

Why Propensity Scores Should Not Be Used For Matching

Gary King¹

Richard Nielsen²

Institute for Quantitative Social Science
Harvard University

MIT

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¹GaryKing.org

²www.mit.edu/~rnielsen

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 - Other uses of propensity scores: E.g., regression adjustment, inverse weighting, stratification, pcores used in other methods
 - The mathematical theorems about propensity scores

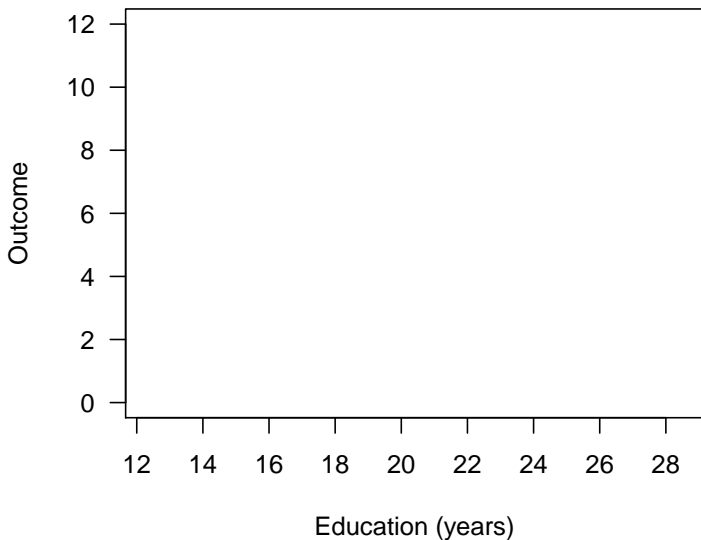
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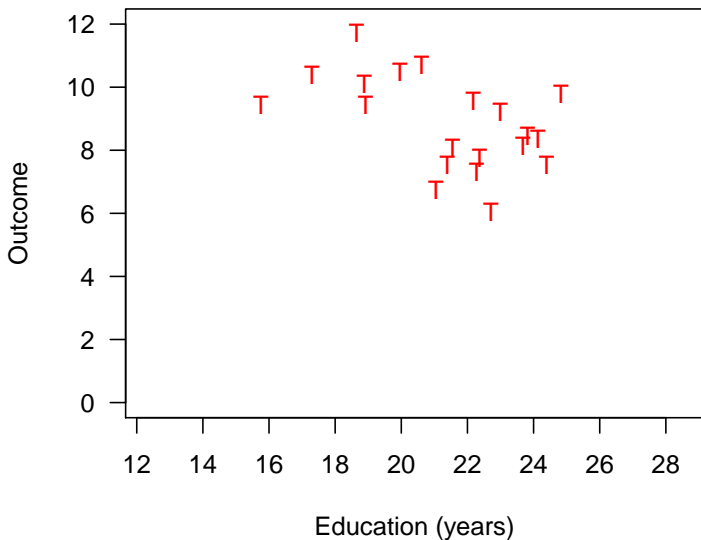
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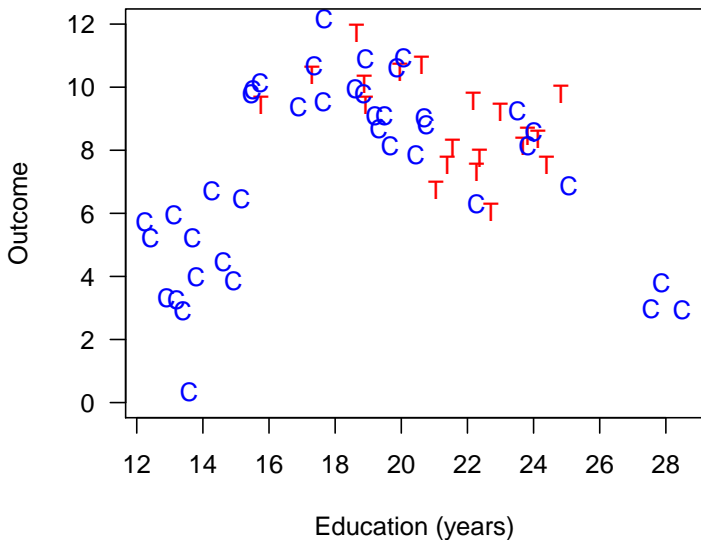
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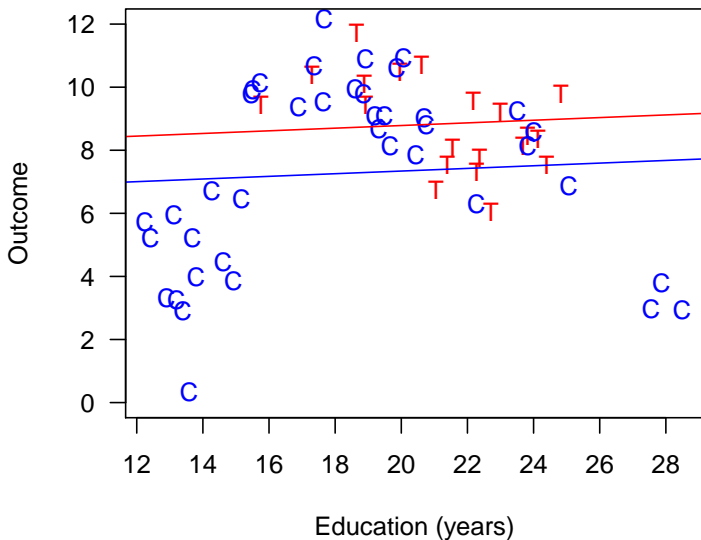
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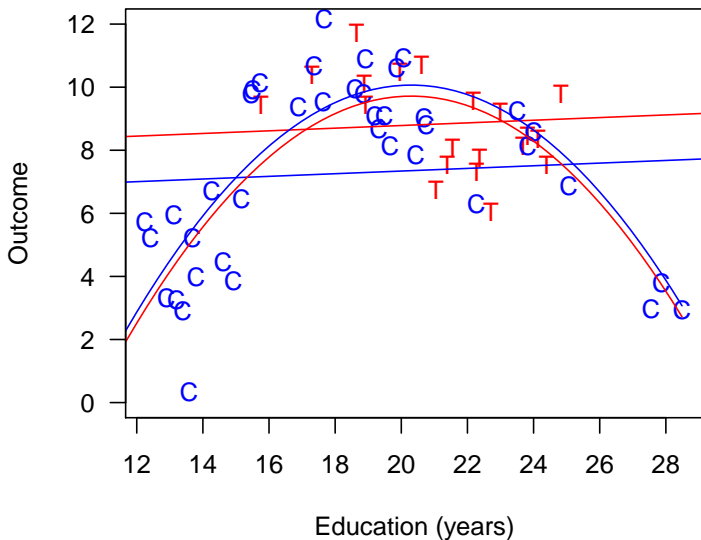
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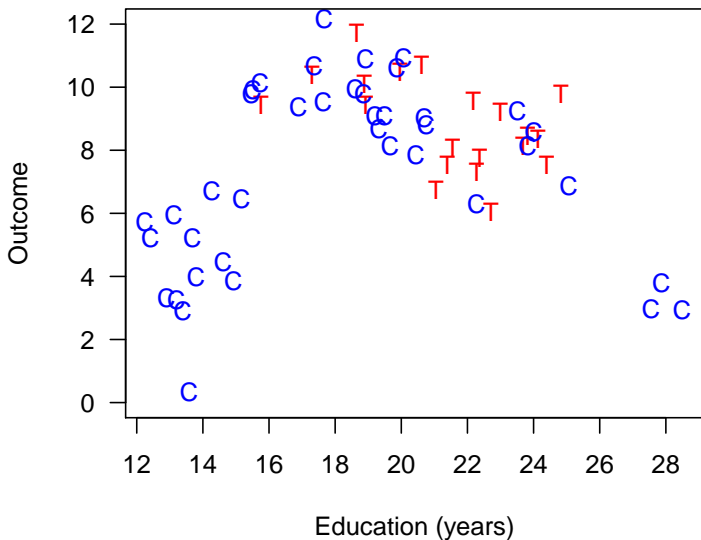
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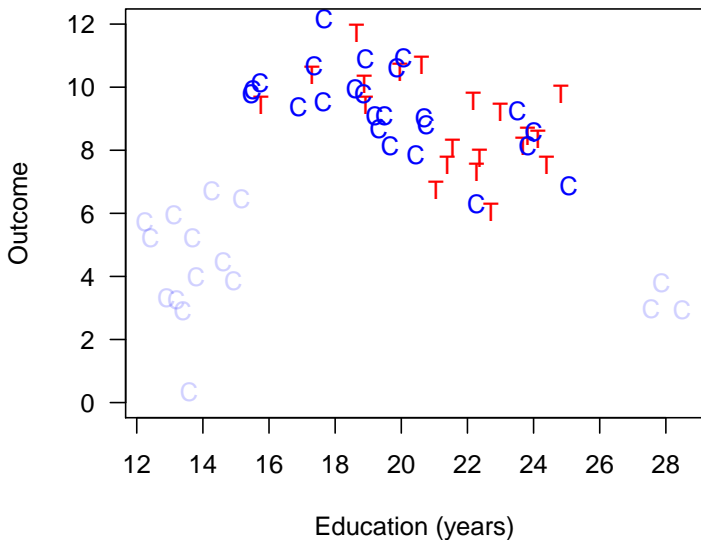
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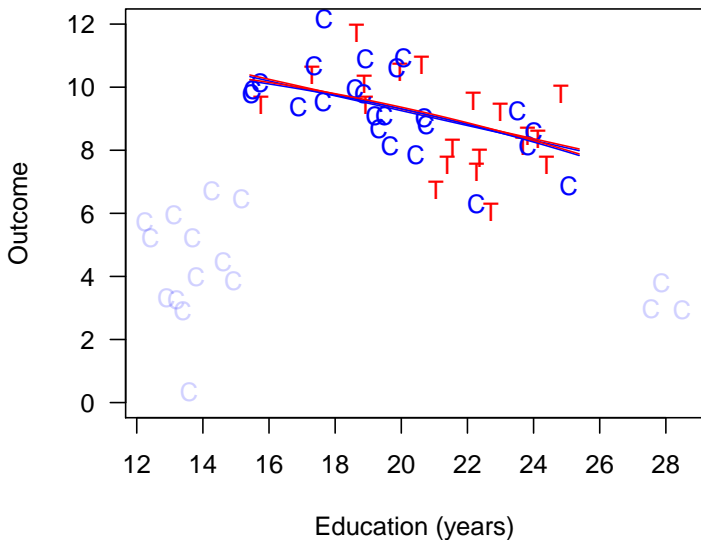
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- “Teaching psychology is mostly a waste of time” (Kahneman 2011)

