

# Simplifying Matching Methods for Causal Inference

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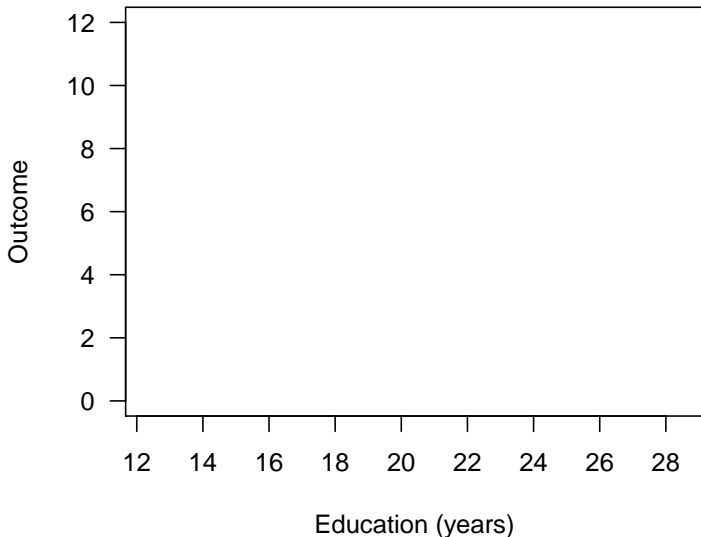
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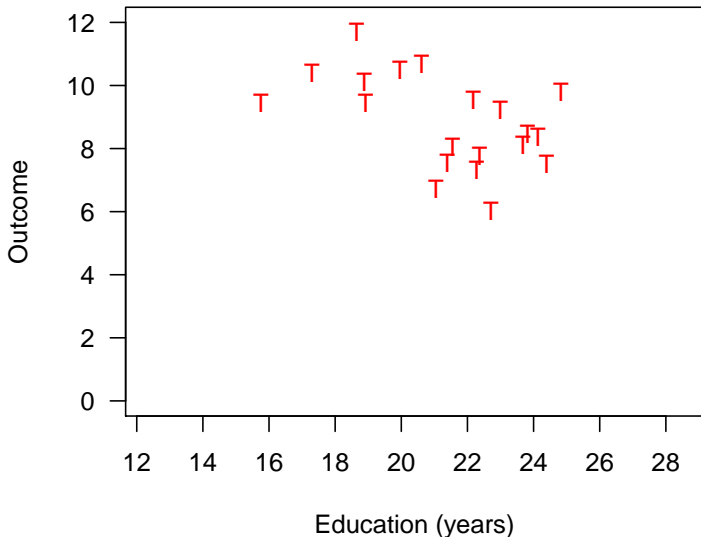
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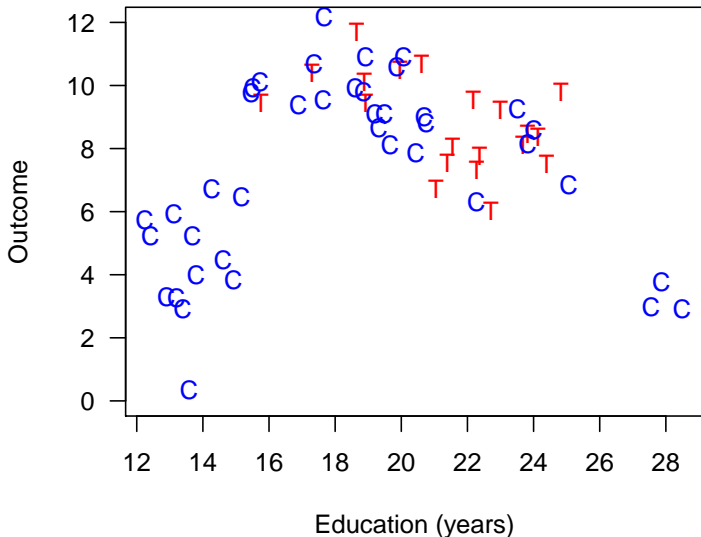
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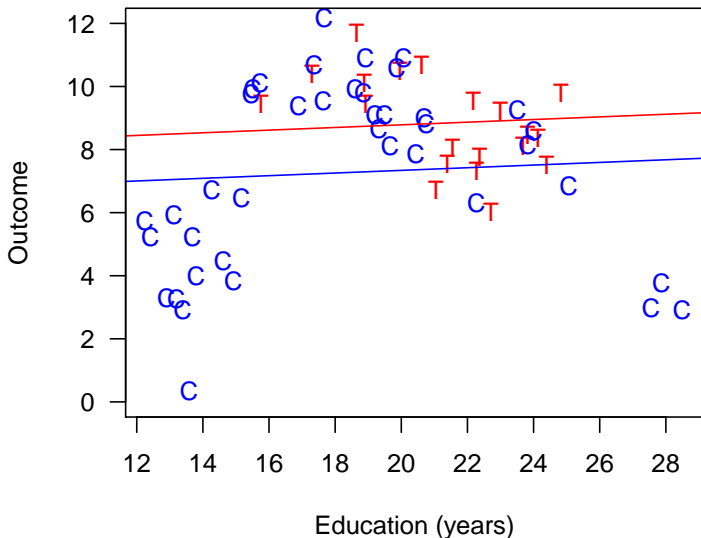
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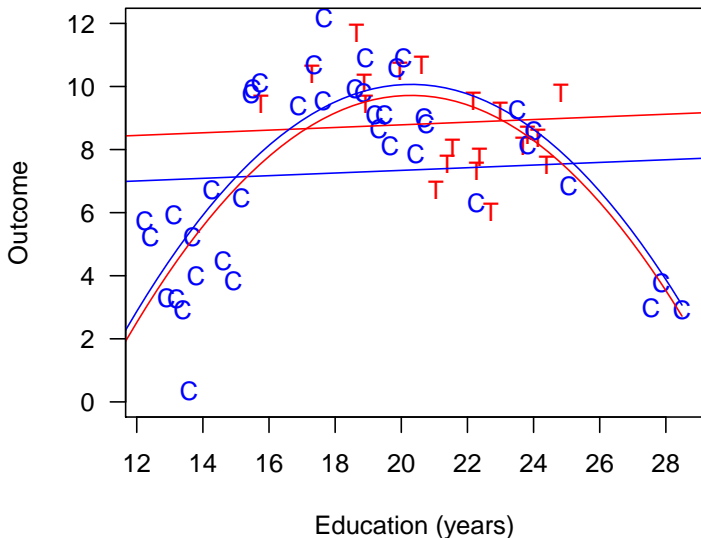
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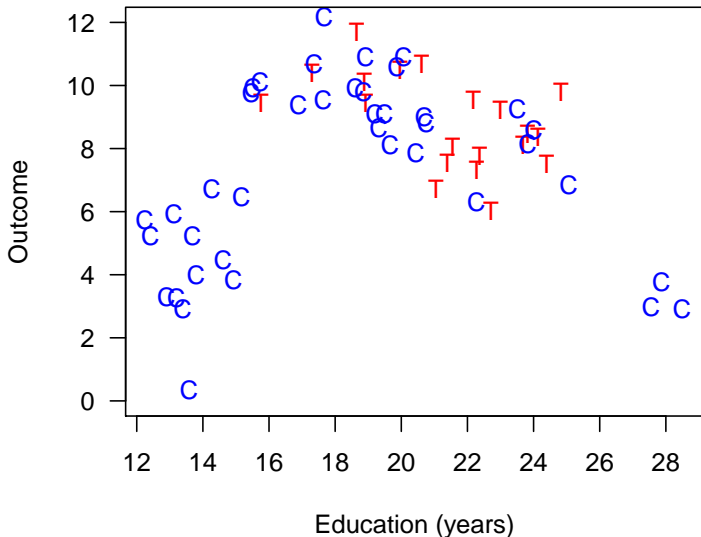
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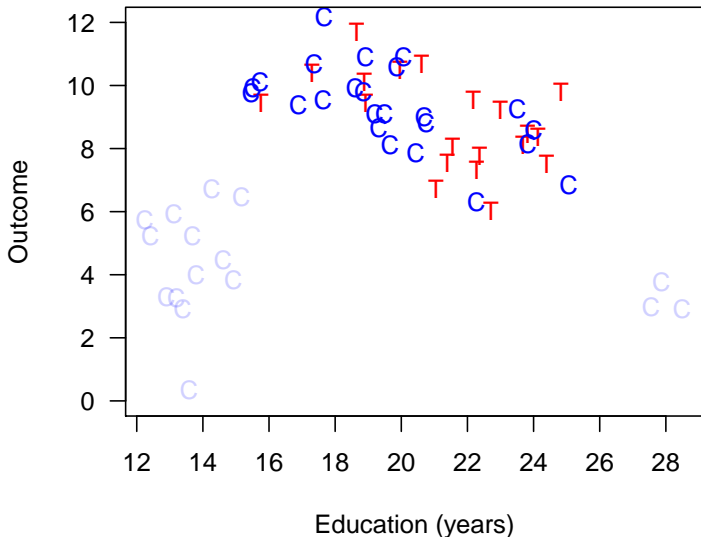
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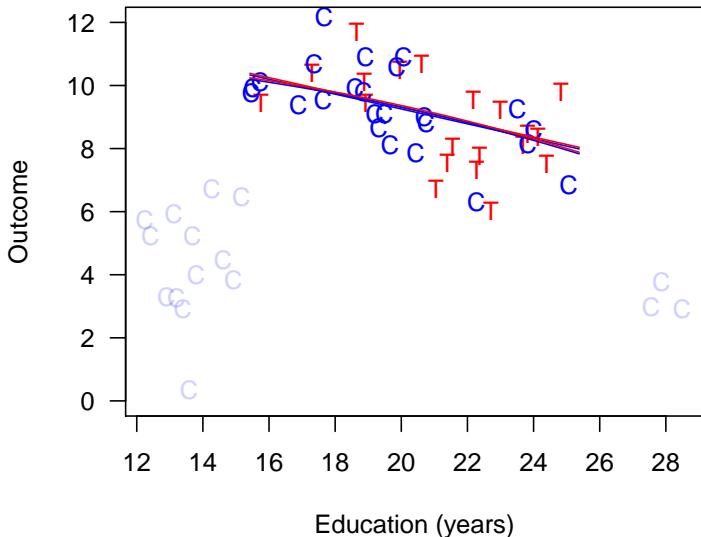
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- “Teaching psychology is mostly a waste of time” (Kahneman 2011)

