FLS 6441 - Methods III: Explanation and Causation

Week 10 - Matching

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Classification of Research Designs

		Independence of Treatment Assignment	**Researcher Controls Treatment Assignment?**
Controlled Experiments	Field Experiments	✓	✓
	Survey and Lab Experiments	✓	✓
Natural Experiments	Natural Experiments	✓	
	Instrumental Variables	✓	
	Discontinuities	✓	
Observational Studies	Difference-in-Differences		
	Controlling for Confounding		
	Matching		
	Comparative Cases and Process Tracing		

Section 1

Matching

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- The solution? **Non-parametric** methods for controlling for confounding
  1. We use *ONLY SOME* of the data
  2. We do not specify the parameters of any model
- **Matching** is a non-parametric method
  - A **pre-processing** stage
  - Analysis of the results is separate and comes later

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    1. One way of forcing balance is by **ajusting** each treated observation to predict what it would 'look like' if it were identical to a control observation - a regression model
    2. An alternative is just to **throw out** all of the treated observations that do not have a comparable control observation - this is matching

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- Matching is **NOT** an experimental method

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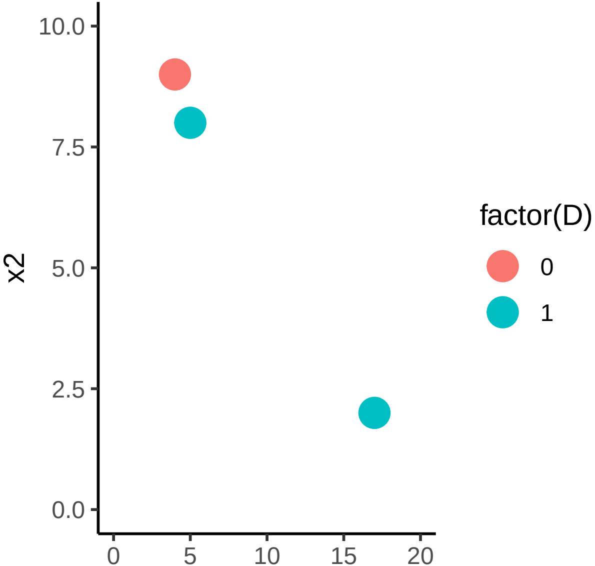
2. Repeat for every treated unit
3. Drop all the unmatched units (eg. ’extra’ treated units that are ’far away’ from any control units)
4. Assess balance - re-run the matching process as many times as you can to maximize balance!

Matching

1. For example:



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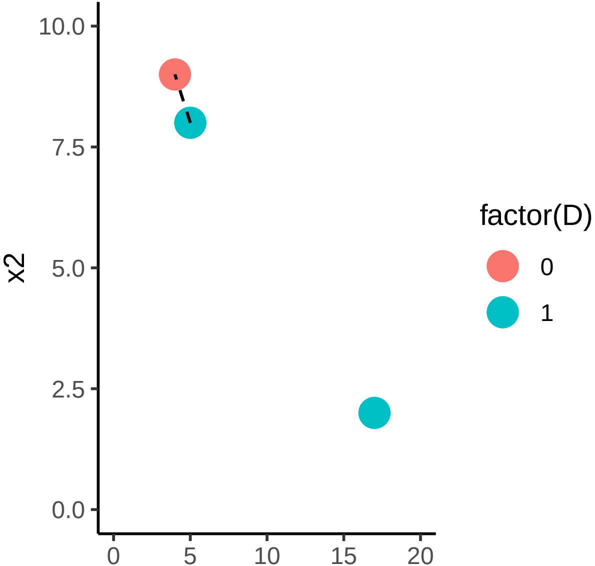

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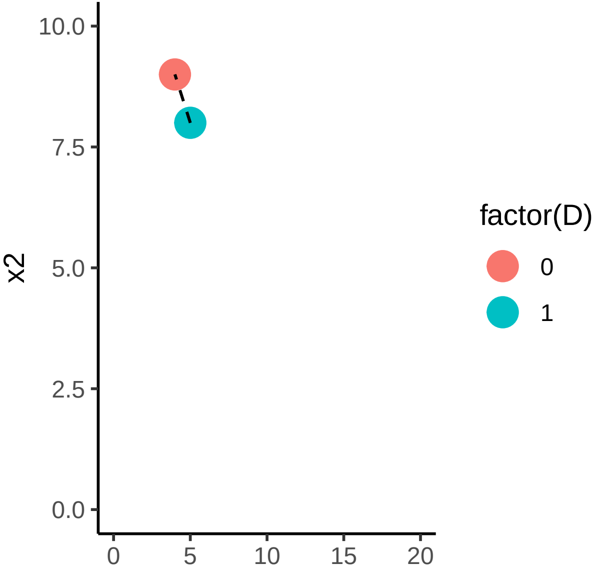

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- After matching, for the analysis we can either:
  1. Calculate the difference in means between treated and control groups
  2. Conduct the normal regression: $Y \sim D$
     - Option to include all our matching variables as controls
     - This will help control for any **residual imbalance** (esp. for continuous variables)

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  - Post-treatment variables? **No!** This will bias our causal effect, just as in regression
  - Pre-treatment Confounders? **Yes!** We want to remove imbalance due to confounders

Matching to Reduce Model Dependence

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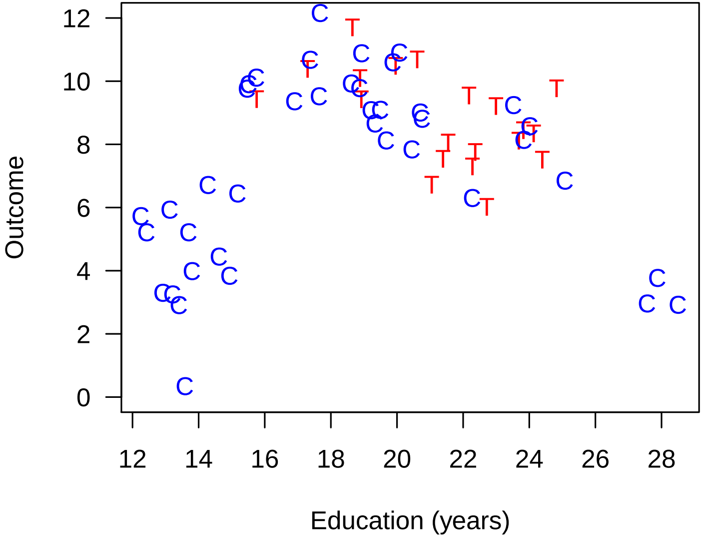

