2. Matching estimators

LPO 8852: Regression II

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Selection bias

Lecture 1 showed why the simple difference in means between the treated and untreated cases does not identify the ATT:

$$E(Y|D=1) - E(Y|D=0) =$$
$$E[Y(1)|D=1] - E[Y(0)|D=0] = ATT + \underbrace{E[Y(0)|D=1] - E[Y(0)|D=0]}_{\text{selection bias}}$$

Selection bias reflects baseline differences in $Y(0)$ between the $D=1$ and $D=0$ groups.

- Randomization of D would help!
- Regression can help under very strong conditions.

Matching

Matching estimators construct comparison groups that are *similar* according to a set of *matching variables*:

- Selecting specific matches
- Constructing a matched weighted sample
- Subclassification

The assumption: once we have conditioned on these matching variables—by selecting matches, constructing weights, or stratifying—treatment assignment and potential outcomes are independent. (The conditional independence assumption).

Weighted average

What is a weighted average? Given a weight for each observation i, the weighted average for Y is:

$$\frac{\sum_{i=1}^{n} w_i Y_i}{\sum_{i=1}^{n} w_i}$$

Weights are used for lots of reasons (Solon, Haider, & Wooldridge, 2015). In matching we may choose weights based on the values of confounders to eliminate differences in X between treated and untreated groups.

Example 1: re-weighting

Imagine a job training program that serves 100 people where the outcome of interest (Y) is employment (0/1).

	Treated ($D_i = 1$)	Untreated ($D_i = 0$)	Diff (Mean Y)
Men	60 $Y = 1$	350 $Y = 1$	
	20 $Y = 0$	150 $Y = 0$	0.05
Women	12 $Y = 1$	275 $Y = 1$	
	8 $Y = 0$	225 $Y = 0$	0.05
Total	100	1000	
Mean(Y)	**0.720**	**0.625**	**0.095**
Mean(Male)	0.800	0.500	

Source: Huntington-Klein ch. 14

Example 1: re-weighting

The simple difference in means is: $E(Y|D = 1) - E(Y|D = 0) = \mathbf{0.095}$. However, you'll notice that for both men and women the treatment effect is only 0.05.

Assuming that *conditional on gender, D* is independent of potential outcomes, then each gender group is like a "randomized trial." The true treatment effect is **0.05** (for both men and women).

The simple difference in means *overstates* the treatment effect because the treatment group is disproportionately male, and males have a higher mean potential outcome in the untreated state (Y_0). There is selection bias (of +0.045).

Example 1: re-weighting

For the ATT: can we re-weight the untreated group so that it "looks like" the treated group?

	Treated	Untreated	Untreated weight
Men	80	500	0.16 (80/500)
Women	20	500	0.04 (20/500)

We want the 500 untreated men to represent the 80 in the treatment group, so each gets a weight of 0.16. We want the 500 untreated women to represent 20 in the treatment group, so each gets a weight of 0.04. Note the weights sum to $(0.16 * 500) + (0.04 * 500) = 100$

Example 1: re-weighting

Using the weights, what the is the proportion male in the untreated group? The proportion employed (Y)?

$$E_w(male|D = 0) = ((500 * 1 * 0.16) + (500 * 0 * 0.04))/100 = 0.80$$

$$E_w(Y|D = 0) = ((350 * 1 * 0.16) + (275 * 1 * 0.04))/100 = 0.67$$

Use this re-weighted mean to get the ATT:

$$ATT = 0.72 - 0.67 = 0.05$$

Note with the weights, the two samples are **balanced** on gender.

Example 1: re-weighting

To re-iterate:

- Gender was the only confounding factor here. Conditional on gender, treatment assignment was "as good as random."
- We adjusted for differences in gender between the treated and untreated groups using weights.
- The weights were chosen based on the distribution of gender in the treatment group (for ATT).
- We could have chosen weights based on the distribution of gender *overall* for ATE.