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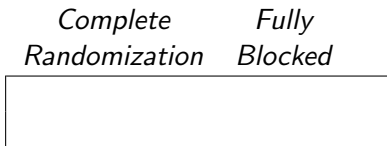
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- **Other matching methods dominate PSM** (wait, it gets worse)

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- Match each treated unit to the nearest control unit

## 2. Estimation Difference in means or a model



# 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!)
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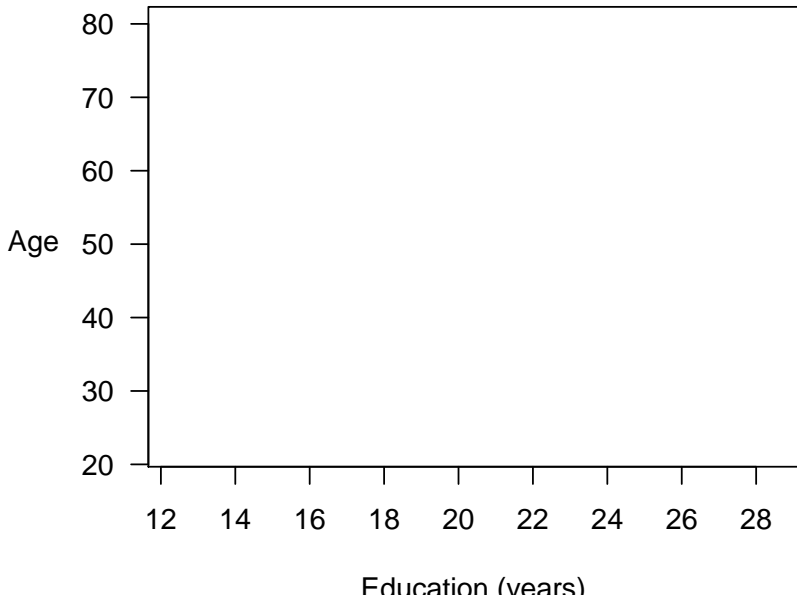
