Advanced Quantitative Research Methodology, Lecture Notes: Matching Methods for Causal Inference[1]

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  - ⇝ "The Balance-Sample Size Frontier in Matching Methods for Causal Inference" (Gary King, Christopher Lucas and Richard Nielsen)

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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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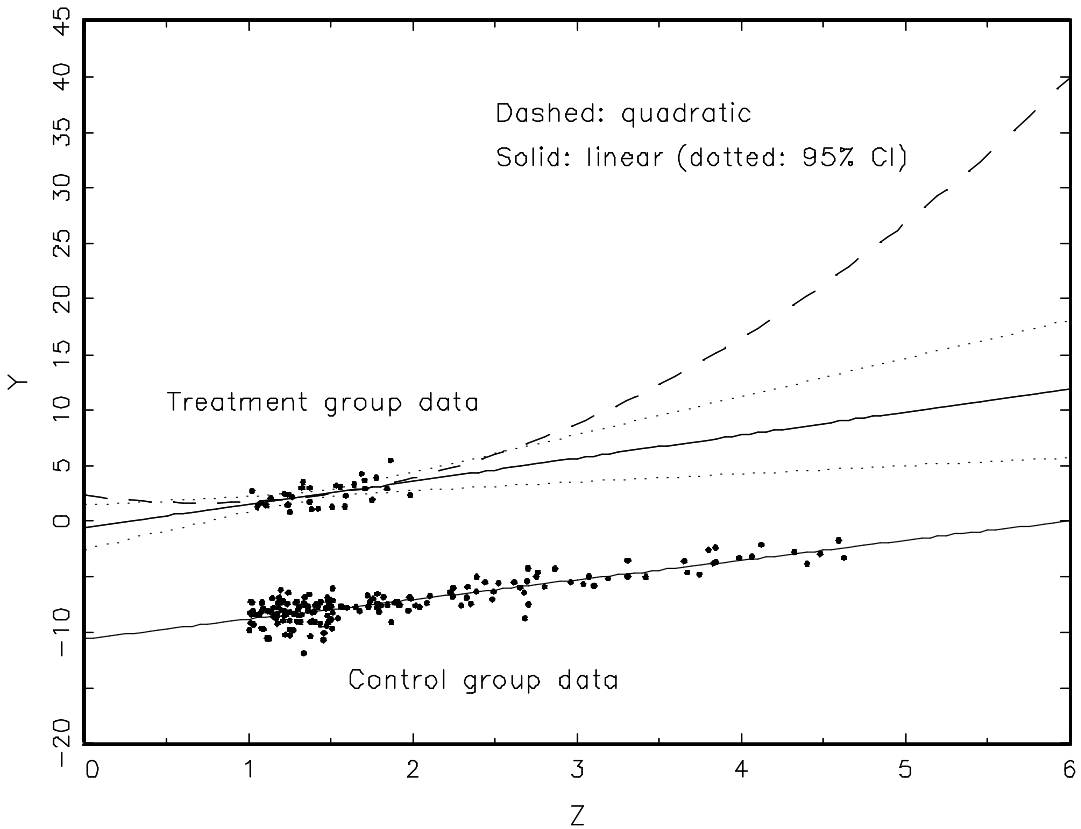

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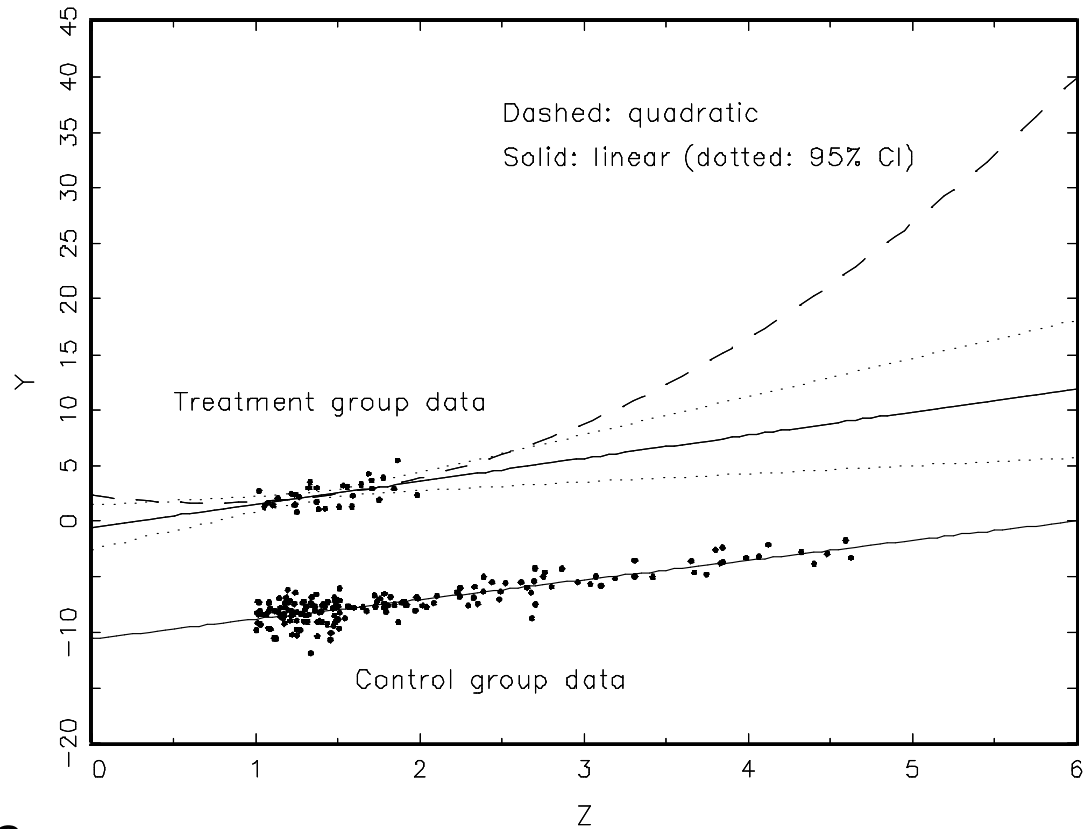

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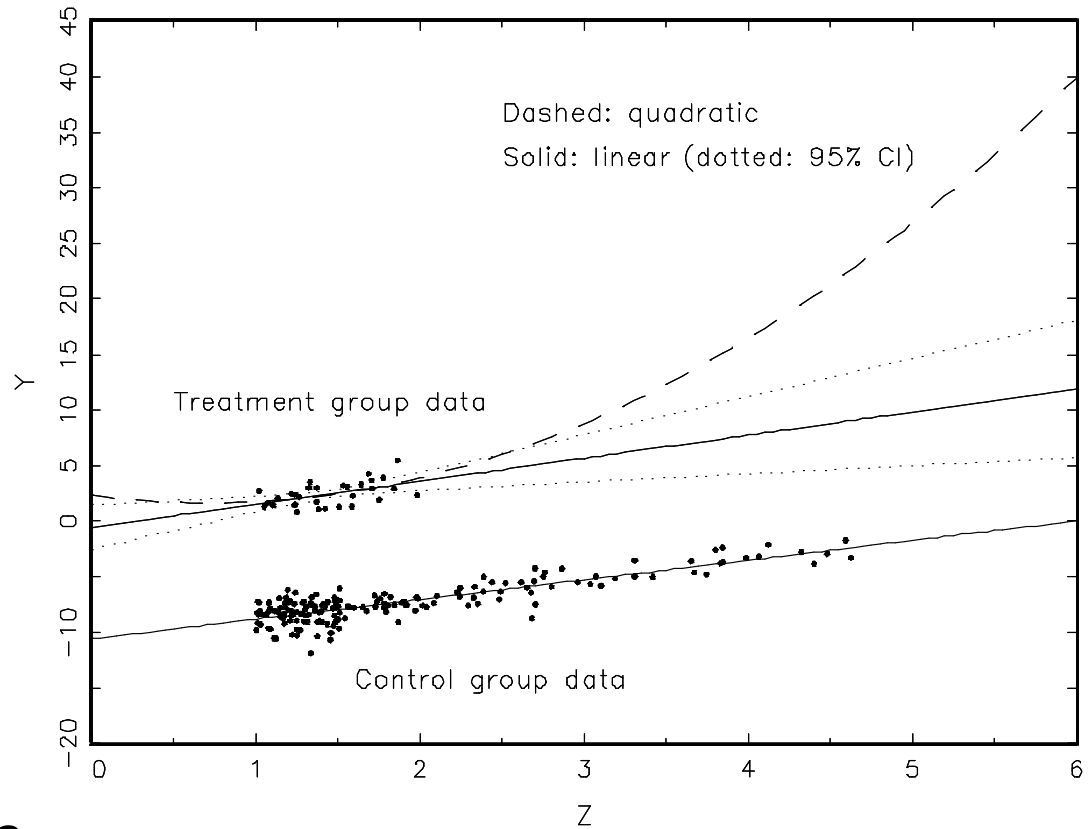

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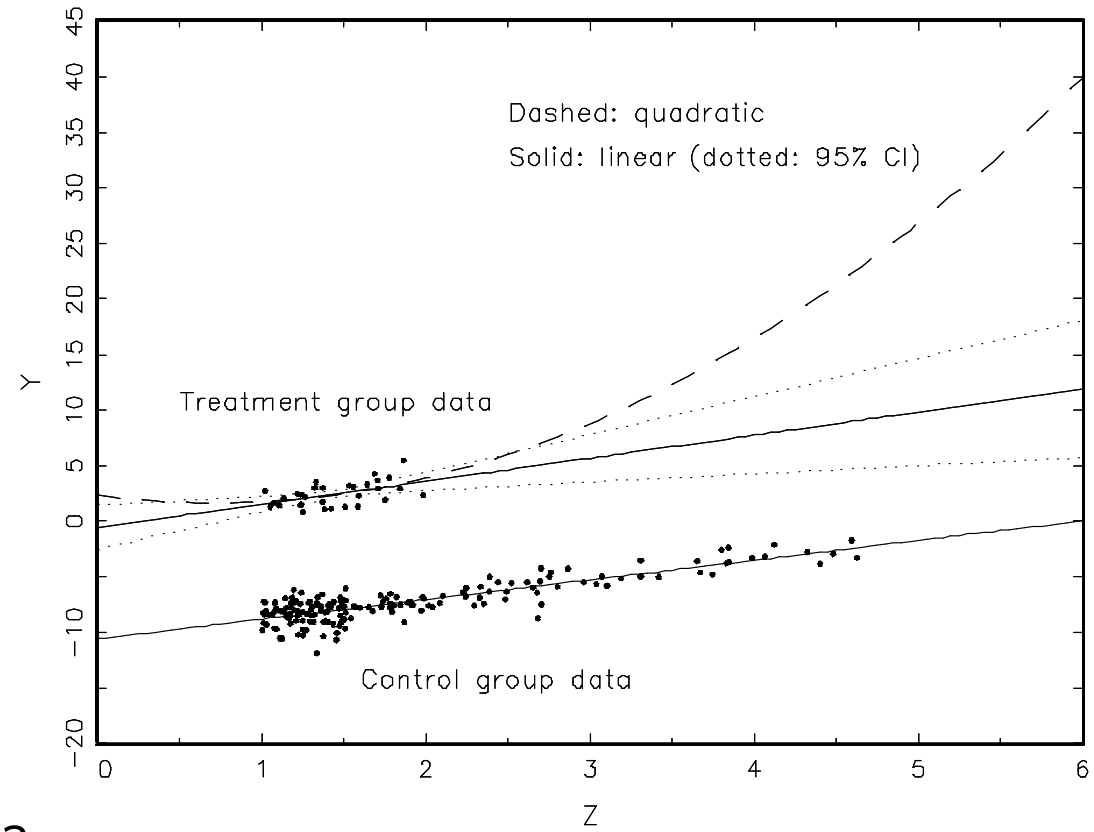

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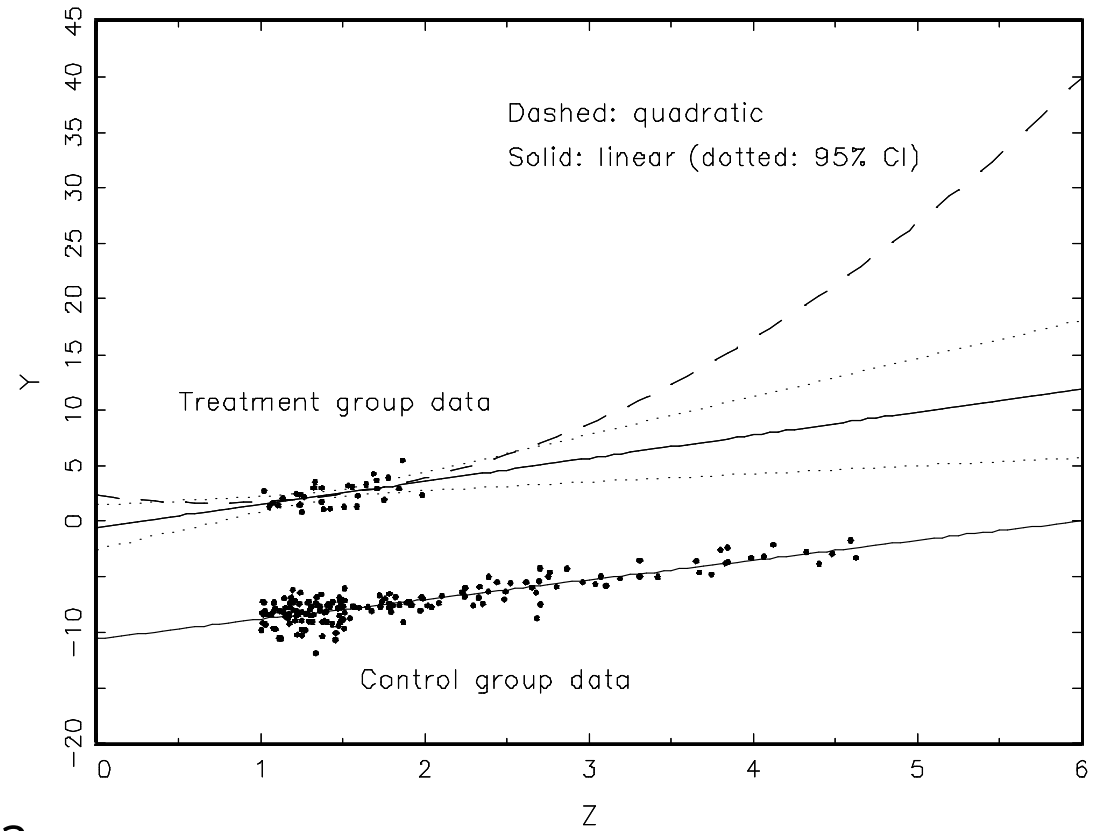

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- Model remaining imbalance (as you would w/o matching)

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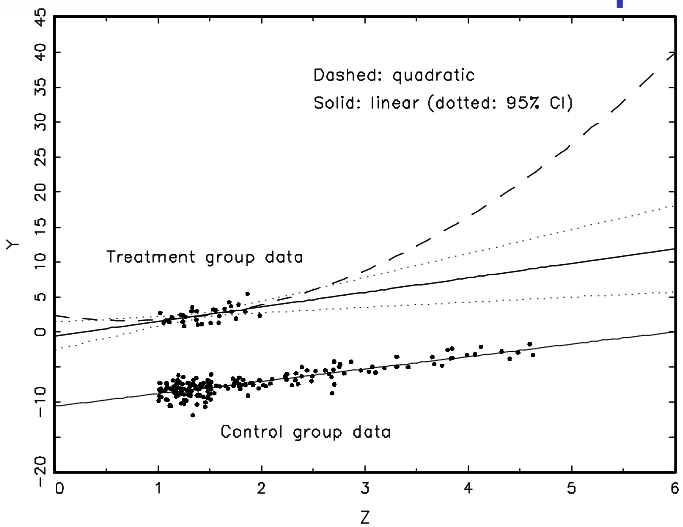

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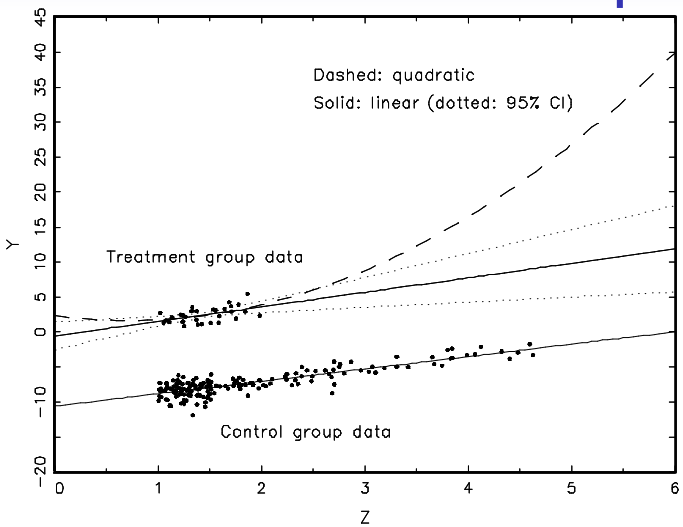

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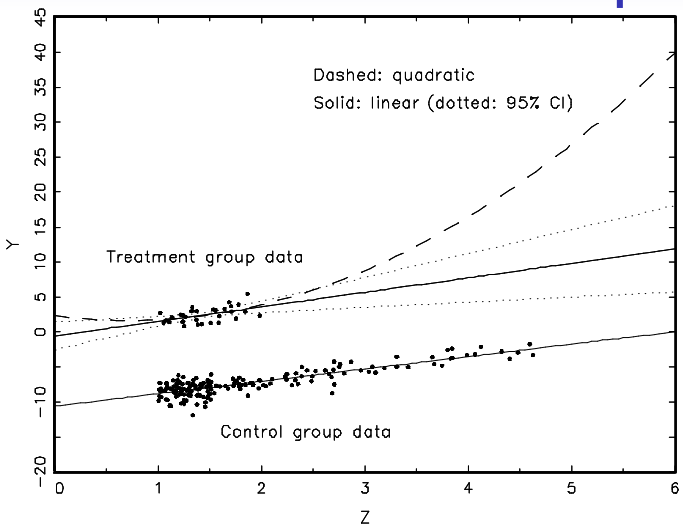

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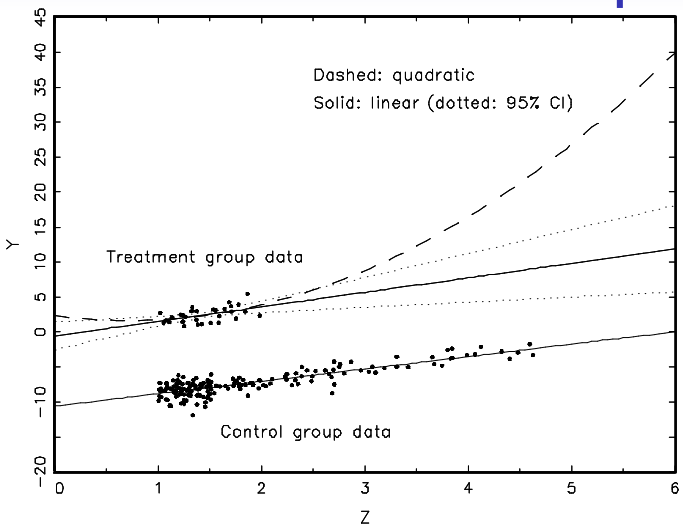

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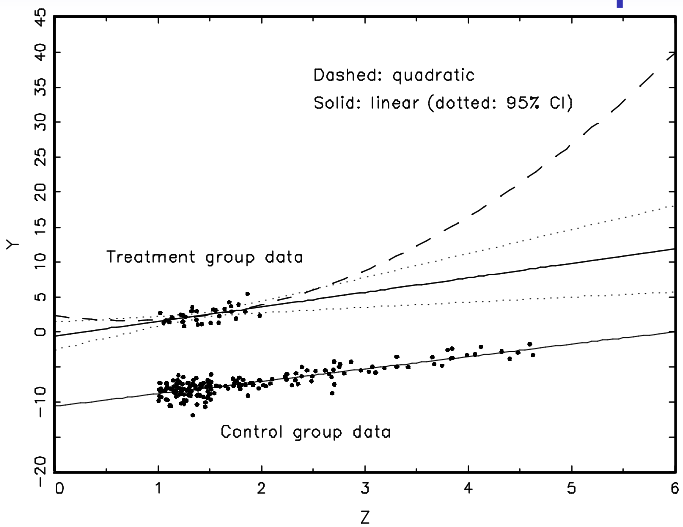

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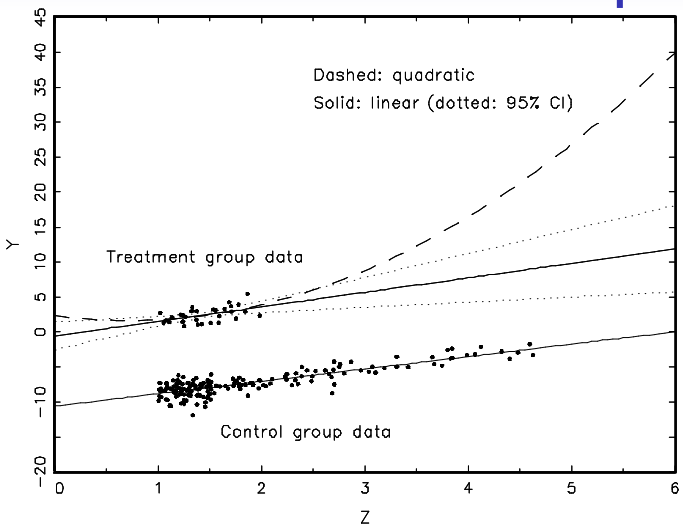

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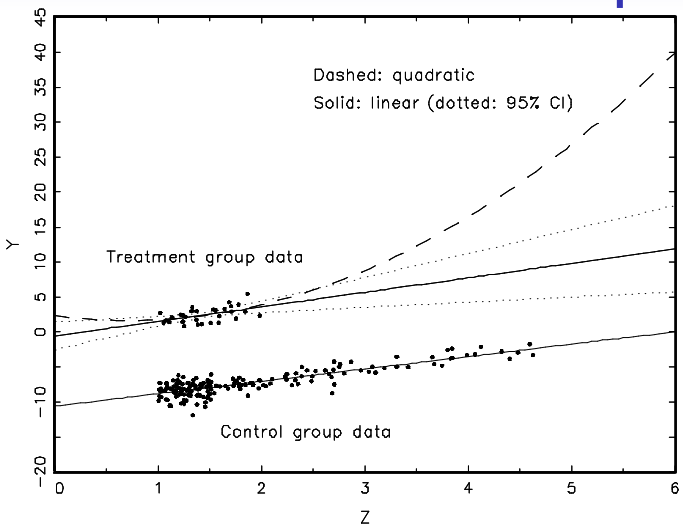

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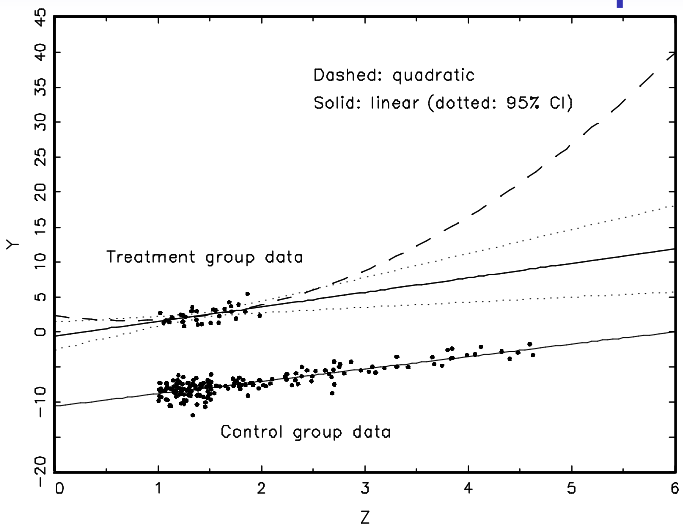

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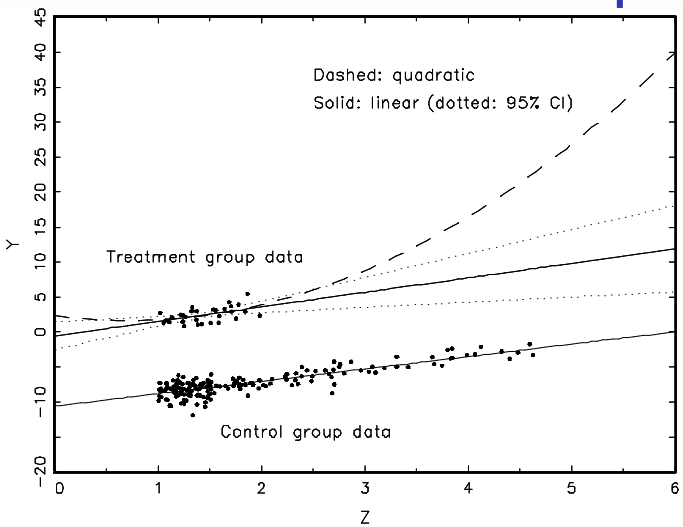

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  4. Easiest: Coarsened Exact Matching, no separate step needed

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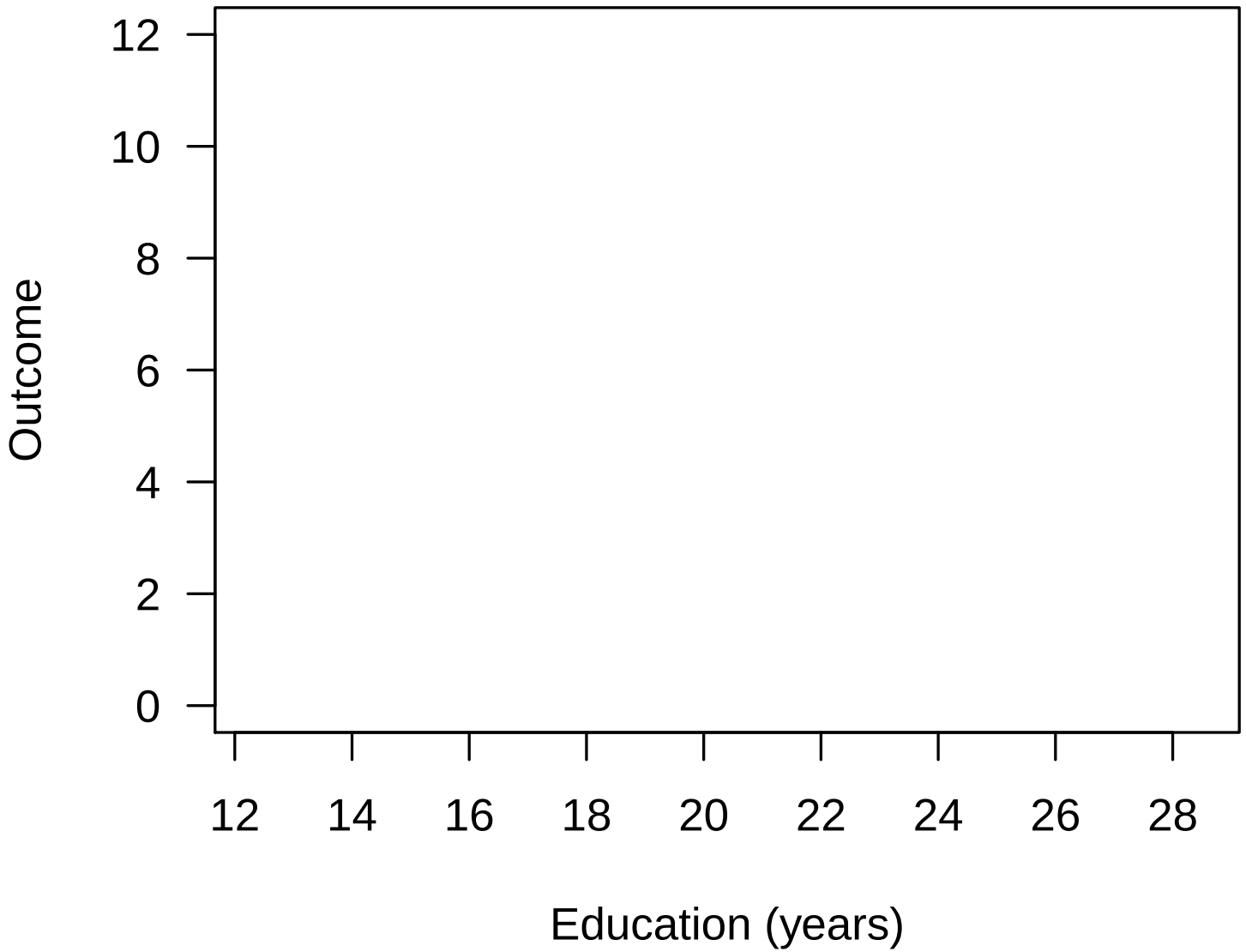

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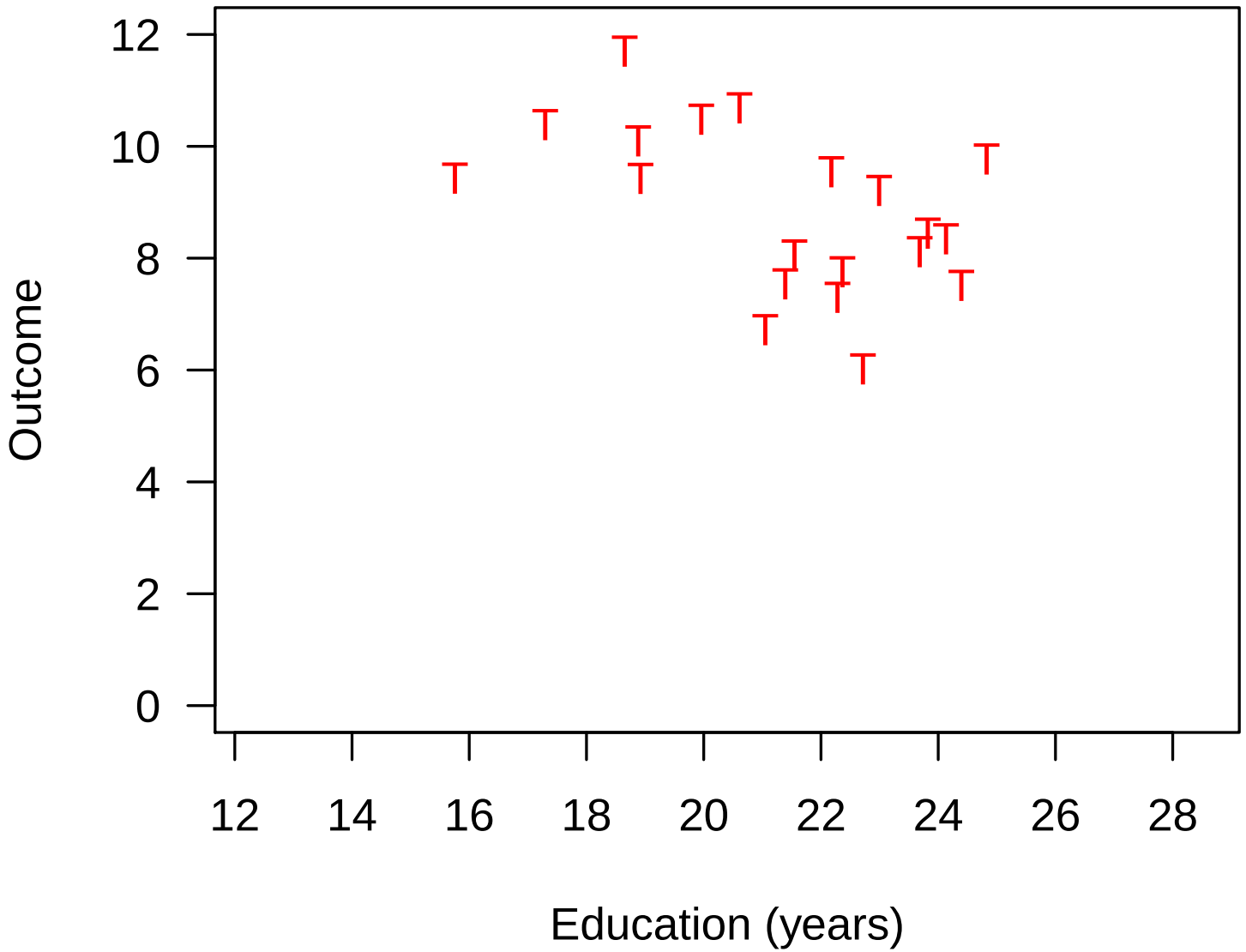

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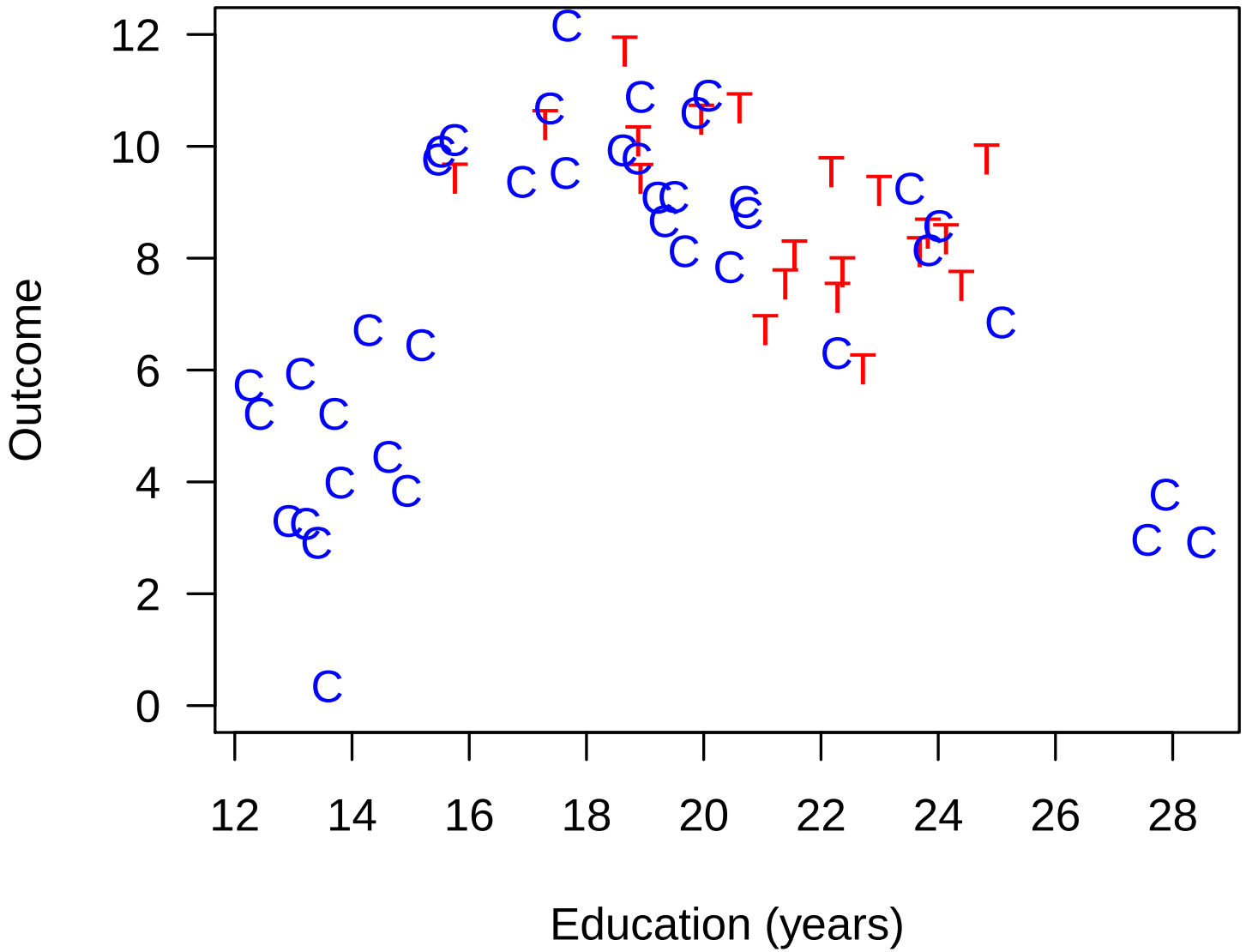

