

CFDR Summer Methods Seminar: Introduction to Propensity Score Analysis

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Outline

1. **Introduction**
2. Matching and Counterfactuals
3. The Propensity Score Matching Process
 - a. Estimate Propensity Scores
 - b. Match Cases
 - c. Estimate Treatment Effects
 - d. Demonstrate Robustness
4. Elaborations and Complications
5. End

A Practical Introduction

This workshop is a practical introduction to propensity score analysis (PSA), a relatively new approach to estimating treatment effects with nonexperimental data.

Whereas regression models attempt to balance data by including controls, PSA involves matching cases based on their predicted likelihood to experience values of the independent variable of interest.

The simplest forms of PSA use discrete treatments (e.g., imprisoned or not; became married or remained unmarried) and is best suited for studies of longitudinal data with few moderating or mediating variables.

The workshop will cover various types of matching, strengths and weaknesses of the approach, and tests of robustness, with examples in Stata.

Matching and Counterfactuals

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Matching and Counterfactuals

Counterfactual reasoning comes at the same kinds of questions we often address with regression. We are often interested estimating treatment effects:

- What was the effect of some life experience, choice or circumstances on some outcome?

Ideally, the causal effect on each case: treated and untreated.

- The perfect study would look at both of your outcomes given the treatment.
- This is Rubin's "fundamental problem of causal inference."

	Y^1	Y^0
Treatment ($W = 1$)	observed	<i>counterfactual</i>
Control ($W = 0$)	<i>counterfactual</i>	observed

- We have a missing data problem.
- So we are going to use our best available data to estimate the missing data.

Matching and Counterfactuals

Take a cue from randomized experiments.

- There, random treatment creates identical groups (well – unimportantly different).

What if we could figure out everything that ‘matters’ and just match people together?

Statistically construct sufficiently identical groups

- Exact matching has been around a long time – but handles very few covariates.
- Propensity score analysis instead extracts the relevant information from those covariates (likelihood to receive treatment) to make its matches.

Before I get into the process, a concluding introductory thought:

- Propensity score analysis is not magical (and see [Shadish 2013](#)).

Estimate Propensity Scores

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 - a. **Estimate Propensity Scores**
 - **Propensity Score**
 - **Model Covariates**
 - **Common Support**
 - b. Match Cases
 - c. Estimate Treatment Effects
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Propensity Scores

A propensity score is the probability of being assigned to a treatment.

- Randomized experiments build this into the design. A coin flip: $P(W_i = 1) = 0.5$
- With observational data, we are instead going to try to estimate it.
- An estimated likelihood, given a vector of observed covariates: $P(W_i = 1|X_i)$
- Matching cases on propensity score will approximately **balance** treated and untreated.

An unbiased estimate of the treatment effects **if** we can satisfy requirements, primarily:

1. Strongly Ignorable Treatment Assumption:
Treatment is independent of outcomes conditional on observed covariates.
2. Stable Unit Treatment Value Assumption:
One version of the treatment; one case's treatment does not affect another's outcome.

Most commonly, a binomial regression model.

- Regress the treatment on the covariates: propensity score is the predicted probability.
- Alternatives are on the way, particularly generalized boosted modeling (*boost* in Stata).

Model Covariates

Which covariates to include? Remember the goal: predicting selection into treatment. As with regression, a lot comes down to this, and quality matters more than quantity.

There is a debate about quantity:

- "Including a variable that is related to treatment, but not outcome, does not improve balance and reduces the number of matched pairs available for analysis" ([Austin et al. 2007](#)). "Familiar econometric rules apply" about the tradeoffs of adding nonsignificant covariates ([Ho et al. 2007](#)).
 - ... as in regression, include covariates jointly related to treatment and outcome.
- "Unless a variable can be excluded because there is a consensus that it is unrelated to the outcome or is not a proper covariate, it is advisable to include it in the propensity score model even if it is not statistically significant." ([Rubin 1997](#))
 - ... when in doubt, toss it in.

Pay attention to time order! Covariates → Treatment → Outcome.

