

Simplifying Matching Methods for Causal Inference

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3 Problems, 3 Solutions

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 - ~> “The Balance-Sample Size Frontier in Matching Methods for Causal Inference” (In press, *AJPS*; Gary King, Christopher Lucas and Richard Nielsen)

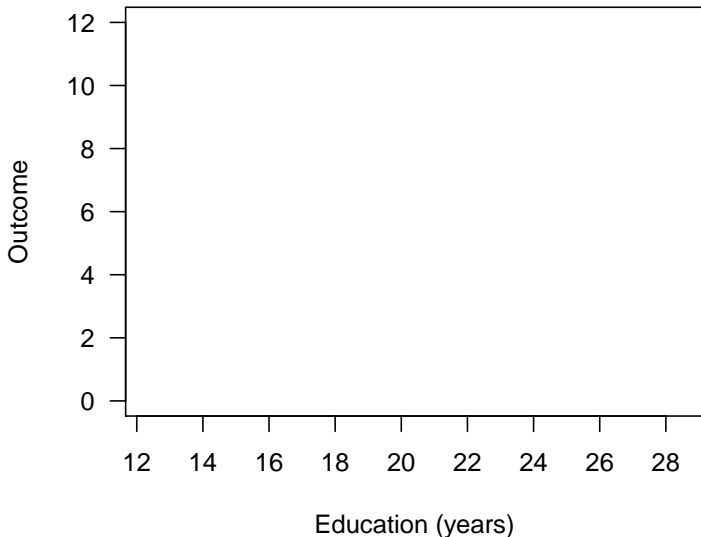
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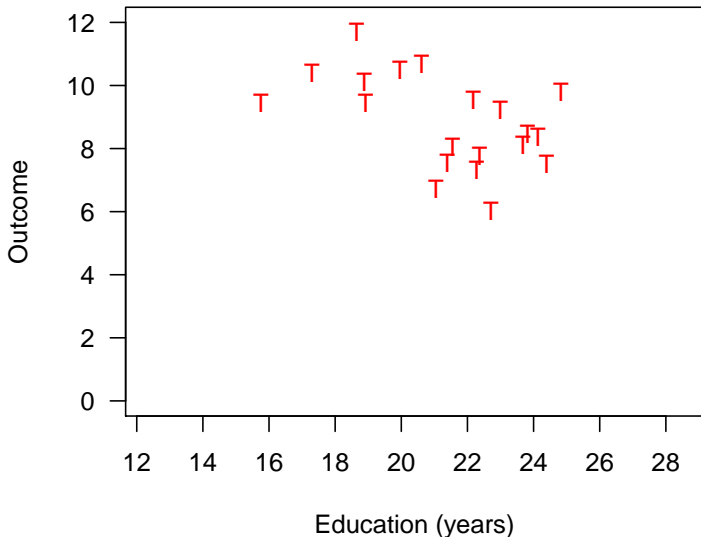
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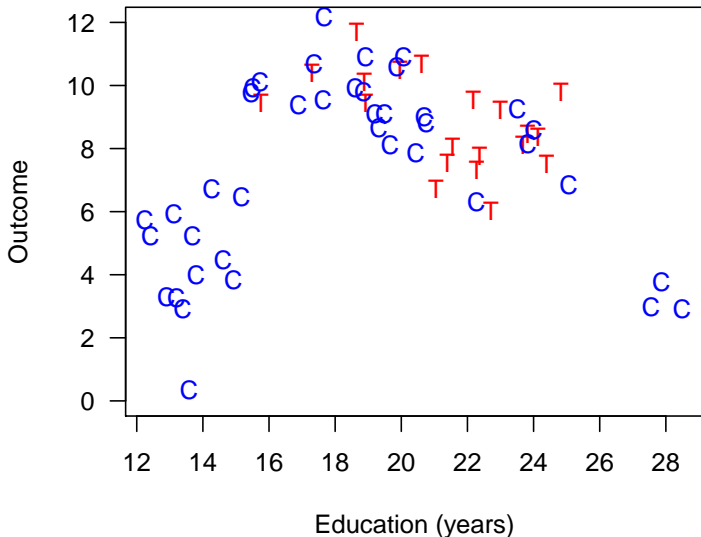
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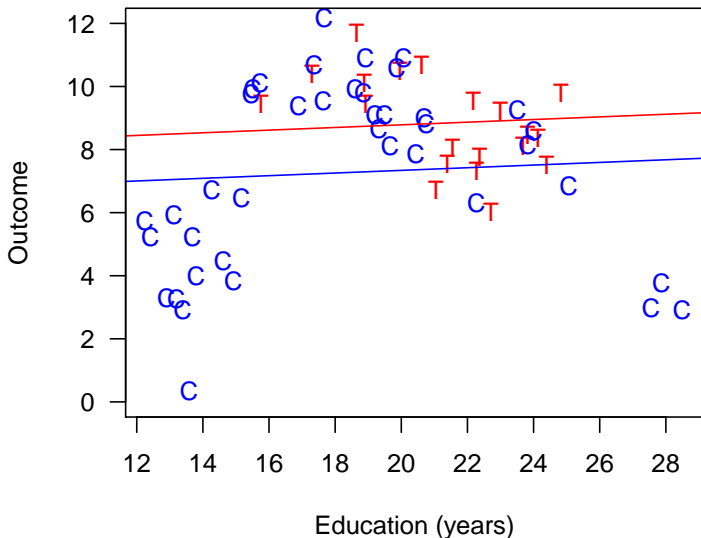
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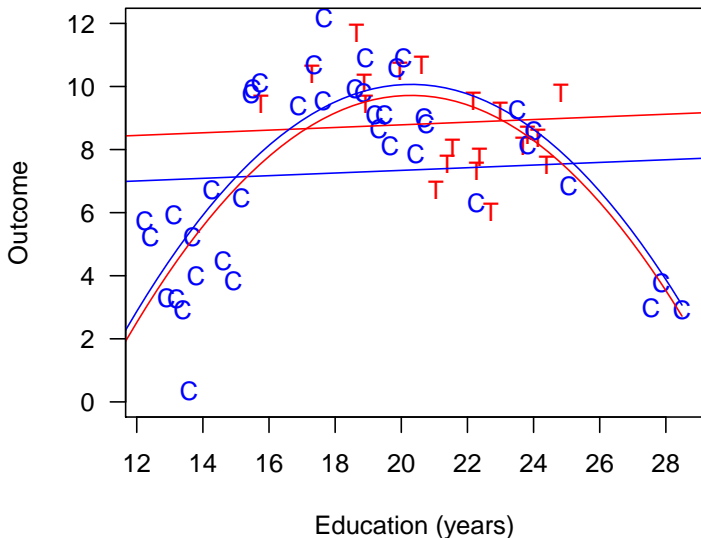
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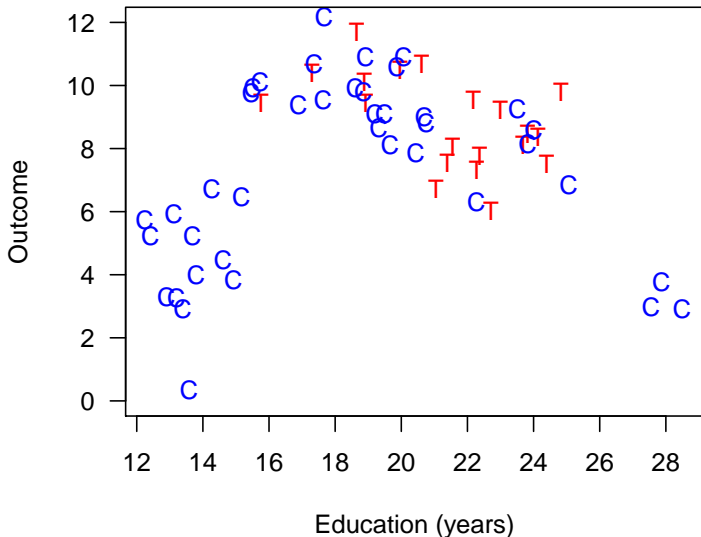
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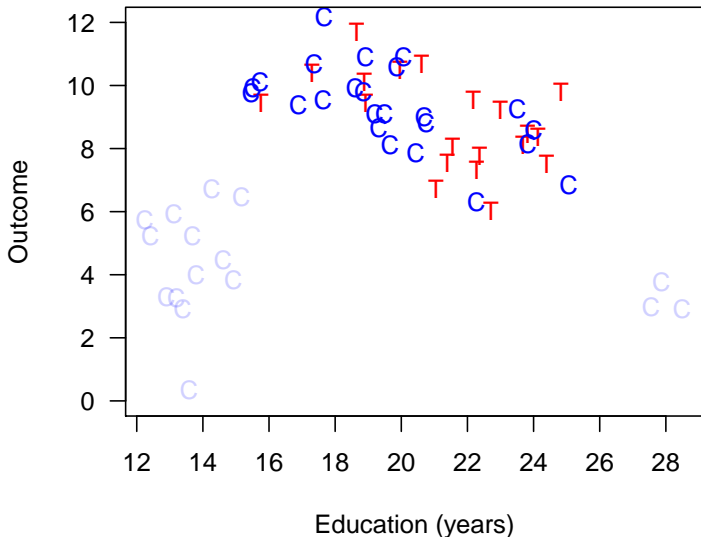
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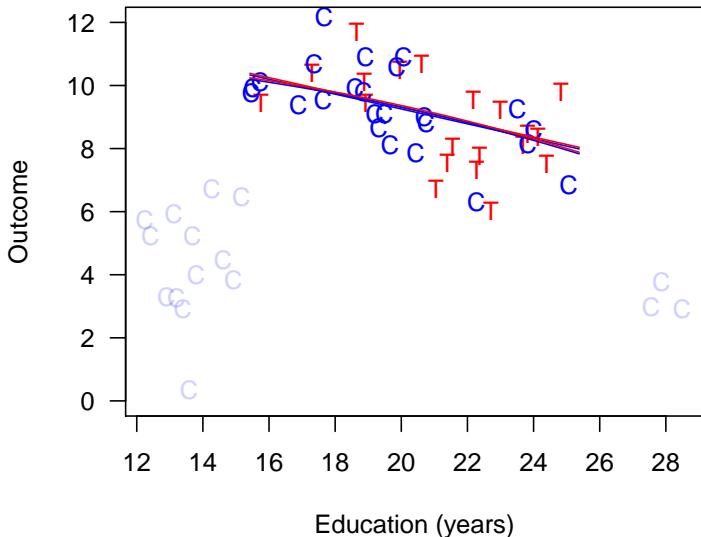
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- “Teaching psychology is mostly a waste of time” (Kahneman 2011)

