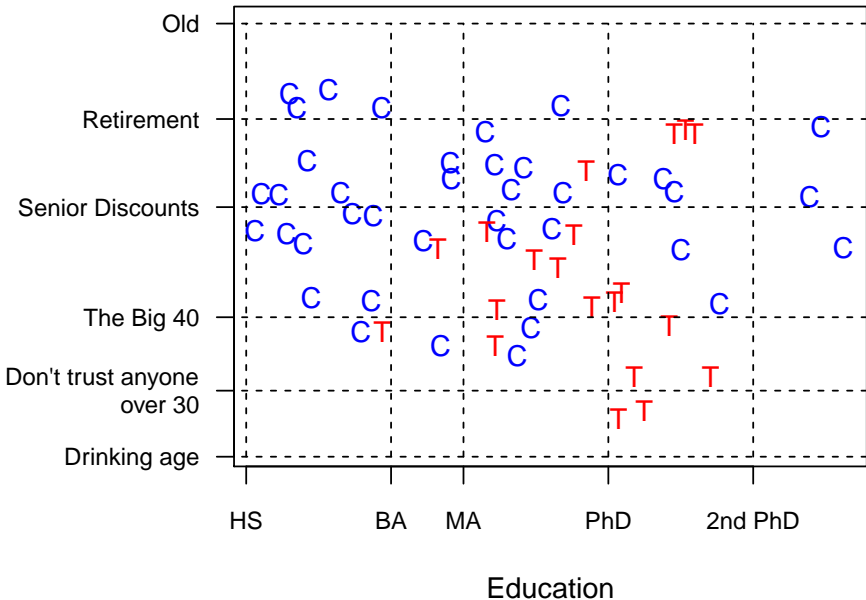
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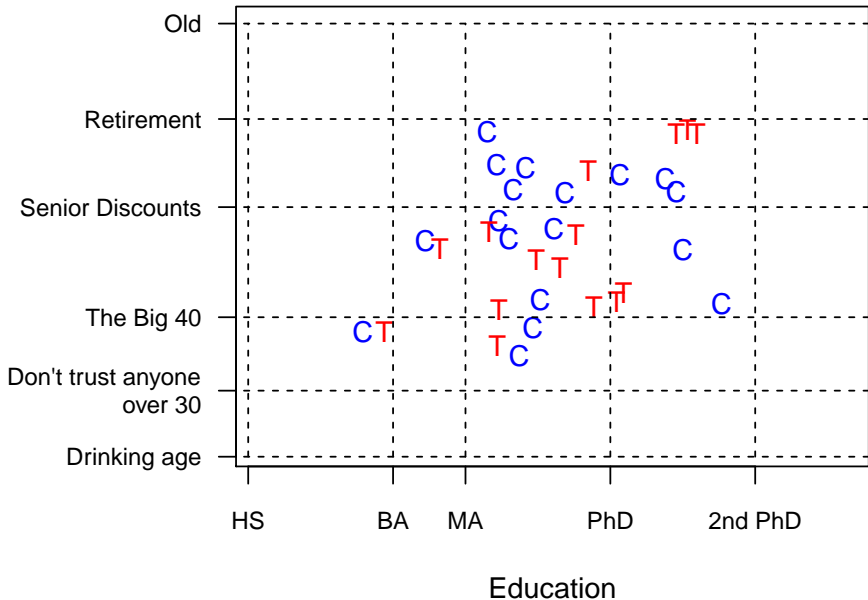
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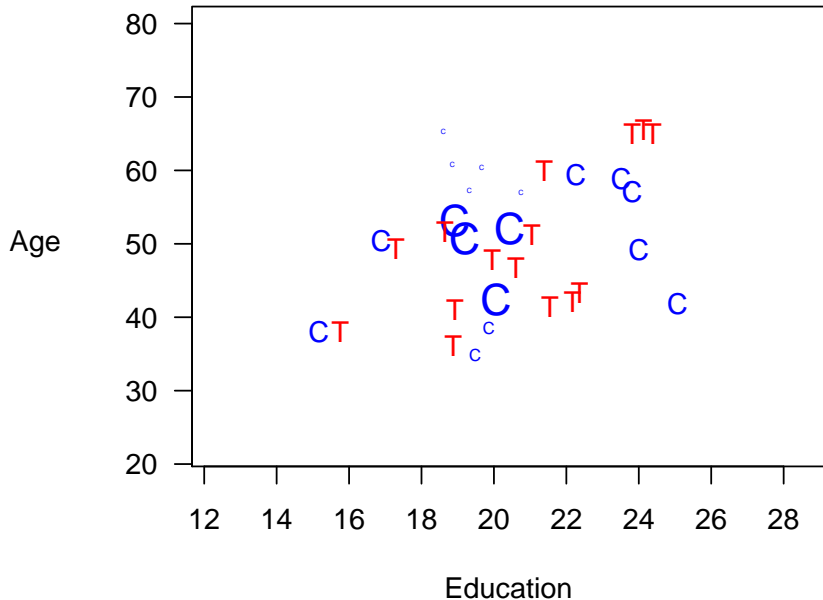
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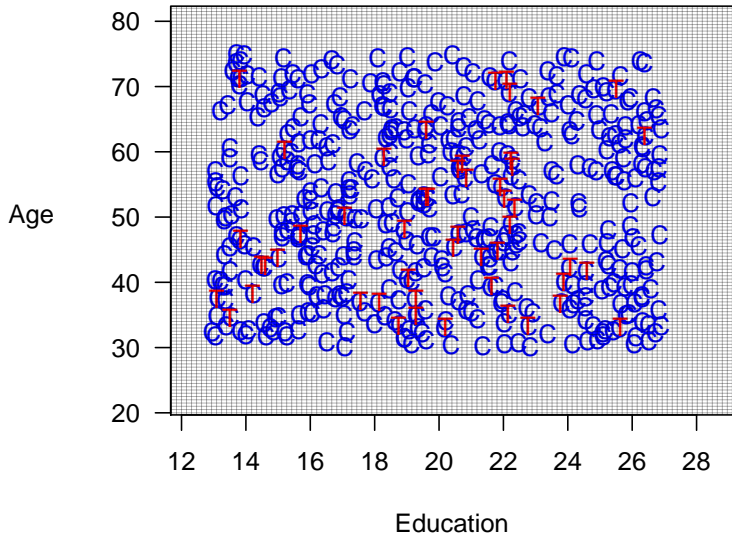