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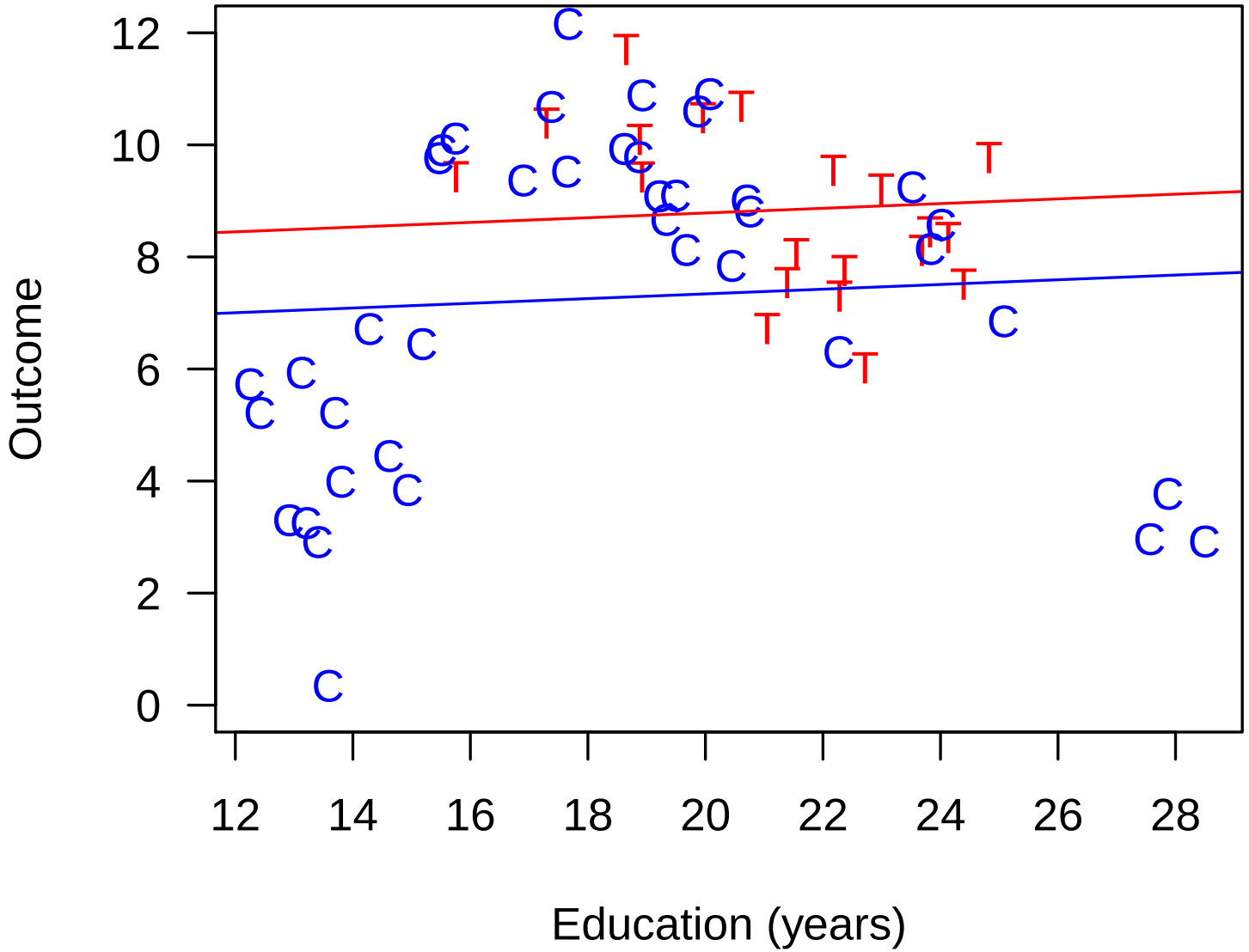

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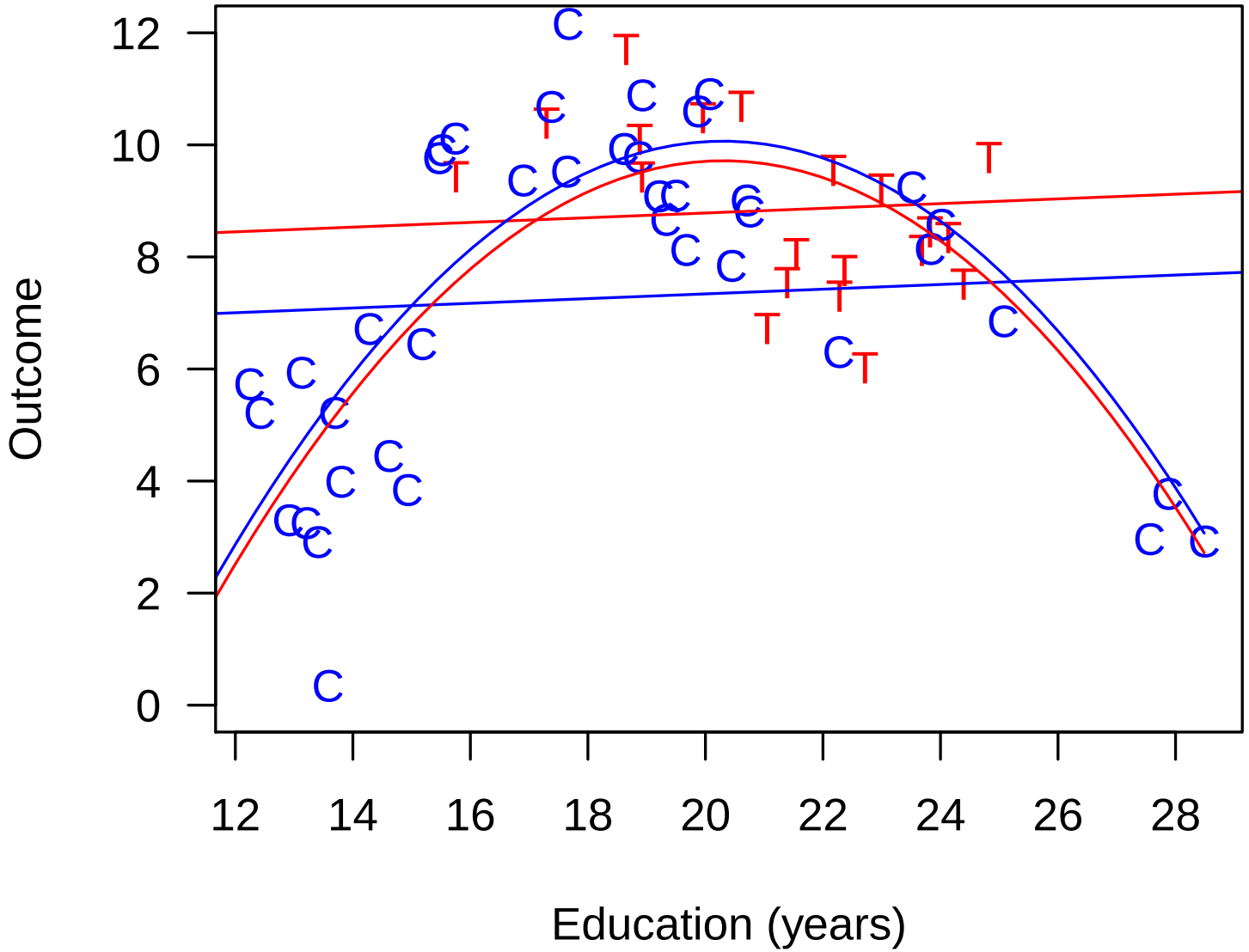

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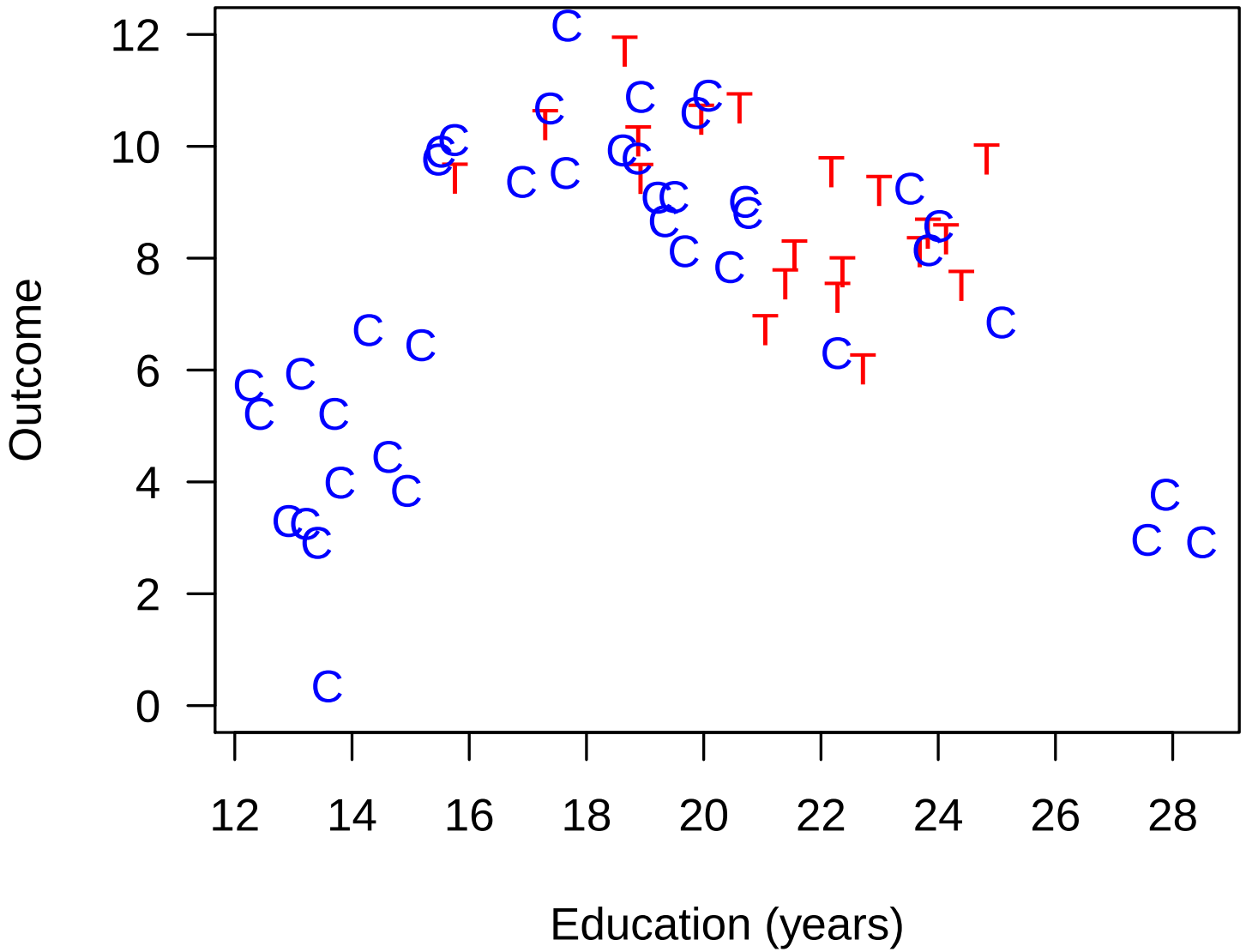

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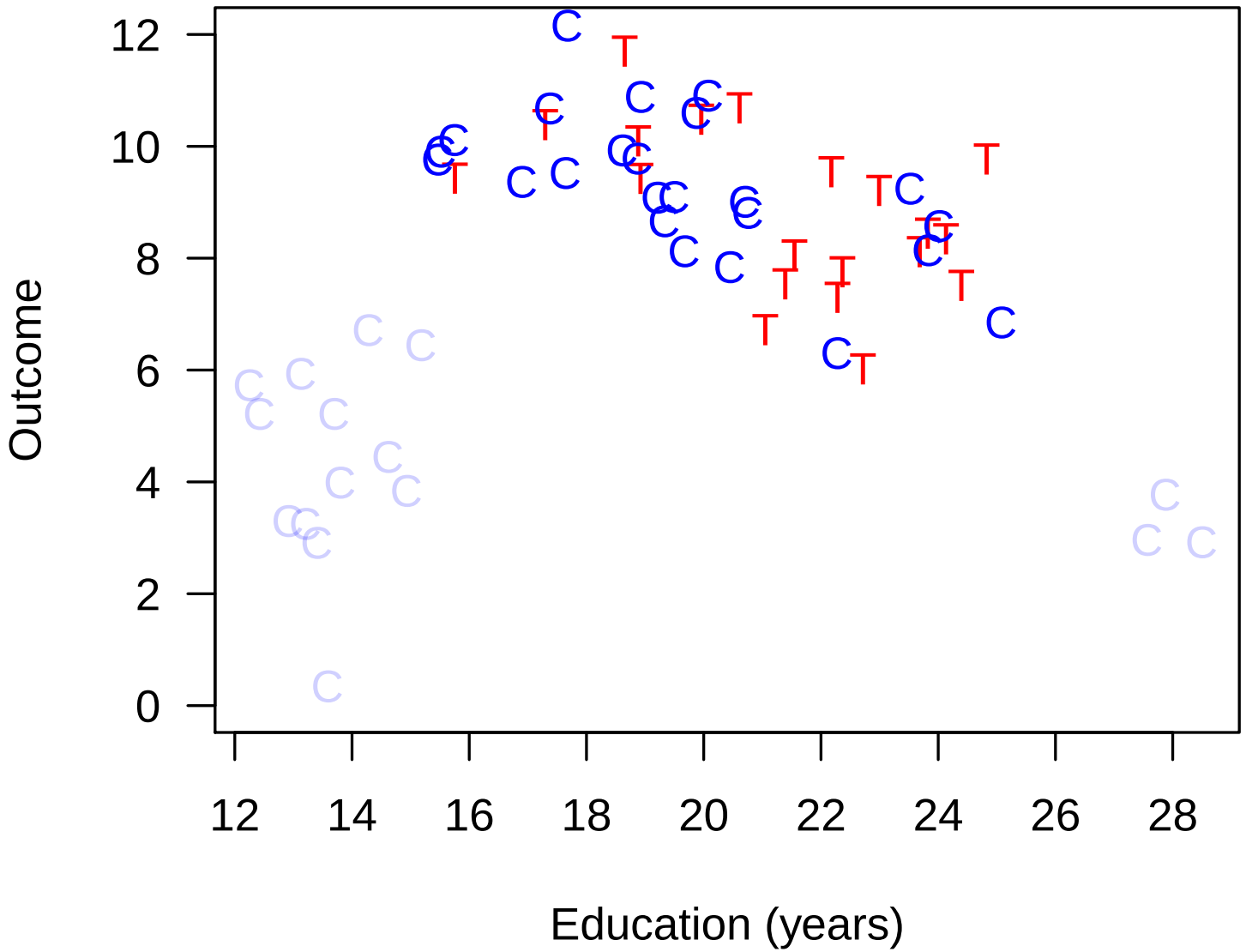

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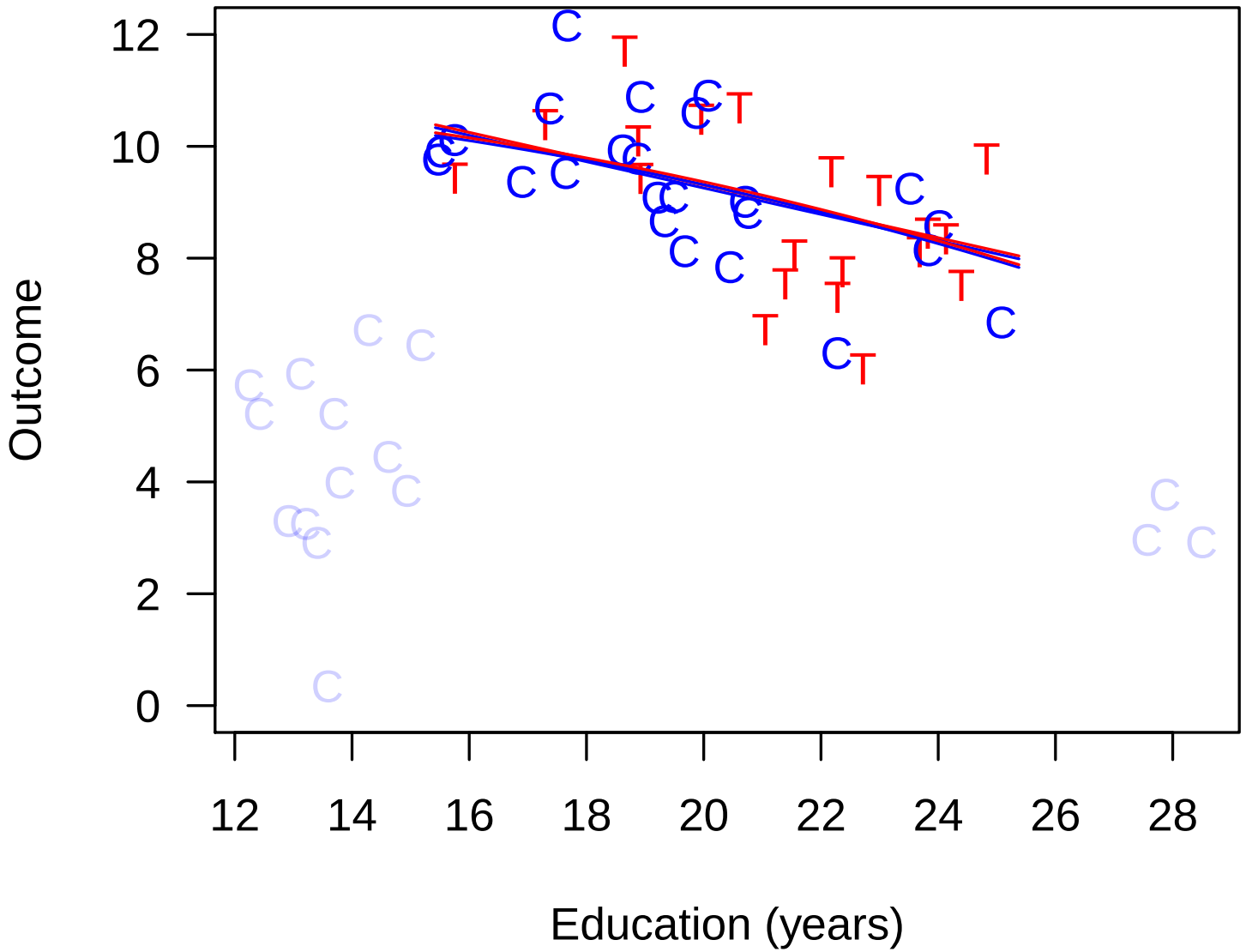

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Matching reduces model dependence, bias, and variance

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

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- (Normal applications would only use one or a few specifications.)

Reducing Model Dependence

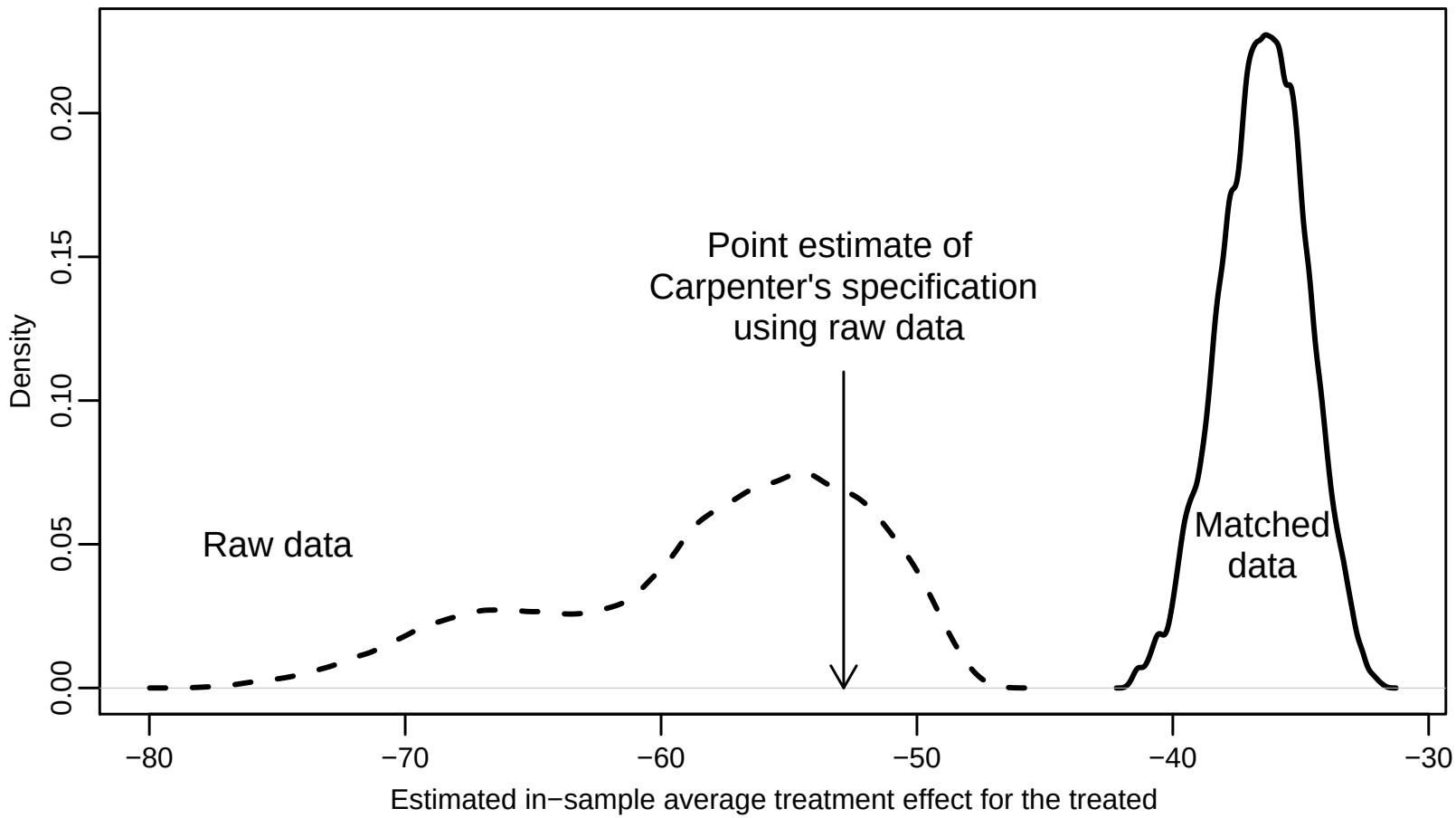

Figure: SATT Histogram: Effect of Democratic Senate majority on FDA drug approval time, across 262,143 specifications.

Another Example: Jeffrey Koch, AJPS, 2002

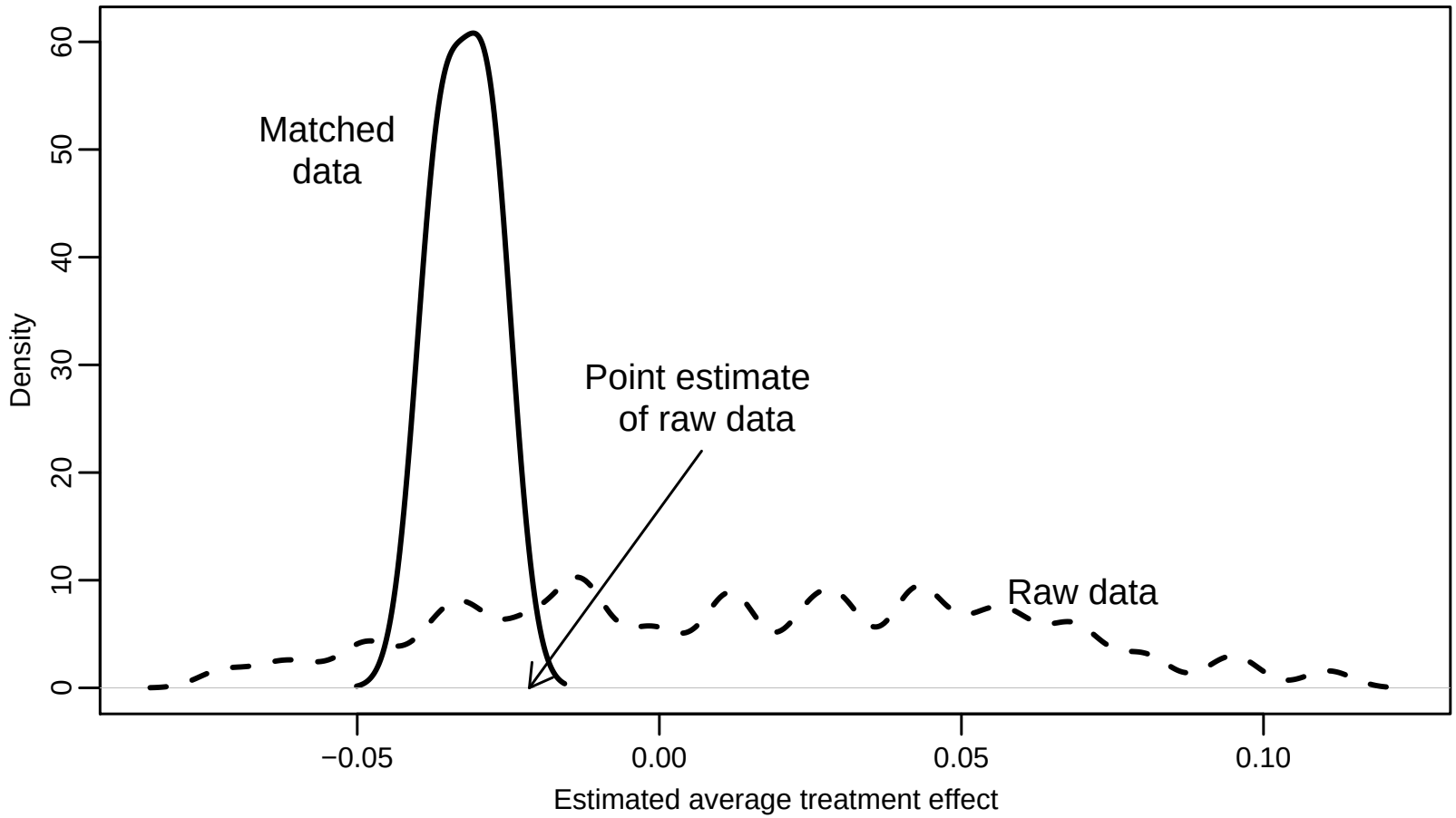

Figure: SATT Histogram: Effect of being a highly visible female Republican candidate across 63 possible specifications with the Koch

The Advantage of Matching

Without Matching:

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Imbalance

The Advantage of Matching

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- Big convenience: Follow preprocessing with whatever statistical method you'd have used without matching

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(Approximates Fully Blocked Experiment)

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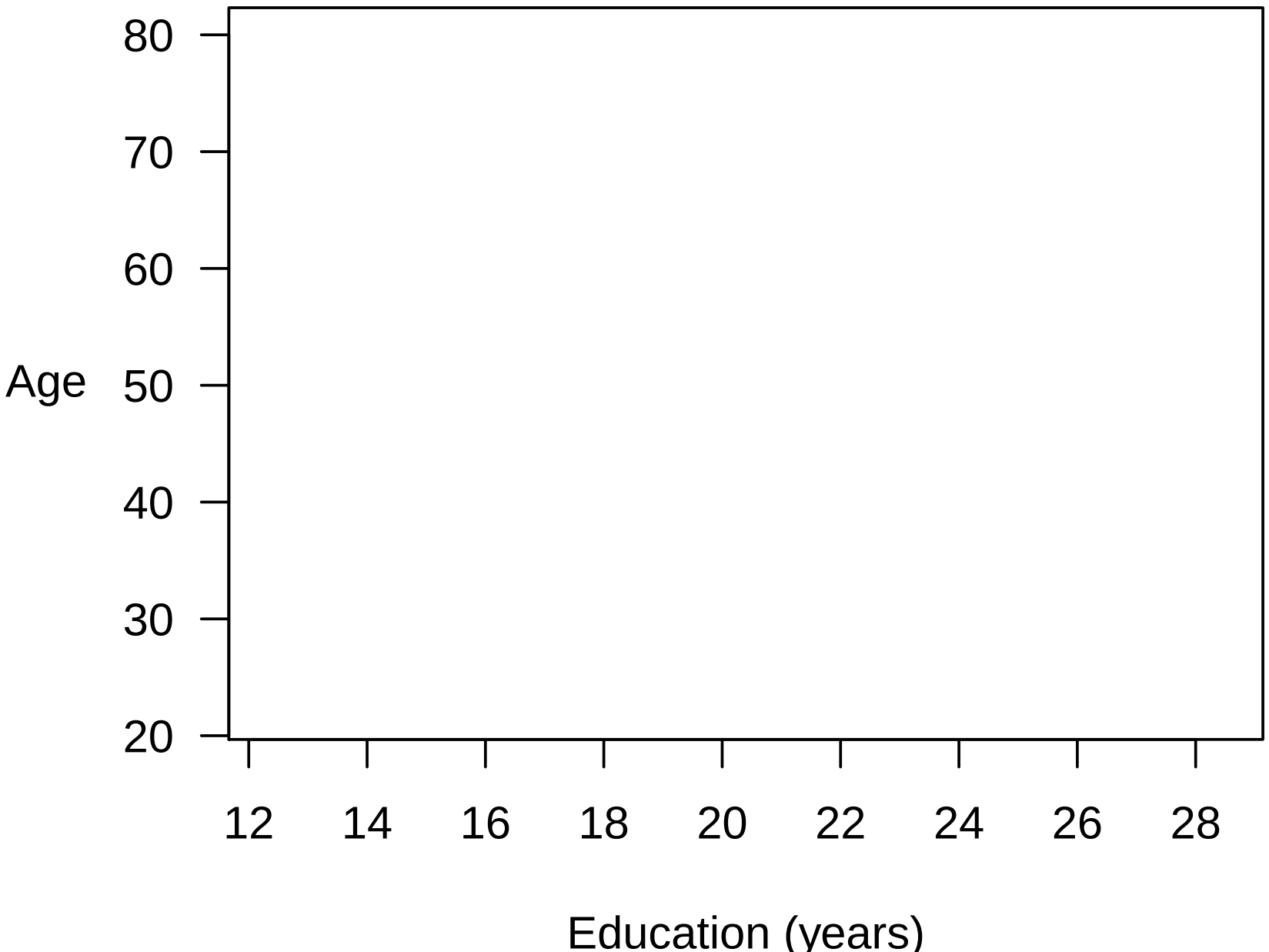

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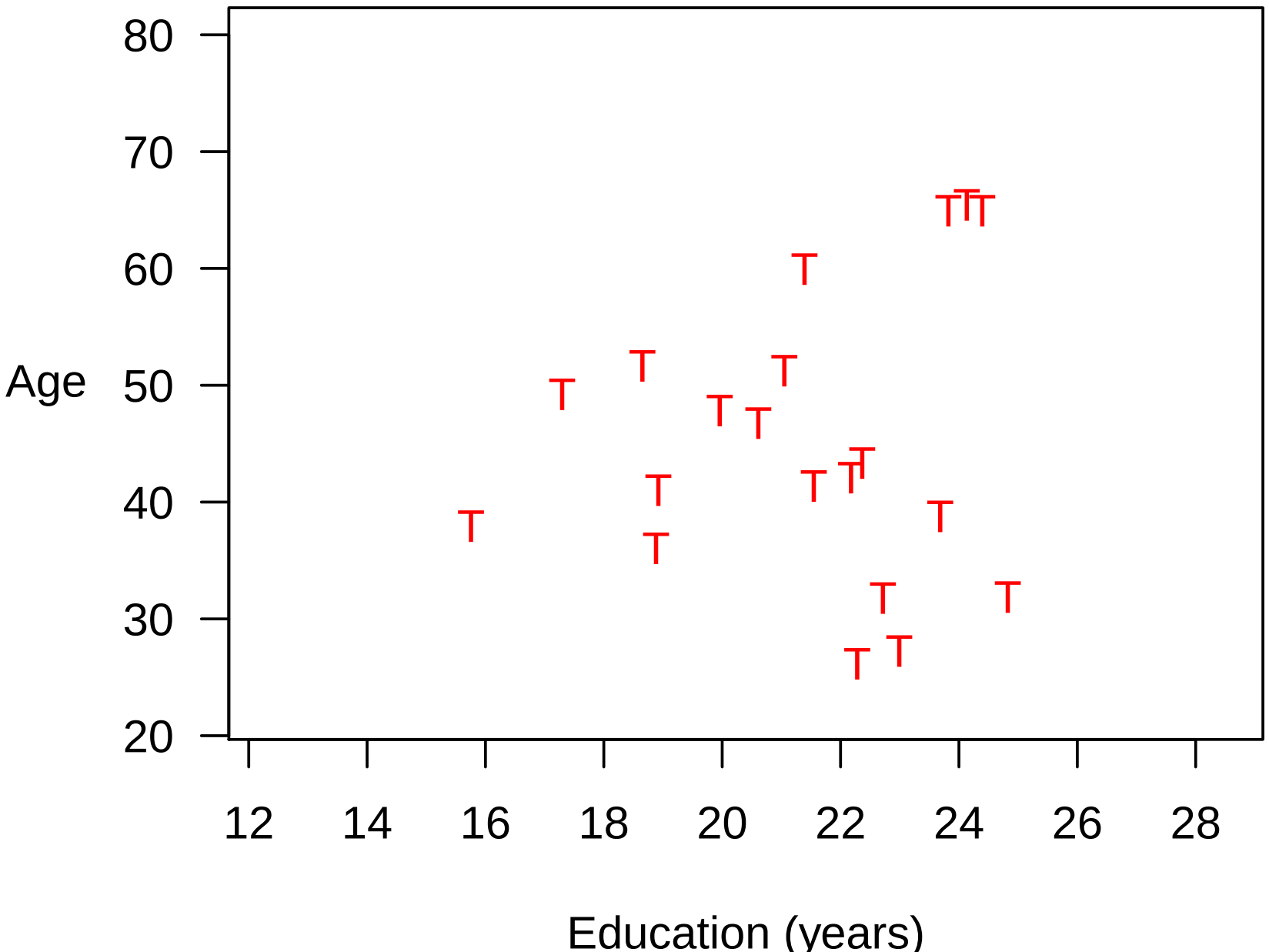

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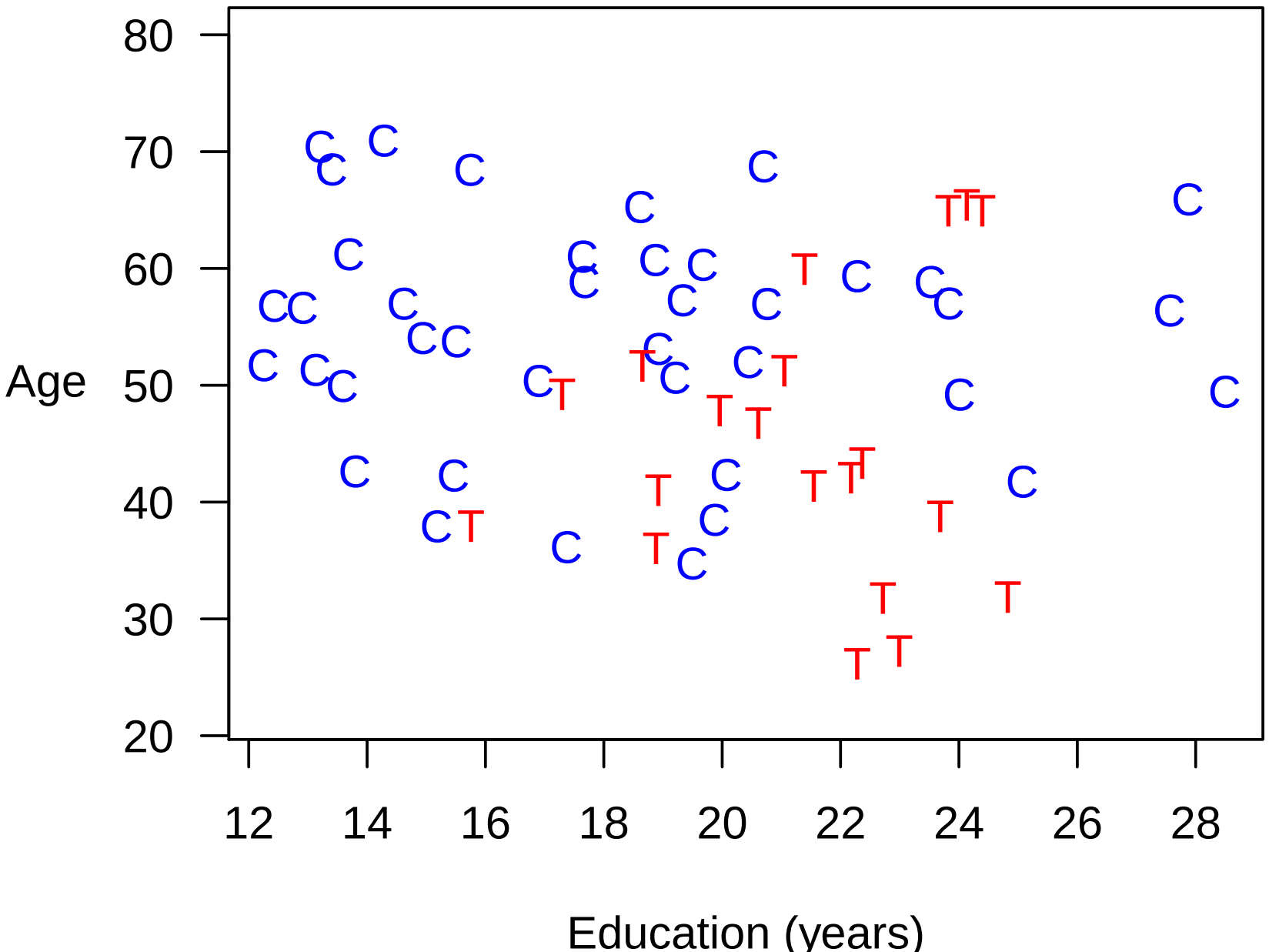