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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

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Types of Experiments



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

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Method 1: Mahalanobis Distance Matching

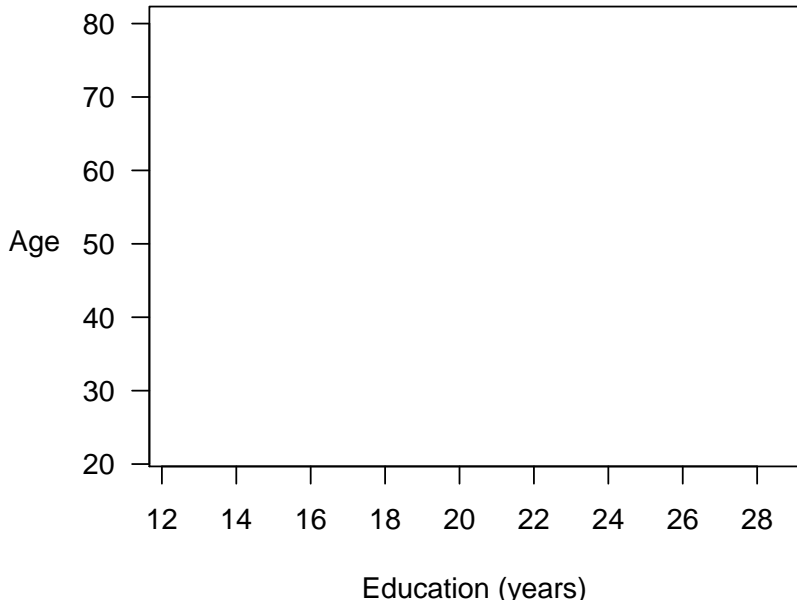
(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)

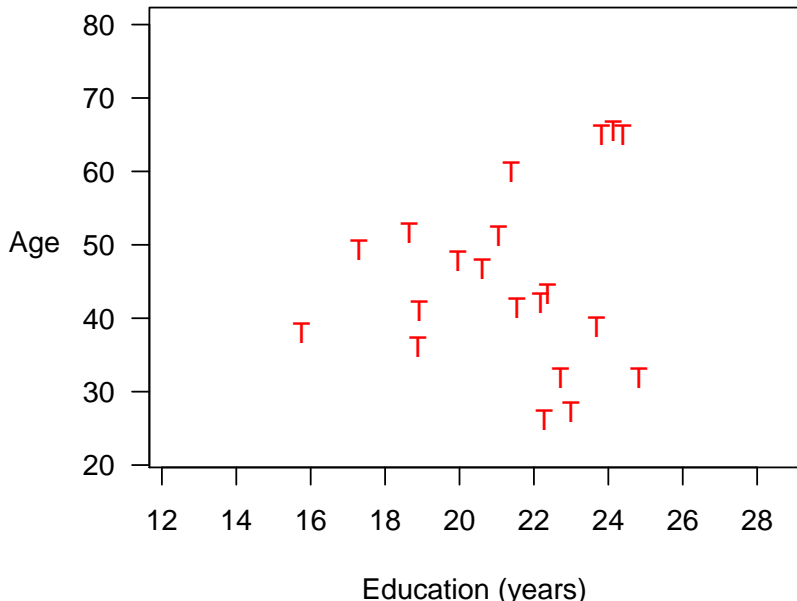
- $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)' S^{-1} (X_c - X_t)}$
- (Mahalanobis is for methodologists; in applications, use Euclidean!)
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if $\text{Distance} > \text{caliper}$
- (Many adjustments available to this basic method)