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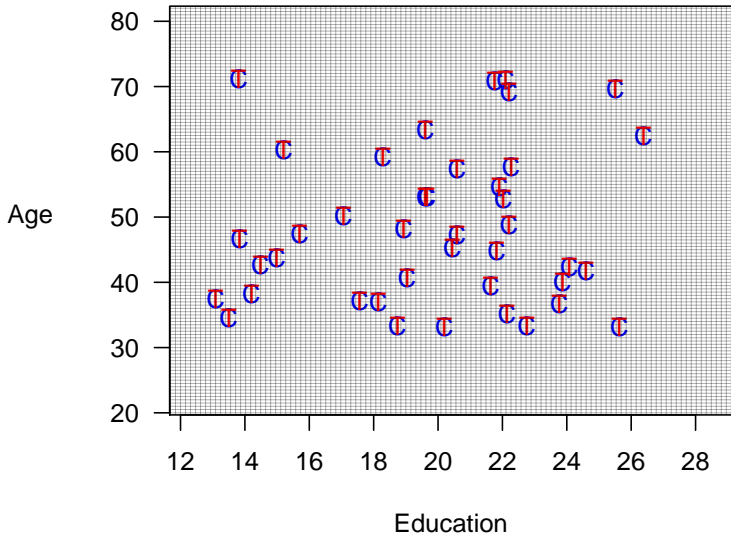