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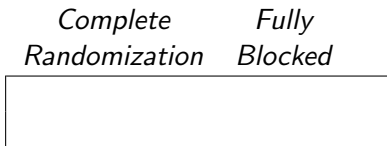
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- Other methods: *fully blocked*
- **Other matching methods dominate PSM** (wait, it gets worse)

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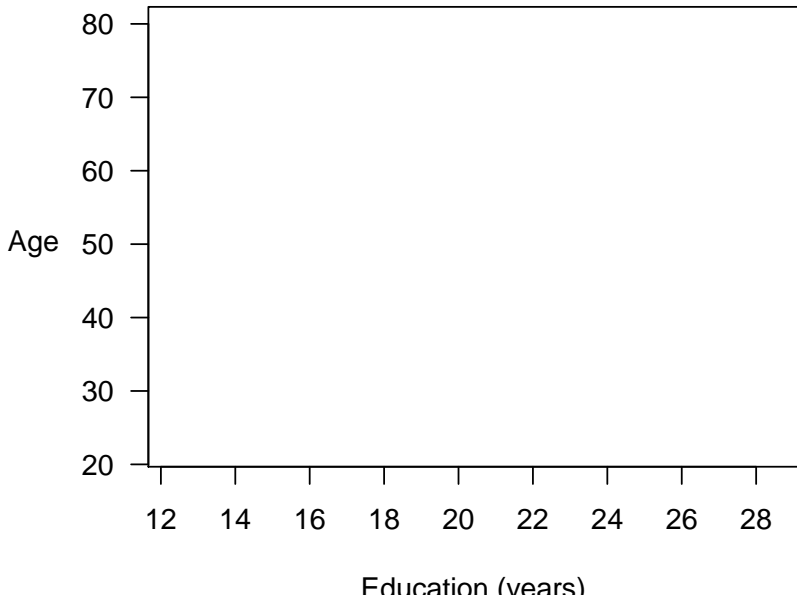
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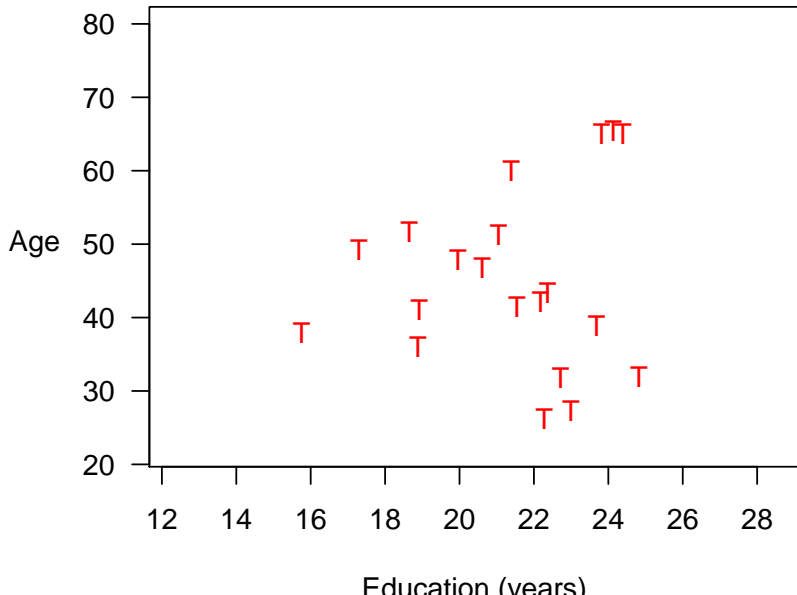
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- (Many adjustments available to this basic method)

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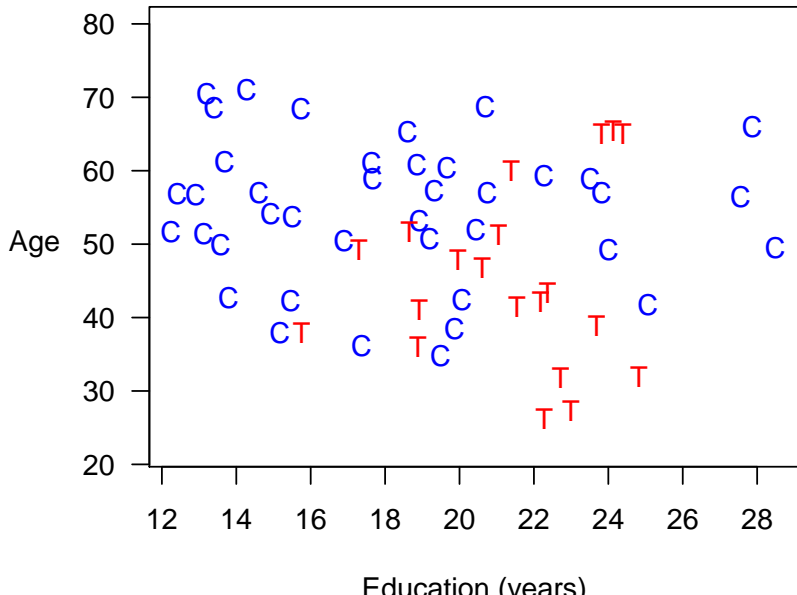
Mahalanobis Distance Matching



