Matching Methods for Causal Inference

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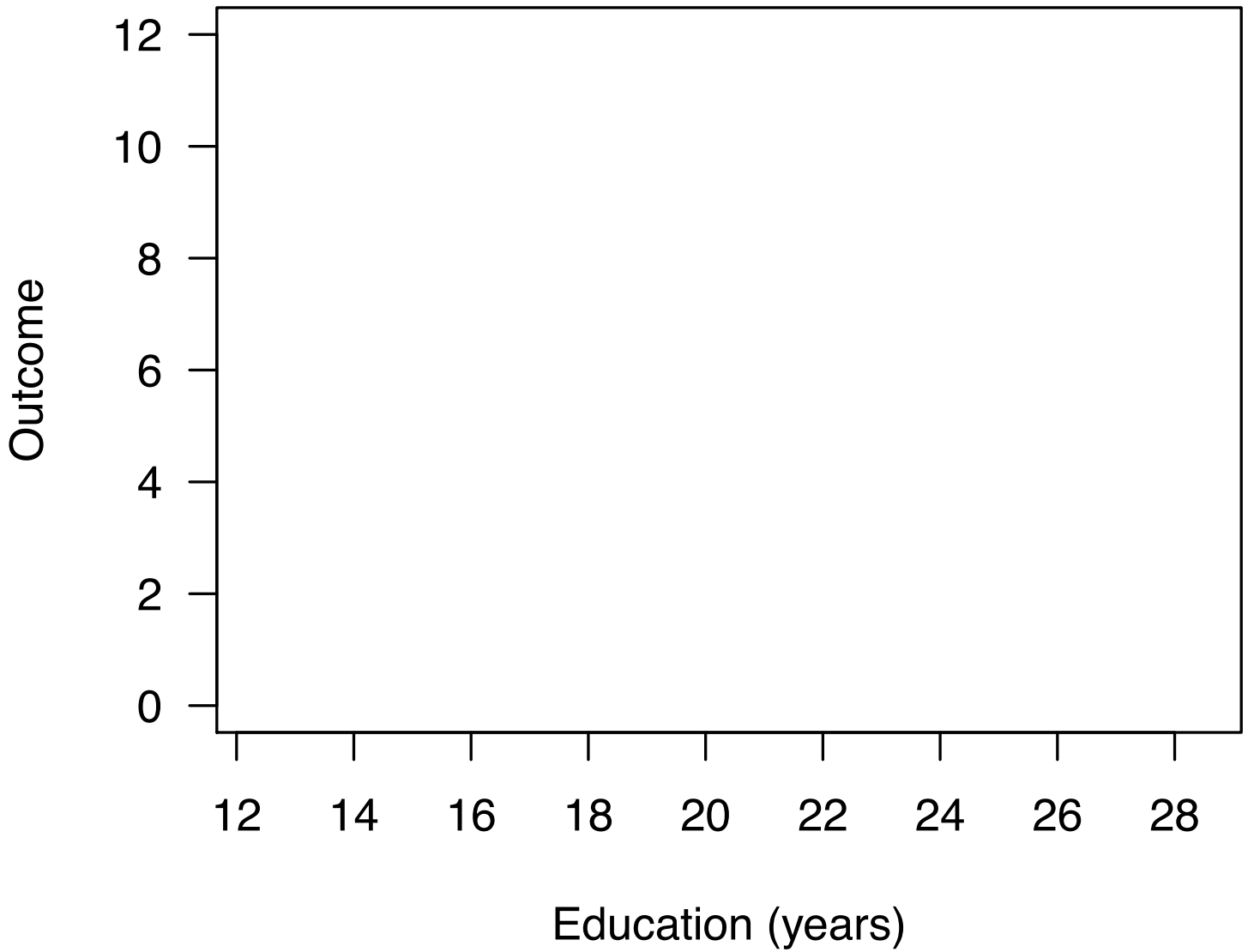
3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 92,900 articles!) sounds magical:
   $\rightsquigarrow$ "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)
2. Do powerful methods have to be complicated?
   $\rightsquigarrow$ "Causal Inference Without Balance Checking: Coarsened Exact Matching" (PA, 2011. Stefano M Iacus, Gary King, and Giuseppe Porro)
3. Matching methods optimize either imbalance ($\approx$ bias) or # units pruned ($\approx$ variance); users need both simultaneously':
   $\rightsquigarrow$ "The Balance-Sample Size Frontier in Matching Methods for Causal Inference" (In press, *AJPS*; Gary King, Christopher Lucas and Richard Nielsen)

Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)



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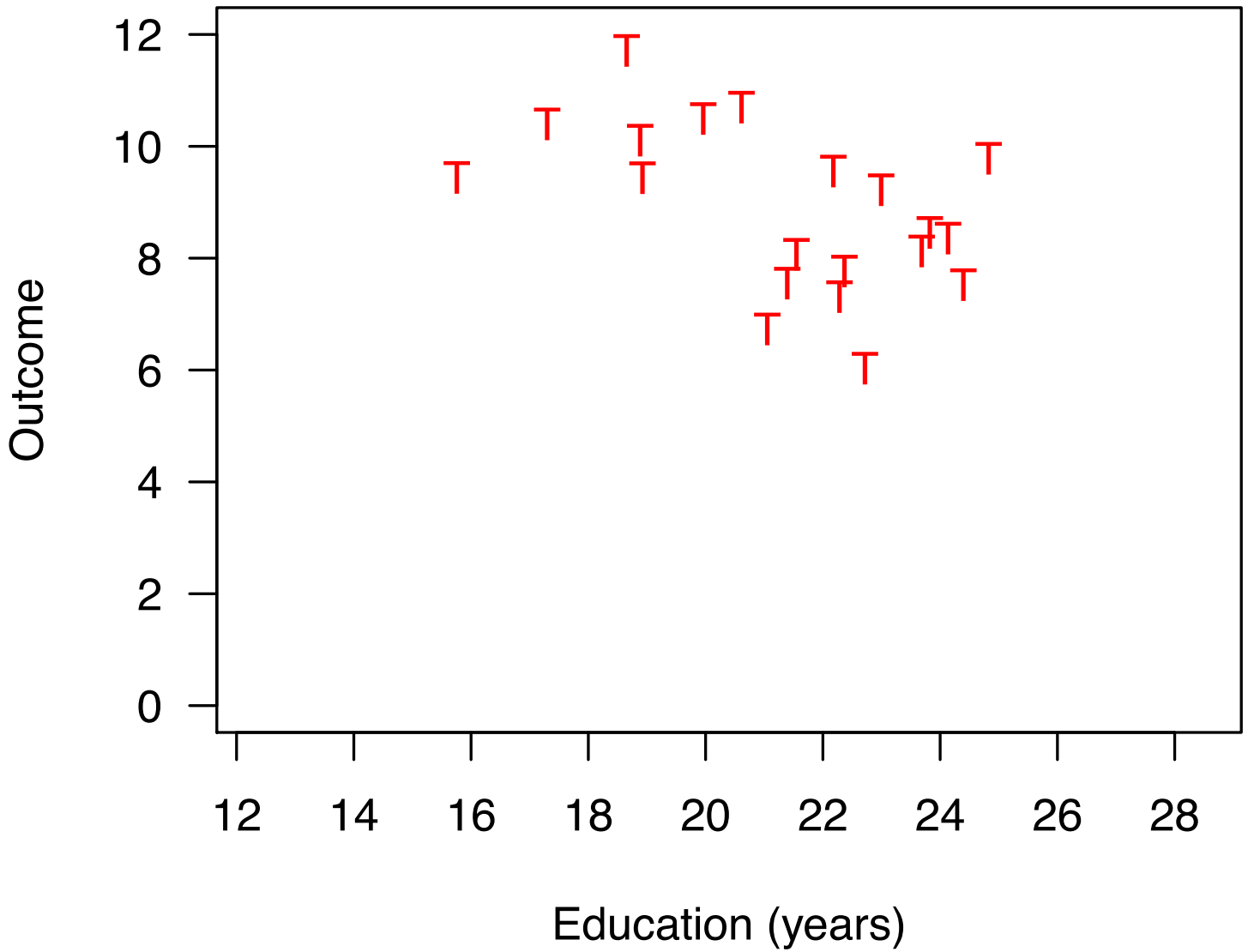

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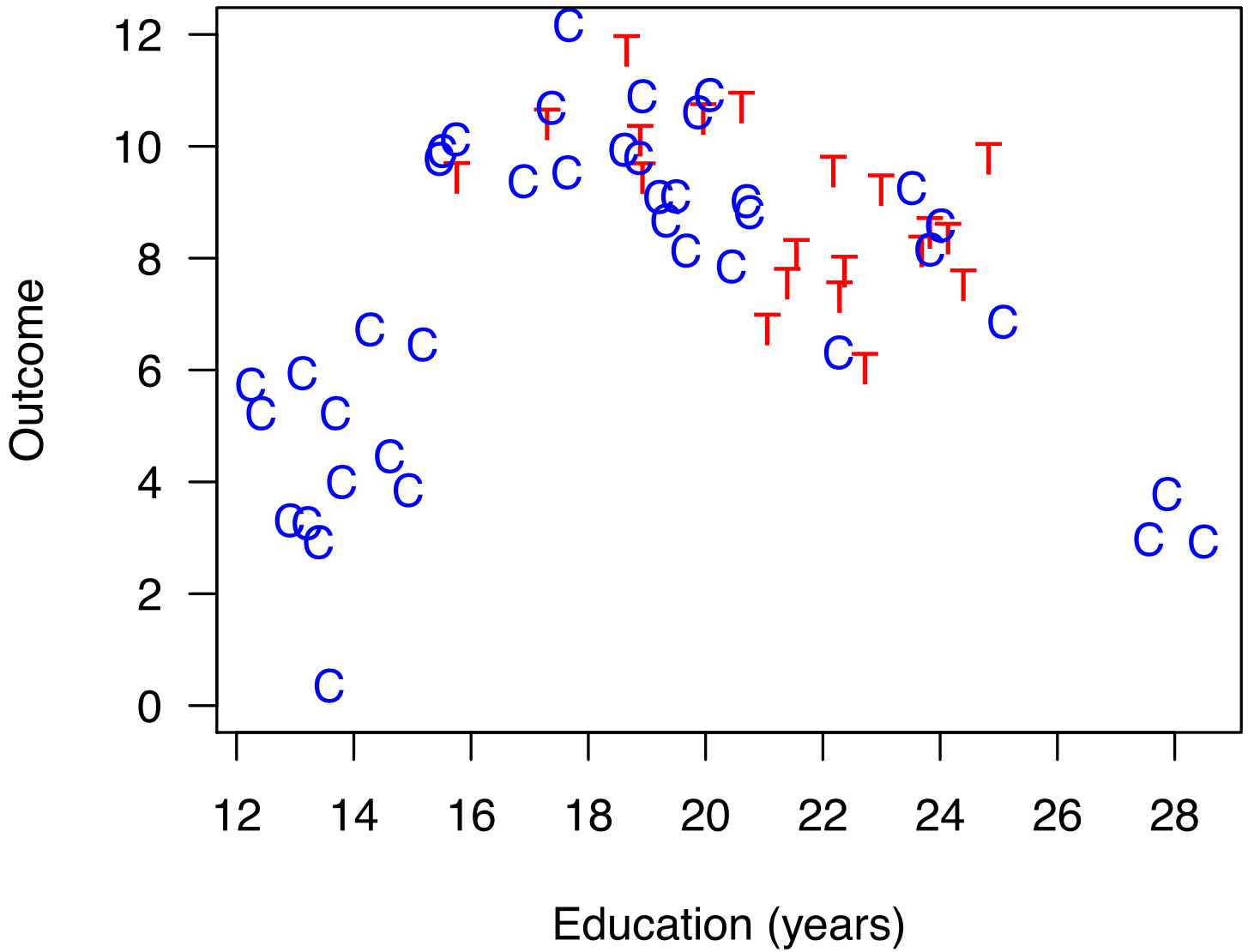

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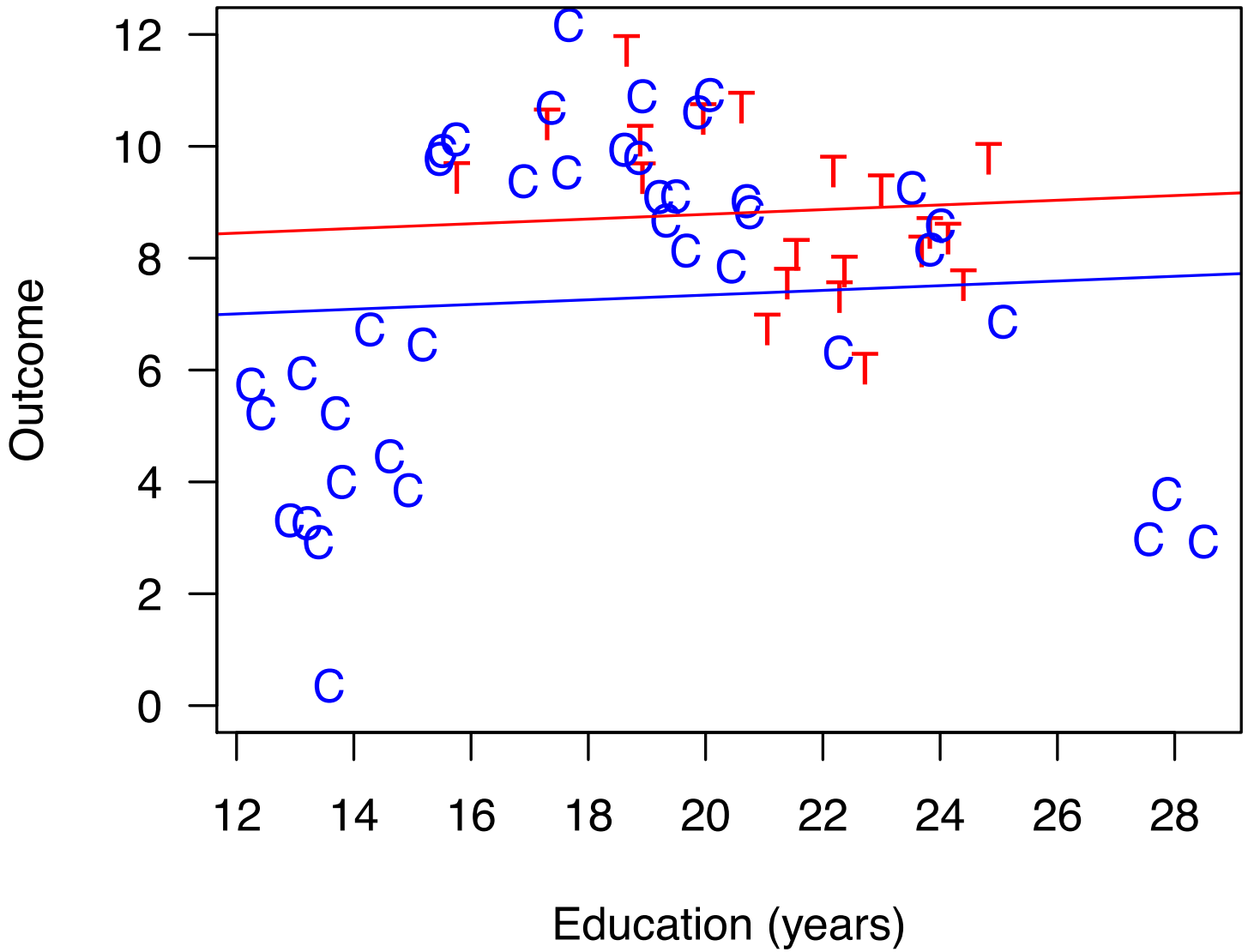

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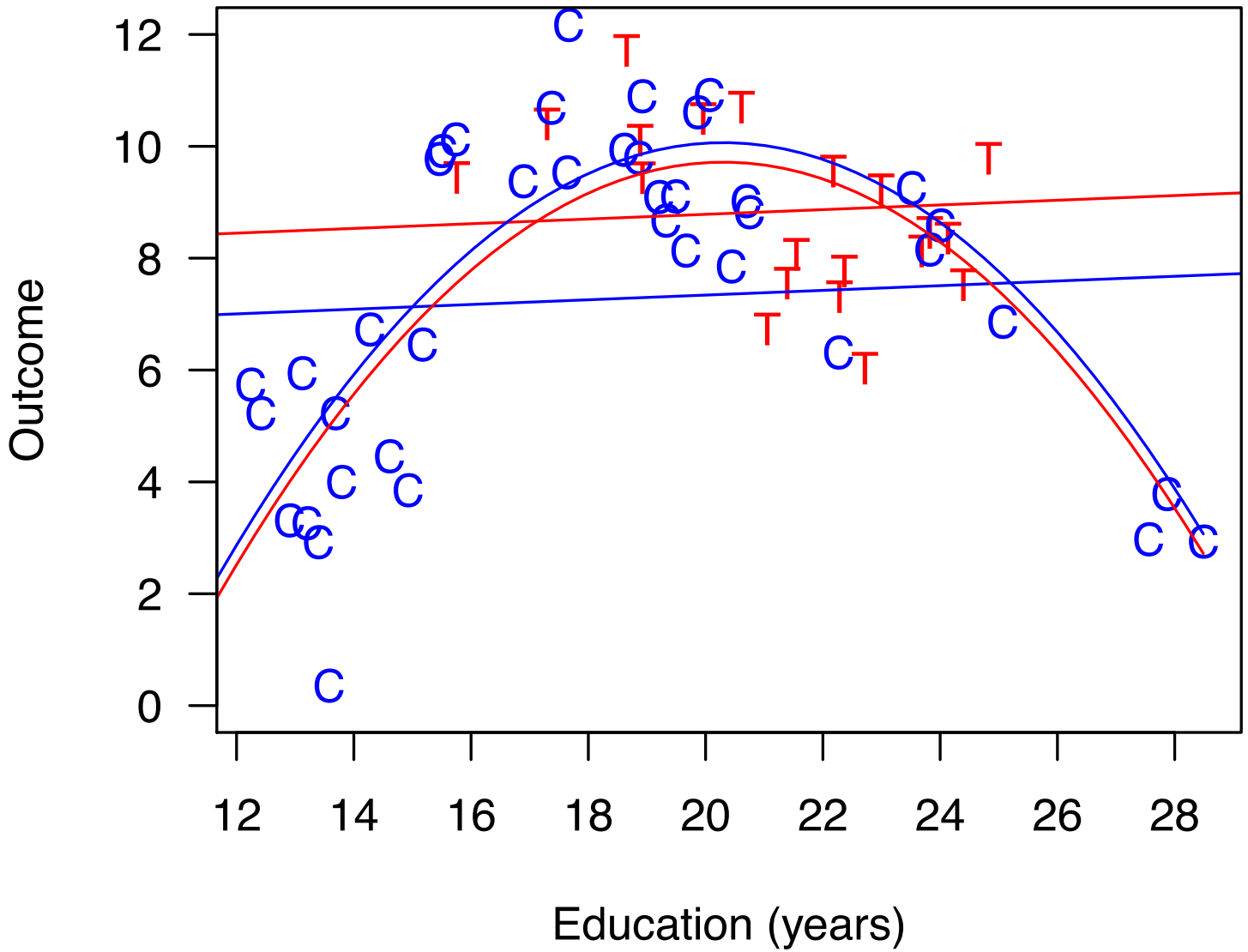

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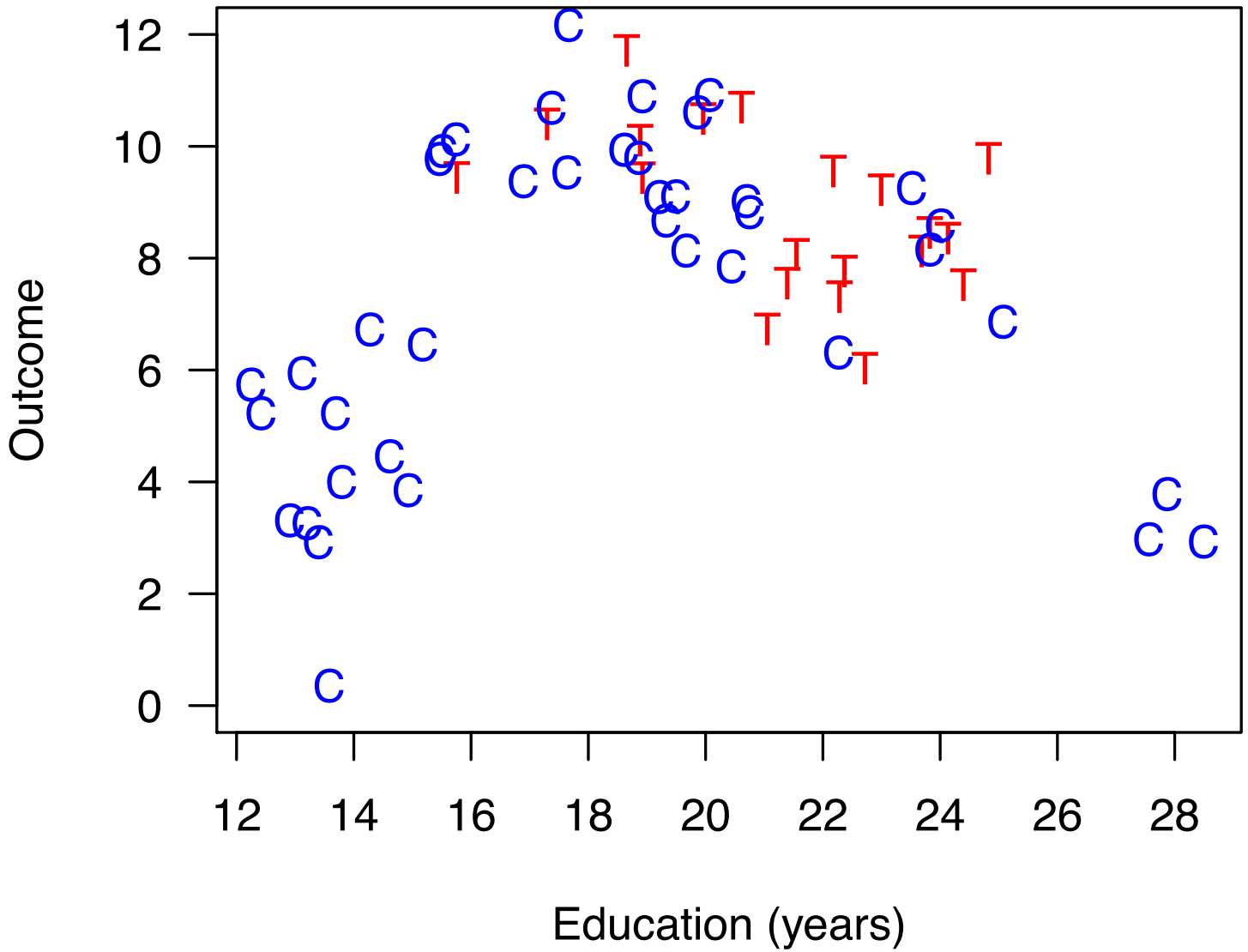