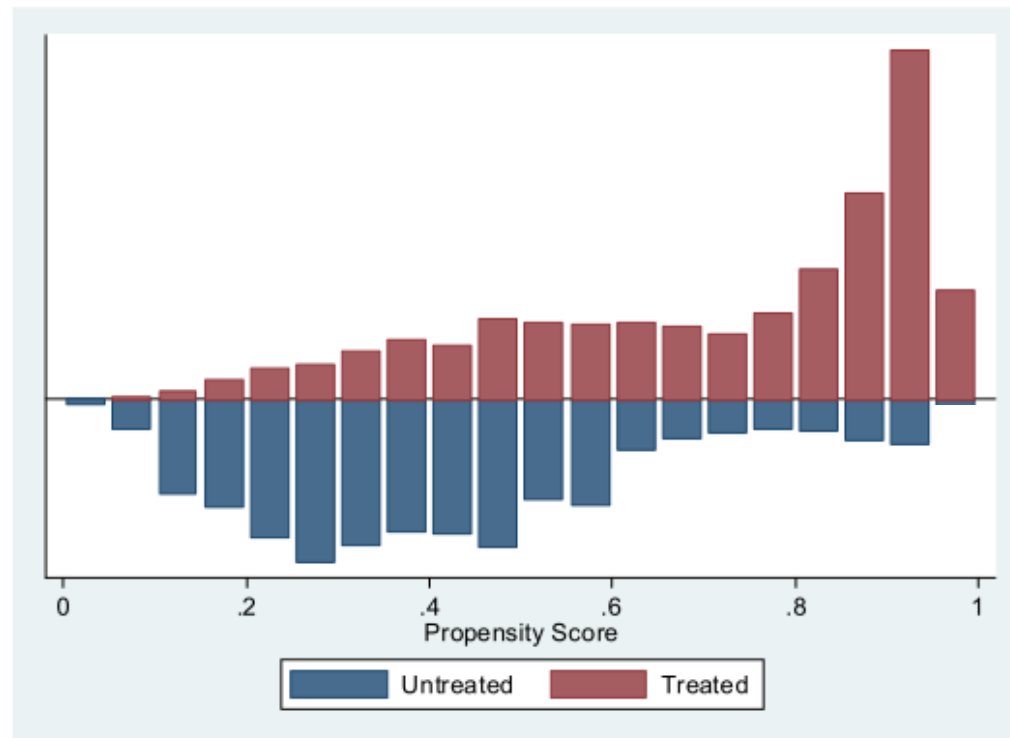
Common Support

Limit inferences to a range with information on both treated and untreated cases.

- Throw out all treated with higher propensity scores than the highest untreated.
- Throw out all untreated with lower propensity scores than the lowest treated.

And now is a good time to look at the distribution of your propensity score.

This is *psgraph* in Stata:



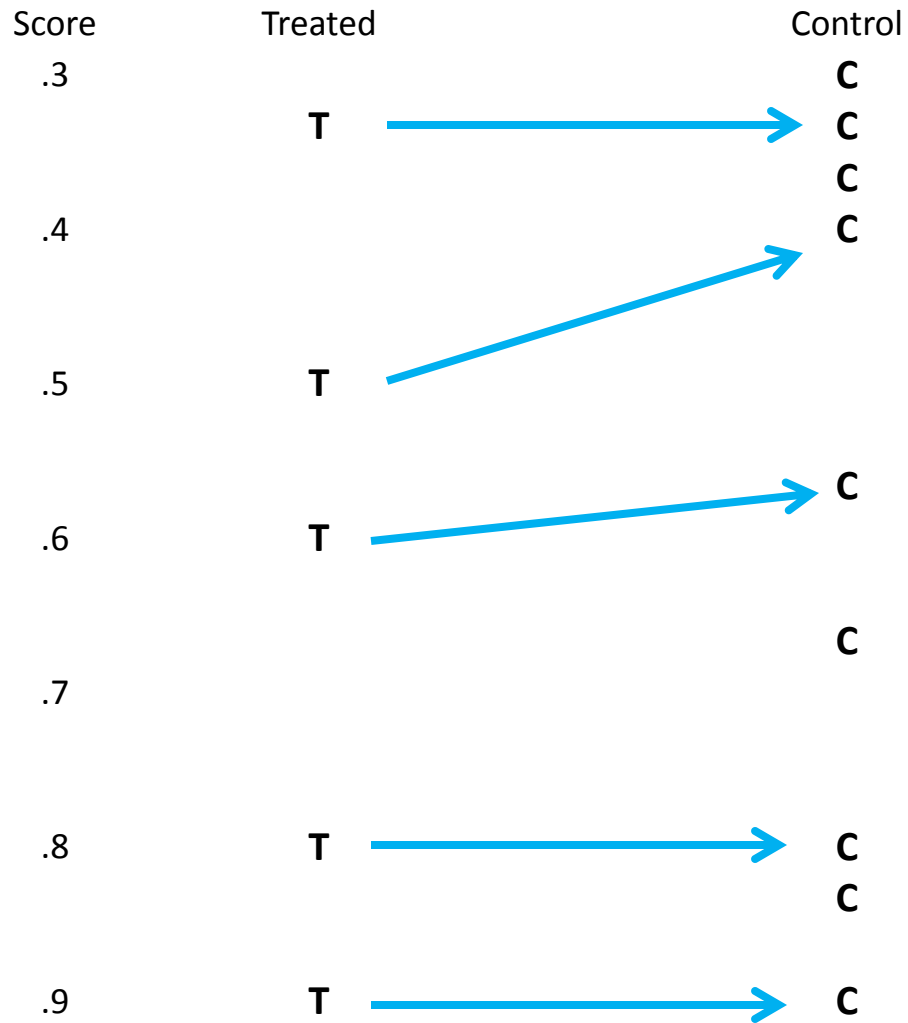
Match Cases

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 - b. Match Cases**
 - **Matching Algorithms**
 - **Check for Balance**
 - c. Estimate Treatment Effects
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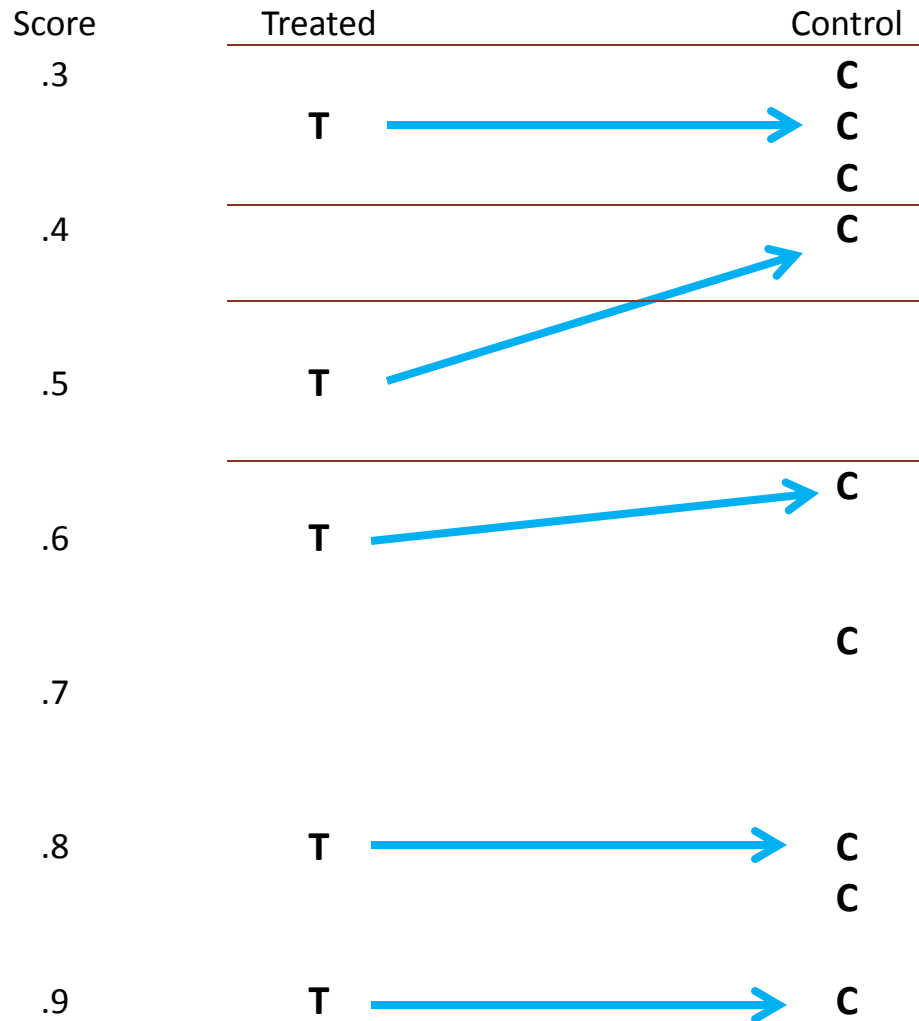
Matching Algorithms

Score	Treated	Control
.3		C
	T	C
		C
.4		C
.5	T	
		C
.6	T	
		C
.7		
.8	T	C
		C
.9	T	C