Best Case: Coarsened Exact Matching

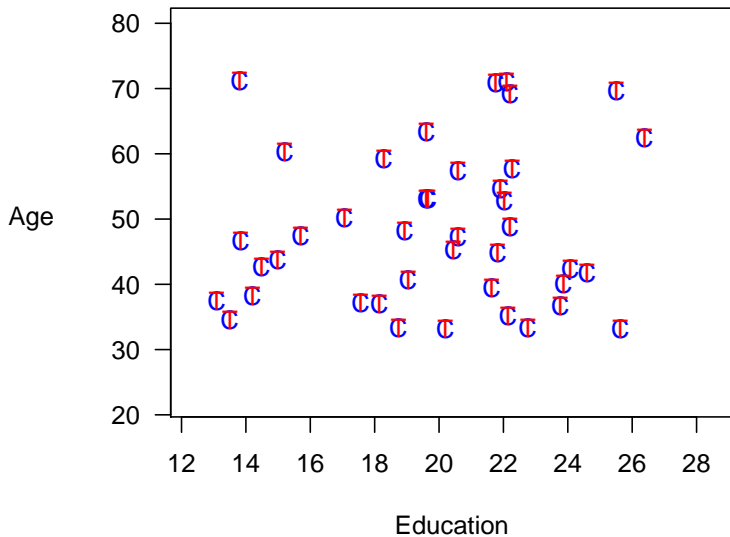
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Method 3: Propensity Score Matching

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(Approximates Completely Randomized Experiment)

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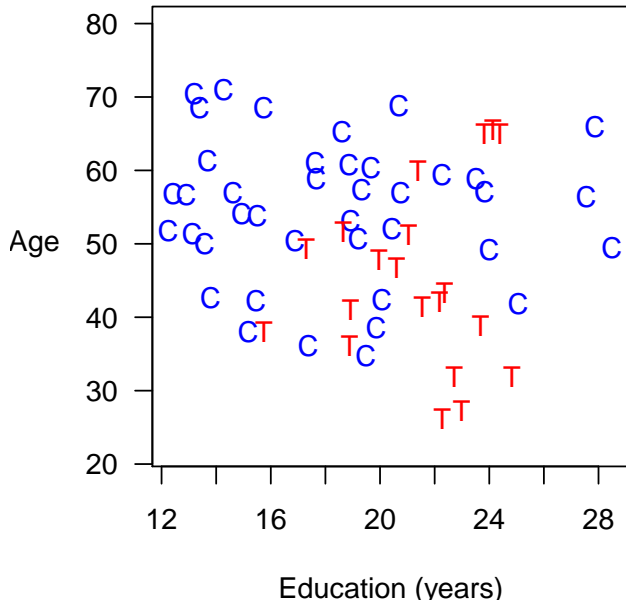
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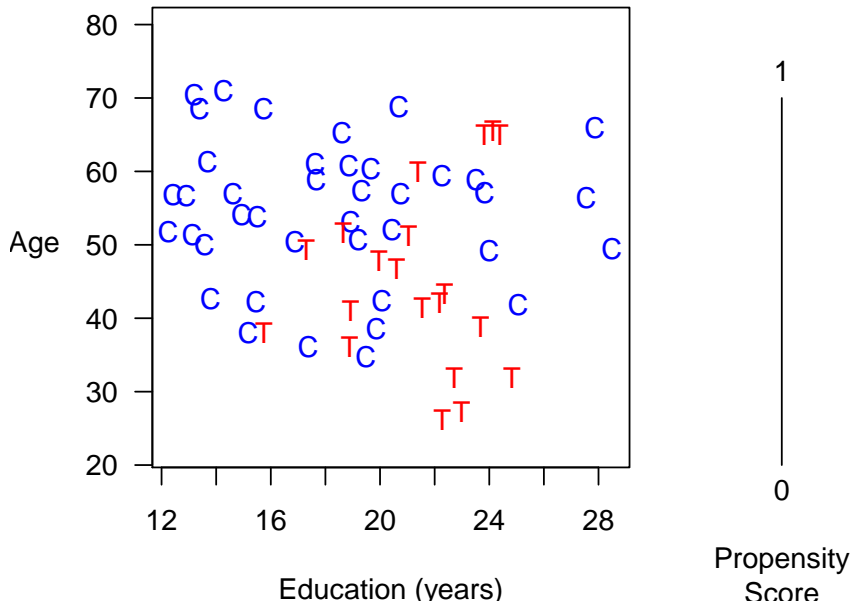
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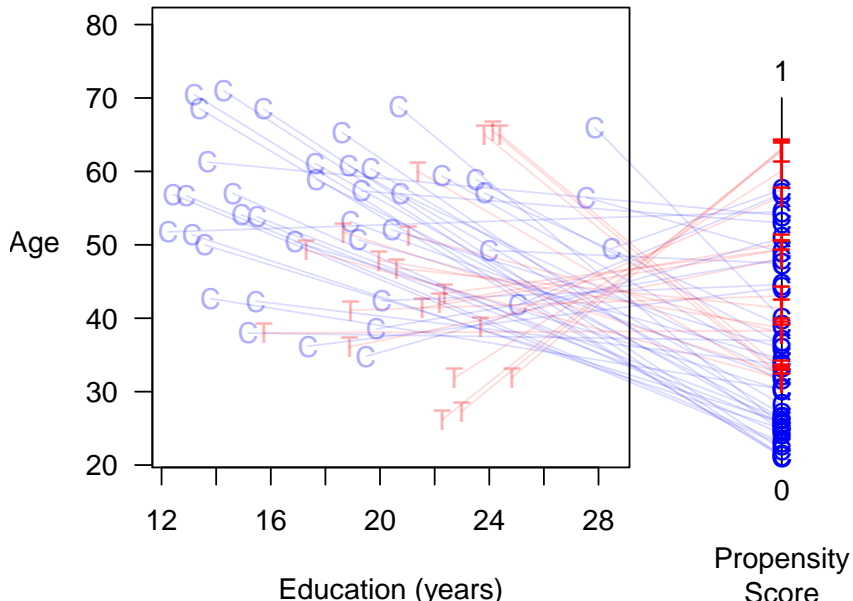
Propensity Score Matching