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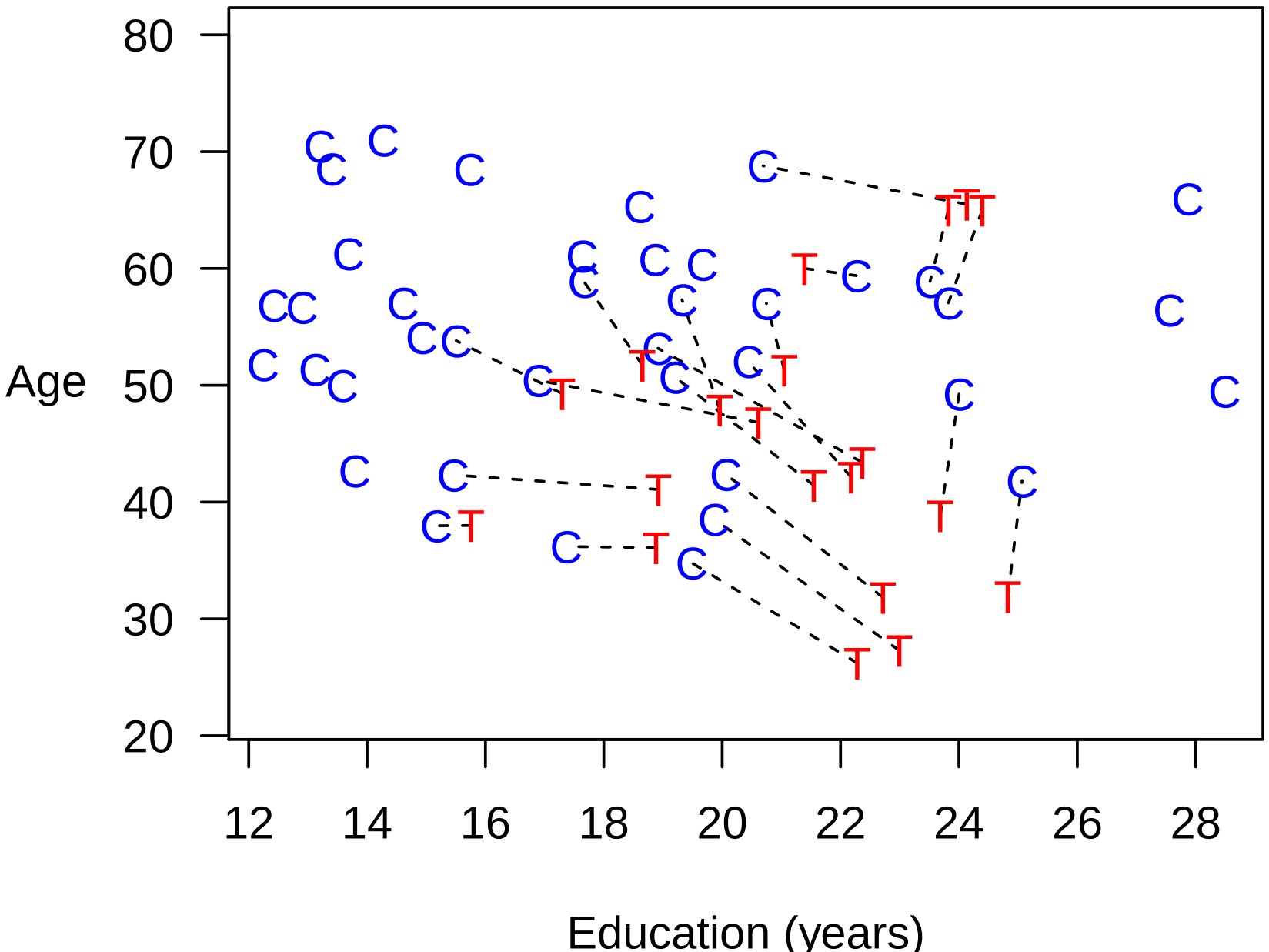

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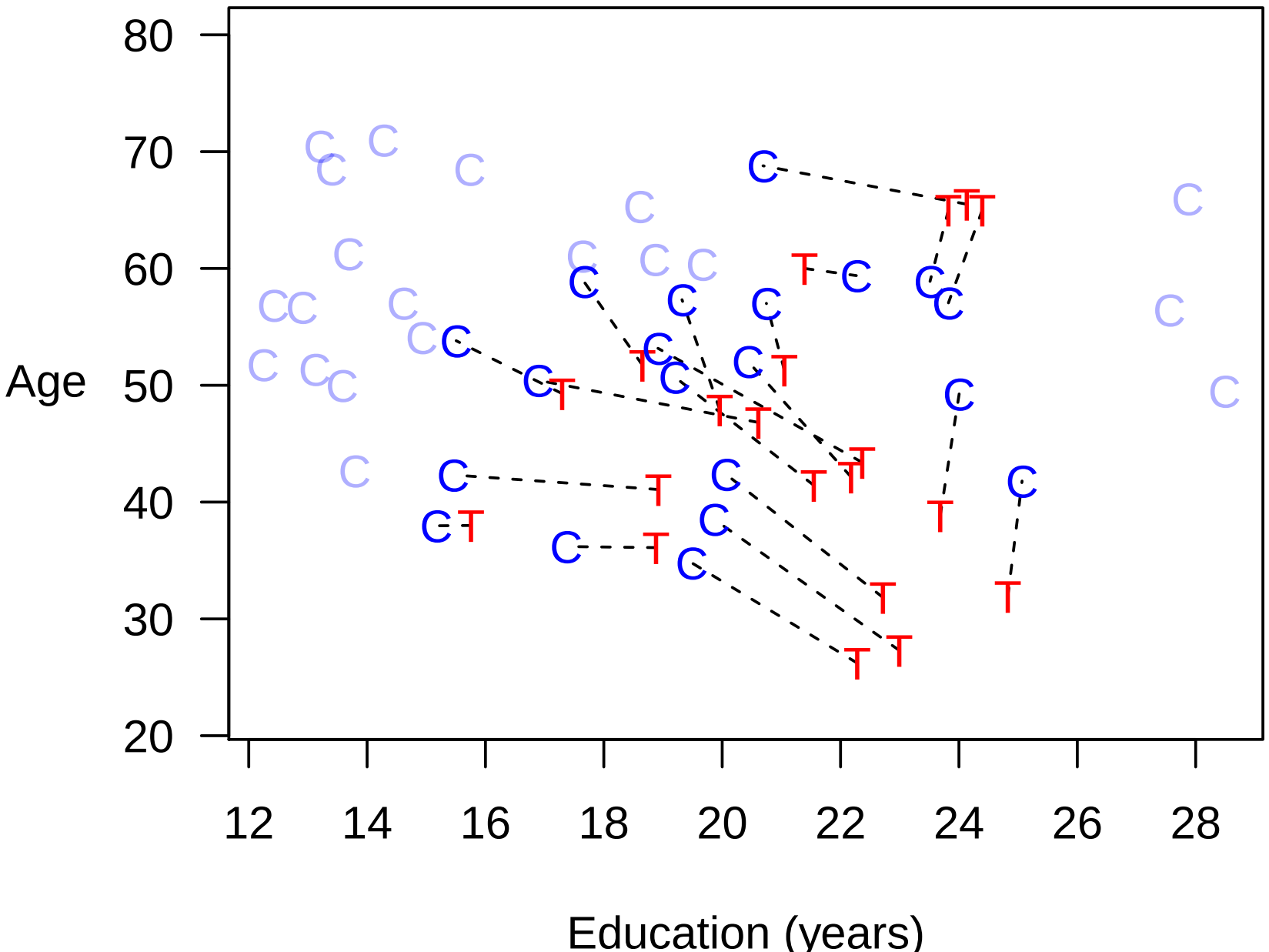

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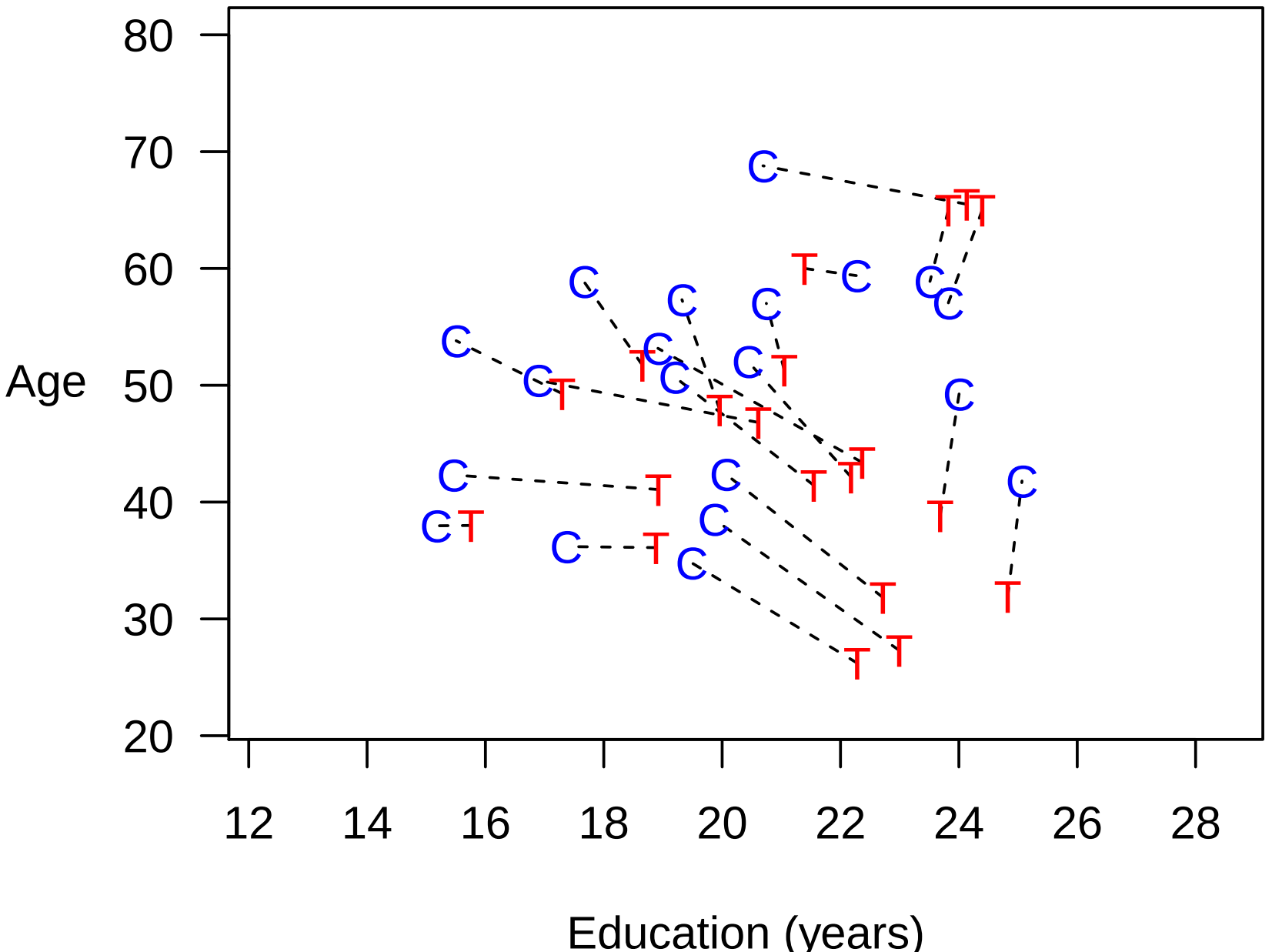

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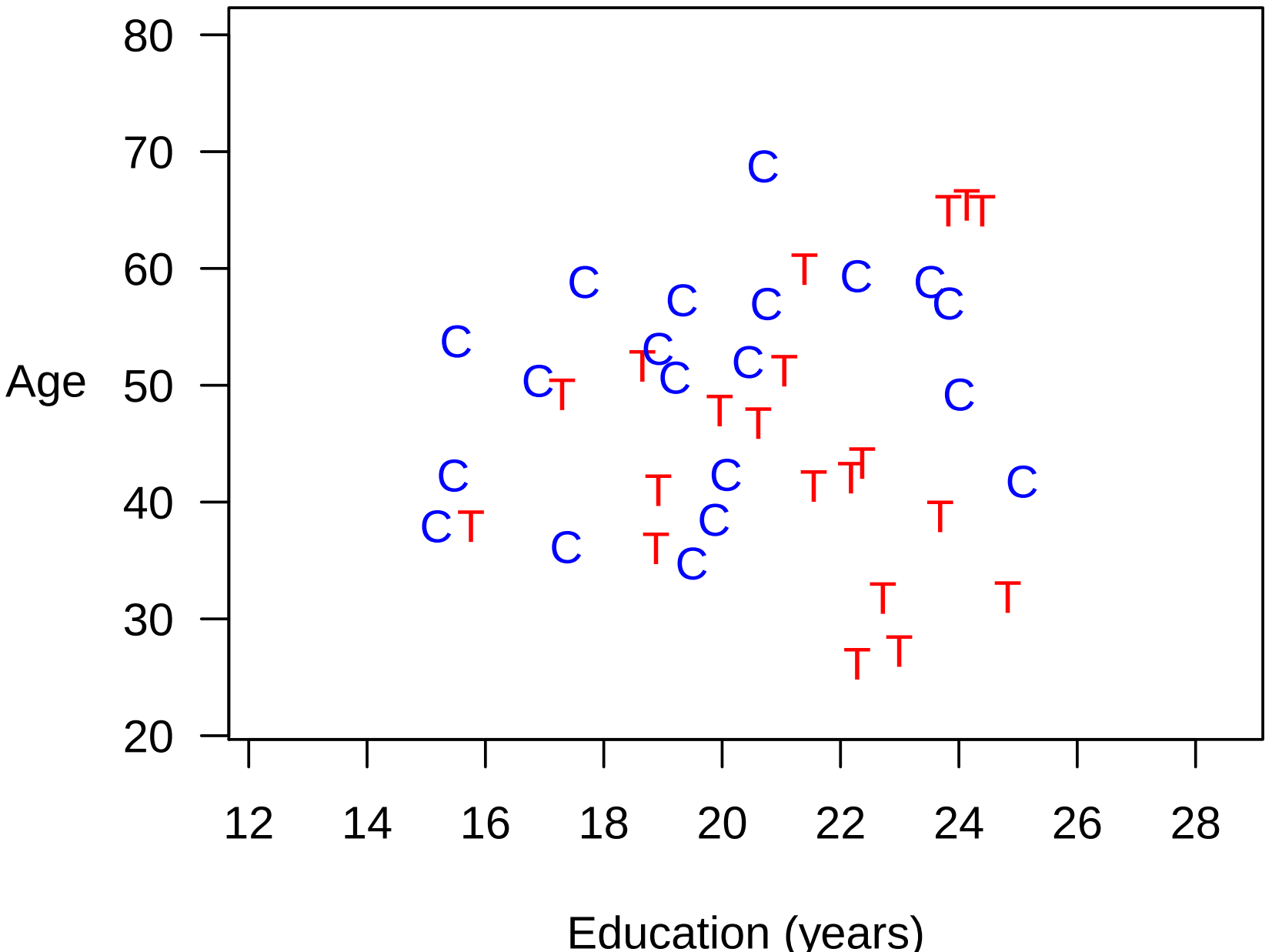

Method 2: Coarsened Exact Matching

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(Approximates Fully Blocked Experiment)

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Method 2: Coarsened Exact Matching

(Approximates Fully Blocked Experiment)

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3. Checking Determine matched sample size, tweak, repeat, ...
   - Easier, but still iterative

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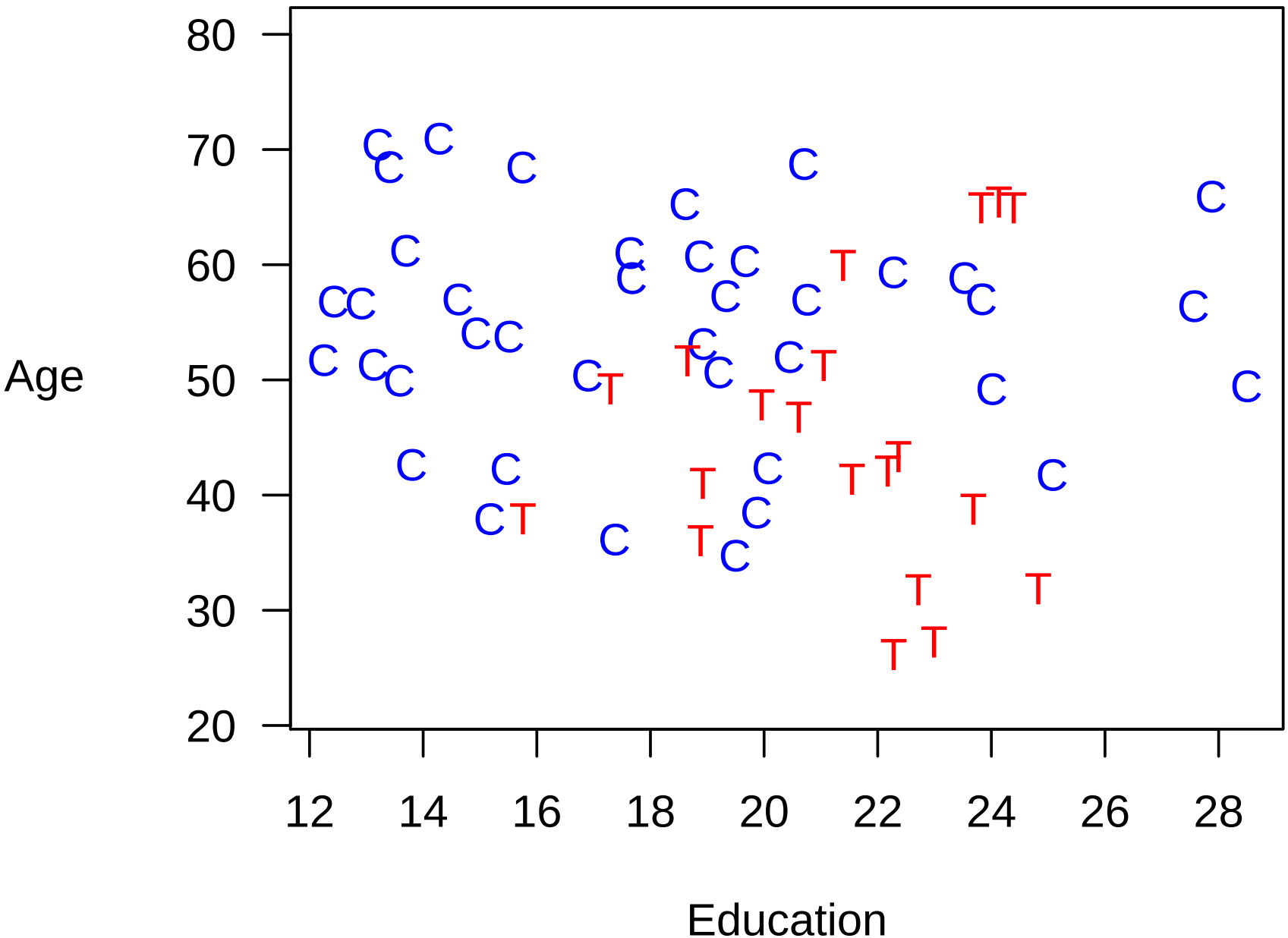

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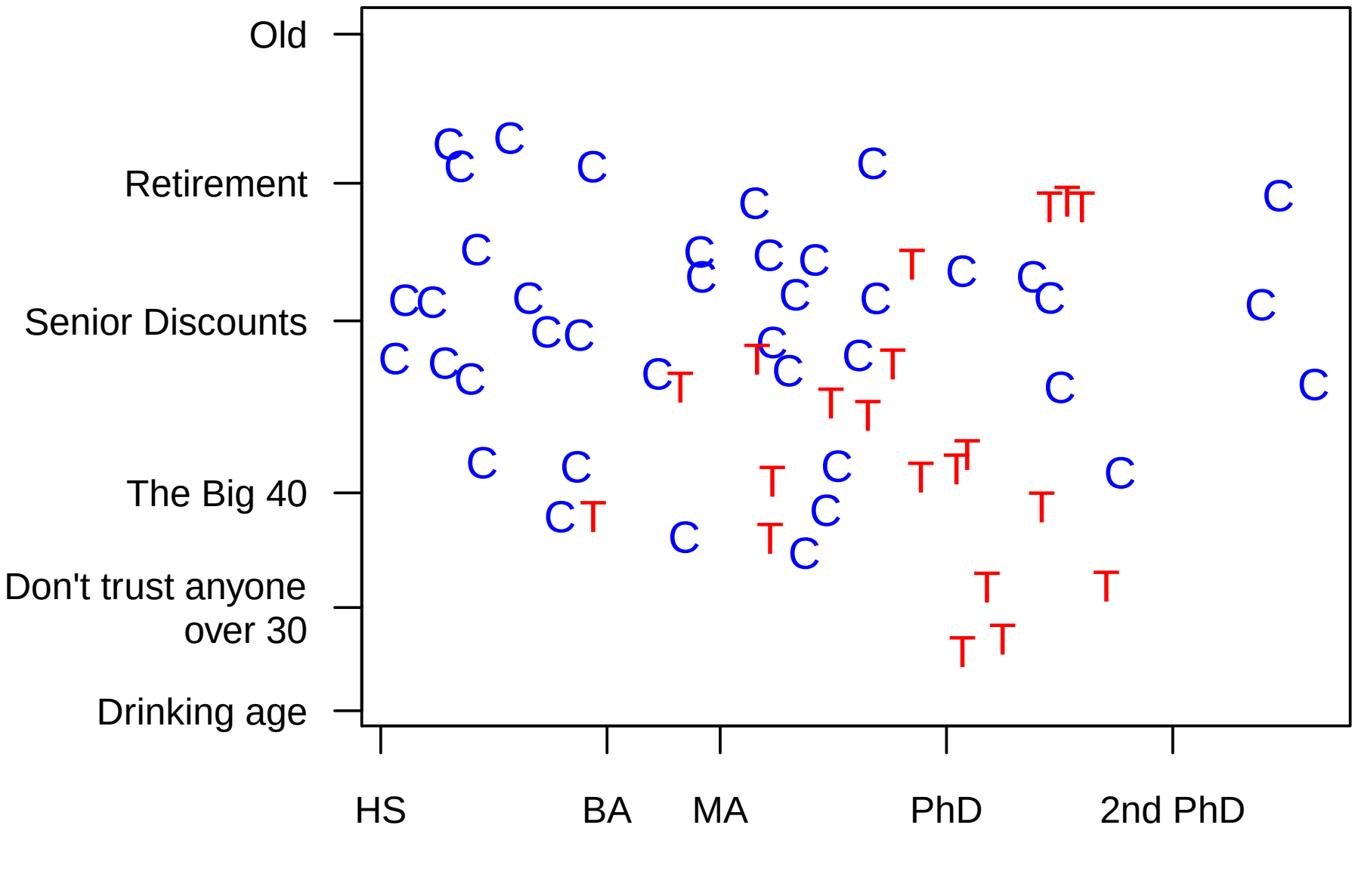

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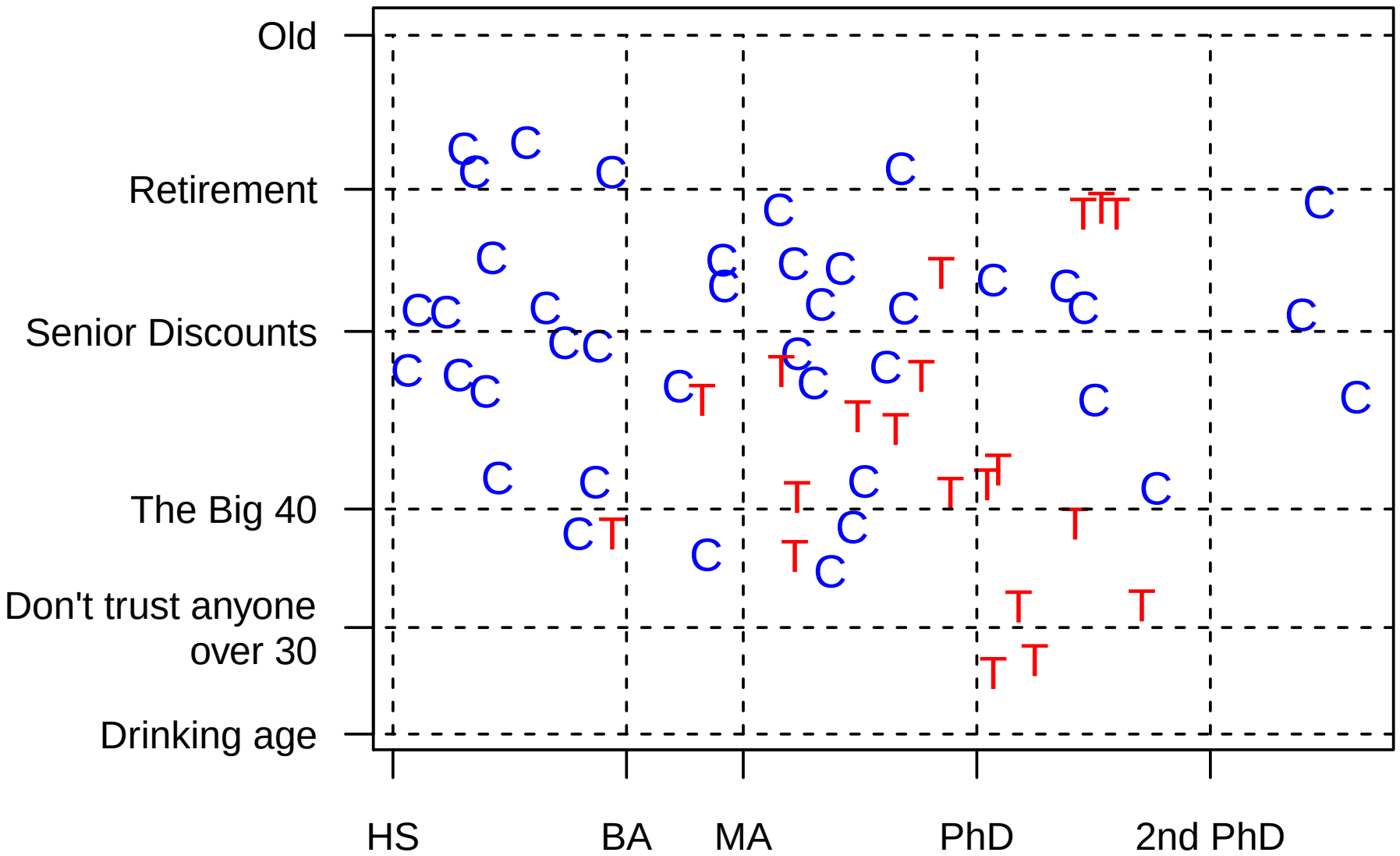

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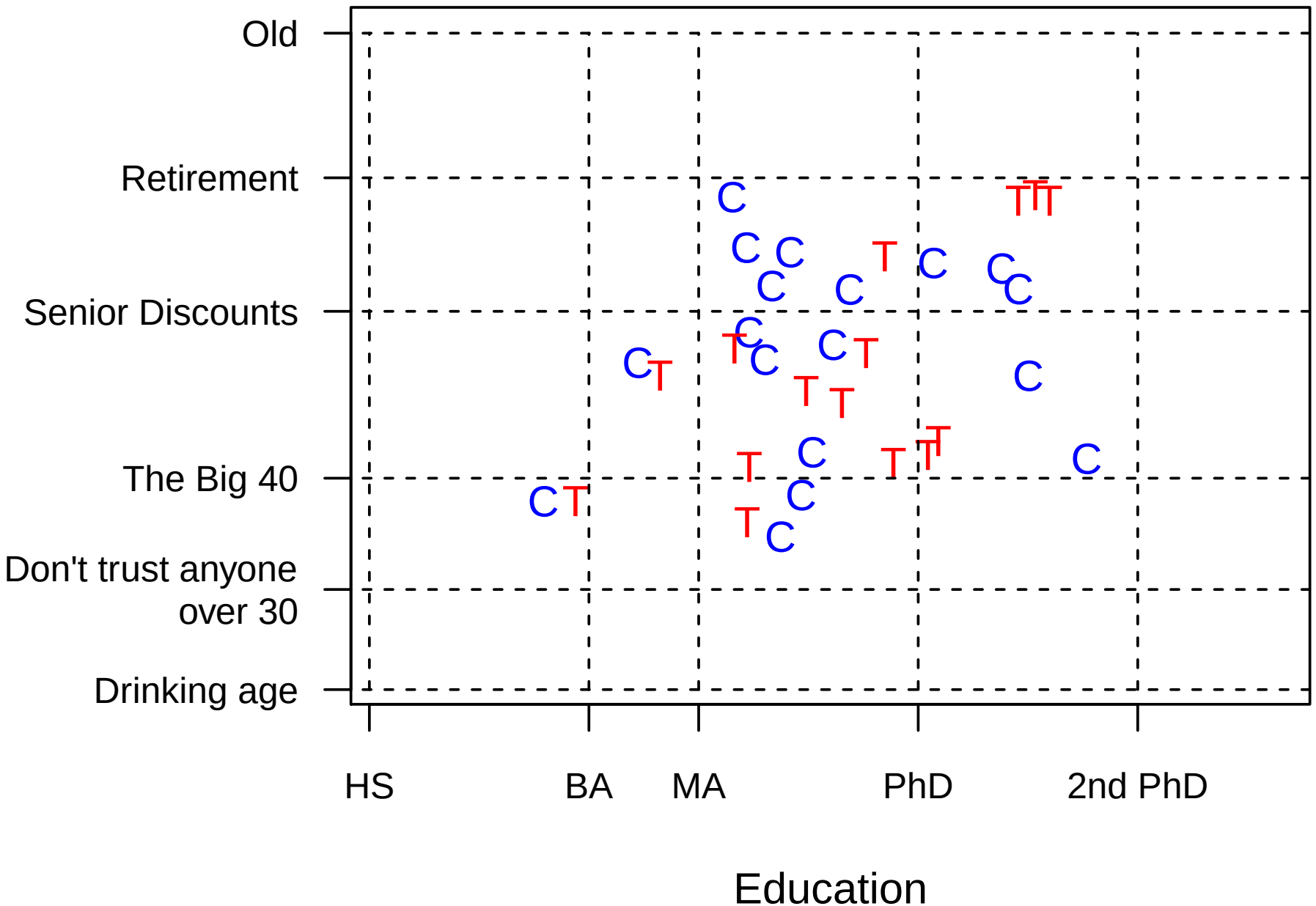

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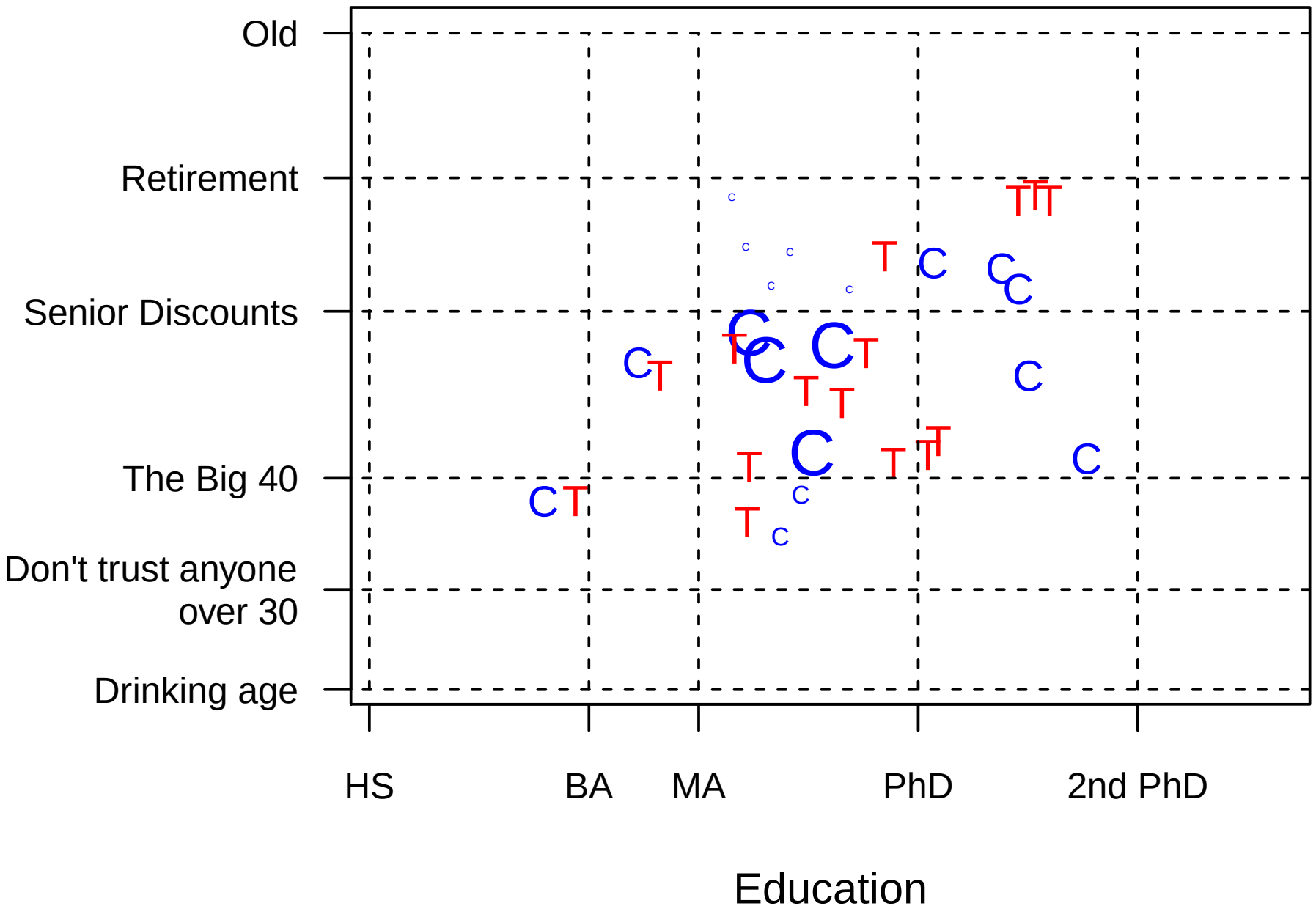

