

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

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Matching Overview

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

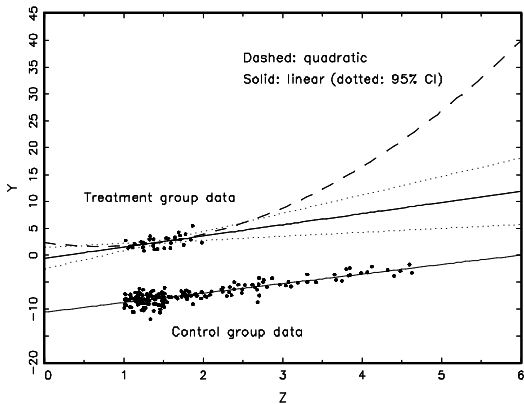
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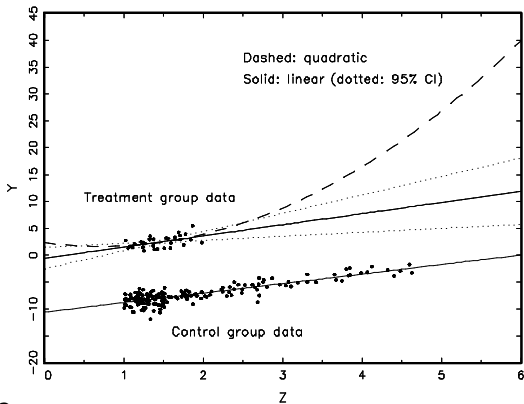
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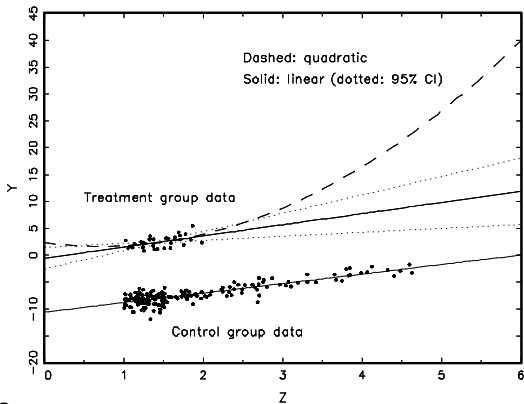
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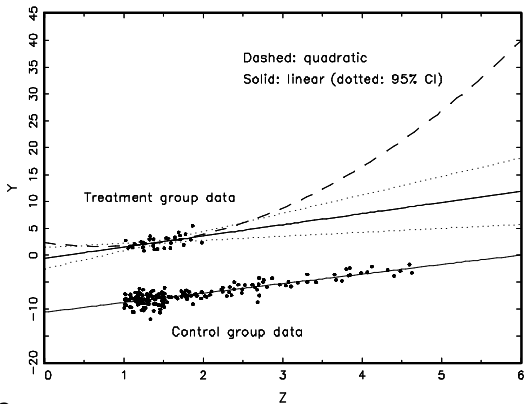


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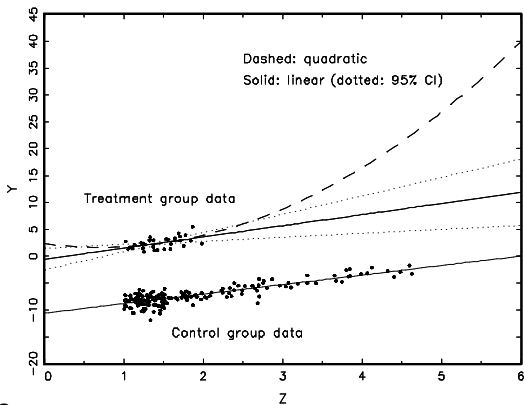


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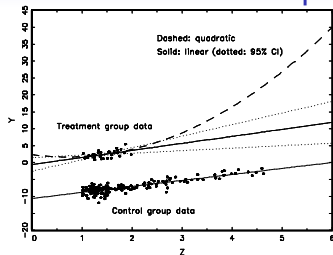


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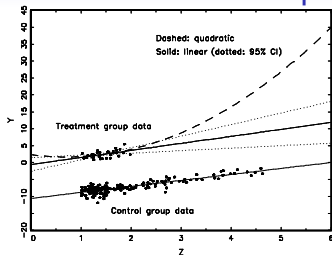
- **Preprocess I:** Eliminate extrapolation region
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- **Model** remaining imbalance (as you would w/o matching)

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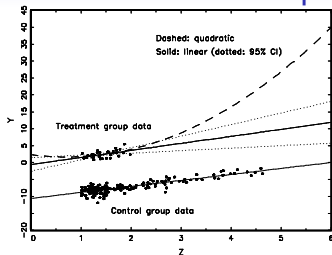


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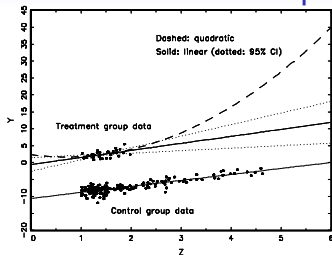
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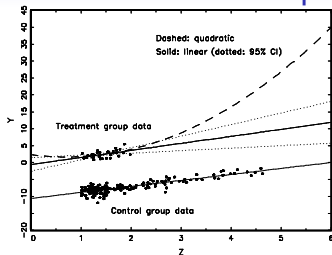
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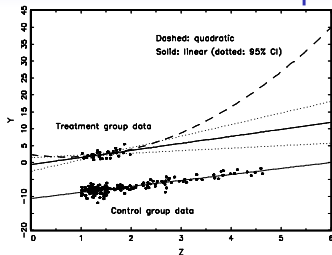
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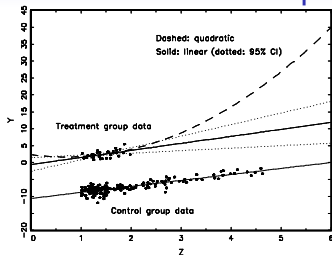
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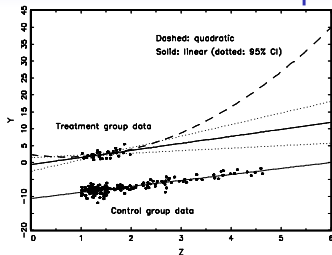
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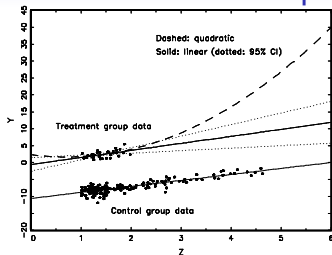
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 4. Easiest: Coarsened Exact Matching, no separate step needed

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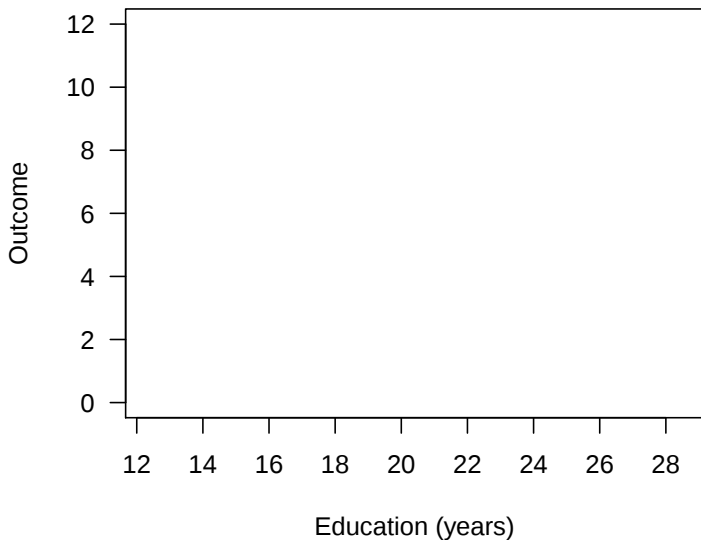
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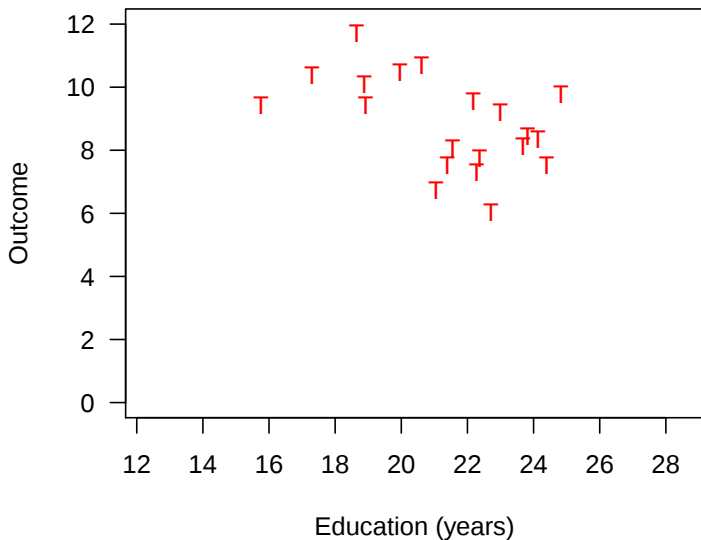
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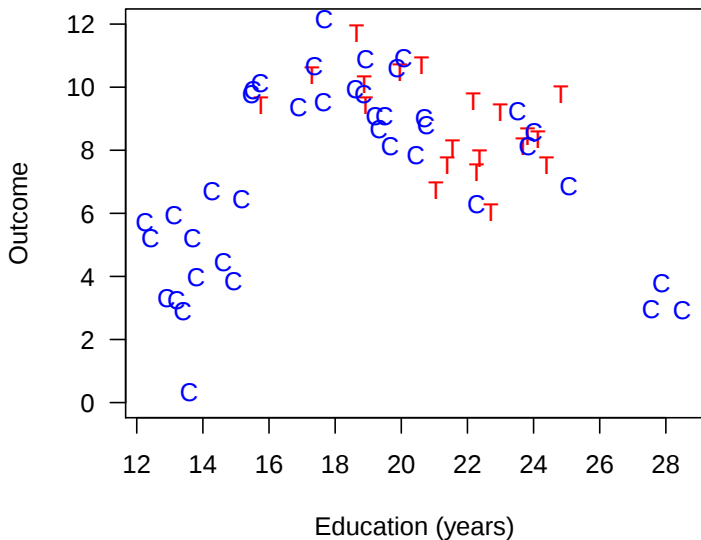
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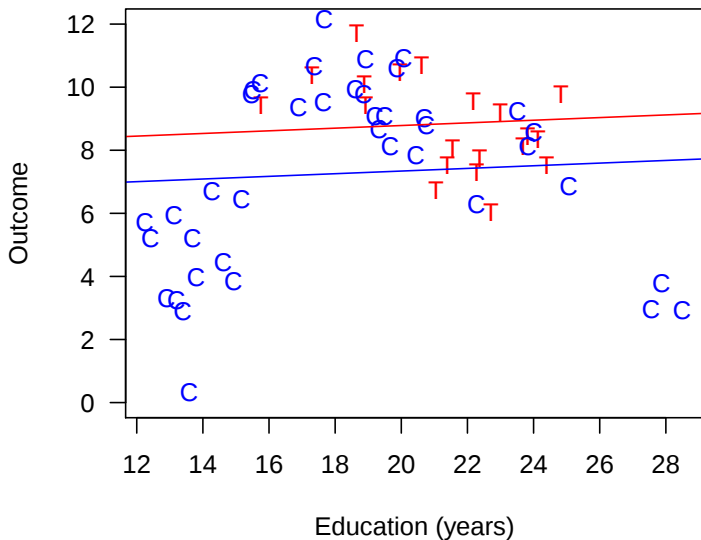
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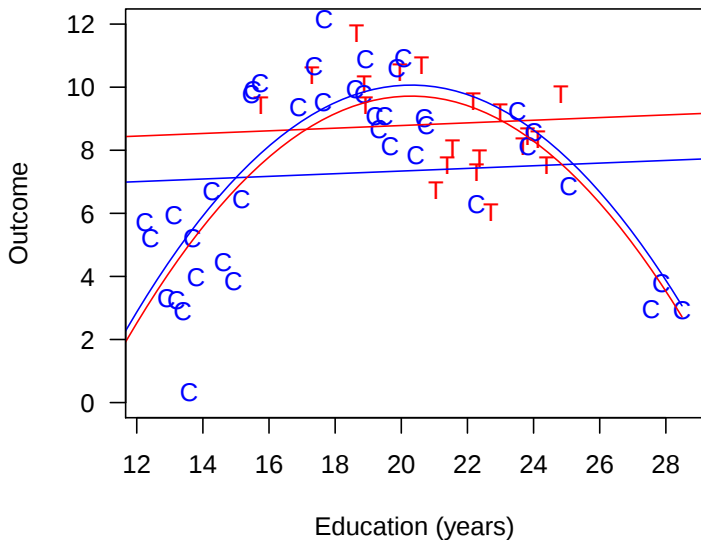
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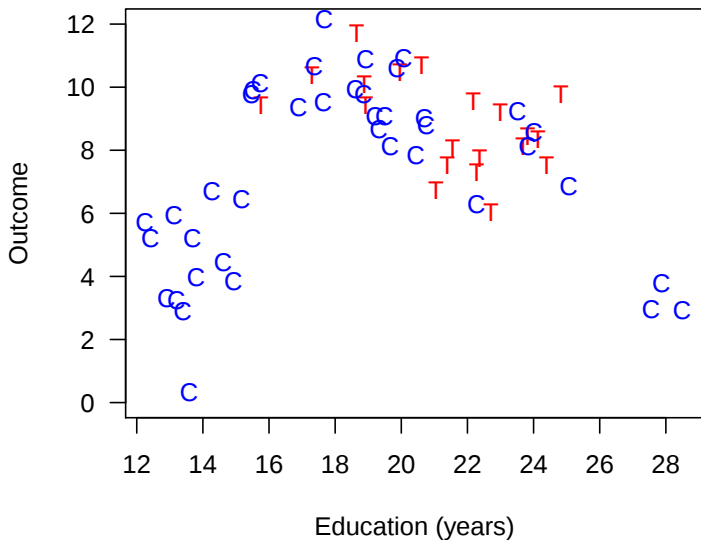
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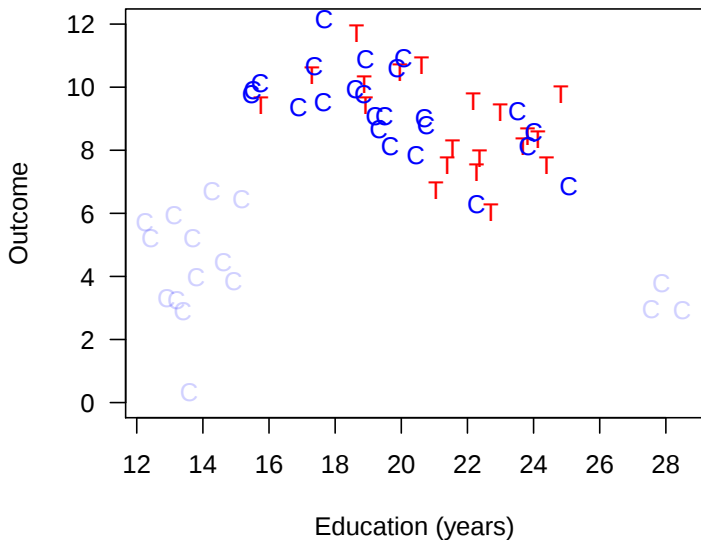
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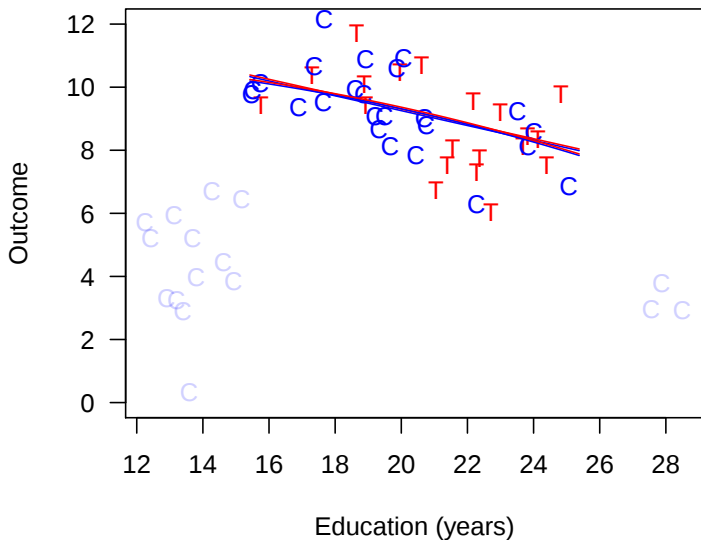
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Matching reduces model dependence, bias, and variance