See the do-file *Lecture 2 weighting example* for more on this example in Stata.

Example 1b: subclassification

In this example we could alternatively use **subclassification**: grouping treated and untreated observations into strata—here, men and women—calculating differences within strata, and then weighting those differences to get a treatment effect estimate. The weights here are chosen based on the full sample (for ATE):

$$ATE = \underbrace{(0.75 - 0.70) * (580/1100)}_{\text{men}} + \underbrace{(0.60 - 0.55) * (520/1000)}_{\text{women}}$$

$$ATE = 0.05$$

Example 2: private vs. public colleges

		Private			Public			
		Ivy	Leafy	Smart	All State	Tall State	Altered State	Earnings
A	1		Reject	**Admit**		Admit		110000
	2		Reject	**Admit**		Admit		100000
	3		Reject	Admit		**Admit**		110000
B	4	**Admit**			Admit		Admit	60000
	5	Admit			Admit		**Admit**	30000
C	6		**Admit**					115000
	7		**Admit**					75000
D	8	Reject			**Admit**	Admit		90000
	9	Reject			Admit	**Admit**		60000

Source: Angrist & Pischke *MM* (2015). Shaded cell represents the student's chosen college, from those they were admitted to. Based on Dale & Krueger (2002).

Example 2: private vs. public colleges

In the above table:

$$E[Y(1)|D=1] - E[Y(0)|D=0] = 92,000 - 72,500 = 19,500$$

$$= ATT + \underbrace{E[Y(0)|D=1] - E[Y(0)|D=0]}_{\text{selection bias}}$$

It is likely the treated group has a higher $Y(0)$ than the untreated group. This is suggested above by the higher mean earnings for students who applied and were admitted to private colleges (esp. groups A and C).

Example 2: private vs. public colleges

What if we could create equivalent groups by conditioning on some X? For example, what if:

$$\underbrace{E[Y(0)|D=1,X]}_{\text{unobserved}} = \underbrace{E[Y(0)|D=0,X]}_{\text{observed!}}$$

In other words, there is no difference in potential outcomes $Y(0)$ between $D=0$ and $D=1$, once we condition on X. Then we could contrast the mean Y for each set of X and then average them.

In the private vs. public college example, assume there is no difference in $Y(0)$ conditional on application/admitted group A-D:

Example 2: private vs. public colleges

		Ivy	Leafy	Smart	All State	Tall State	Altered State	Earnings
A	1		R	A		A		110000
	2		R	A		A		100000
	3		R	A		A		110000
B	4	A			A		A	60000
	5	A			A		A	30000
C	6		A					115000
	7		A					75000
D	8	R			A	A		90000
	9	R			A	A		60000

Avg(Y|D=1, Group=A)=105,000
Avg(Y|D=0, Group=A)=110,000. Difference = 105,000 - 110,000 = -5,000

Avg(Y|D=1, Group=B)=60,000
Avg(Y|D=0, Group=B)=30,000. Difference = 60,000 - 30,000 = 30,000

Example 2: private vs. public colleges

The simple average of the within-group differences (groups A and B) is:

$$(-5,000 + 30,000)/2 = \$12,500$$

A *weighted* average gives more weight to the group with more individuals:

$$(-5,000) * (3/5) + (30,000) * (2/5) = \$9,000$$

The weighted average uses the data more efficiently, and also generalizes appropriately to the groups included in the calculation. Note groups C and D are either all treated (private college) or all untreated (public college). There is no **common support** here. This term will come up again.

Example 2: private vs. public colleges

Note in this case that neither the weighted nor unweighted average of groups A and B estimates the ATE or ATT. This is due to the lack of common support.

- Without a counterfactual for the treated in group C, we can't estimate ATT (or ATE)
- Without a counterfactual for the untreated in group D, we can't estimate ATU (or ATE)

An illustration of the importance of being attentive to the population to which you are able to generalize with the data you have.