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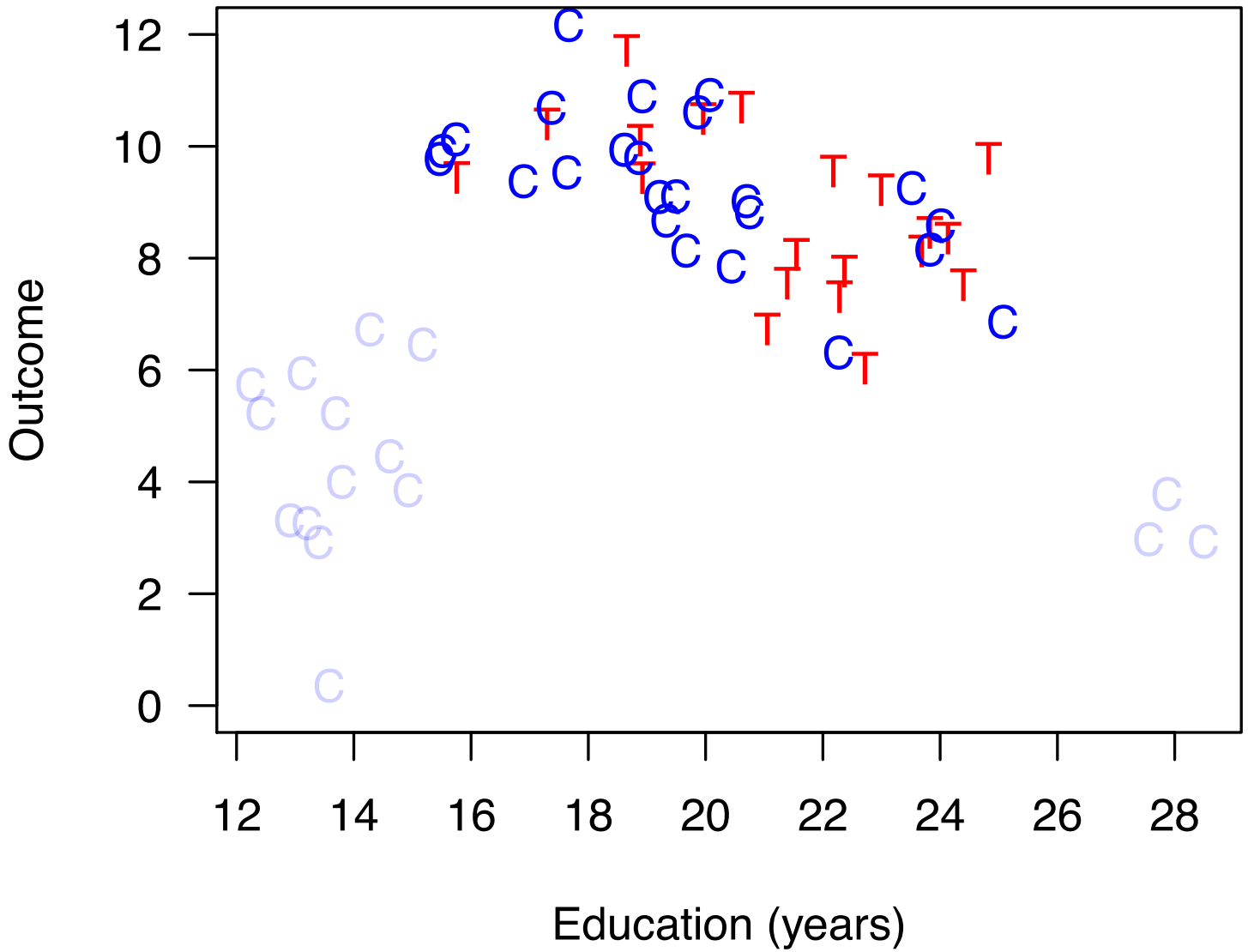

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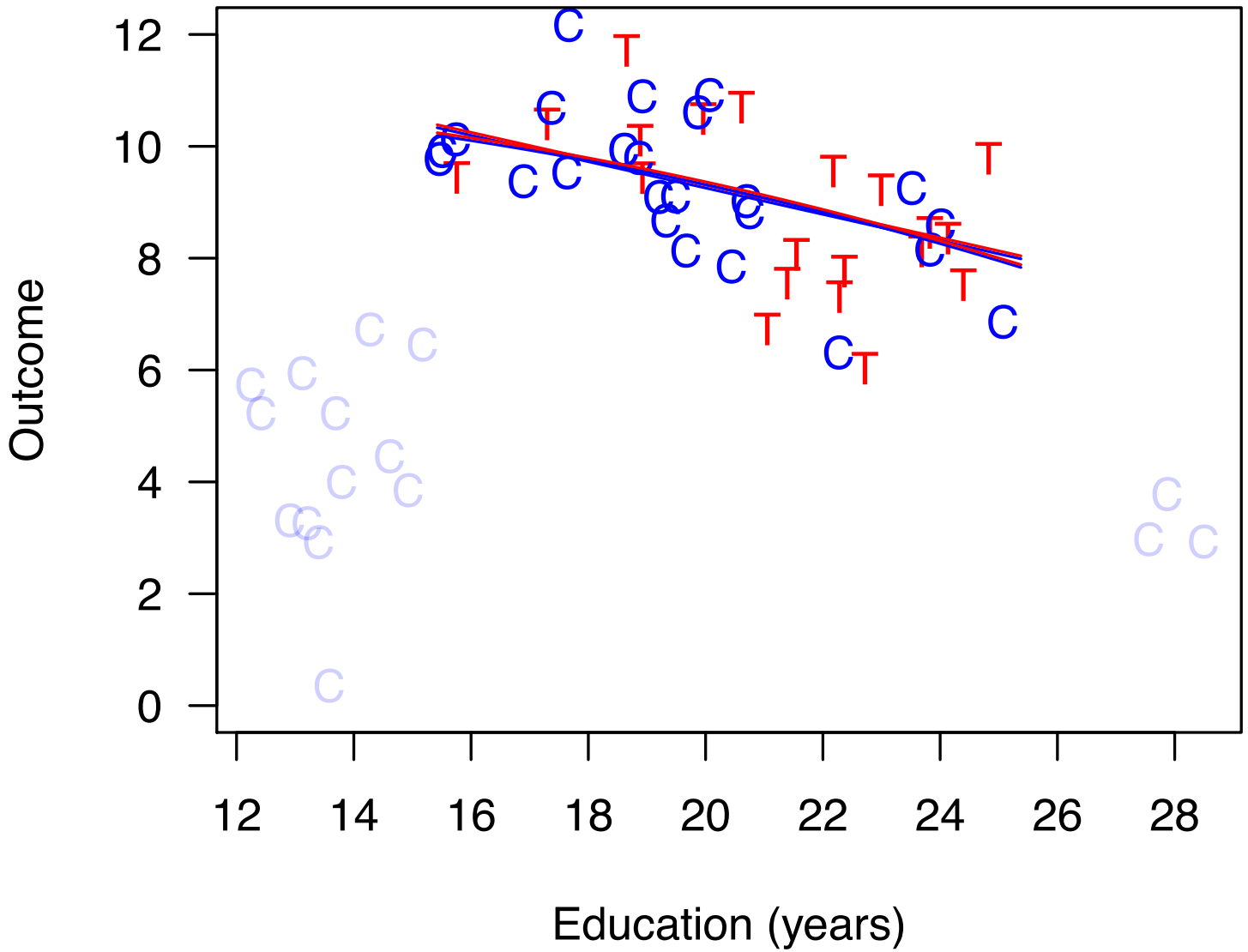


The Problems Matching Solves

Without Matching:

Imbalance $\rightsquigarrow$ Model Dependence $\rightsquigarrow$ Researcher discretion $\rightsquigarrow$ Bias

- Qualitative choice from unbiased estimates = biased estimator
  - e.g., Choosing from *results* of 50 randomized experiments
  - Choosing based on "plausibility" is probably worse[effrt]
- conscientious effort doesn't avoid biases (Banaji 2013)[acc]
- People do not have easy access to their own mental processes or feedback to avoid the problem (Wilson and Brekke 1994)[exprt]
- Experts overestimate their ability to control personal biases more than nonexperts, and more prominent experts are the most overconfident (Tetlock 2005)[tch]
- "Teaching psychology is mostly a waste of time" (Kahneman 2011)

The Problems Matching Solves

Without Matching:

~~Im~~balance $\rightsquigarrow$ ~~Model Dependence~~ $\rightsquigarrow$ ~~Researcher discretion~~ $\rightsquigarrow$ ~~Bias~~

A central project of statistics: Automating away human discretion

What's Matching?

- Y_i dep var, T_i (1=treated, 0=control), X_i confounders
- Treatment Effect for treated observation i:

$$\begin{aligned} \text{TE}_i &= Y_i - Y_i(0) \\ &= \text{observed} - \textit{unobserved} \end{aligned}$$

- Estimate $Y_i(0)$ with Y_j with a matched ($X_i \approx X_j$) control
- Quantities of Interest:
  1. SATT: Sample Average Treatment effect on the Treated:

$$\text{SATT} = \underset{i \in \{T_i = 1\}}{\text{Mean}} (\text{TE}_i)$$

  2. FSATT: Feasible SATT (prune badly matched treateds too)
- Big convenience: Follow preprocessing with whatever statistical method you'd have used without matching
- Pruning nonmatches makes control vars matter less: reduces imbalance, model dependence, researcher discretion, & bias

Matching: Finding Hidden Randomized Experiments

Types of Experiments

Balance Covariates:	*Complete Randomization*	*Fully Blocked*
Observed	On average	Exact
Unobserved	On average	On average

$\rightsquigarrow$ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

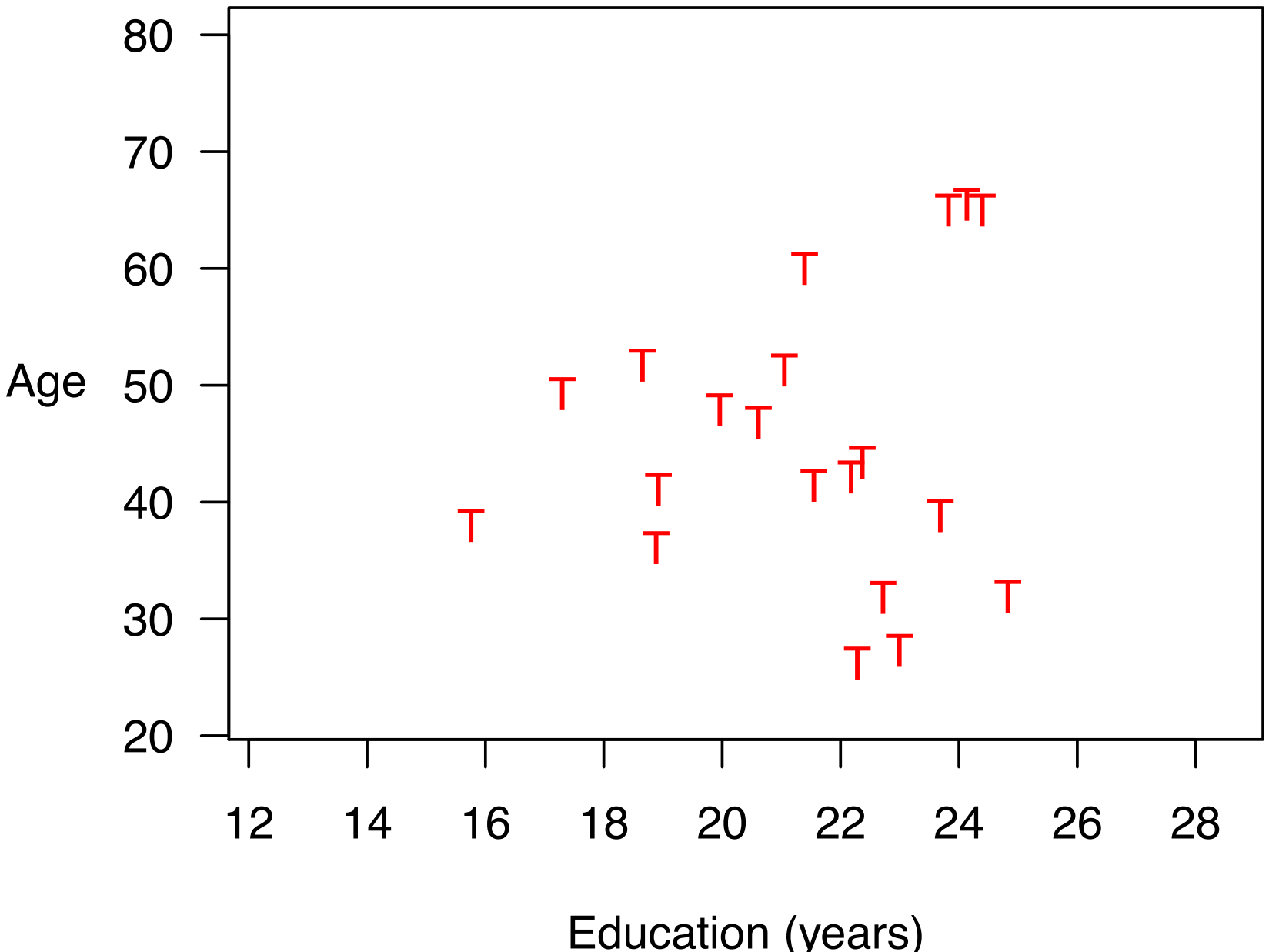
- PSM: *complete randomization*
- Other methods: *fully blocked*
- Other matching methods dominate PSM (wait, it gets worse)

Method 1: Mahalanobis Distance Matching

(Approximates Fully Blocked Experiment)

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

Mahalanobis Distance Matching



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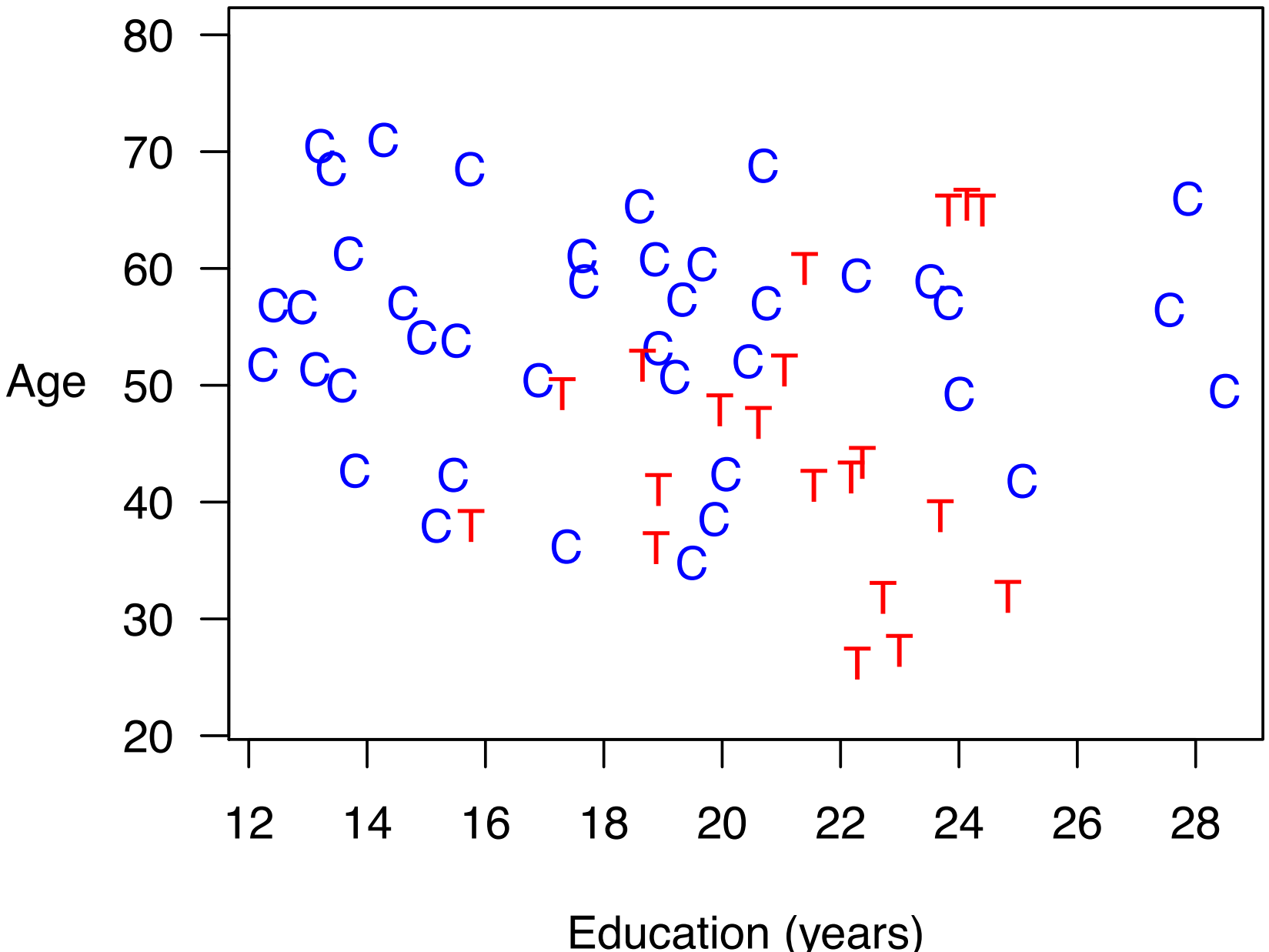

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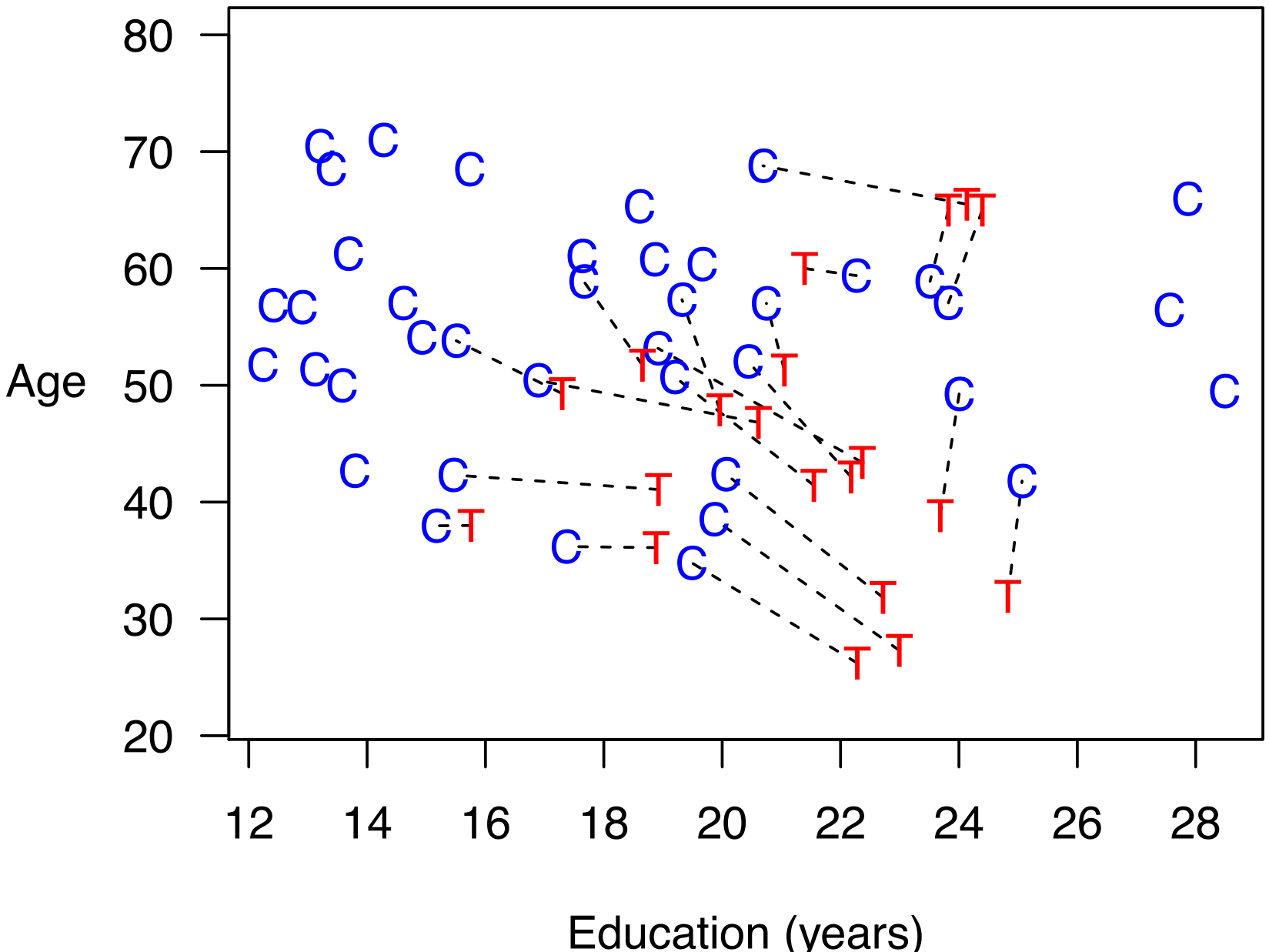