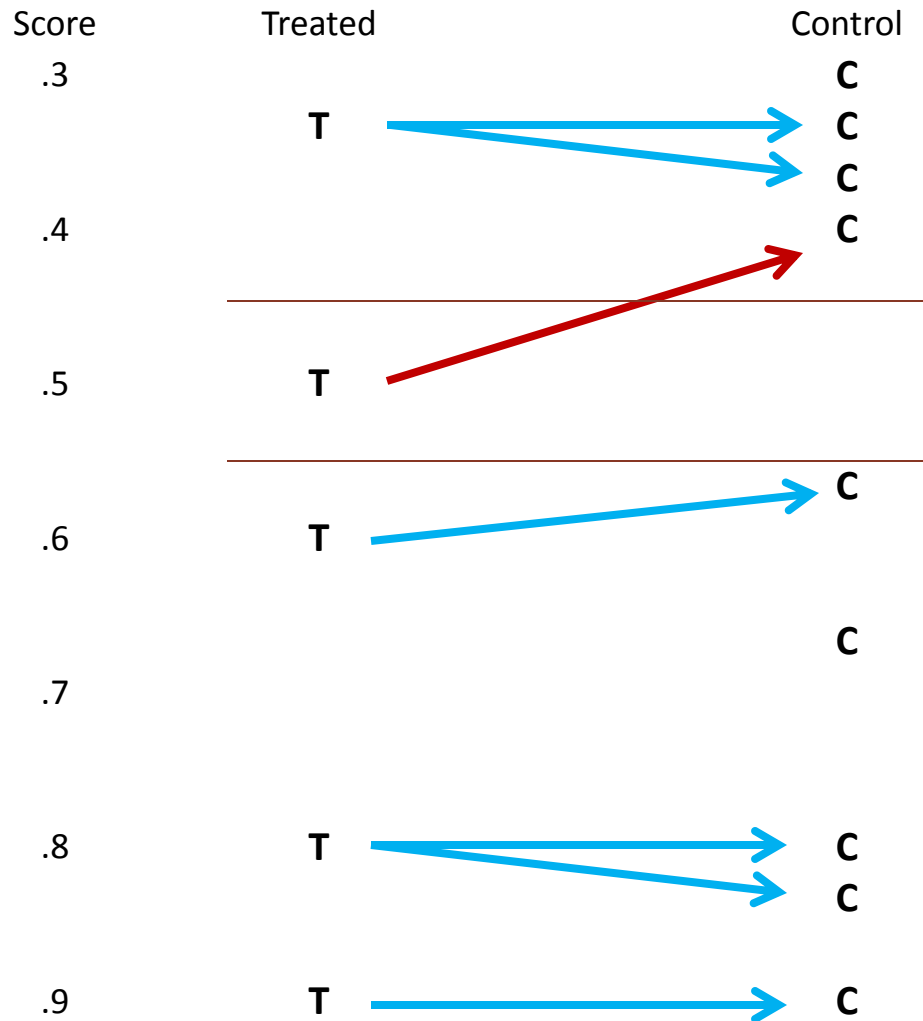
Nearest-Neighbor



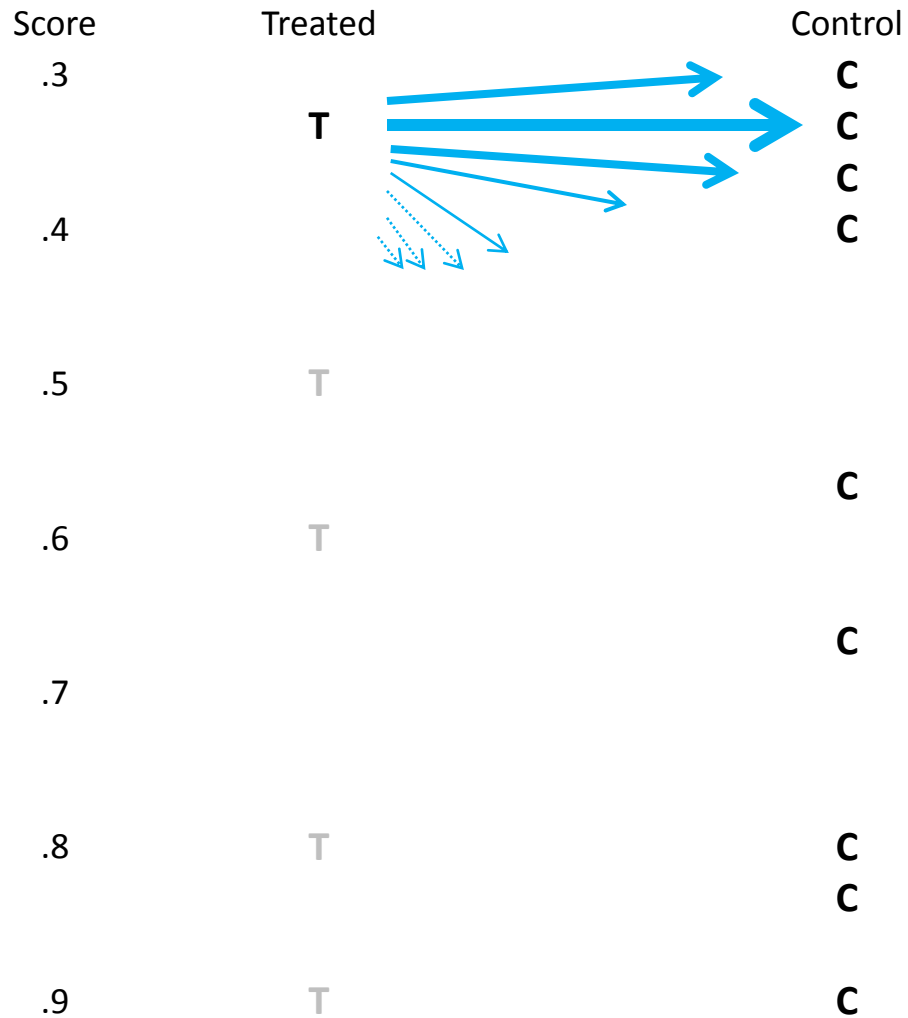