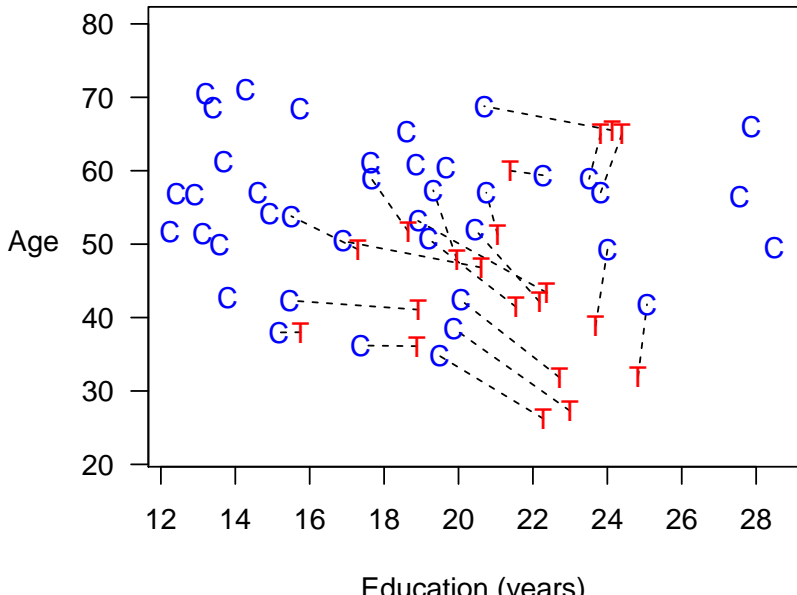
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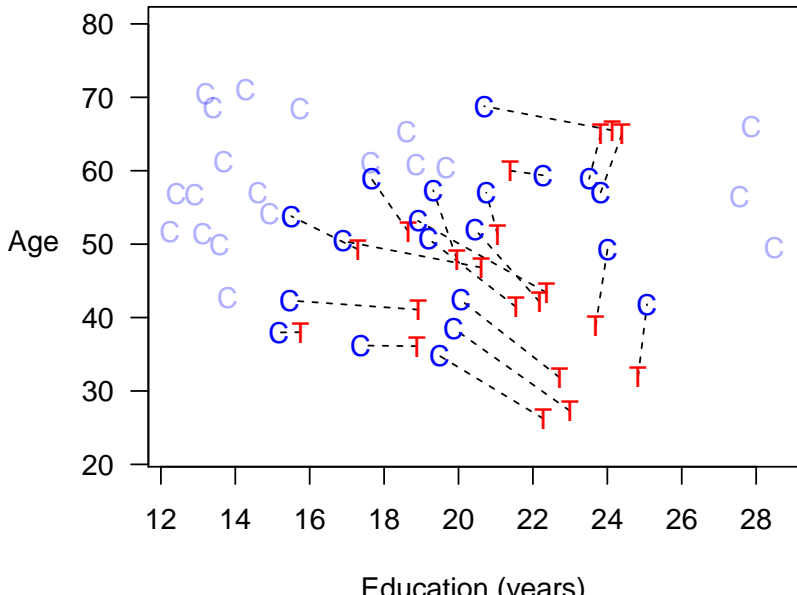
Mahalanobis Distance Matching



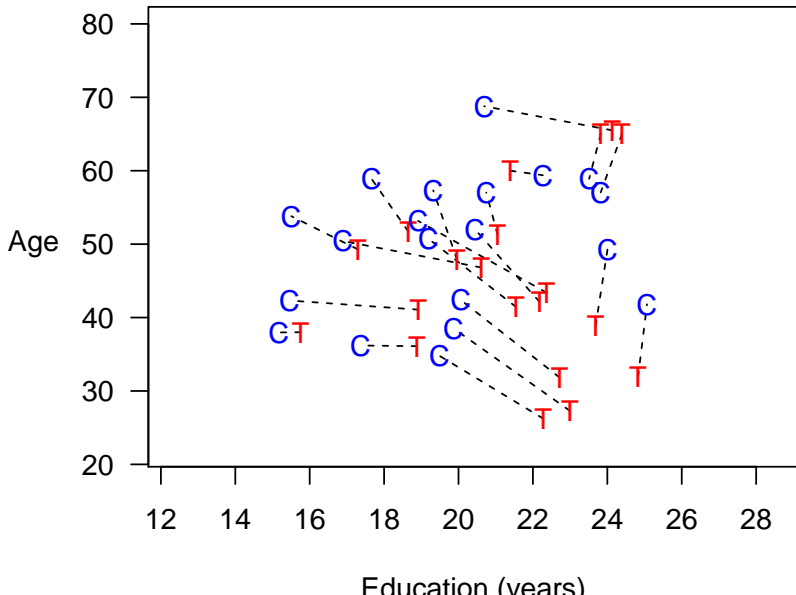
Mahalanobis Distance Matching



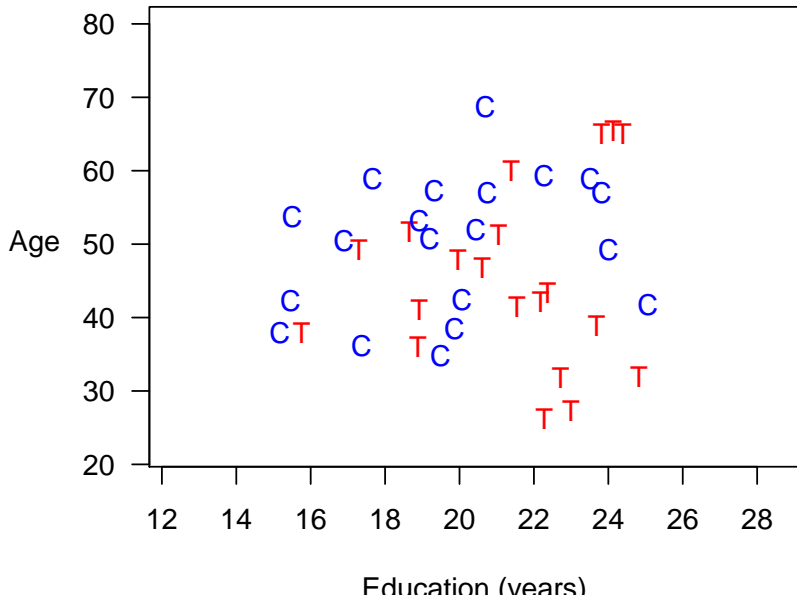
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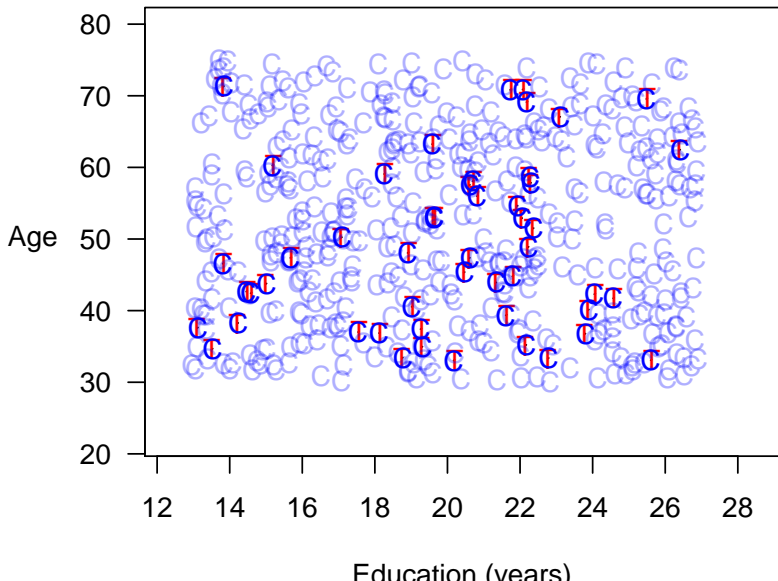