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

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- Look at *variability* in ATE estimate across specifications.
- (Normal applications would only use one or a few specifications.)

Reducing Model Dependence

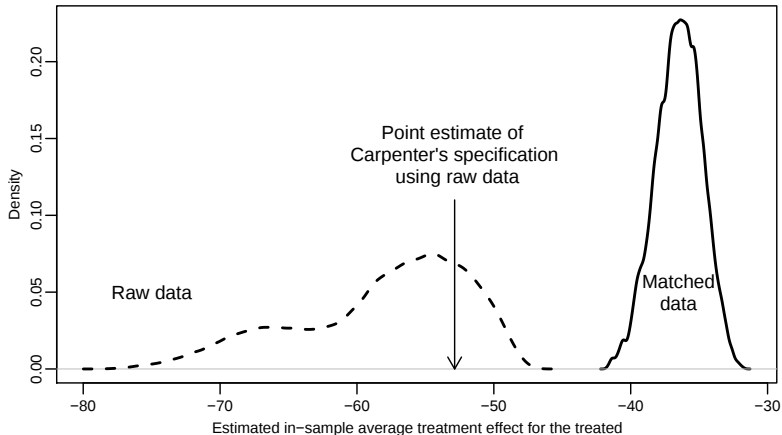


Figure: SATT Histogram: Effect of Democratic Senate majority on FDA drug approval time, across 262,143 specifications.

Another Example: Jeffrey Koch, AJPS, 2002

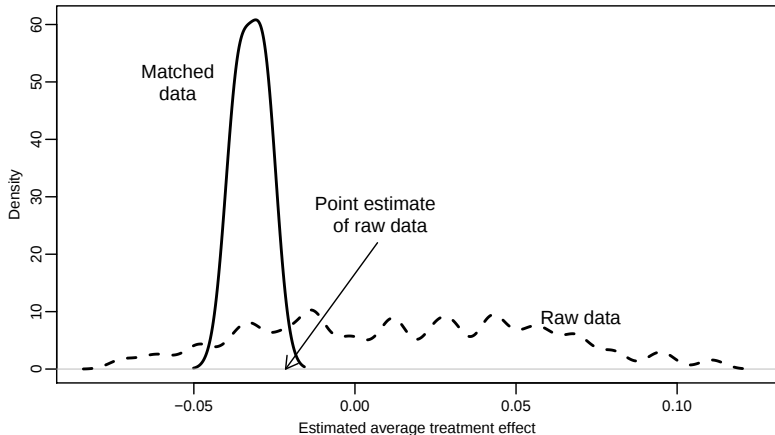


Figure: SATT Histogram: Effect of being a highly visible female Republican candidate across 63 possible specifications with the Koch

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Imbalance

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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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$$\begin{aligned} TE_i &= Y_i(1) - Y_i(0) \\ &= \text{observed} - \text{unobserved} \end{aligned}$$

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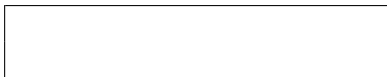
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 - **Pruning nonmatches makes control vars matter less:** reduces imbalance, model dependence, researcher discretion, & bias

Matching: Finding Hidden Randomized Experiments

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Types of Experiments



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Types of Experiments

*Complete
Randomization*



Matching: Finding Hidden Randomized Experiments

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<i>Complete Randomization</i>	<i>Fully Blocked</i>

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Goal of Each Matching Method (in Observational Data)

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

Method 1: Mahalanobis Distance Matching

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(Approximates Fully Blocked Experiment)

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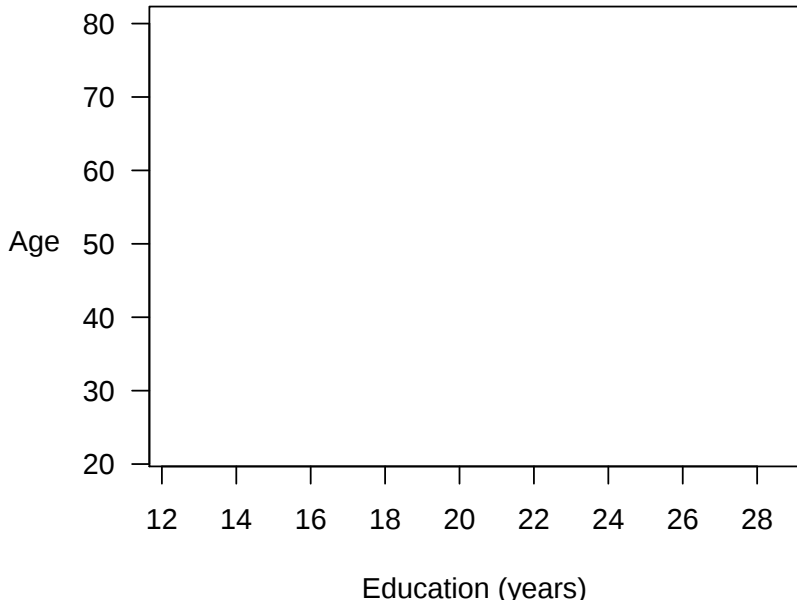
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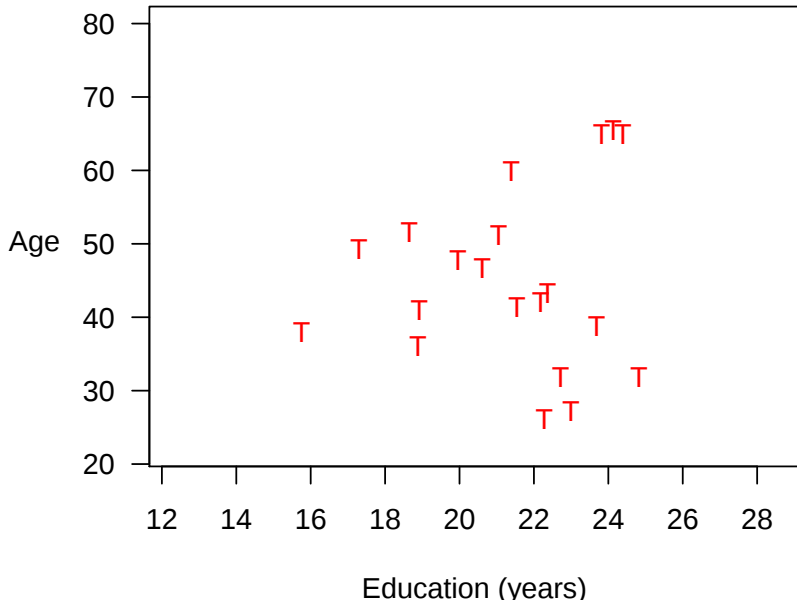
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- (Many adjustments available to this basic method)