NN within Caliper



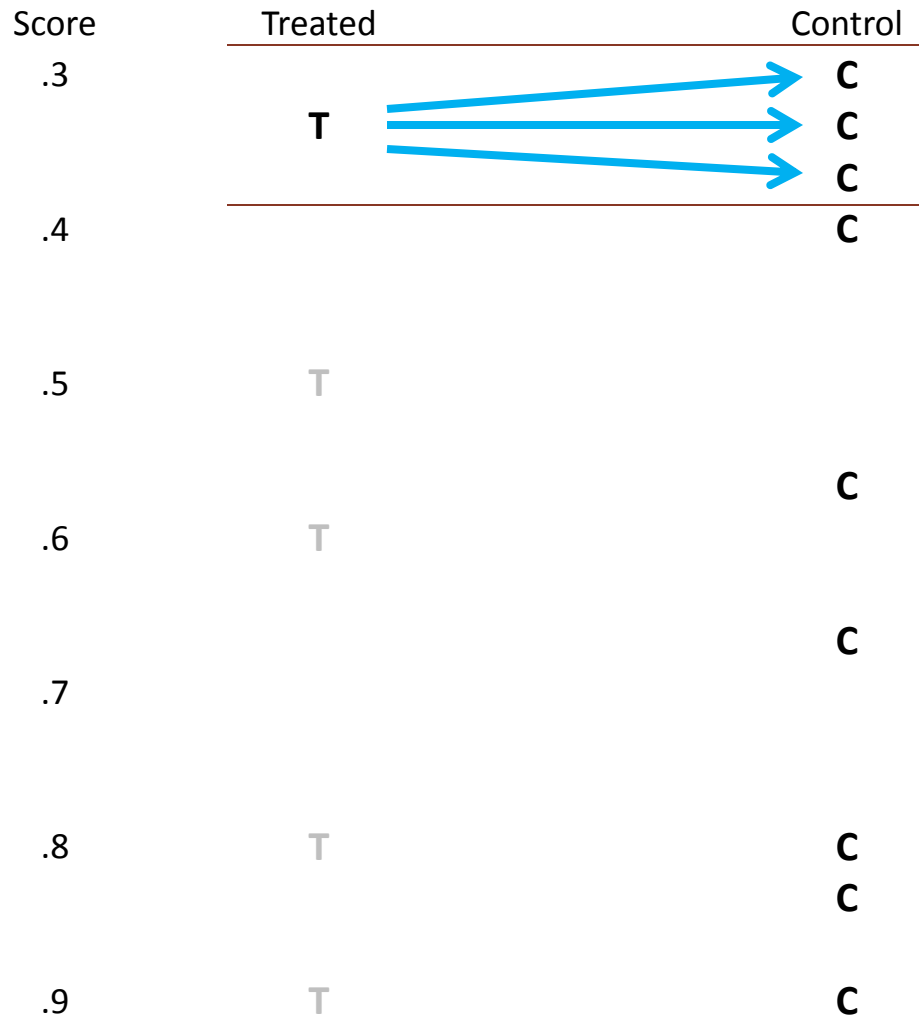