Mahalanobis Distance Matching

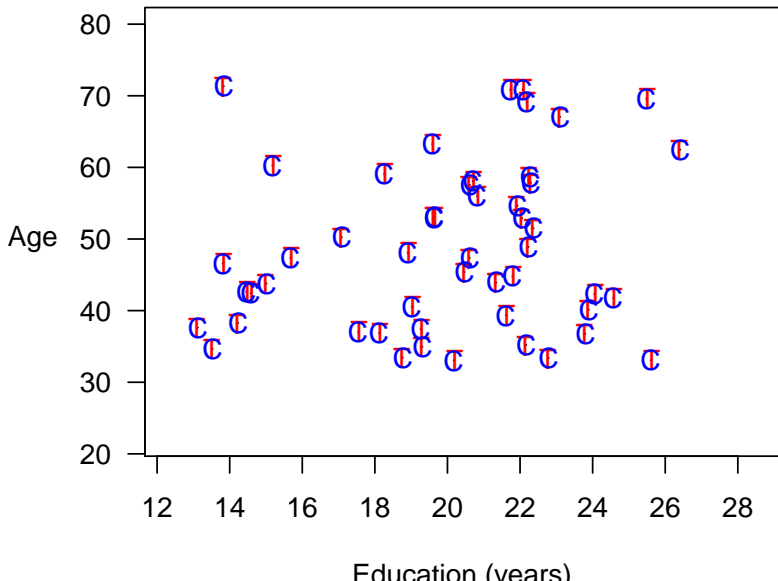


Best Case: Mahalanobis Distance Matching

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Best Case: Mahalanobis Distance Matching



Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

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(Approximates Fully Blocked Experiment)

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1. **Preprocess** (Matching)
2. **Estimation** Difference in means or a model

Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

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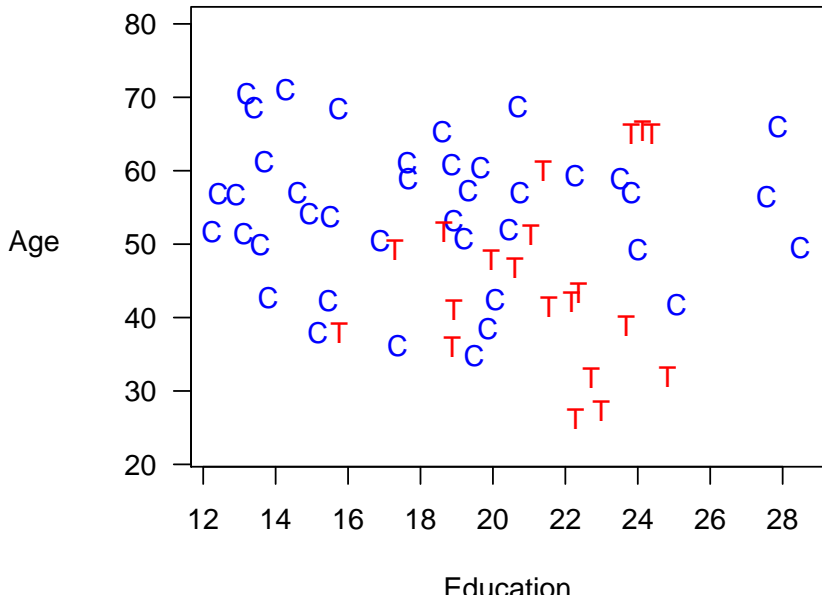
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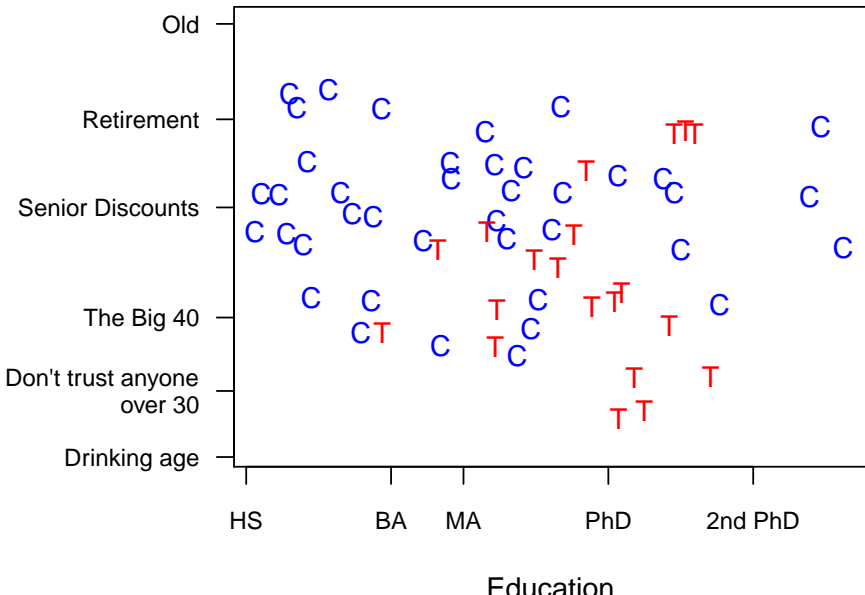
- Weight controls in each stratum to equal treated

Coarsened Exact Matching

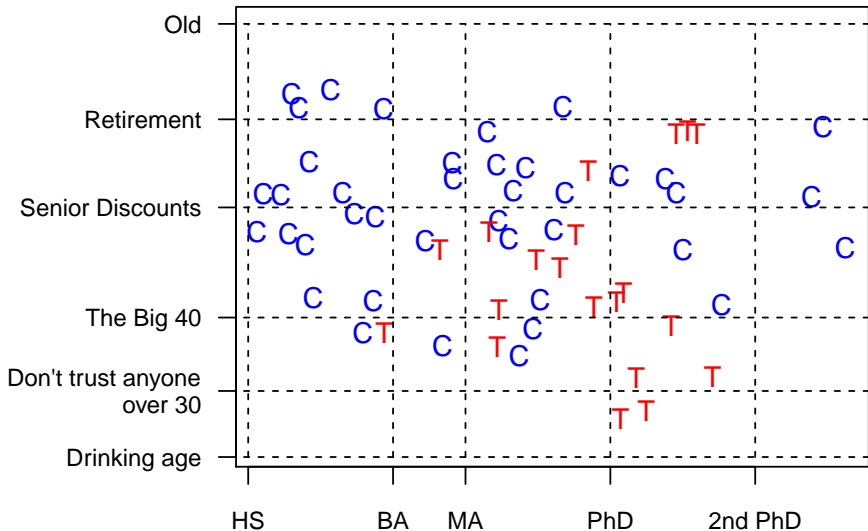
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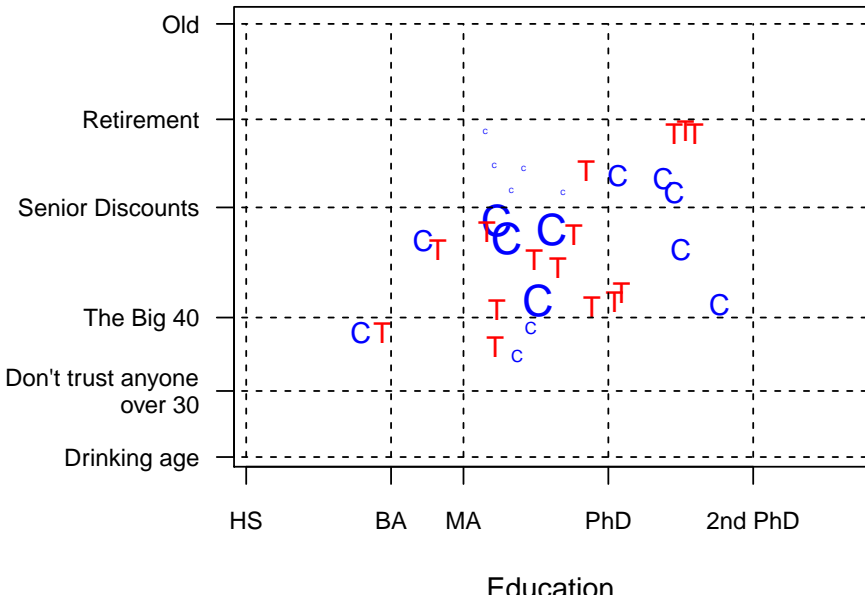
Coarsened Exact Matching