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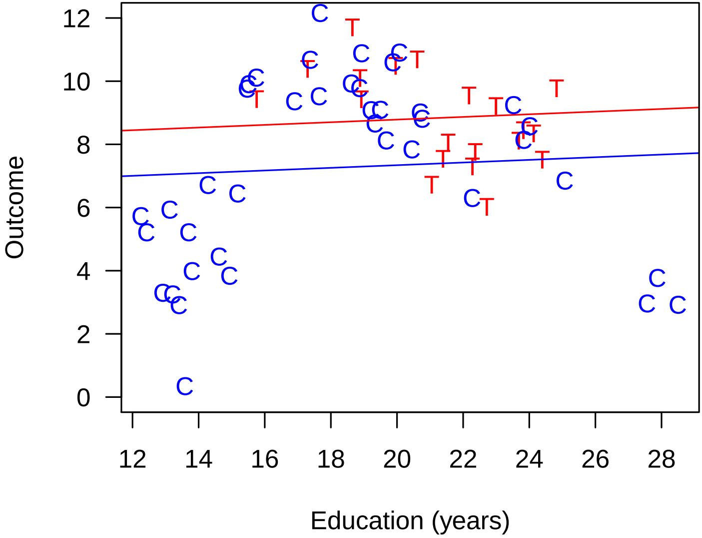

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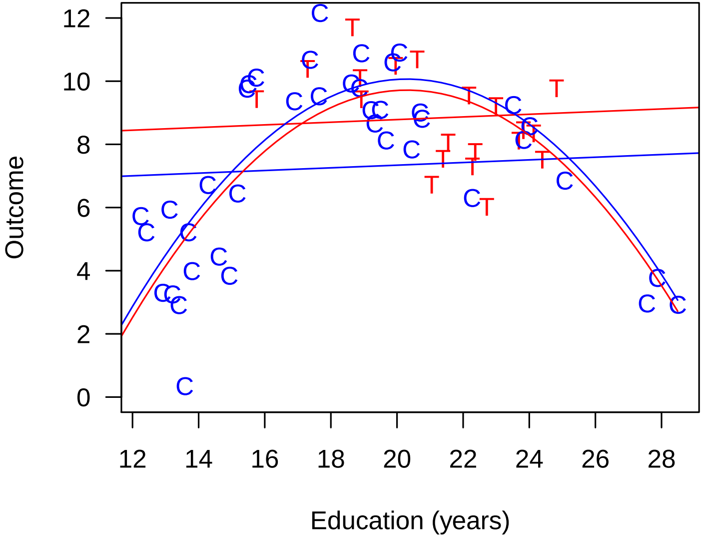

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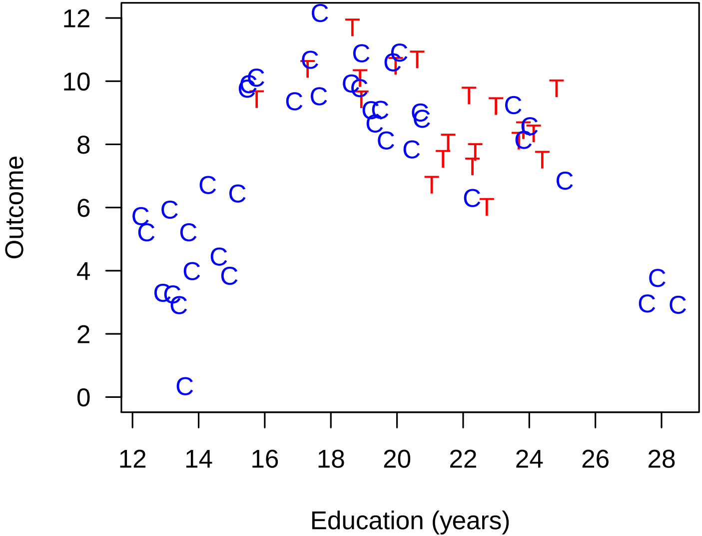

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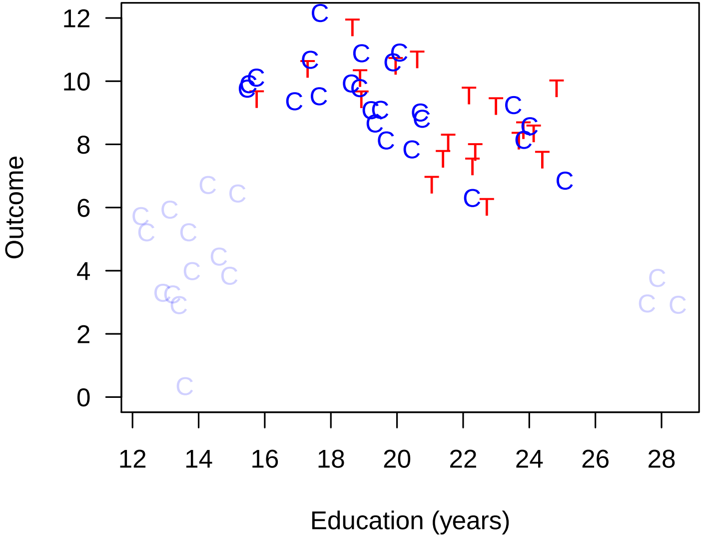

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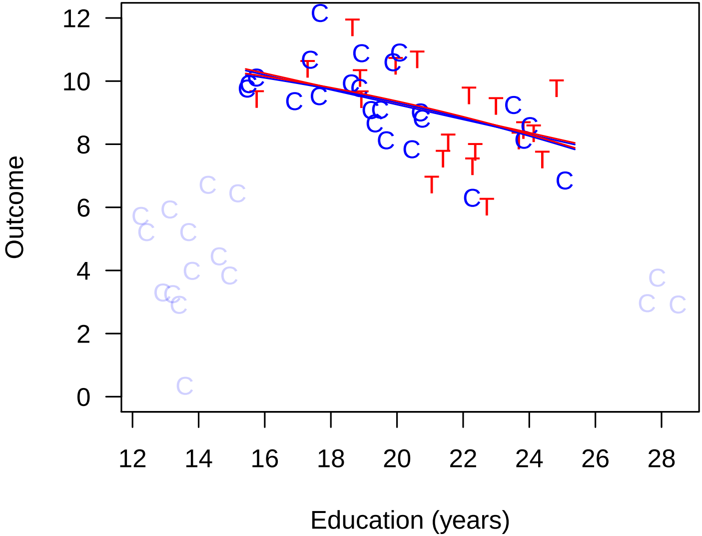

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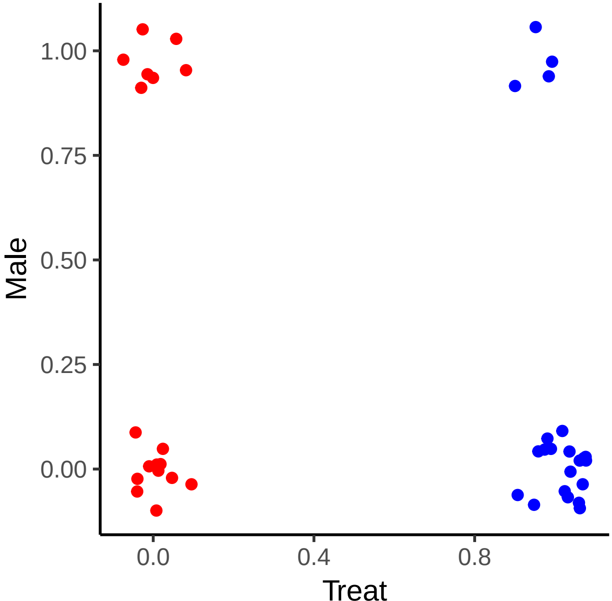
2. Matching on continuous variables (sequential): **Nearest-Neighbour Matching**
3. Matching to maximize balance: **Optimal/Genetic Matching**
4. Matching on the probability of treatment: **Propensity Score Matching**