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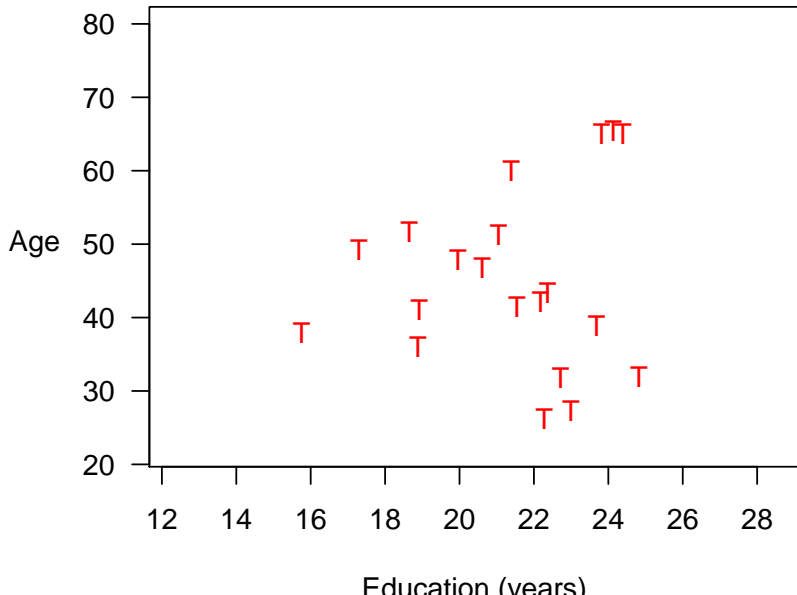
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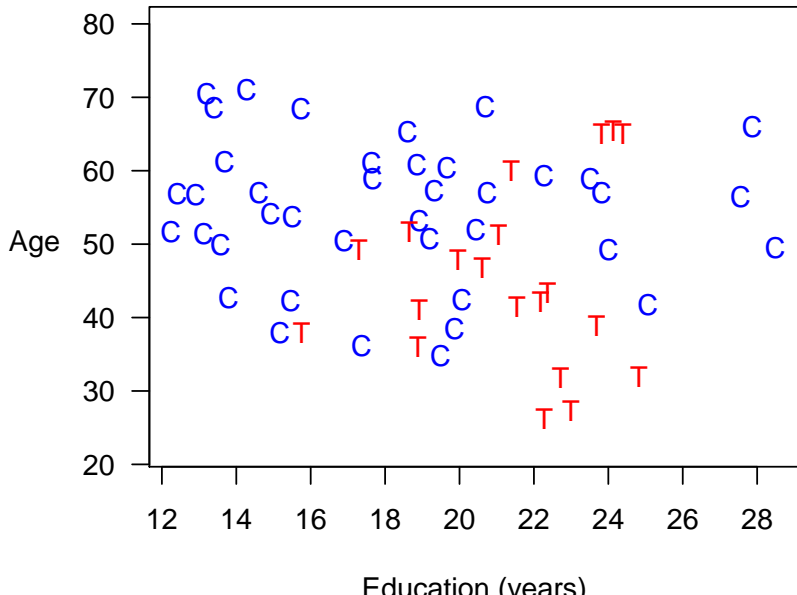
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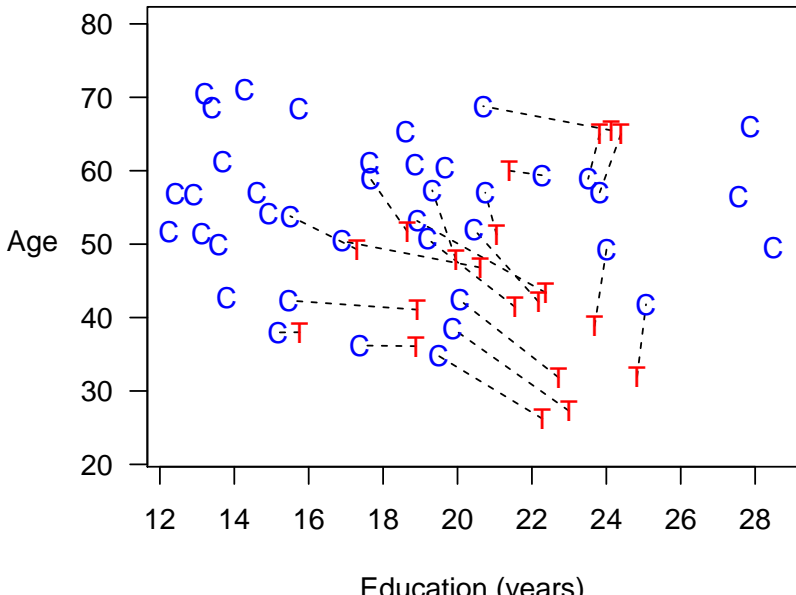
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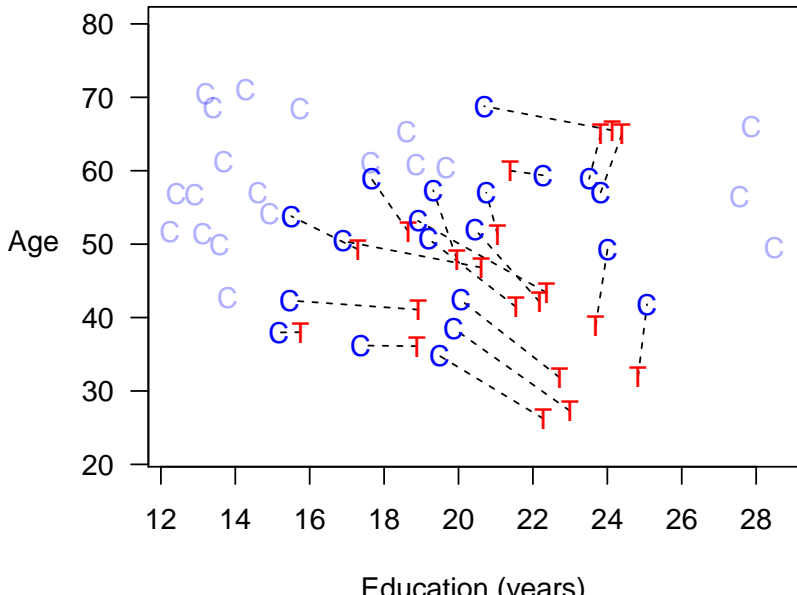
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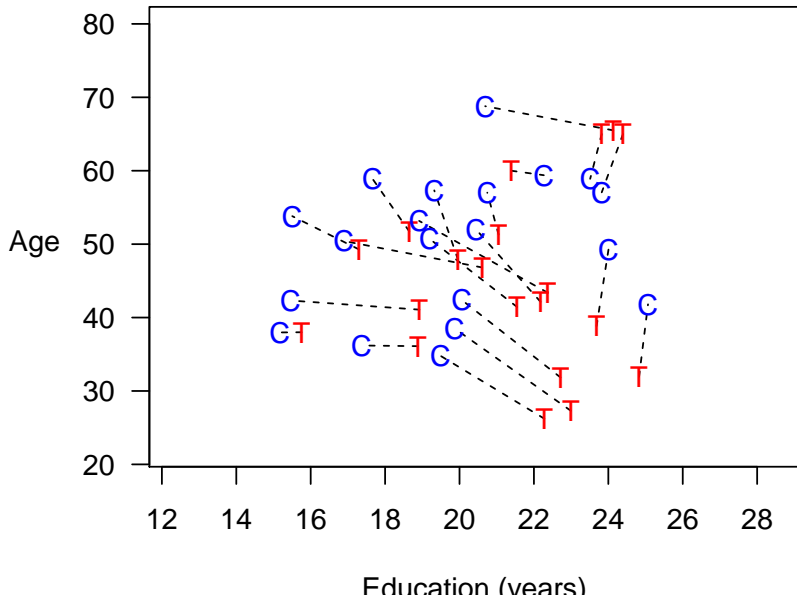


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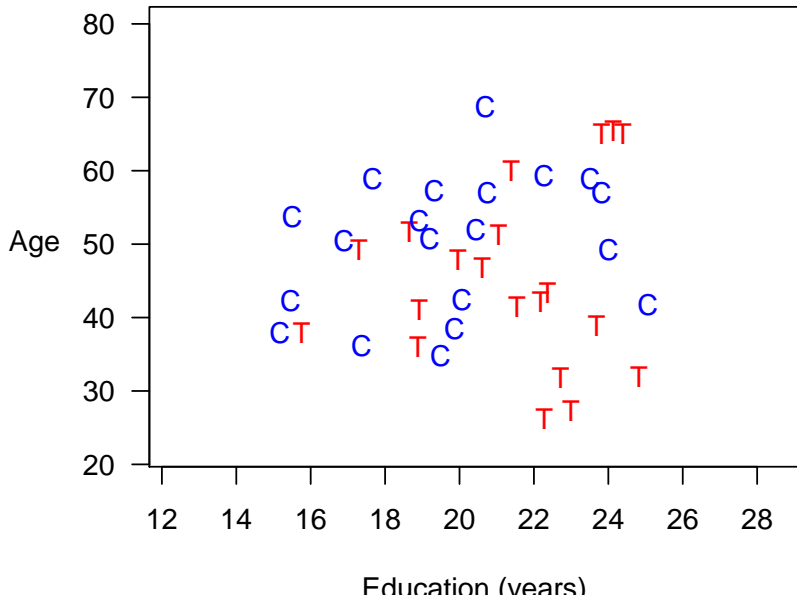