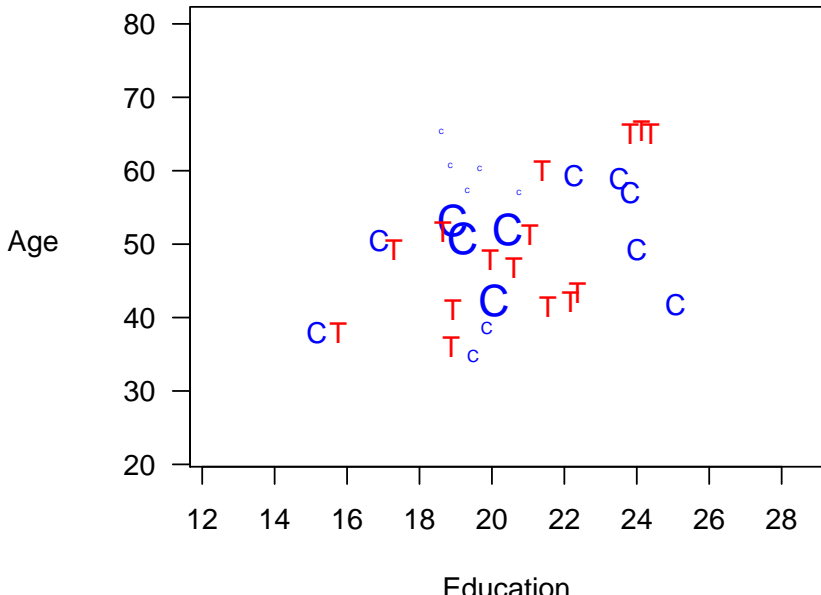
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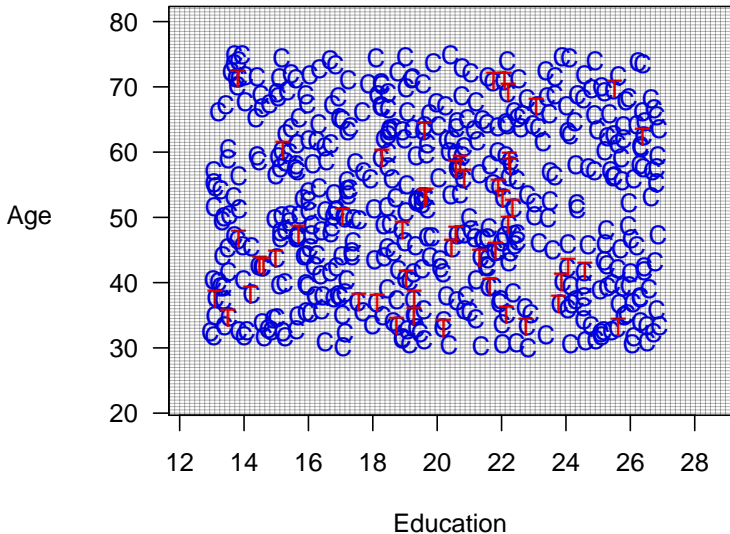


Coarsened Exact Matching

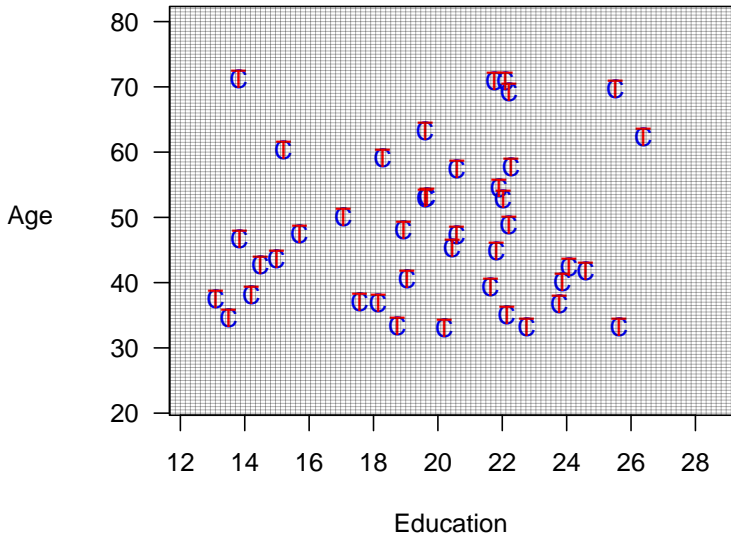


Best Case: Coarsened Exact Matching

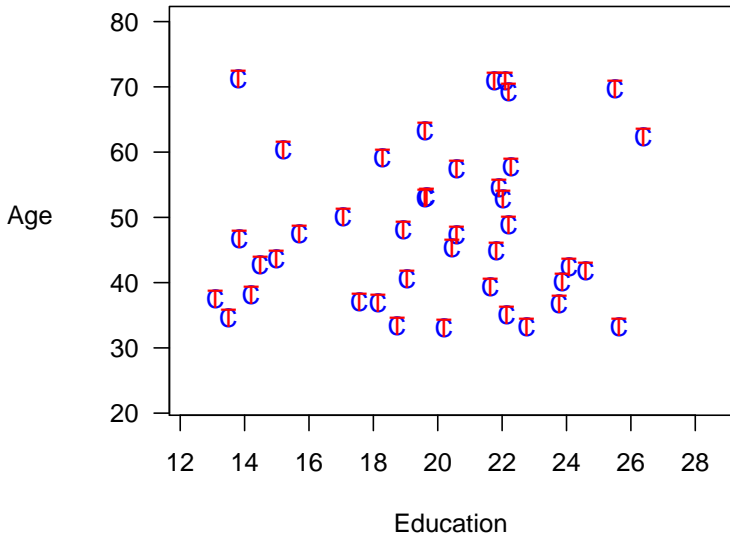
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Method 3: Propensity Score Matching

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(Approximates Completely Randomized Experiment)

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Method 3: Propensity Score Matching

(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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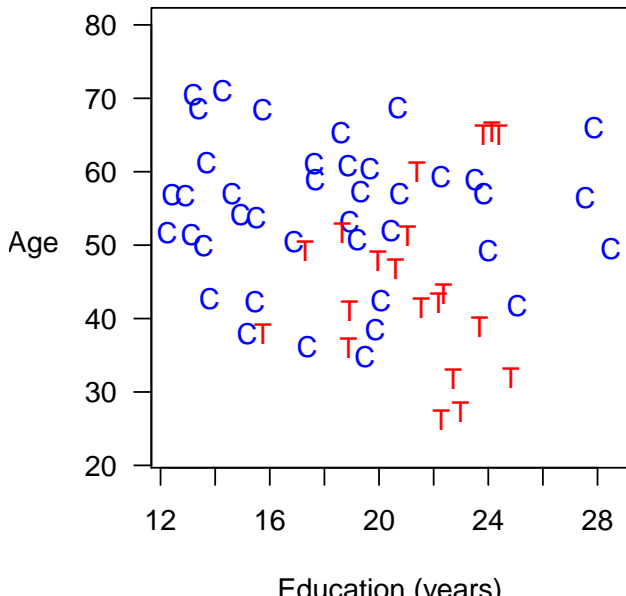
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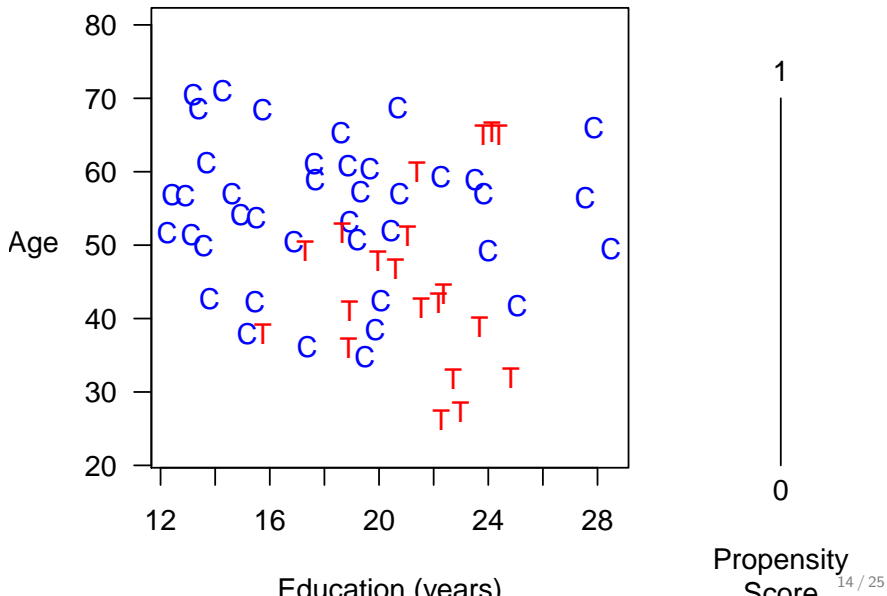
- Distance(X_c, X_t) = $|\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit
- Control units: not reused; pruned if unused
- Prune matches if Distance > *caliper*
- (Many adjustments available to this basic method)