2. Estimation Difference in means or a model

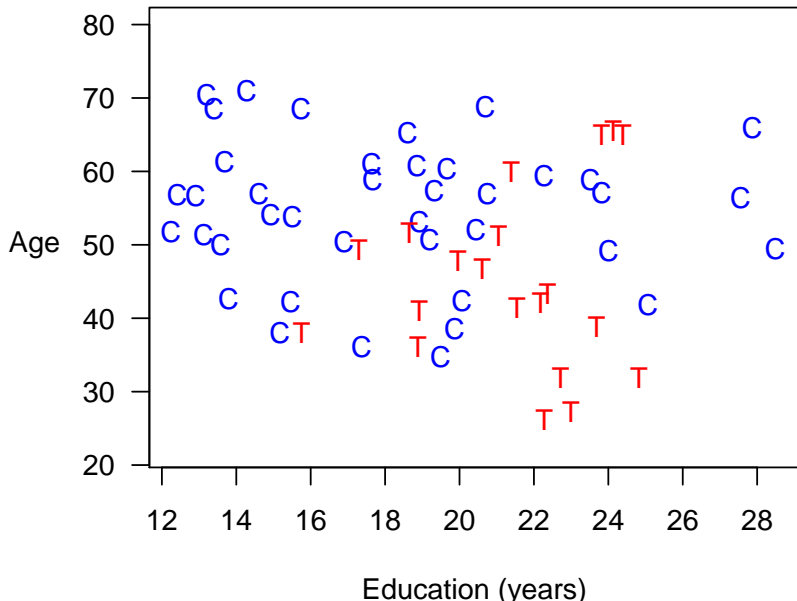
Mahalanobis Distance Matching



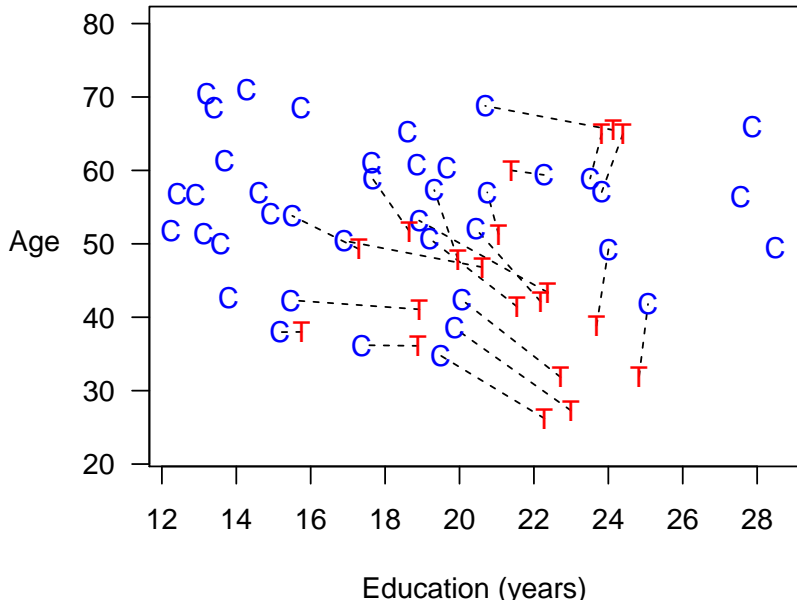
Mahalanobis Distance Matching



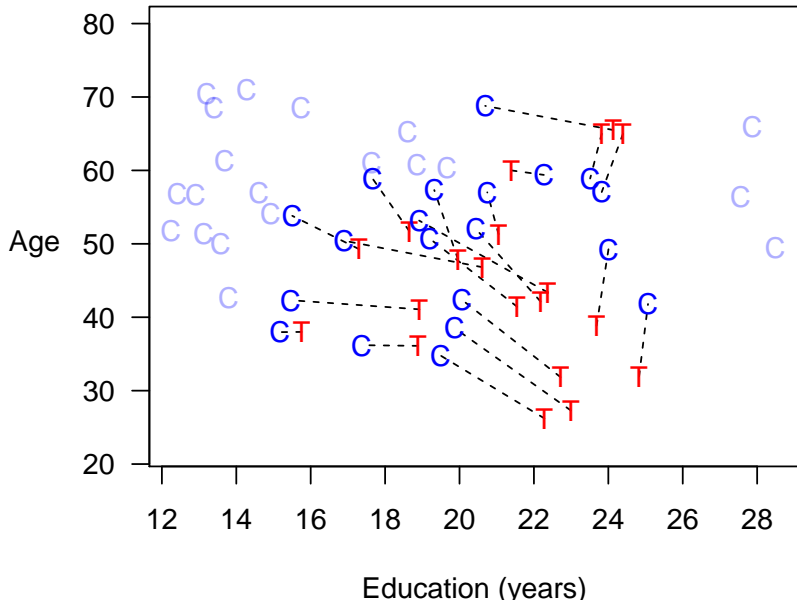
Mahalanobis Distance Matching



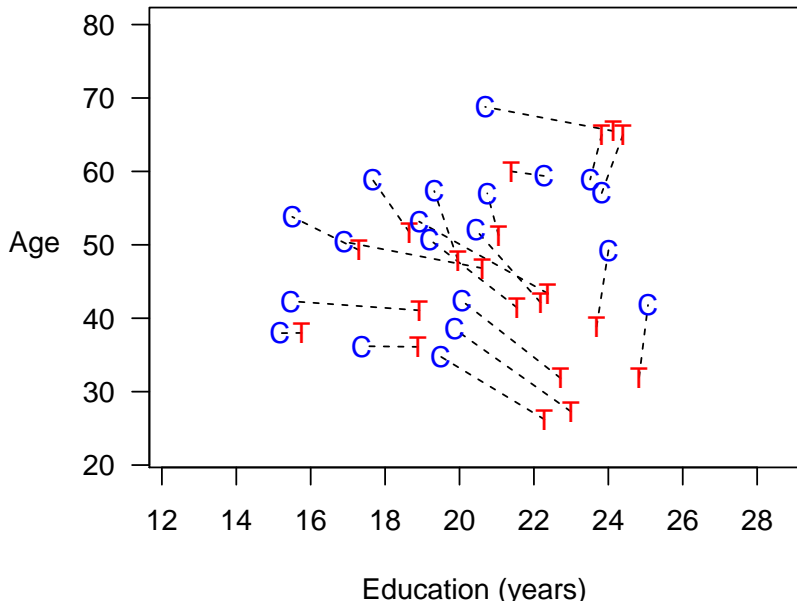
Mahalanobis Distance Matching



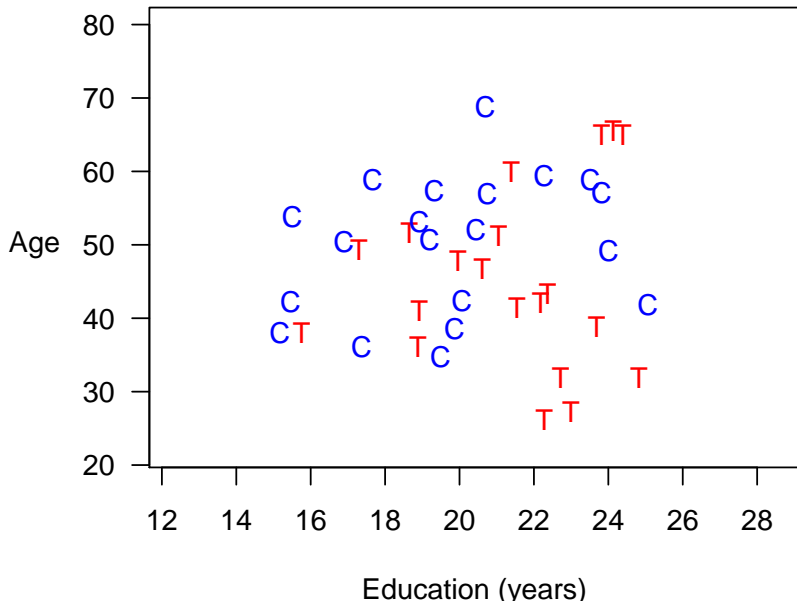
Mahalanobis Distance Matching



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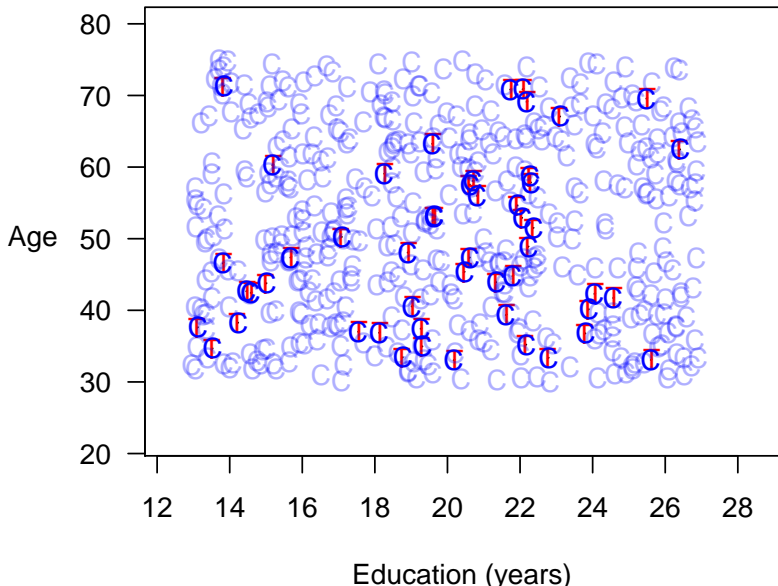