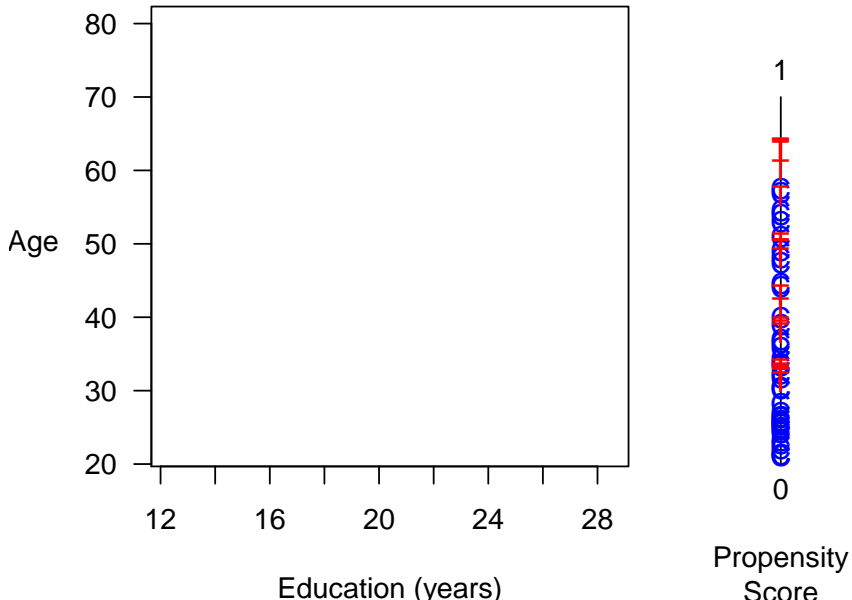
Propensity Score Matching



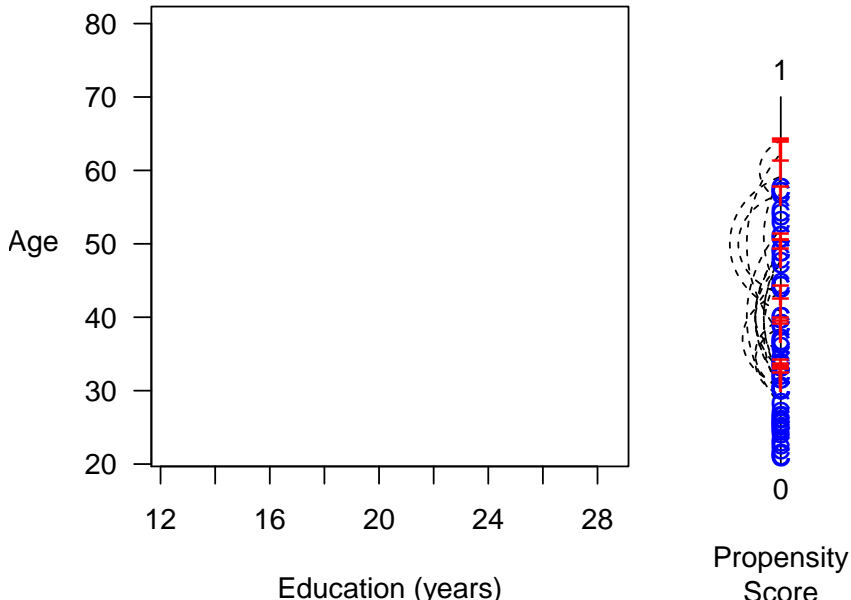
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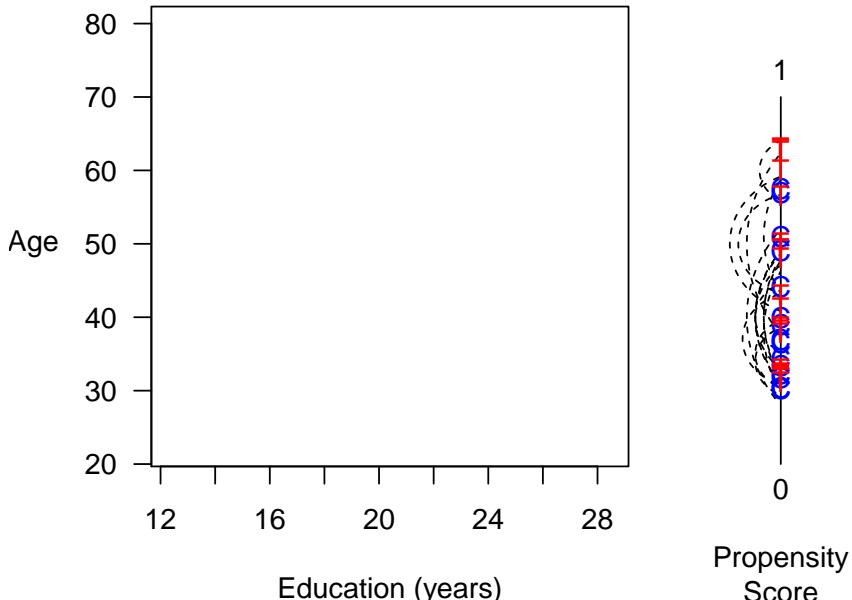
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