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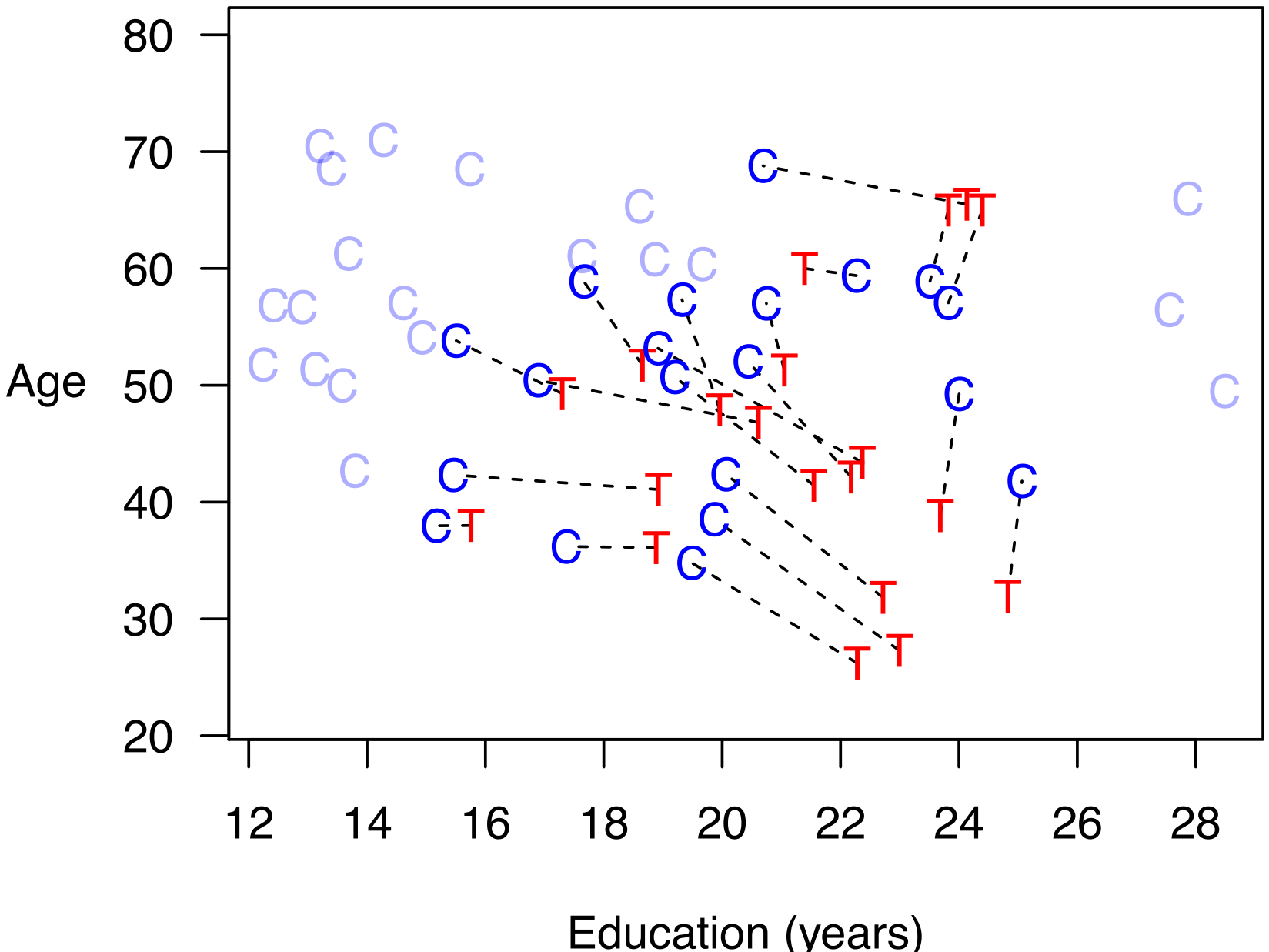

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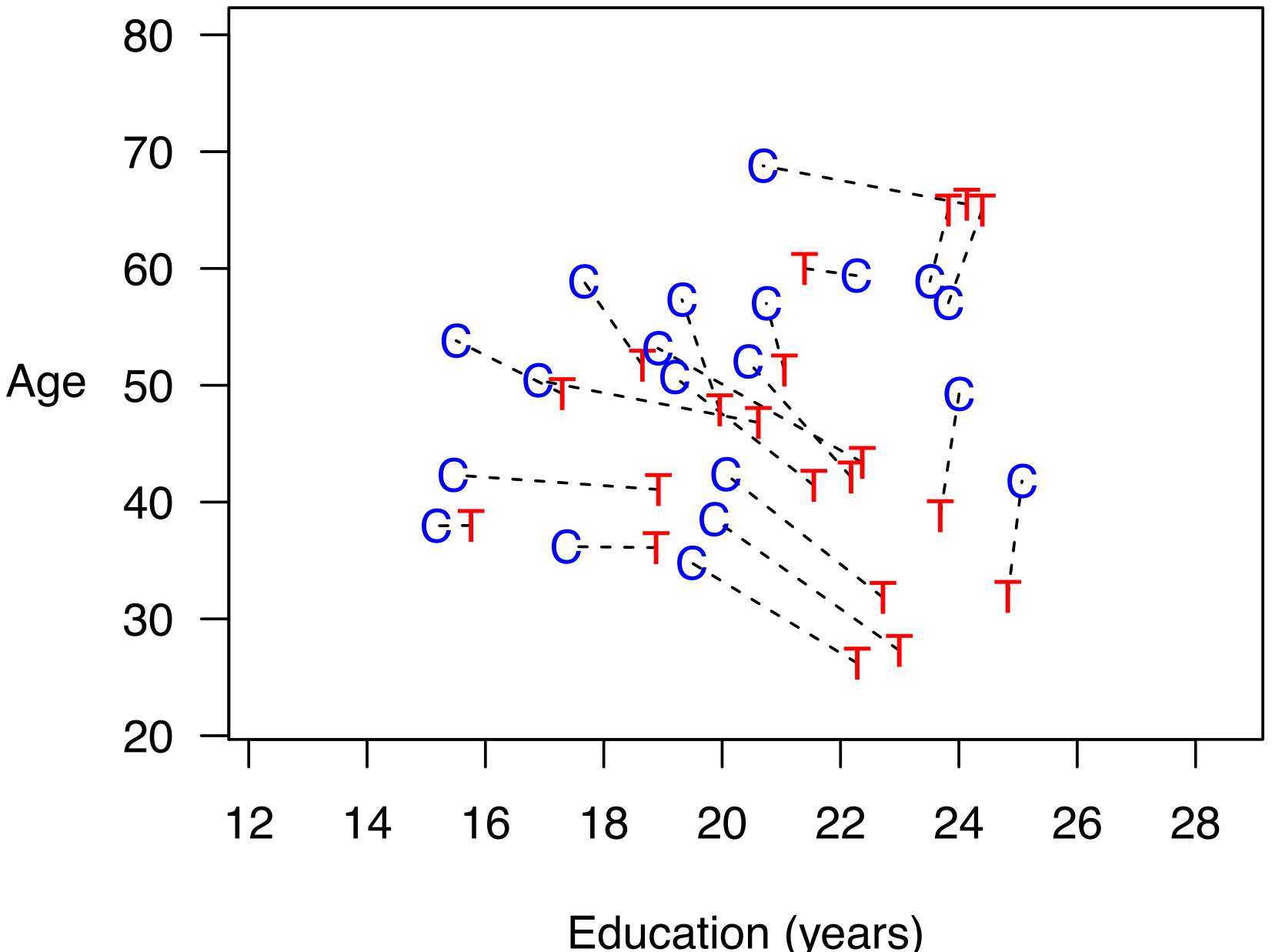

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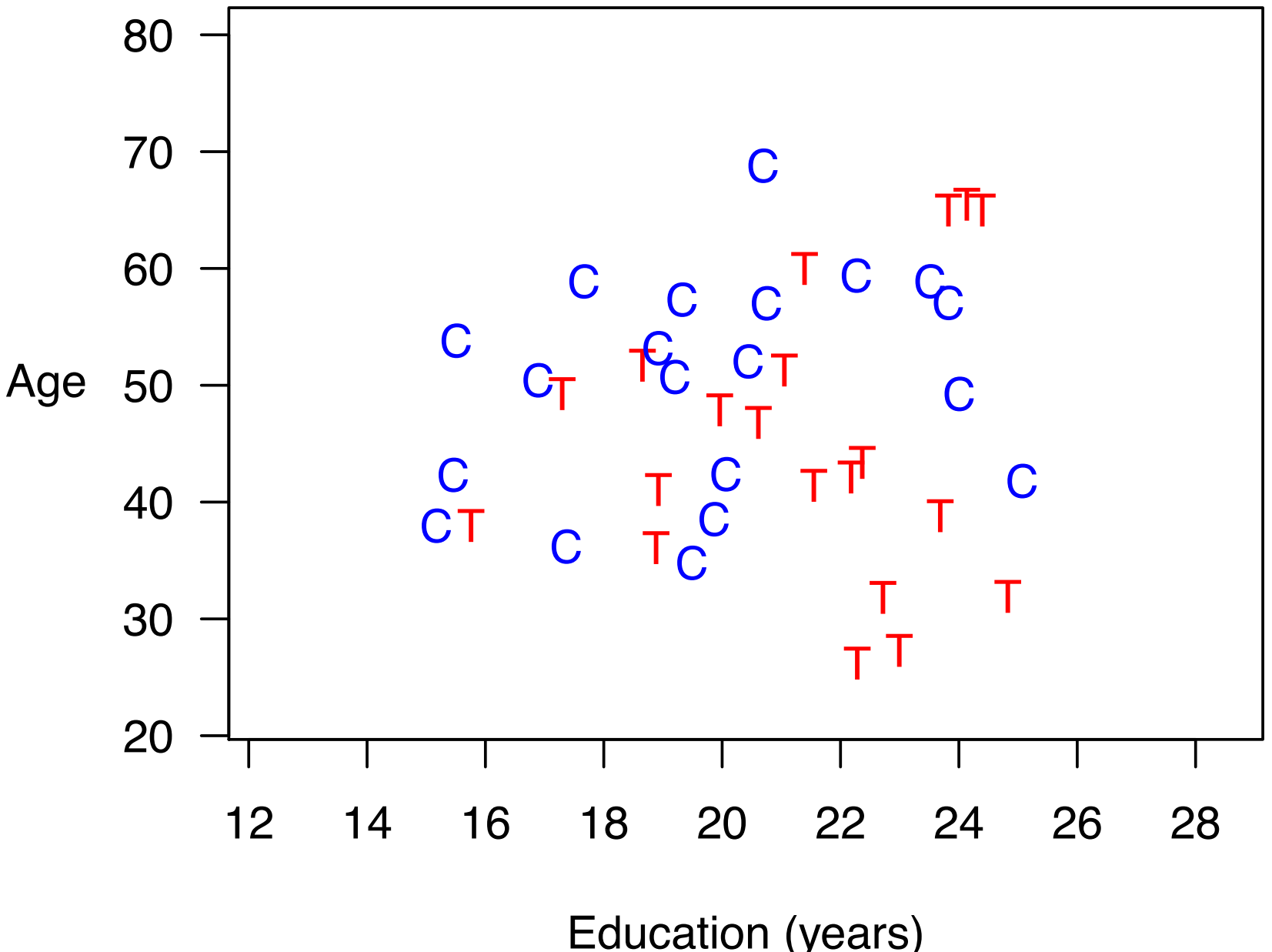
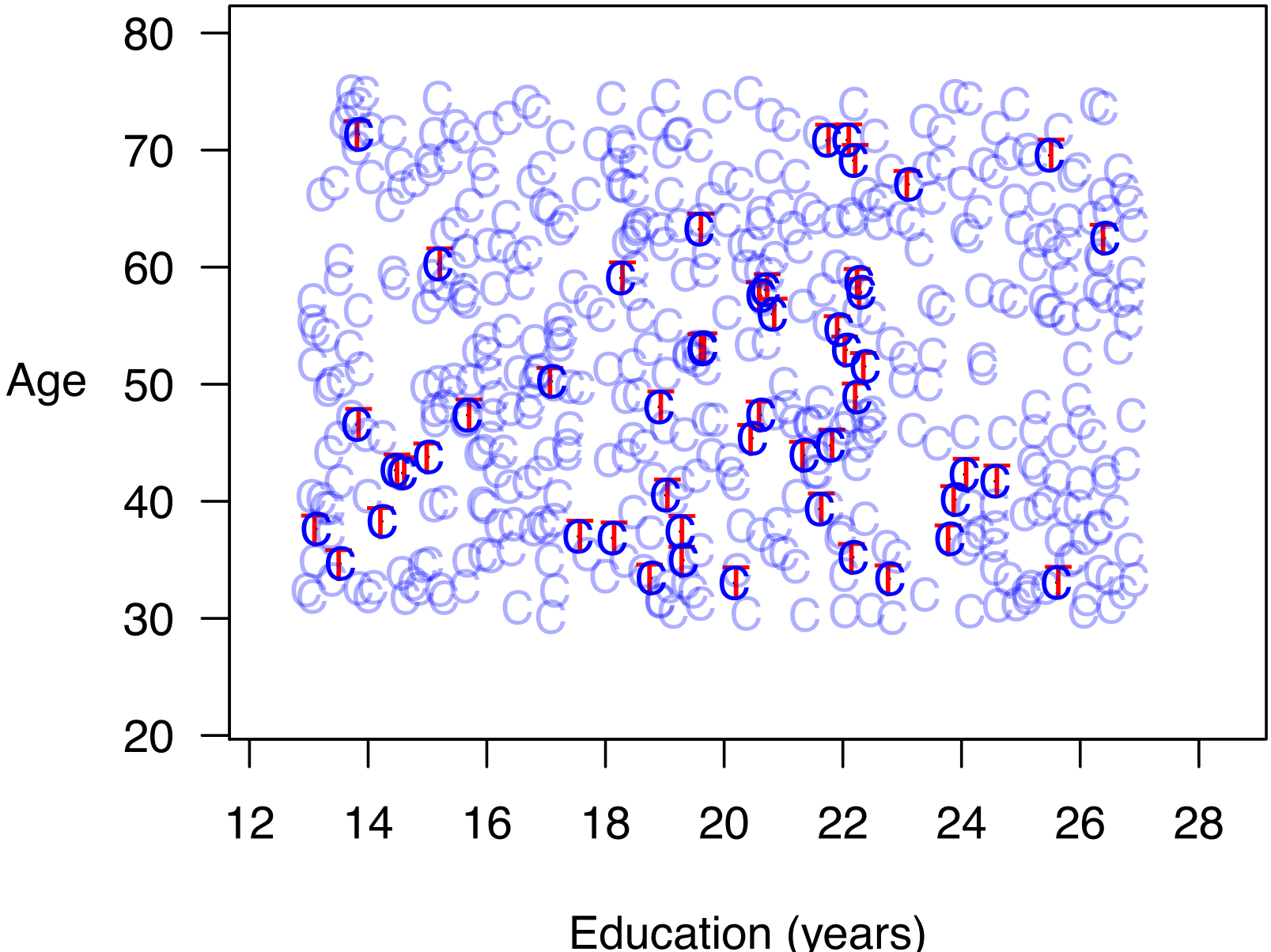


Best Case: Mahalanobis Distance Matching



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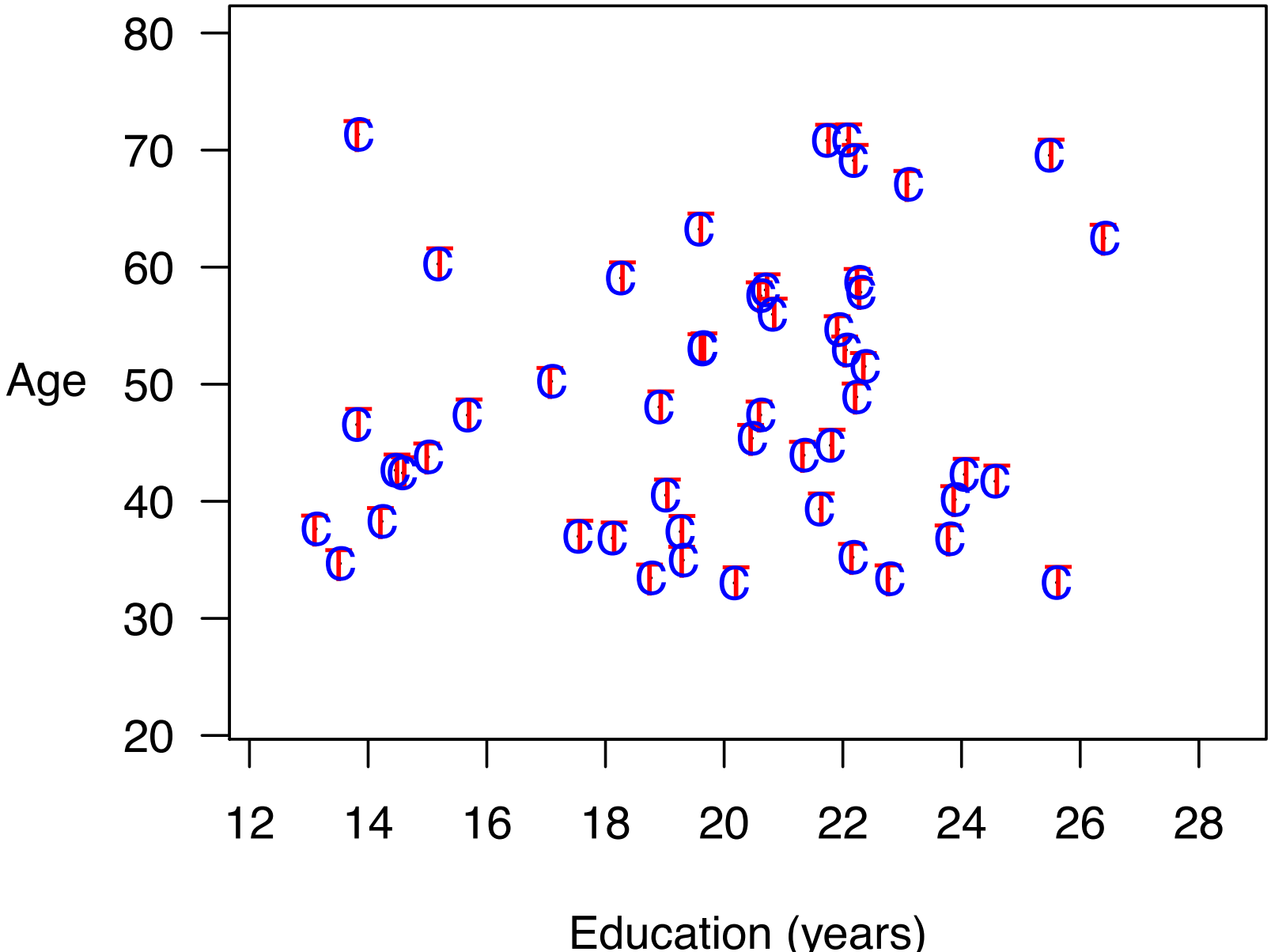
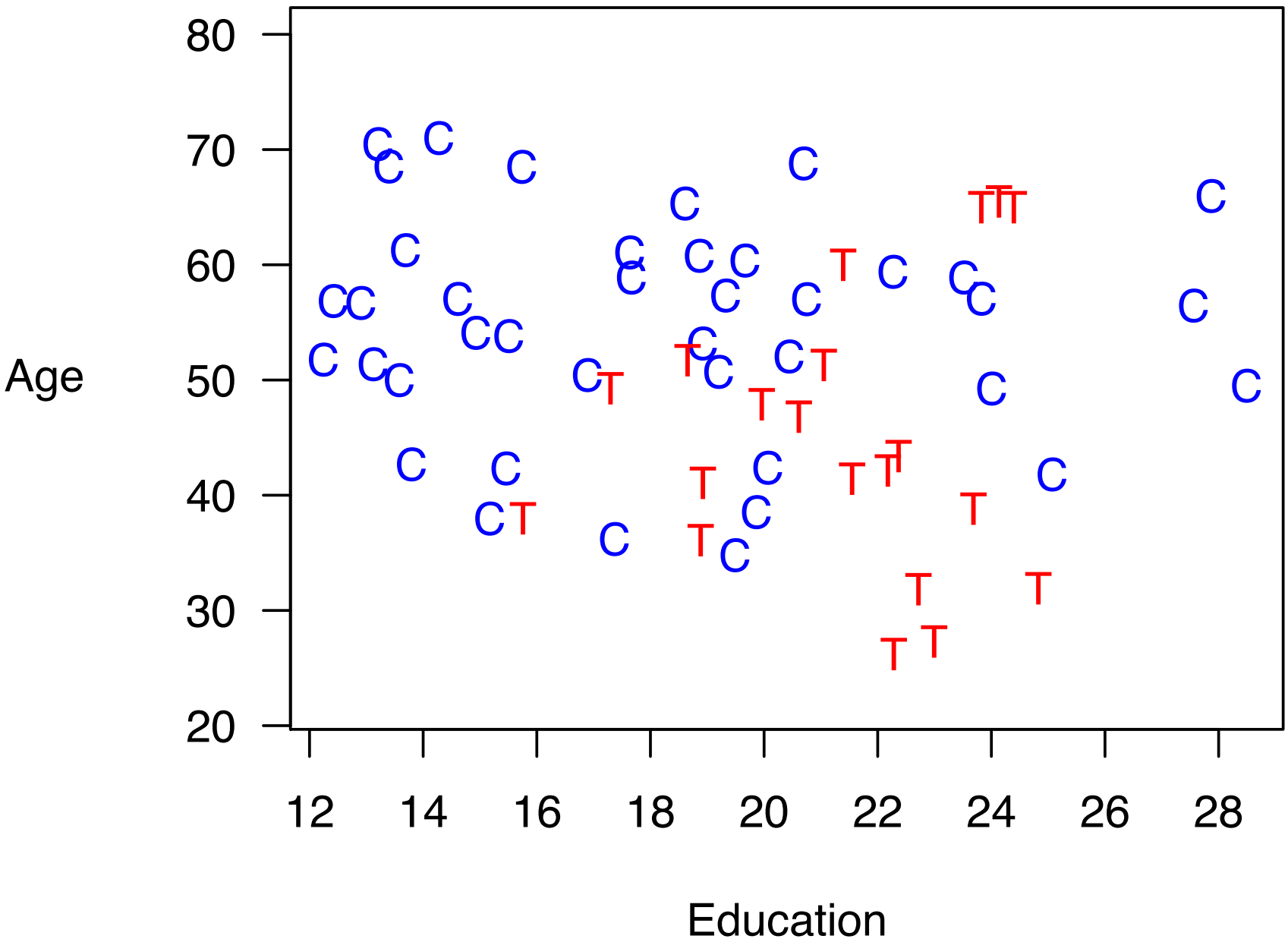