Mahalanobis Distance Matching

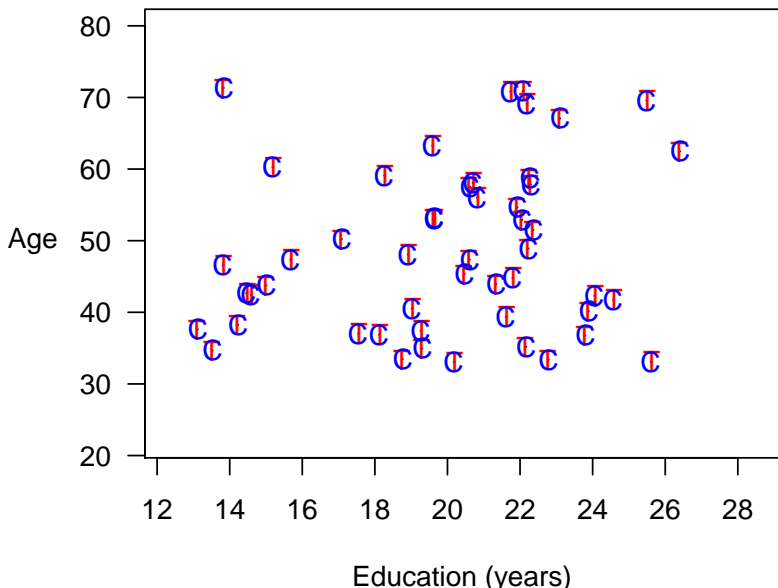


Best Case: Mahalanobis Distance Matching

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Best Case: Mahalanobis Distance Matching



Method 2: Coarsened Exact Matching

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(Approximates Fully Blocked Experiment)

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1. **Preprocess** (Matching)
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Method 2: Coarsened Exact Matching

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1. **Preprocess** (Matching)
 - Temporarily coarsen X as much as you're willing
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Method 2: Coarsened Exact Matching

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1. Preprocess (Matching)

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 - e.g., Education (grade school, high school, college, graduate)

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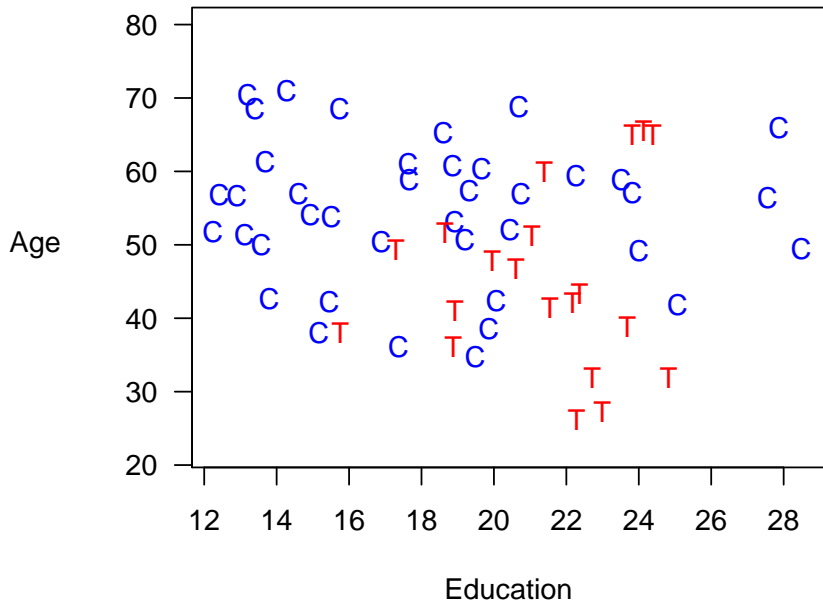
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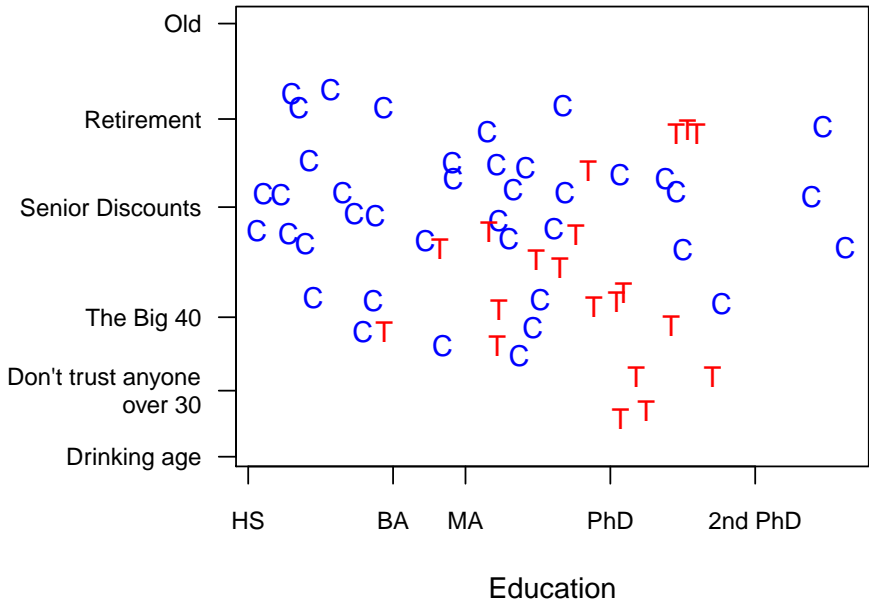
- Weight controls in each stratum to equal treateds