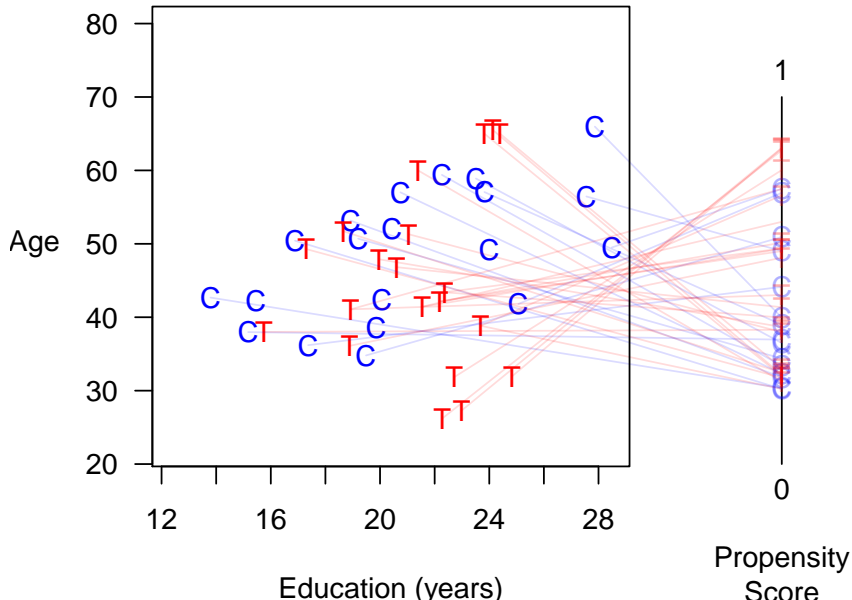
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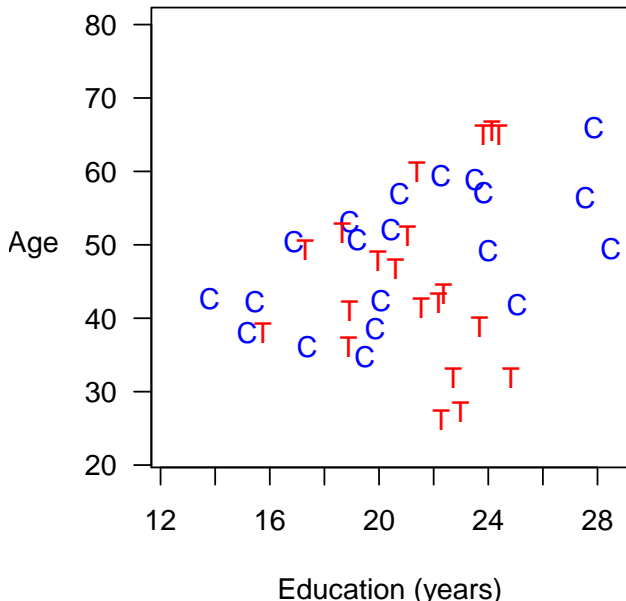
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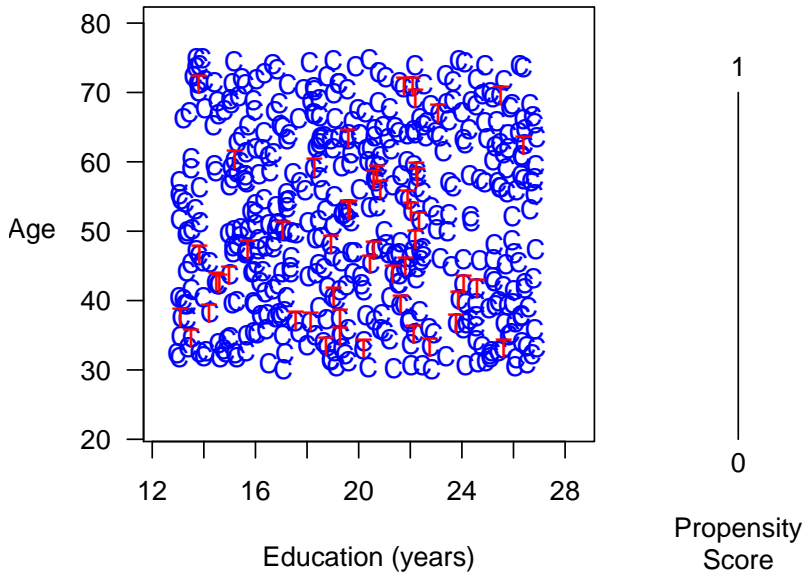