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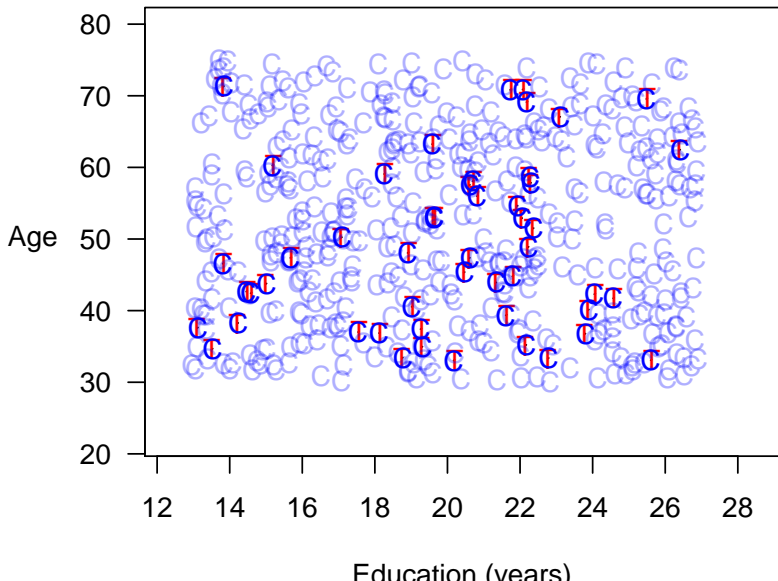


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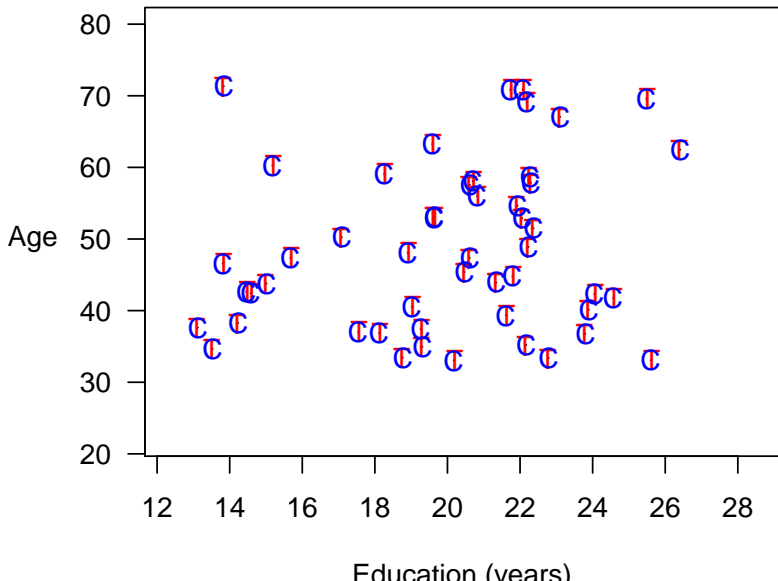


## Best Case: Mahalanobis Distance Matching

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

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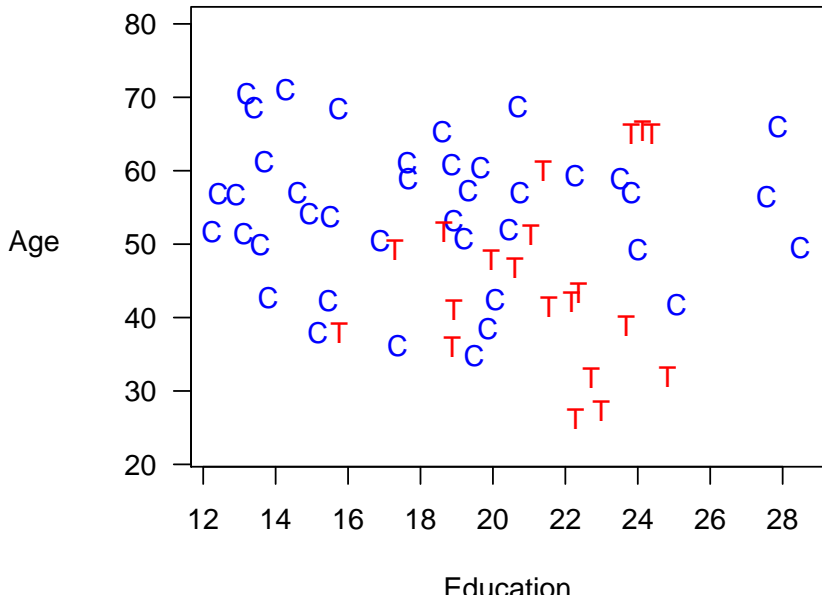
## 2. Estimation Difference in means or a model

- Weight controls in each stratum to equal treated

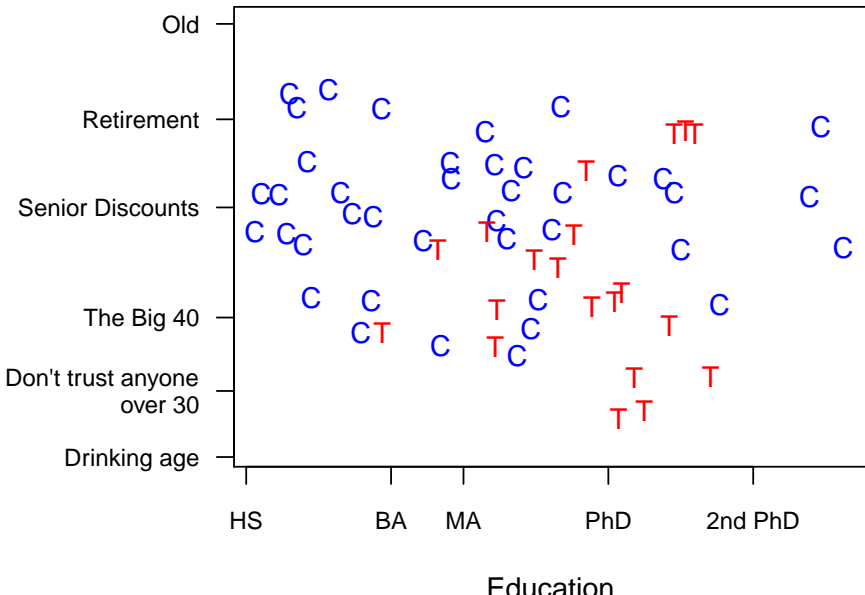
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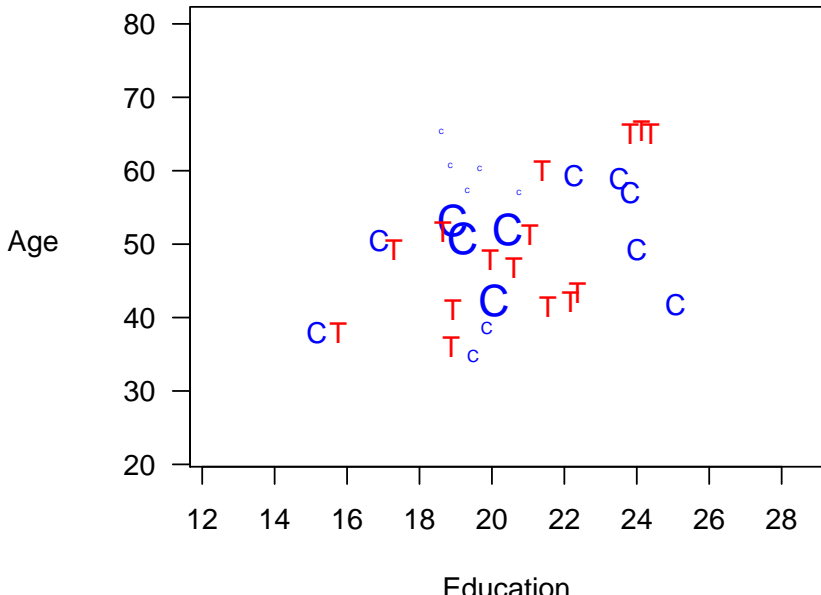