Section 2

Alternative Matching Methods

Exact Matching



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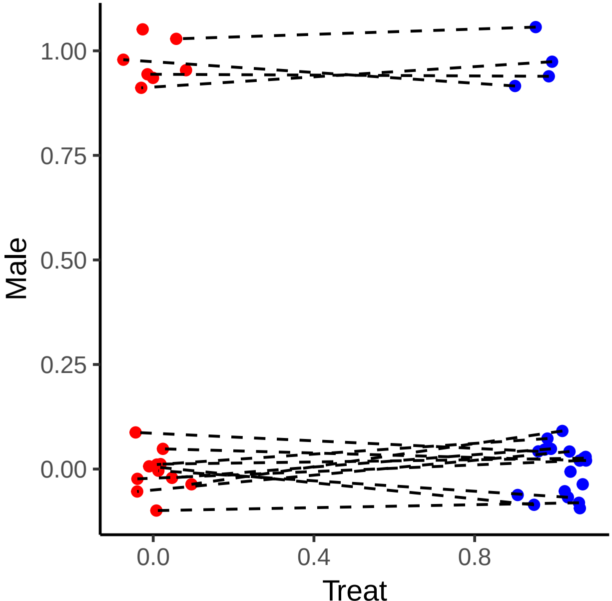

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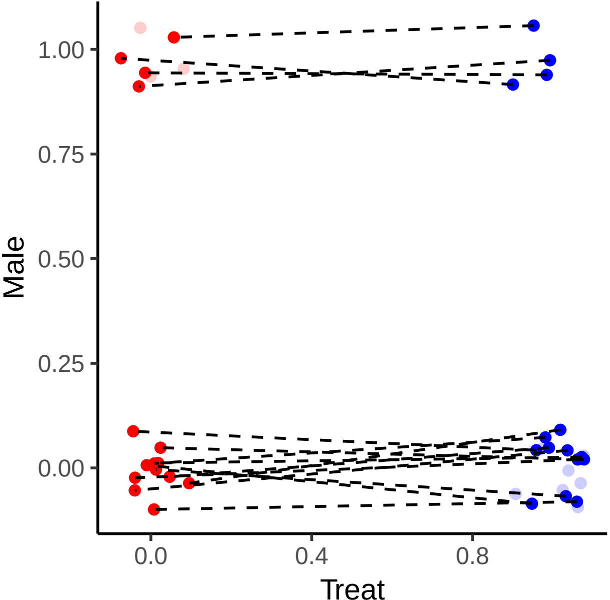

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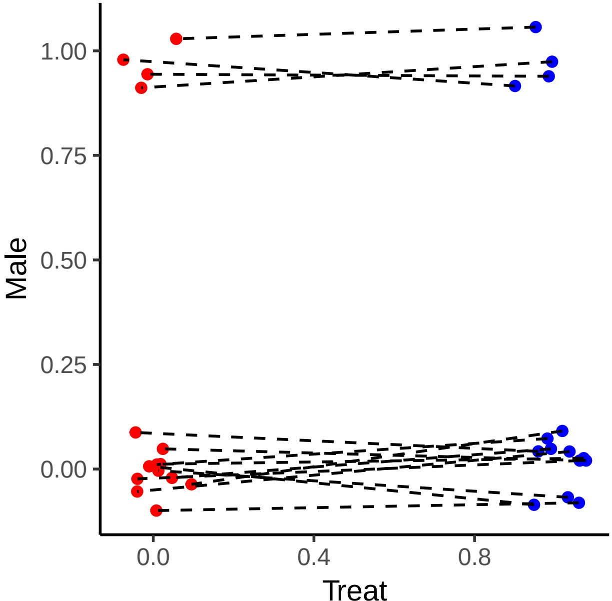

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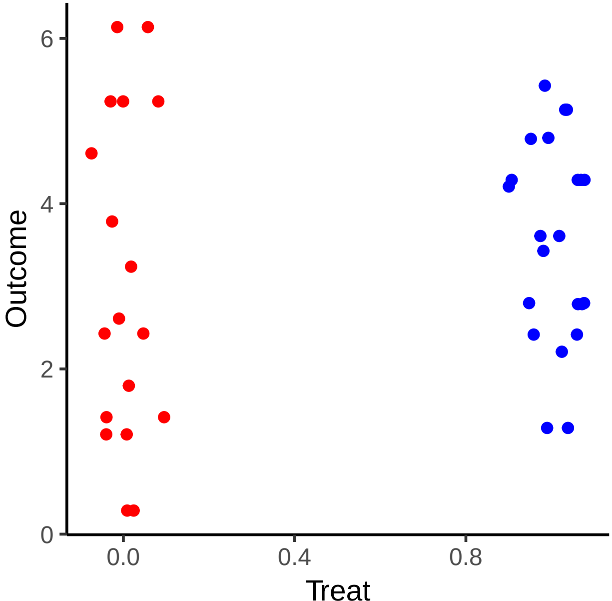
- Then compare the outcome of the **remaining** treated and control units
  - Difference in means
  - Or regression of outcome on treatment

Exact Matching

	Units	Means Treated	Means Control	Mean Diff
1	All	0.18	0.39	-0.21
2	Matched	0.27	0.27	0.00

Exact Matching Analysis



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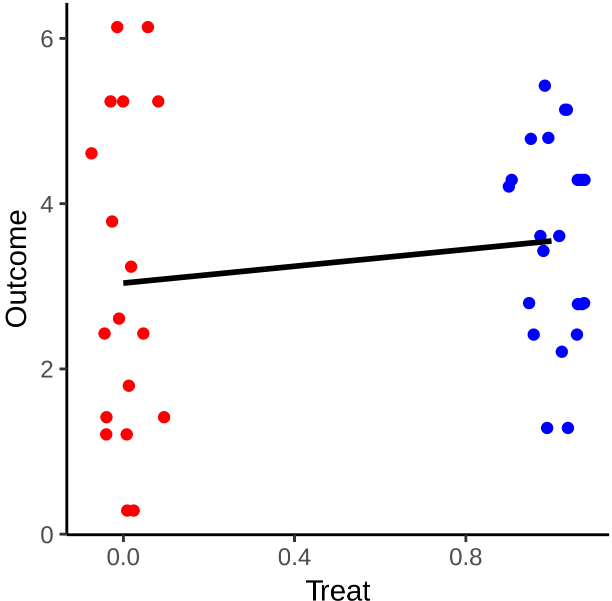