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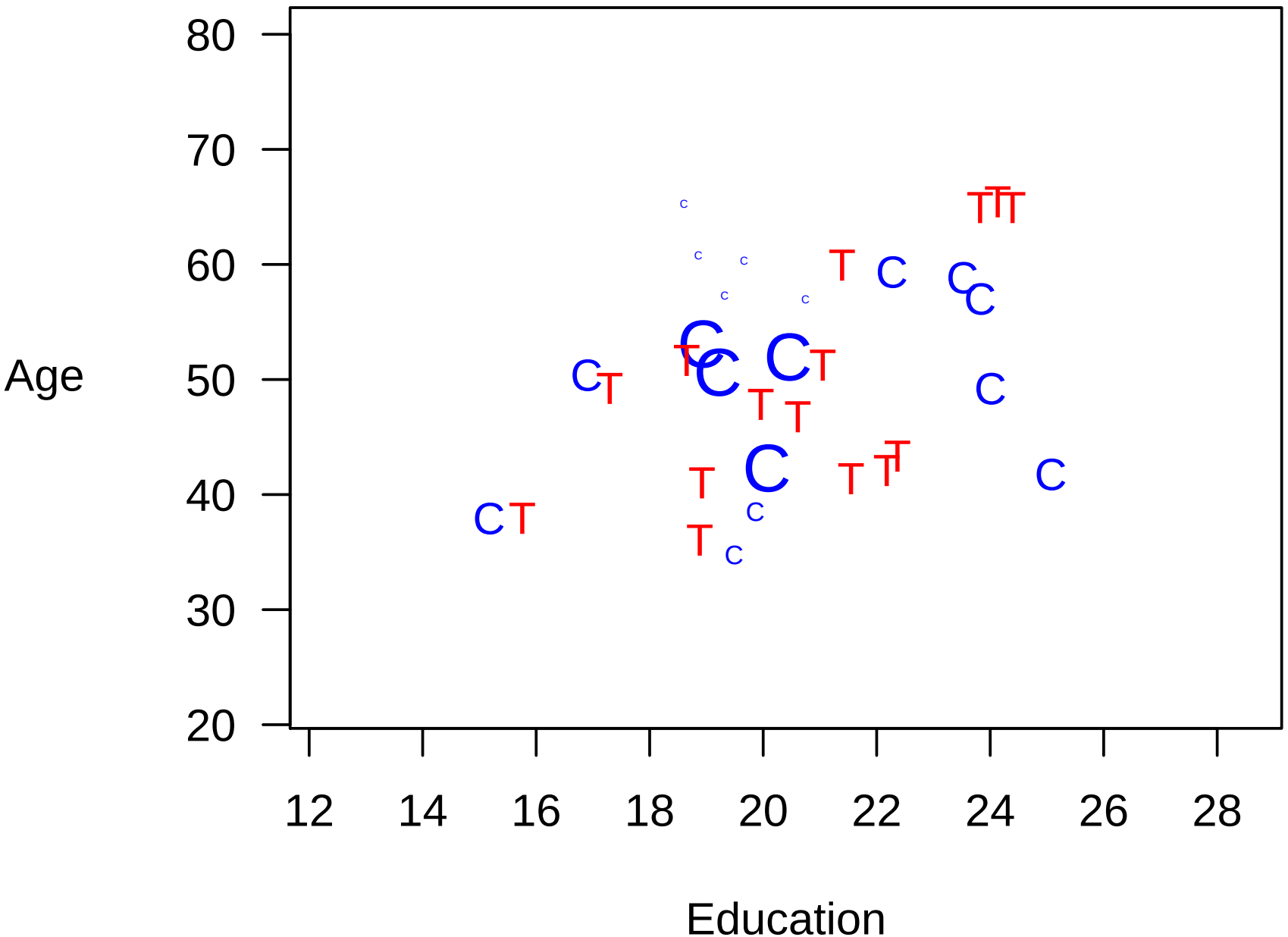

Method 3: Propensity Score Matching

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   - 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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(Approximates Completely Randomized Experiment)

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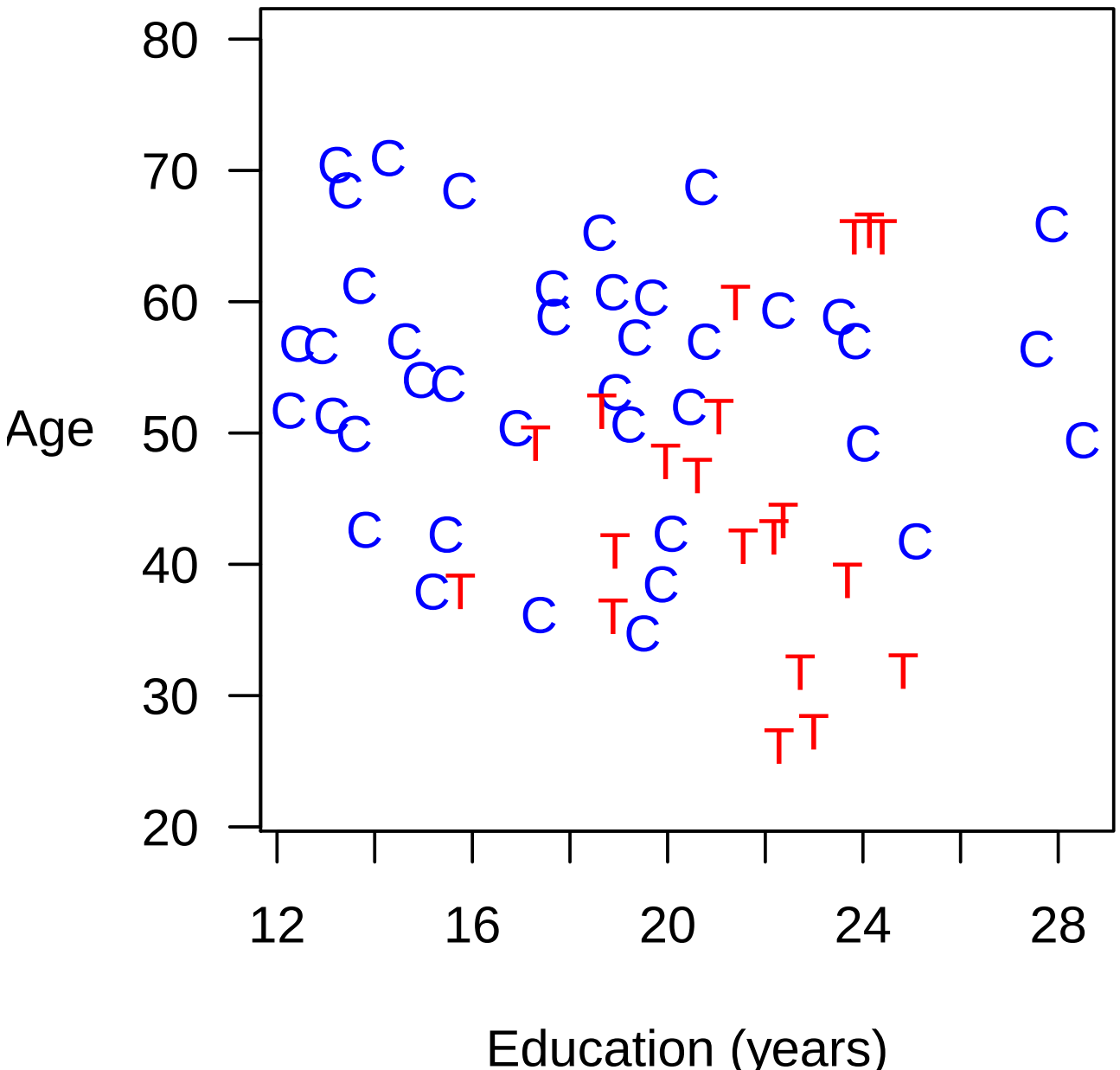

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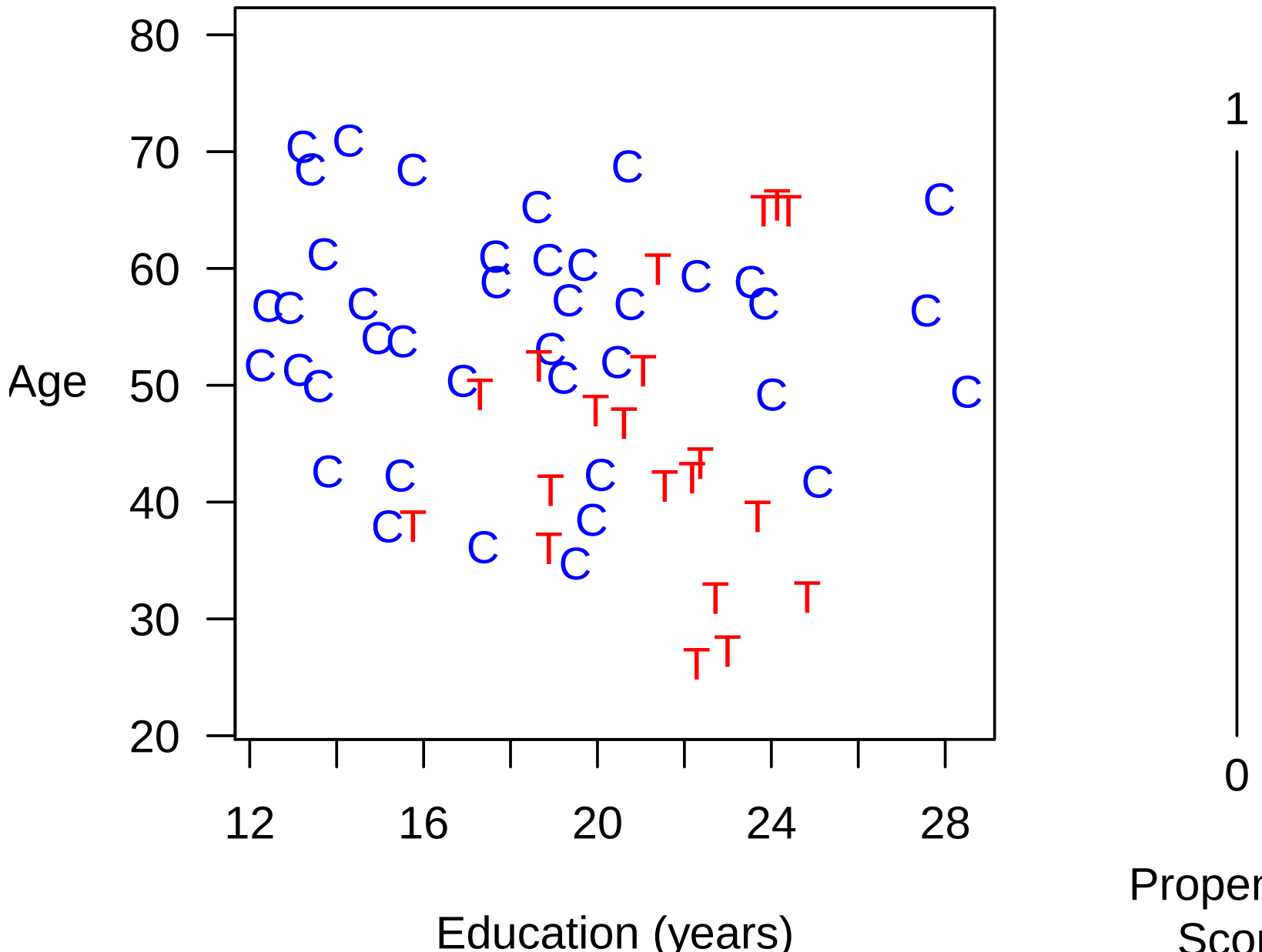

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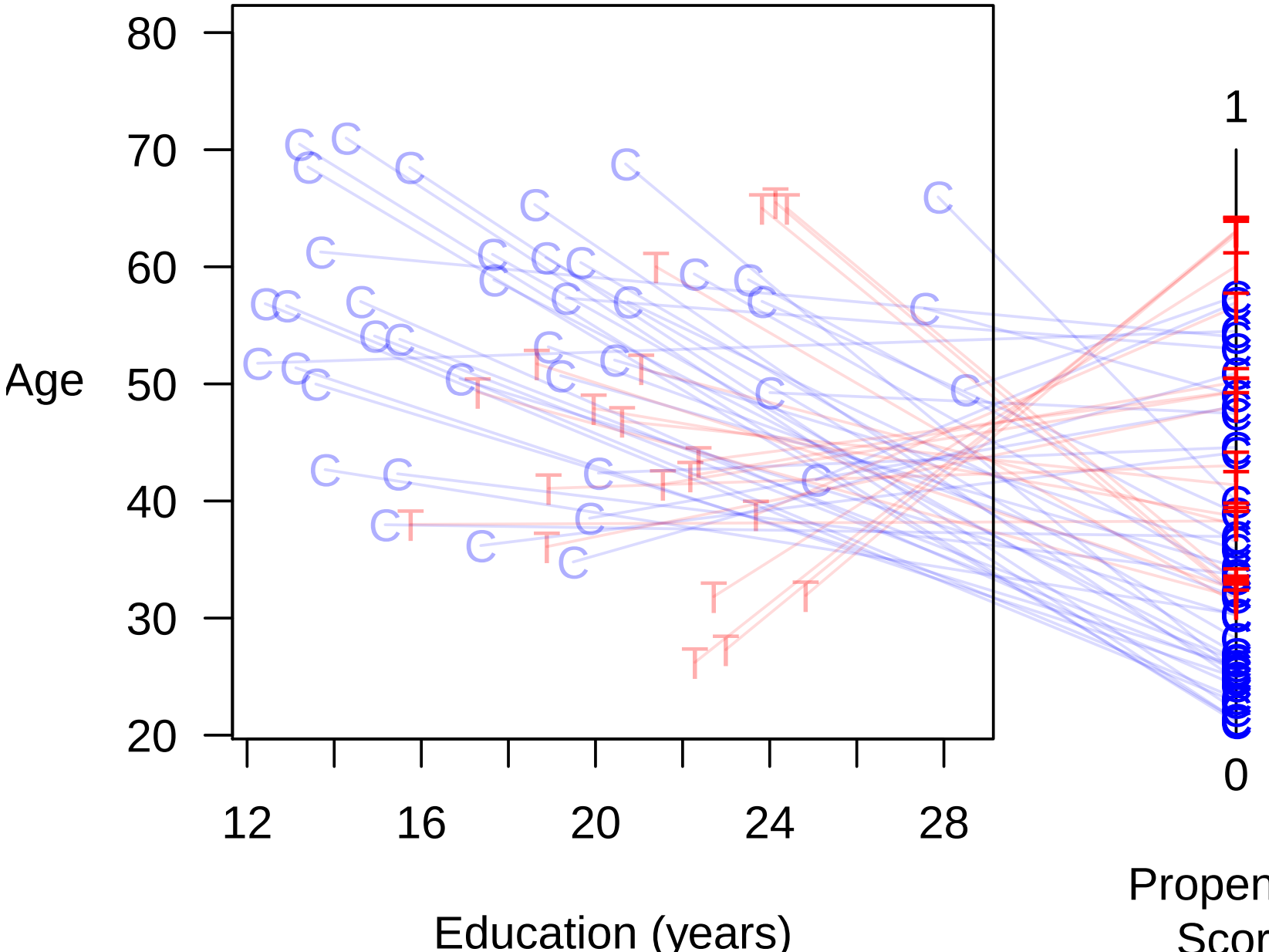

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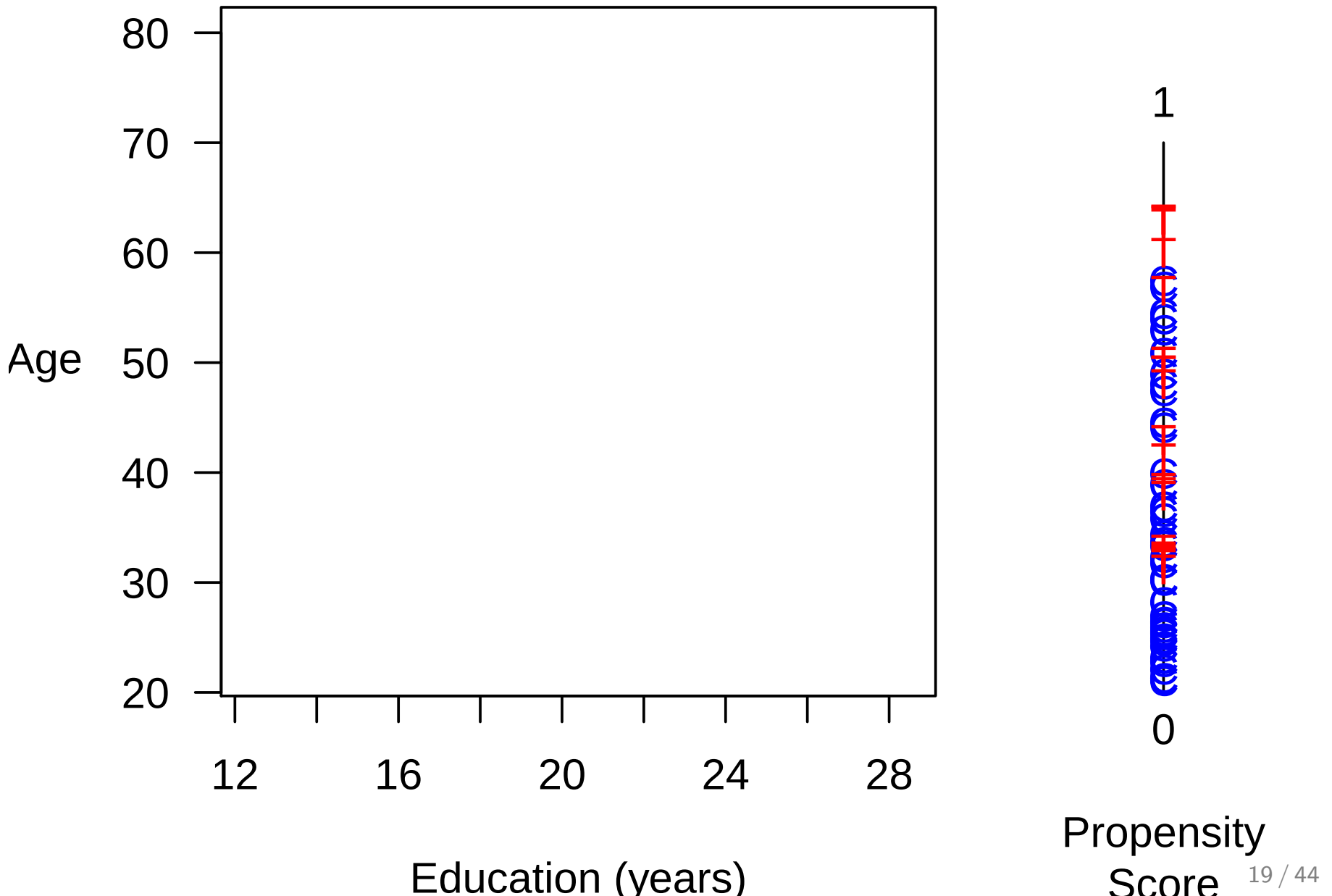

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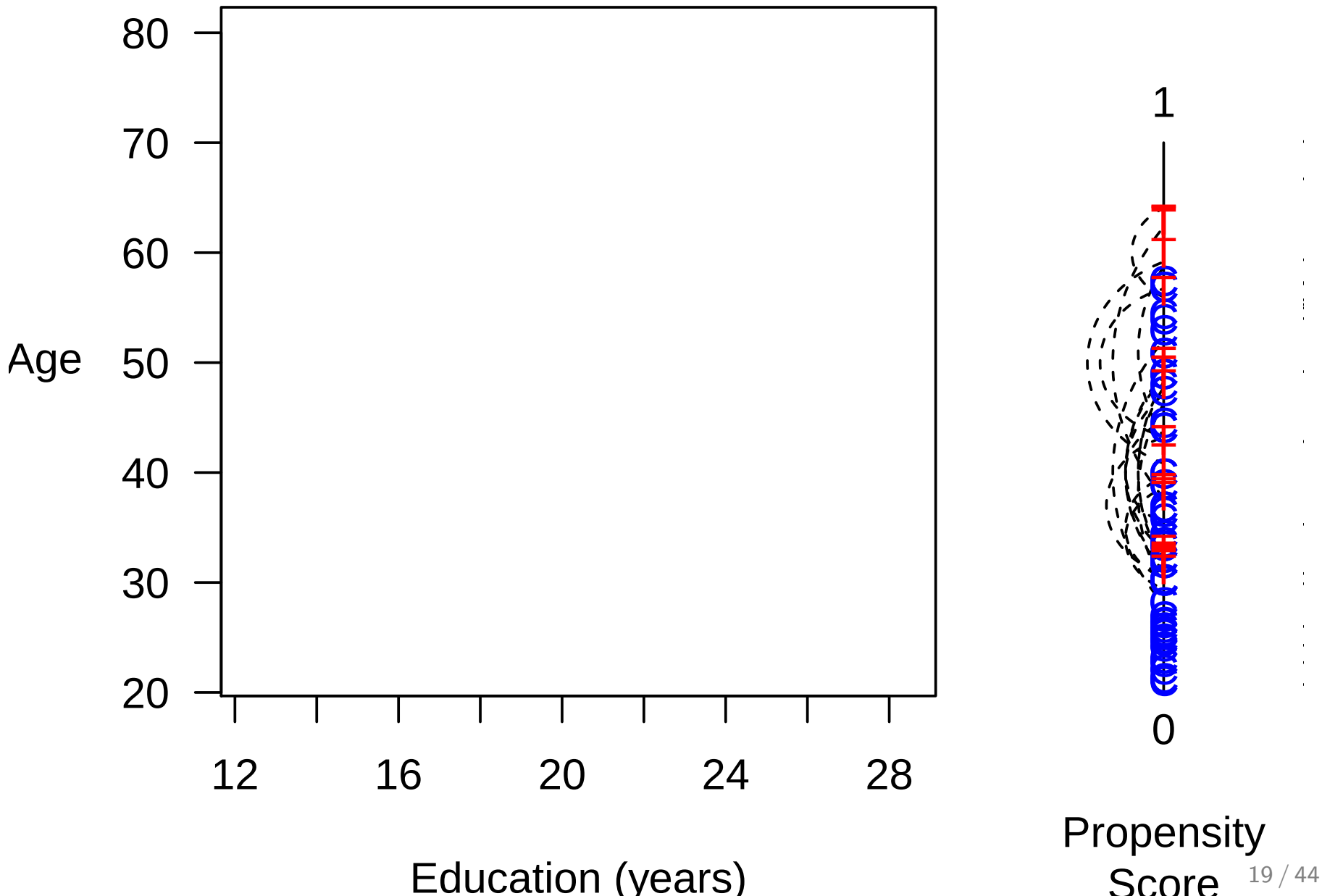

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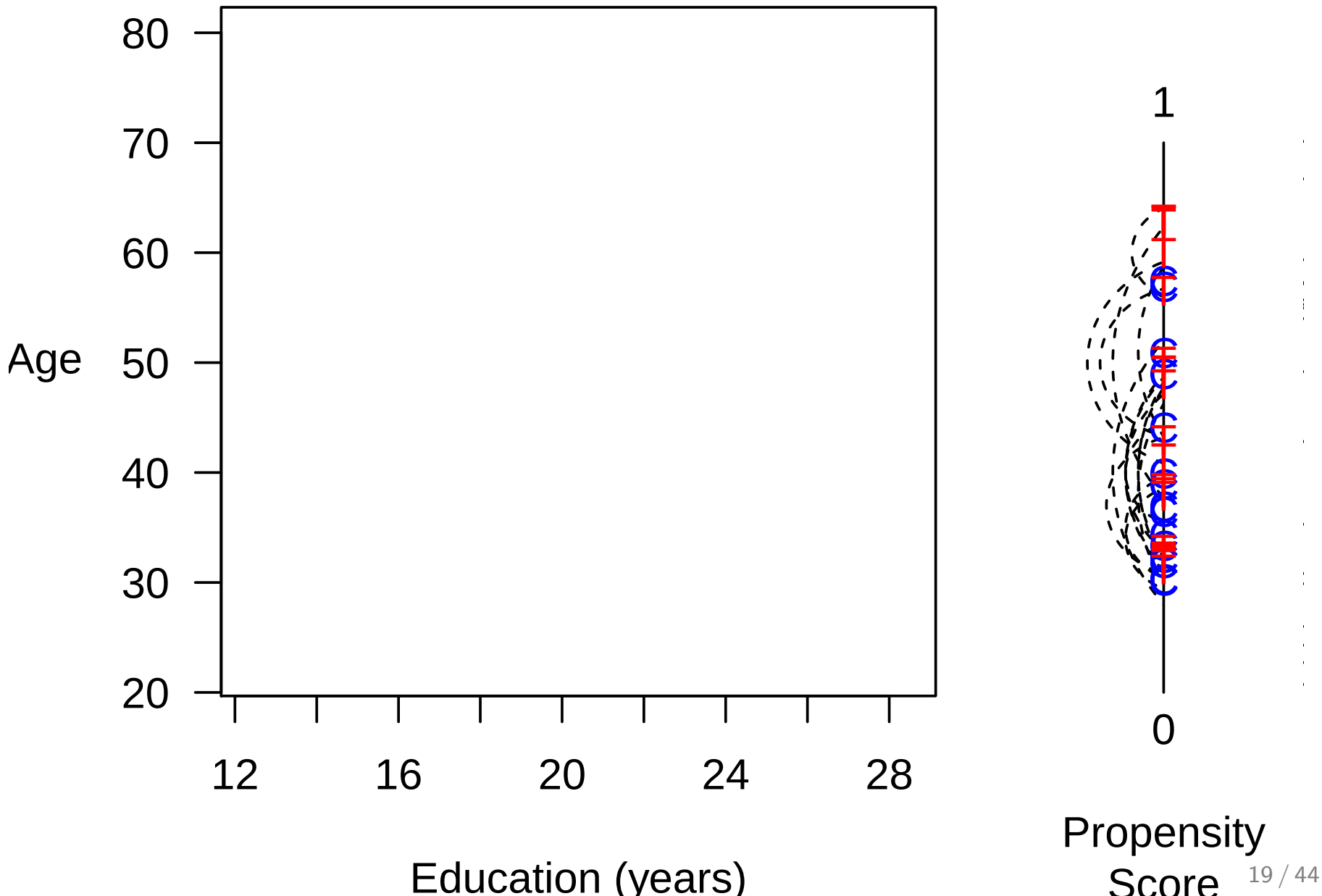

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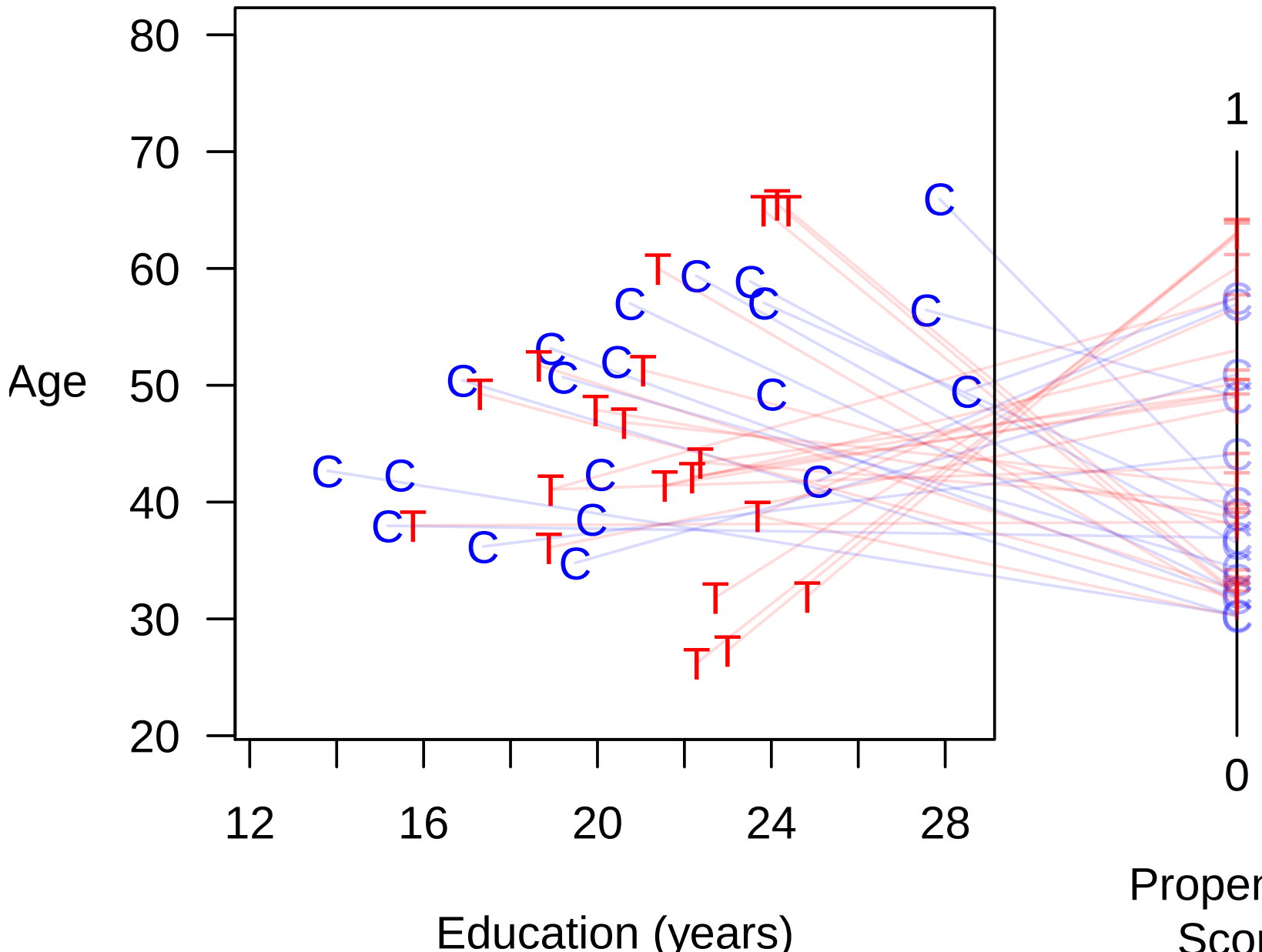

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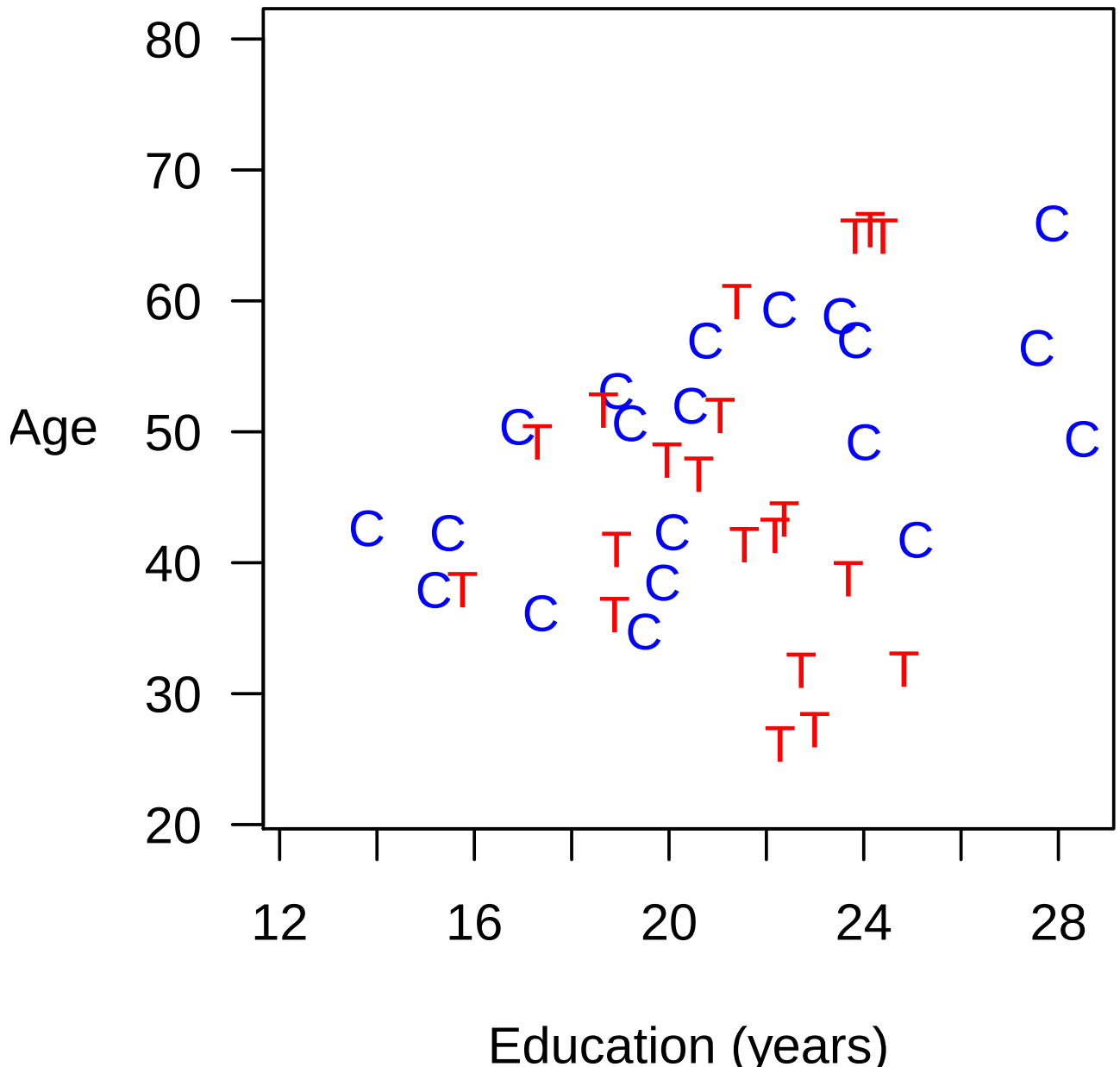

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  - The Reality: The PSM Paradox is bigger with more covariates

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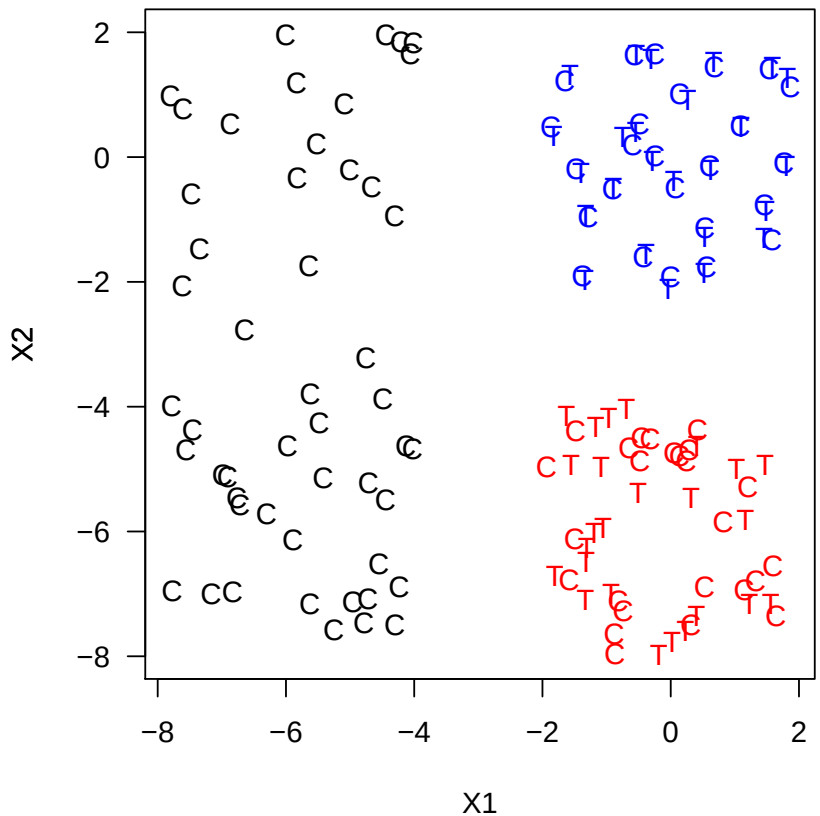

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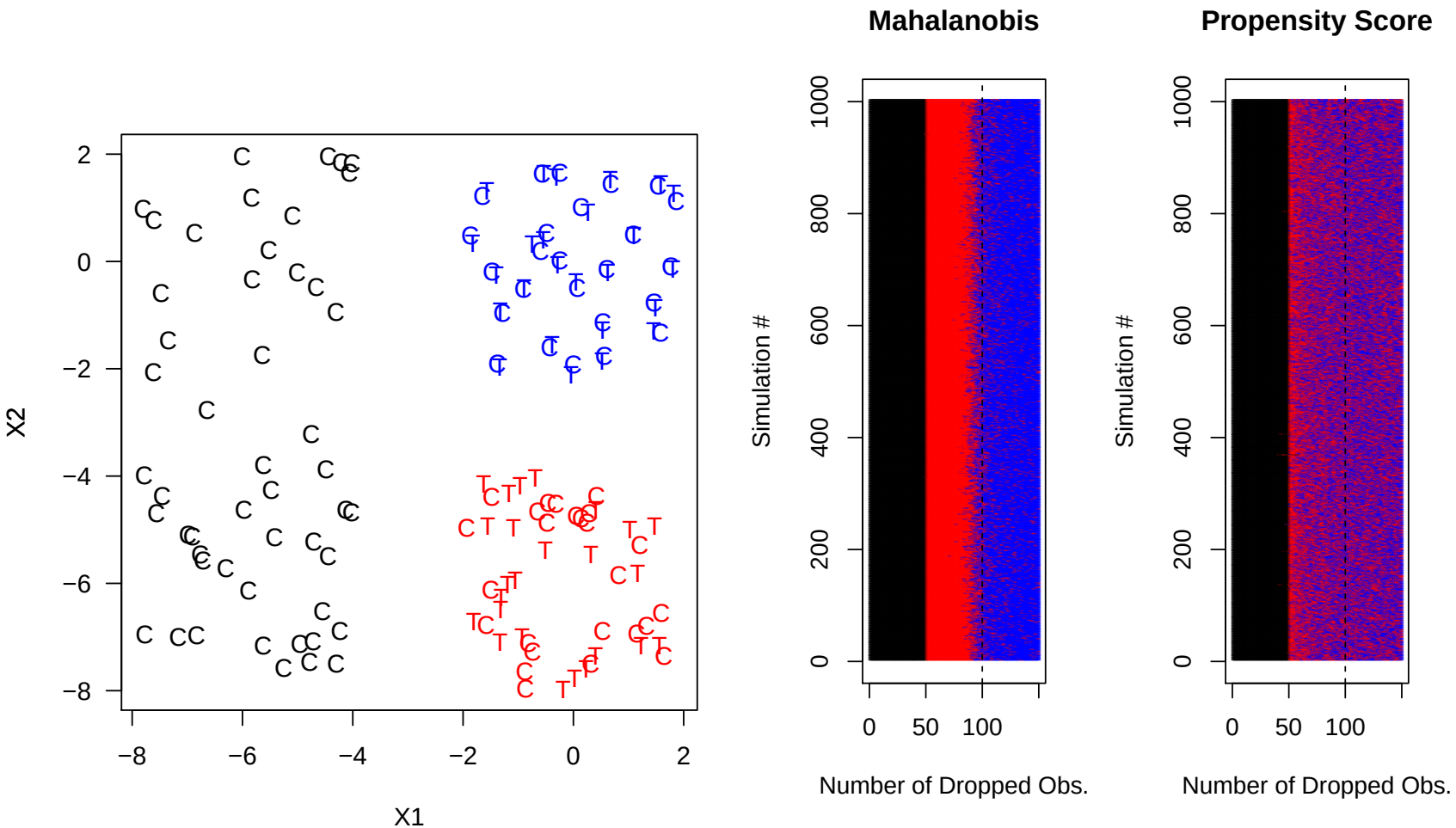
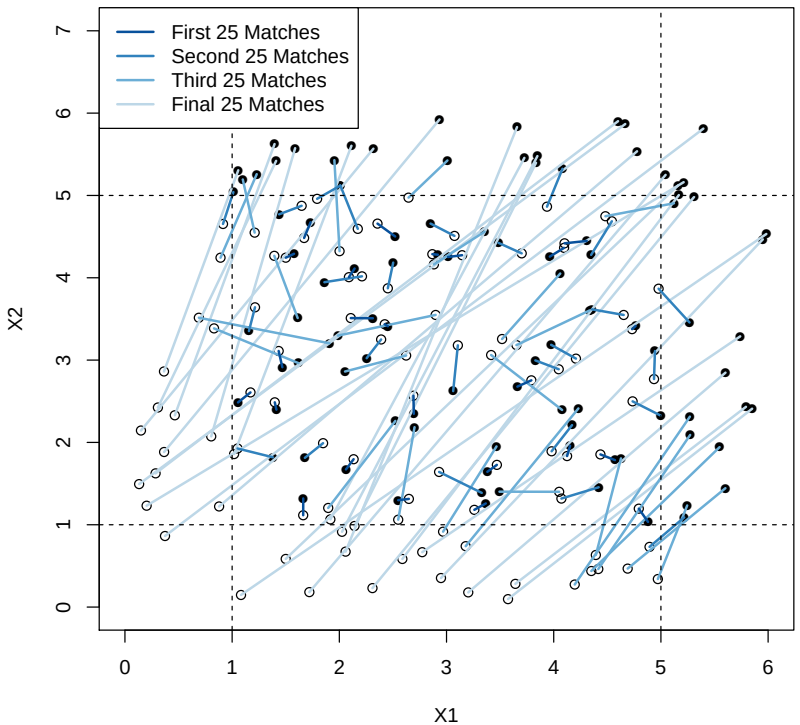


What Does PSM Match?