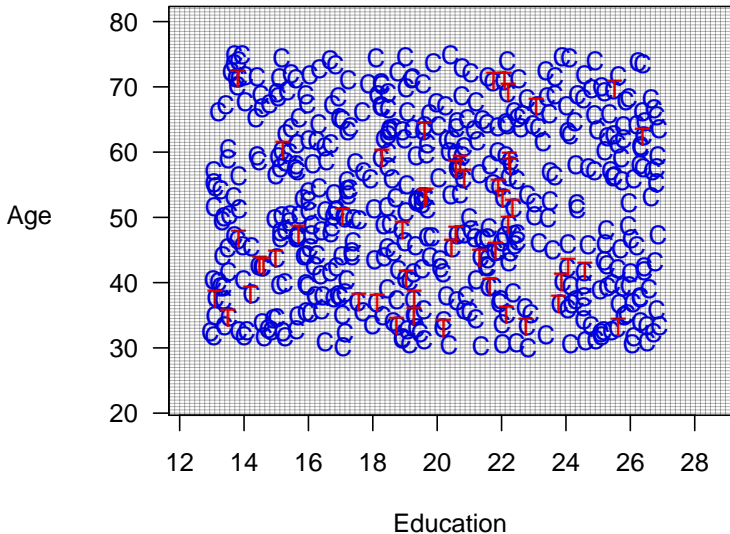


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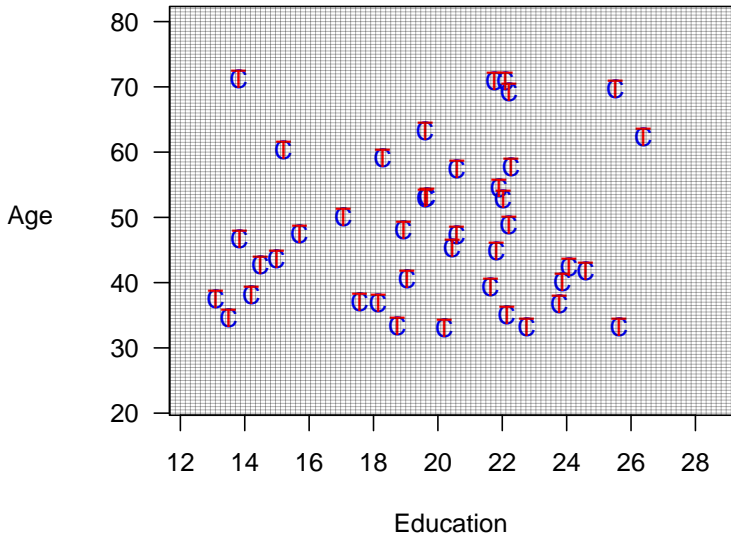
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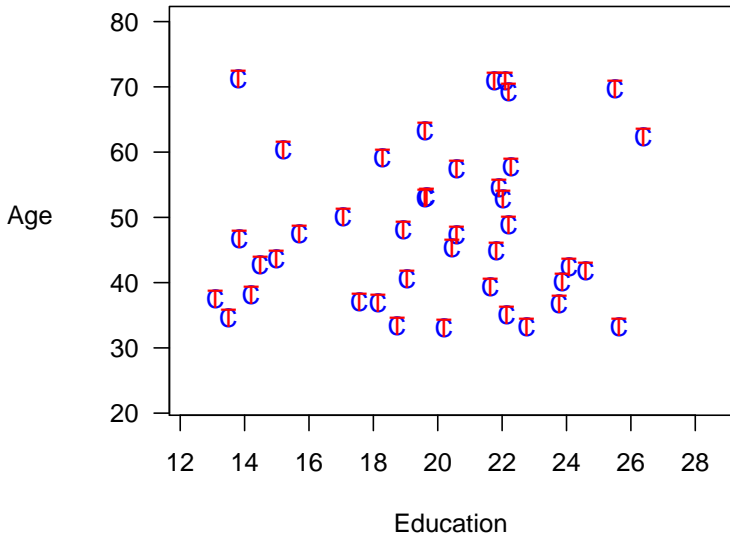




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## Method 3: Propensity Score Matching