Coarsened Exact Matching

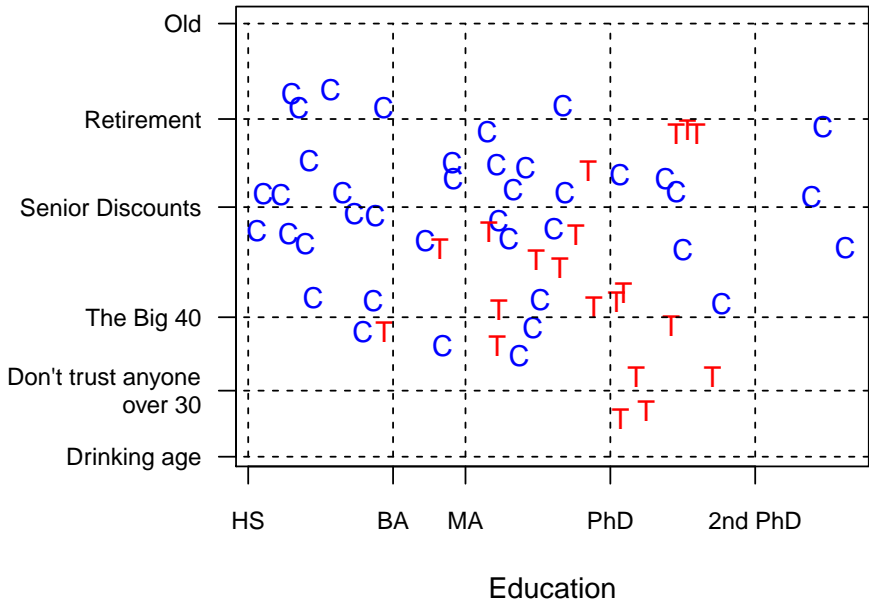
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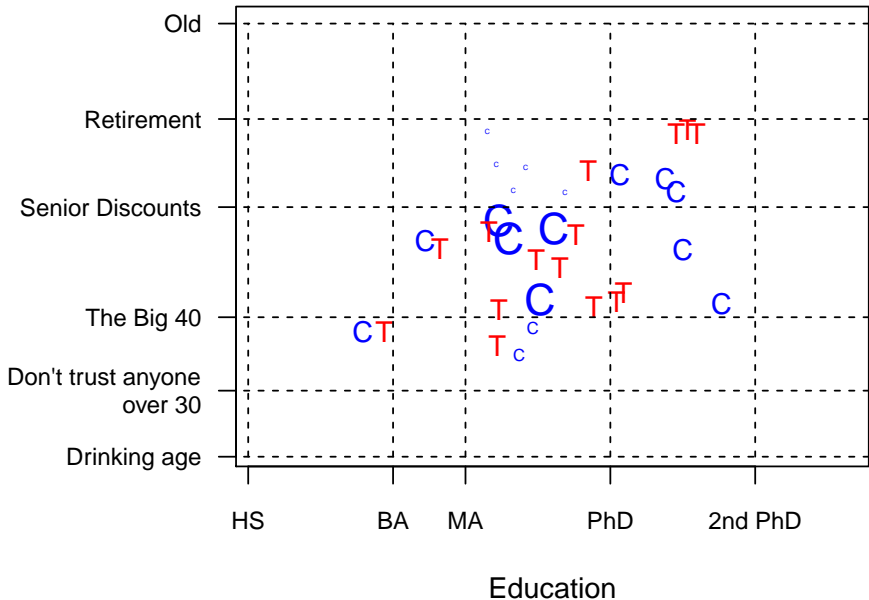
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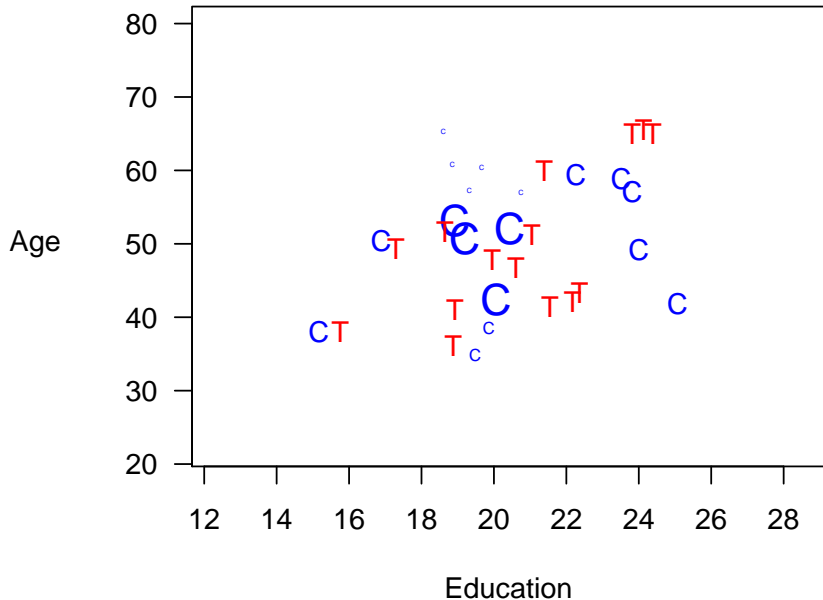
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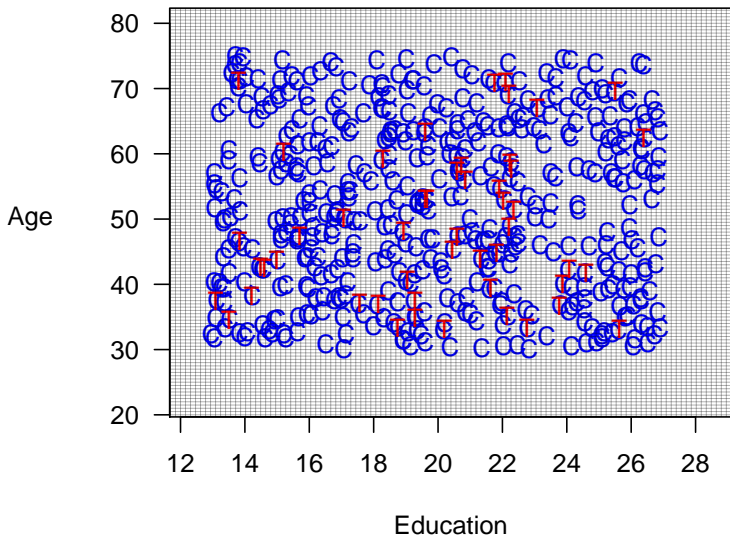


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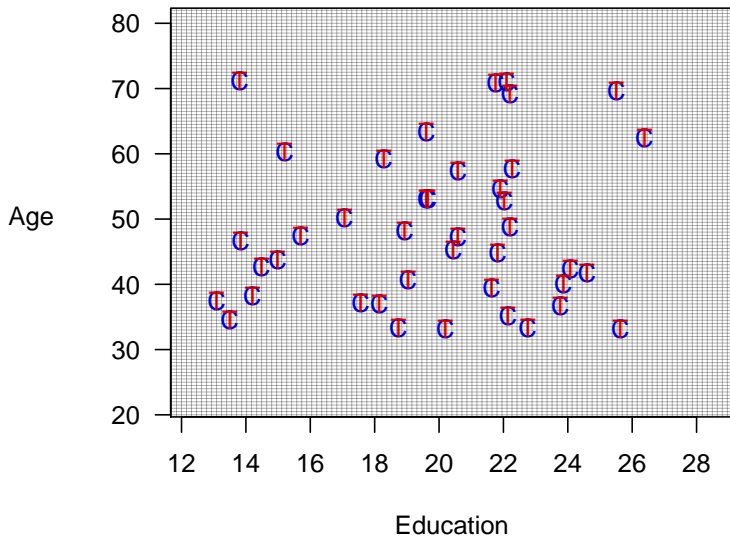


Best Case: Coarsened Exact Matching

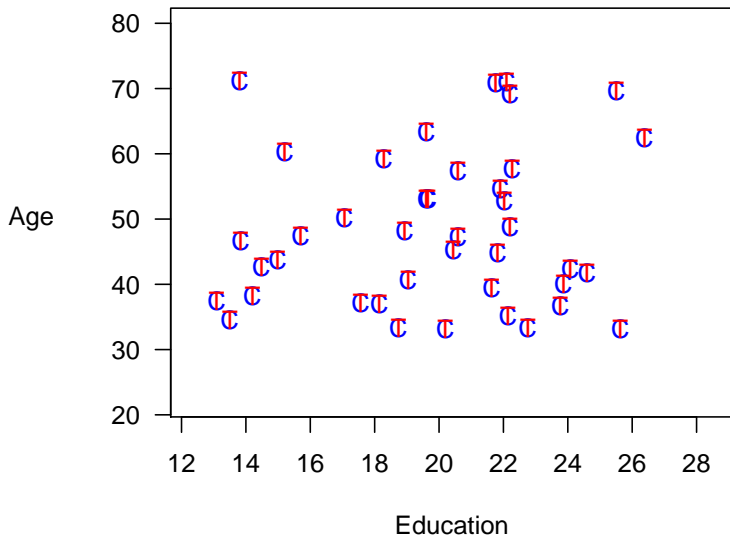
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Method 3: Propensity Score Matching

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(Approximates Completely Randomized Experiment)

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1. **Preprocess** (Matching)
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(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