MDM Matches



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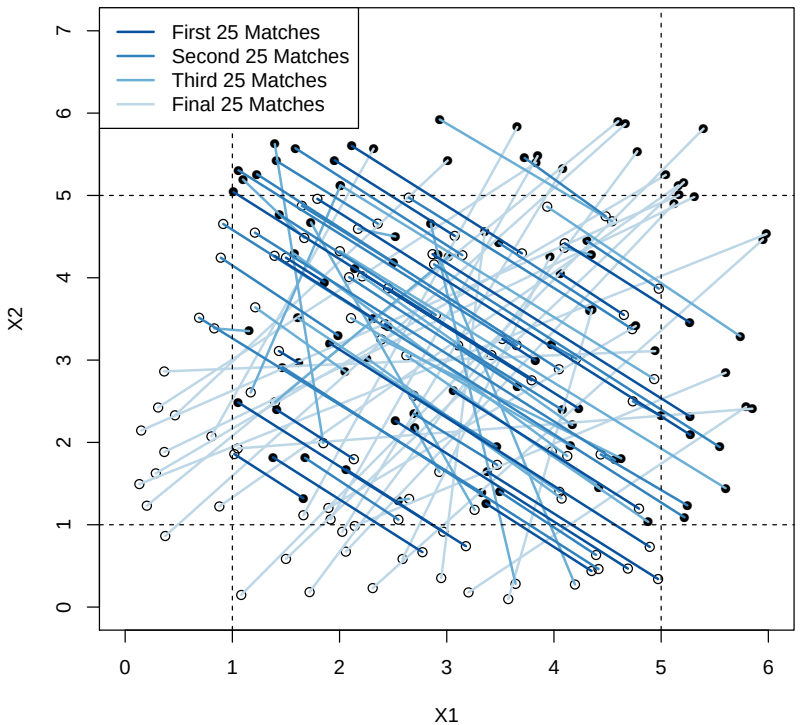
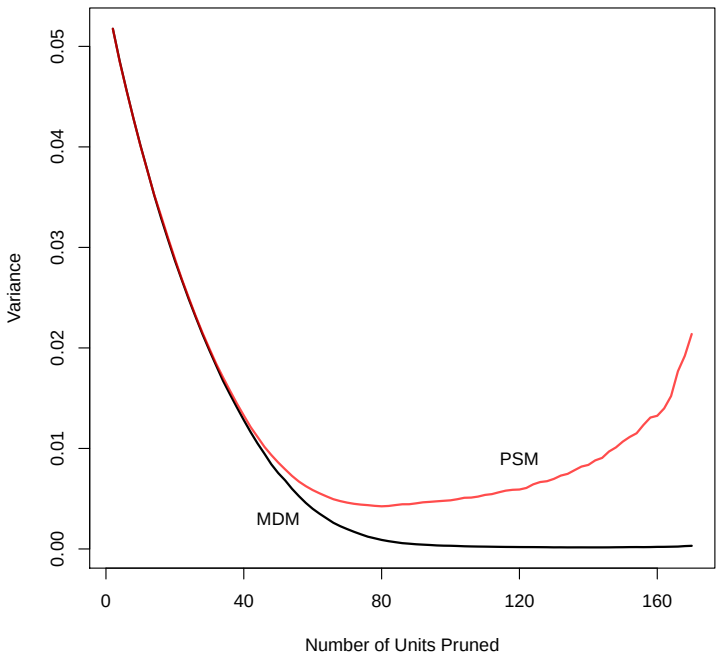


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

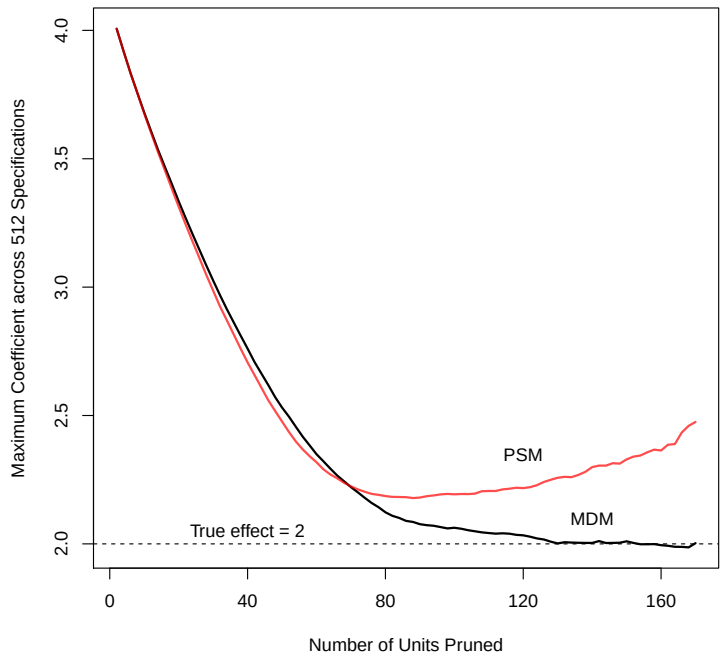
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



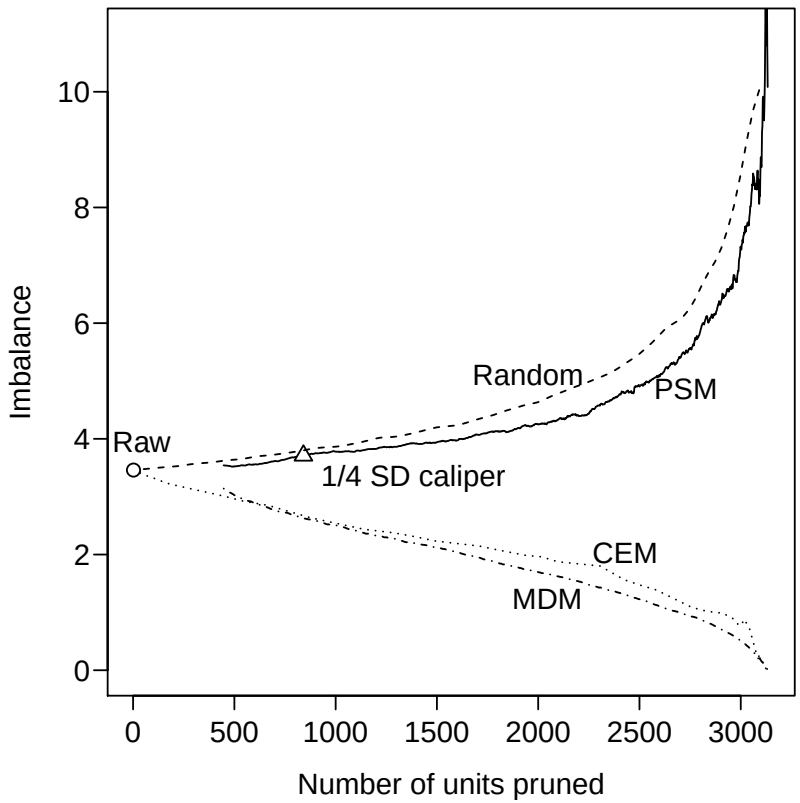
Bias



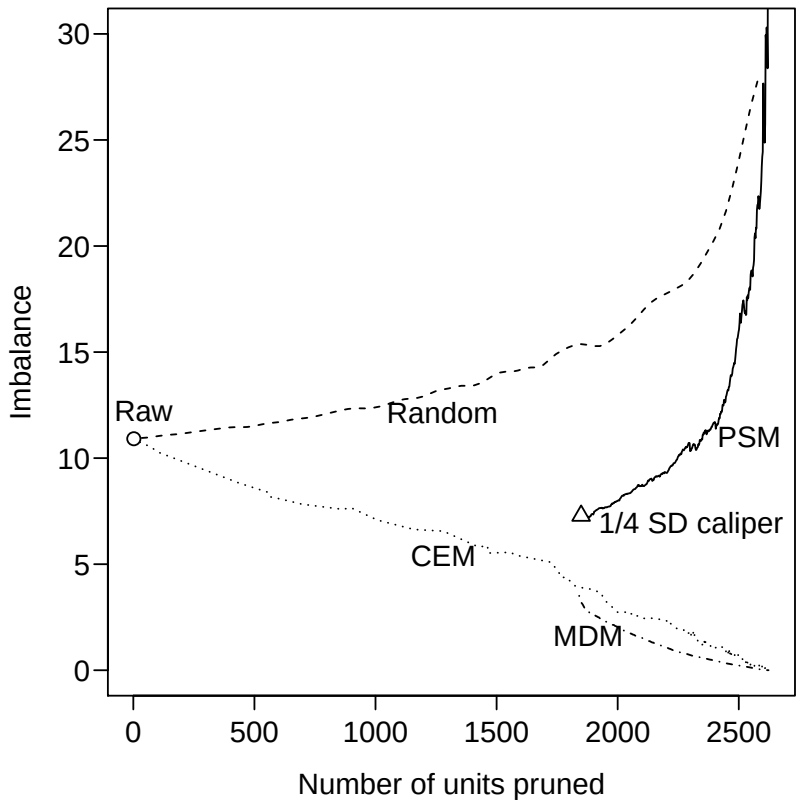
$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

The Propensity Score Paradox

Finkle et al. (2012)



Nielsen et al. (2011)



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  - $\binom{N}{n}$ evaluations for each sample size $n = N, N-1, \ldots, 1$
  - The combination is the (gargantuan) "power set"
  - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
  - $\rightsquigarrow$ It's **hard** to calculate!
- We develop algorithms for the (optimal) frontier which:
  - runs very fast
  - operate as "greedy" but we prove are optimal
  - do not require evaluating every subset
  - work with very large data sets
  - is the exact frontier (no approximation or estimation)

How hard is the frontier to calculate?

- Consider 1 point on the SATT frontier:
  - Start with matrix of N control units X_0
  - Calculate imbalance for all $\binom{N}{n}$ subsets of rows of X_0
  - Choose subset with lowest imbalance
- Evaluations needed to compute the entire frontier:
  - $\binom{N}{n}$ evaluations for each sample size $n = N, N-1, \ldots, 1$
  - The combination is the (gargantuan) "power set"
  - e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe
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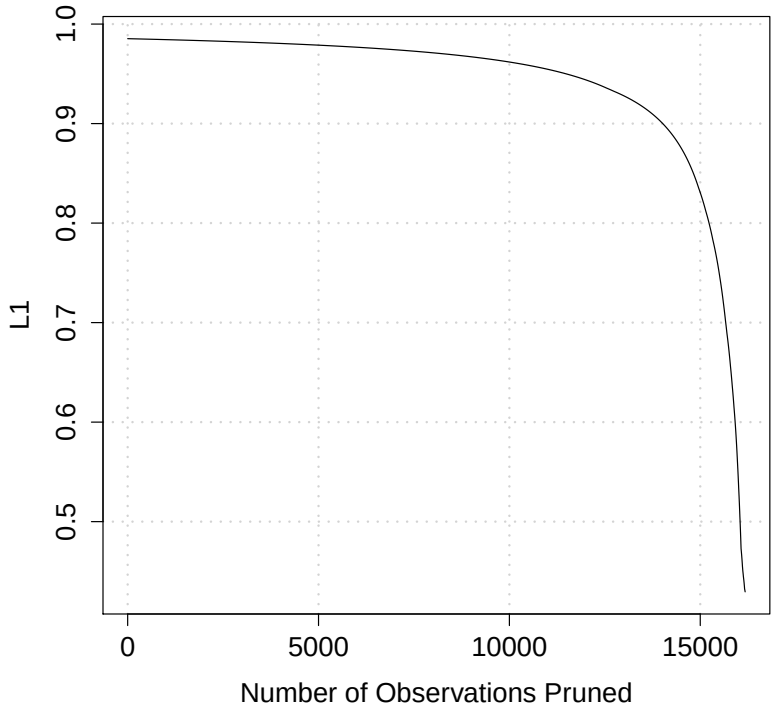
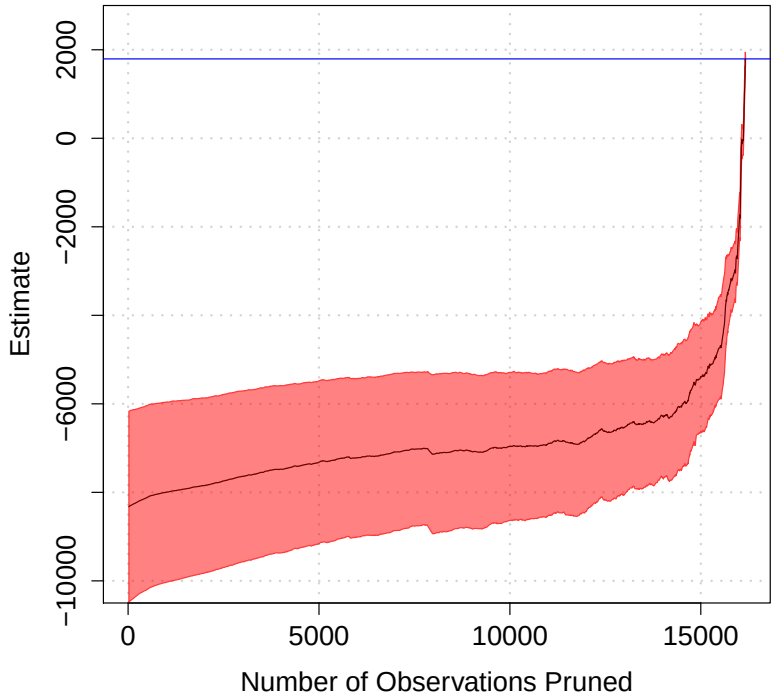
Job Training Data: Frontier and Causal Estimates

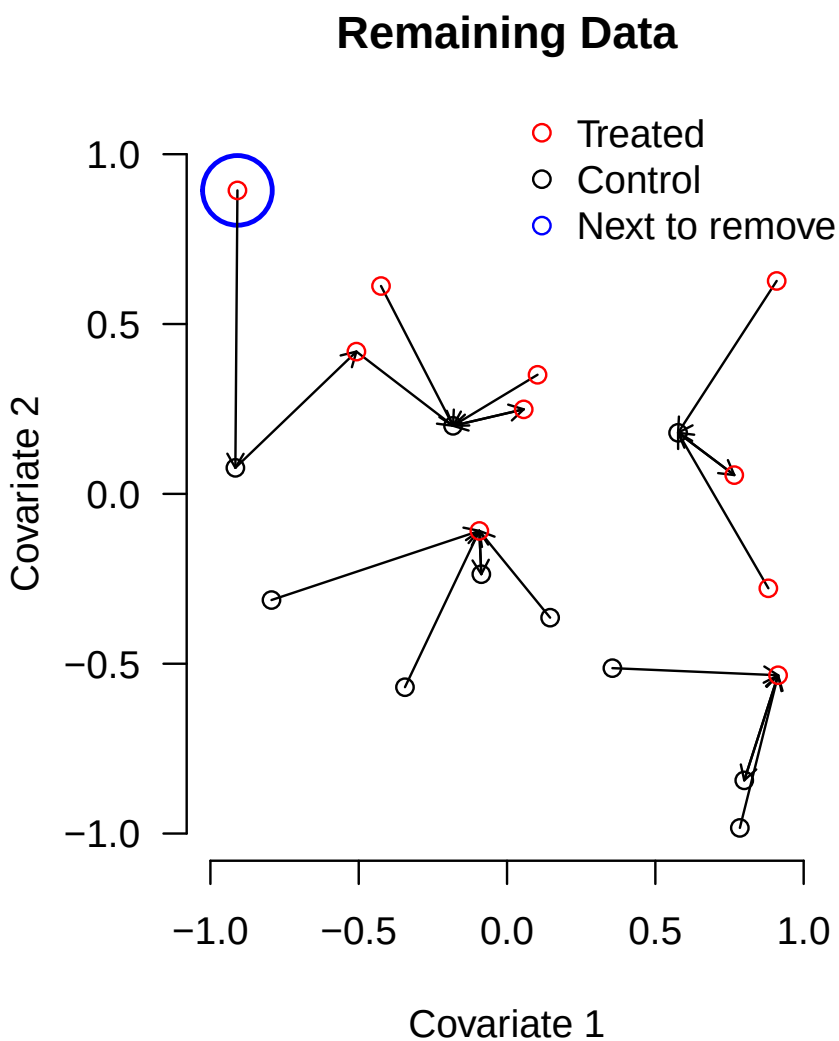


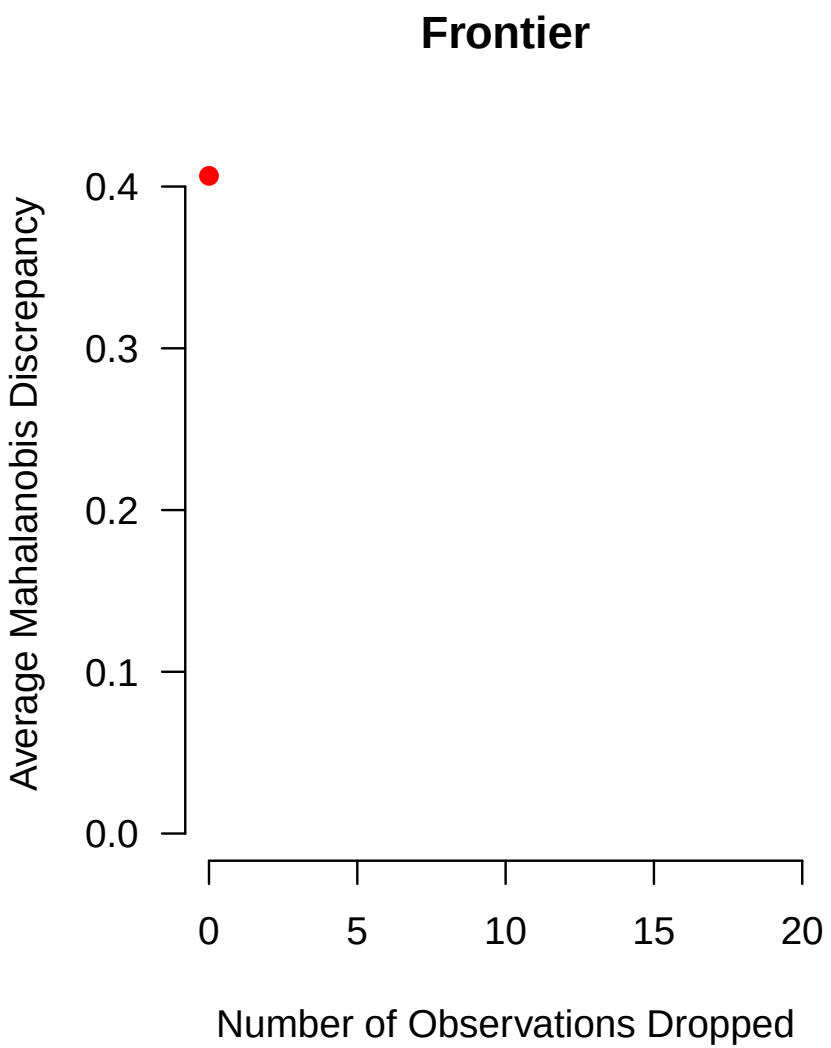


- 185 Ts; pruning most 16,252 Cs won't increase variance much
- Huge bias-variance trade-off after pruning most Cs
- Estimates converge to experiment after removing bias
- No mysteries: basis of inference clearly revealed

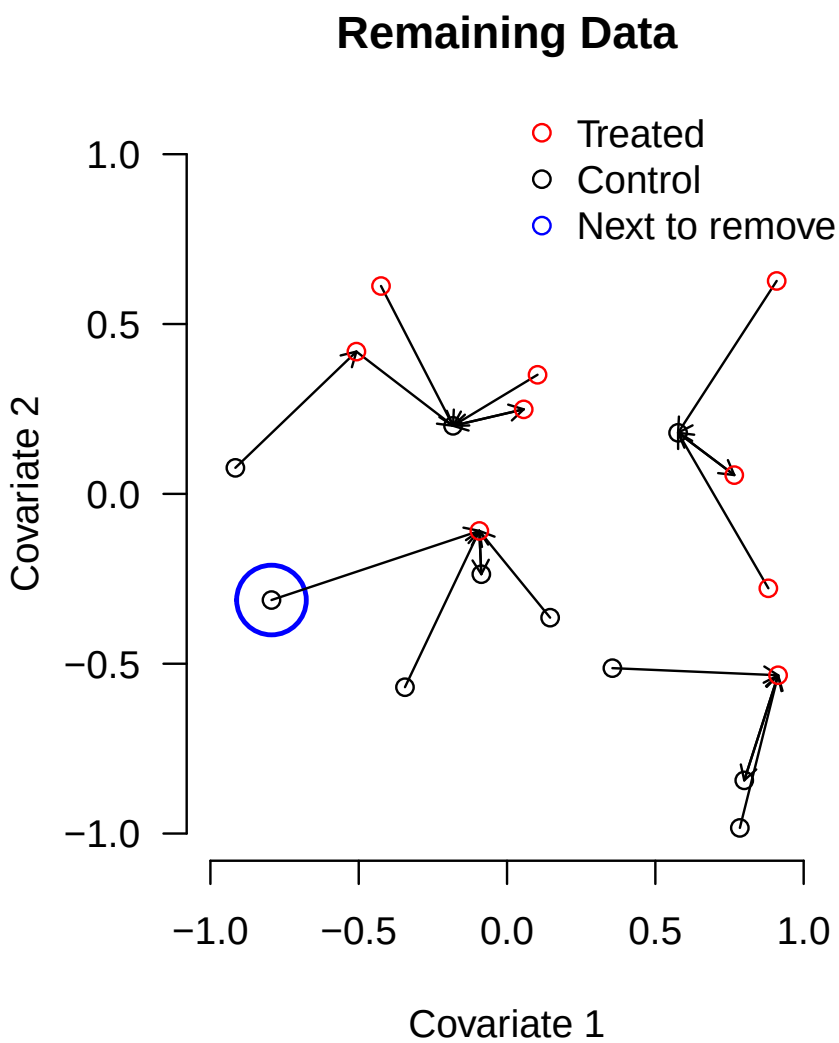
Constructing the FSATT Mahalanobis Frontier

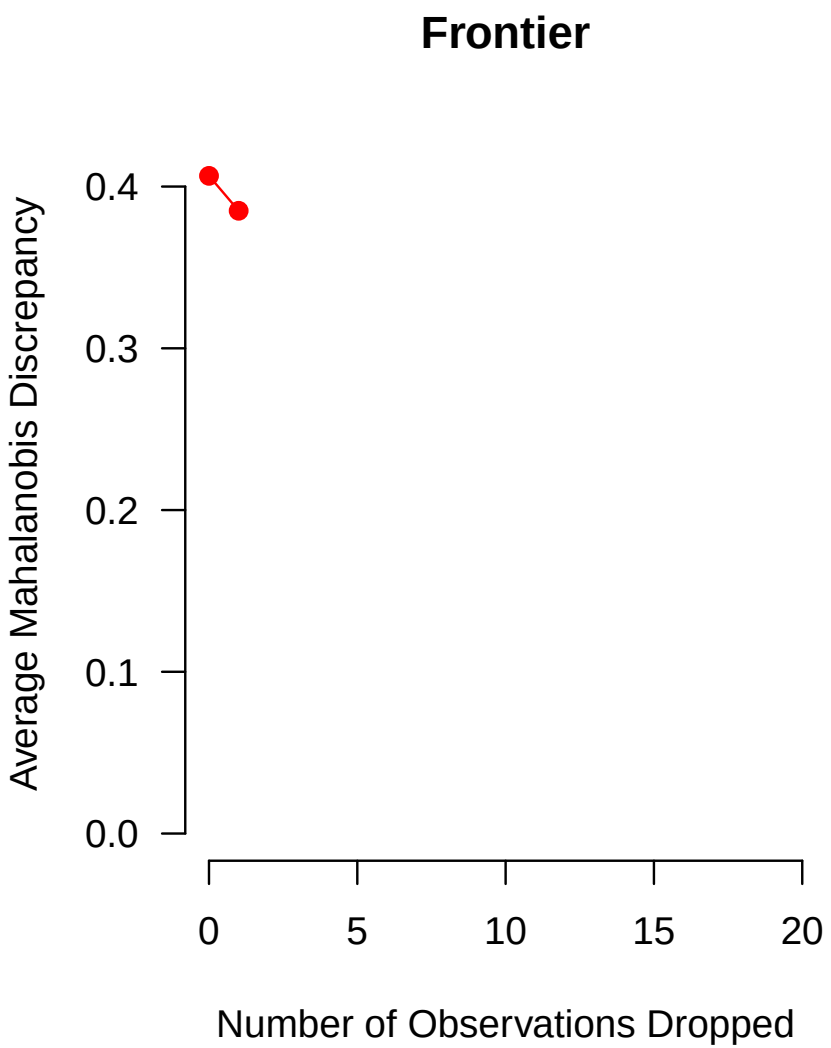
Constructing the FSATT Mahalanobis Frontier





Constructing the FSATT Mahalanobis Frontier





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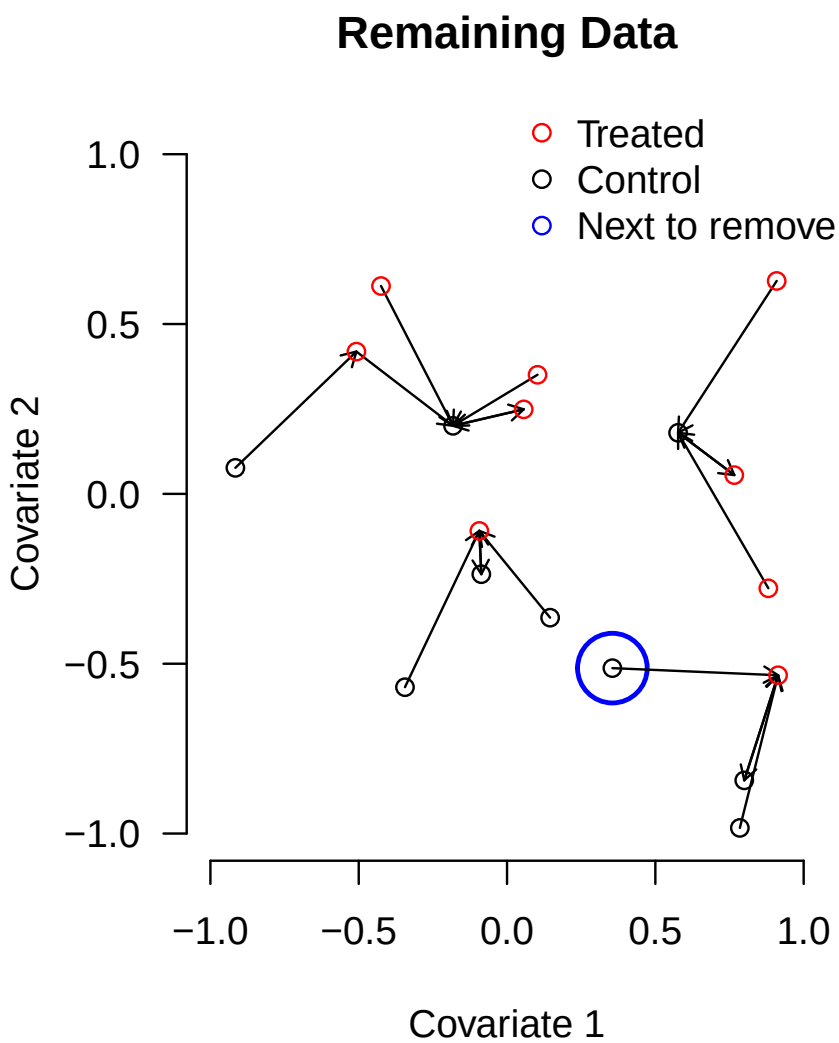

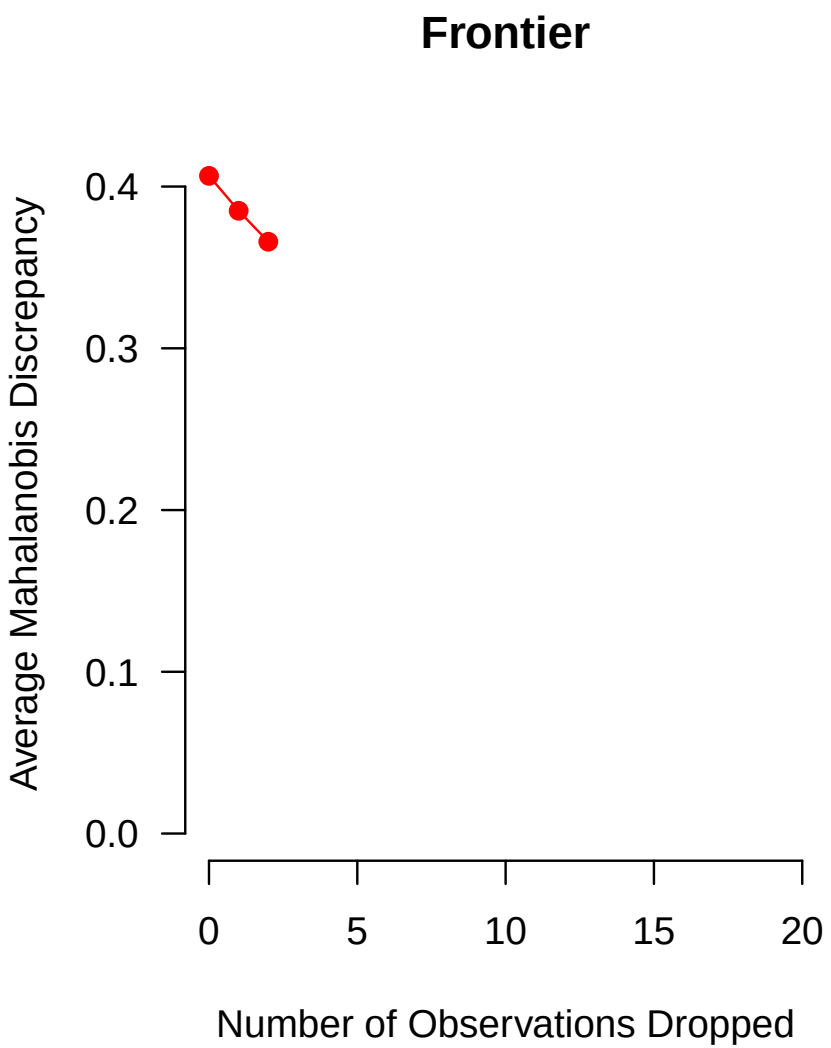

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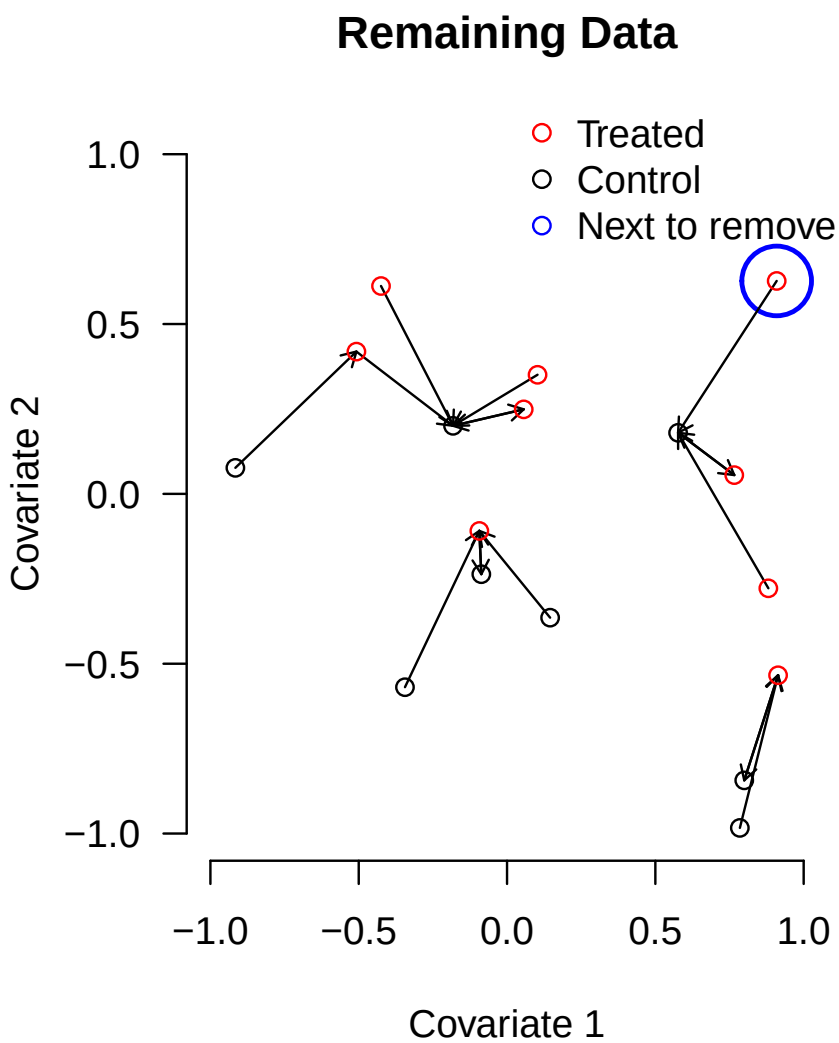