Method 2: Coarsened Exact Matching (Most powerful easy-to-use approach)

(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)
   - Temporarily coarsen X as much as you're willing
     - e.g., Education (grade school, high school, college, graduate)
   - Apply exact matching to the coarsened X, $C(X)$
     - Sort observations into strata, each with unique values of $C(X)$
     - Prune any stratum with 0 treated or 0 control units
   - Pass on original (uncoarsened) units except those pruned
2. Estimation Difference in means or a model
   - Weight controls in each stratum to equal treateds

Coarsened Exact Matching



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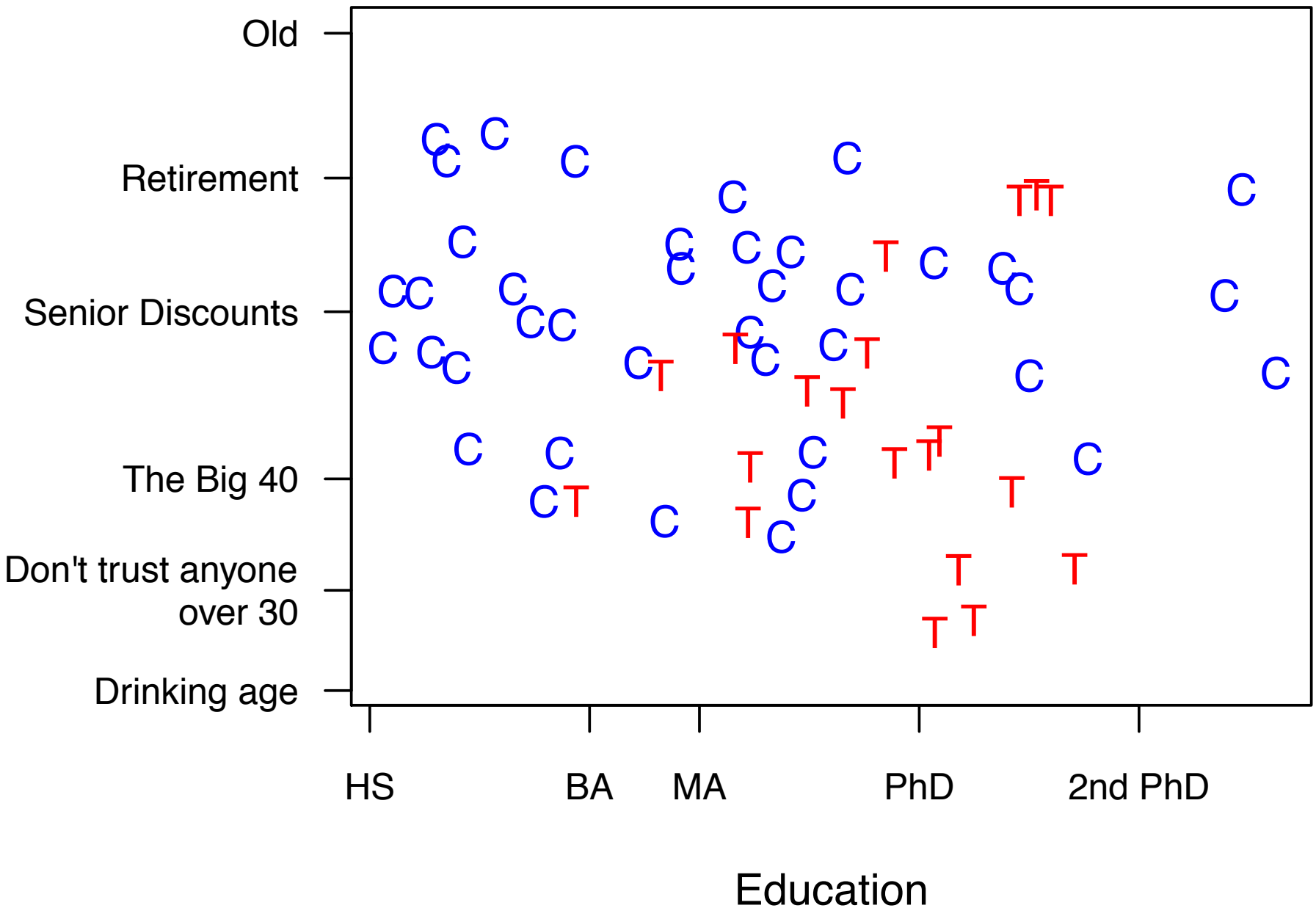

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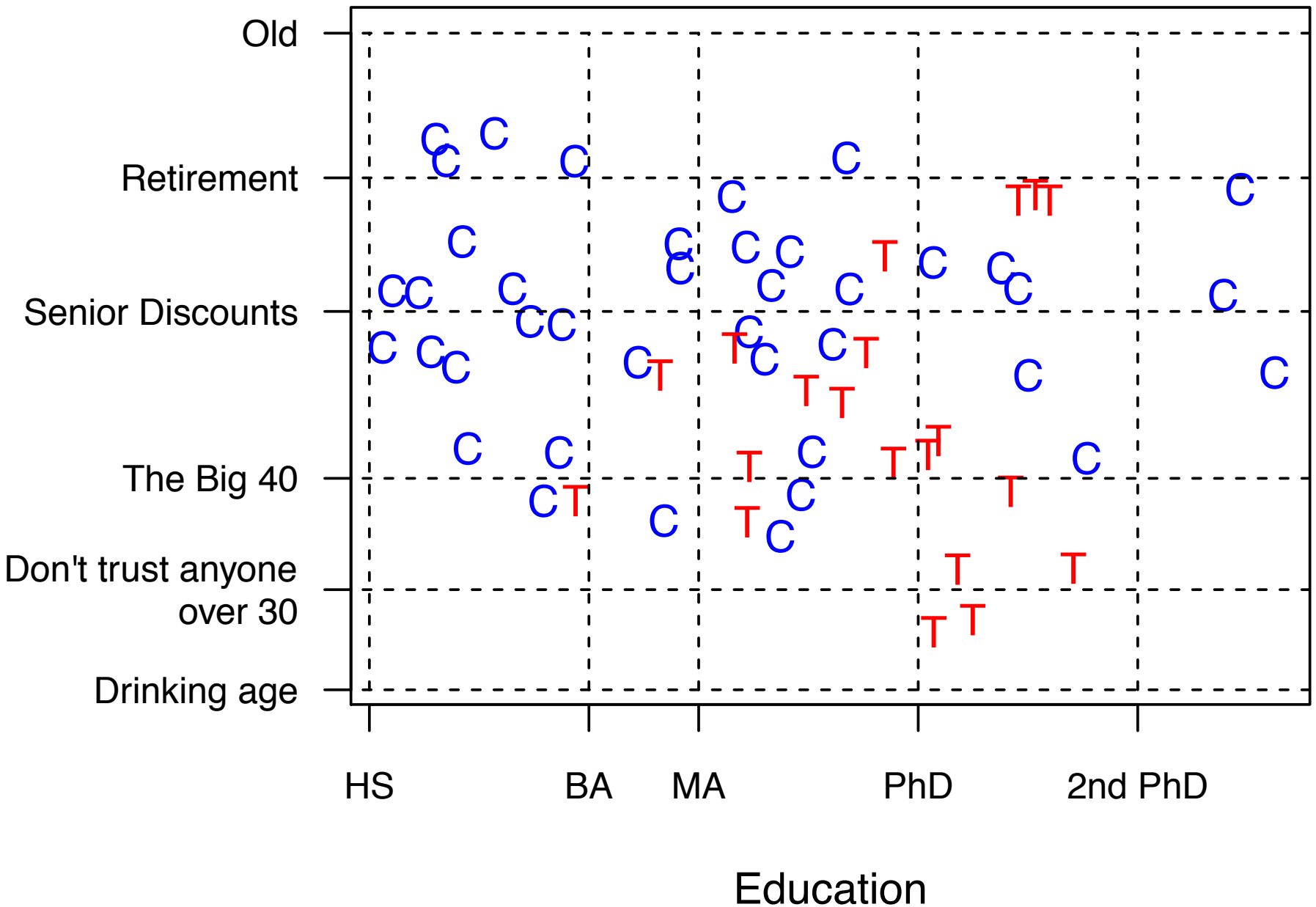

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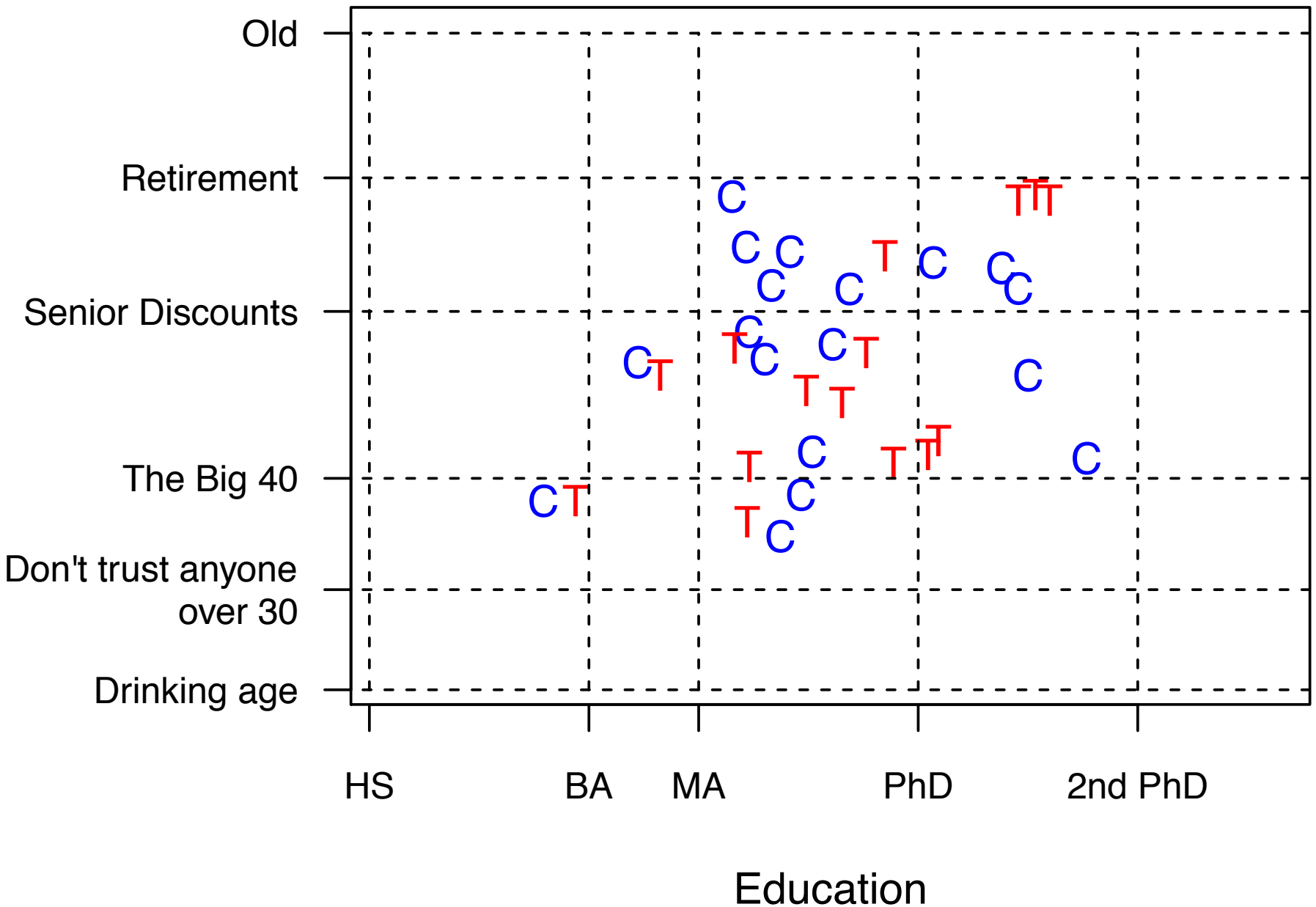

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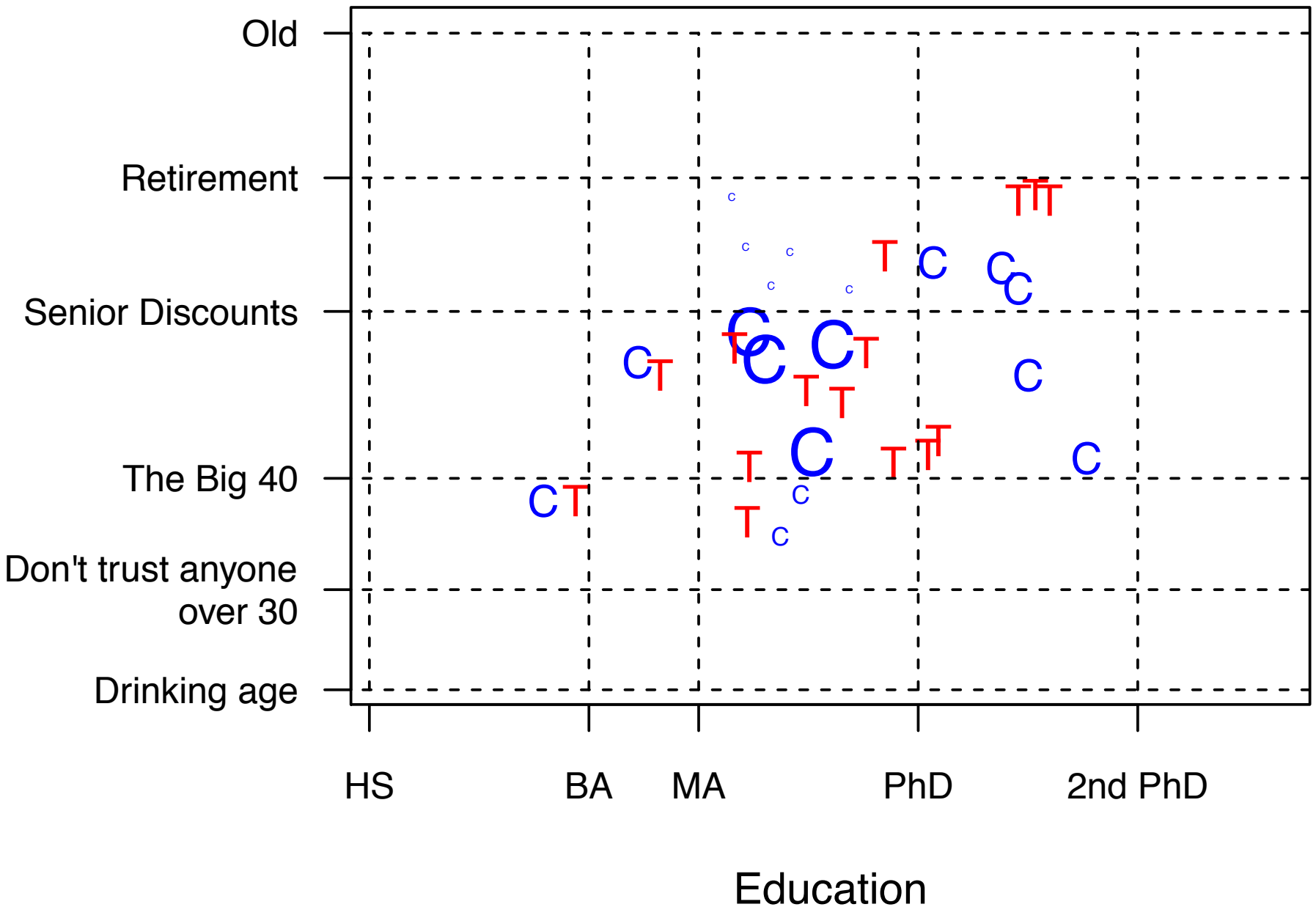

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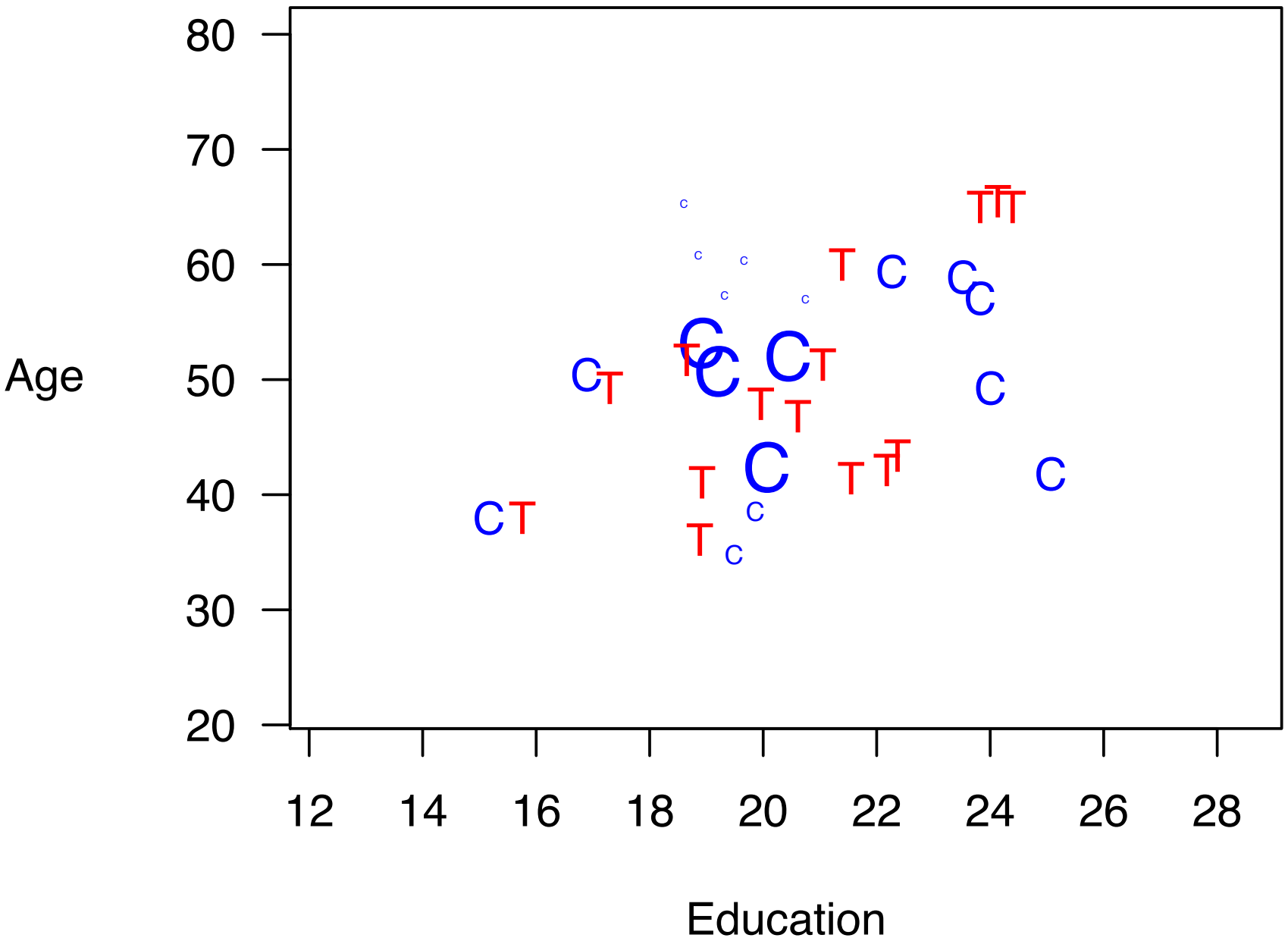