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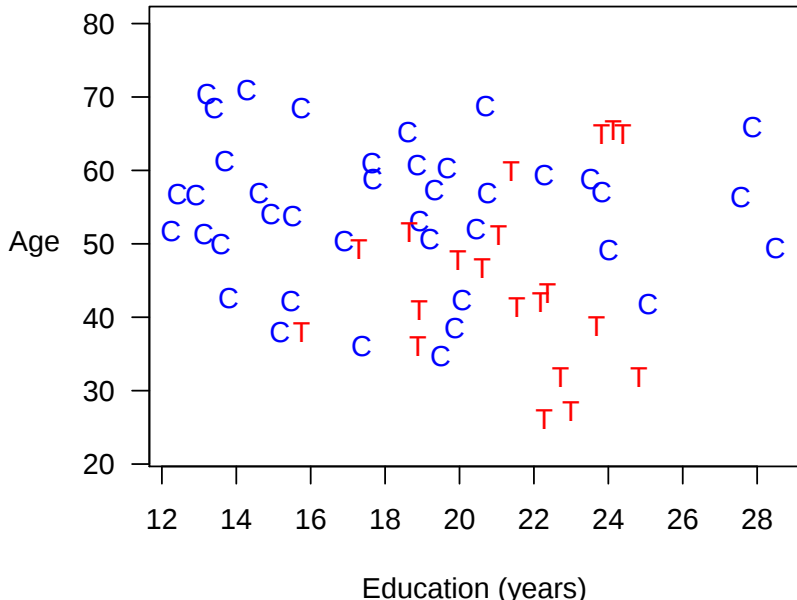
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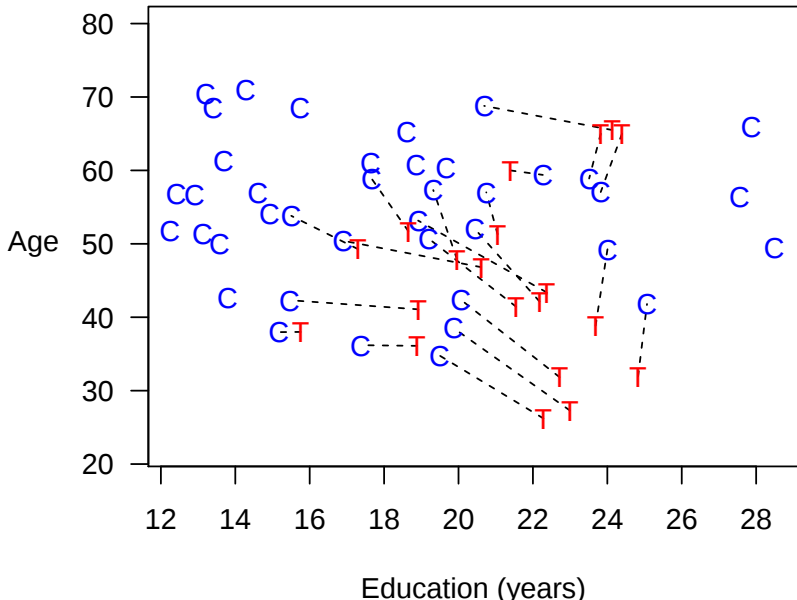
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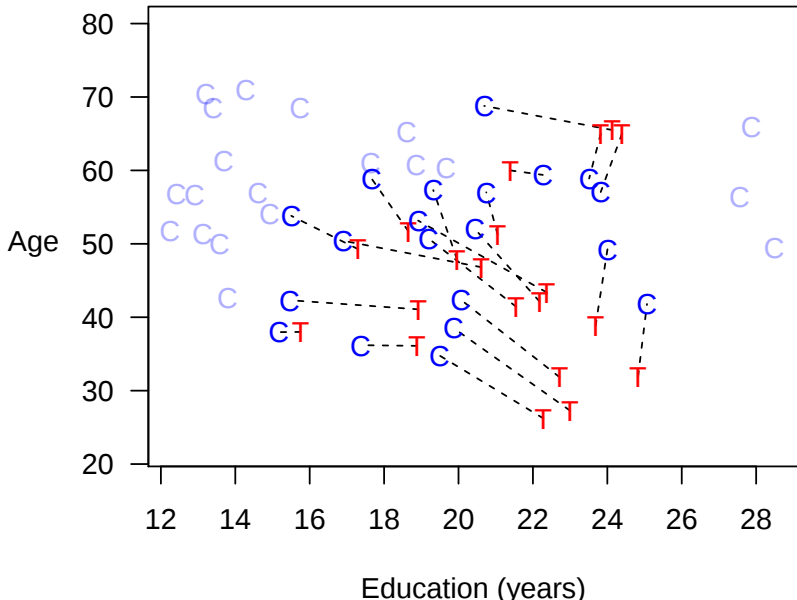
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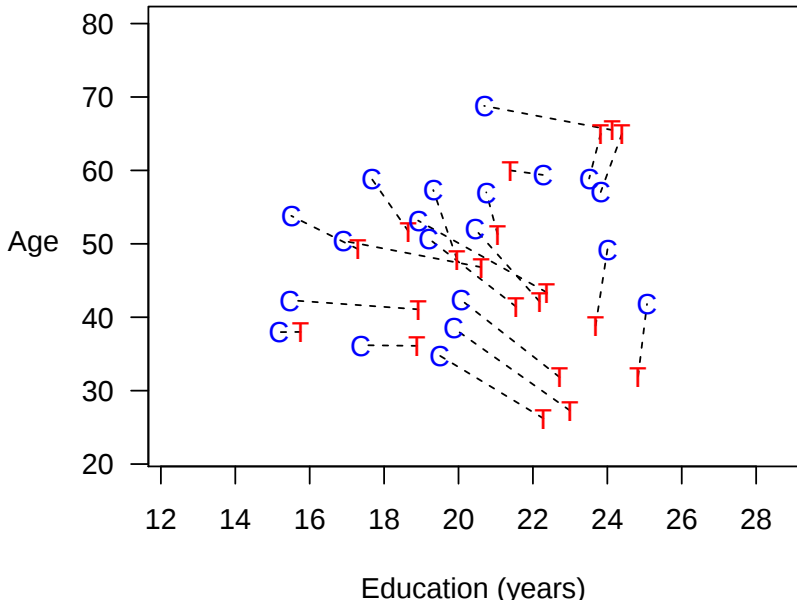
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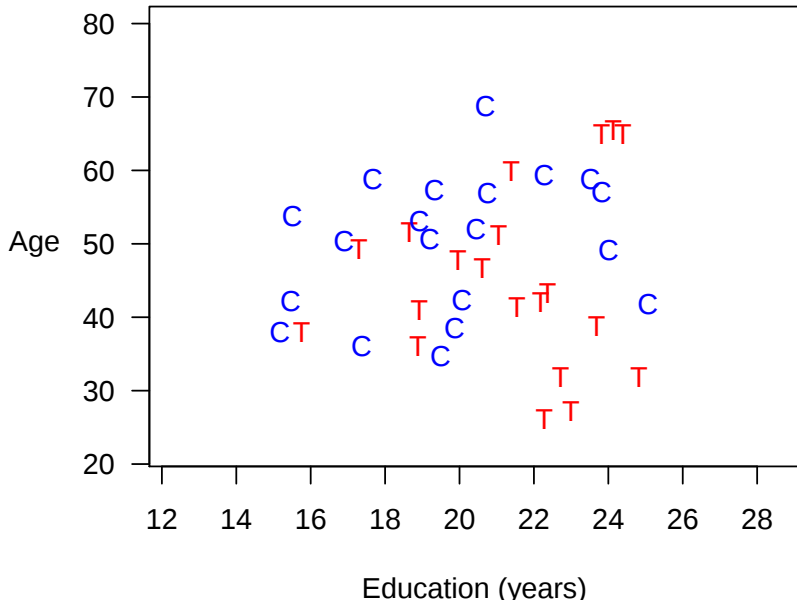
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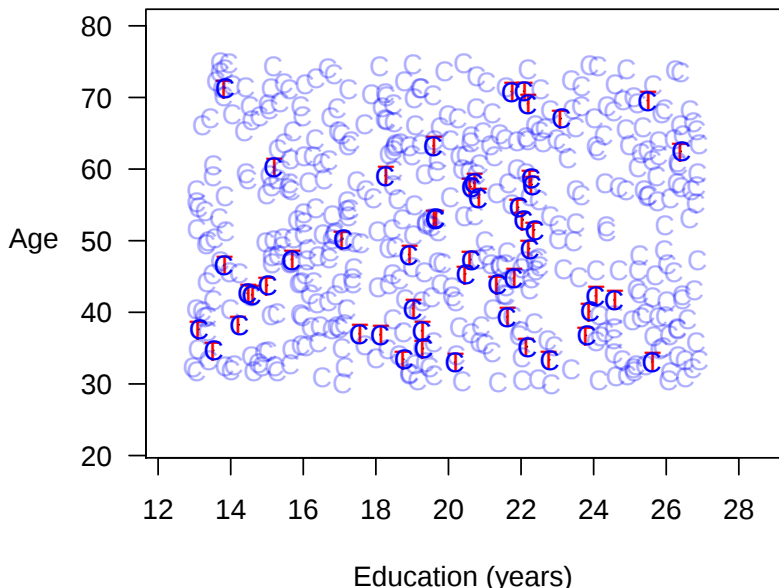


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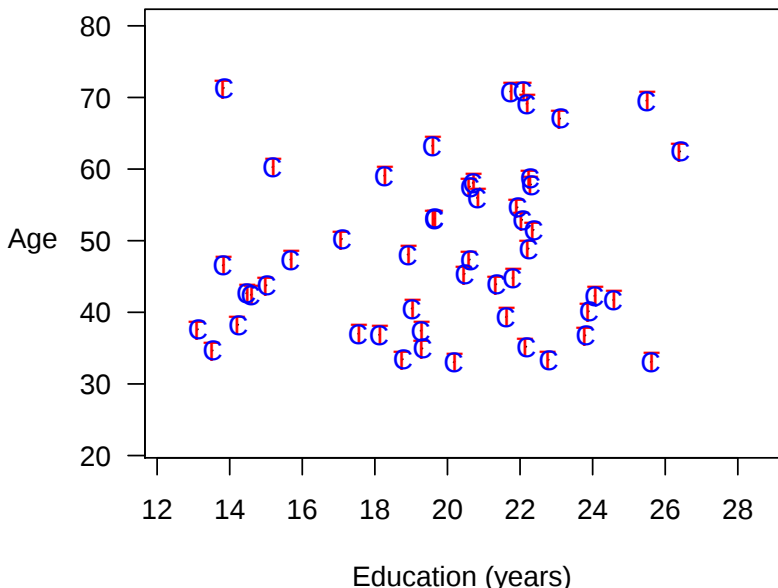


Best Case: Mahalanobis Distance Matching

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Method 2: Coarsened Exact Matching

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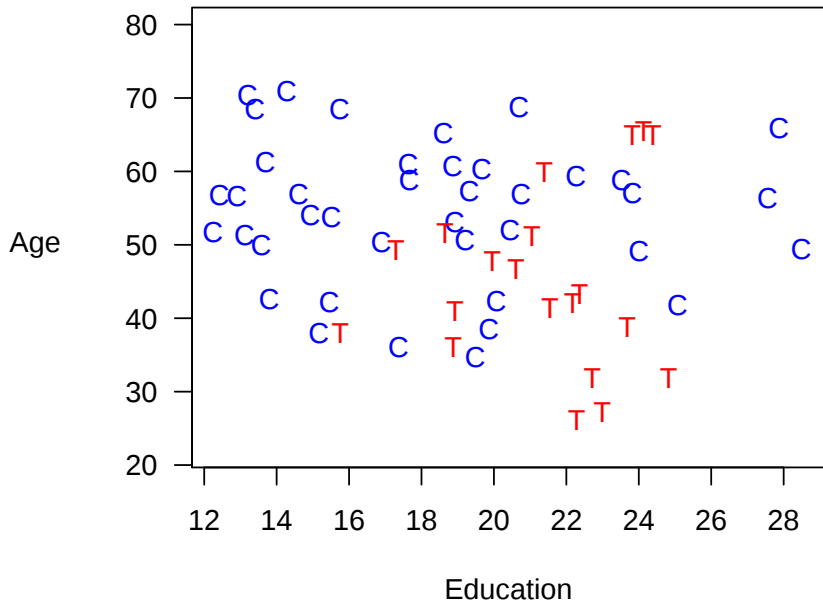
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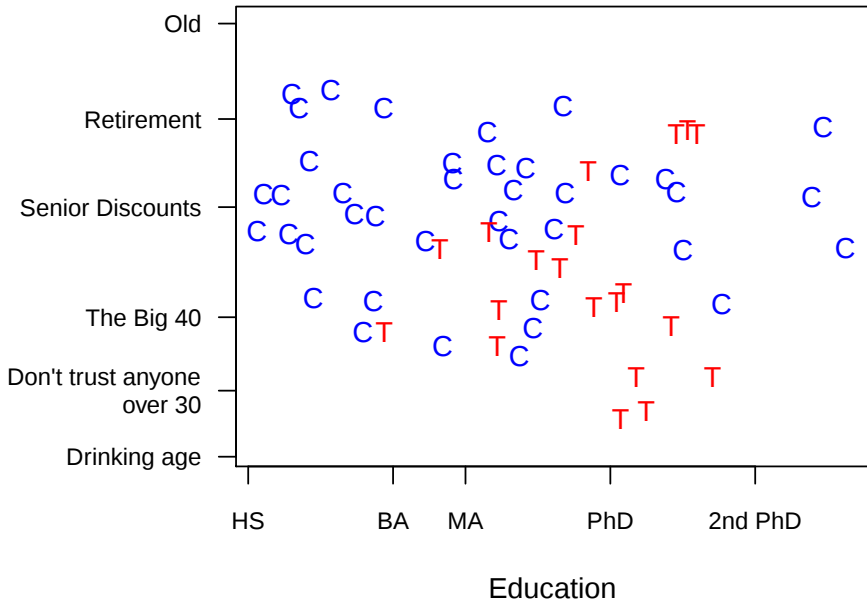
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Coarsened Exact Matching