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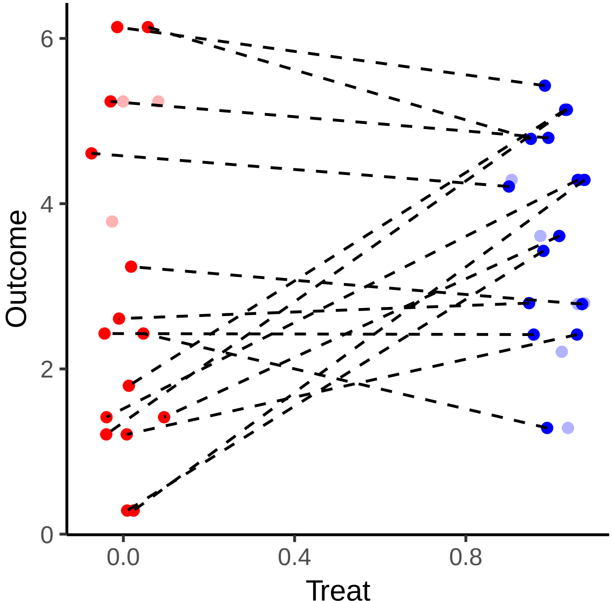

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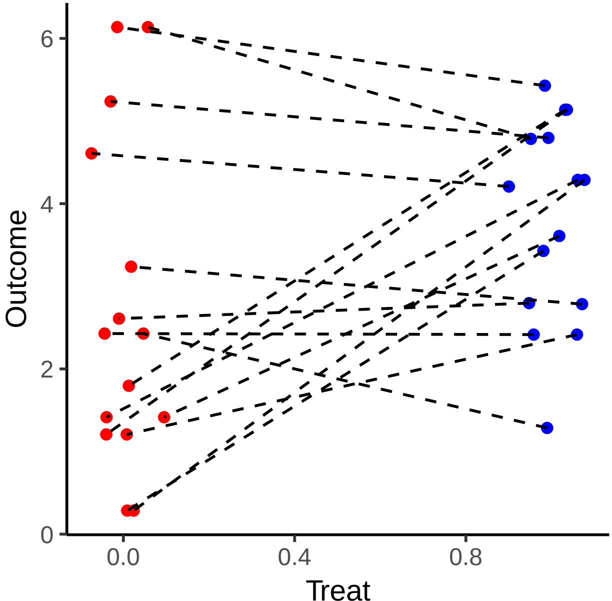

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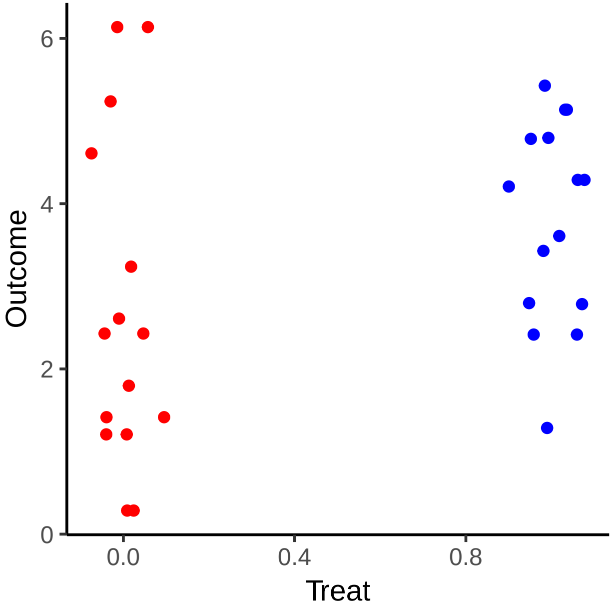

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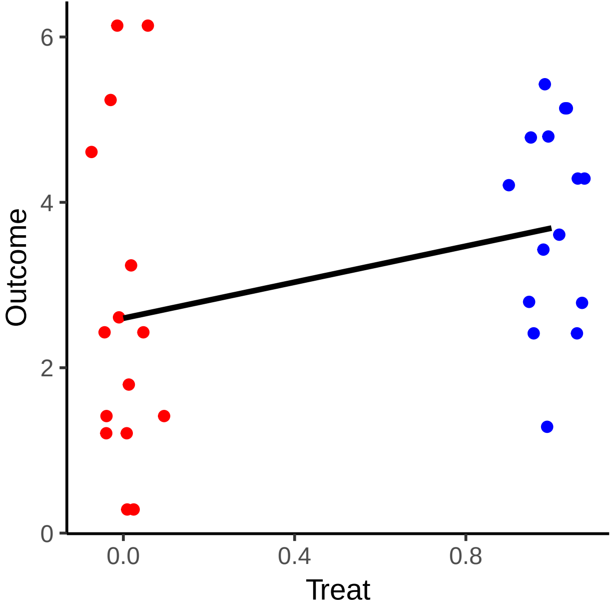

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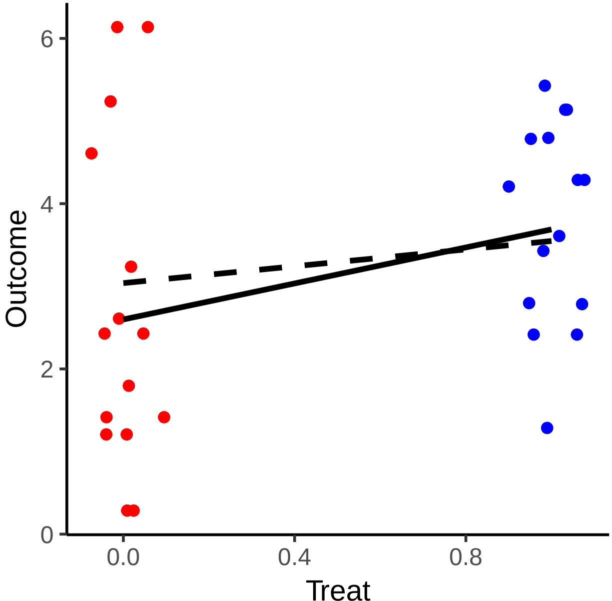

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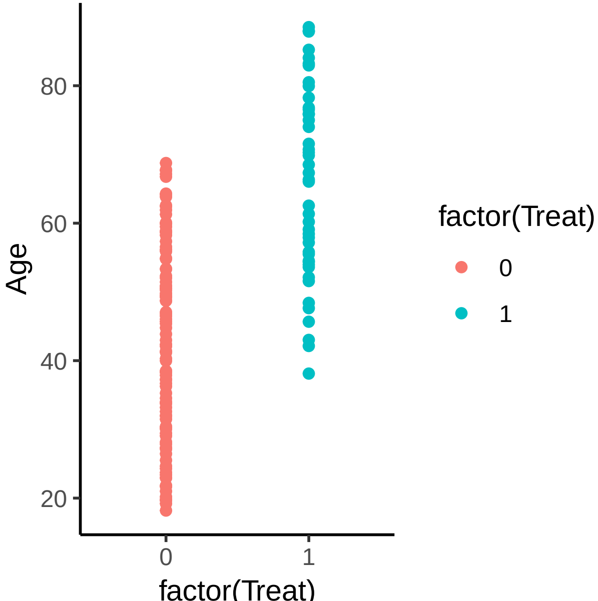