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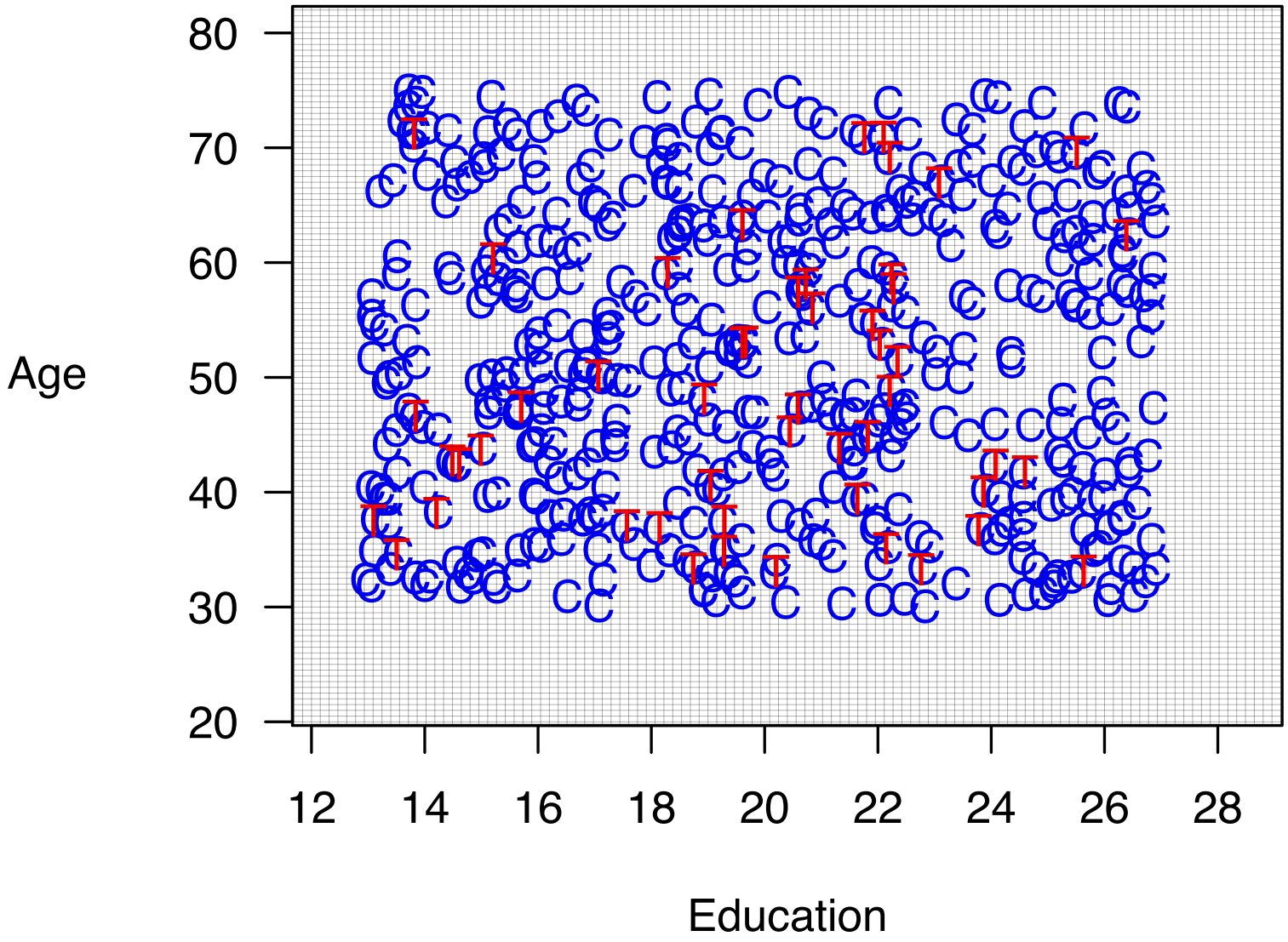

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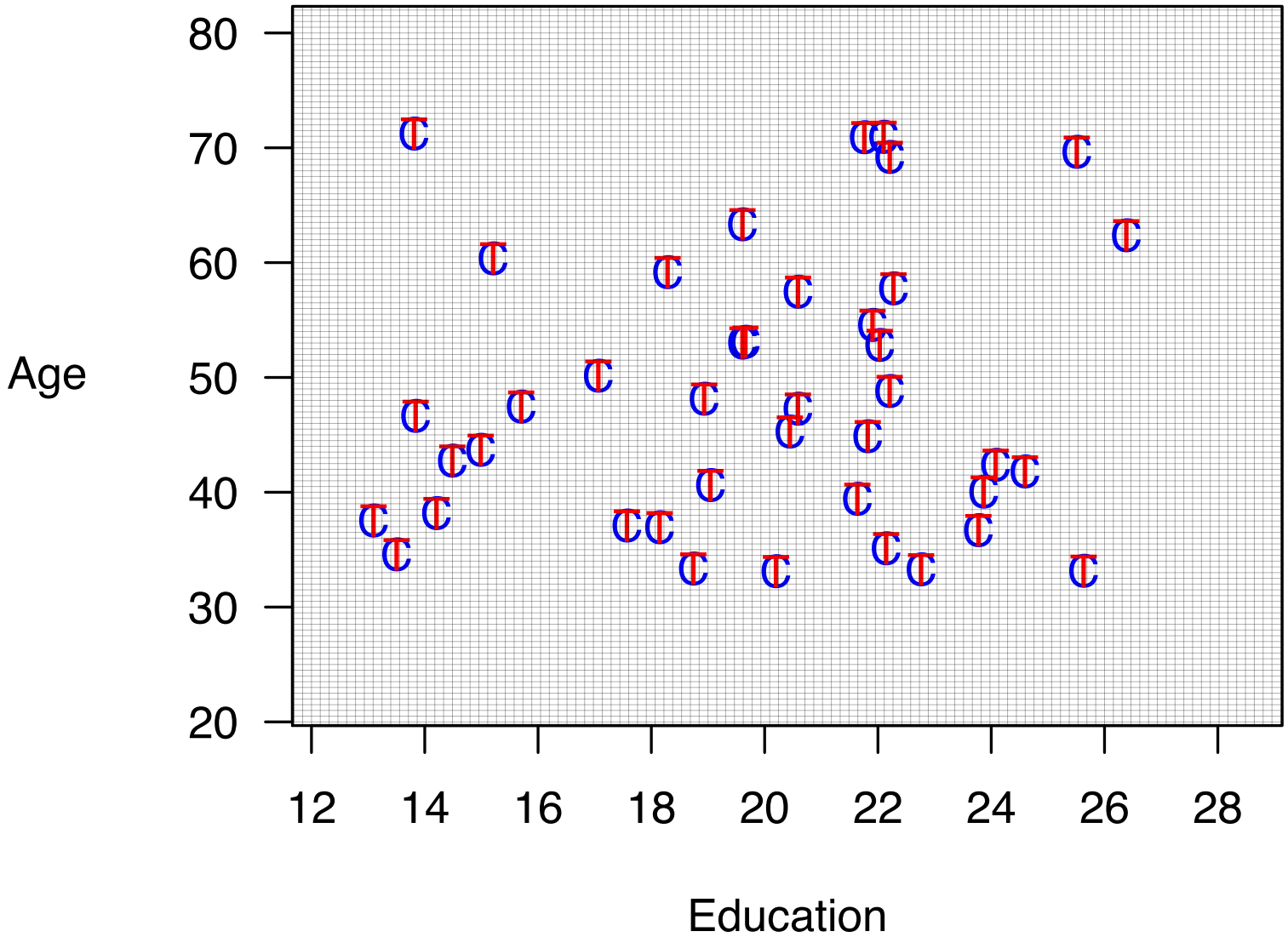

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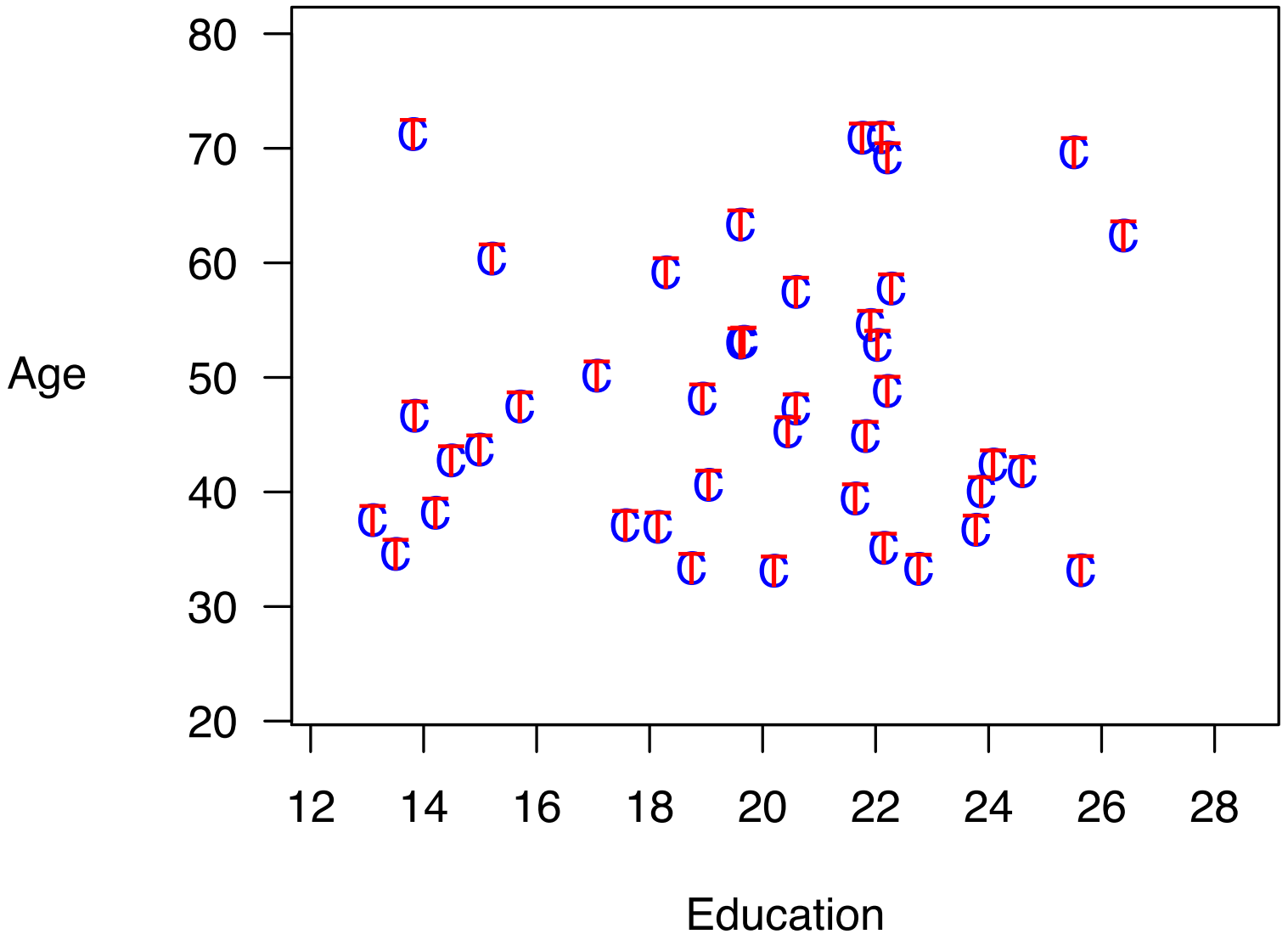

Method 3: Propensity Score Matching

(Approximates Completely Randomized Experiment)

1. Preprocess (Matching)
   - Reduce k elements of X to scalar $\pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-X_i\beta}}$
   - 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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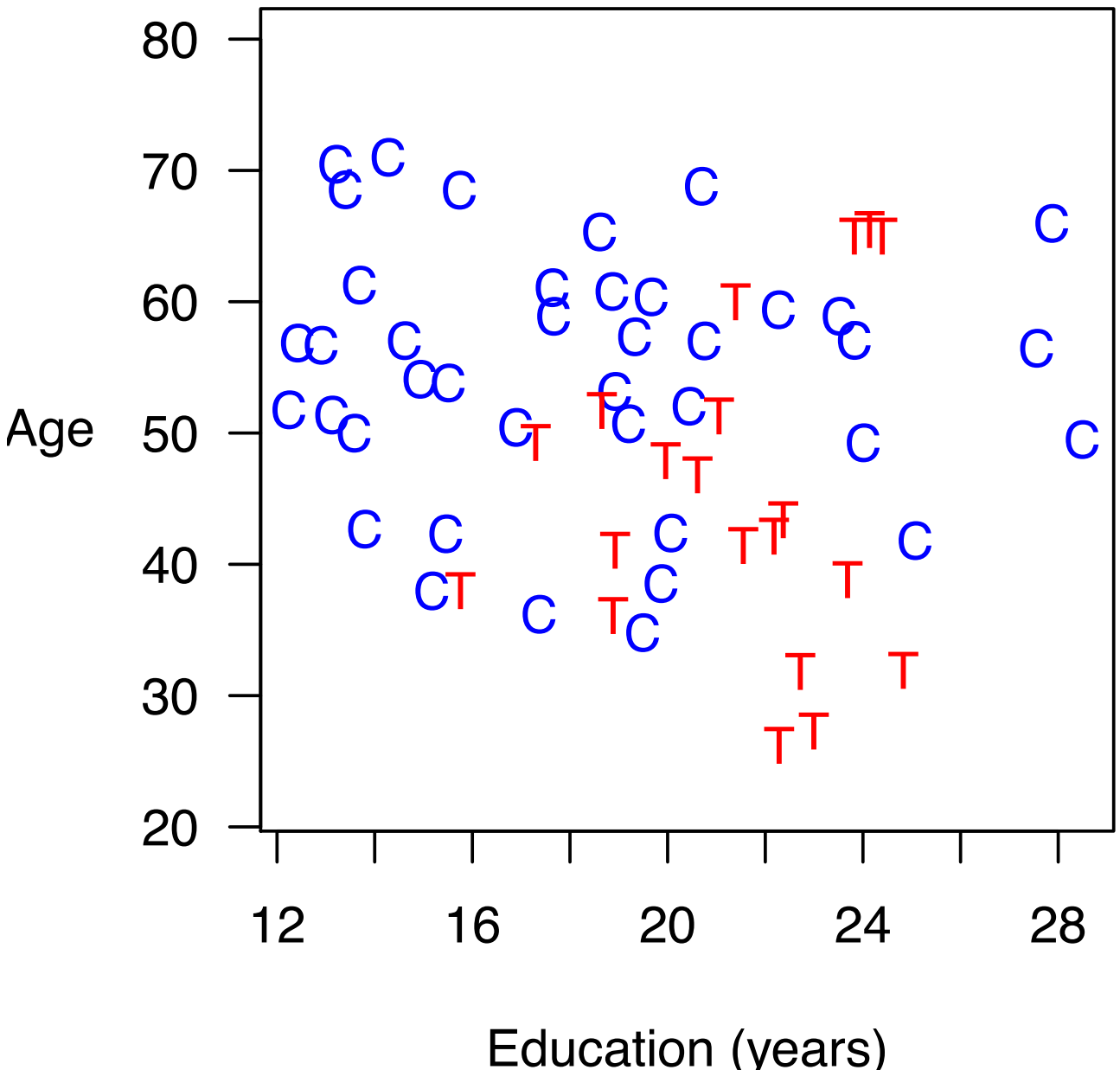

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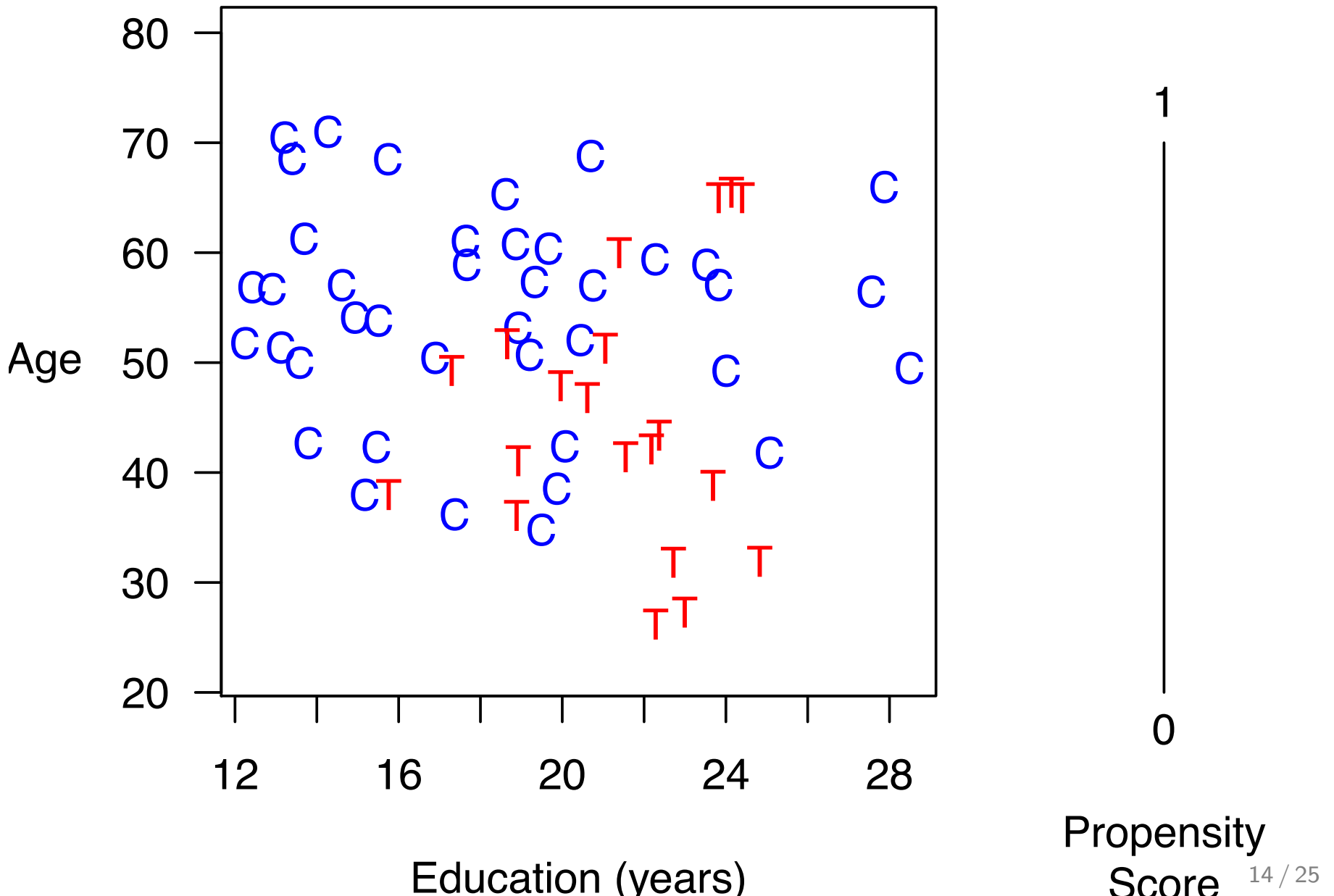