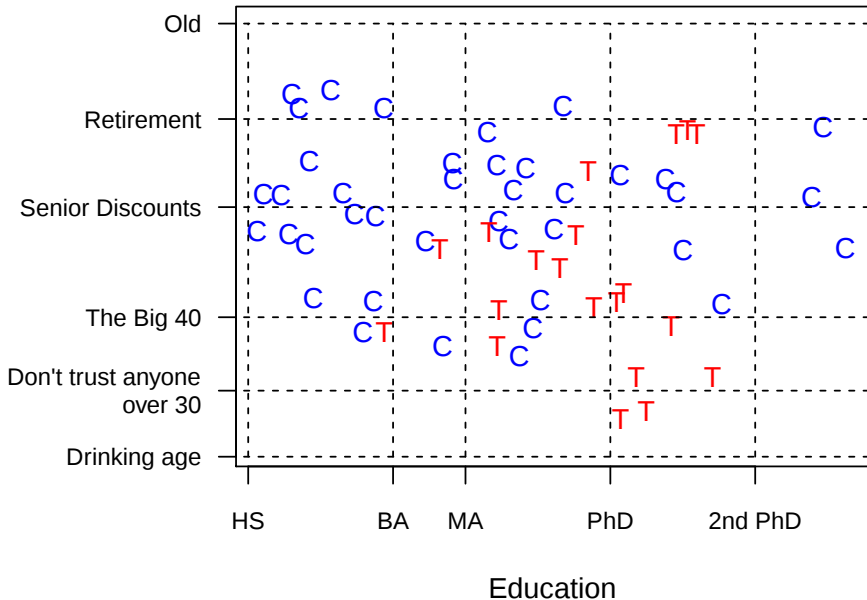
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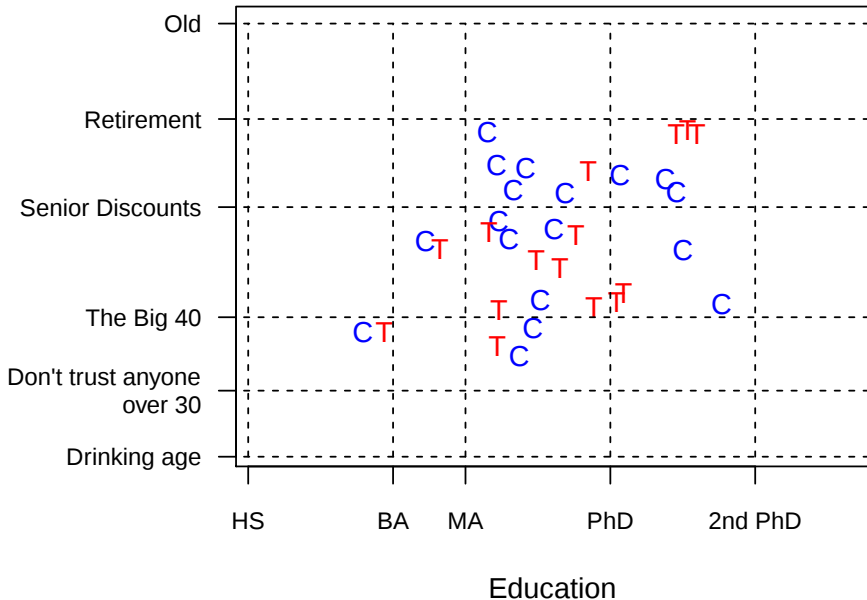
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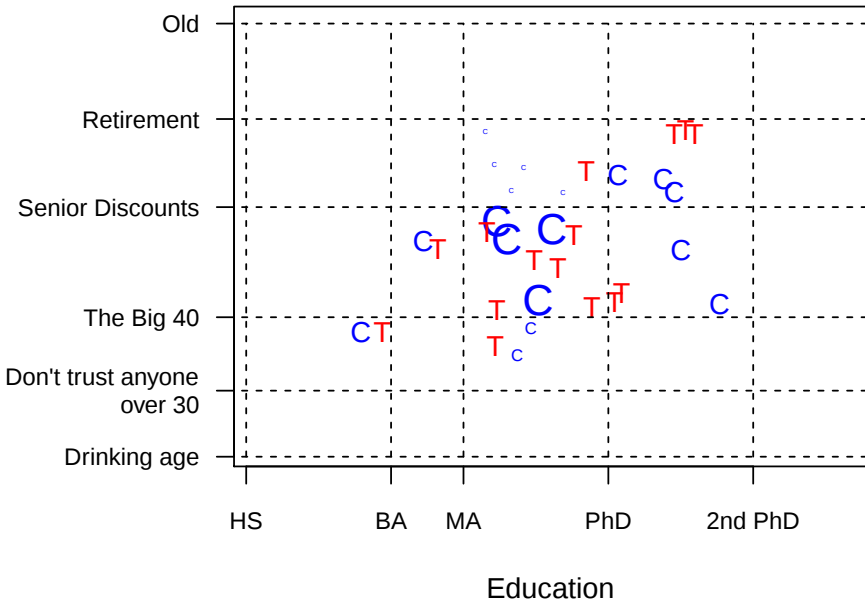
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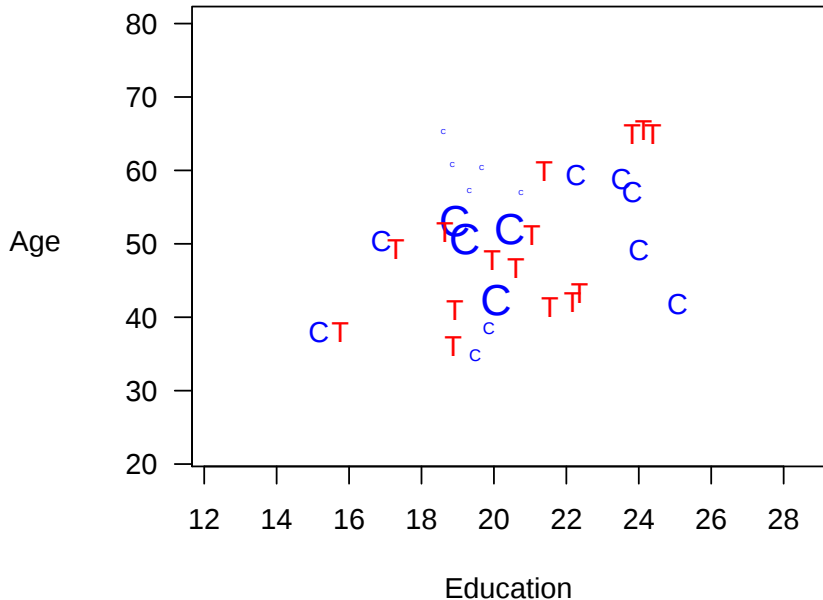
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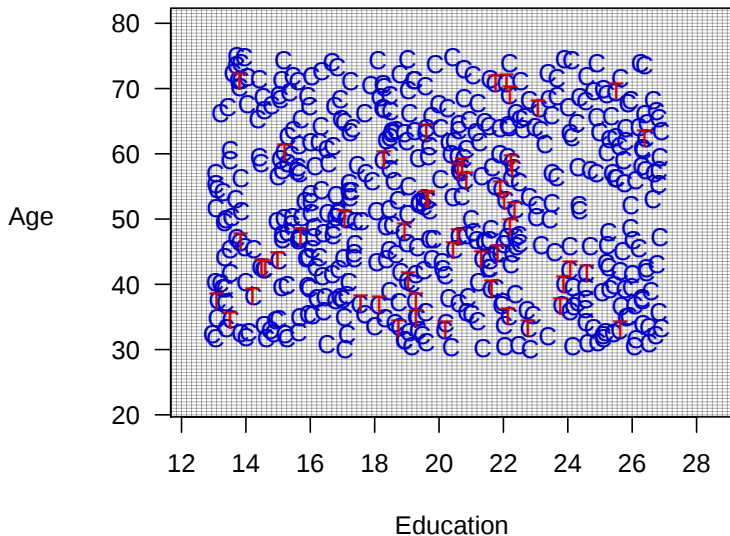


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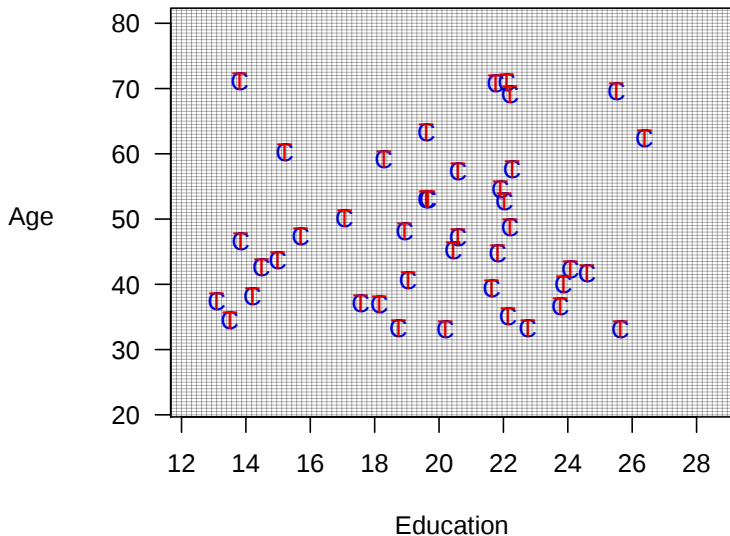


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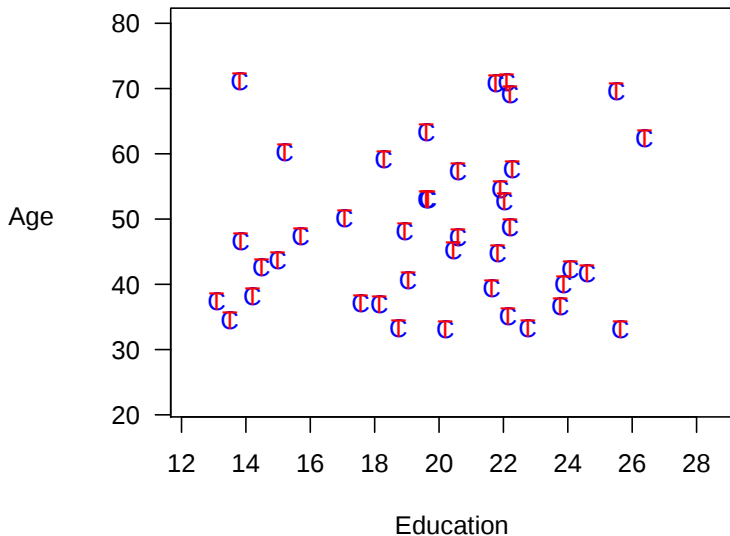
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Method 3: Propensity Score Matching

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(Approximates Completely Randomized Experiment)

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

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- Prune matches if $\text{Distance} > \text{caliper}$

2. Estimation Difference in means or a model

Method 3: Propensity Score Matching

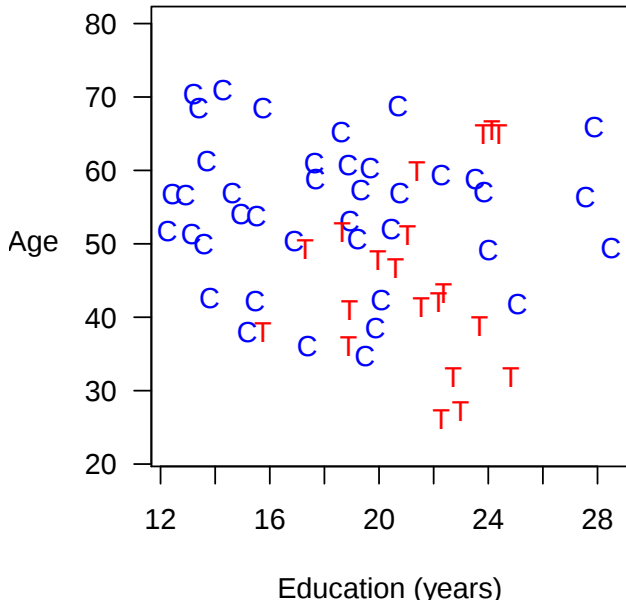
(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)

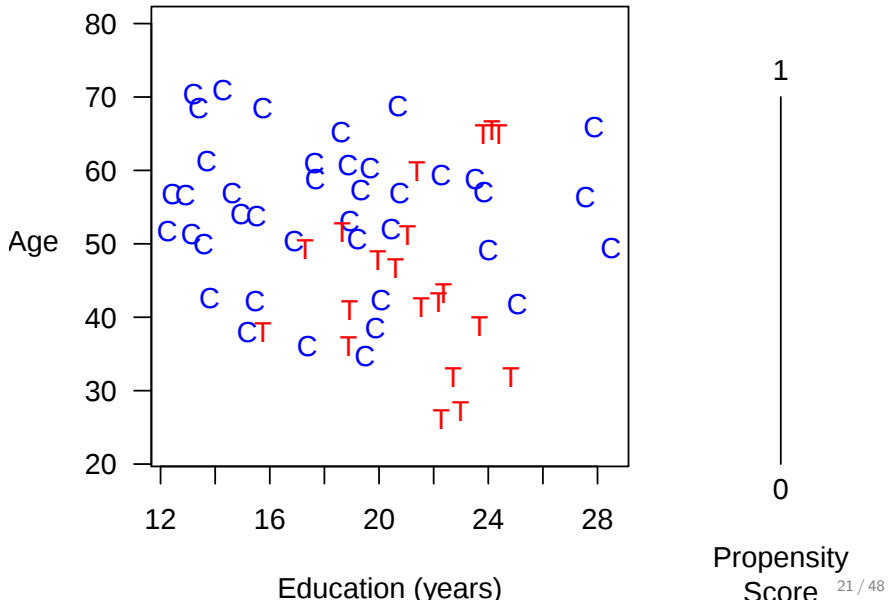
- Reduce k elements of X to scalar
$$\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$$
- $\text{Distance}(X_c, X_t) = |\pi_c - \pi_t|$
- Match each treated unit to the nearest control unit
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- (Many adjustments available to this basic method)

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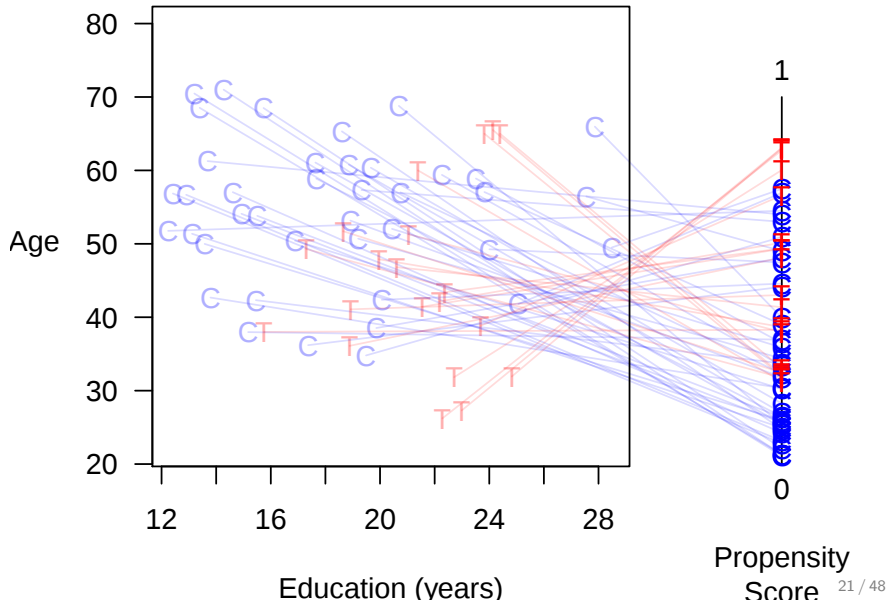
Propensity Score Matching