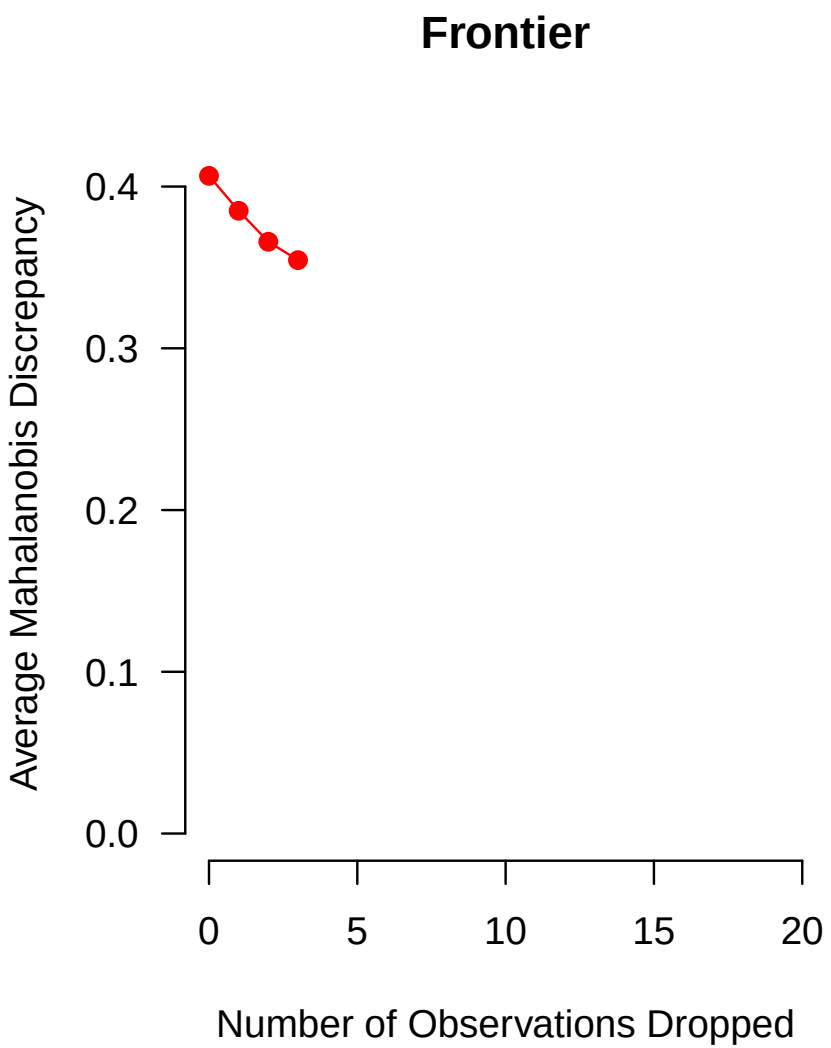

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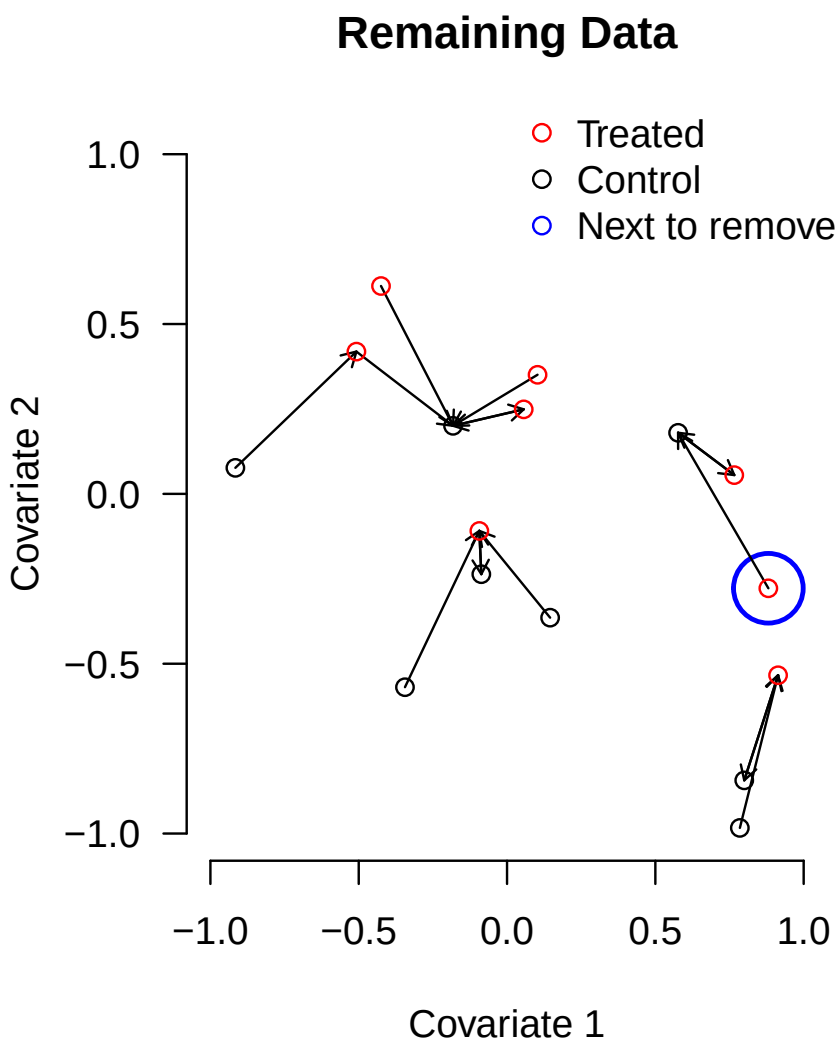

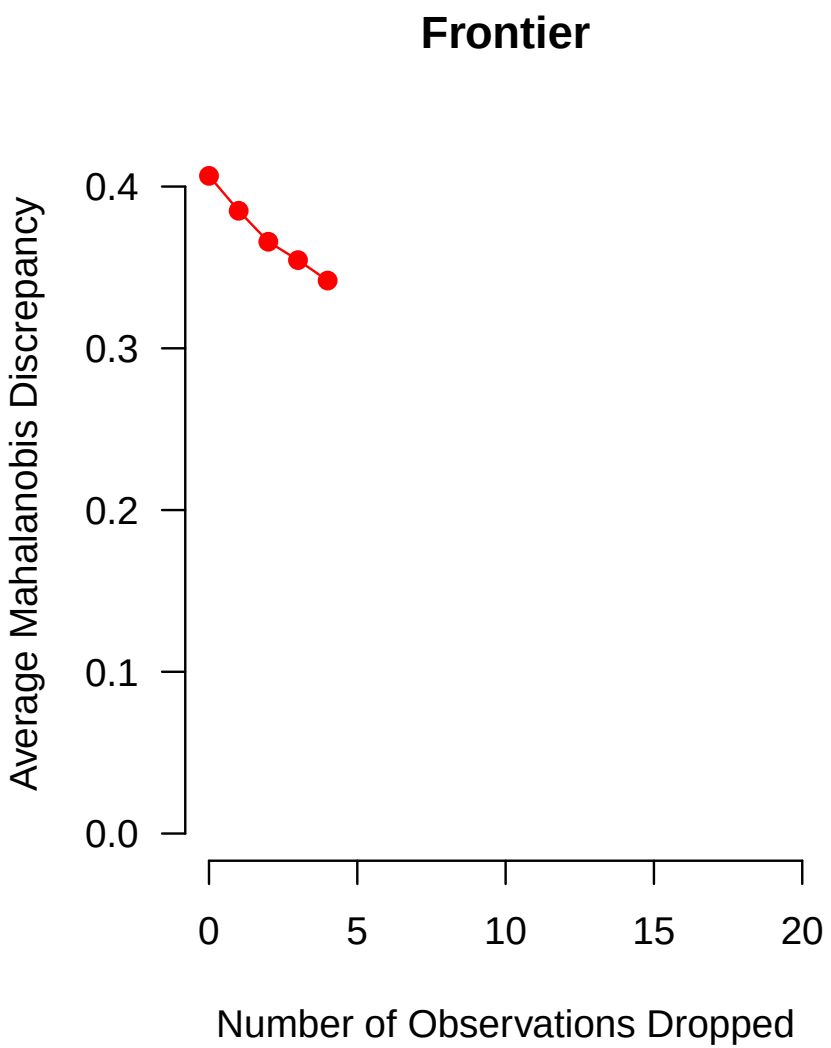

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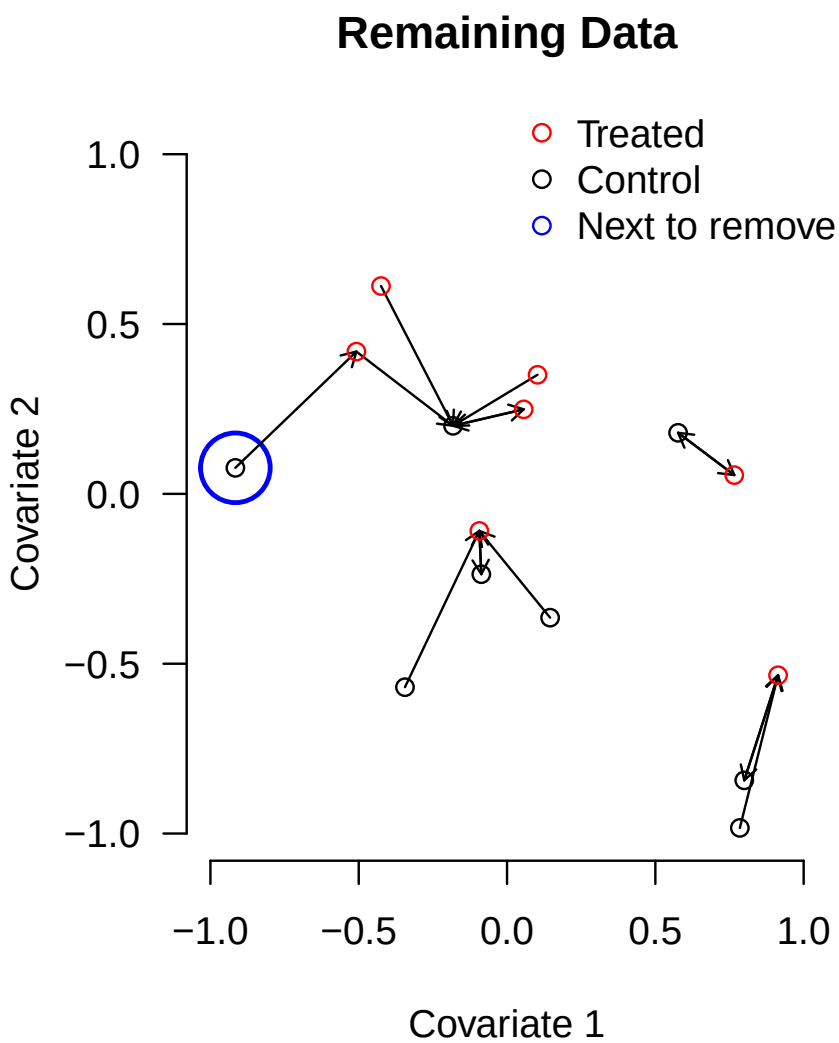

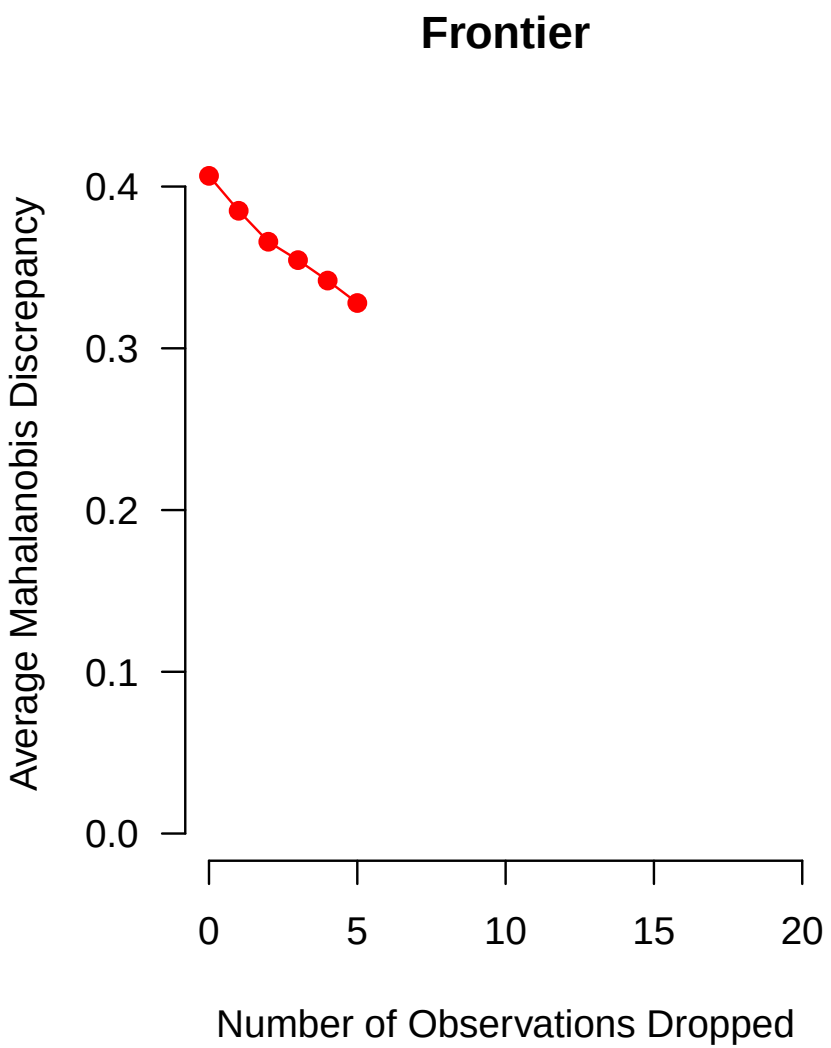

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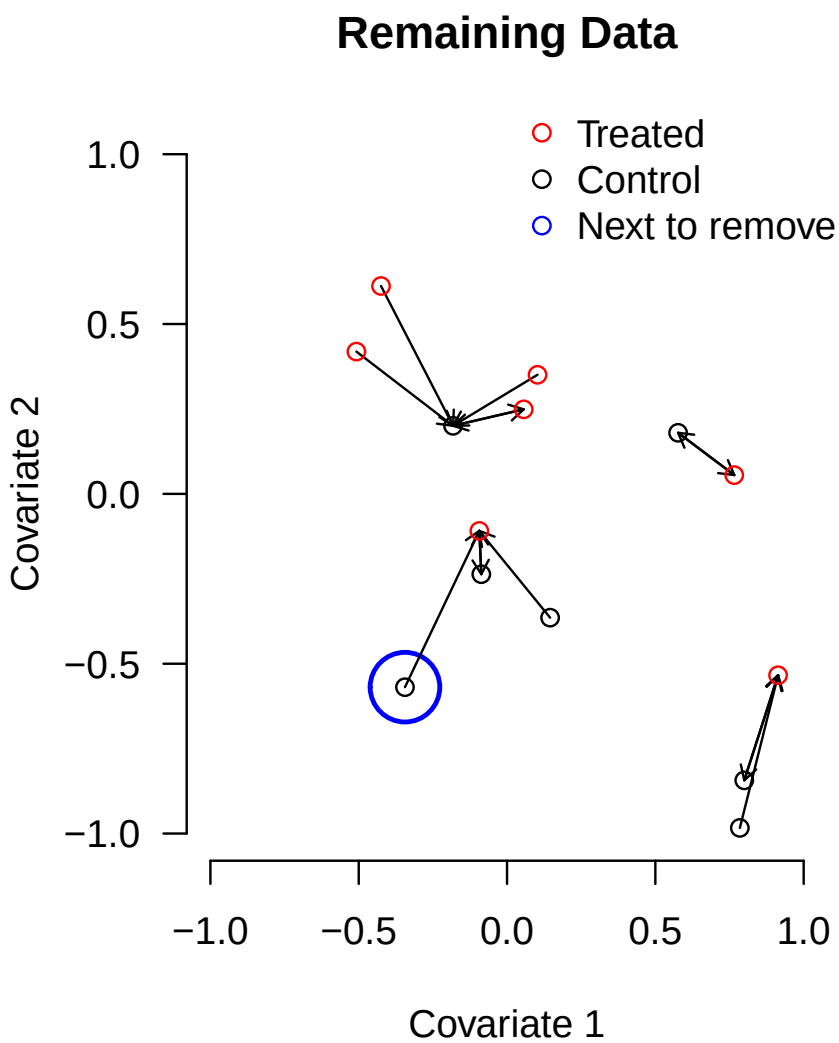

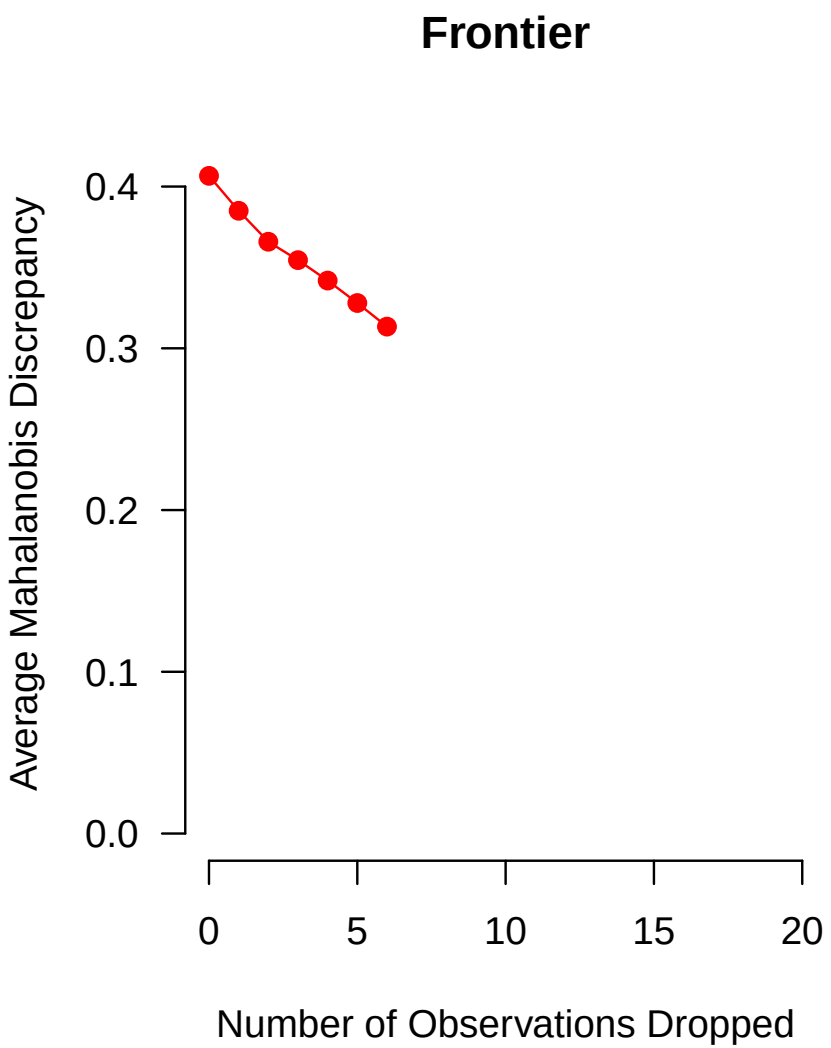

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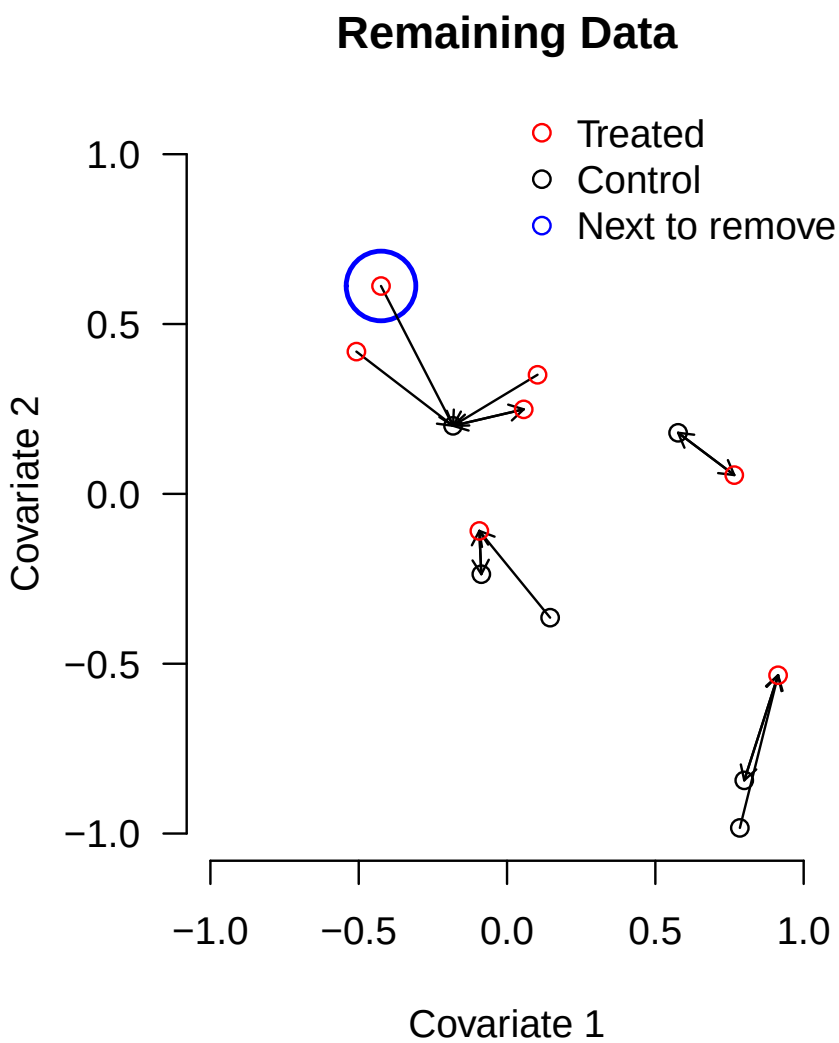

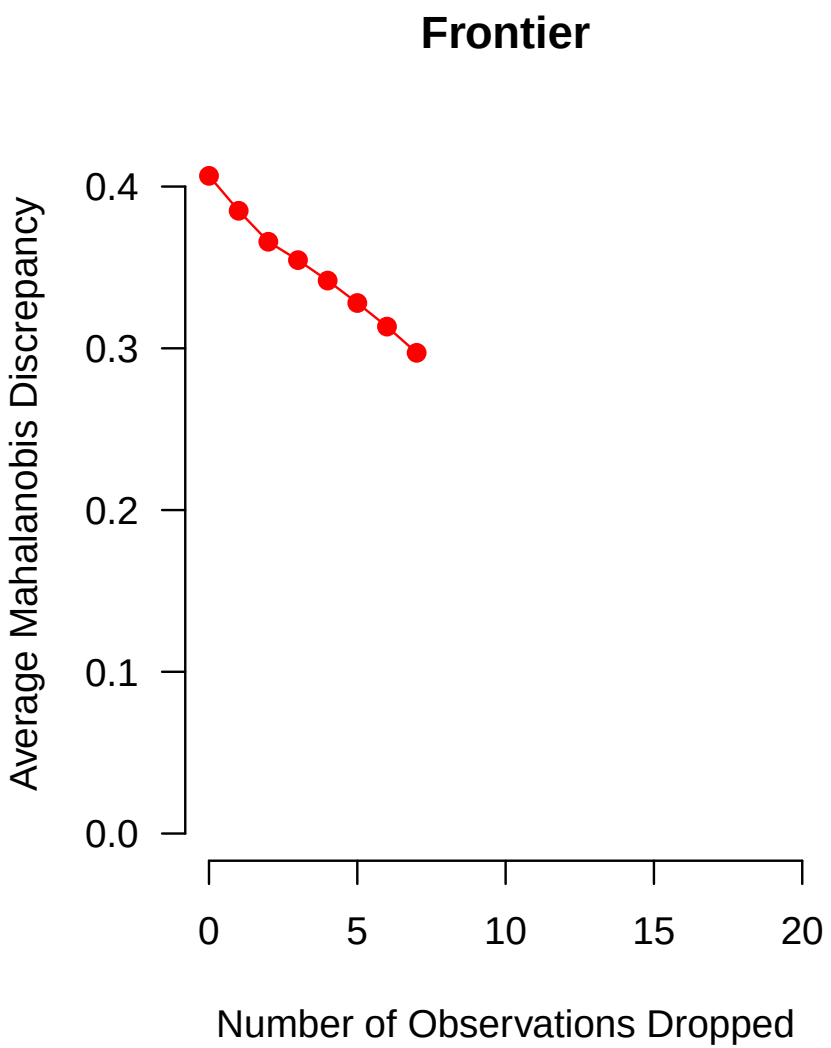

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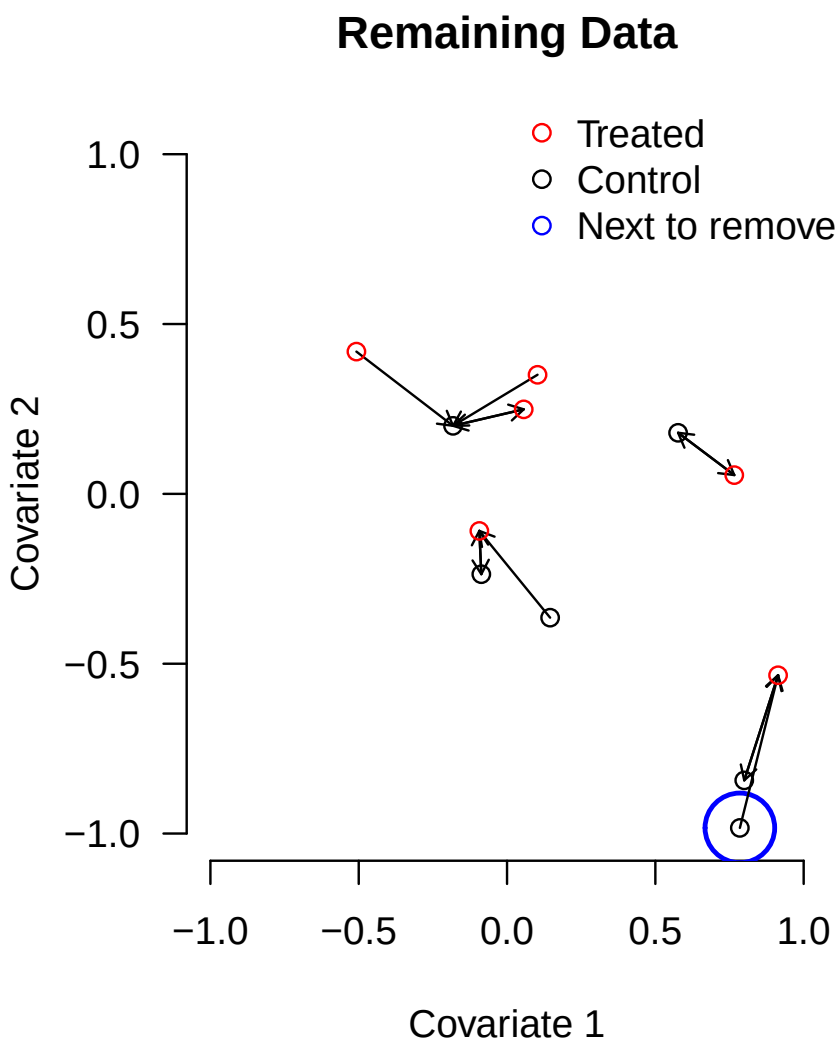

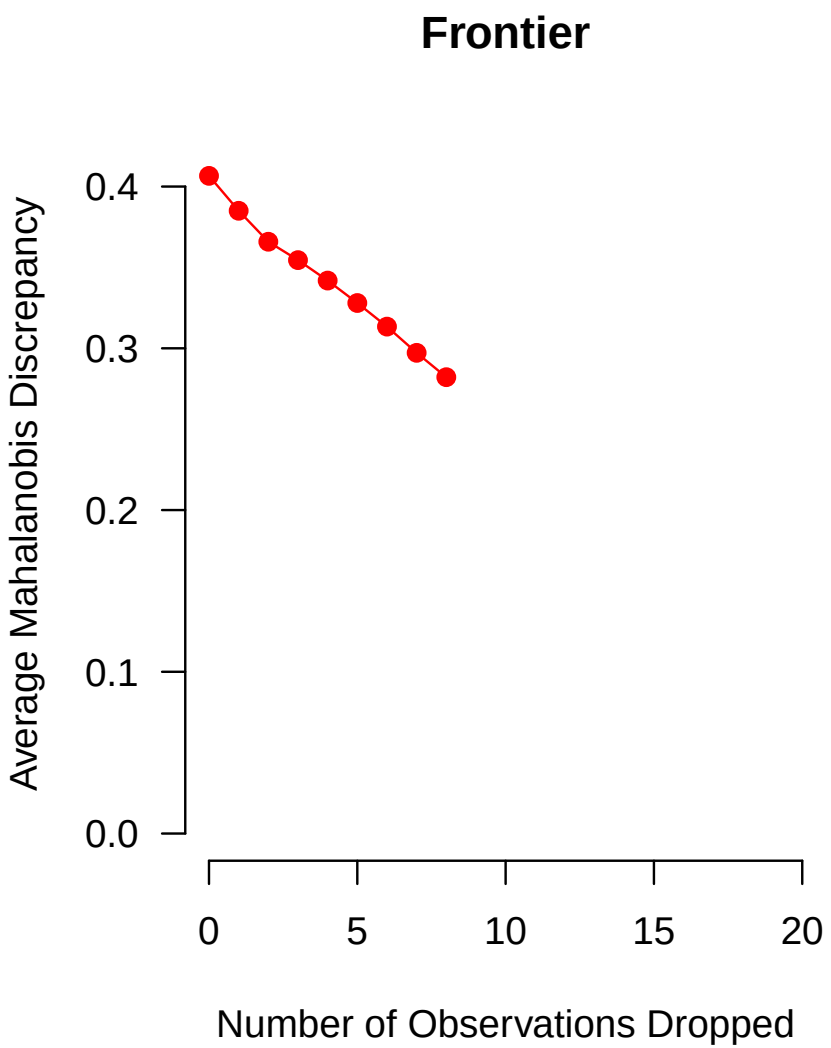

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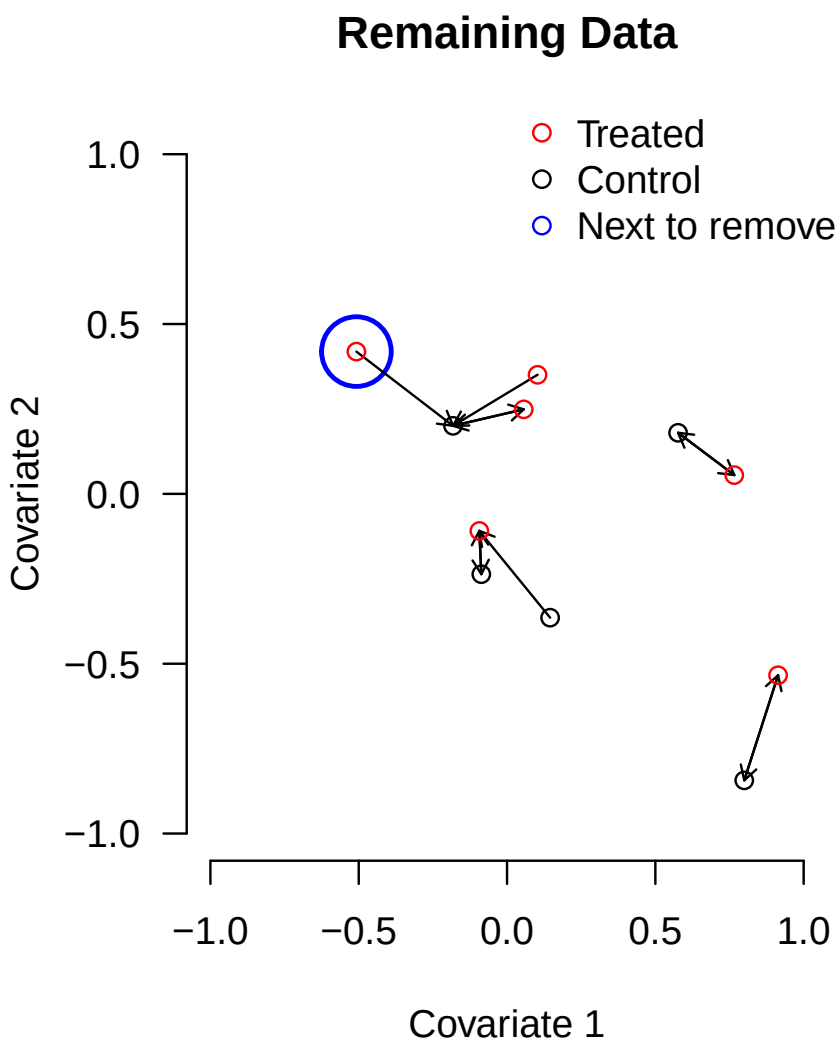