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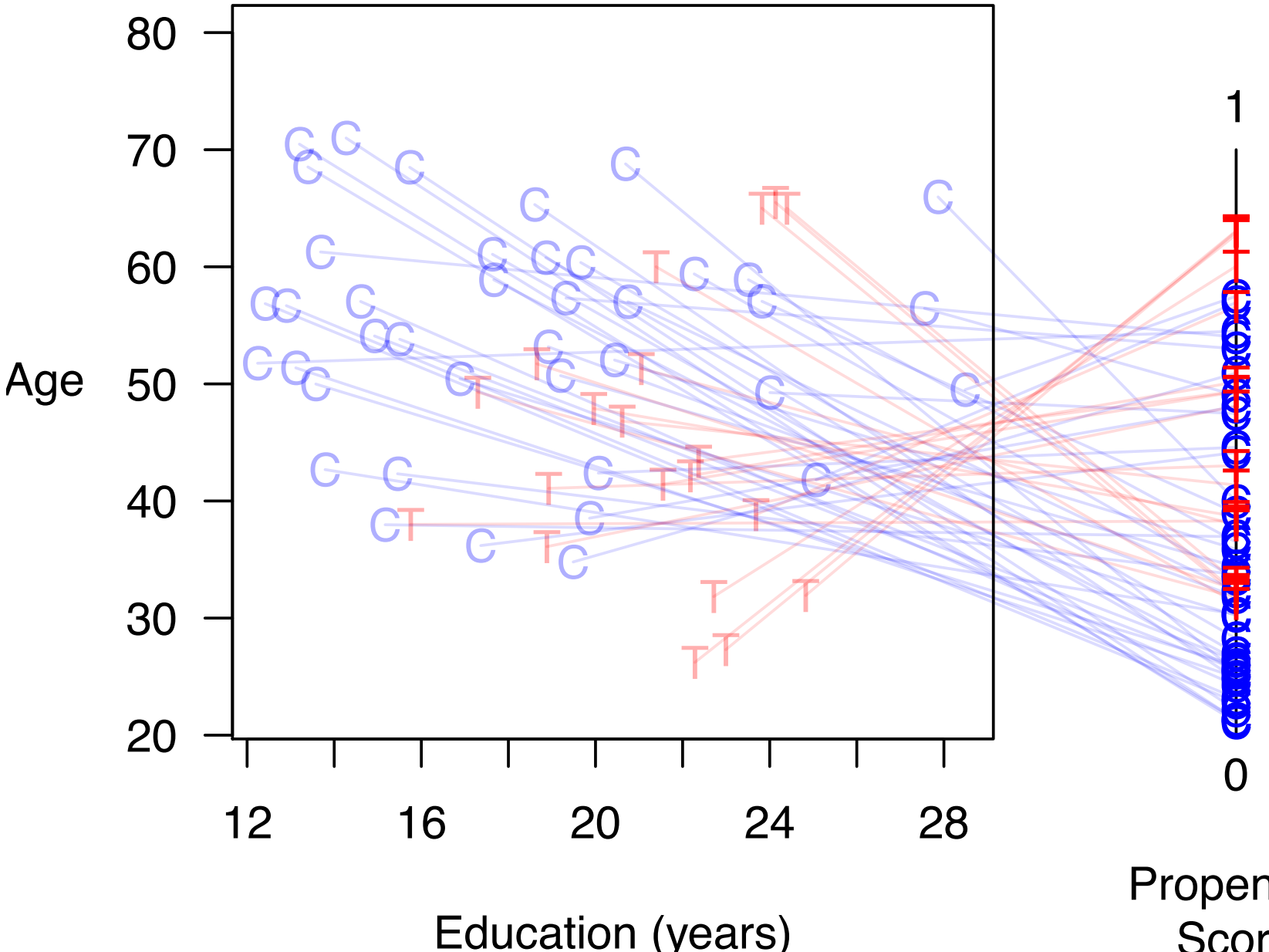

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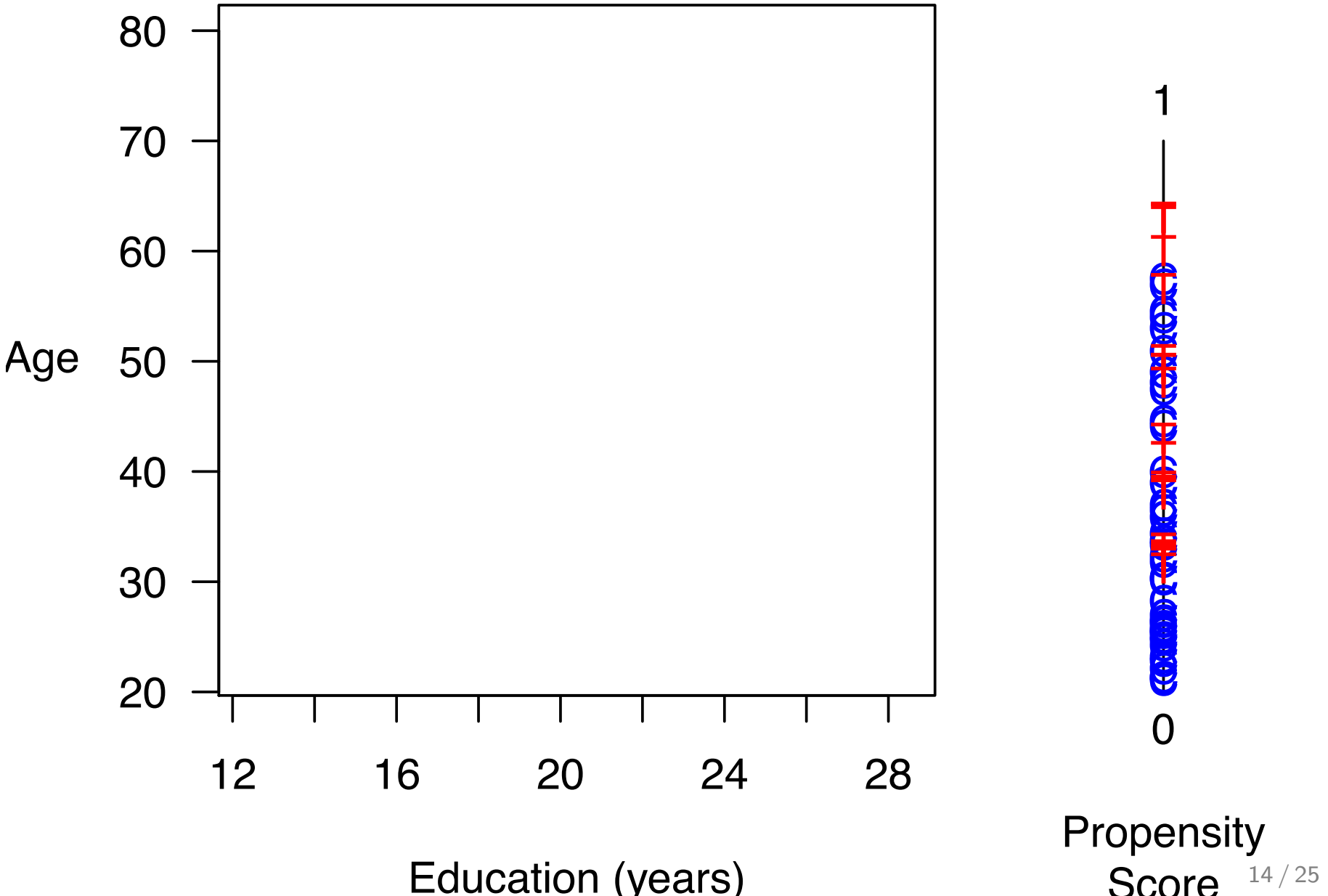

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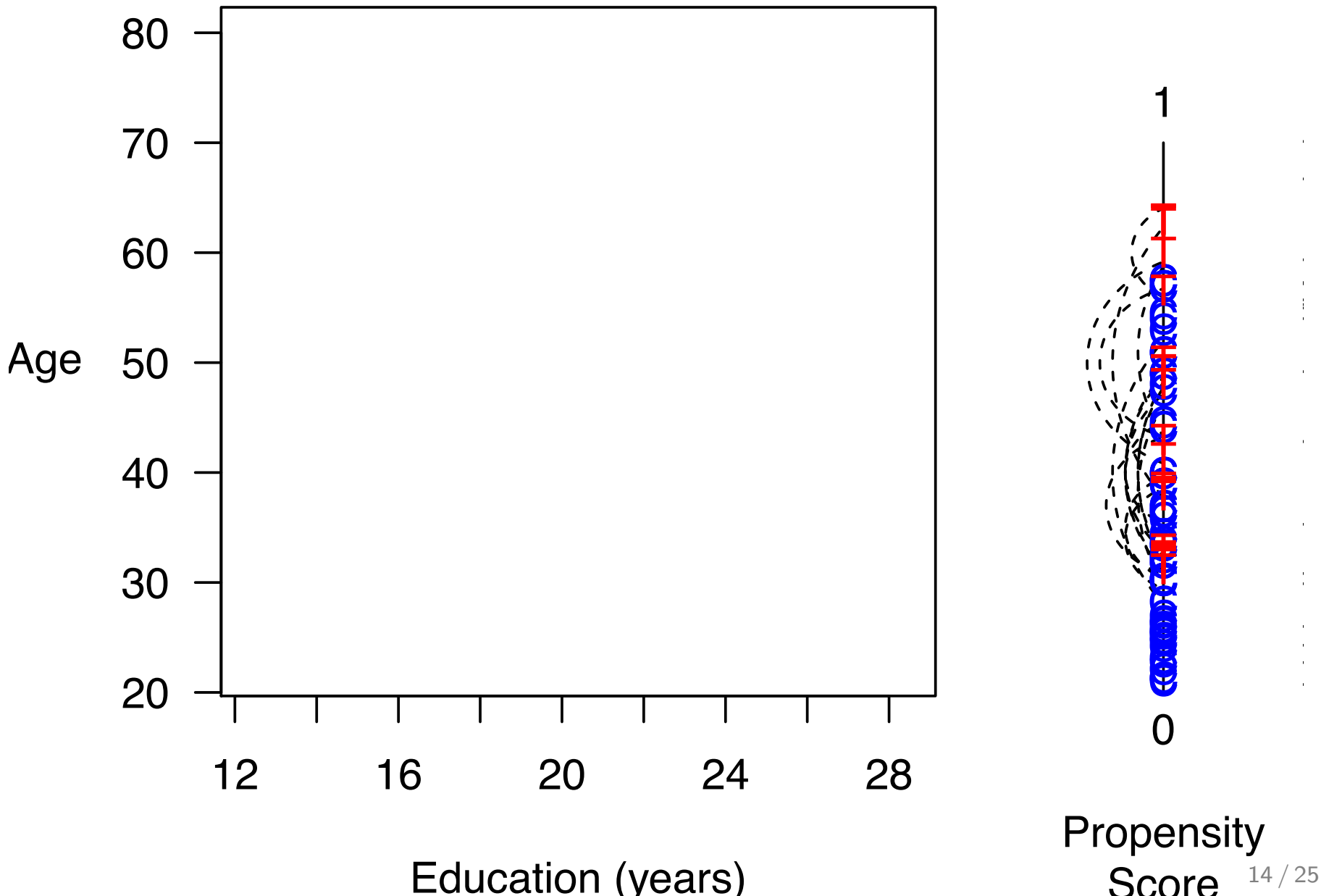

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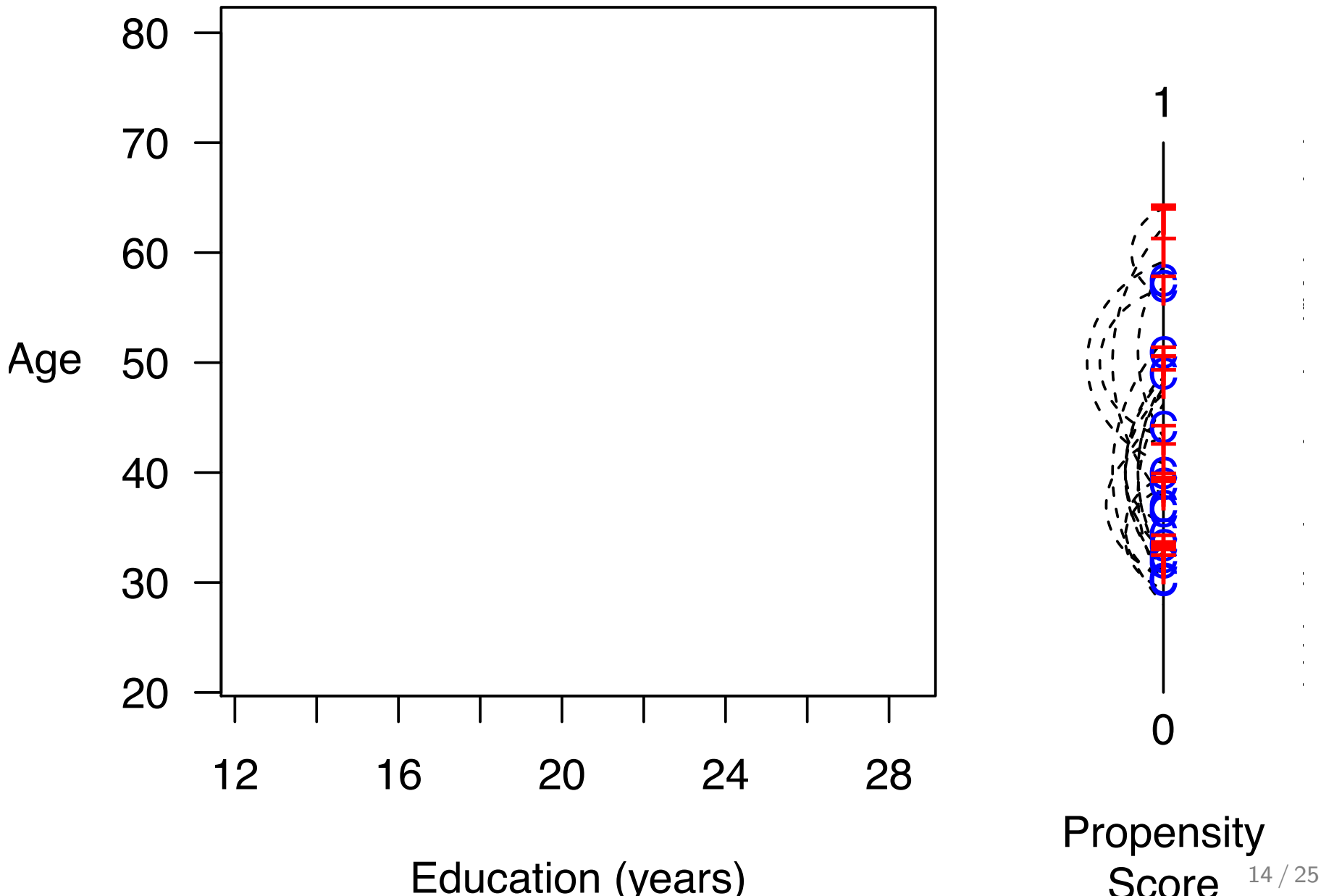

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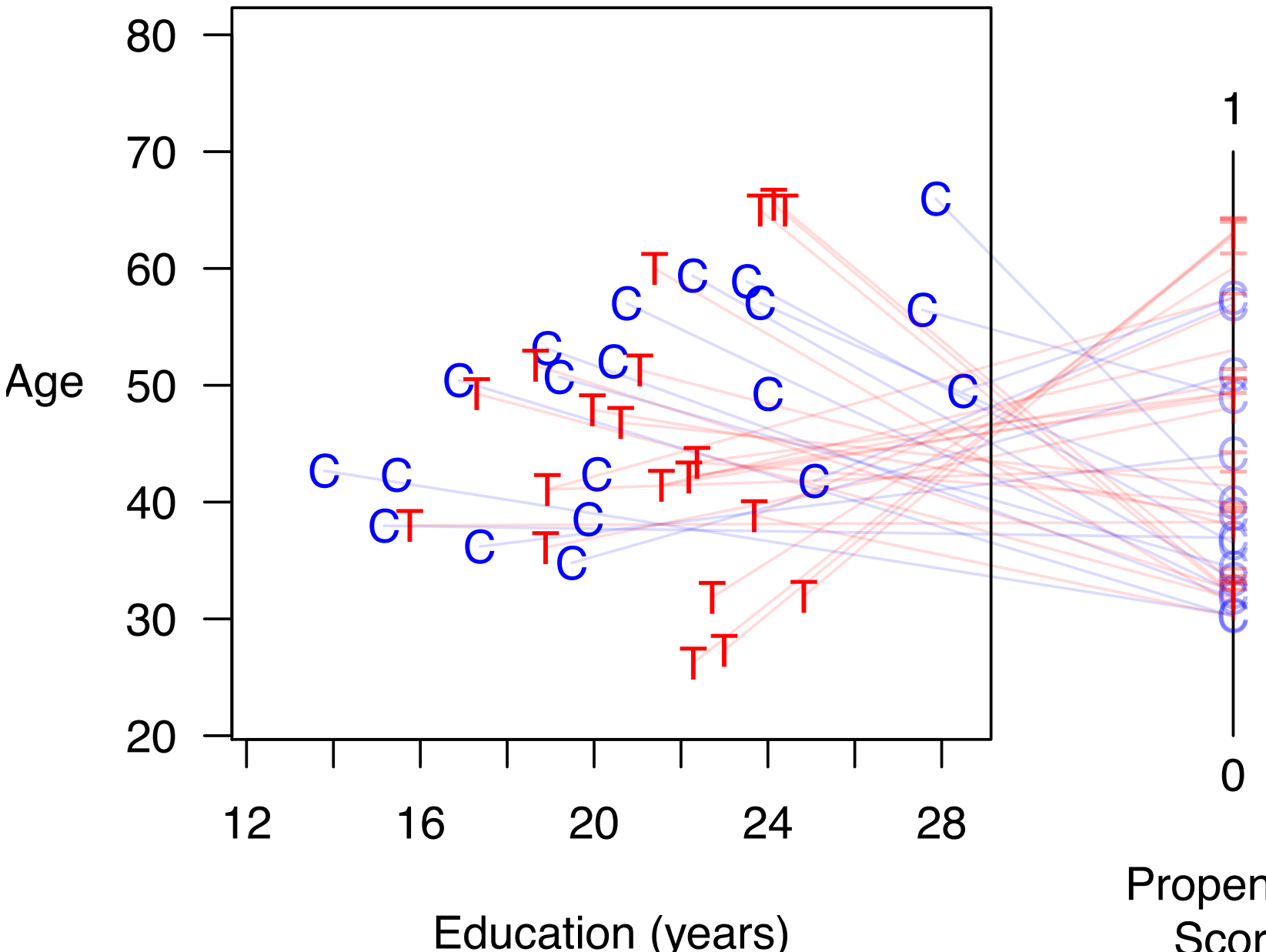

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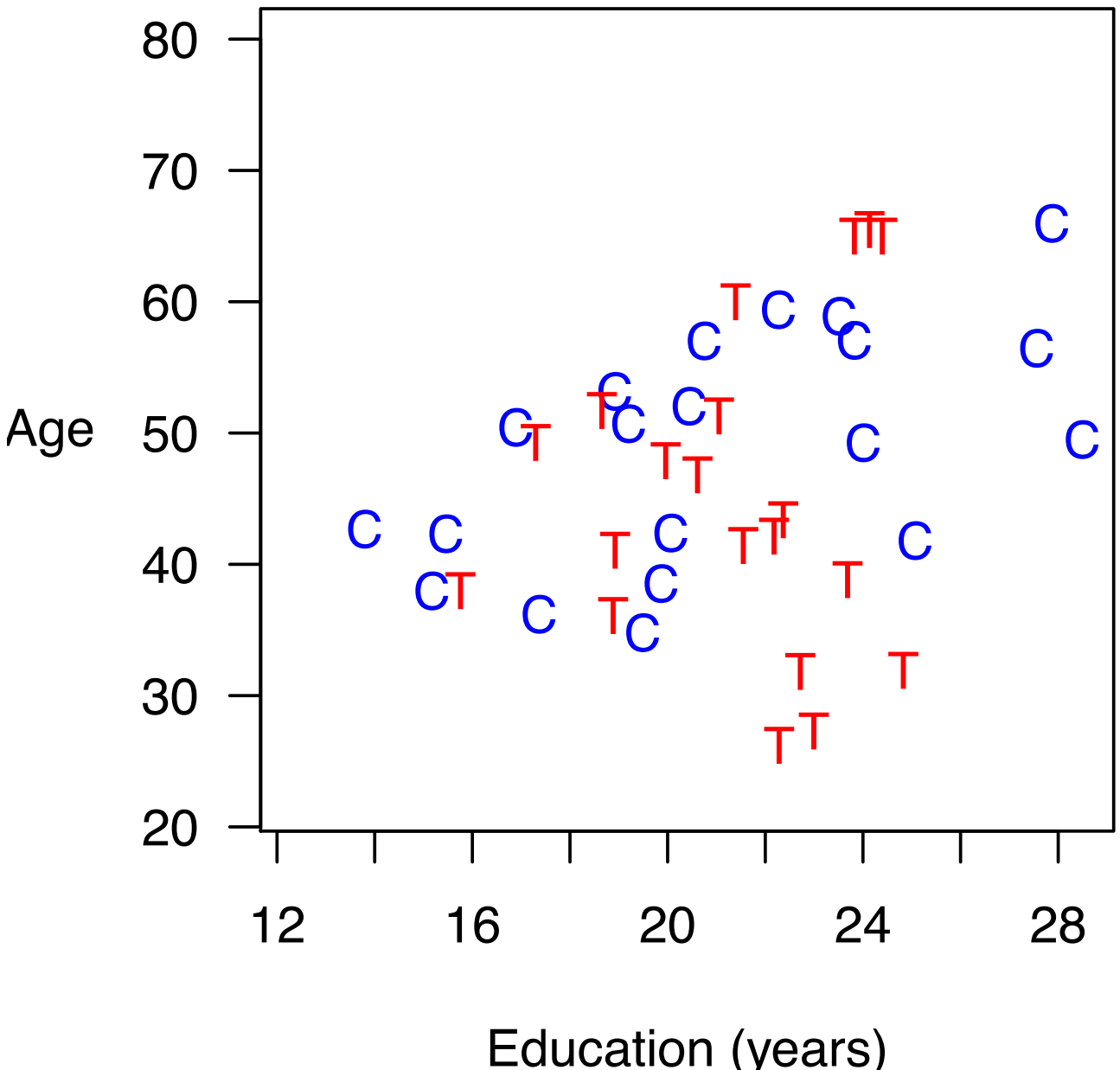