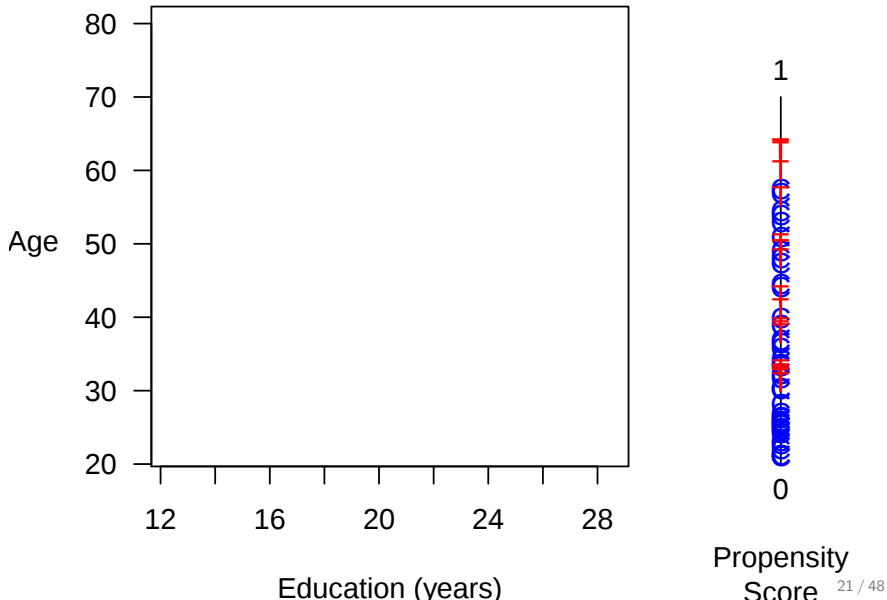
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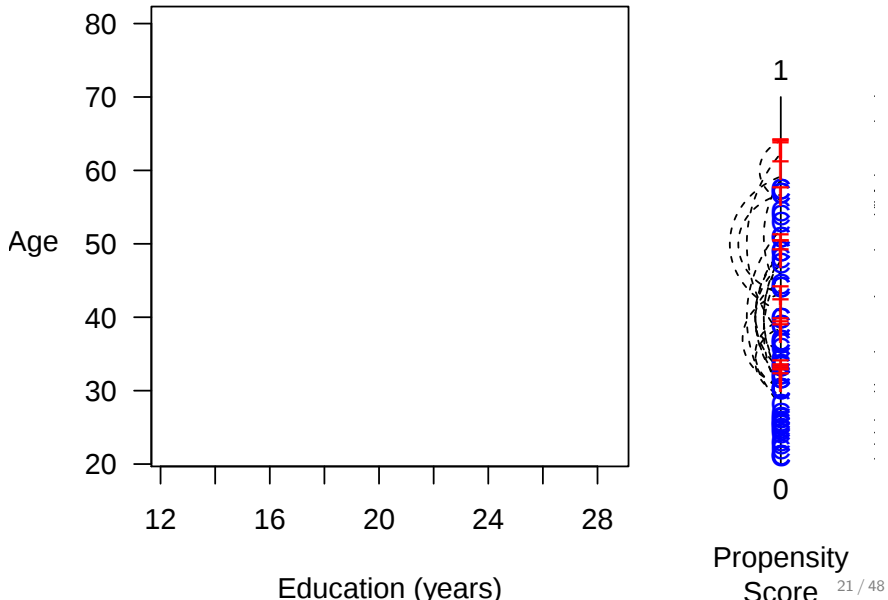
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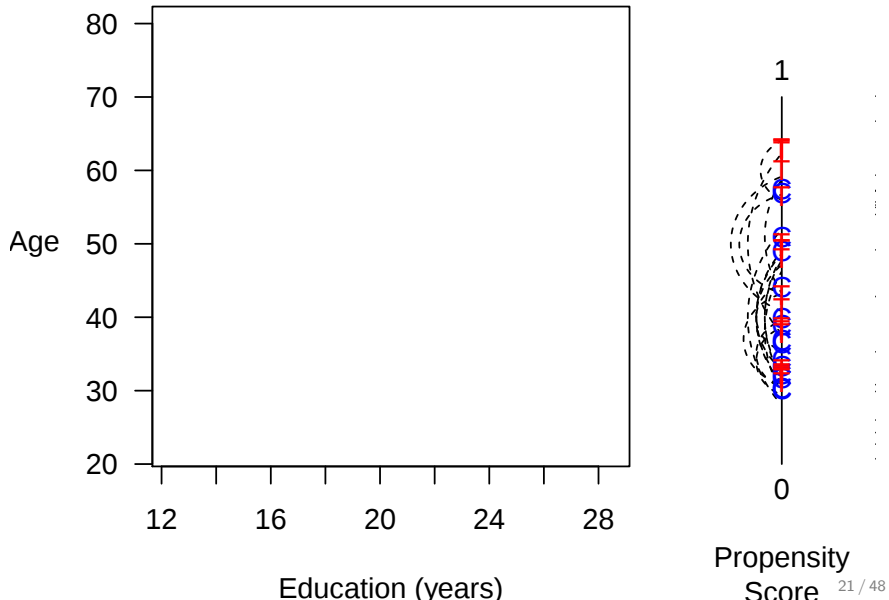
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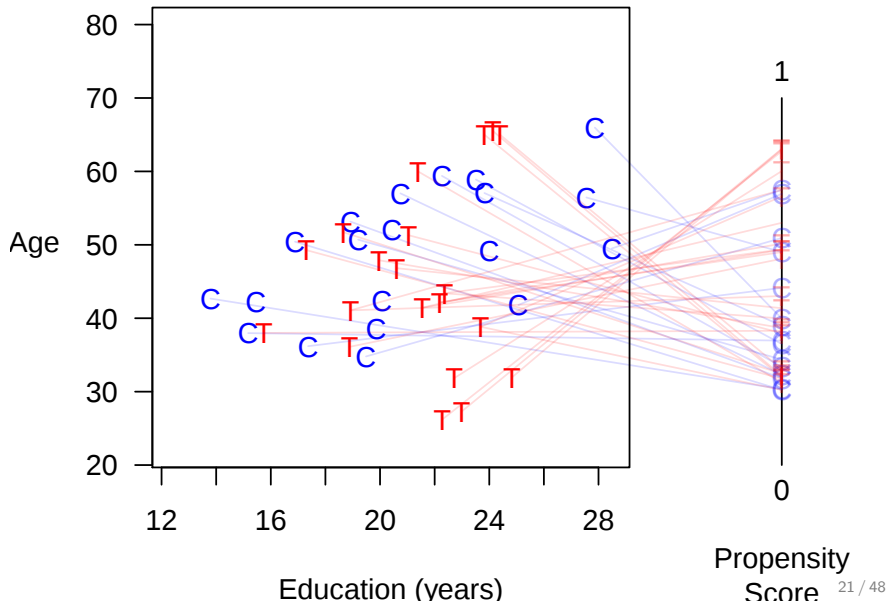
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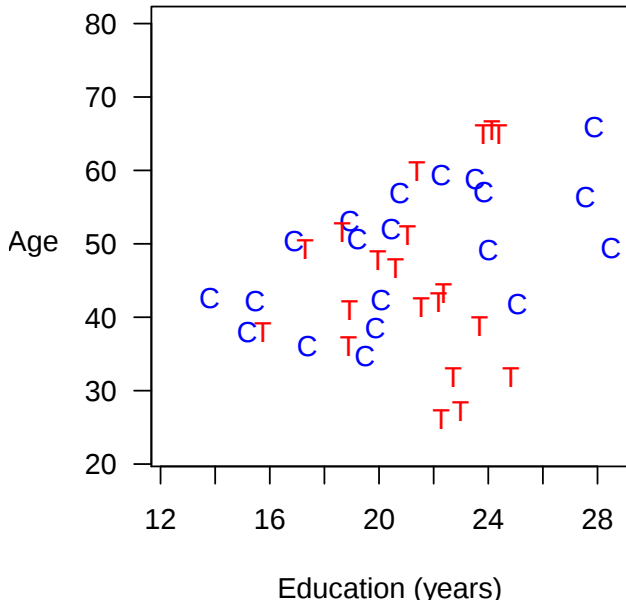
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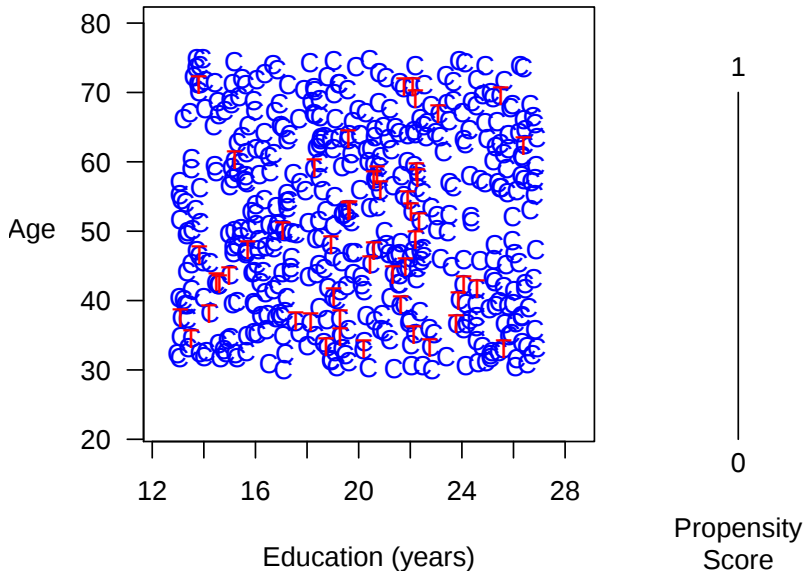


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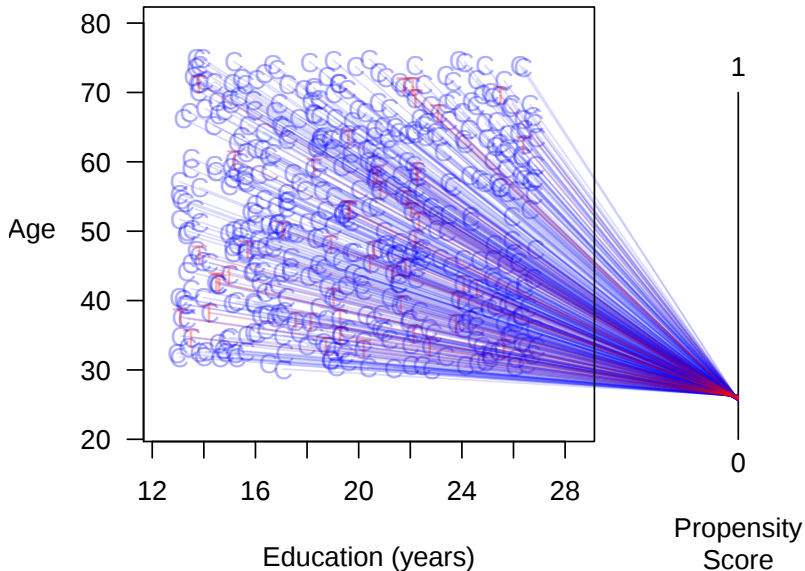


Best Case: Propensity Score Matching

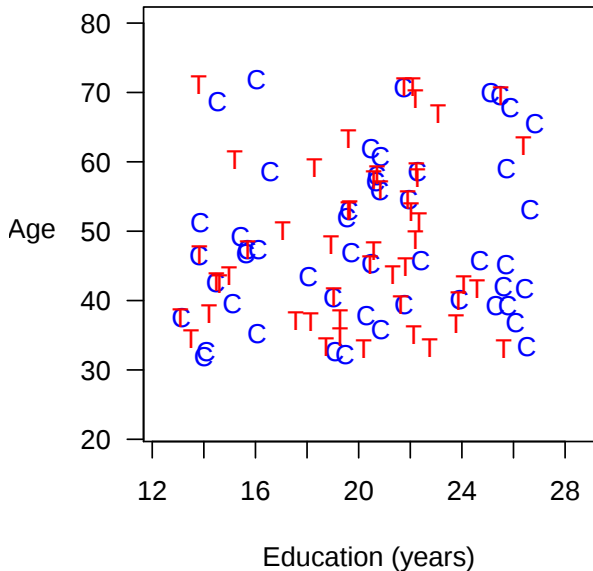
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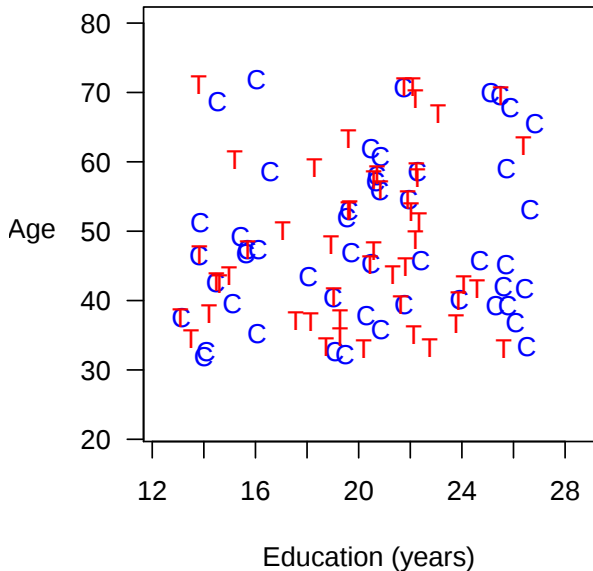
Best Case: Propensity Score Matching