Example 2: private vs. public colleges

Angrist & Pischke *MM* (2015) explain how regression estimates are weighted averages of multiple matched comparisons. E.g., consider the regression:

$$Y_i = \alpha + \beta P_i + \gamma A_i + e_i$$

where $P_i = 1$ if the student attended a private college and $A_i = 1$ if the student was in group A (versus B). Students in groups C and D are excluded.

Using the Example 2 data, $\hat{\beta} = 10,000$. This is comparable to the averages on the previous slide, but not identical to either. Regression effectively applies different weights, but the idea is the same. (See *MM* for details).

We will return later to the differences between matching and regression.

Example 3: Catholic schools

Murnane & Willett (ch. 12) stratify the NELS sample by family income to estimate the effect of Catholic high school attendance on 12th grade math achievement:

Table 12.1 Descriptive statistics on annual family income, by stratum, overall and by type of high school attended, and average twelfth-grade mathematics achievement by income stratum and by high-school type (n = 5,671)

Stratum		Average Base-Year Annual Family Income *(1988 dollars, 15-point ordinal scale)*			Cell Frequencies		Average Mathematics Achievement (12th grade)		
Label	Income Range	Sample Variance	Sample Mean		Public	Catholic (% of stratum total)	Public	Catholic	Diff.
			Public	Catholic					
Hi_Inc	$35,000 to $74,999	0.24	11.38	11.42	1,969	344 (*14.87%*)	53.60	55.72	2.12***,†
Med_Inc	$20,000 to $34,999	0.22	9.65	9.73	1,745	177 (*9.21%*)	50.34	53.86	3.52***,†
Lo_Inc	≤$19,999	3.06	6.33	6.77	1,365	71 (*4.94%*)	46.77	50.54	3.76***,†
							Weighted Average ATE		***3.01***
							Weighted Average ATT		***2.74***

^{-}p <0.10; $^{*}p$ <0.05; $^{**}p$ <0.01; $^{***}p$ <0.001
†One-sided test.

Example 3: Catholic schools

Take the difference within each strata and then take the weighted average of these differences across strata.

The ATE uses *total* cell sizes as weights; ATT uses counts of *treated* cases in each cell as weights. These are smaller than the unconditional mean differences in math scores ($\hat{\beta}_{CATH} = 3.895$), suggesting upward bias.

Note income is a continuous variable. M&W created three strata with the aim of (1) creating balance in family income within each strata; (2) maintaining common support.

Again, we are appealing to the conditional independence assumption. Conditional on income (strata), enrollment in Catholic school is "as good as random" (!).

Return of the "unobservables"

Example 3: Catholic schools

Can also stratify on multiple covariates, as M&W do here with income and a measure of prior achievement (12 total cells):

Table 12.2 Sample frequencies and average twelfth-grade mathematics achievement, by high-school type, within 12 strata defined by the crossing of stratified versions of base-year annual family income and mathematics achievement (n = 5,671)

Stratum		Cell Frequencies		Average Mathematics Achievement (12th Grade)		
Base-Year Family Income	Base-Year Mathematics Achievement	Public	Catholic	Public	Catholic	Diff.
Hi_Inc	*Hi_Ach*	1,159	227	58.93	59.66	0.72
	MHi_Ach	432	73	49.18	50.71	1.53*,†
	MLo_Ach	321	38	42.75	44.23	1.48
	Lo_Ach	57	6	39.79	40.40	0.62
Med_Inc	*Hi_Ach*	790	93	57.42	59.42	2.00**,†
	MHi_Ach	469	49	47.95	50.14	2.19**,†
	MLo_Ach	390	33	41.92	44.56	2.64*,†
	Lo_Ach	96	2	37.94	39.77	1.83
Lo_Inc	*Hi_Ach*	405	36	56.12	56.59	0.47
	MHi_Ach	385	13	47.12	48.65	1.53
	MLo_Ach	433	21	40.99	41.70	0.71
	Lo_Ach	142	1	36.81	42.57	5.76
				Weighted Average ATE		***1.50***
				Weighted Average ATT		***1.31***

$^{\cdot}p$ <0.10; $^{*}p$ <0.05; $^{**}p$ <0.01; $^{***}p$ <0.001
†One-sided test.