2-to-1 within Caliper



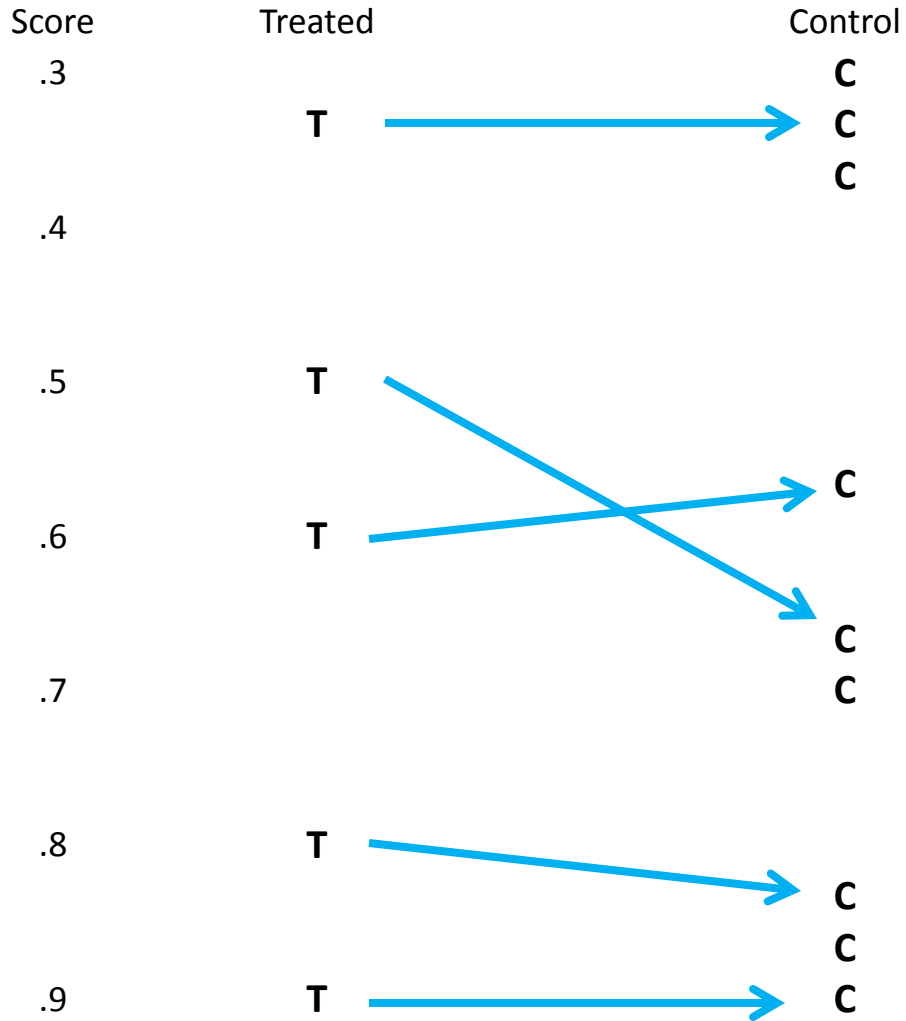
Kernel (Gaussian)