Best Case: Propensity Score Matching



Best Case: Propensity Score Matching is Suboptimal



Background: Random Pruning Increases Imbalance

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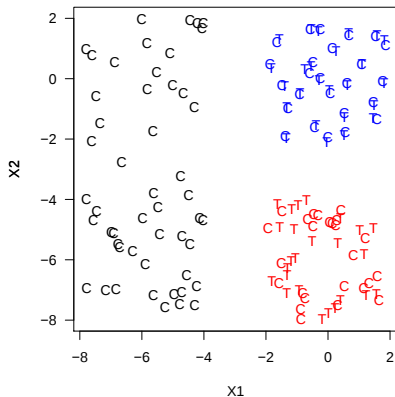
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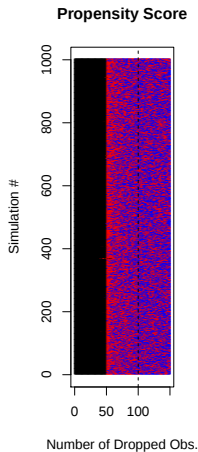
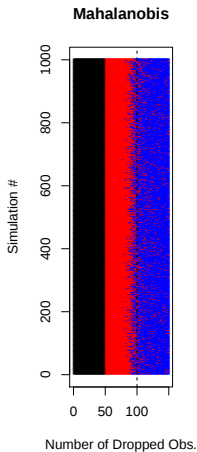
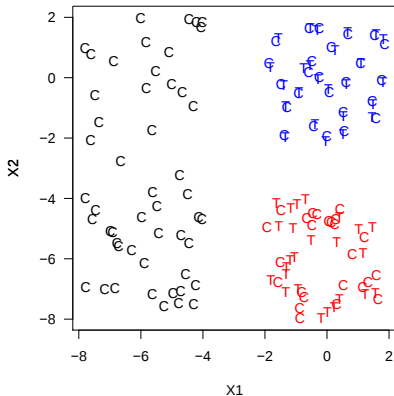
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PSM is Blind Where Other Methods Can See

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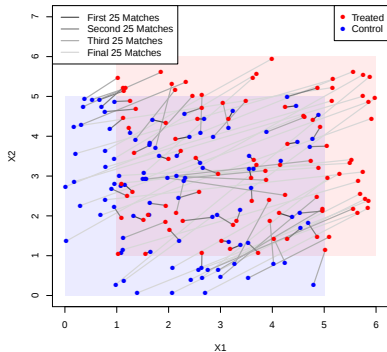


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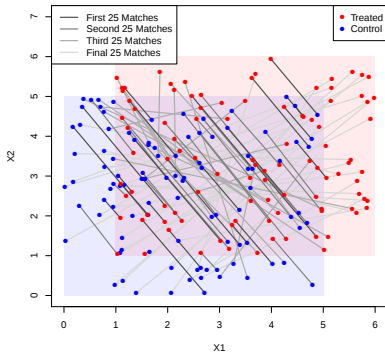


What Does PSM Match?

MDM Matches



PSM Matches

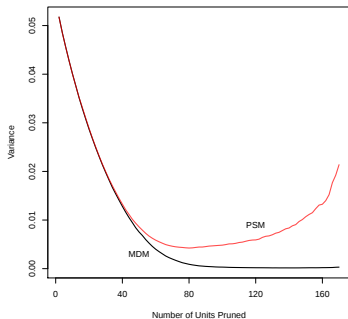


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

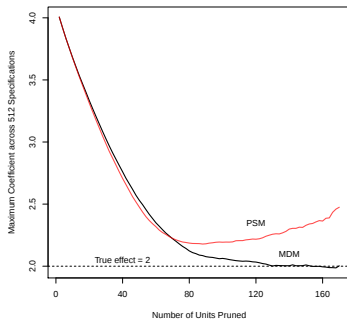
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

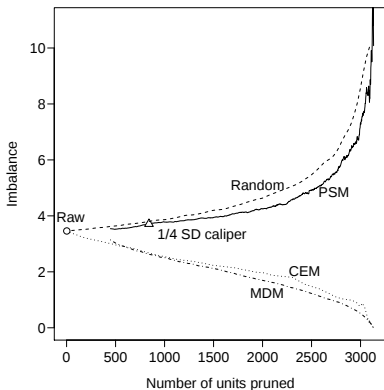


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

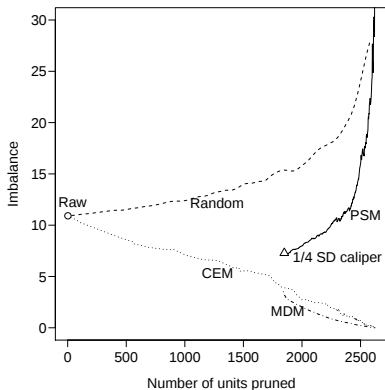
The Propensity Score Paradox in Real Data

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Finkel et al. (JOP, 2012)

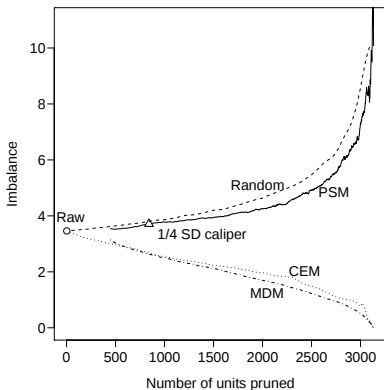


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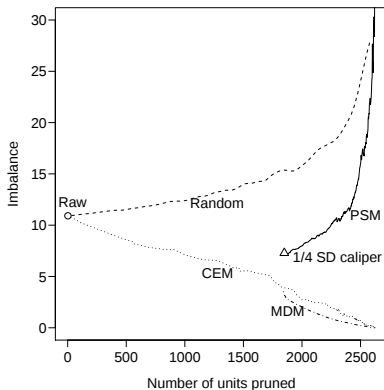


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Similar pattern for > 20 other real data sets we checked

The Matching Frontier

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Frontier = matched dataset with lowest imbalance for each n

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- Average Mahalanobis Distance (average distance from each unit to the closest in the other treatment regime)
- Difference of multivariate histograms (L_1):

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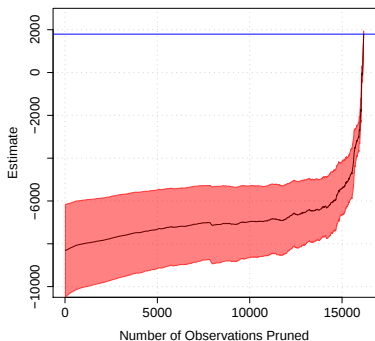
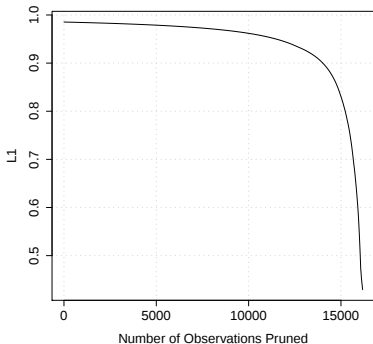
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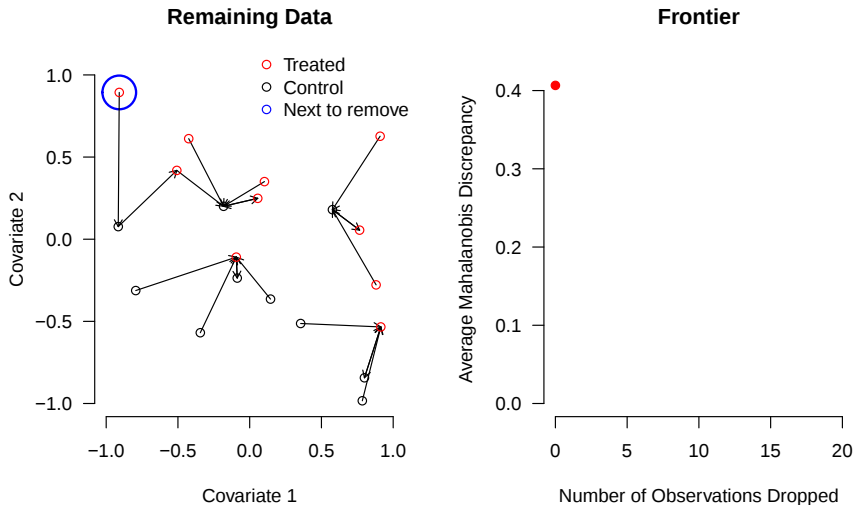
Job Training Data: Frontier and Causal Estimates



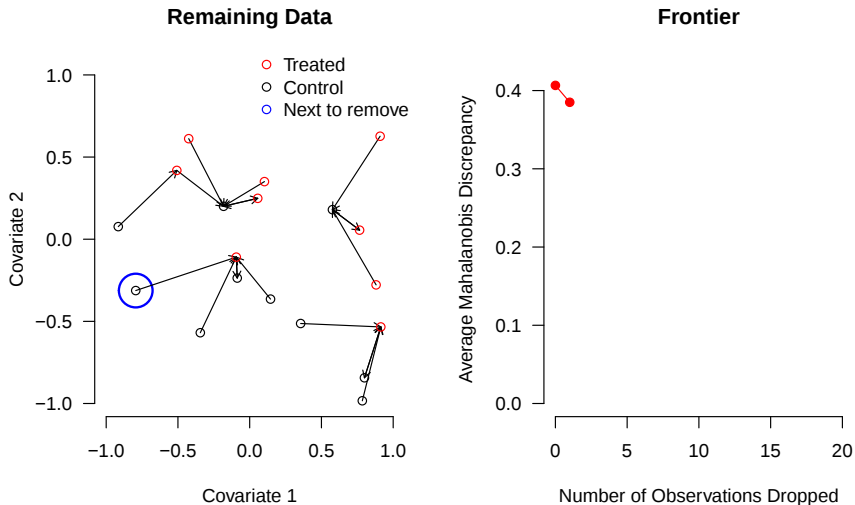
- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after pruning most Cs
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

Constructing the FSATT Mahalanobis Frontier

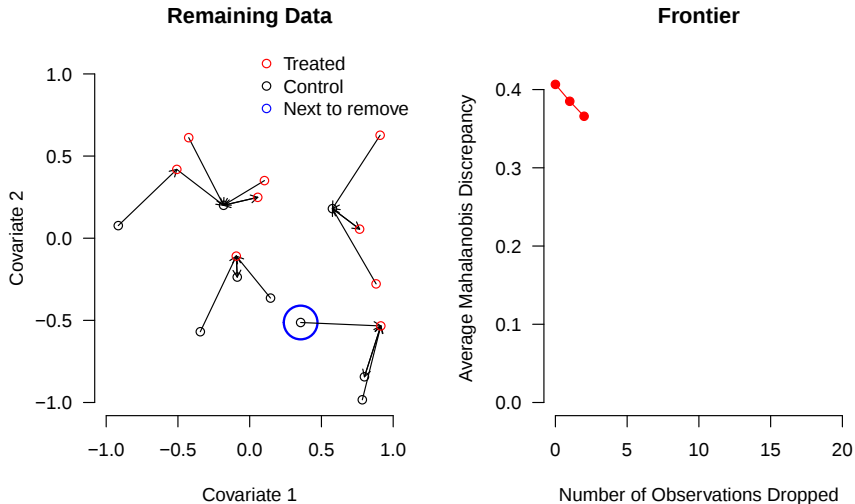
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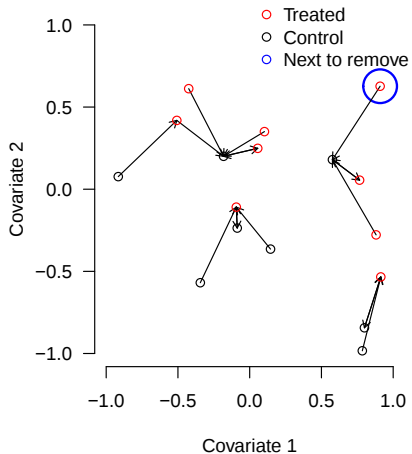


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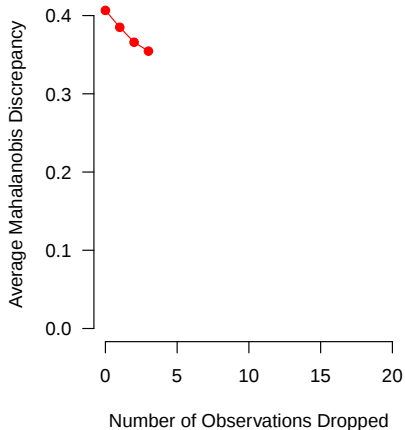