Best Case: Propensity Score Matching

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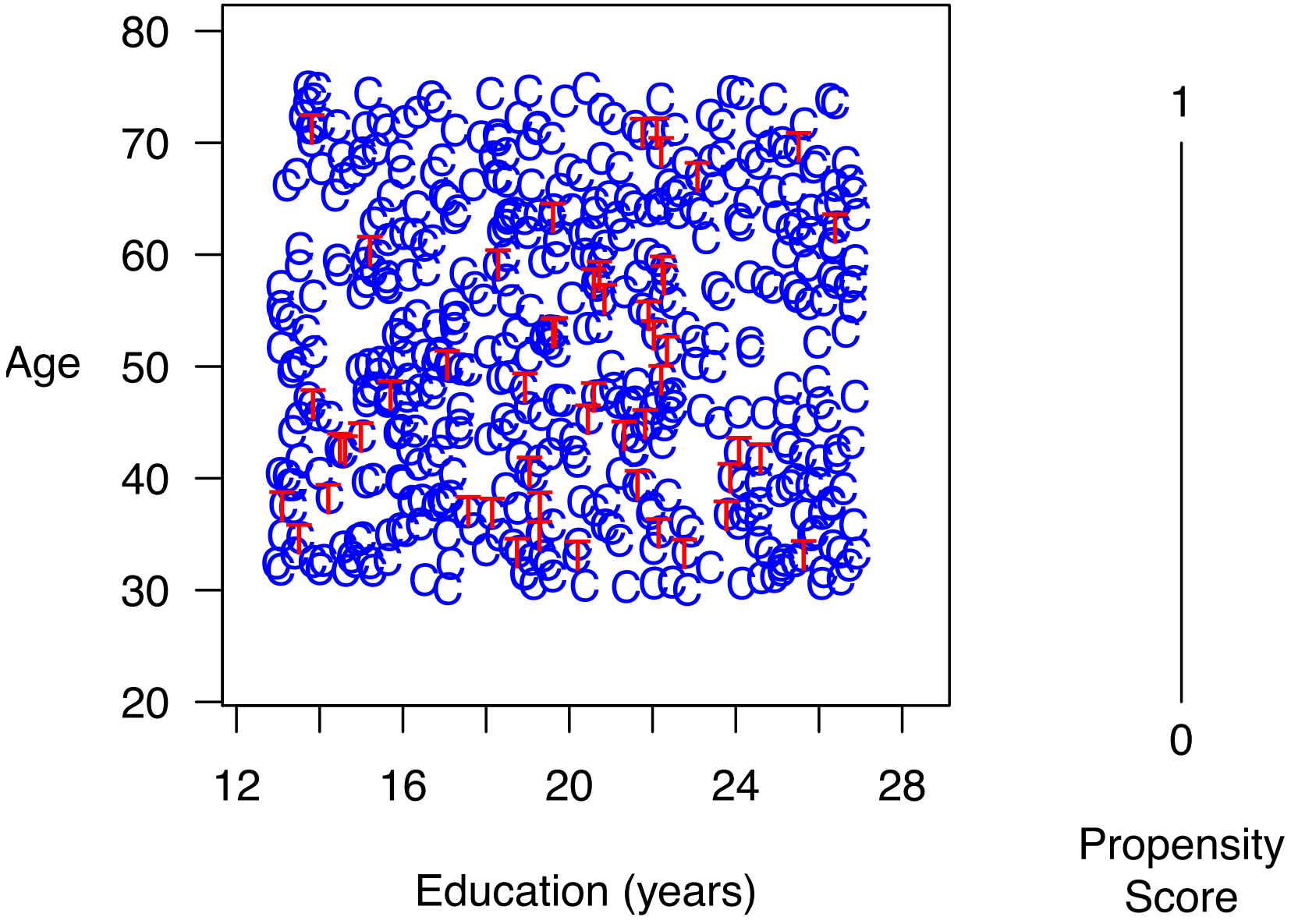

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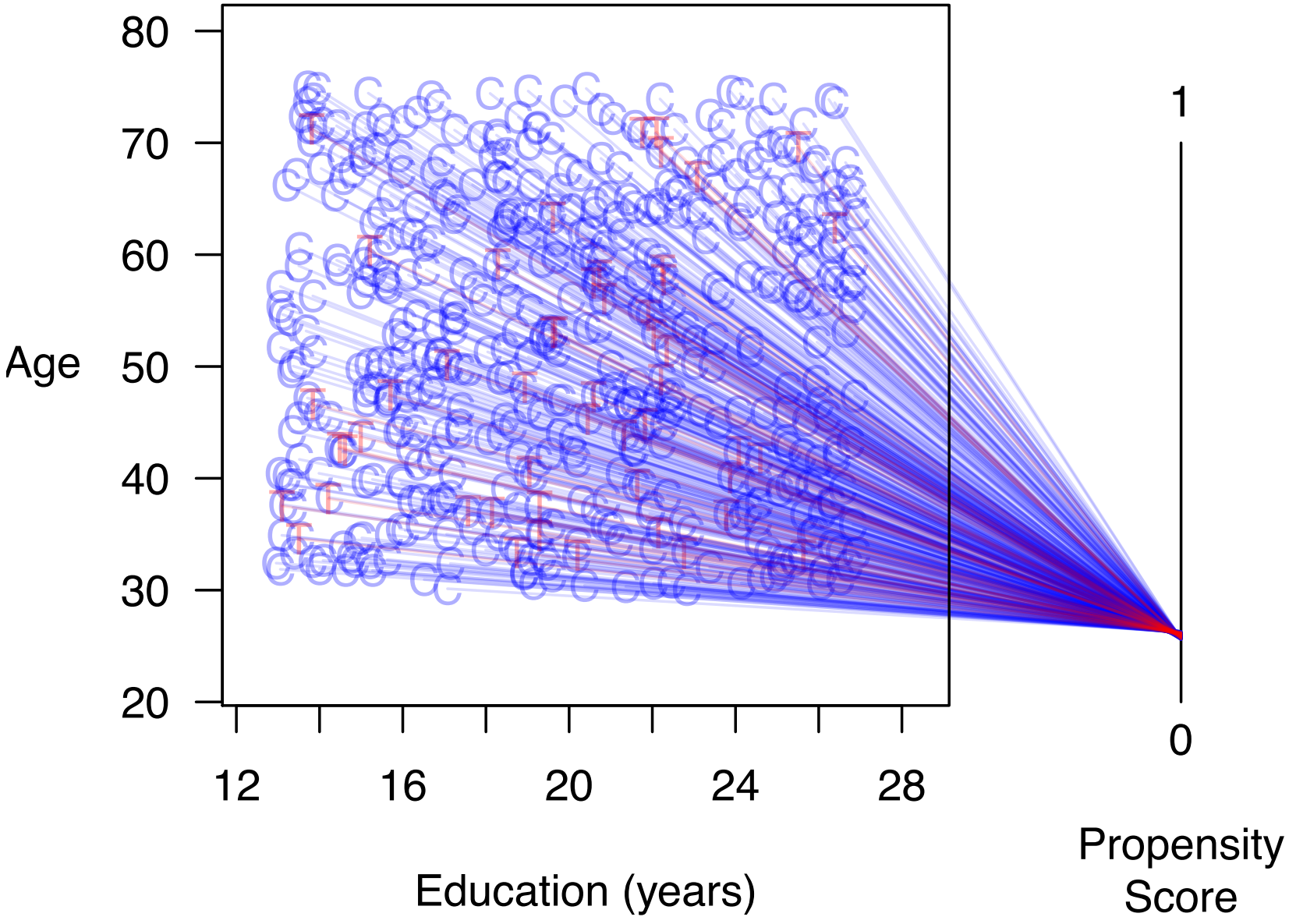

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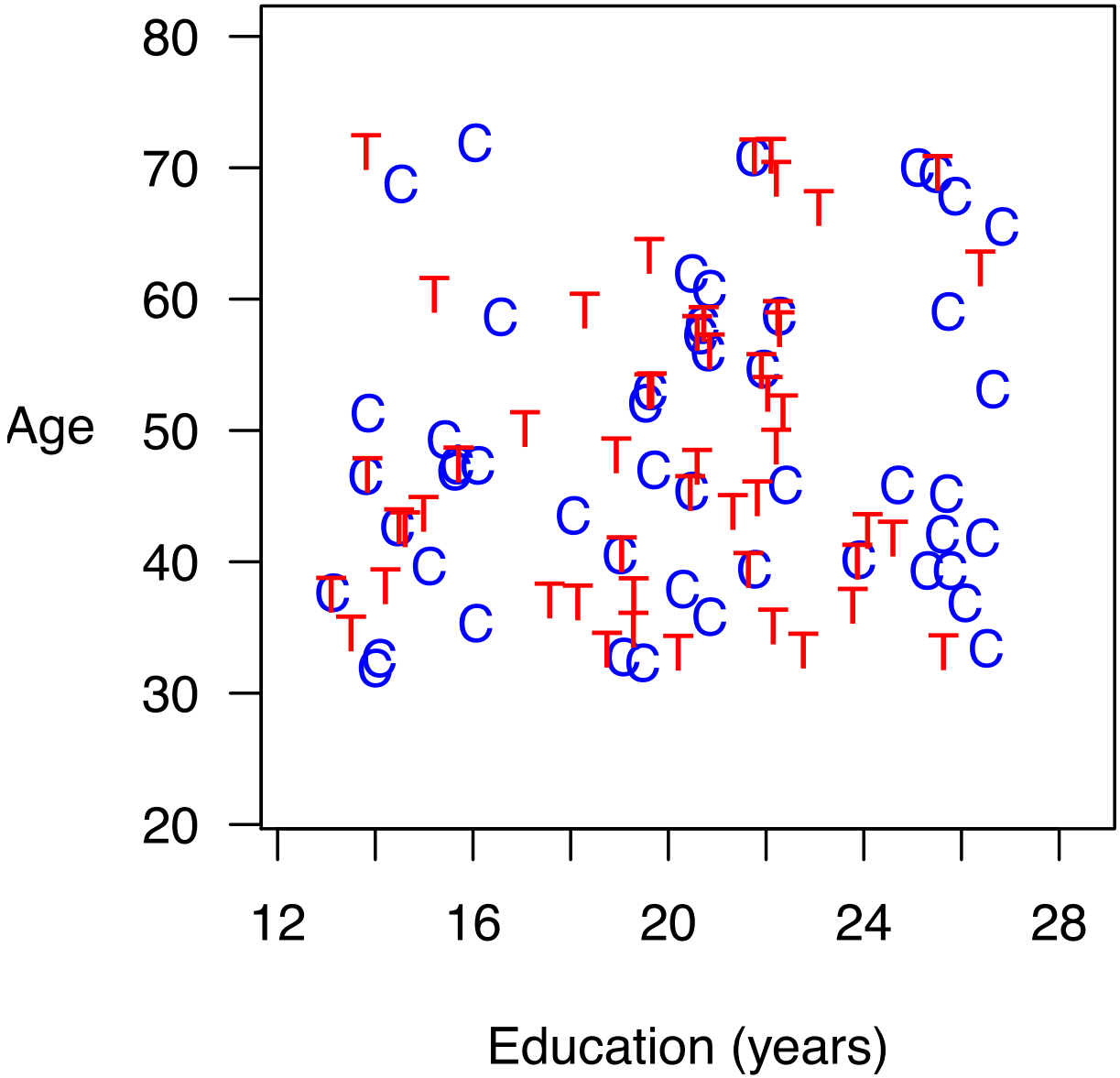
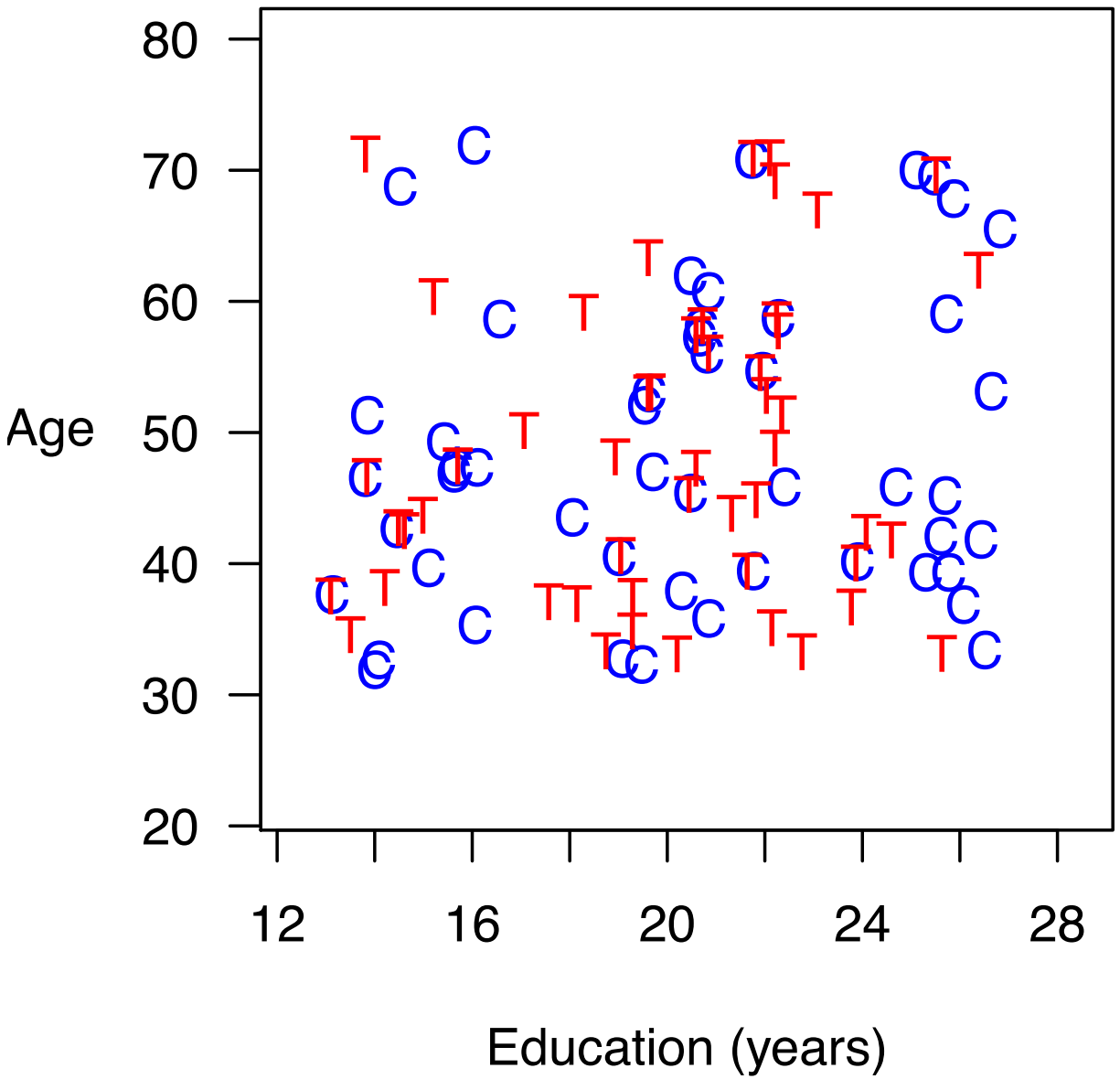


Best Case: Propensity Score Matching is Suboptimal

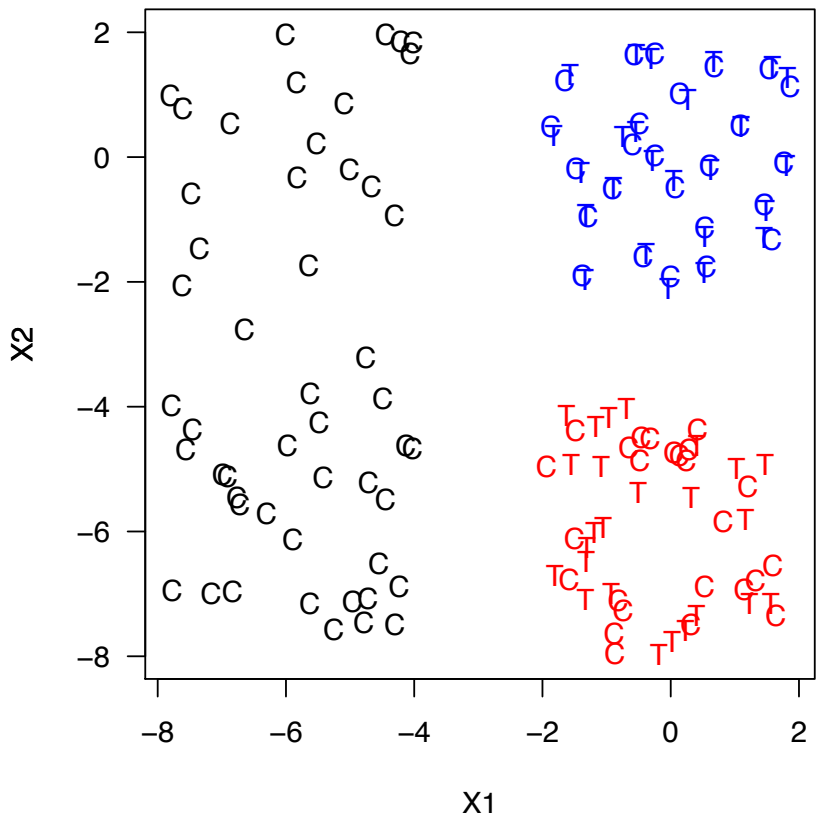


PSM's Statistical Properties

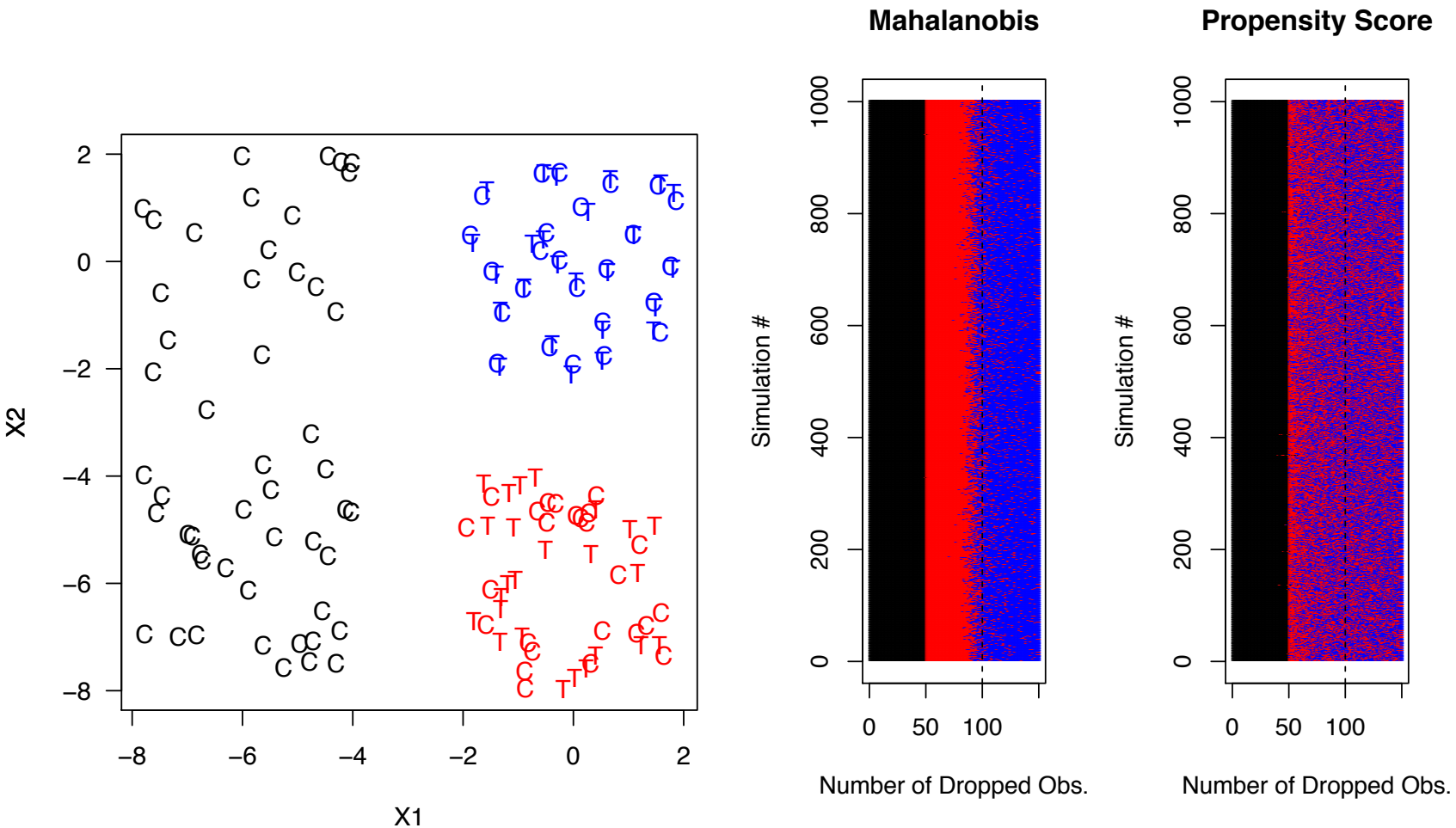
1. Low Standards: Sometimes helps, never optimizes
   - *Efficient* relative to complete randomization, but
   - *Inefficient* relative to (the more powerful) full blocking
   - Other methods usually dominate:
     $X_c = X_t \implies \pi_c = \pi_t$ but
     $\pi_c = \pi_t \not\implies X_c = X_t$
2. 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 $\rightsquigarrow$ Inefficency $\rightsquigarrow$ 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