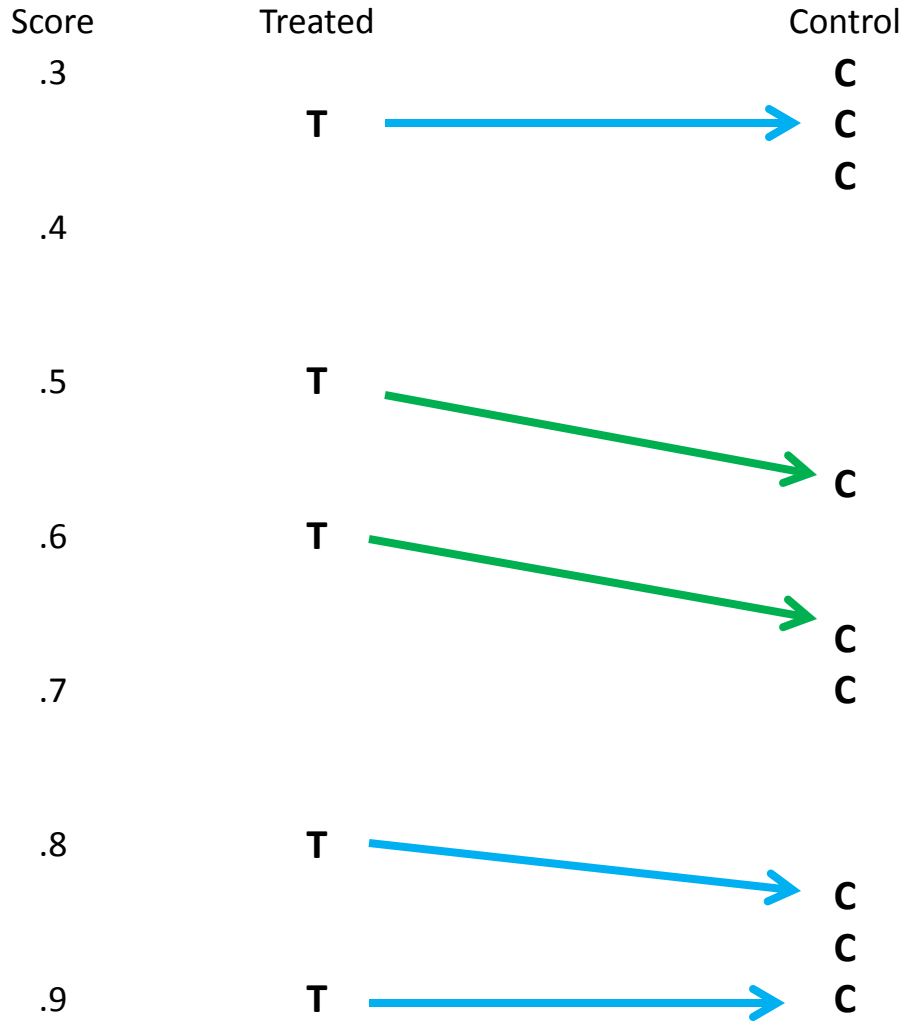
Kernel (Uniform)



Greedy vs. Optimal



Greedy vs. Optimal



Matching Algorithms

A range of matching protocols... so how do you decide?

Tradeoffs between variance and bias, completeness and accuracy.

With many untreated, many-to-one improves efficiency.

Kernel is preferred when treated and control groups have “quite different” distributions (Apel and Sweeten 2010).

Nearest-neighbor, without replacement, with caliper is a good default.

Recommended width: 0.2 of the SD of the logit of the propensity score ([Austin 2011](#))

For us, availability probably matters. See references for software links.

In Stata, *pscore* supports nearest-neighbor, kernel, and radius matching.

And *psmatch2* adds Mahalanobis to that list.

Optimal matching is available in R, but not Stata (yet).

And as always, consult your field’s literature for standard expectations.

Check for Balance

A critical evaluation of the Strongly Ignorable Treatment Assumption:

Conditional on covariates X , the assignment to treatment W will be independent of the potential outcomes Y if observable covariates are held constant.

This also known as unconfoundedness, selection on observables, conditional independence, exogeneity... the same concern underlies controls in OLS.

Did the propensity score successfully balance the data on **observed** covariates? Compare differences between treated and untreated for each covariate before and after matching.

- Can use standardized bias ([Rosenbaum and Rubin 1985b](#)): under 10 as a rule of thumb
 - Available for Stata in *pstest*.
- Can use a general guideline: less than 25% of the SD of X ([Ho et al. 2007](#))
- No hard rules. You'll see t-tests being used, though they're debatable here.
- In Stata, *pscore* can test for balance by strata: don't make it angry.

Estimate Treatment Effects

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 - **Average Treatment Effect on the Treated (ATT)**
 - **Alternatives to Matching**
 - d. Demonstrate Robustness
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Treatment Effect Estimate

Really estimating **average treatment effect on the treated** (ATT).

- Methodologically, we have been matching controls to our treated cases.
- Conceptually, the treated could have gone untreated (more than the other way around).

The most commonly used packages in Stata are *pscore* and *psmatch2*.

Becker, Sascha O. and Andrea Ichino. 2002. “Estimation of Average Treatment Effects Based on Propensity Scores.” *The Stata Journal* 2(4): 358–377.

Alternatives to Matching

Stratification on the propensity score.

- Bin the sample into quintiles (or finer) by propensity score.
- Five subclasses are expected to remove 90% of bias from modeled covariates.
- Favored not for the overall estimate as much as the substantive value.

Stratification

Score	Treated	Control	Strata
.3	T	C	1
.4		C	
		C	2
.5	T	C	
	T	C	3
.6	T	C	
	T	C	4
.7		C	
	T	C	5
.8	T	C	
	T	C	
.9	T	C	

Alternatives to Matching

Stratification on the propensity score.