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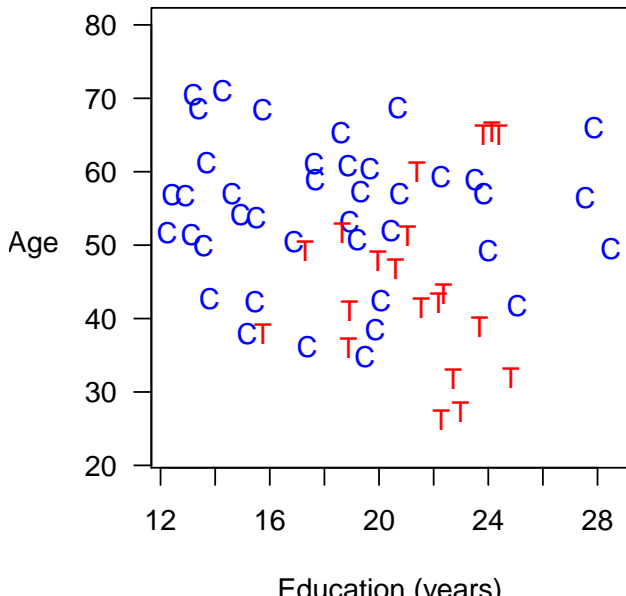
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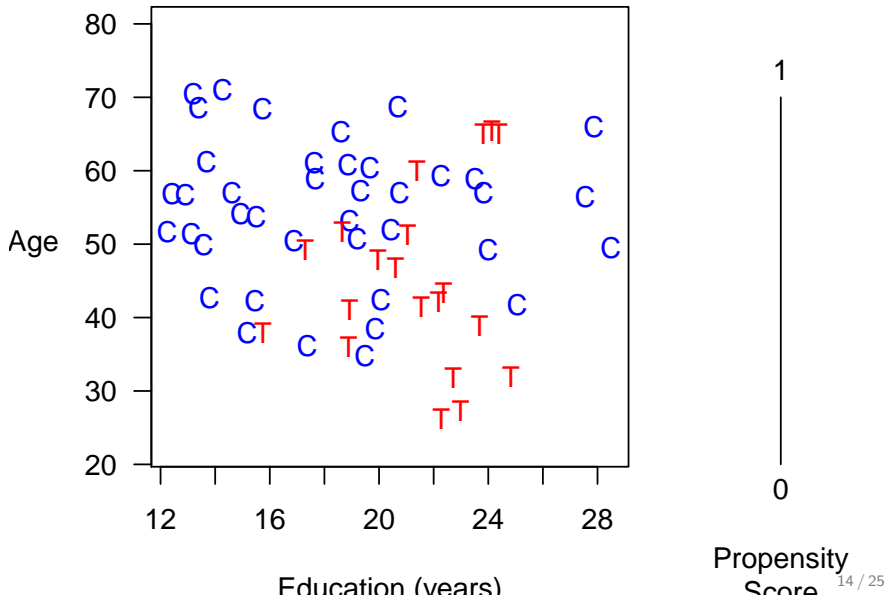
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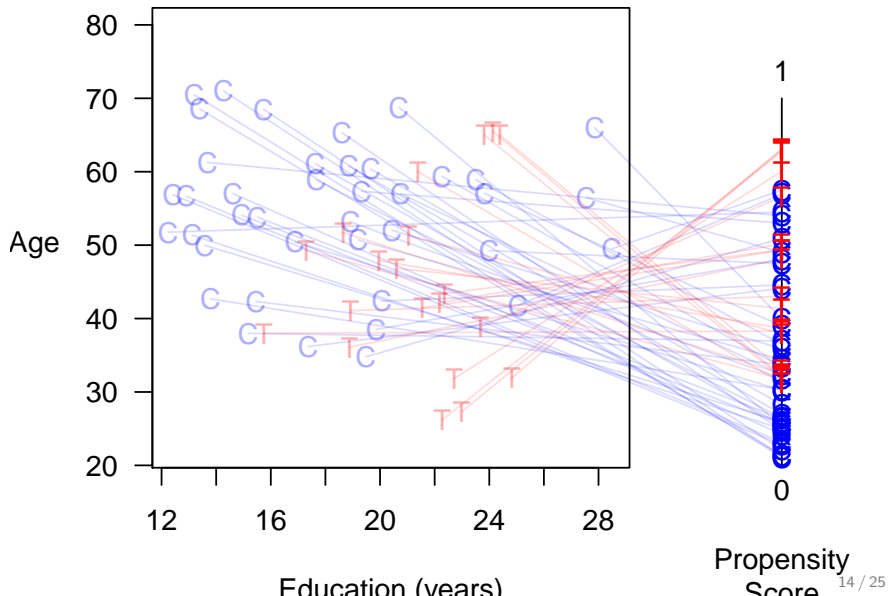
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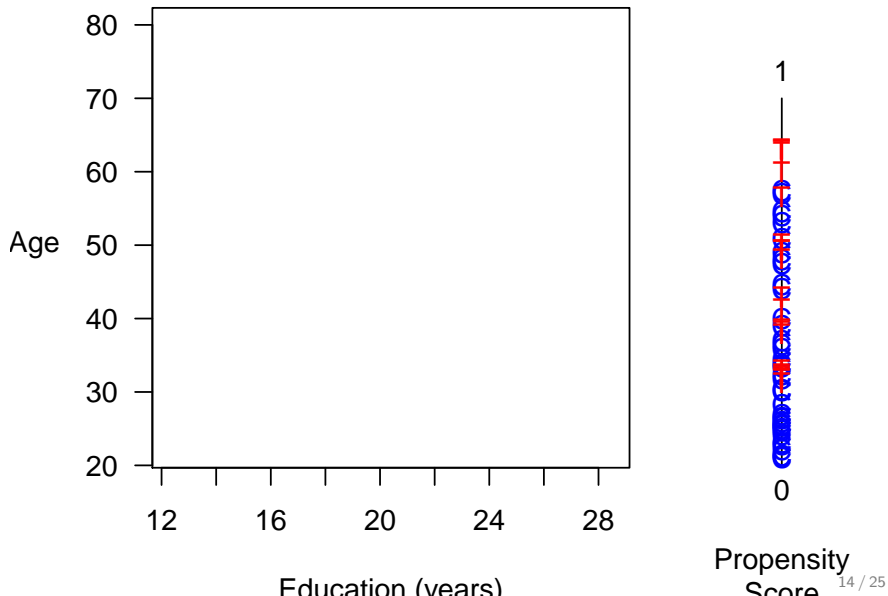
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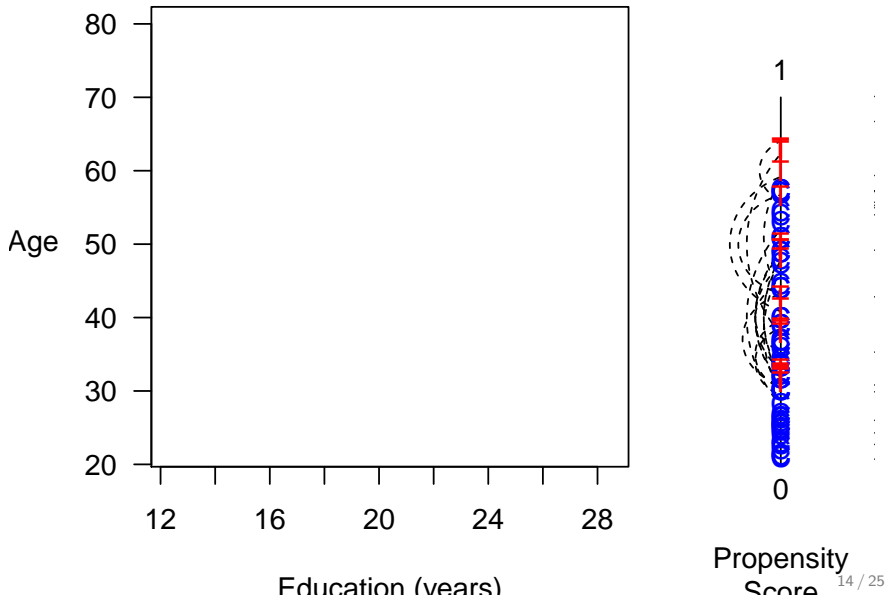
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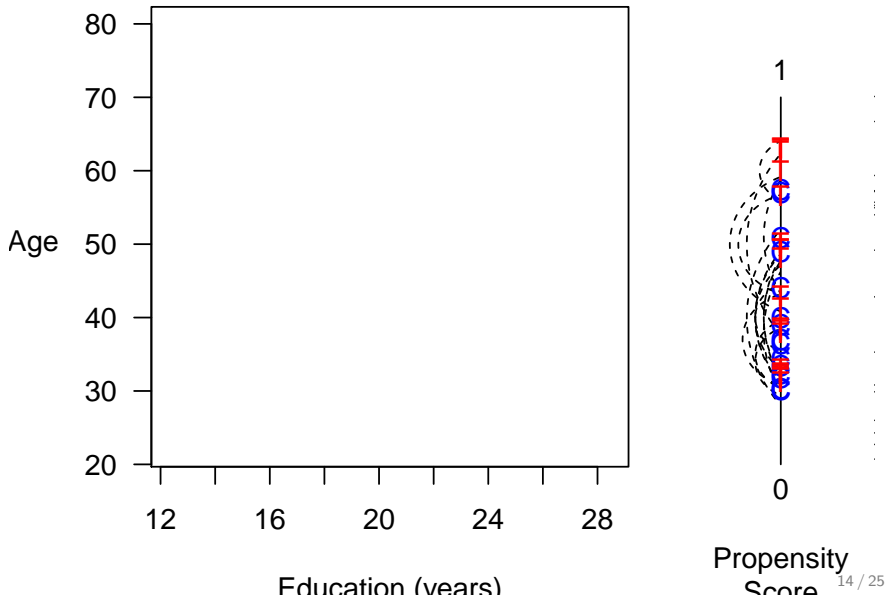