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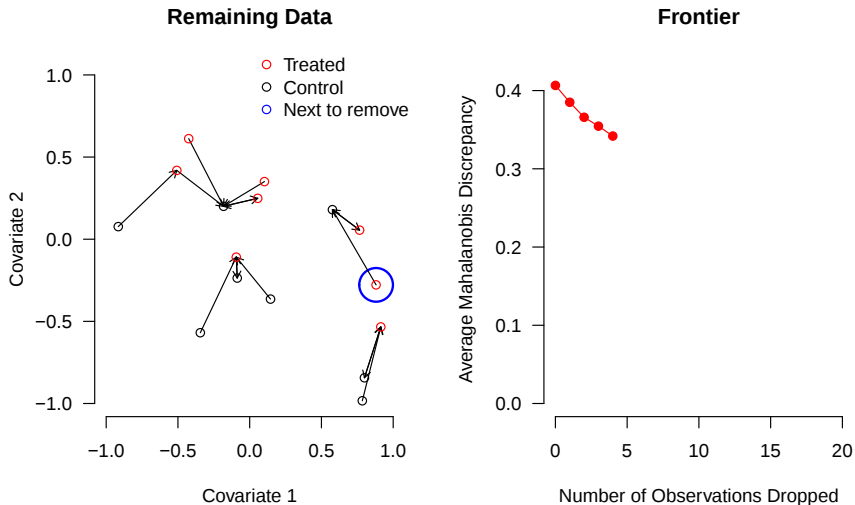
Remaining Data



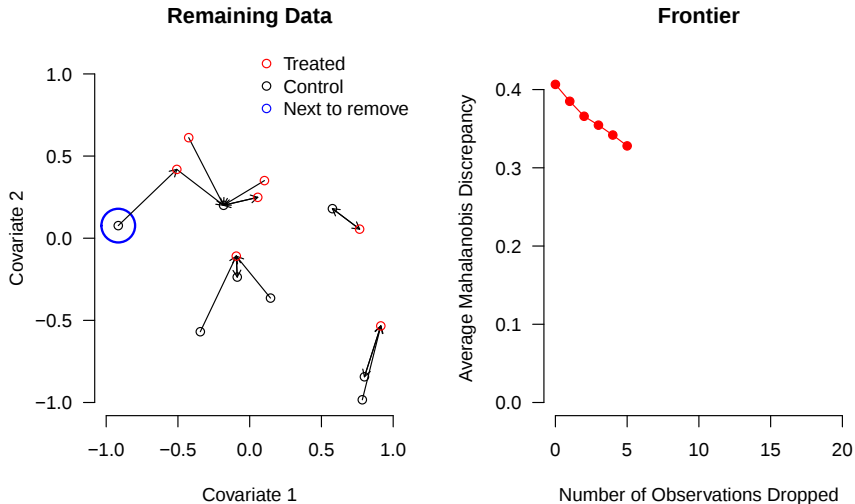
Frontier



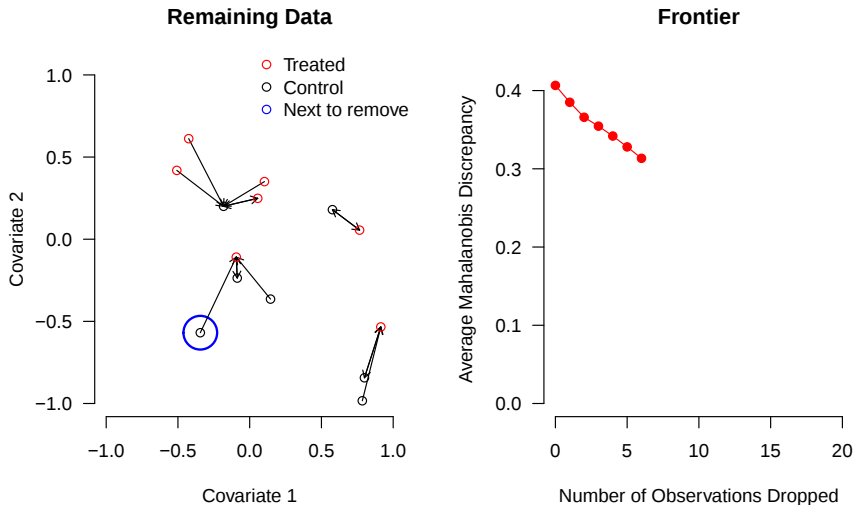
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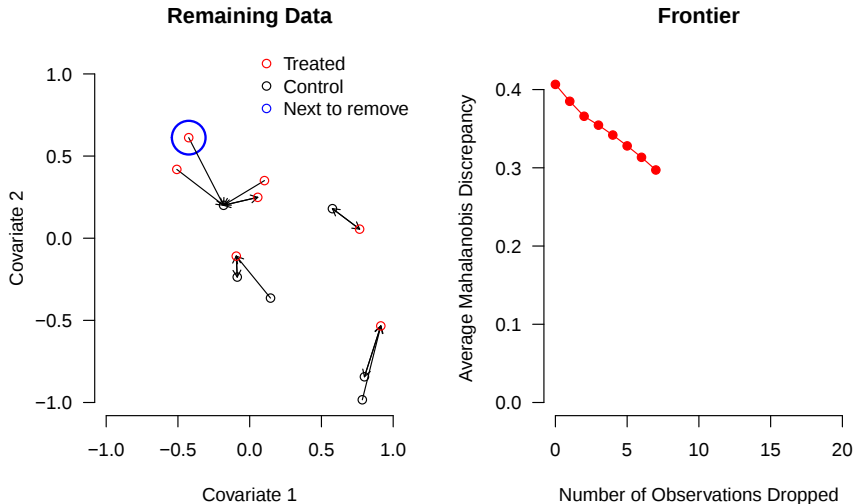
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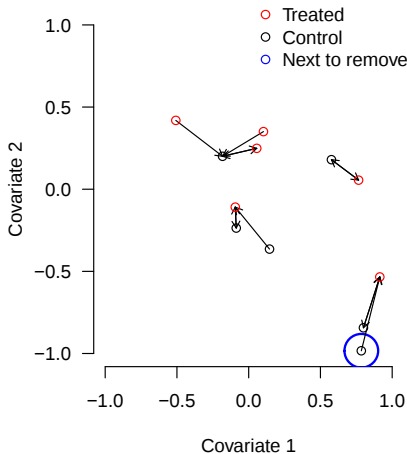


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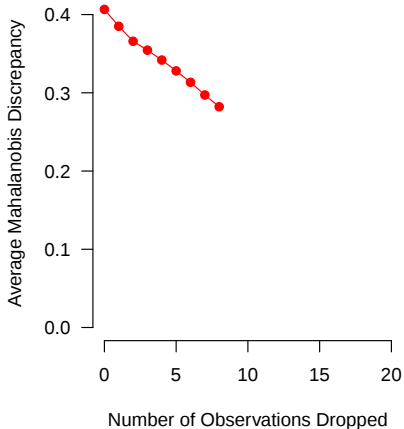


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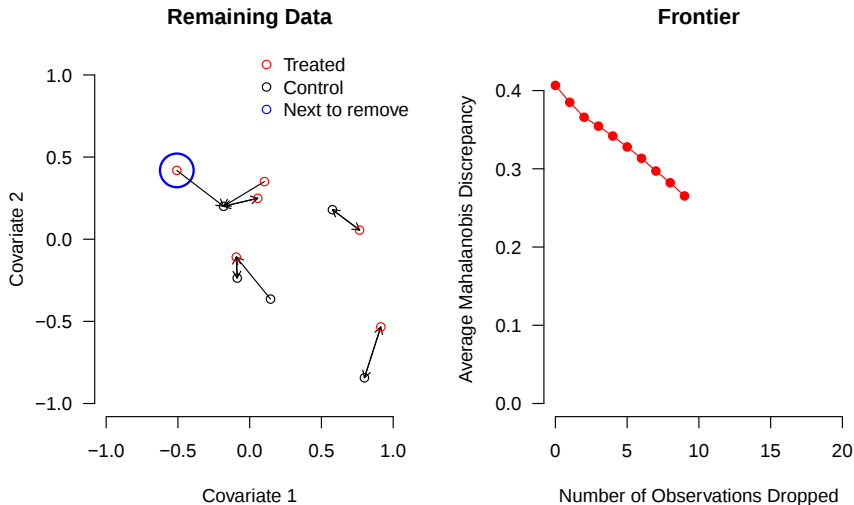
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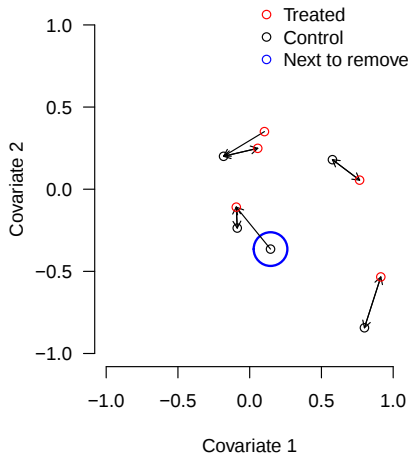


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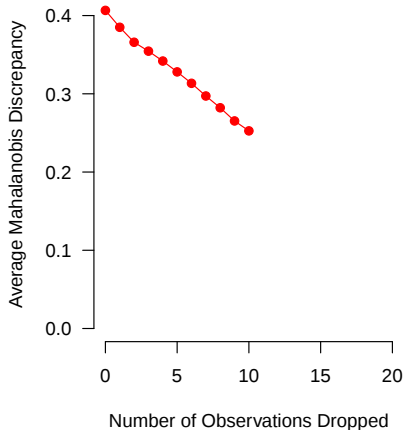


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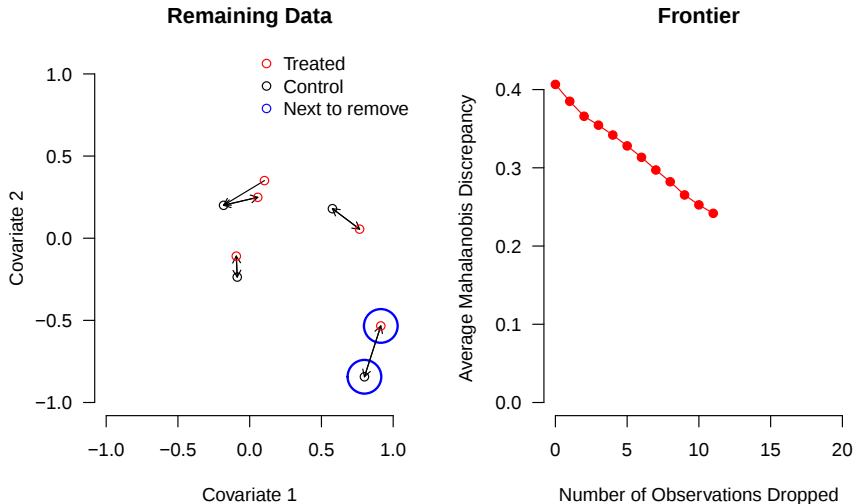
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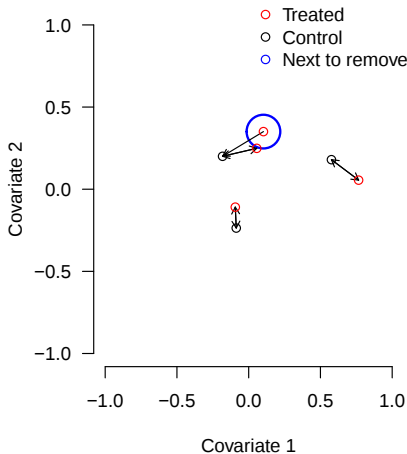


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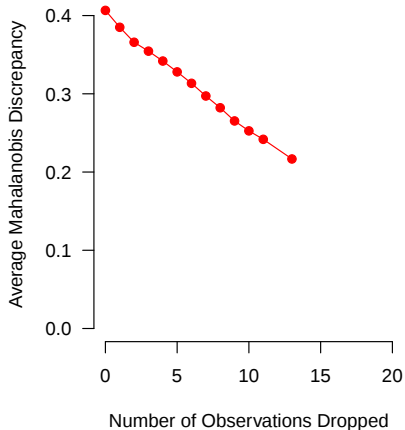


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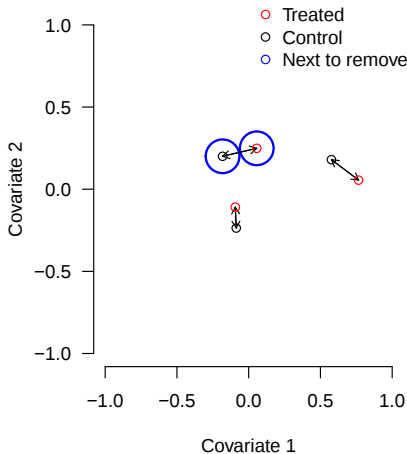


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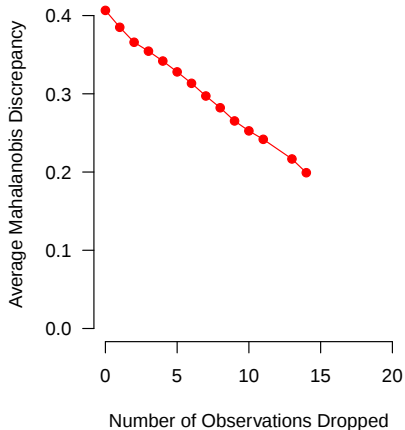