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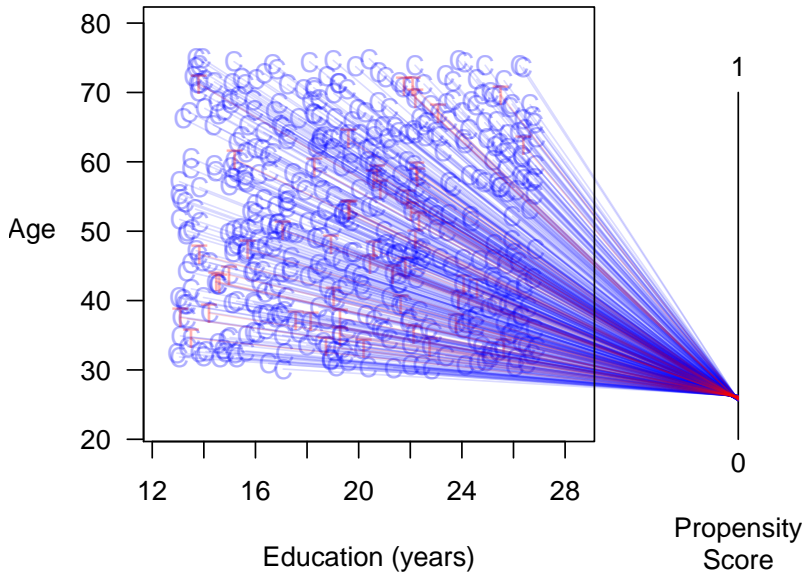