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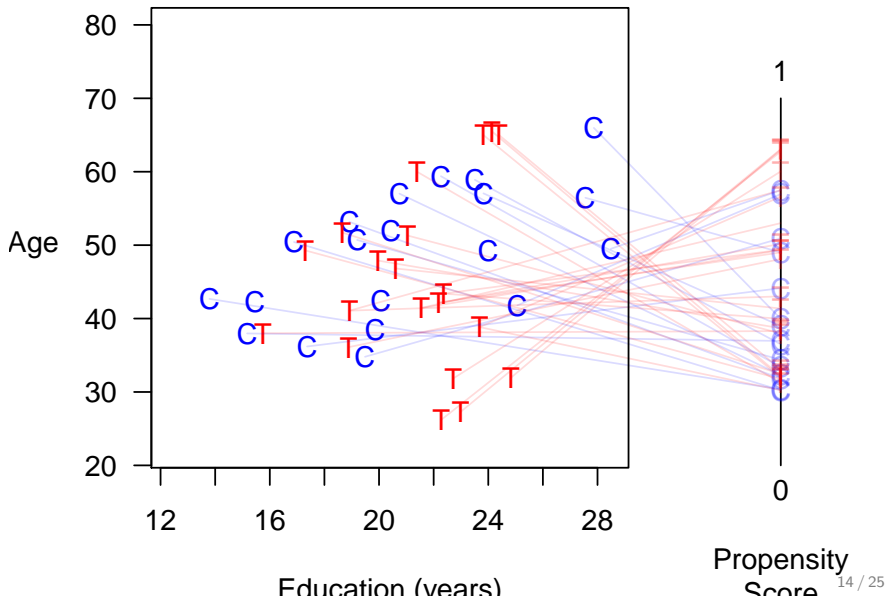




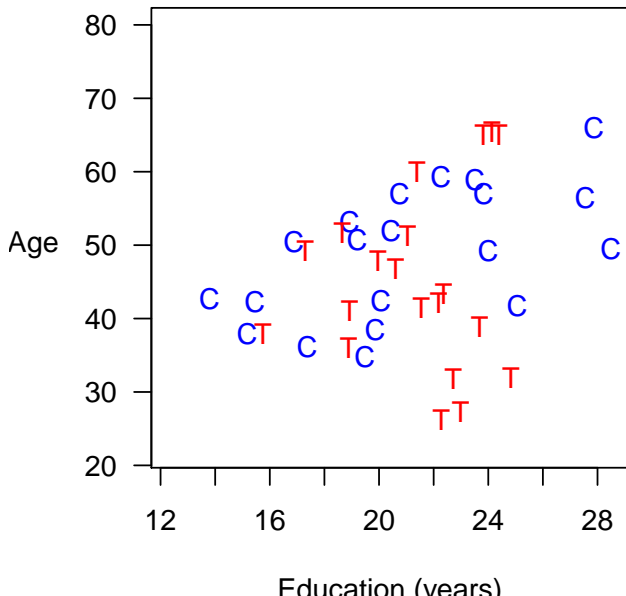
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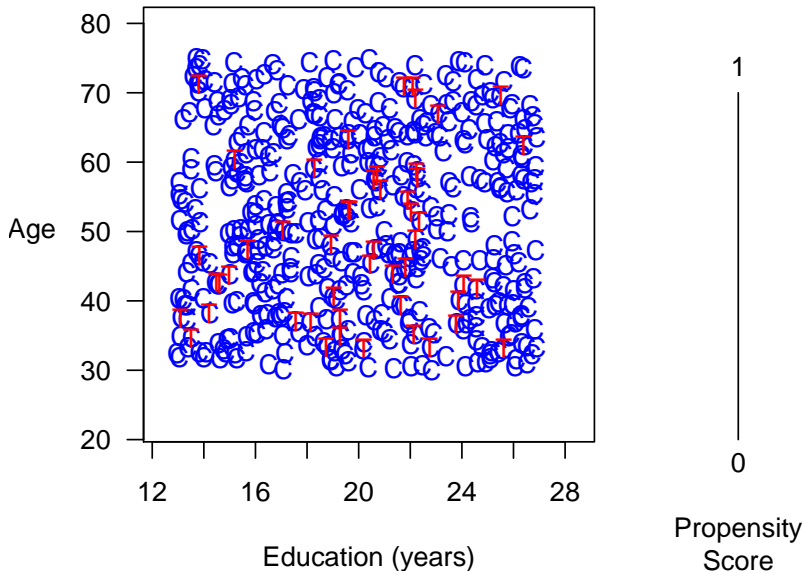


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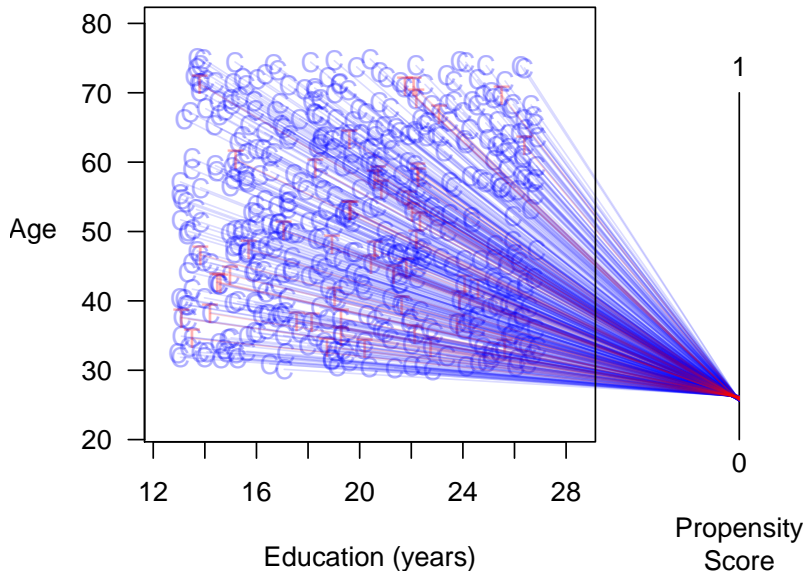


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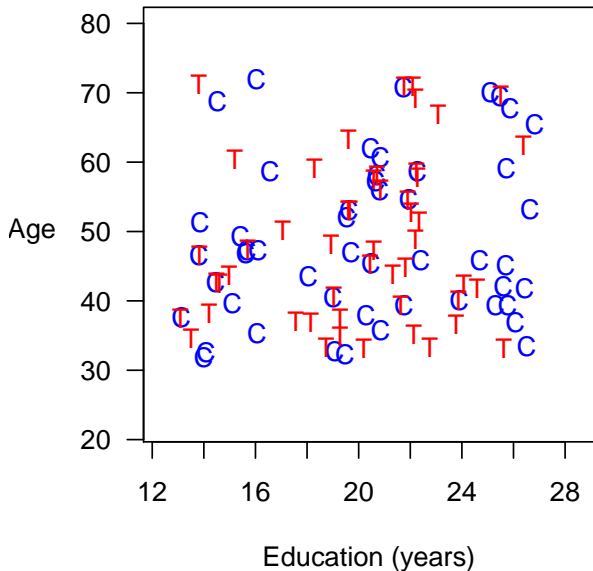
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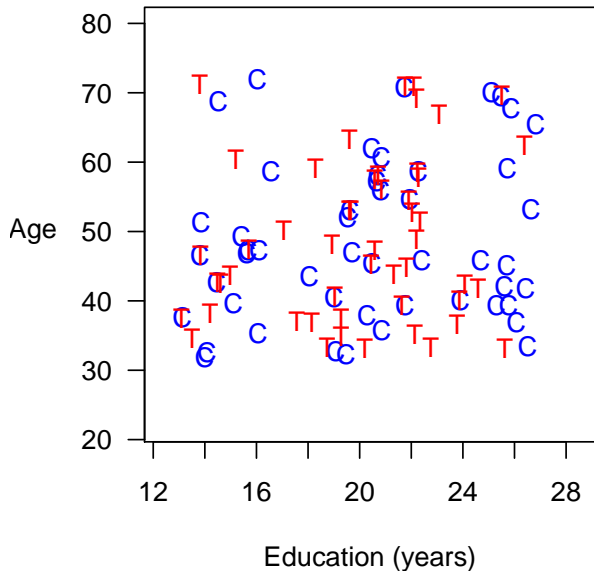
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## Best Case: Propensity Score Matching is Suboptimal