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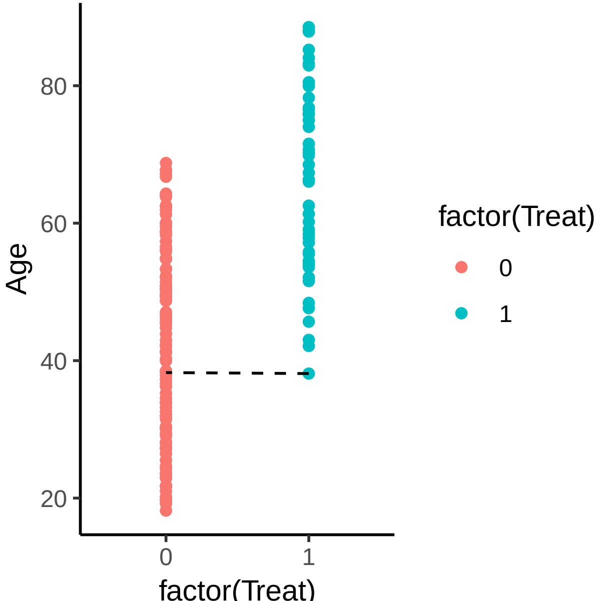

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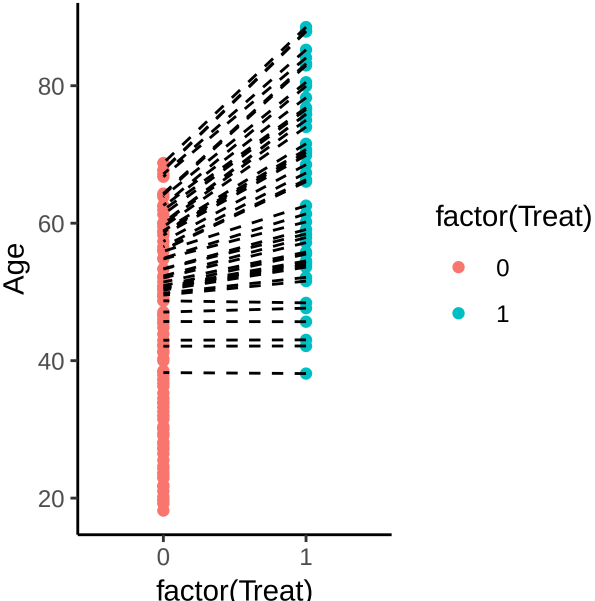

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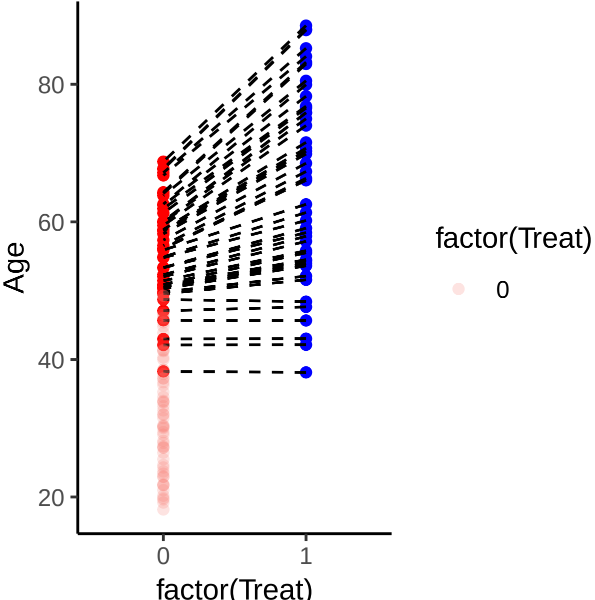

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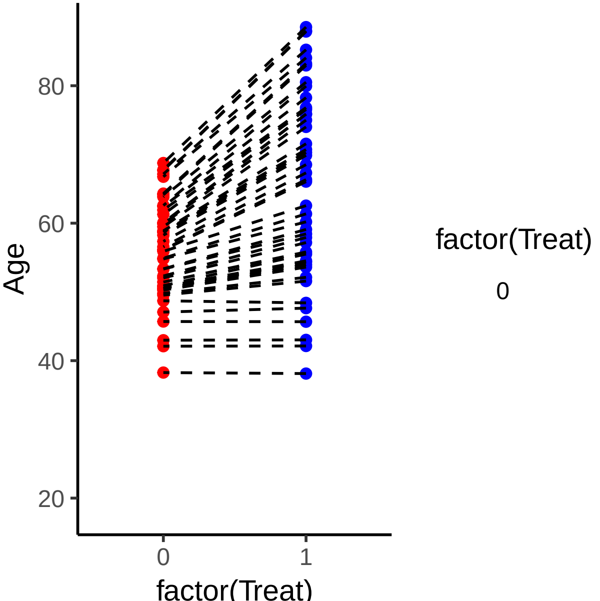

Nearest Neighbour Matching

	Units	Means Treated	Means Control	Mean Diff
1	All	65.70	42.67	23.03
2	Matched	65.70	56.09	9.61

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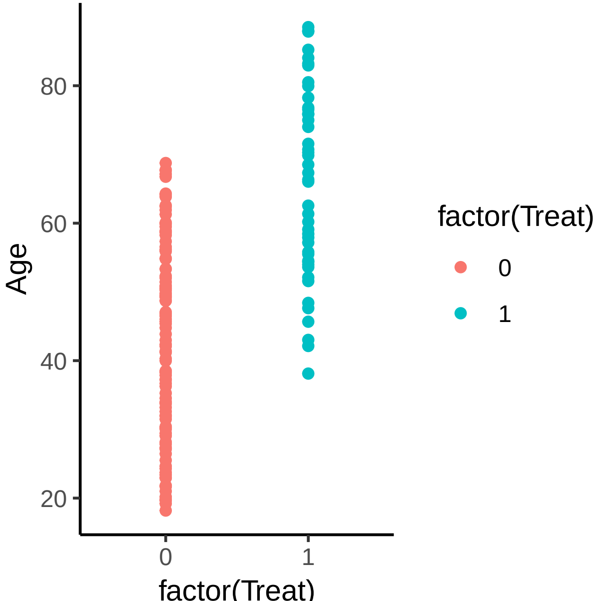
  2. **The order of matching matters:** The first matches use up units that might make better matches for later treated units
     - To maximize balance we need to ’look ahead’ and match in the right order
     - For this we can use optimal or genetic matching, which is fully automated

Nearest Neighbour Matching with Caliper



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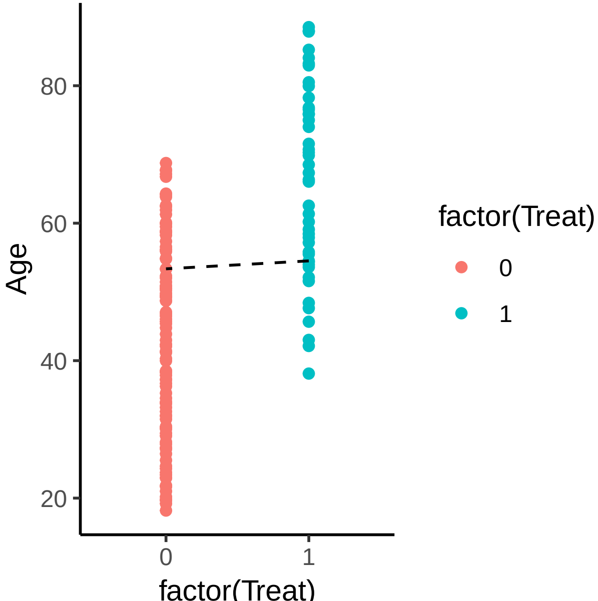