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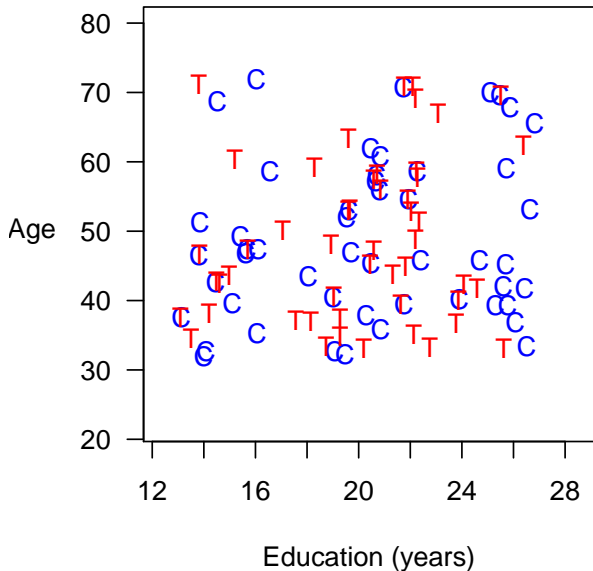
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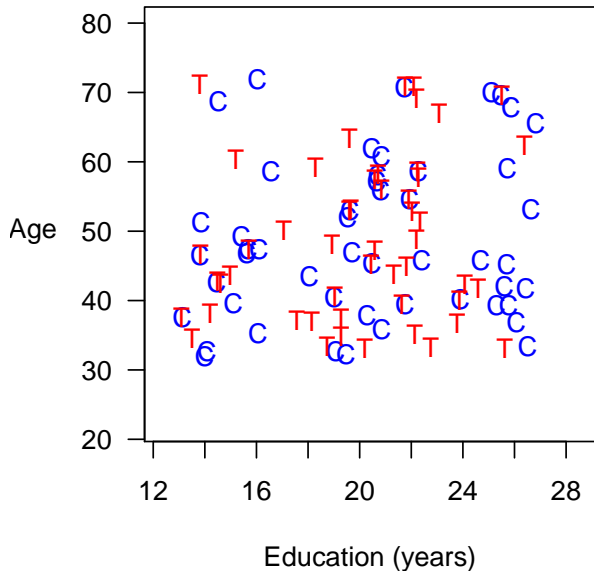
Best Case: Propensity Score Matching



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Best Case: Propensity Score Matching is Suboptimal



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- *Efficient* relative to complete randomization, but
- *Inefficient* relative to (the more powerful) full blocking
- Other methods dominate:

$$X_c = X_t \implies \pi_c = \pi_t \text{ but}$$

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2. The PSM Paradox: When you do “better,” you do worse

- When PSM approximates complete randomization (to begin with or, after some pruning) \rightsquigarrow all $\hat{\pi} \approx 0.5$ (or constant within strata) \rightsquigarrow pruning at random \rightsquigarrow Imbalance \rightsquigarrow Inefficiency \rightsquigarrow Model dependence \rightsquigarrow Bias

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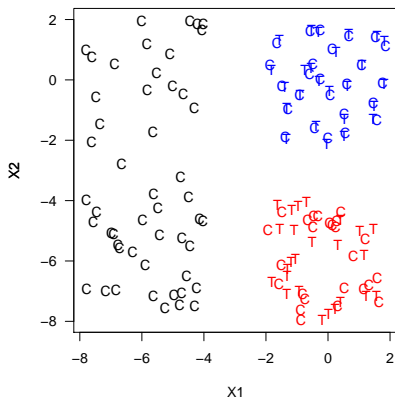
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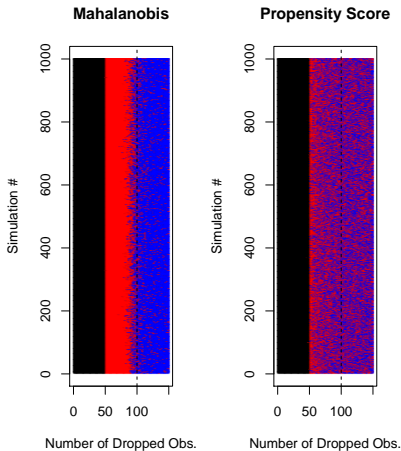
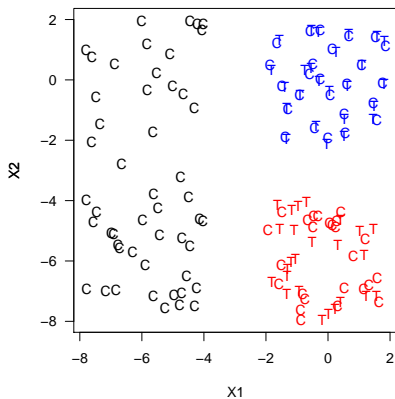
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PSM is Blind Where Other Methods Can See