Curse of dimensionality

Finer strata may provide a stronger argument for the conditional independence assumption that treatment group membership is unrelated to potential outcomes (within strata), but they make it more and more difficult to achieve common support—the **curse of dimensionality**.

Matching on a single variable

Examples 1-3 all created balance on a single variable (gender, sets of colleges, income). There are *lots* of ways to do this. When matching, there are a lot of choices to make:

1. What will the matching criteria be?
2. Will you *select* matches, or use weights to create a matched sample?
3. If selecting matches, how many?
4. If constructing a matched weighted sample, how will weights decay with distance?
5. What is the *worst* acceptable match?

Treatment effect estimation is usually the easy part. The hard part is finding the right matched comparison groups.

What will the matching criteria be?

The goal is to construct comparison groups that are "similar" on matching variables. What does "similar" mean?

- Exact matching
- Coarsened exact matching
- Distance matching (e.g. nearest neighbor)
- Propensity score matching (observations with similar *propensity* to be treated)

Select matches or use weights?

Selecting matches:

- Literally picking observations to be "in" or "out" based on some criteria.
- Usually if an observation is "in" it gets equal weight.
- Intuitively appealing and avoids situation where some observations get very large weights.

Constructing a matched weighted sample:

- Determine how close untreated observations are to treated observations.
- Weight based on similarity, or to make matched sample "look like" treated group.
- Has nice statistical properties and is less sensitive/noisy.

If selecting matches, how many?

- Nearest neighbor? k nearest neighbors? **Radius** matching (all neighbors within a given radius)?
- With replacement or without?

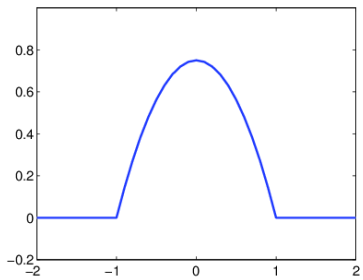
There is typically a **bias-variance tradeoff** in these decisions. More matches = larger sample size = less sampling variation. But more matches typically means "worse" matches, so more opportunity for bias.

With replacement = better matches. But matching with replacement may mean less variability. (The same matched observation may be used multiple times).

How will weights decay with distance?

Typically a distance measure or propensity score is used to construct weights. We often want "less similar" observations to receive less weight.

A **kernel function** can do this. For example, the Epanechnikov kernel is $K(x) = \frac{3}{4}(1 - x^2)$ for $-1 \leq x \leq 1$ and 0 otherwise:



where x is a standardized distance measure. Note the weight is largest when the distance is 0 and then decays as you move away from 0.

How will weights decay with distance?

Propensity scores are often used to construct **inverse probability weights** where (for ATE) each *treated* observation gets a weight of 1 divided by their probability of treatment (p_i) and each *untreated* observation gets a weight of 1 divided by their probability of non-treatment ($1 - p_i$).

As we will see, IPW makes the treated and untreated groups more similar:

- Treated observations with the biggest weights ($1/p_i$) are those that are more like the *untreated* group.
- Untreated observations with the biggest weights ($1/(1 - p_i)$) are those that are more like the *treated* group.

What is the worse acceptable match?

How dissimilar will matches be allowed to be?

- Can choose a **caliper** or **bandwidth** for acceptable matches (in terms of the distance measure or propensity score).
- Note a kernel implies a bandwidth, since the weight is 0 beyond a certain distance.
- Exact matching requires exact matches (as the name implies!)
- Coarsened exact matching requires exact matches on the coarsened continuous variable(s).