2. Estimation Difference in means or a model

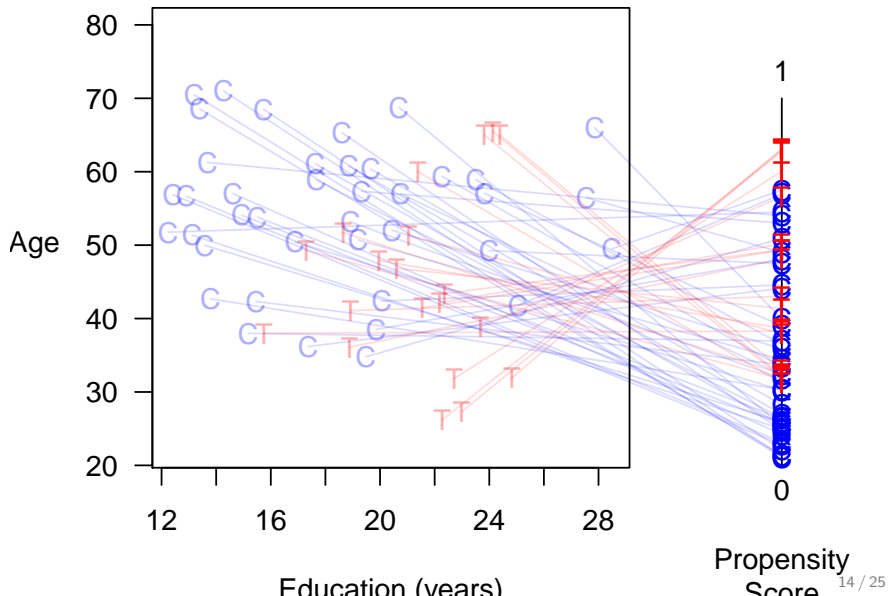
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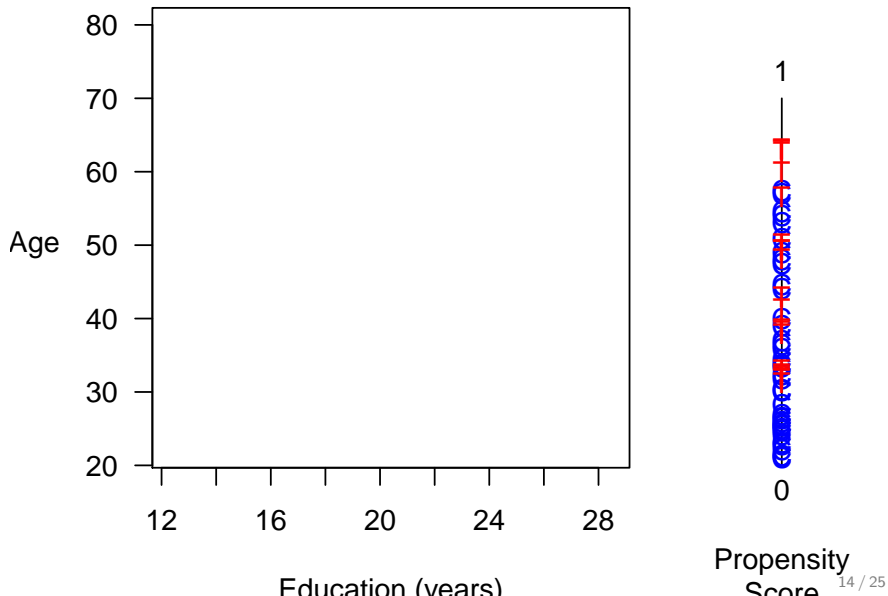
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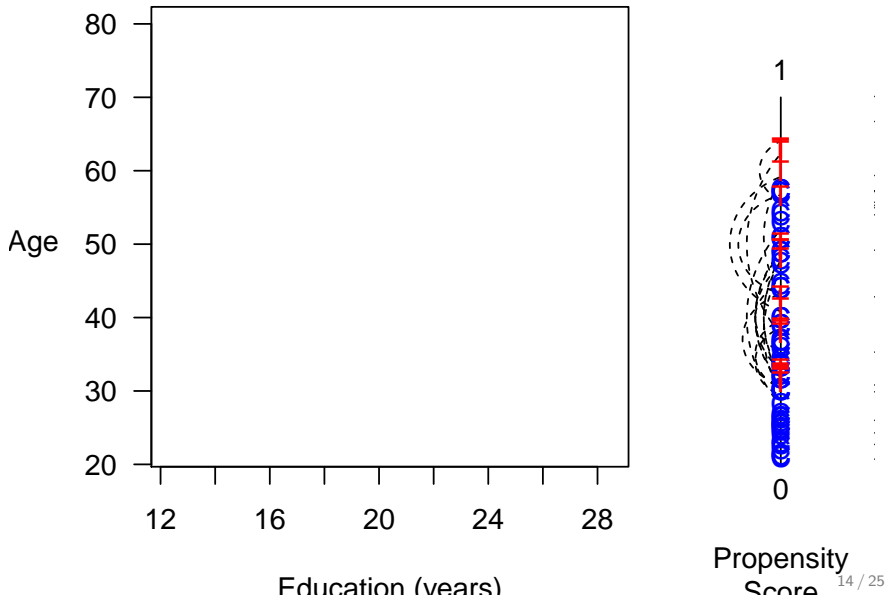
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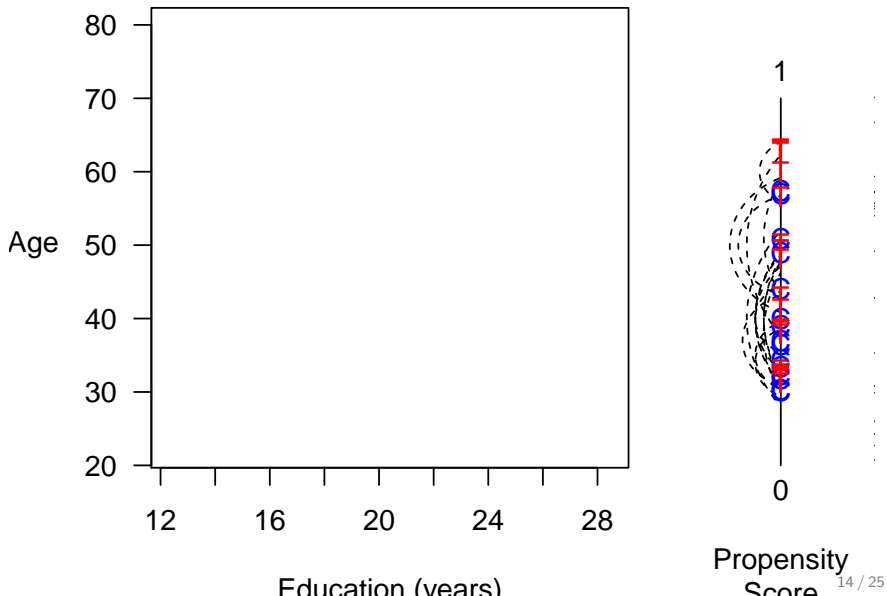
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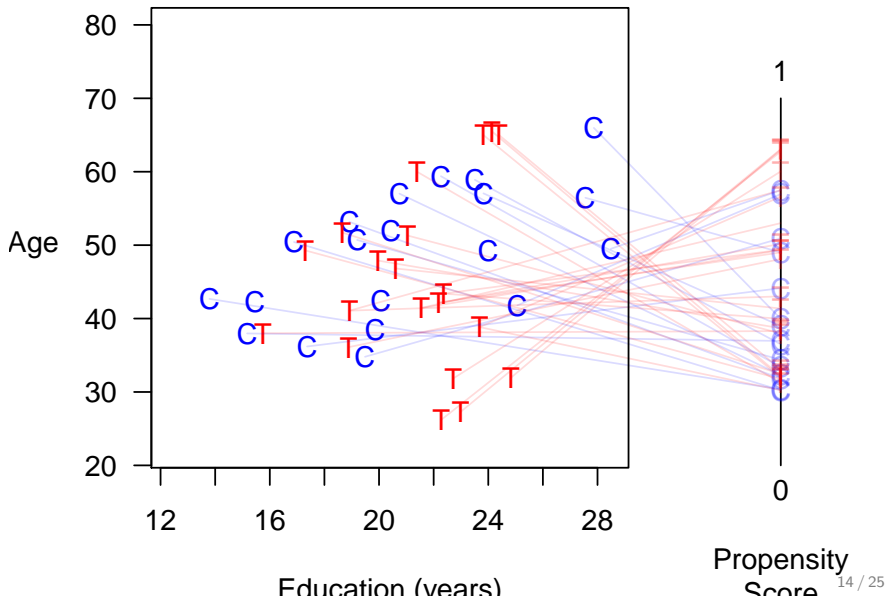
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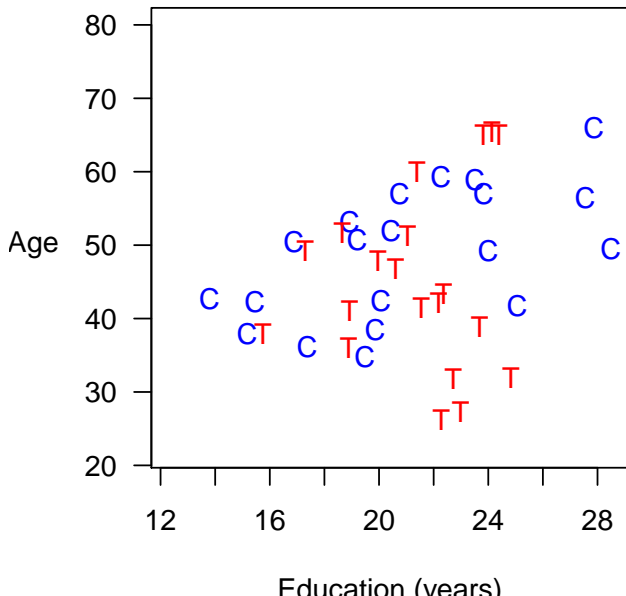
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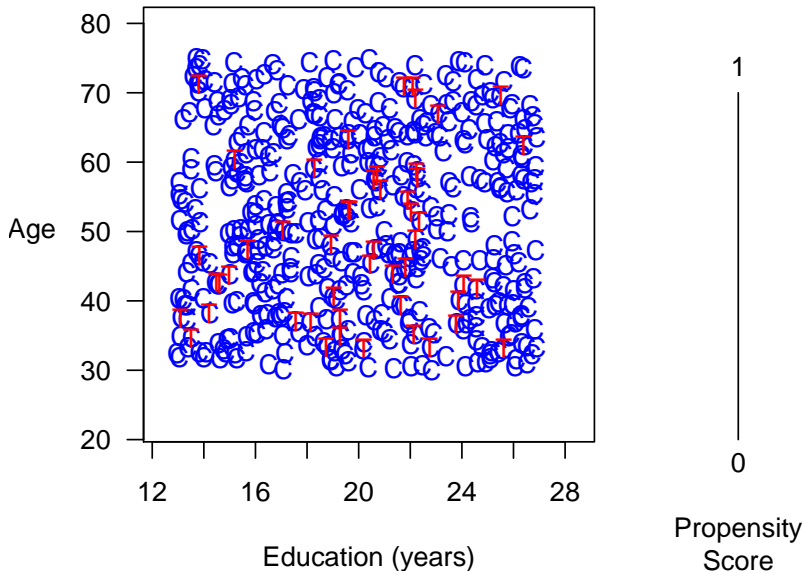