- Reduce k elements of X to scalar

$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$

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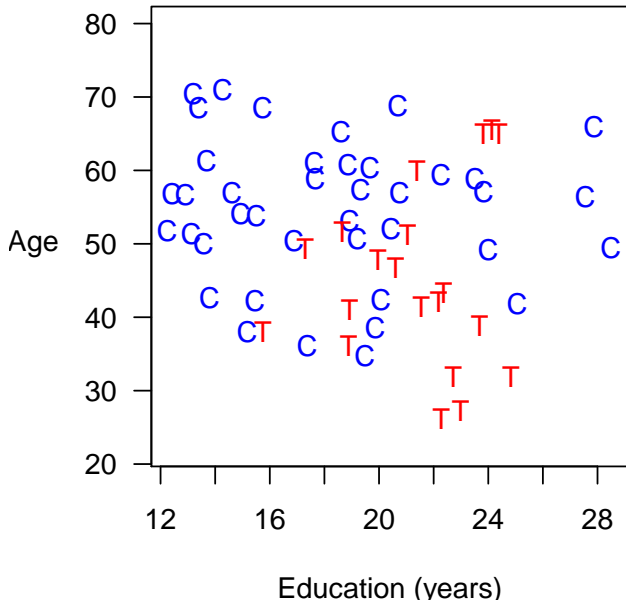
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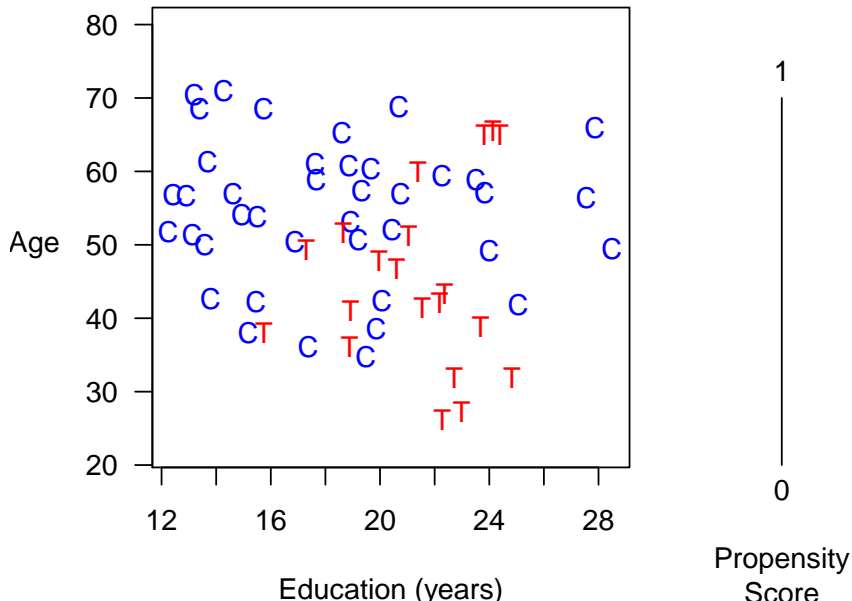
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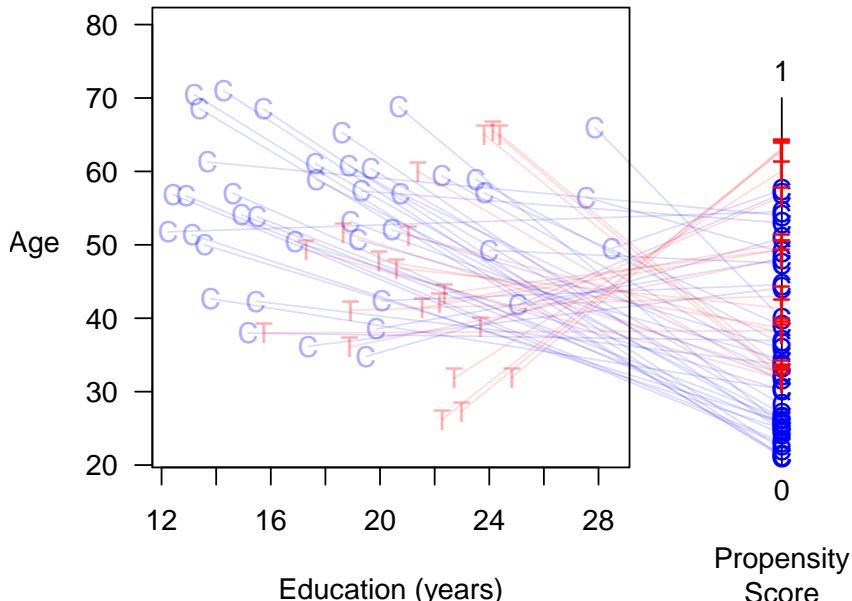
Propensity Score Matching