Again this decision involves a bias-variance tradeoff. Methods do exist for choosing an optimal bandwidth based on some criteria.

Matching on multiple variables

When matching on *multiple* variables, we have all of the same decisions above to make. But we will need to reduce multiple differences into one dimension. Common approaches:

- Euclidean distance $||X_i - X_j|| = \sqrt{\sum_{m=1}^{k}(X_{mi} - X_{mj})^2}$, though variables are on different scales
- *Normalized* Euclidean distance—scales each variable by its variance: $\sqrt{\sum_{m=1}^{k} \frac{(X_{mi}-X_{mj})^2}{\sigma_m^2}}$
- **Mahalanobis distance**—adjusts for any covariance between x's
- **Propensity scores**

With multiple matching variables, we can even combine criteria, like exact matching for one or more variables and distance matching for the others.

Mahalanobis distance

Take two observations (1 & 2) with X vectors of values X_1 and X_2. The Mahalanobis distance measure is:

$$d(X_1, X_2) = \sqrt{(X_1 - X_2)' C^{-1} (X_1 - X_2)}$$

Loosely, this is the sum of squared distances between values in X_1 and X_2 divided by the covariance. (C is the covariance matrix for the matching variables in X). If there is no covariance between the X, this reduces to the normalized Euclidean distance. Why "take out" the covariance?

- Suppose there is some latent characteristic that shows up in multiple matching variables. If those multiple variables are used to calculate distance, we may be "double-counting" by using distance on all of those variables.

Propensity scores

Think of the **propensity score** as a "one-number summary" capturing the relationship between a binary treatment and X: $P(X_i) = Pr(D_i = 1|X_i)$. It is the probability of treatment given X.

The propensity score can be estimated using a logistic model:

$$P(D_i|X_i) = \frac{1}{1 + e^{-X_i\beta}}$$

Taking the logit tranformation results in a linear function of X:

$$log\left(\frac{P}{1-P}\right) = X_i\beta$$

Other options are available for estimating propensity scores (probit, machine learning methods like regularized regression, boosted regression.)

Curse of dimensionality, revisited

The curse of dimensionality comes up again when trying to match on multiple variables. The more matching variables you have, the less likely it is you will find a "close" match on all variables. Getting a better match on one variable x_1 may entail a worse match on x_2.

Selecting matches in practice

Let's see some examples of matching when our aim is to *select specific matches* (i.e., we are not just creating weights for the purpose of re-weighting).

NOTE: there are lots of methods and decision points. It is easy to get lost in the weeds. But the objective is ultimately the same throughout:

- **Create balance so that you can appeal to the CIA**!

You also want common support. For example, if you are estimating the ATT, you want overlap between your treated group (their X's, or propensity scores) and your untreated group.

Exact matching

As the name suggests, **exact matching** entails pairing each treated observation with one or more untreated observations with the same X (one or more matching variables). Estimate the ATT with:

$$\widehat{ATT} = \frac{1}{N_T} \sum_{D_i=1} (Y_i - Y_{j(i)})$$

where $Y_{j(i)}$ represents the Y for the matched case(s) for treated observation i. If multiple exact matches are used, $Y_{j(i)}$ stands in for the average of these.

Nearest neighbor matching

Nearest neighbor, approximate, or distance matching relaxes the demand for an exact match and identifies "nearest neighbors" based on one or more matching variables.

- Euclidean distance
- *Normalized* Euclidean distance
- Mahalanobis distance

Stata's `teffects` commands

Stata's `teffects` commands implement a wide array of treatment effect estimators using matching, weighting, regression adjustment, etc.

- `teffects nnmatch`: exact or nearest neighbor matching
- `teffects psmatch`: propensity score matching
- `teffects ipw`: inverse probability weighting
- ...and others

The `teffects` manual on Stata is actually worth reading.