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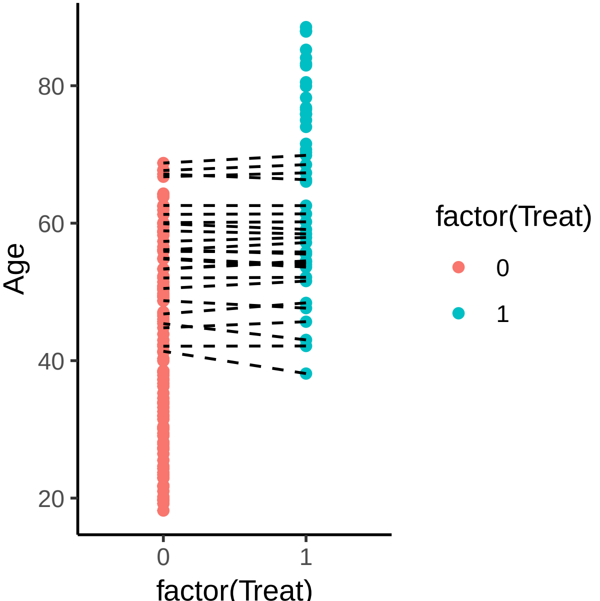

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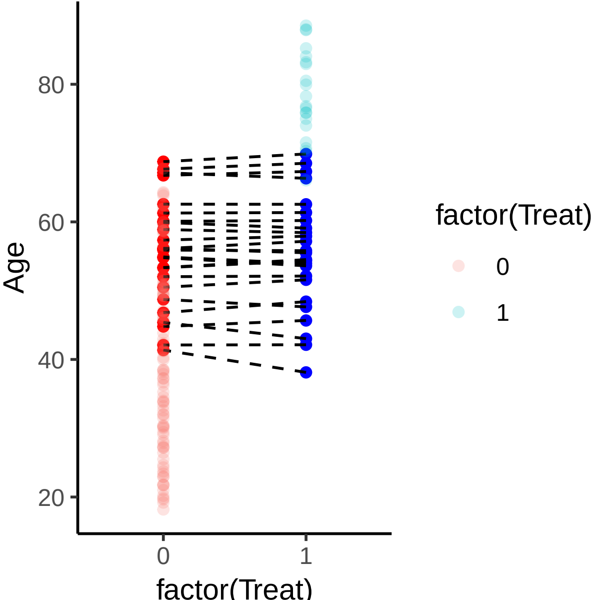

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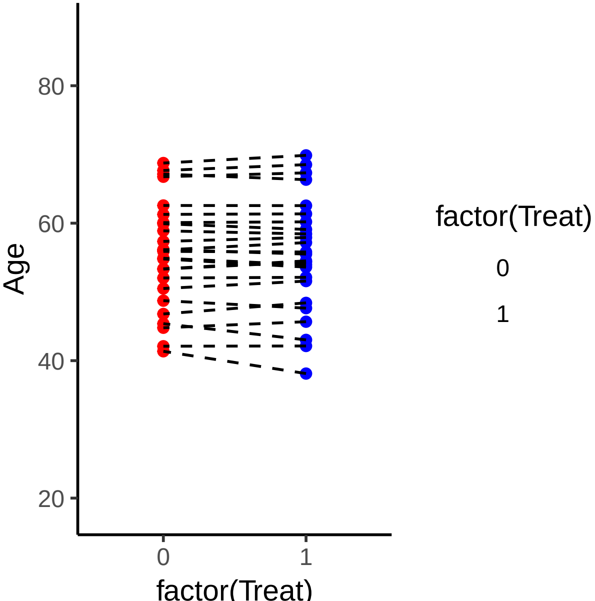

Nearest Neighbour Matching with Caliper

	Units	Means Treated	Means Control	Mean Diff
1	All	65.70	42.67	23.03
2	Matched	55.41	55.46	-0.06

- Note: p-values don't mean so much for balance tests

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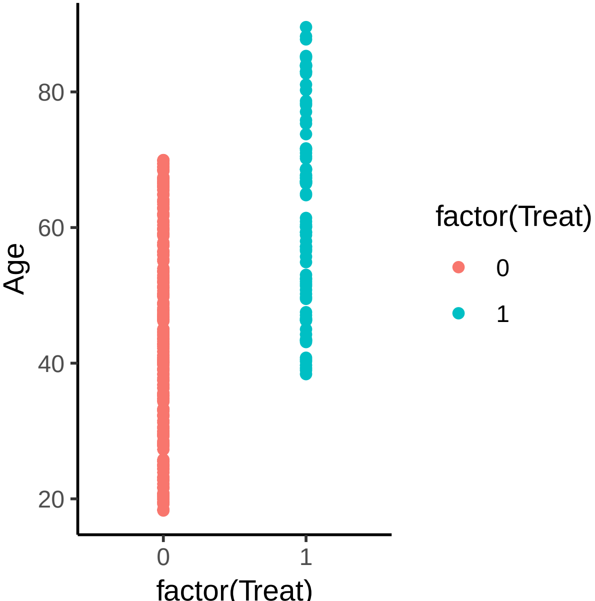
- We always want to improve balance as much as possible
- Better to compare (standardized) difference in means

Optimal Matching



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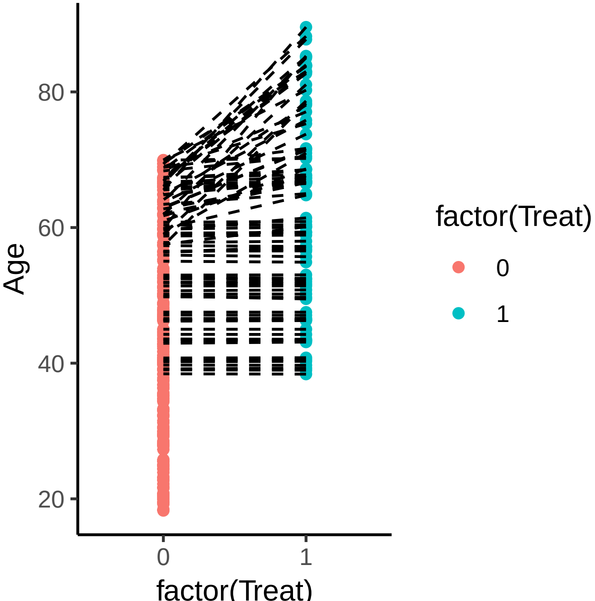