PSM is Blind Where Other Methods Can See

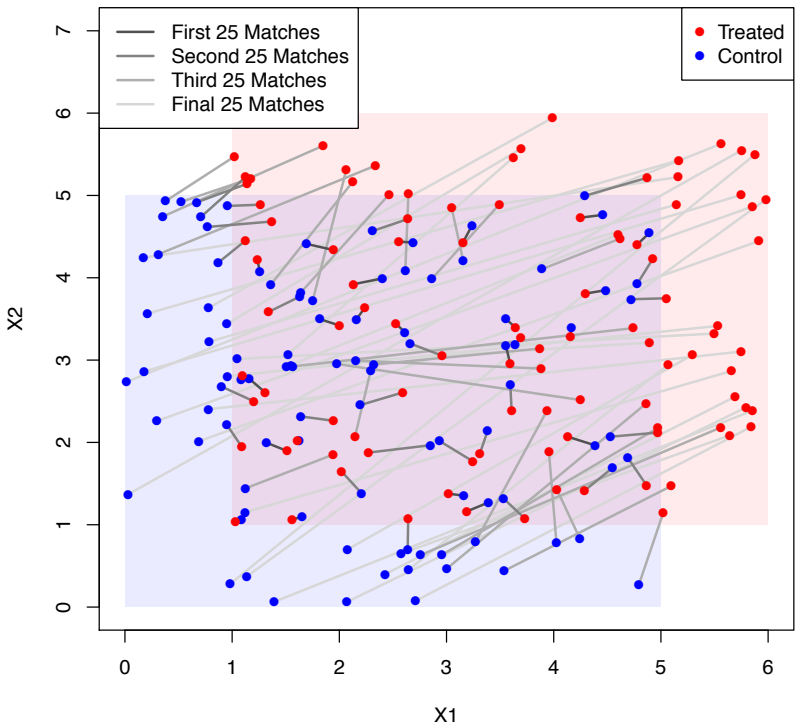


PSM is Blind Where Other Methods Can See

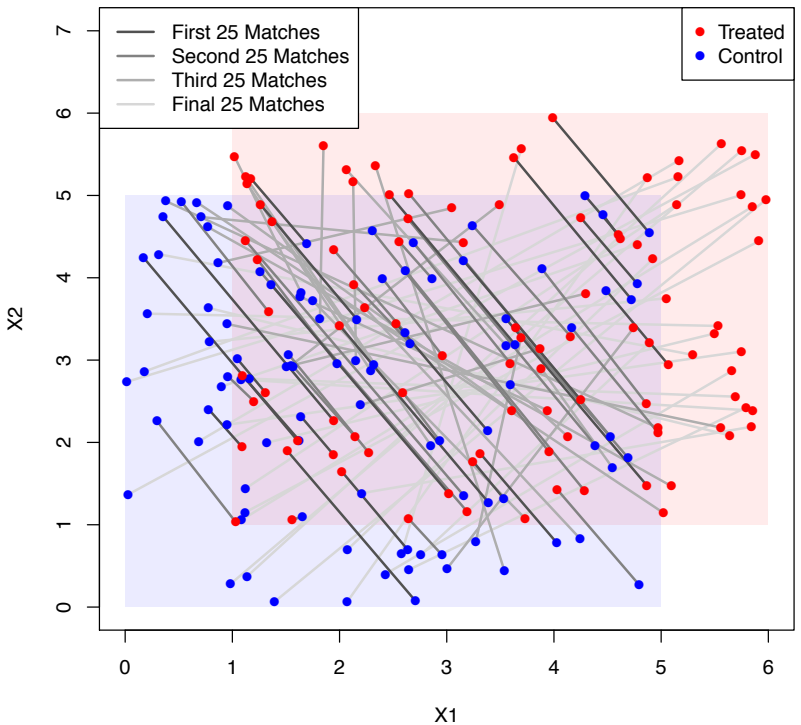


What Does PSM Match?

MDM Matches



PSM Matches

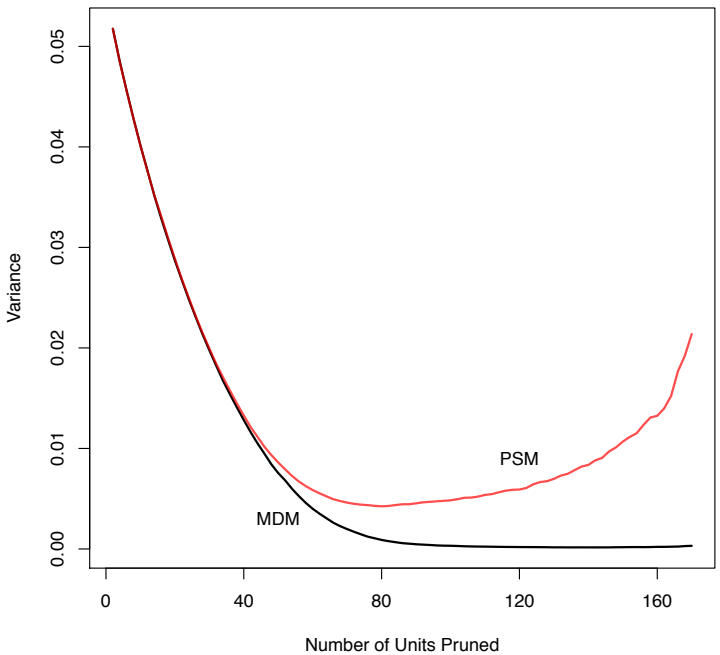


Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

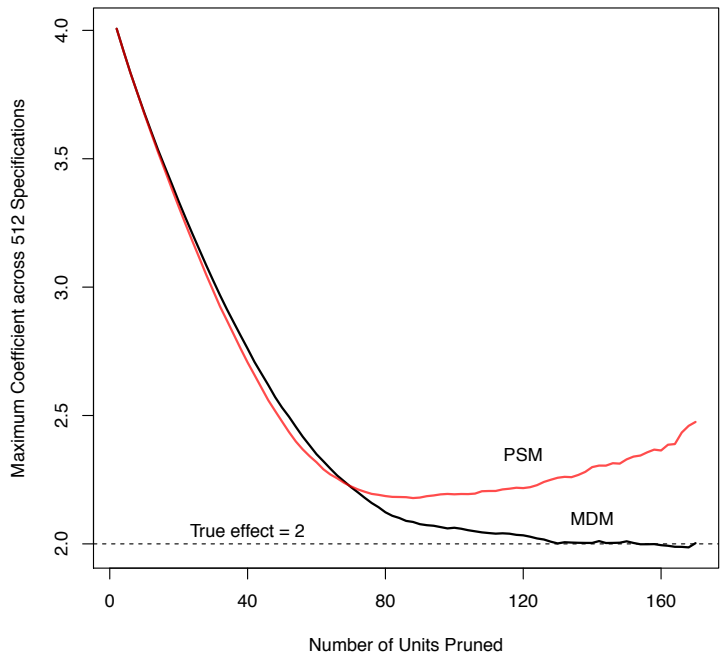
Treateds: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Increases Model Dependence & Bias

Model Dependence



Bias

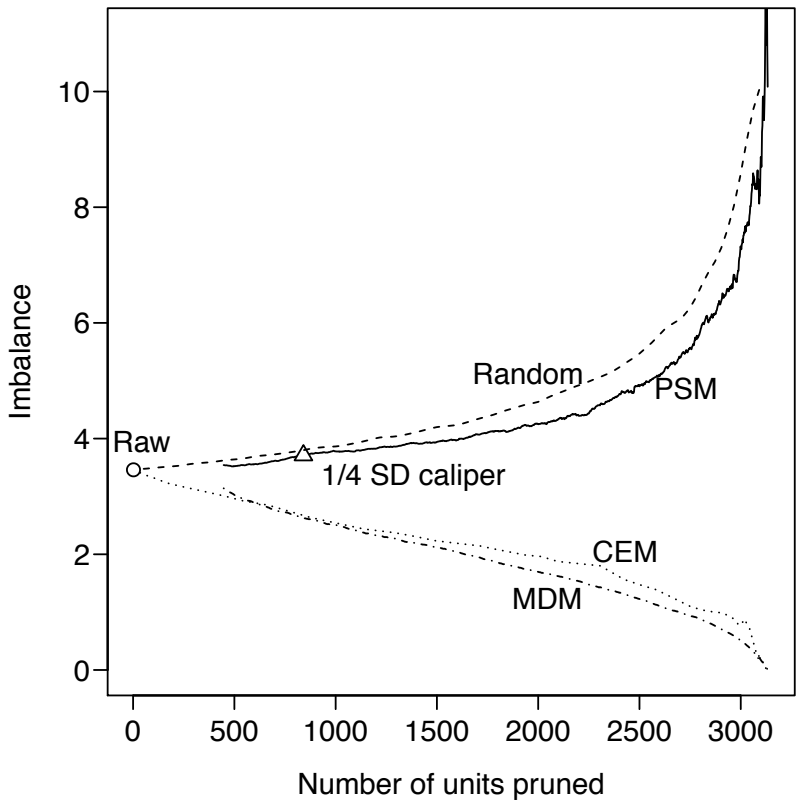


$$Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i$$
$$\epsilon_i \sim N(0, 1)$$

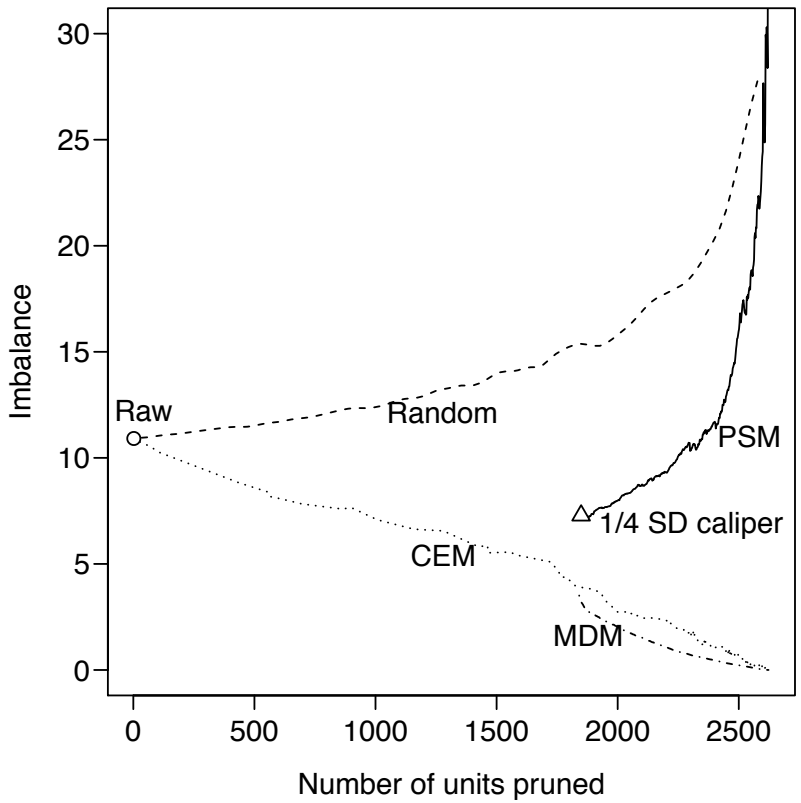
The Propensity Score Paradox in Real Data

The Propensity Score Paradox in Real Data

Finkel et al. (JOP, 2012)

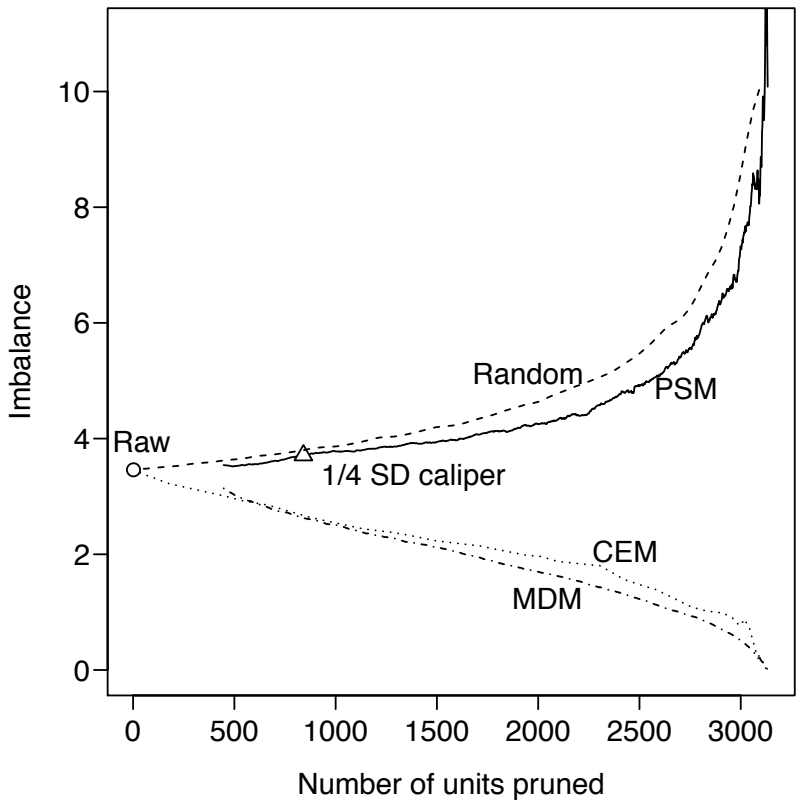


Nielsen et al. (AJPS, 2011)

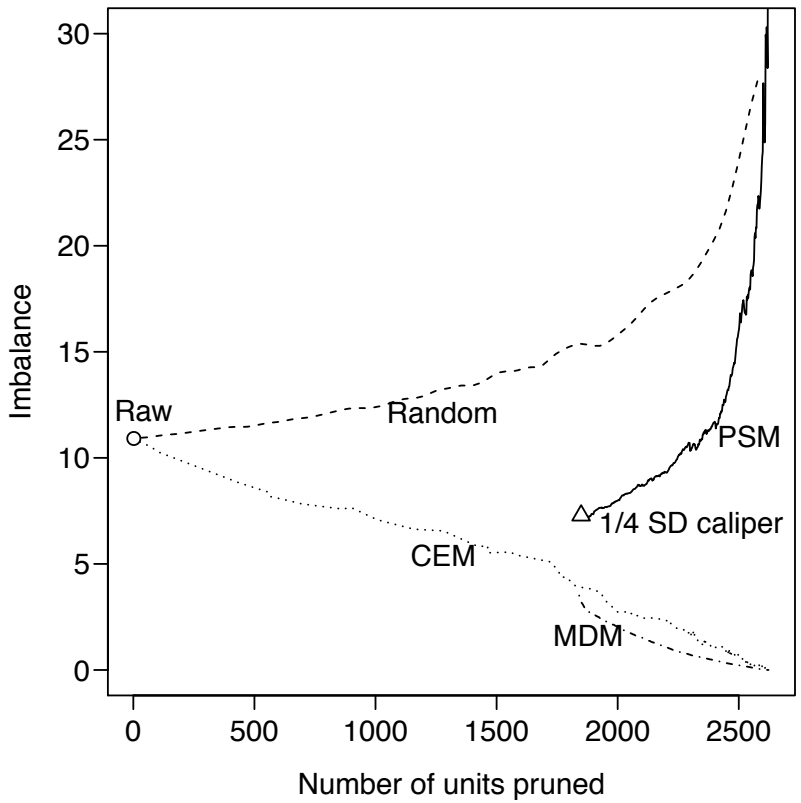


The Propensity Score Paradox in Real Data

Finkel et al. (JOP, 2012)



Nielsen et al. (AJPS, 2011)



Similar pattern for $>$ 20 other real data sets we checked

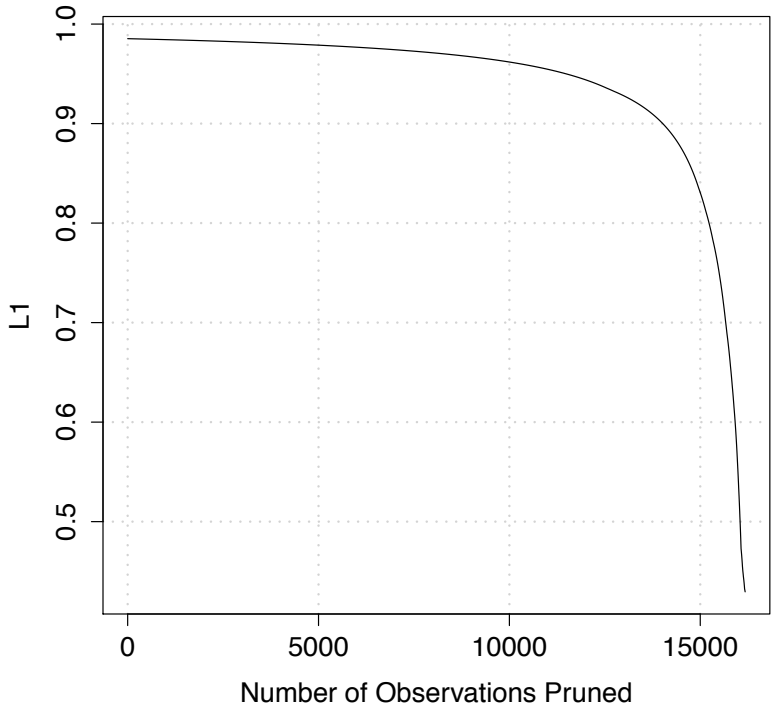
The Matching Frontier

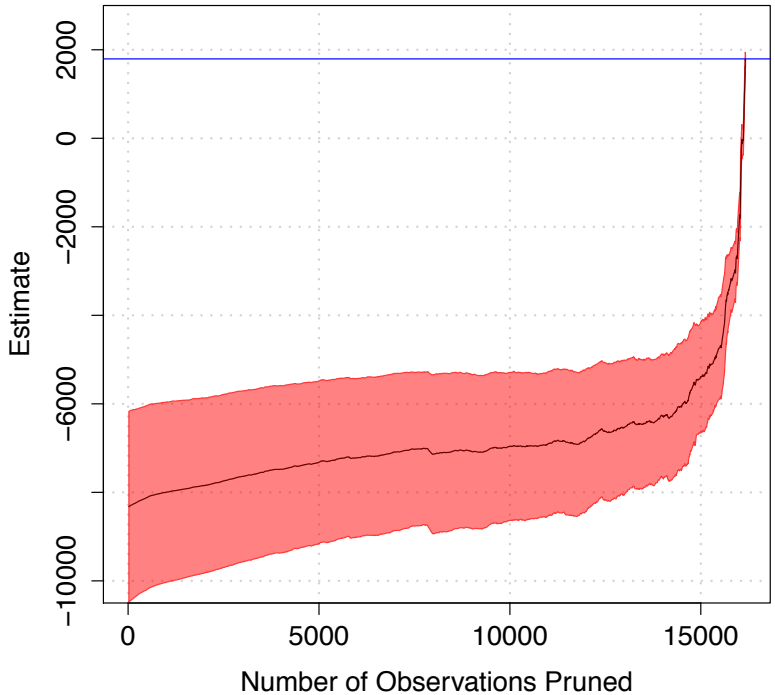
- Frontier = matched dataset with lowest imbalance for each n
- Bias-Variance trade off $\rightsquigarrow$ Imbalance-n Trade Off
- Simple to use
- No need to choose or use a matching method
- All solutions are optimal
- No iteration or diagnostics required
- No cherry picking possible; you see everything optimal
- Choose an imbalance metric, then run.

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
  - $\rightsquigarrow$ 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)
  - $\rightsquigarrow$ It's **easy** to calculate!

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

Conclusions

- Propensity score matching:
  - Approximates complete, not fully blocked, experiments
  - Ignores information; exacerbates model dependence
  - Some mistakes with PSM: Controlling for irrelevant covariates; Adjusting experimental data; Reestimating propensity score after eliminating noncommon support; 1/4 caliper on propensity score; Not switching to other methods.
- A Simple and Powerful Method: CEM
- A New General Approach: The Matching Frontier
  - Fast; easy; no iteration; Software: MatchingFrontier
  - No need to choose among matching methods
  - Optimal results from your choice of imbalance metric
- $\rightsquigarrow$ Using more information is simpler and more powerful

For more information, articles, & software

GaryKing.org