Stata's `teffects nnmatch`

`teffects nnmatch` uses exact or nearest neighbor matching—or a combination of these.

`teffects nnmatch` *(y x) (t), options*

y is the outcome, *x* are the matching variables, and *t* is the treatment indicator. In the options can use `ematch(`*vars*`)` to specify a list of variables on which you desire an exact match. For nearest neighbor matching you can specify the distance metric used, e.g., `metric(euclidean)`. There are lots of other options.

See matching examples on Github using NHIS and simulated data.

A word of advice: requesting treatment effects

`teffects` will automatically give you a treatment effect estimate based on the procedure you request (e.g., nearest neighbor matching). Include `ate` or `atet` in the options to request the ATE or ATT, respectiveity.

A word of advice: matching and weighting often involve trial and error as you tweak the matching model, adjust the number of neighbors, etc., to obtain better balance. It is not good practice to allow estimates of the treatment effect to guide your decisions about matching!!

You can preceded `teffects` with the prefix `quietly:` to suppress the output. It will do all of the necessary matching—allowing you to do balance diagnostics—without letting you "cheat" by looking at the ATE.

Some use alternative commands like `psmatch2` to perform matching before requesting a treatment effect with `teffects`.

Stata's `teffects nnmatch`

More on `teffects nnmatch`:

- The default distance metric is Mahalanobis.
- The default number of nearest neighbor matches is 1, but in the case of *exact* matching, `teffects` will use *all* available exact matches. Note for exact matching to work for ATT, there must be at least one exact match for every treated observation.
- Can include `nneighbor(#)` option to specify the minimum number of nearest neighbors. Note when there are *ties* for distance (or exact matches), `teffects` will take all of the ties as matches.
- Uses matching *with replacement*, so a nearest neighbor can be used more than once.

Stata's `teffects nnmatch`

More on `teffects nnmatch`:

- Can choose a `caliper(#)` in the options to specify "how bad" the nearest neighbor match can be.
- Can include the option `gen(`*`stubname`*`)` to have Stata create new variables with the observation numbers of nearest neighbor matches. *Note a change in sort order will change observation numbers*. You may wish to assign an id to your observations (and sort by this) to keep your sort order fixed.
- Can use postestimation command `predict` *`stubname*`*`, distance` to have Stata create new variables with the distance to nearest neighbors.

See example syntax on Github using NHIS data.

Using `mahapick` for Mahalanobis matching

An alternative command for identifying k nearest neighbors using Mahalanobis distance is `mahapick`. It automatically creates the list of matches and can output them to a file.

`mahapick` *`x1 x2 x3...`*`, idvar(`*`id`*`) treated(`*`treat`*`) nmatches(#) genfile(`*`filename`*`) score`

The *x1, x2, x3...* are the matching variables, *id* is the unique observation ID (see advice on previous slide), *treat* is the treatment indicator, and *filename* is where you want to save the resulting list of matches. `score` tells Stata to include the distance score in the output file.

As always with nearest neighbor matching, be aware of how ties are handled, and whether and how sort order matters.

Using psmatch2 for Mahalanobis matching

Another alternative for Mahalanobis matching is psmatch2, which is also used for propensity score matching.

```
psmatch2 treat , mahalanobis(x1 x2 x3...) neighbor(#)
```

The *x1, x2, x3...* are the matching variables, and *treat* is the treatment indicator. There are lots of options, including radius matching, matching *without* replacement, and more.

As always with nearest neighbor matching, be aware of how ties are handled, and whether and how sort order matters.

Coarsened exact matching

Iacus, King, and Porro (2012) make a case for coarsened exact matching, in which exact matches are required on continuous variables that have been binned ("coarsened"). See the user-written Stata command cem. Ex:

```
cem x1 (#5), treatment(treat)
```

This command performs the matching and creates weights, but does not estimate the treatment effect. You can do this yourself using the provided weights (*cem_weights*):

```
reg y treat [iweight=cem_weights]
```

Propensity scores

Rosenbaum & Rubin (1983) showed that if $Y(0), Y(1)$ are independent of D conditional on X, then they are also independent of D conditional on a **propensity score** constructed using X.