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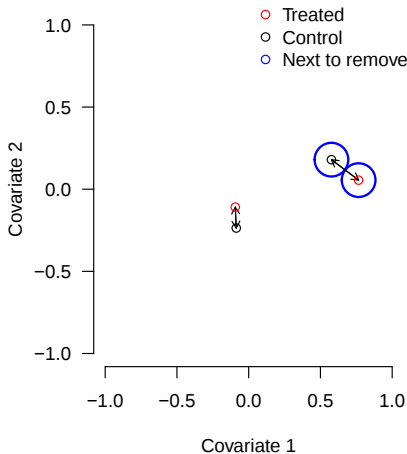


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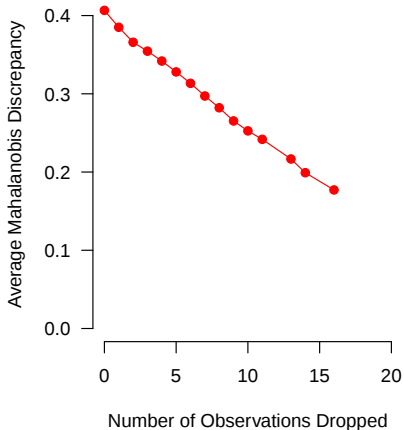


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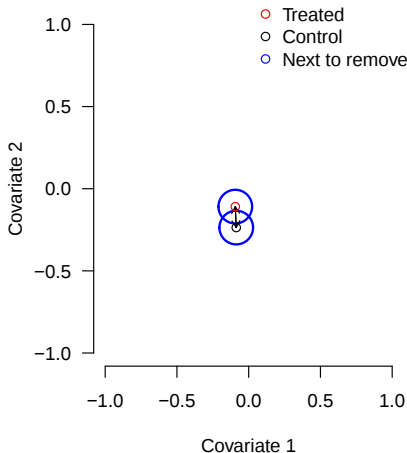


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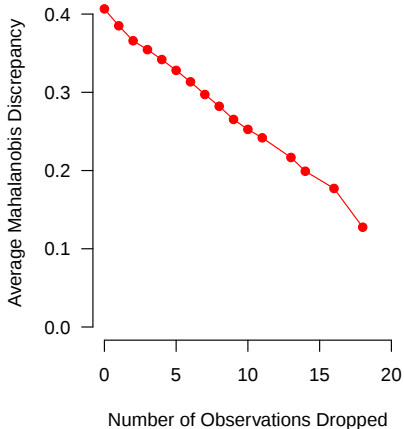


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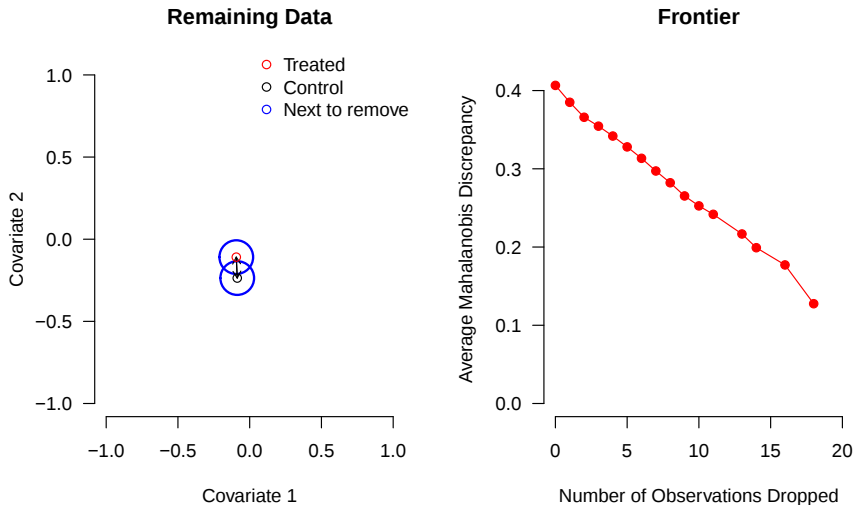
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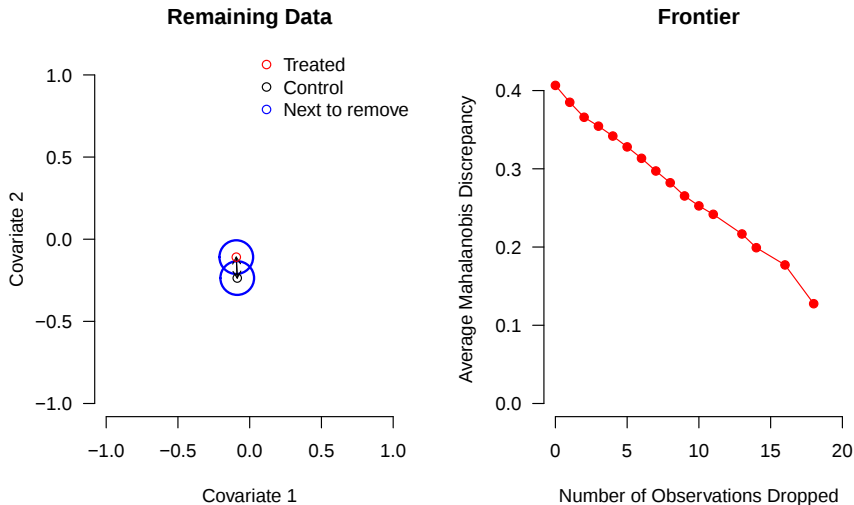


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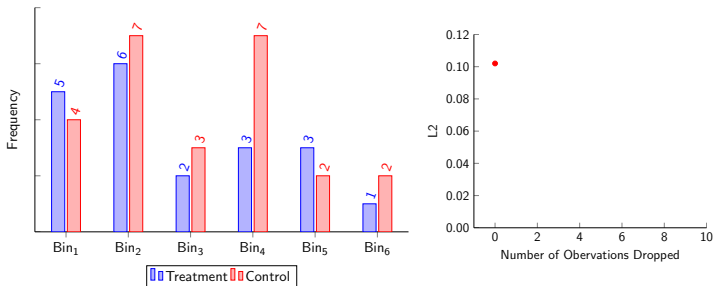
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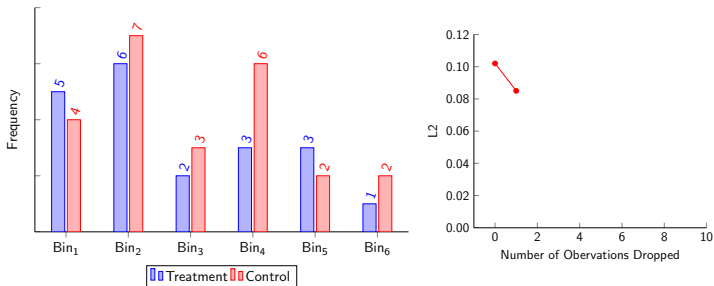


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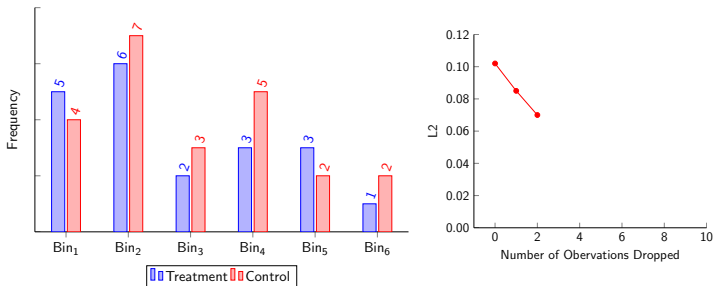
Constructing the L1/L2 SATT Frontier



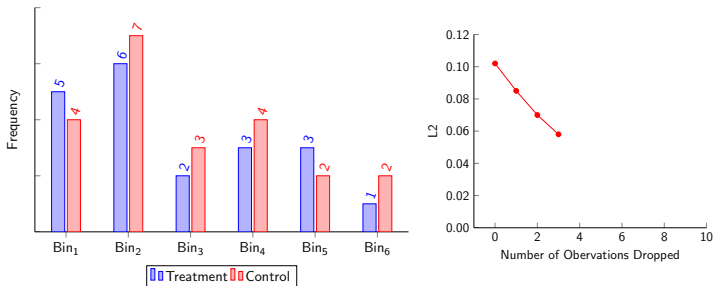
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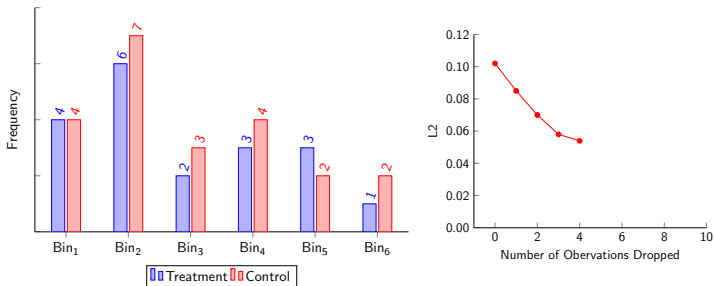
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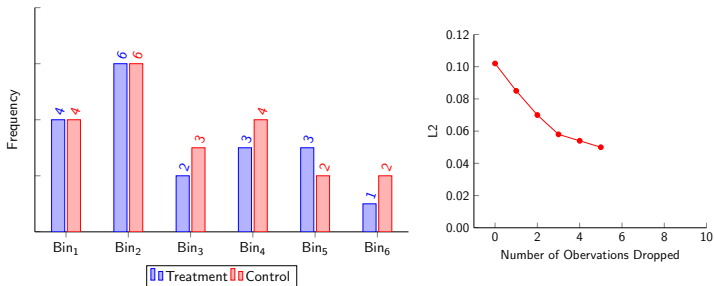
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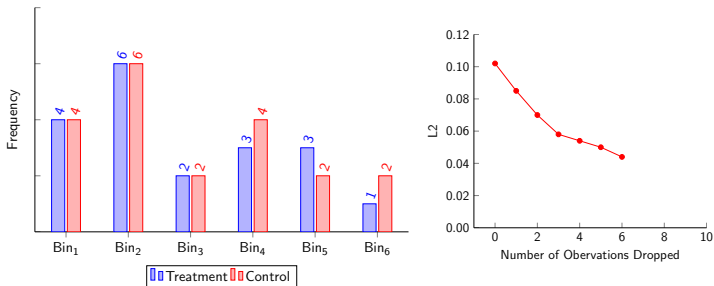
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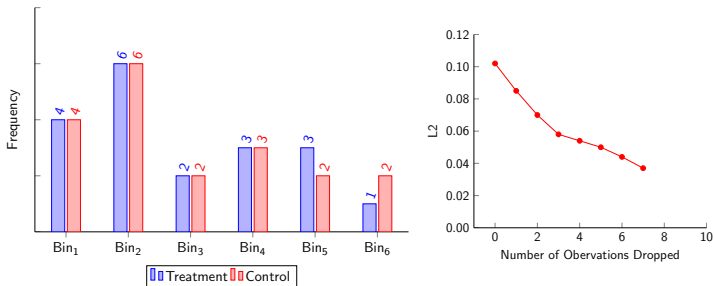
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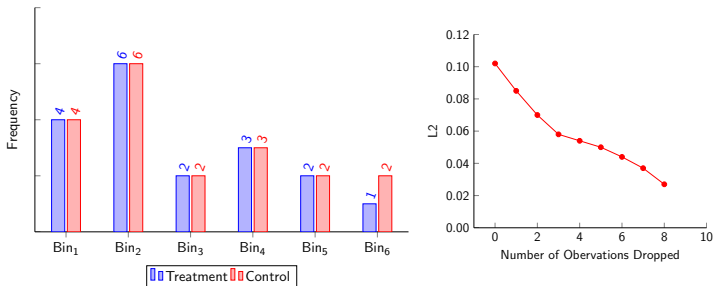
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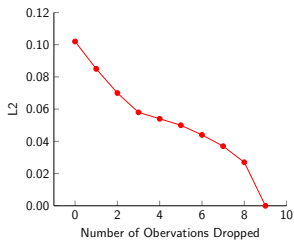
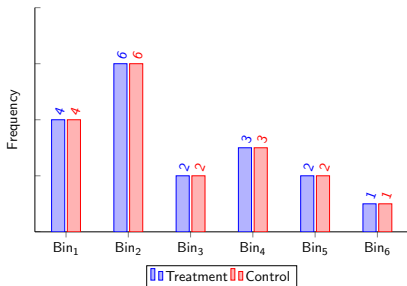
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- **Fundamental problem of causal inference:** $Y_i(0)$ and $Y_i(1)$ are never both observed for any i
- **Observed outcome:** $Y_i = T_i Y_i(1) + (1 - T_i) Y_i(0)$
- **Pretreatment control variables:** X_i (k -vector)
- **Simplification we will use:** focus on TE for treated units; so $Y_i(0)$ is unobserved; $Y_i(1) = Y_i$

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- Other QOIs: PATT, FPATT; SATE, FSATE; PATE, FPATE

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