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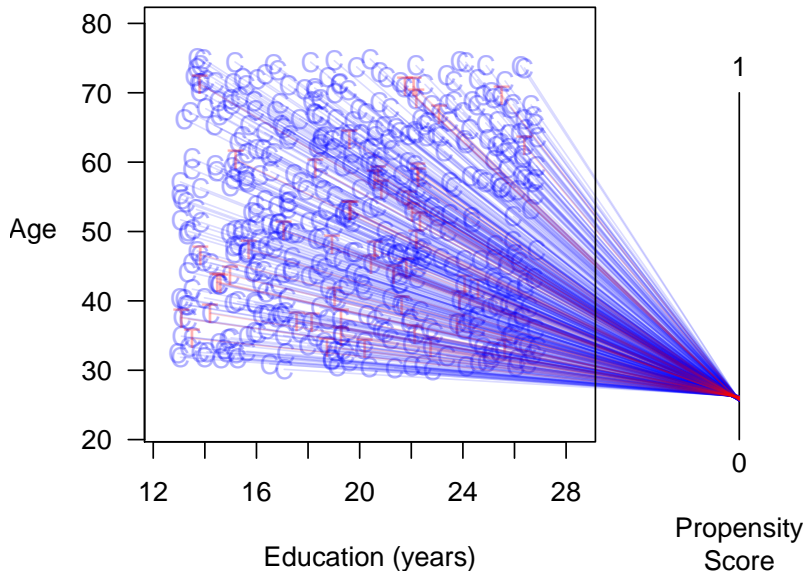


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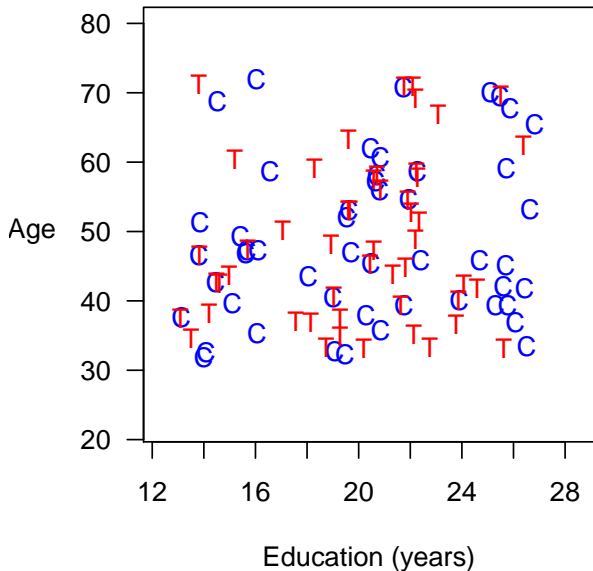
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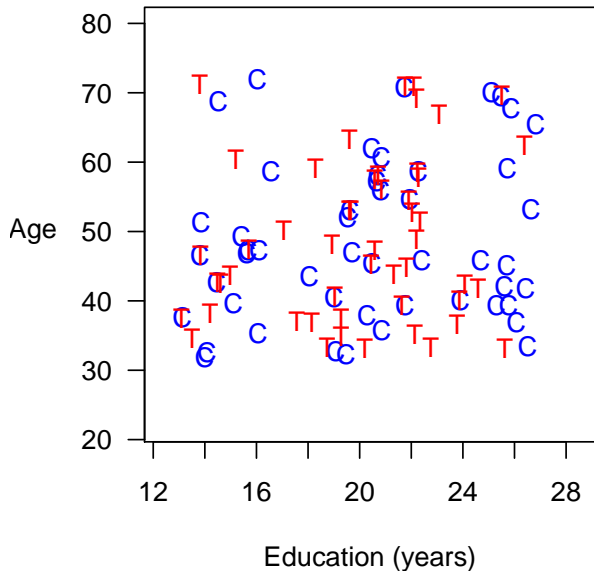
Best Case: Propensity Score Matching