- Rather than stratifying or matching on all of the variables in X, it is sufficient to use the "one-number summary" of the relationship between treatment and X: $P(X_i) = Pr(D_i = 1|X_i)$
- $P(X_i)$ can be estimated using a logit, probit, or LPM regression from which one can obtain predicted probabilities $\widehat{P(X_i)}$. LPM is not advised if predicted probability falls outside of [0,1].

Stata also refers to the propensity score as the probability of treatment.

Propensity scores

The propensity score estimator for ATT can be written as:

$$E_{P(X)|D=1}\left(\underbrace{E[Y(1)|D=1,P(X)]}_{\text{treated}} - \underbrace{E[Y(0)|D=0,P(X)]}_{\text{untreated}}\right)$$

In theory, *for each propensity score* we calculate the difference in mean outcomes for the treated and untreated with that $P(X)$. We then take a weighted average of these over the different propensity score values. The subscript $_{P(X)|D=1}$ means we are taking a weighted average over the area of common support (same propensities to be treated).

Compare logic to Example 2 where we averaged the group differences in earnings across two groups with common support (A and C), weighting as appropriate.

Propensity scores

In practice $P(X)$ takes on a continuum of values and thus stratifying on $P(X)$ itself—in the manner we did with subclassification—is not feasible.

Thus, we can do other things with the propensity score, including matching and re-weighting. Even when propensity scores are not used to estimate treatment effects, they can be useful diagnostic tools since they force you to think about balance between the treated and untreated groups, and the model of selection into treatment.

Note: King & Nielson (2019) advise against using propensity scores for matching. (See link to seminar video on Github). Preferred use for propensity scores these days is IPW.

Stata's `teffects psmatch`

`teffects psmatch` can estimate propensity scores and produce ATT and ATE using nearest neighbor matches based on propensity scores.

`teffects psmatch` *`(y) (t x, tmodel), options`*

Again y is the outcome, x are the covariates, and t is the treatment indicator. *tmodel* is the type of propensity score model you would like to estimate (e.g., logit, probit). In the options can specify `ate` or `atet` for the treatment effect estimation, the number of nearest neighbors, the caliper, etc. (like `nnmatch`)

Again, it is best practice to *not* look at the treatment effect estimate until you have settled on a matching model/matched sample!

Stata's `teffects psmatch`

Can obtain predicted propensity scores after `teffects psmatch` using the `predict` postestimation command. Requires the `gen()` option in the `teffects psmatch` command, which creates variables containing the index of the nearest neighbor(s):

`predict` *`(newvar)`*`, ps` *`options`*

Can also predict *potential outcomes* (`po`), individual treatment effects given potential outcomes (`te`), and distance to nearest neighbor (`distance`).

See example syntax on Github using NHIS data.

Using `psmatch2` for propensity score matching

I also recommend the older user-written package `psmatch2`, which is useful for refining your propensity score model *before* requesting the ATT estimate. This package should not be used for treatment effects, however, as the standard errors are incorrect. Use `teffects` for the final treatment effect estimation.

Using psmatch2 for propensity score matching

psmatch2 can estimate propensity scores, find matches, and estimate treatment effects.

psmatch2 *treat x* , outcome(*y*) ate

treat is the treatment indicator, x are the covariates, and y is the outcome variable. There are lots of options, including type of propensity score model (probit is the deafult, can type logit for logit), number of nearest neighbors, caliper, etc. See help menu for details.