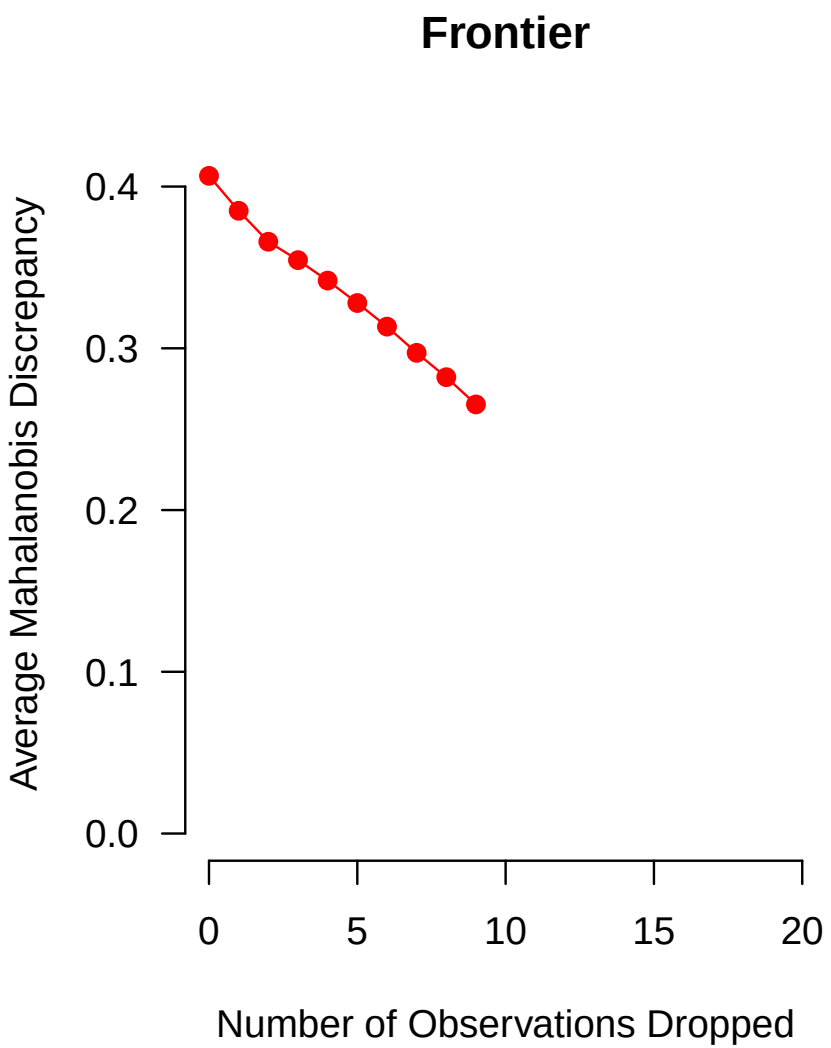

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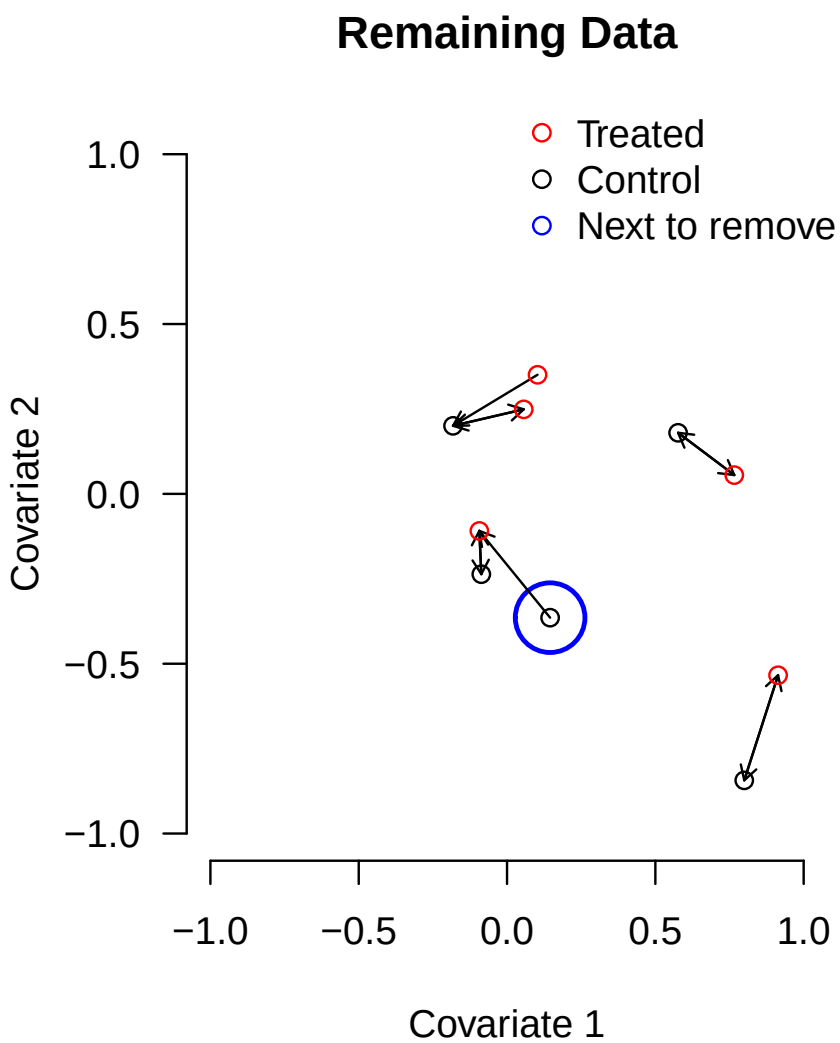

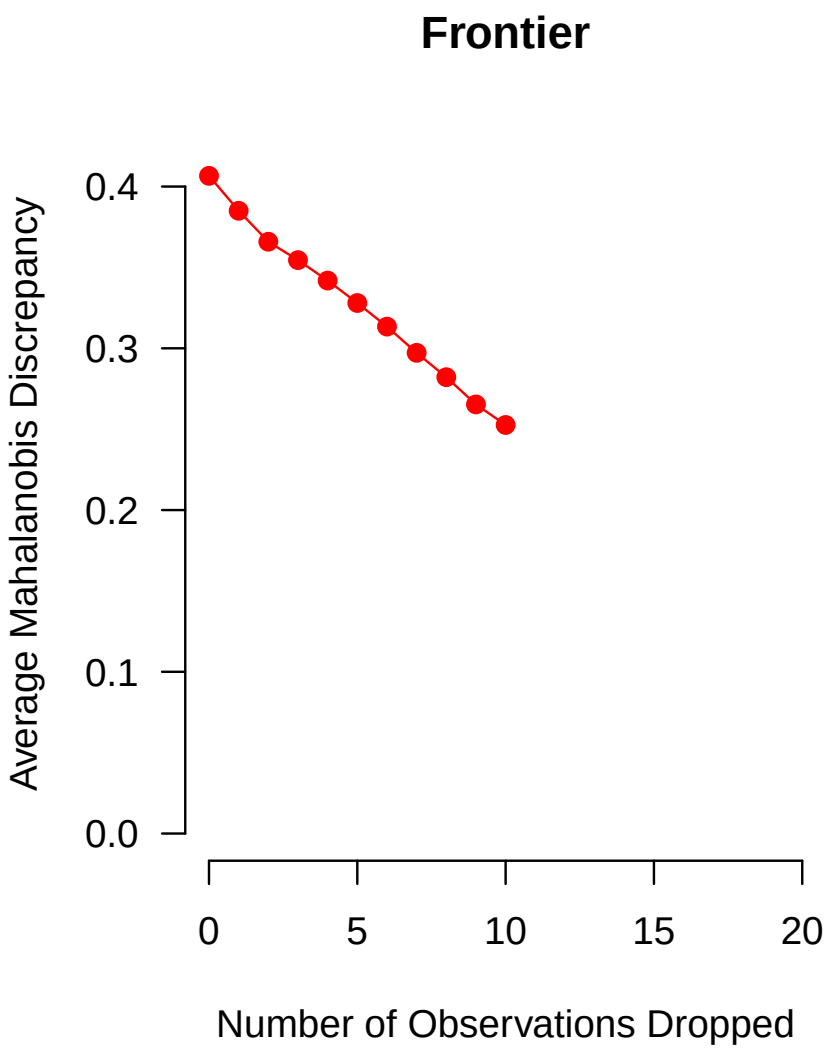

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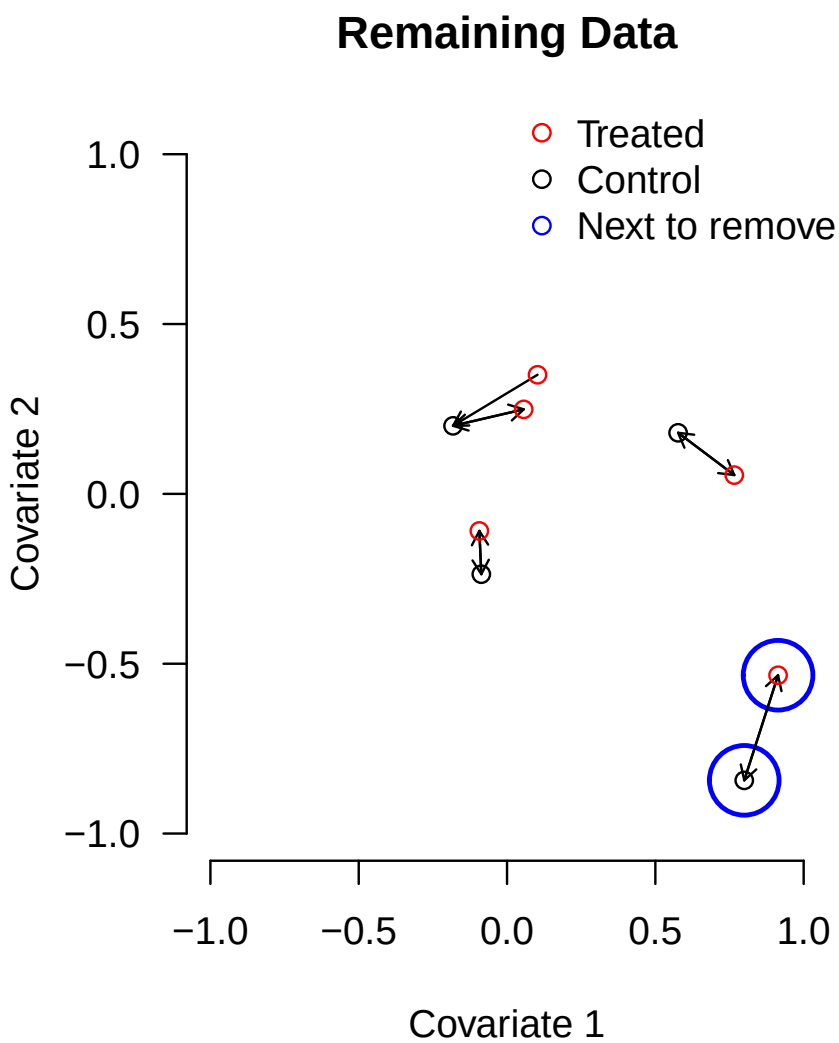

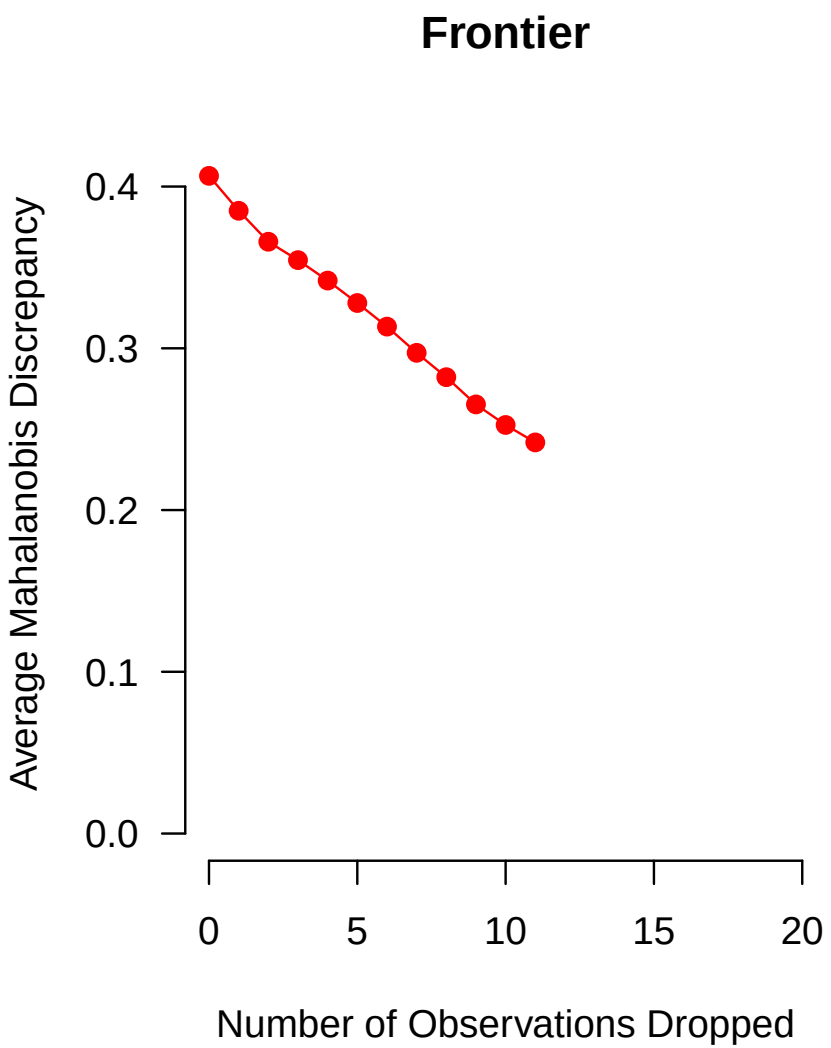

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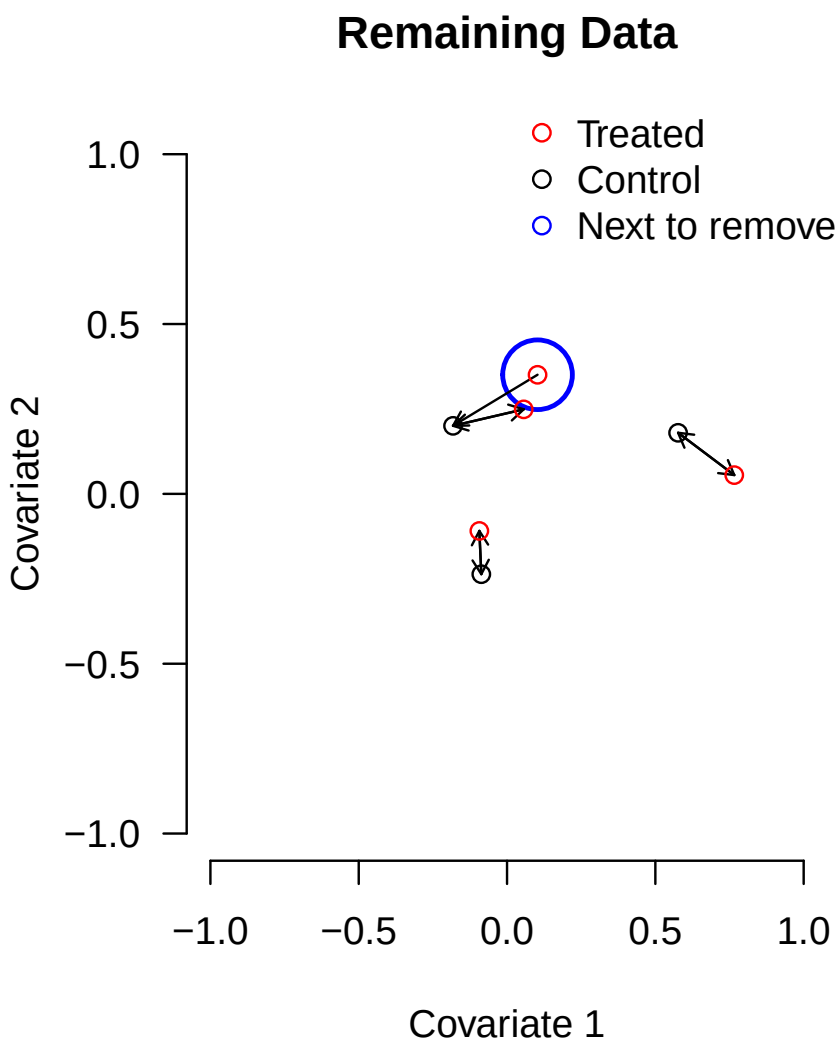

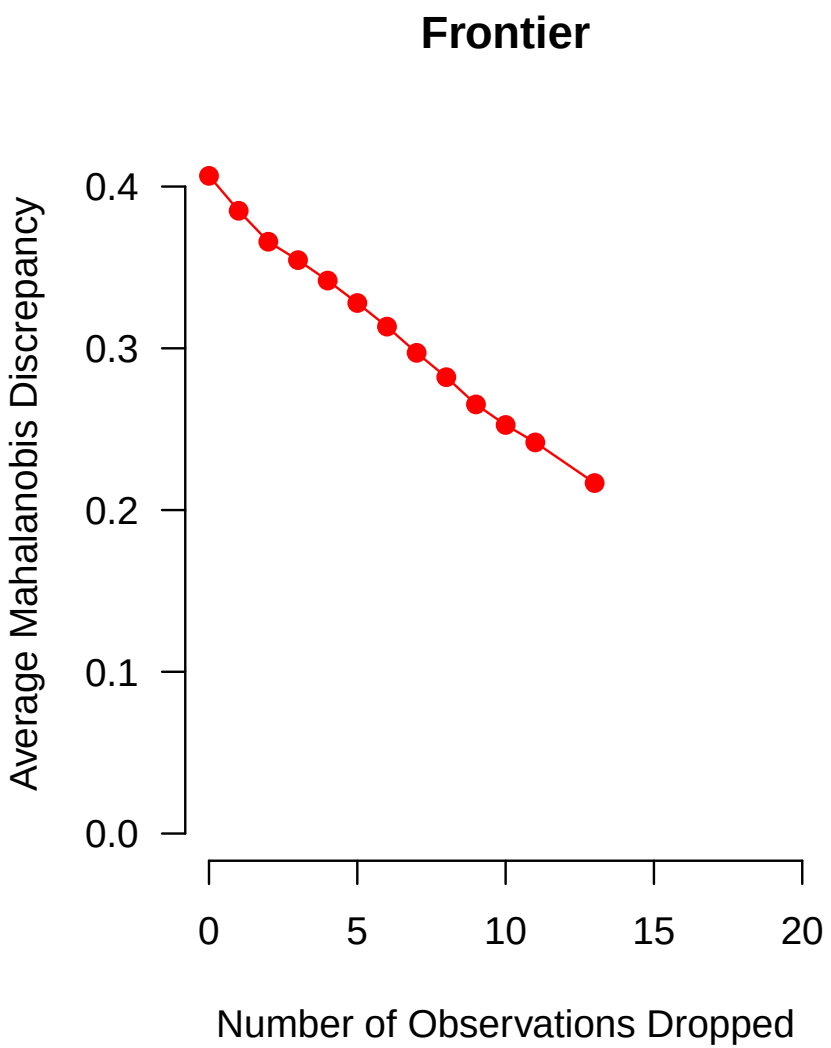

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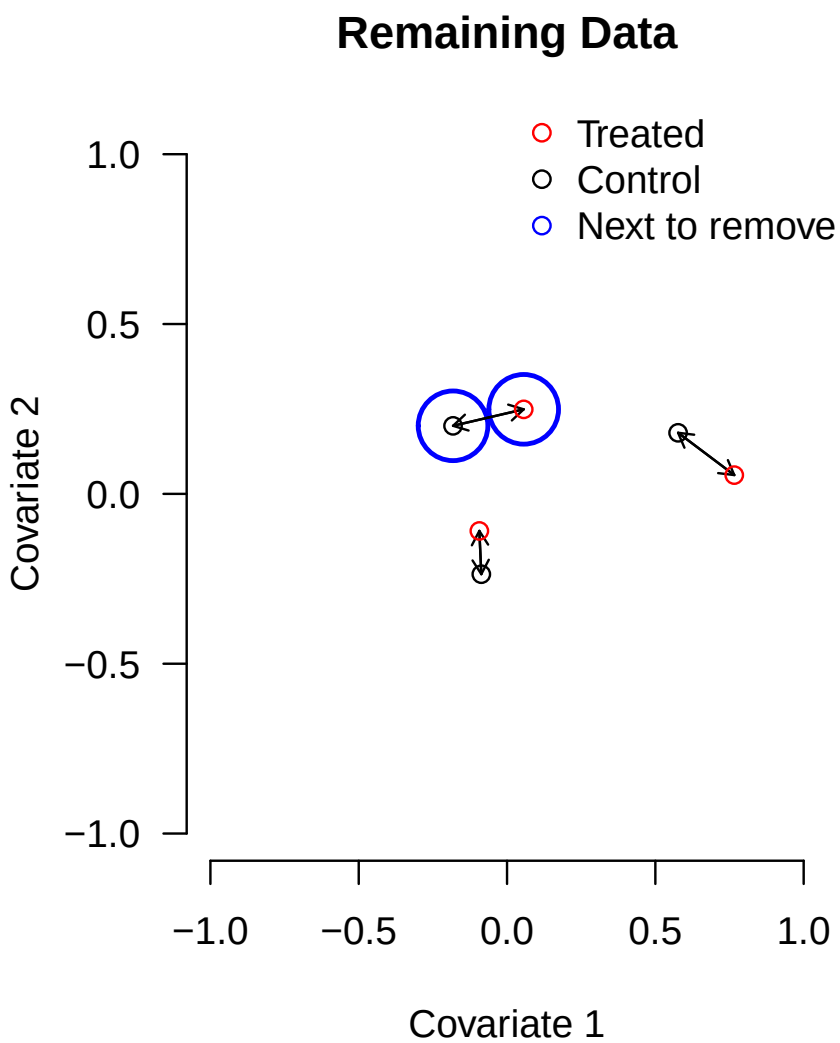

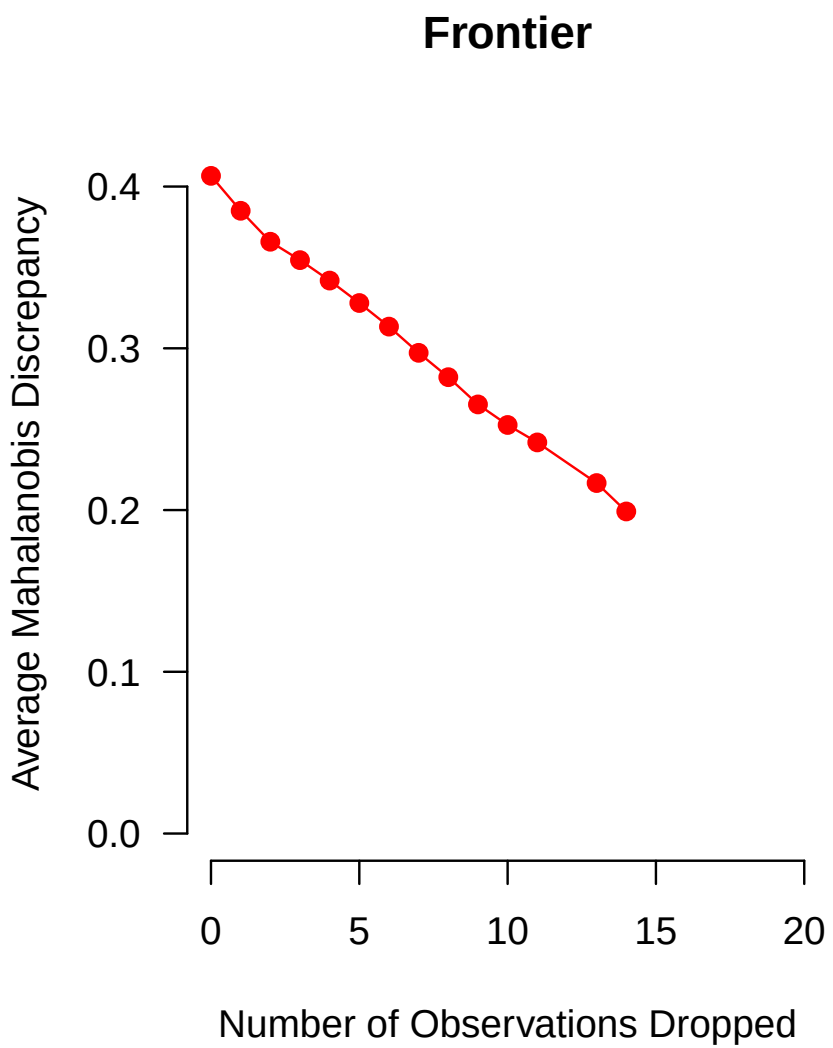

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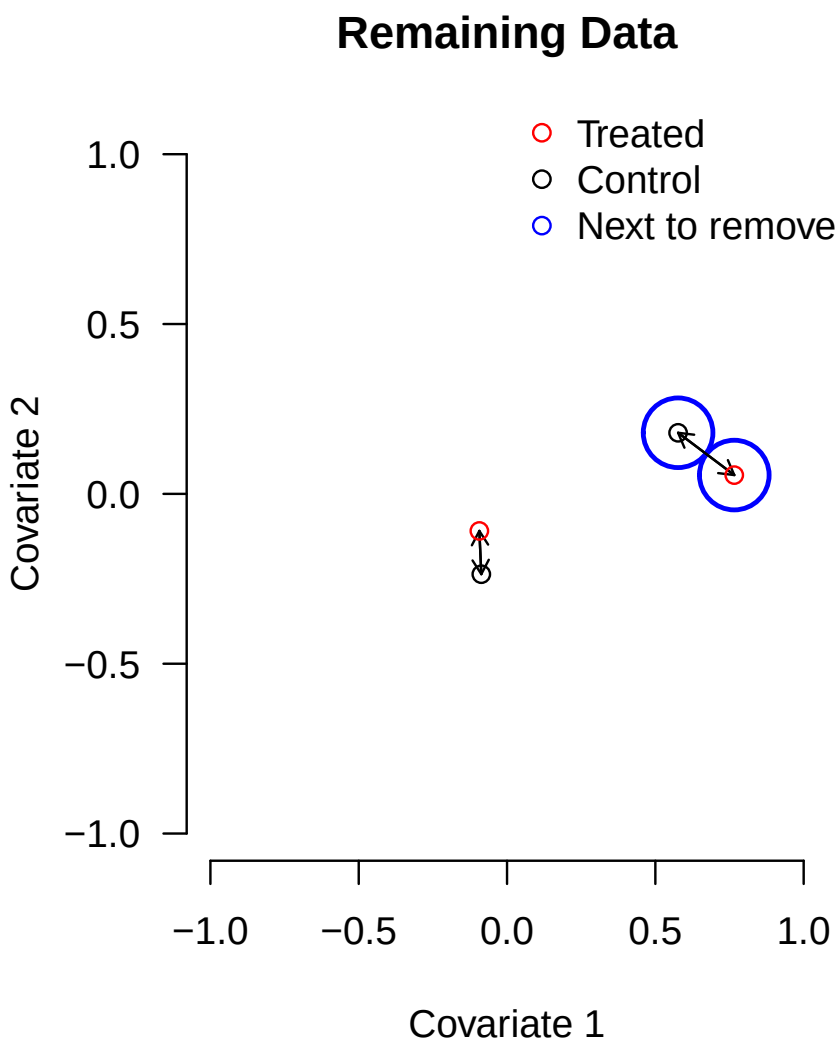

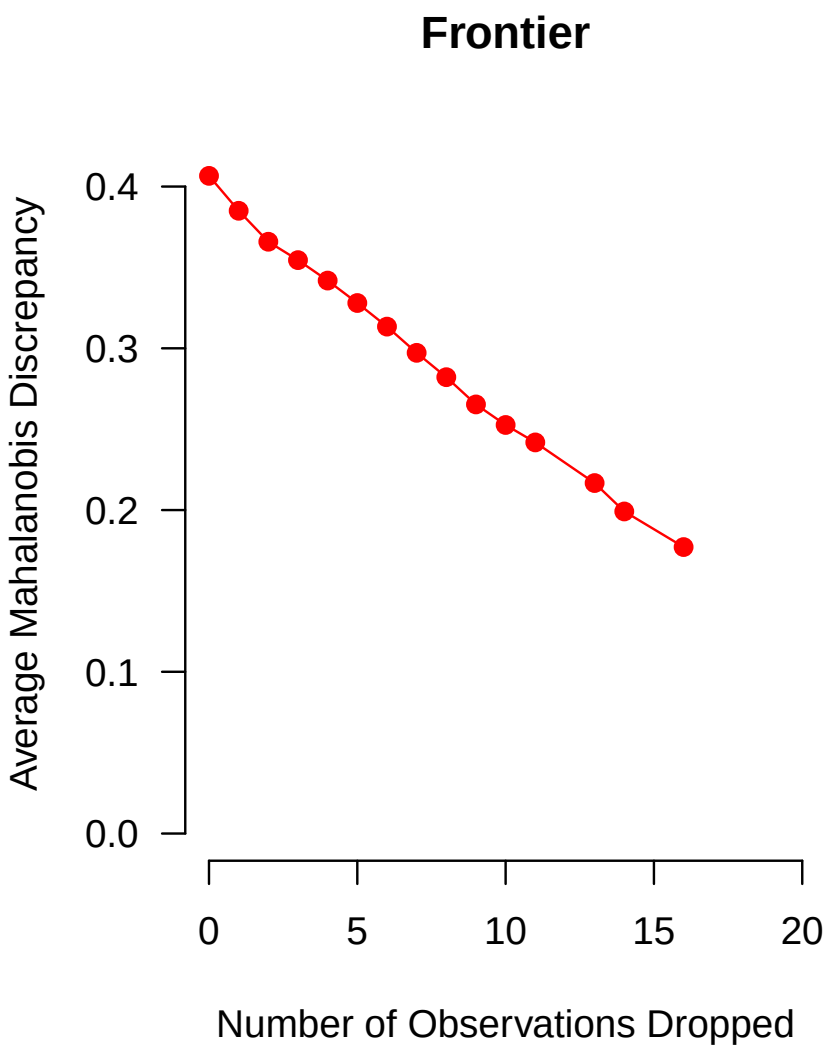

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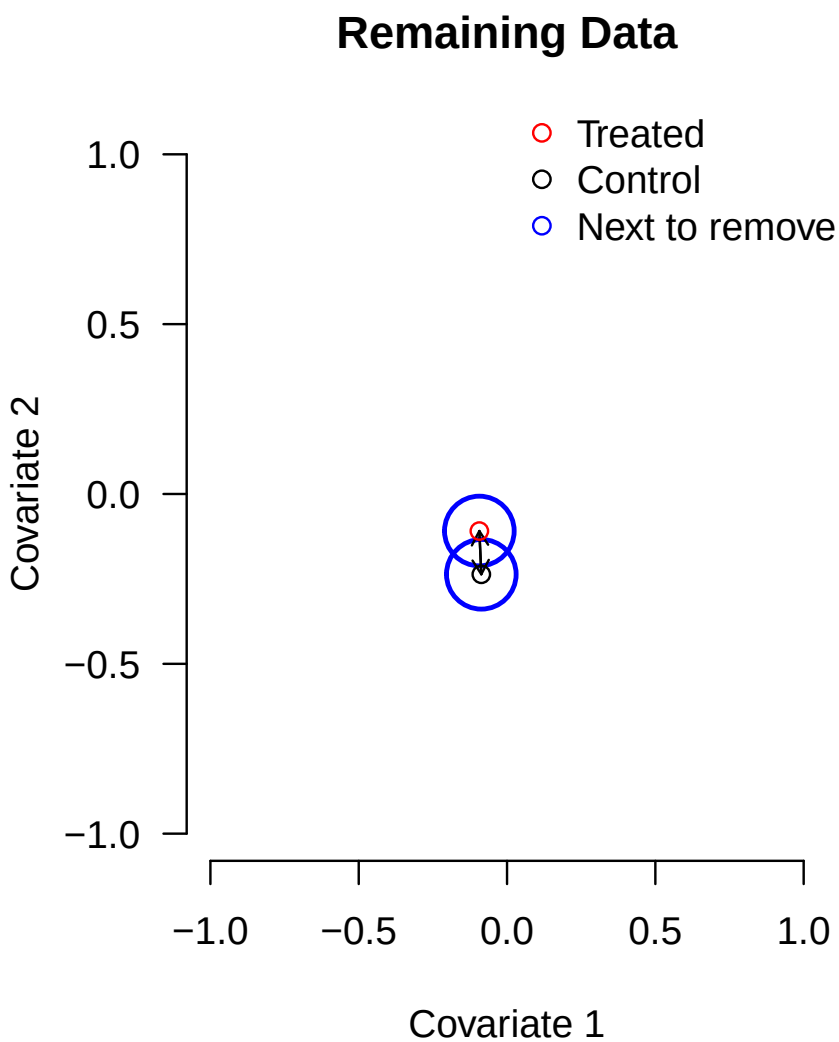
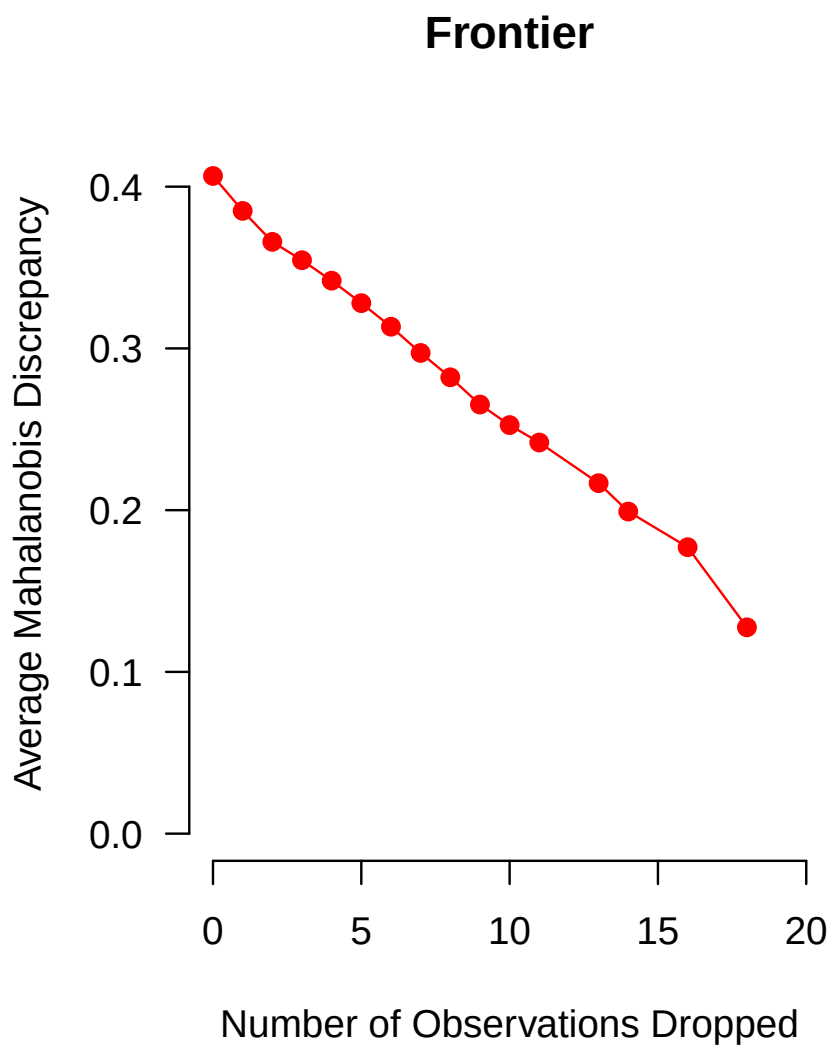
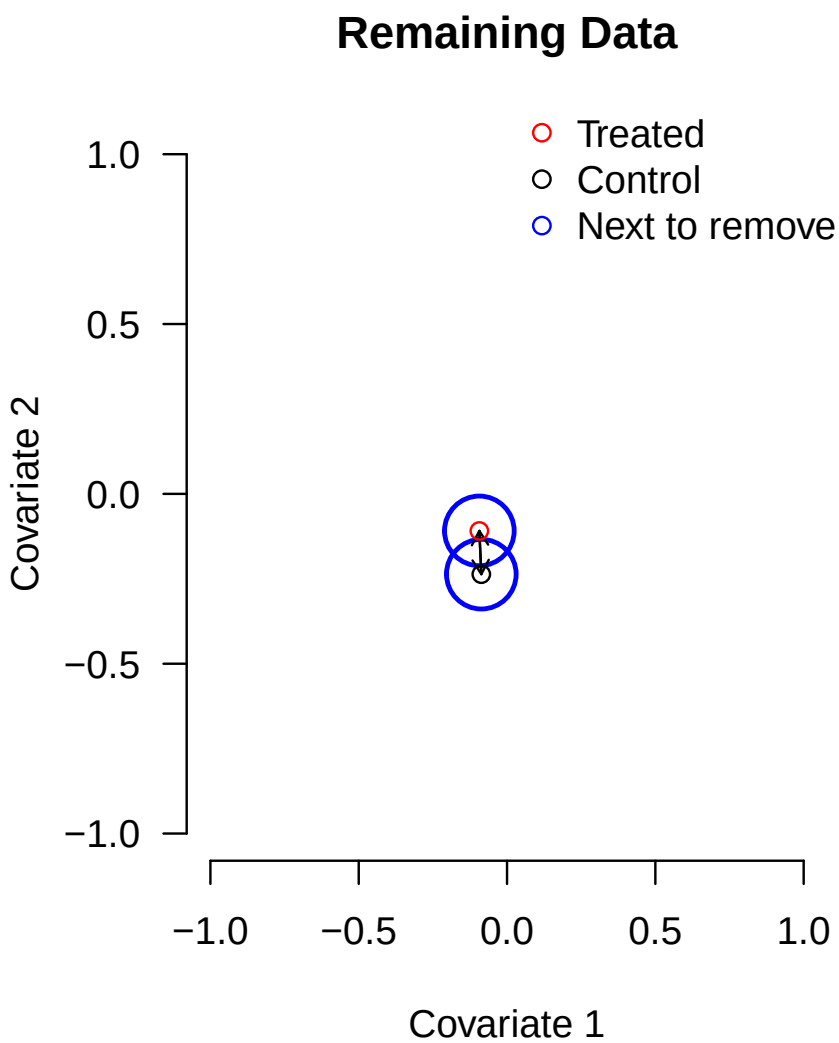
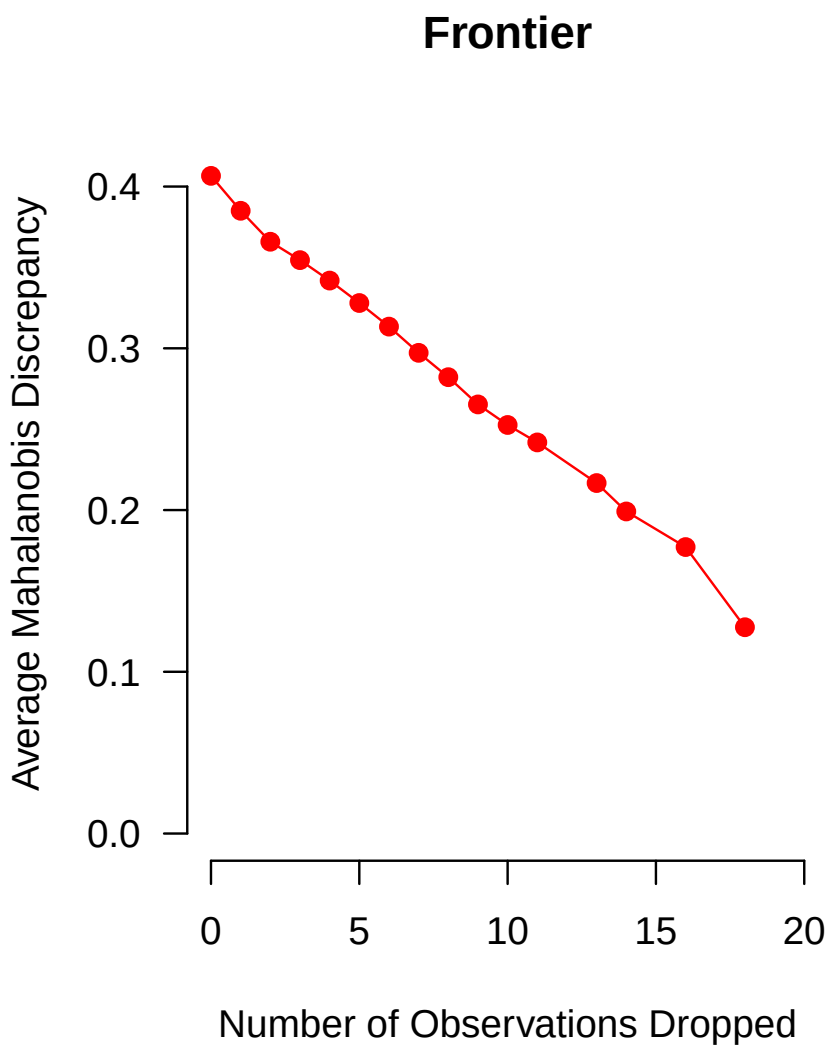