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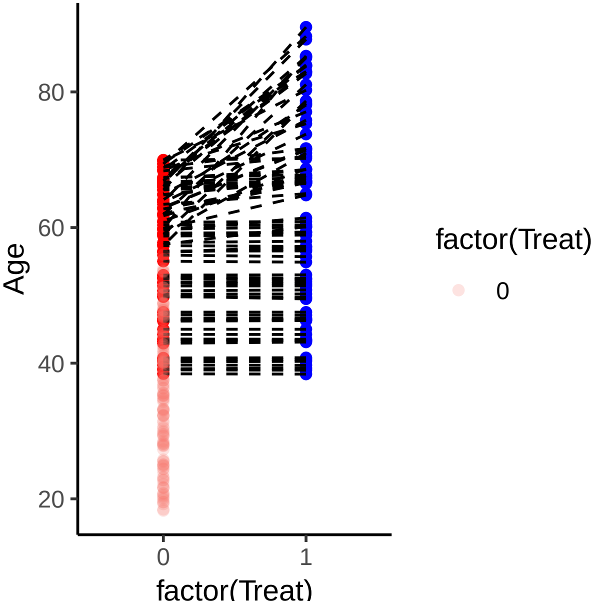

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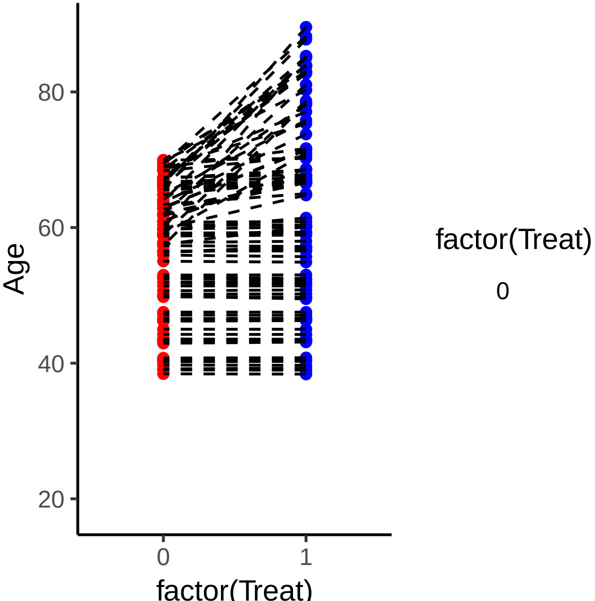

Optimal Matching

	Units	Means Treated	Means Control	Mean Diff
1	All	62.60	44.64	17.96
2	Matched	62.60	57.57	5.03

Propensity Score Matching

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- Then use the propensity score (probability 0-1) to match treated and control units which have the same ex ante probability of treatment

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- We have to get the functional form of the treatment explanation right (linear, quadratic etc.) so we remain vulnerable to model dependence!

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- Logit model predicting treatment:

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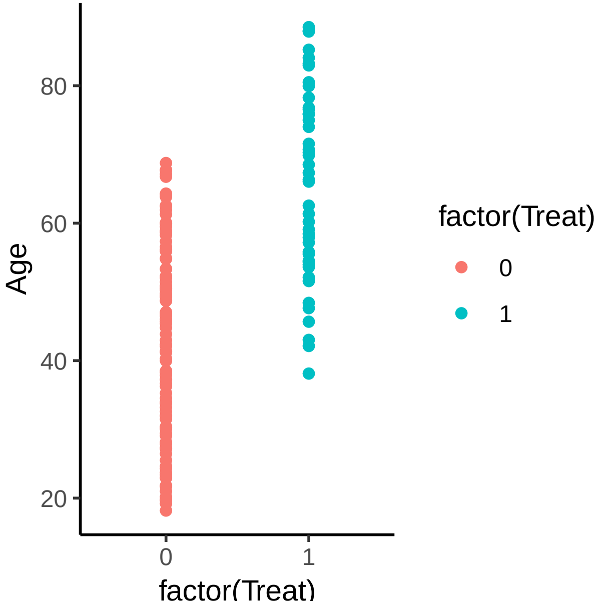
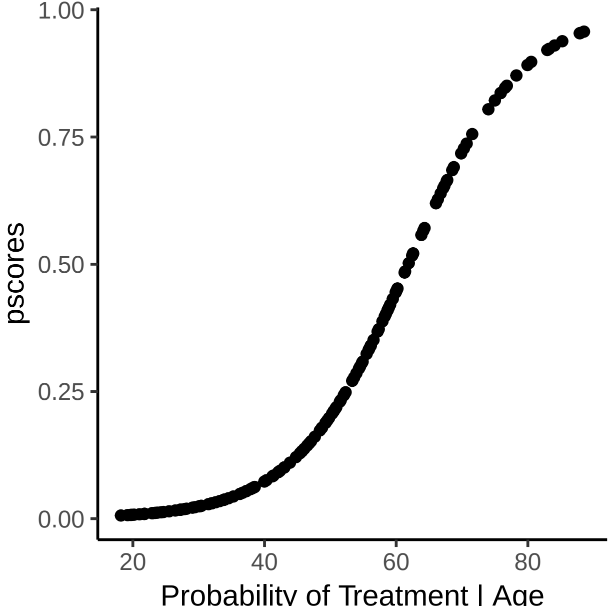
- I.e. match units with a similar *probability* of treatment
- ...Regardless of whether they actually get treated

Propensity Score Matching



Propensity Score Matching



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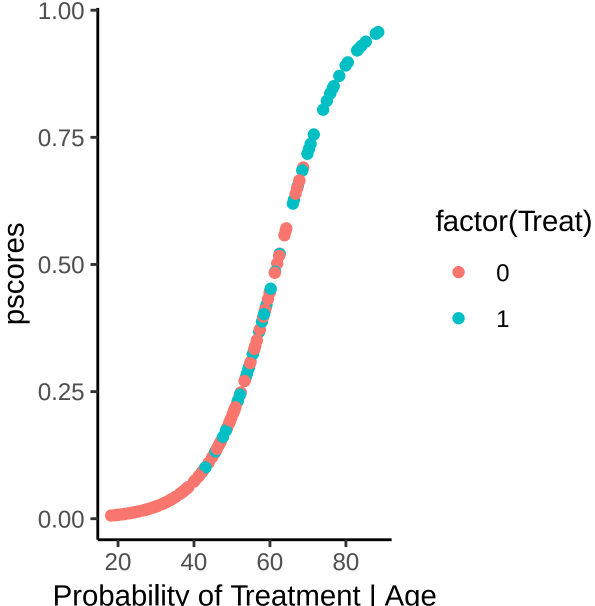