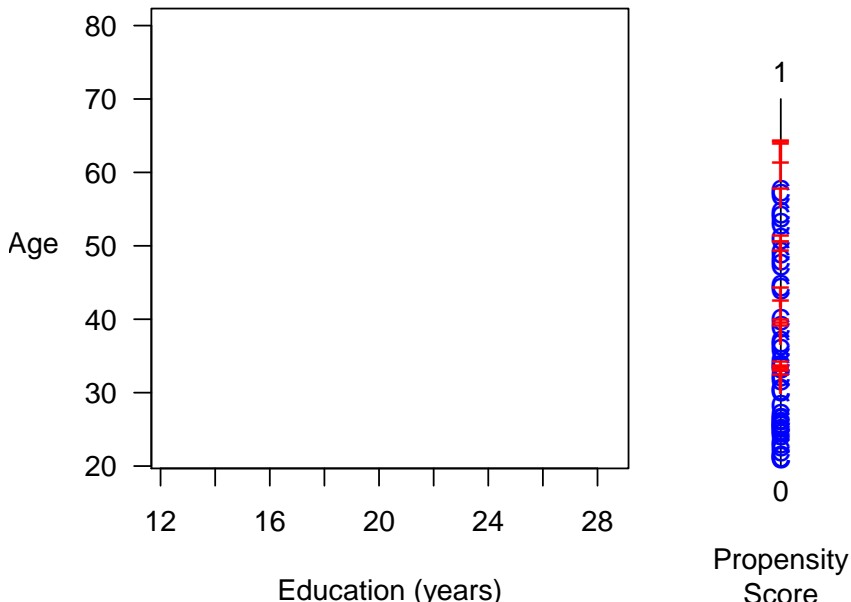
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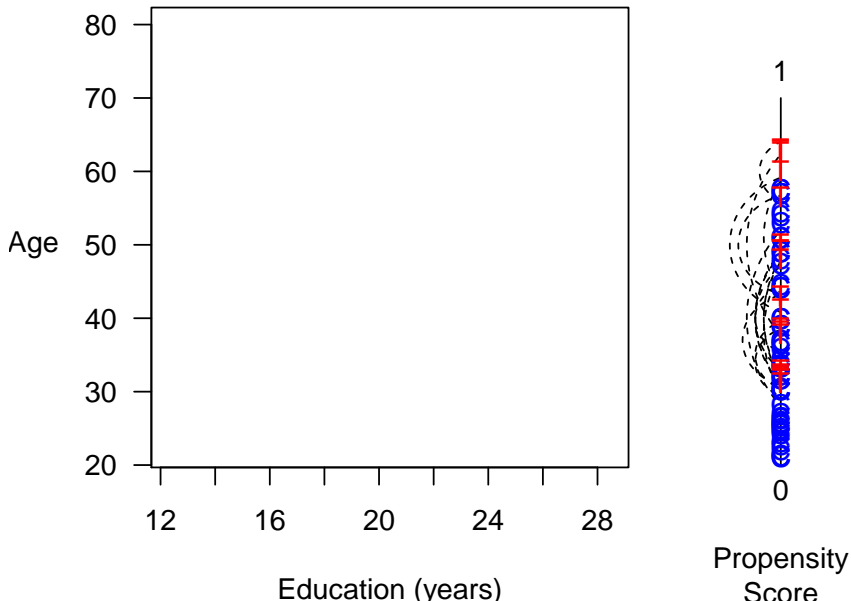
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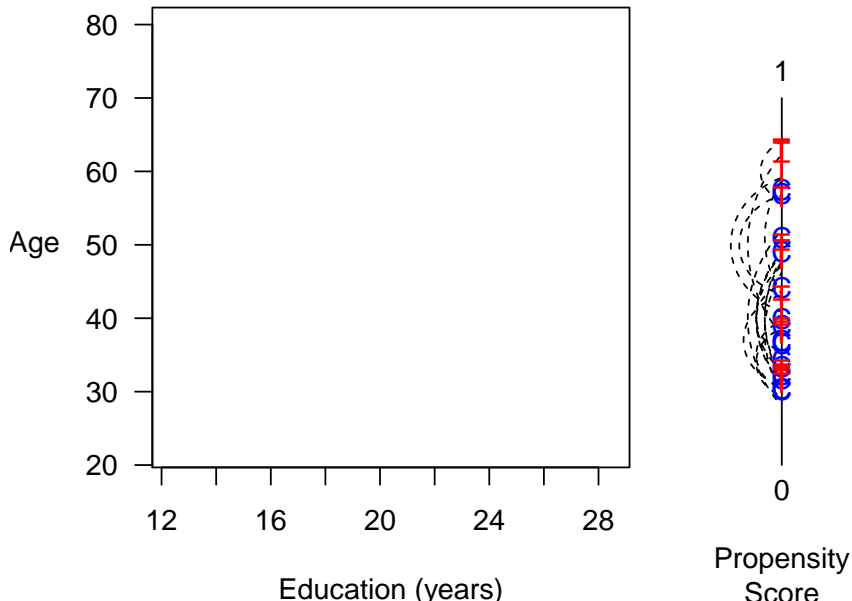
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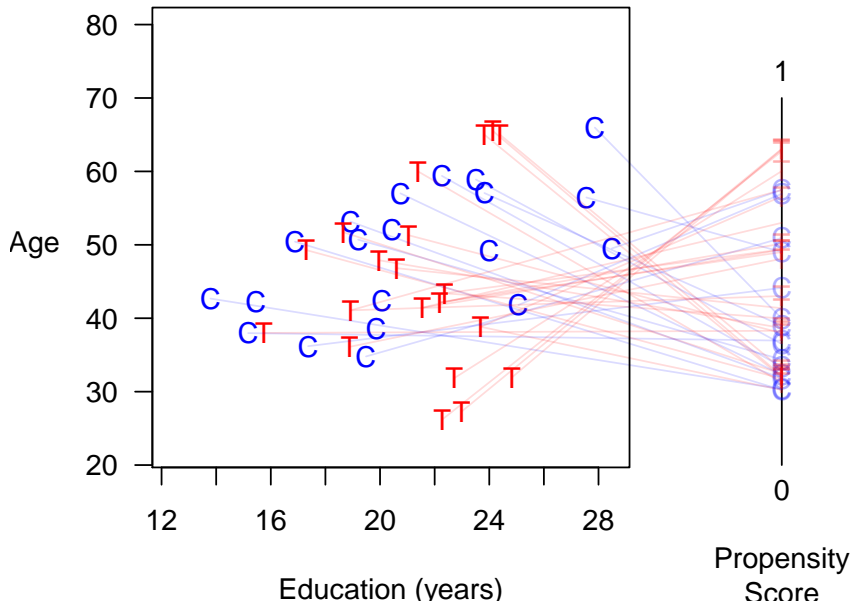
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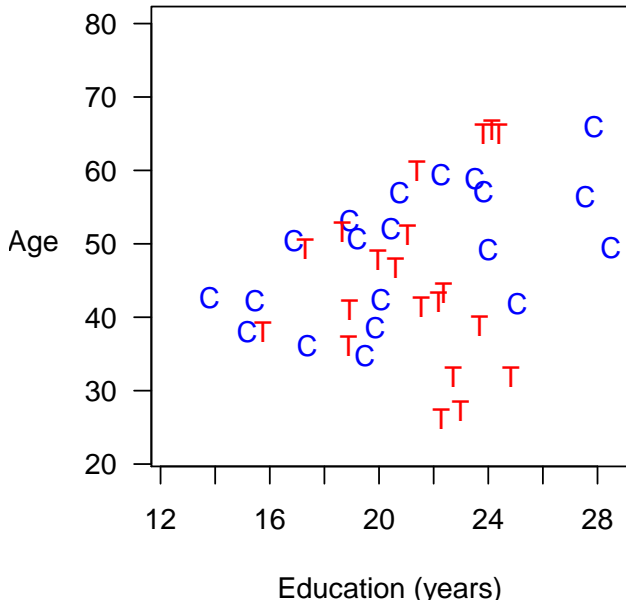
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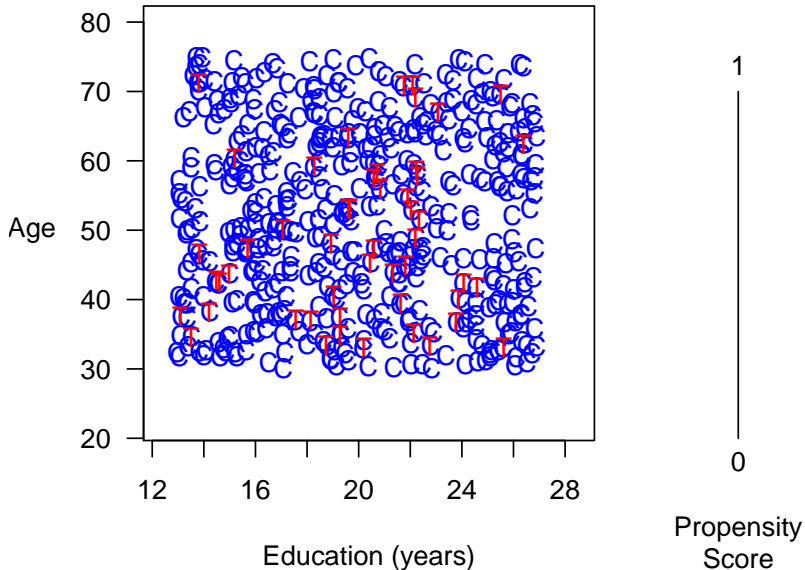