- Bin the sample into quintiles (or finer) by propensity score.
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- Favored not for the overall estimate as much as the substantive value.

Covariate adjustment on the propensity score.

- Regress the outcome on the treatment, controlling for the propensity score.
- Restrict to on-support cases; can also trim the sample; can add controls.
- Will usually give you results extremely similar to ordinary regression approach.

Demonstrate Robustness

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 - **Rosenbaum Bounds**
 - **Modifications and Variations**
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Rosenbaum Bounds

Rosenbaum (2002): A sensitivity analysis for observational studies should ask “what the unmeasured covariate would have to be like to alter the conclusions of the study.”

- Really showing us “what happens when we violate ignorable treatment assumption”?
- The standard formal sensitivity analysis for propensity score matching in sociology.

Gamma (Γ) is a hypothetical odds ratio of an increase in odds of the outcome for treated cases due to unobserved covariate(s).

- 1.0 (no bias) up by intervals to 2.0.
- “How bad does it have to be?”
- “When do I lose confidence in my effect?”
- Better to show confidence intervals.

Available for Stata as *rbounds*.

Table 5

Rosenbaum Bounds of Positive Selection for Tr

Intensive Work vs. No Work (p-values)

Γ	Sex	Pregnancy	Union Formation
1.0	.000	.042	.000
1.2	.001	.202	.004
1.4	.016	.466	.022
1.6	.107	.713	.071
1.8	.325	.872	.161
2.0	.599	.951	.285

Modifications and Variations

Some (like in a regression approach) depends on your research question.
Different formulations of outcomes? Definitions of treatment? Subgroups?

Especially important covariate(s)?

- Might separate analyses into subgroups
- Might include covariate as an exact match

Shenyang Guo recommends a “3 x 2 x 2” design, for twelve total treatment estimates

- 3 alternative propensity score models
- 2 different matching algorithms
- 2 variations in matching specifications
- “Which choice should I make?” “Both!”

Elaborations and Complications

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What About...

Sample size?

- At least 1,000–1,500 is recommended ([Shadish 2013](#)).

Missing data?

- Some disagreement. Listwise is most common. [Multiple imputation might be okay](#).

Clustered data?

- Still an open issue. Multilevel matching is on the way. (Within-group or within-person.)

Weighting?

- You can use population weights on the final estimates if it makes sense.
- Sampling weights are generally out.

Non-binary treatment variable?

- Multinomial, ordinal, continuous... on the way, and examples in the literature.

End

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Points for Review

1. Why is propensity score matching appropriate for this research question and data?
2. Was the treatment adequately conceptualized and measured?
3. Did the propensity score model include appropriate covariates?
4. Was the support condition addressed and enforced?
5. Were all covariates shown to be successfully balanced?
6. Did the authors justify their choices of matching procedures and their parameters?
7. Did the authors demonstrate the robustness of their results?

For longer lists, see Apel and Sweeten (2010:559–560), Guo and Fraser (2010:321–326).

Key Features

The reasons *I* find propensity score matching especially advantageous or compelling:

- Counterfactual framework.
- Common support and “apples to apples” comparisons.
- Nonparametric estimates of treatment effects.
- Rosenbaum bounds and sensitivity testing.
- Generally promotes good habits.

Morgan, Winship, and Harding (2007): "Matching represents an intuitive method for addressing causal questions, primarily because it pushes the analyst to confront the process of causal exposure as well as the limitations of available data."

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My Stata example uses data from Add Health, a program project directed by Kathleen Mullan Harris and designed by J. Richard Udry, Peter S. Bearman, and Kathleen Mullan Harris at the University of North Carolina at Chapel Hill, and funded by grant P01-HD31921 from the Eunice Kennedy Shriver National Institute of Child Health and Human Development, with cooperative funding from 23 other federal agencies and foundations. Special acknowledgment is due Ronald R. Rindfuss and Barbara Entwisle for assistance in the original design. Information on how to obtain the Add Health data files is available on the Add Health website. No direct support was received from grant P01-HD31921 for this analysis.

Examples in Handout

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King, Ryan D., Michael Massoglia, and Ross Macmillan. 2007. “The Context of Marriage and Crime: Gender, the Propensity to Marry, and Offending in Early Adulthood.” *Criminology* 45:33–65. **OLS comparison, gender subgroups, stratification within gender.**

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Full-Scale Coverage

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References

Elizabeth Stuart maintains a page with information on propensity score procedures available to researchers. This will be a good place to look if you go beyond Stata:

<http://www.biostat.jhsph.edu/~estuart/propensityscoresoftware.html>

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