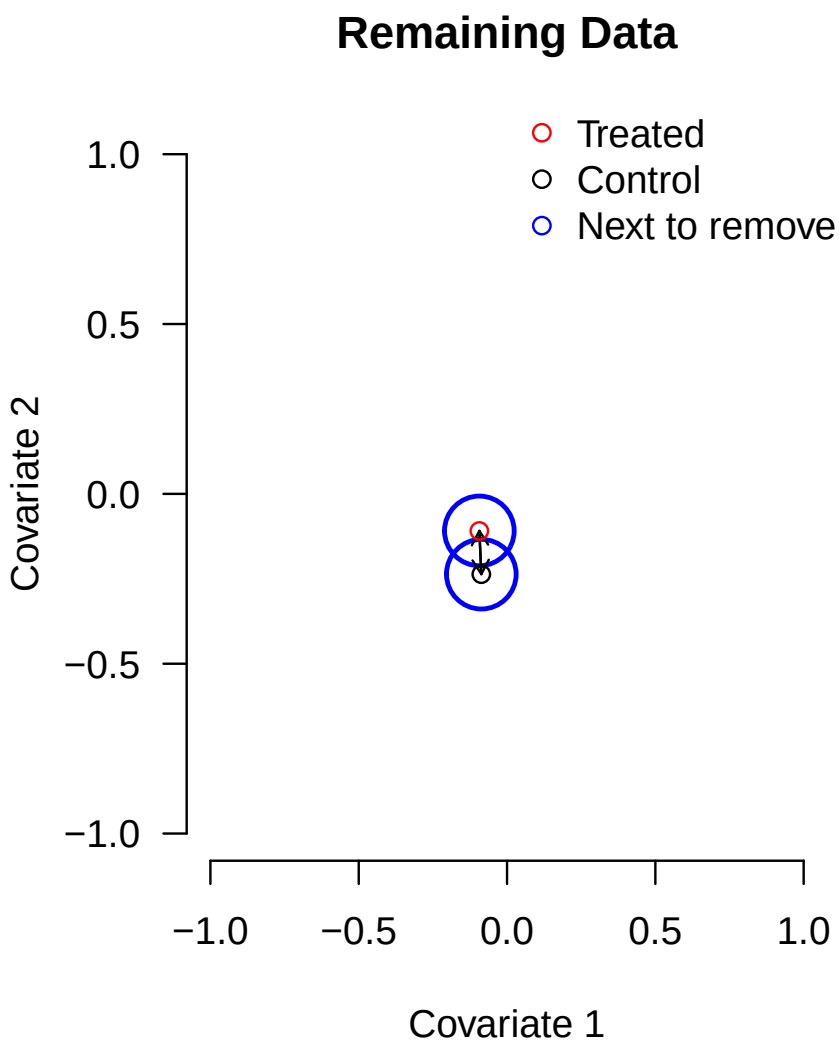
Constructing the FSATT Mahalanobis Frontier

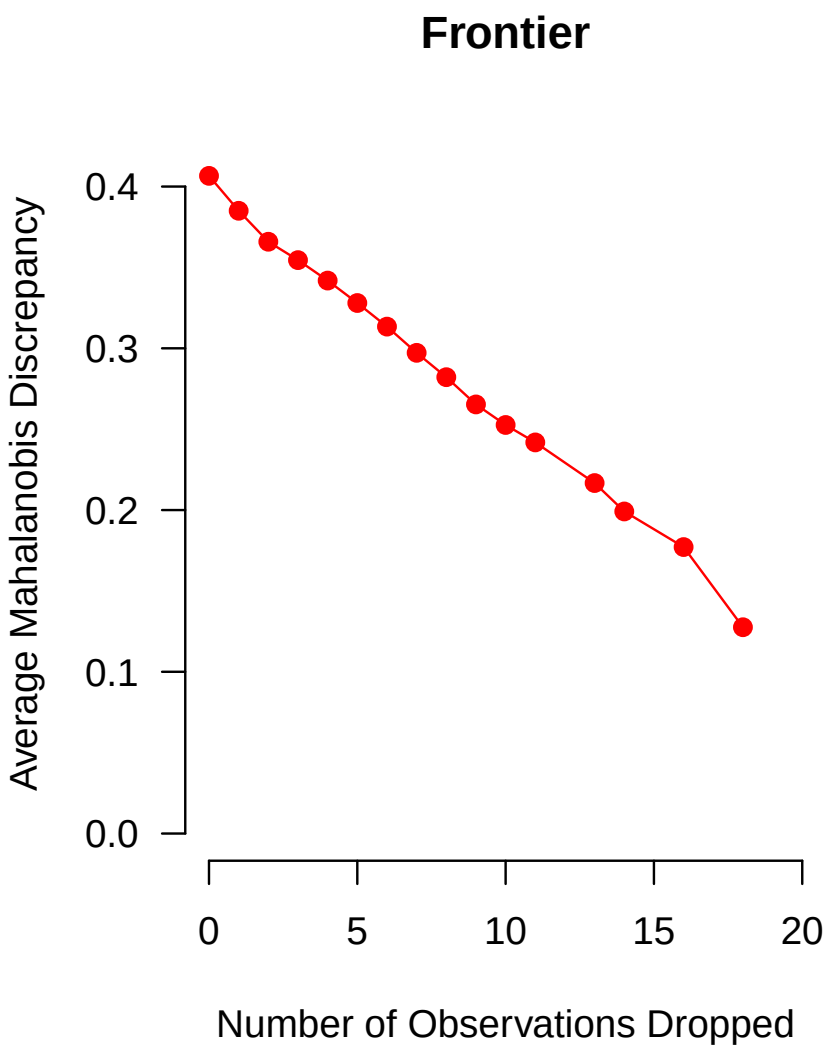




- Warning: figure omits some details!

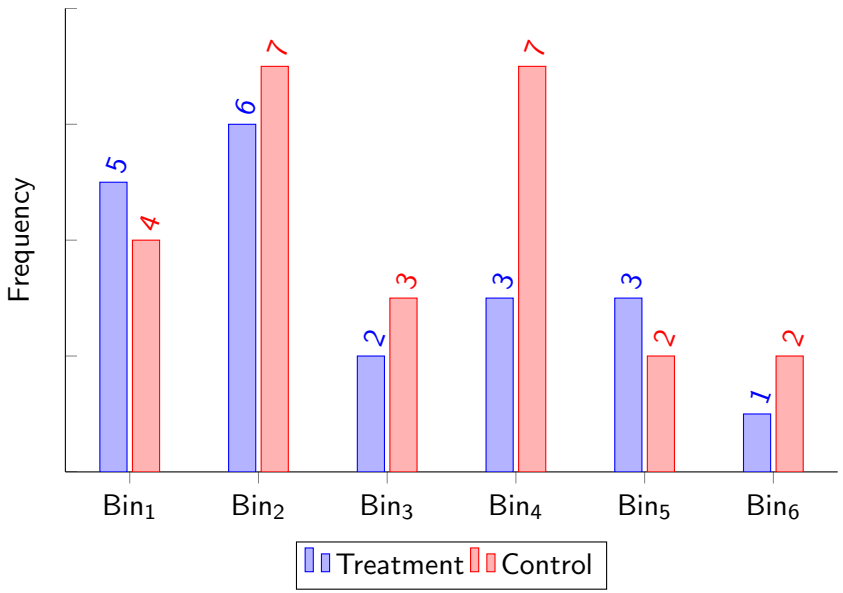
Constructing the FSATT Mahalanobis Frontier

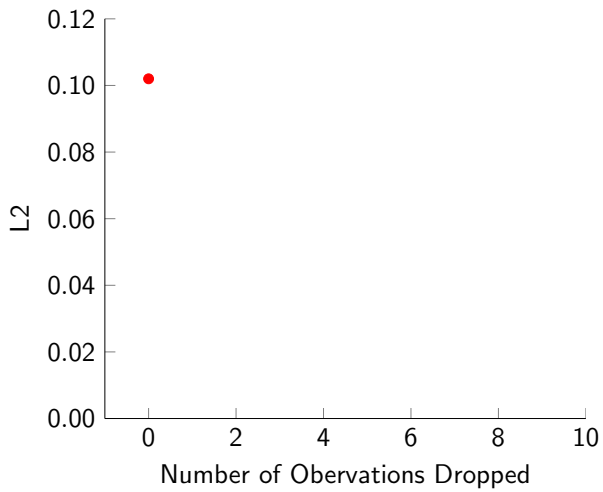




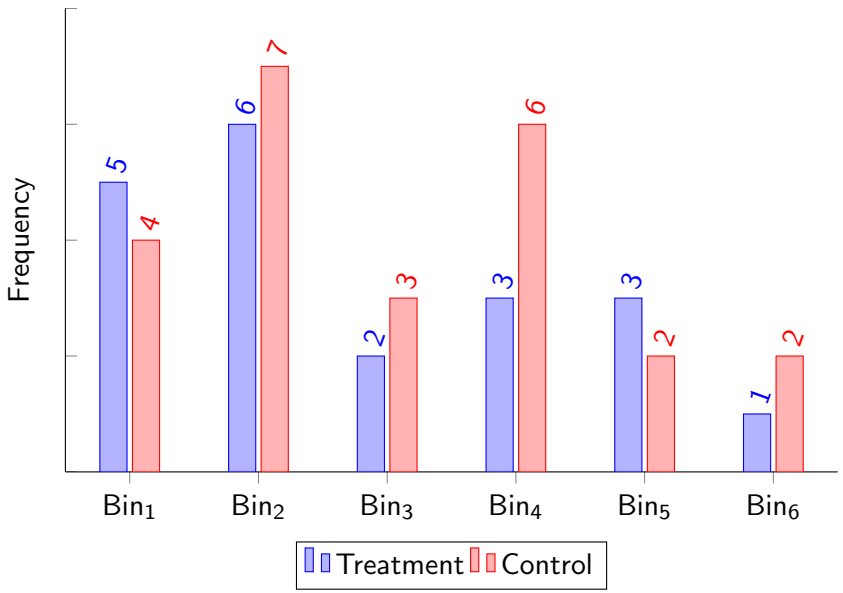
- Warning: figure omits some details!
- Very fast; works with any continuous imbalance metric

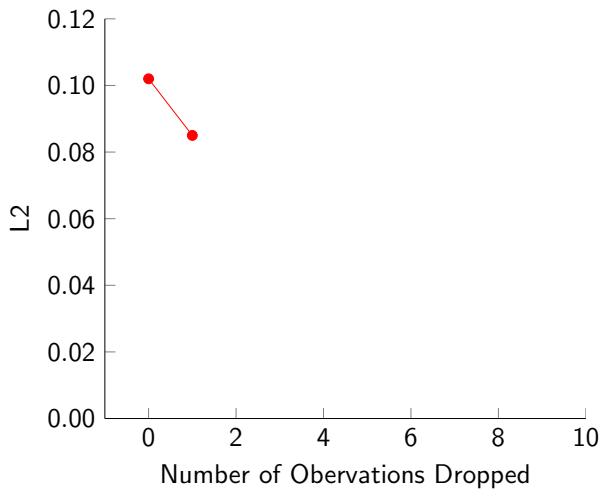
Constructing the L1/L2 SATT Frontier





Constructing the L1/L2 SATT Frontier





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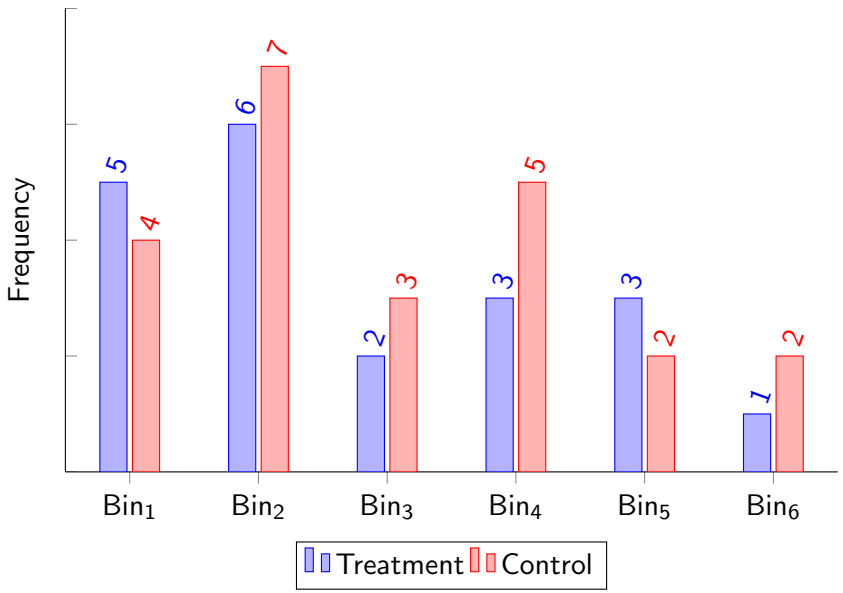

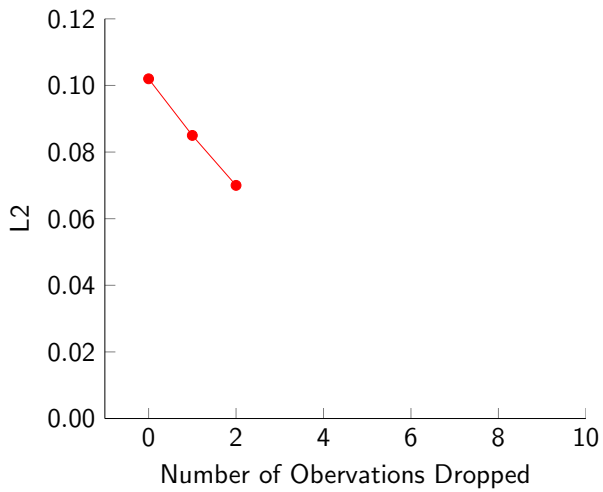

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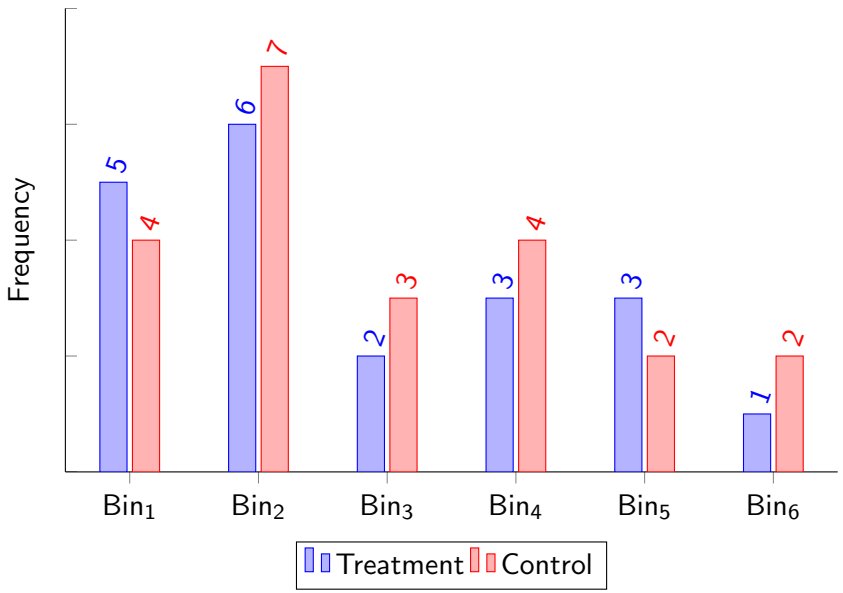

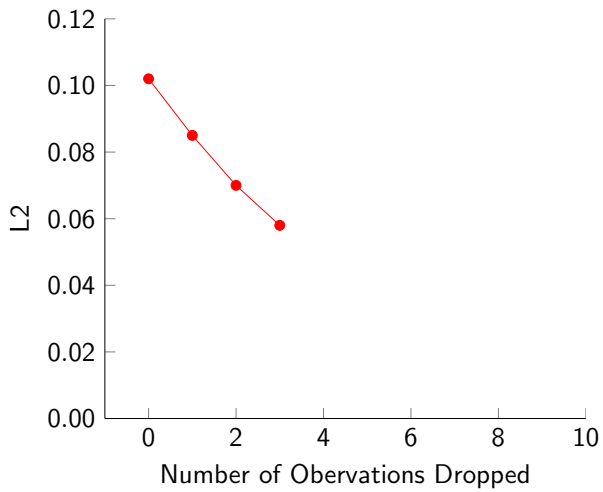

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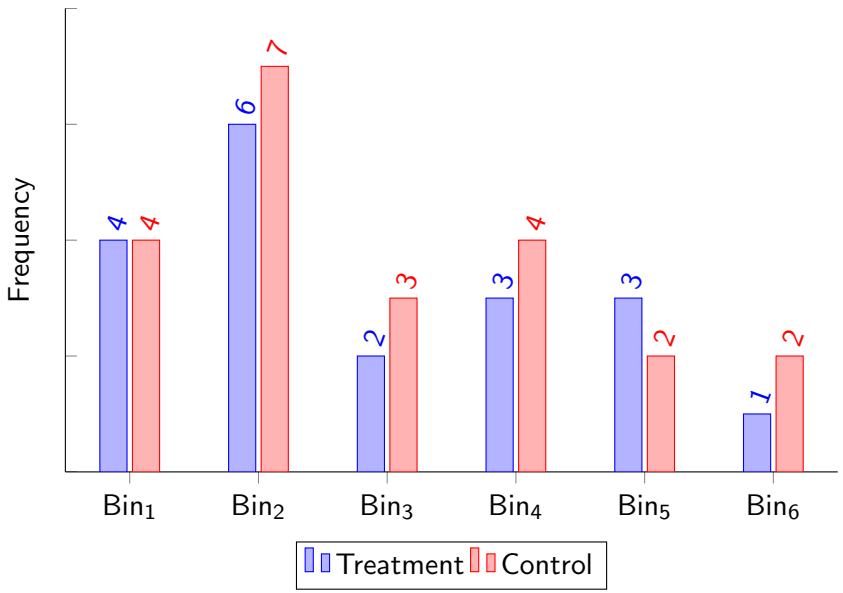

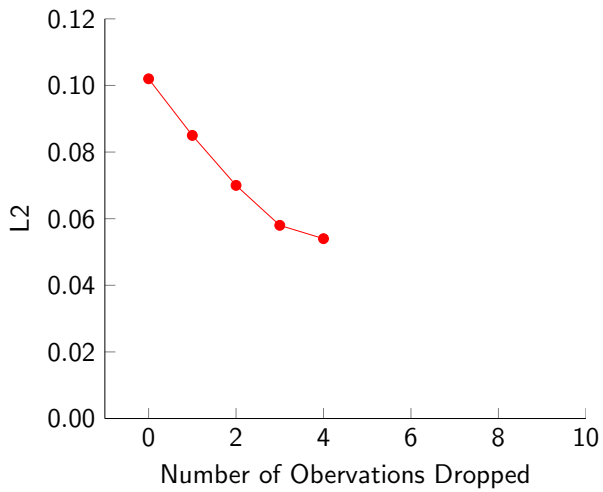

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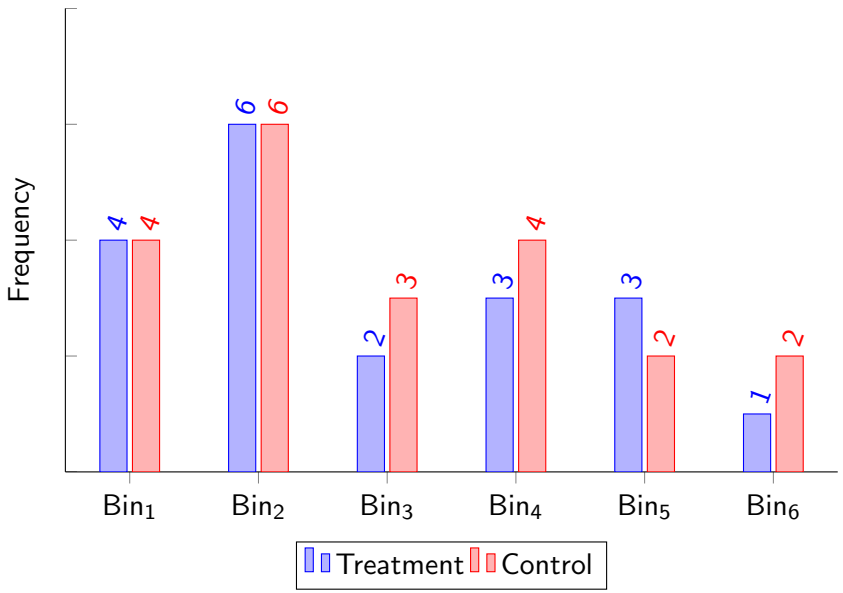

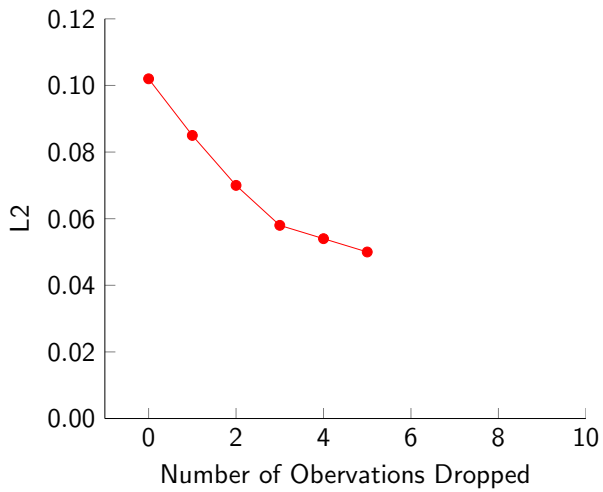

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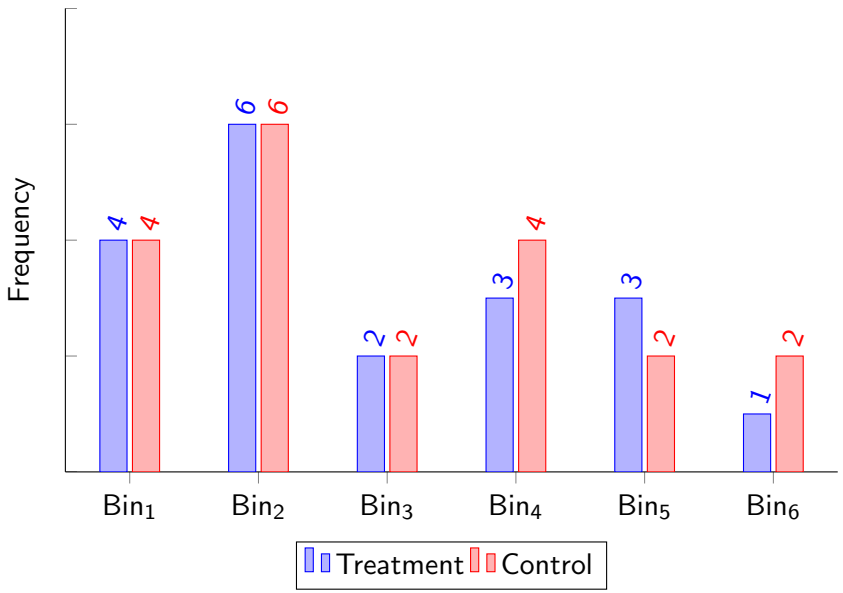

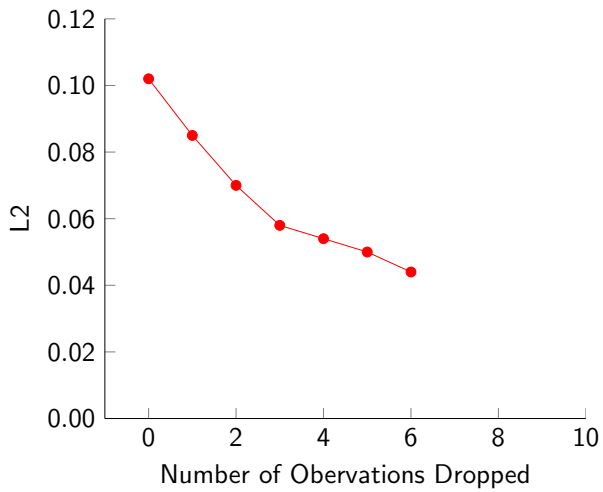

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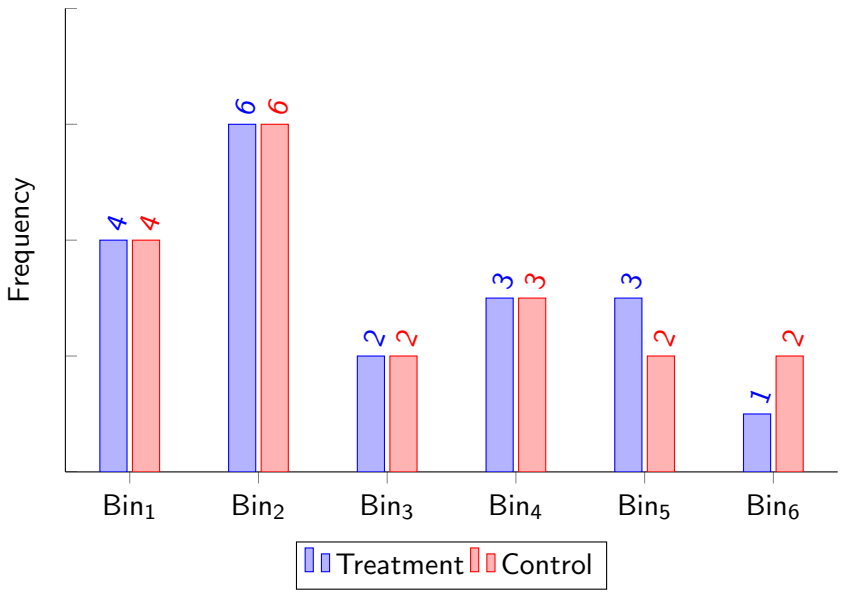
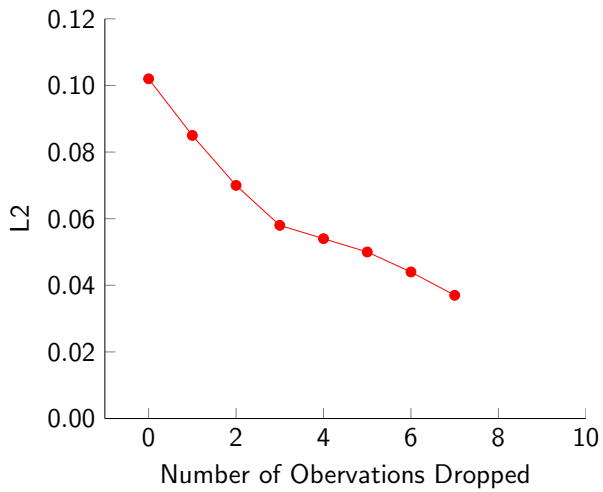
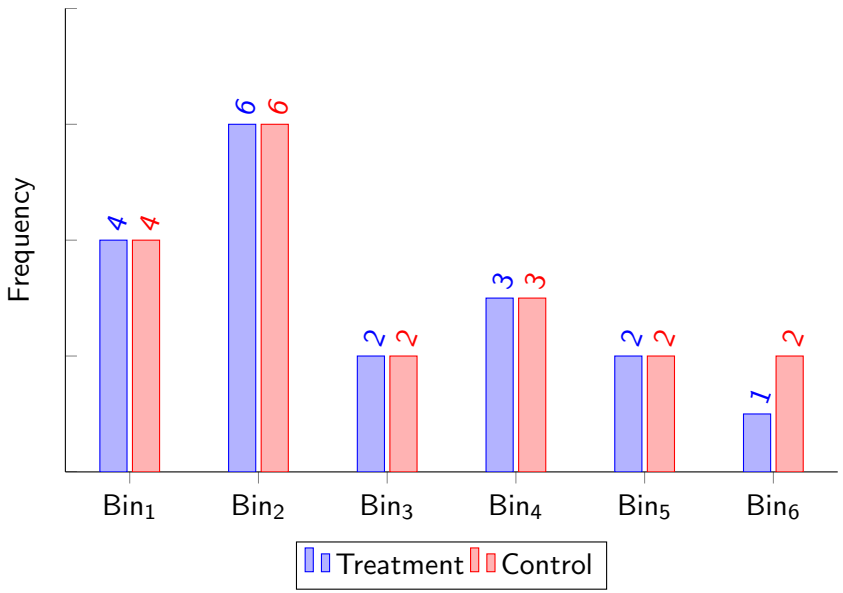
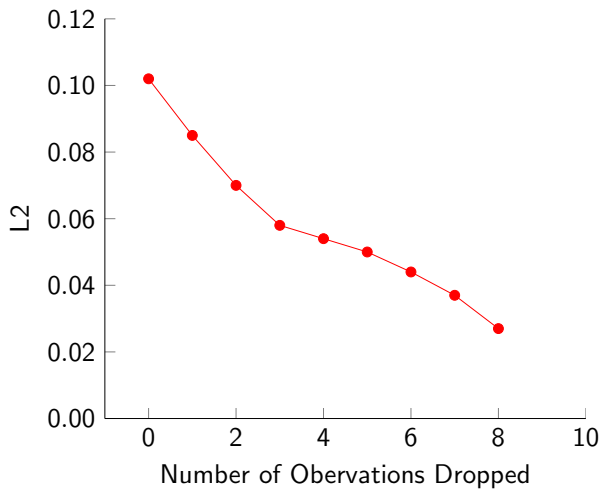




Constructing the L1/L2 SATT Frontier





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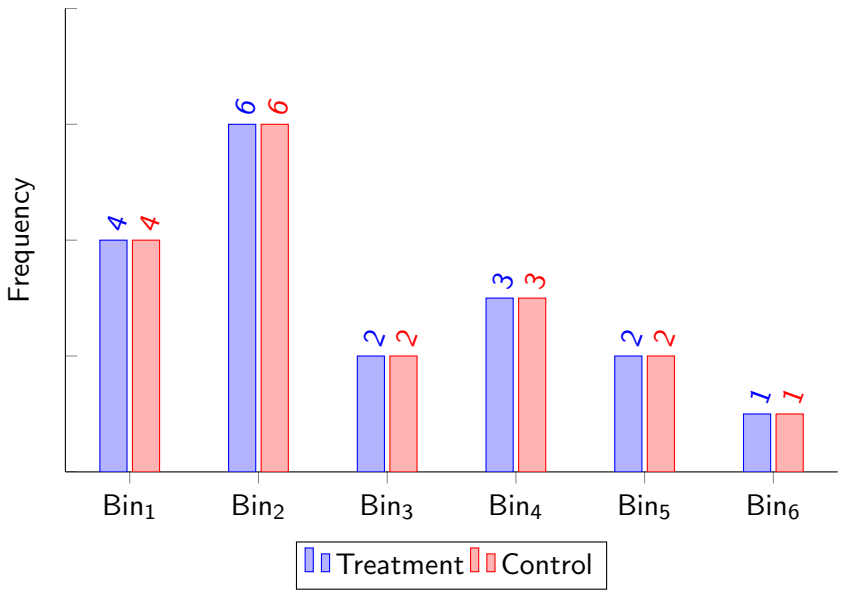

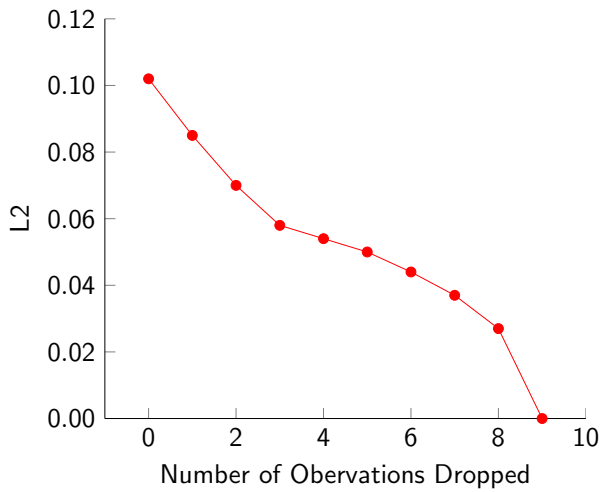

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- Simplification we will use: focus on TE for treated units; so $Y_i(0)$ is unobserved; $Y_i(1) = Y_i$

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

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  - Simpler special case under 1-to-1 matching on X: $\text{mean}(Y_i(0)|T_i = 1) = \text{mean}(Y_j|T_j = 0)$

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- Easy extensions for: multi-level, continuous, & mismeasured treatments; A too wide, n too small