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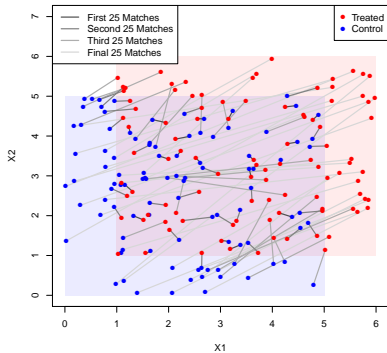


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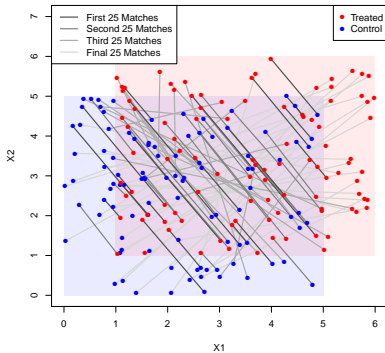


What Does PSM Match?

MDM Matches



PSM Matches

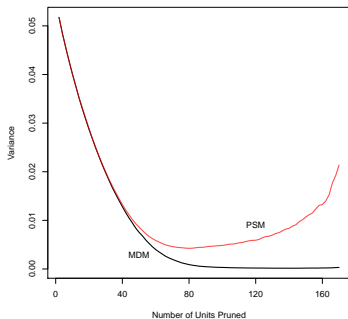


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

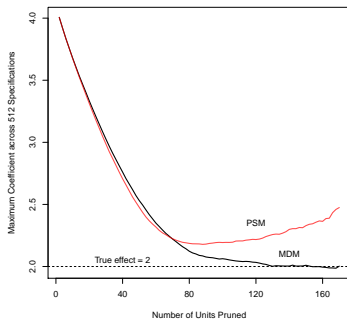
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

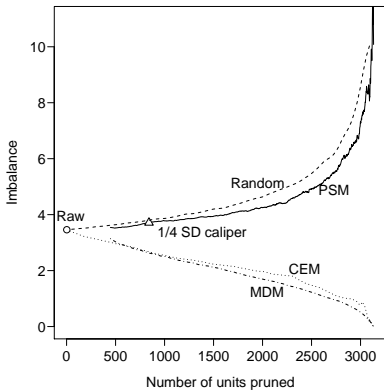


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

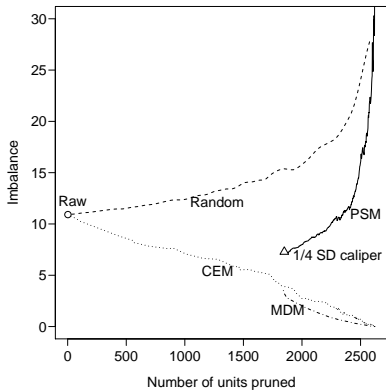
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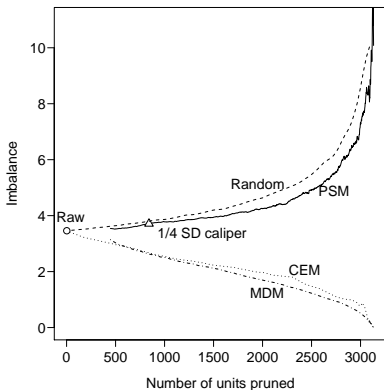


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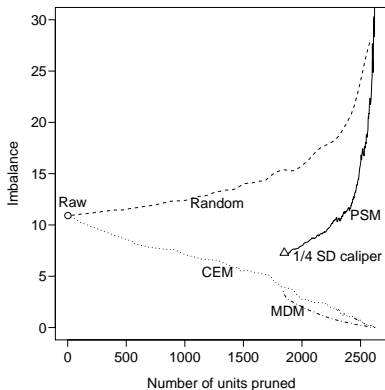


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Similar pattern for > 20 other real data sets we checked

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- **Matching methods still highly recommended; choose one with higher standards**

For more information, papers, & software



GaryKing.org
www.mit.edu/~rnielsen