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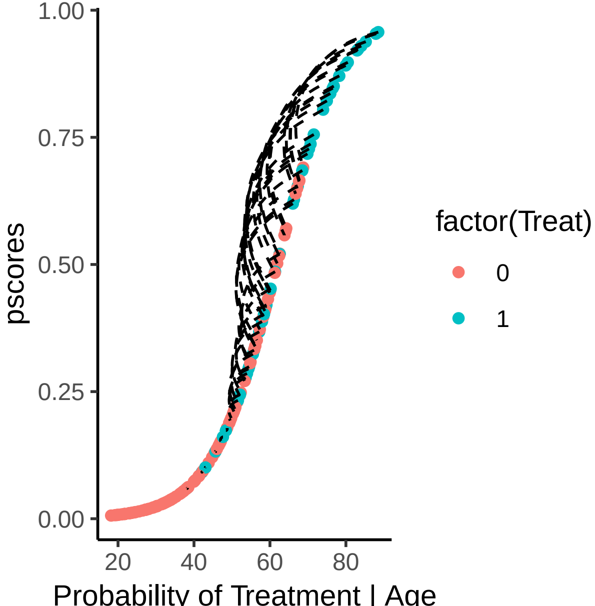

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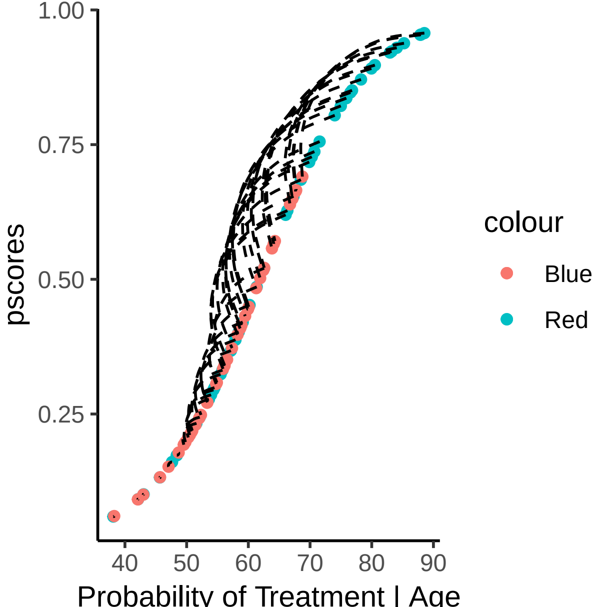
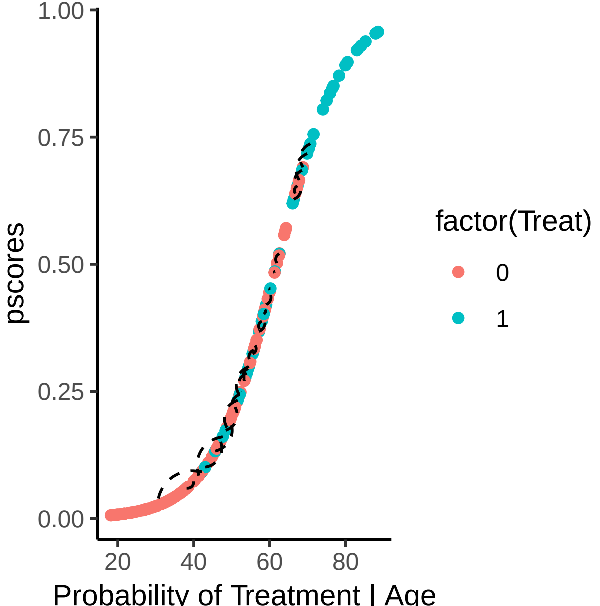


Propensity Score Matching

	Units	Means Treated	Means Control	Mean Diff
1	All	0.57	0.18	0.39
2	Matched	0.57	0.36	0.21

Propensity Score Matching with Caliper



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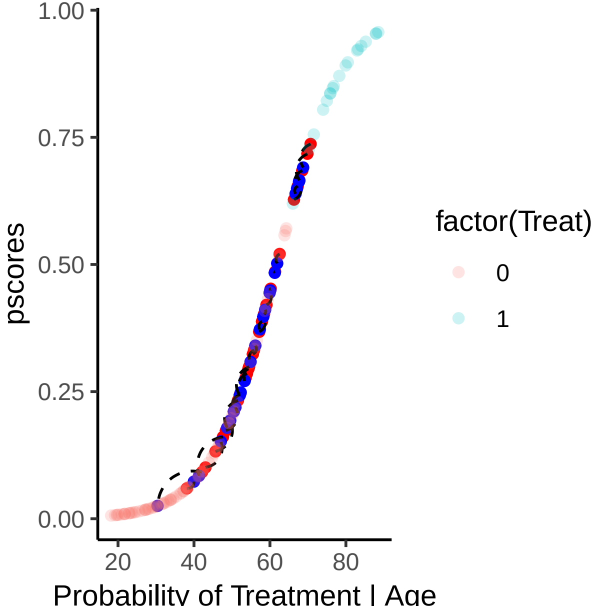

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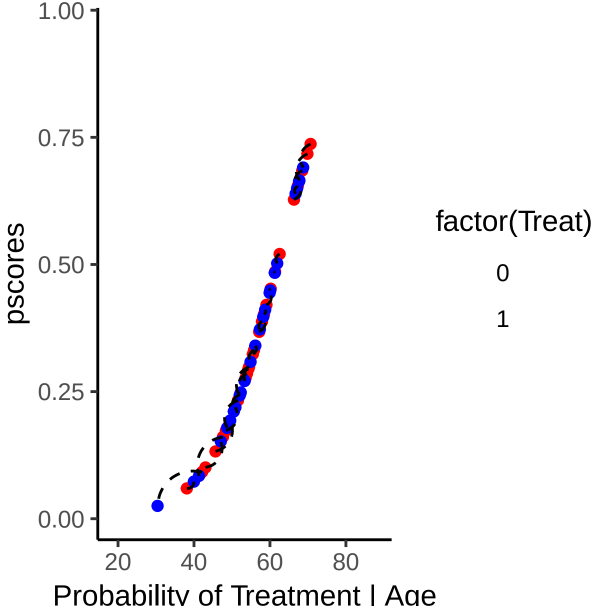

Propensity Score Matching with Caliper

	Units	Means Treated	Means Control	Mean Diff
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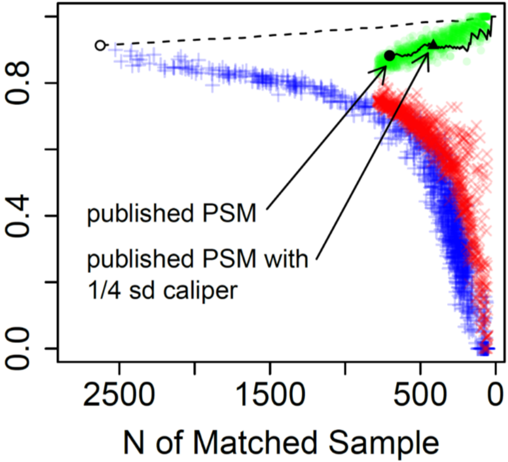
- Try alternative specifications

Matching



0.0
0.4
0.8
published PSM
published PSM with
1/4 sd caliper
2500
1500
500
0
N of Matched Sample

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- Matching + Regression = "Doubly Robust"
  - If **either** matching produces balance **OR** we have the correct functional form for regression, we can make causal inference

Section 3

Matching vs. Experiments

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- Lots of controls
- But unobserved confounders mean matching can't recover causal estimates

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- Matching still relies on **measuring all confounders**