Propensity Score Matching

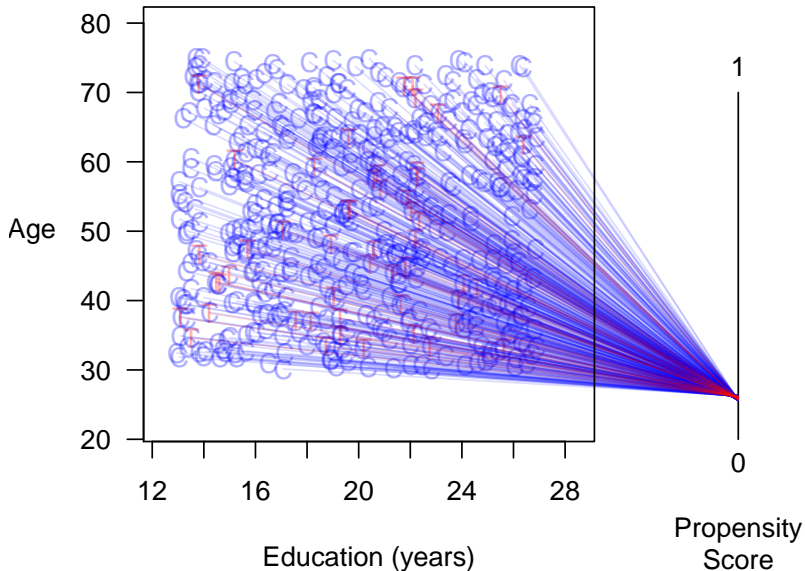


Best Case: Propensity Score Matching

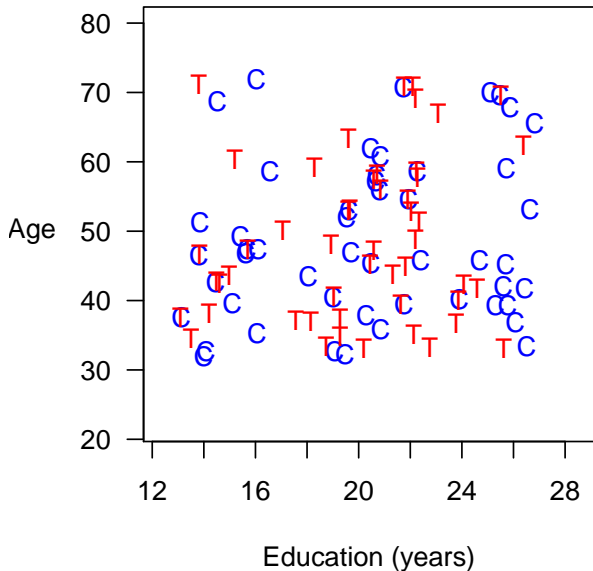
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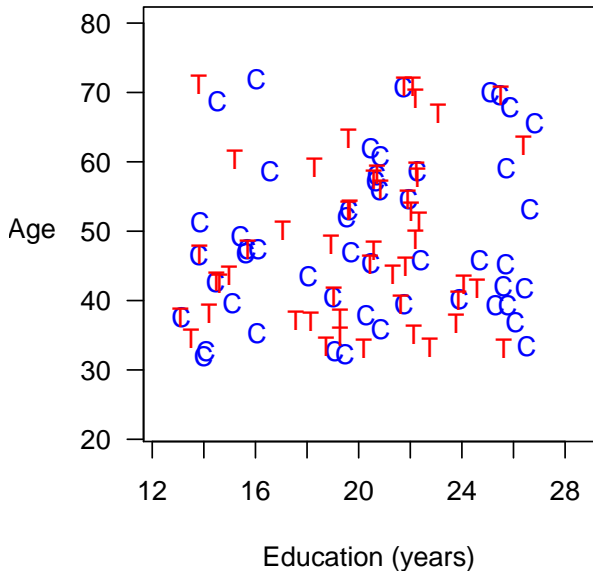
Best Case: Propensity Score Matching



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Best Case: Propensity Score Matching is Suboptimal



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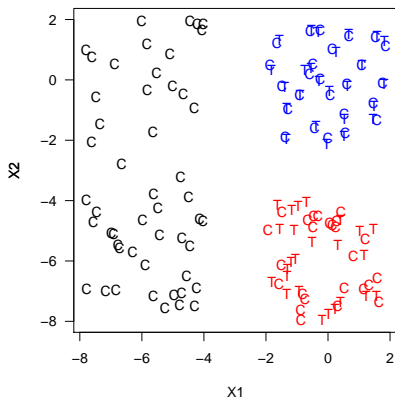
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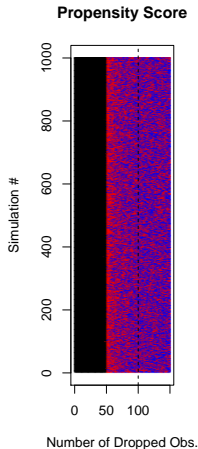
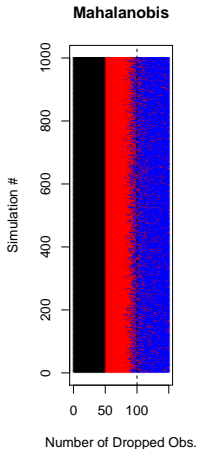
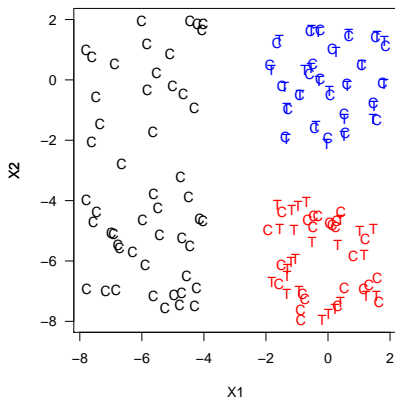
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PSM is Blind Where Other Methods Can See

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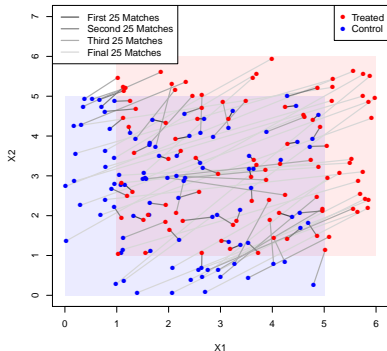


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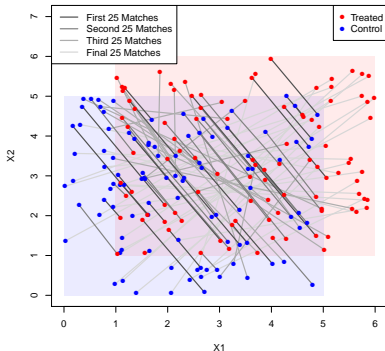


What Does PSM Match?

MDM Matches



PSM Matches

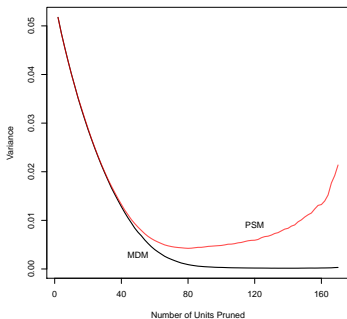


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

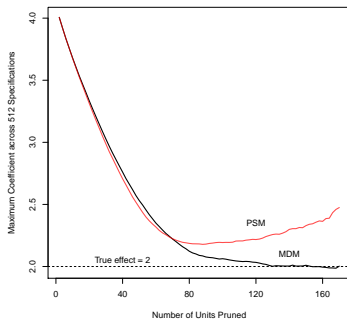
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

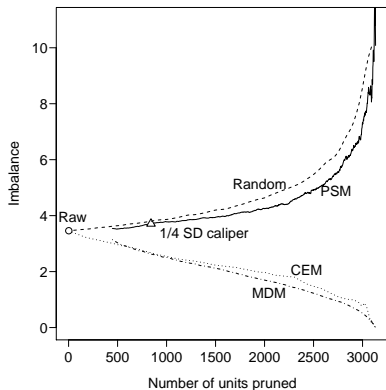


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

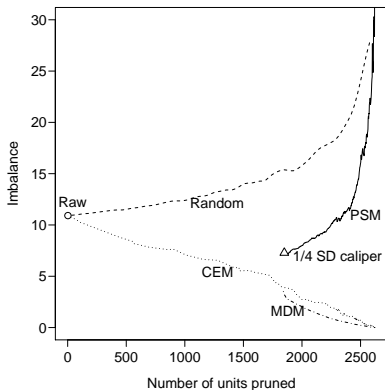
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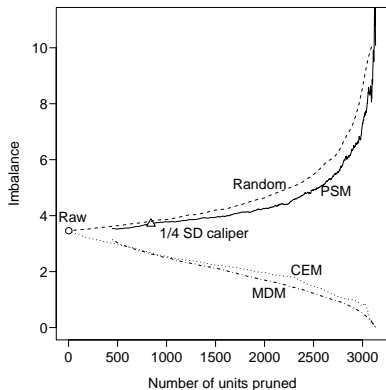


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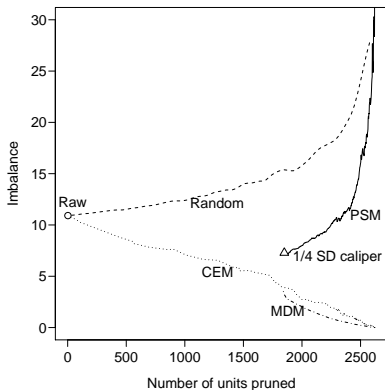


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Similar pattern for > 20 other real data sets we checked

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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