Best Case: Propensity Score Matching



Best Case: Propensity Score Matching is Suboptimal



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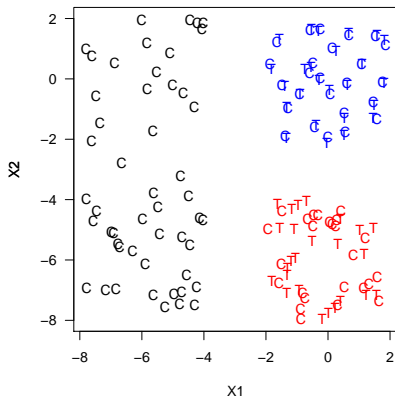
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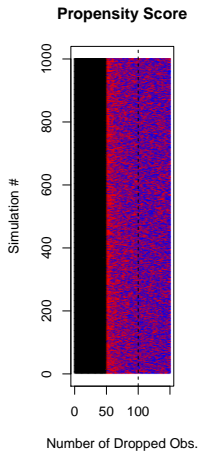
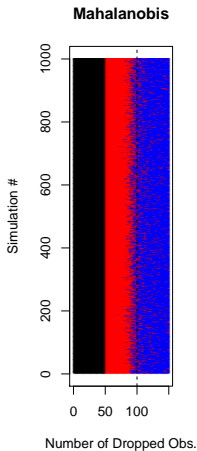
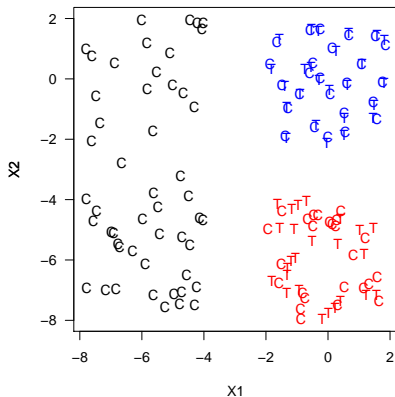
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- If the data have no good matches, the paradox won't be a problem but you're cooked anyway.
- Doesn't PSM solve the curse of dimensionality problem? Nope. The PSM Paradox gets worse with more covariates

PSM is Blind Where Other Methods Can See

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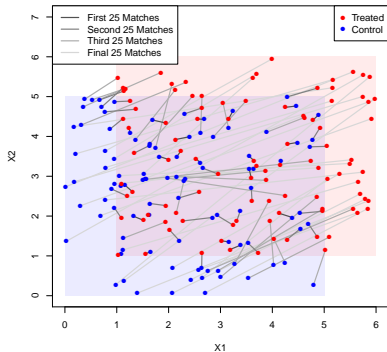


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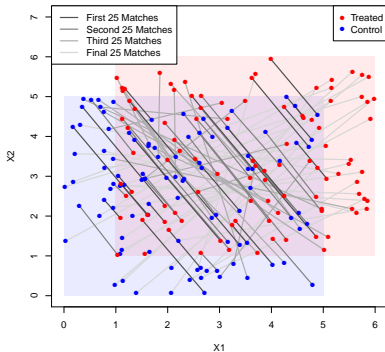


What Does PSM Match?

MDM Matches



PSM Matches

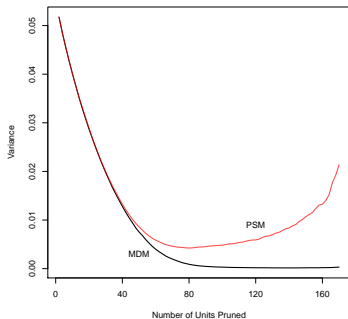


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

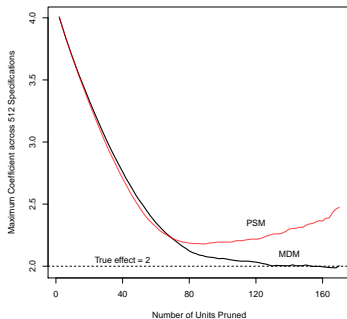
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

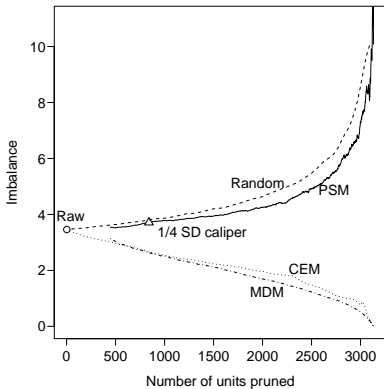


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

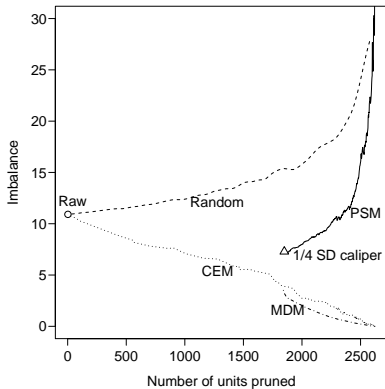
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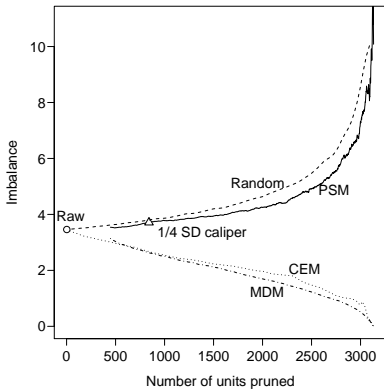


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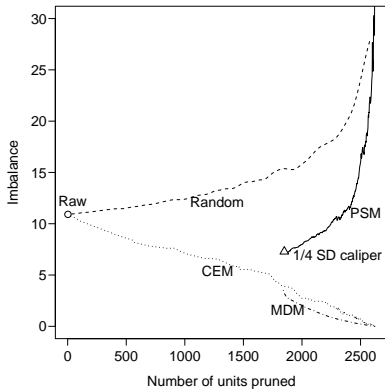


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Similar pattern for > 20 other real data sets we checked

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- Choose an imbalance metric, then run.

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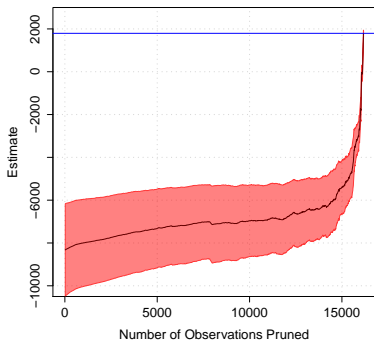
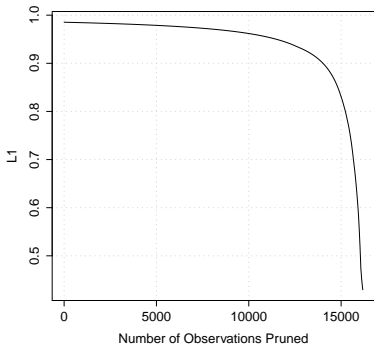
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Job Training Data: Frontier and Causal Estimates



- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after pruning most Cs
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

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For more information, articles, & software

GaryKing.org