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

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

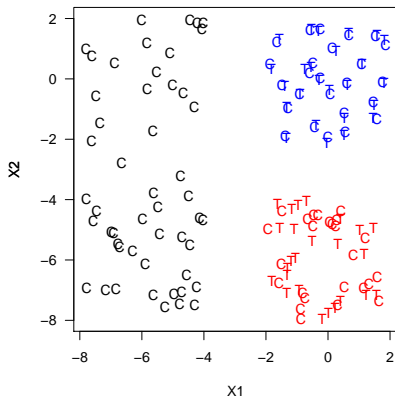
$$\pi_c = \pi_t \not\implies X_c = X_t$$

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

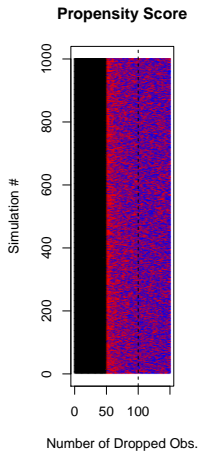
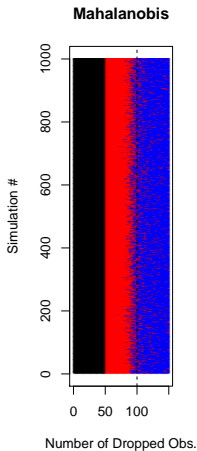
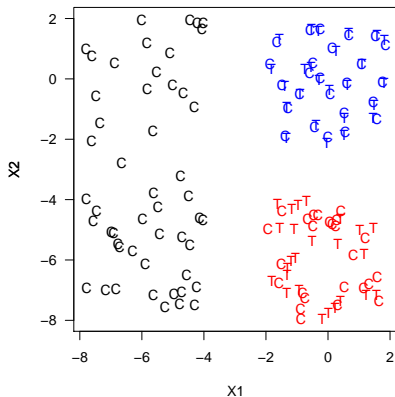
- Background: Random matching increases imbalance
- When PSM approximates complete randomization (to begin with or, after some pruning)  $\rightsquigarrow$  all  $\hat{\pi} \approx 0.5$  (or constant within strata)  $\rightsquigarrow$  pruning at random  $\rightsquigarrow$  Imbalance  $\rightsquigarrow$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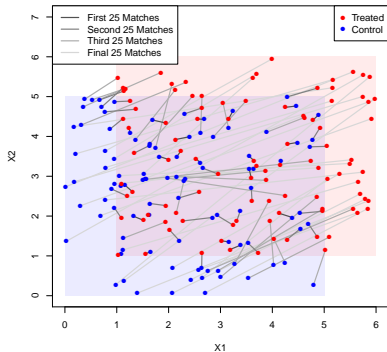


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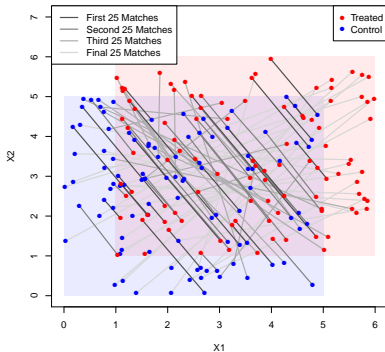


# What Does PSM Match?

## MDM Matches



## PSM Matches



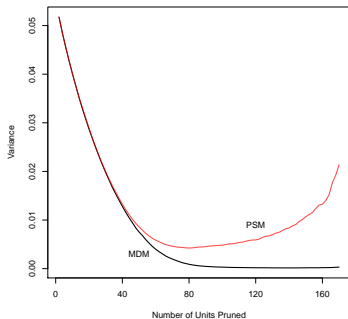
Controls:  $X_1, X_2 \sim \text{Uniform}(0,5)$

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

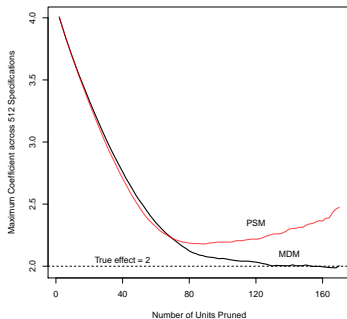


# PSM Increases Model Dependence & Bias

## Model Dependence



## Bias

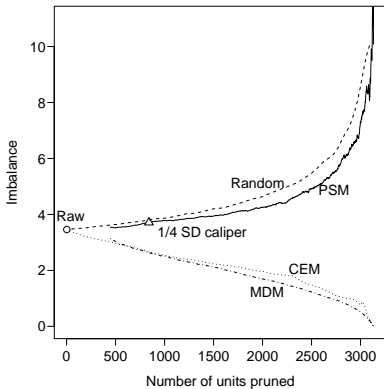


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

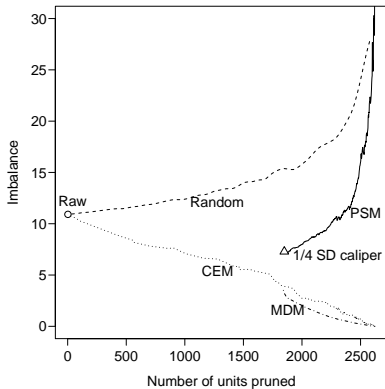
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Finkel et al. (JOP, 2012)

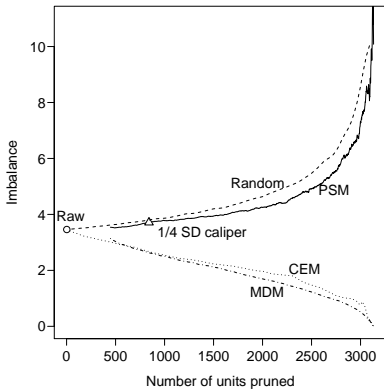


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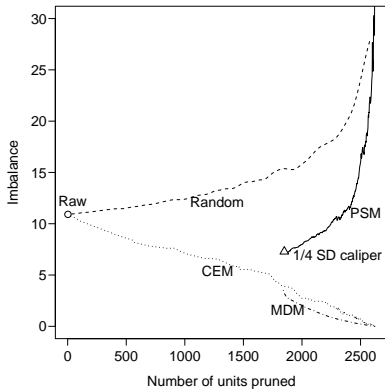


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Similar pattern for > 20 other real data sets we checked

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- Choose an imbalance metric, then run.

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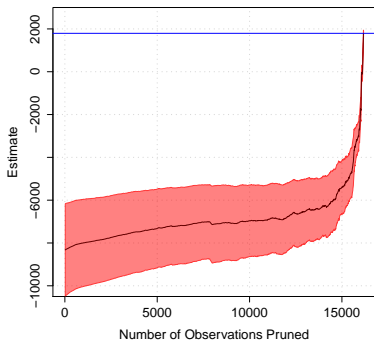
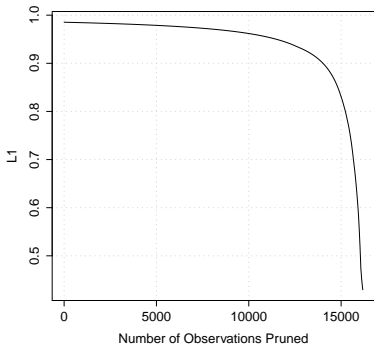
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## Job Training Data: Frontier and Causal Estimates



- 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