Using psmatch2 for propensity score matching

psmatch2 creates several variables in your dataset: _pscore, _treated, _support, _weight, _id, _n1, _nn, _pdif

- _pscore: estimated $P(X)$
- _treated: flags observations Stata recognized as treated
- _support: flags observations on common support
- _weight: weight for matched controls (untreated obs only)
- _id: id number assigned for identifying matches
- _n1: id of nearest neighbor (treated obs only)
- _nn: number of matched neighbors
- _pdif: absolute value of diff between $P(X)$ and $P(X)$ of NN

As noted earlier, teffects psmatch can be augmented with options (and used with the predict command to get similar information)

Checking balance

The whole point of matching methods is to construct comparison groups that are balanced so that we can appeal to the conditional independence assumption. *Before estimating treatment effects*, one should do diagnostics to check for balance on matching variables and/or propensity scores.

Compare means, but also other features of the distribution (e.g., variance).

Stata's `tebalance summarize`

Can use `tebalance summarize` following `teffects nnmatch` (or `pstest` after `psmatch`):

```
. tebalance summarize
note: refitting the model using the generate() option

  Covariate balance summary
                                                Raw              Matched
                     Number of obs =             200                  168
                     Treated obs   =              84                   84
                     Control obs   =             116                   84

------------------------------------------------------------------------------
             |  Standardized differences      Variance ratio
             |        Raw        Matched              Raw        Matched
-------------+----------------------------------------------------------------
         age |   .5124947      .0095797            .8829962    1.011965
        educ |   .1125516       .20222             1.038685     1.08452
------------------------------------------------------------------------------
```

Note: the *standardized difference* is the difference in means between the treated and untreated groups, divided by the square root of a pooled variance. They can be interpreted in standard deviation units.

Stata's `tebalance summarize`

Try `tebalance summarize, baseline` following `teffects` to see baseline differences in covariates in original units.

```
. tebalance summarize, baseline
note: refitting the model using the generate() option

  Covariate balance summary
                                              Raw        Matched
                      Number of obs =         750            556
                      Treated obs   =         278            278
                      Control obs   =         472            278
```

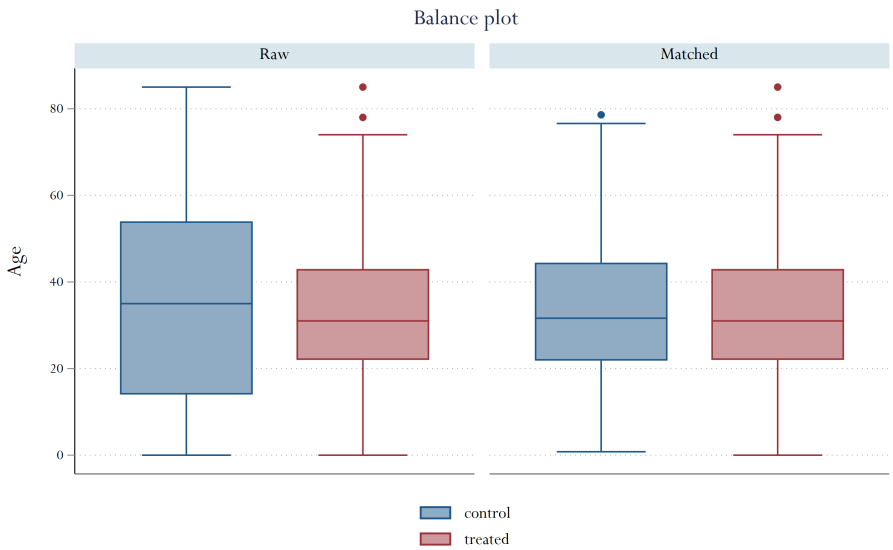
	Means		Variances	
	Control	Treated	Control	Treated
age	27.49364	30.3705	41.56259	38.57342

Stata's `tebalance summarize`

Note: when there are *multiple* nearest neighbor matches, they should be appropriately weighted so that the sum of the weights of one's neighbors equals one. (In other words, if one treatment observation has five matched untreated neighbors, they will each count as 1/5). Stata should do this automatically in `tebalance`.

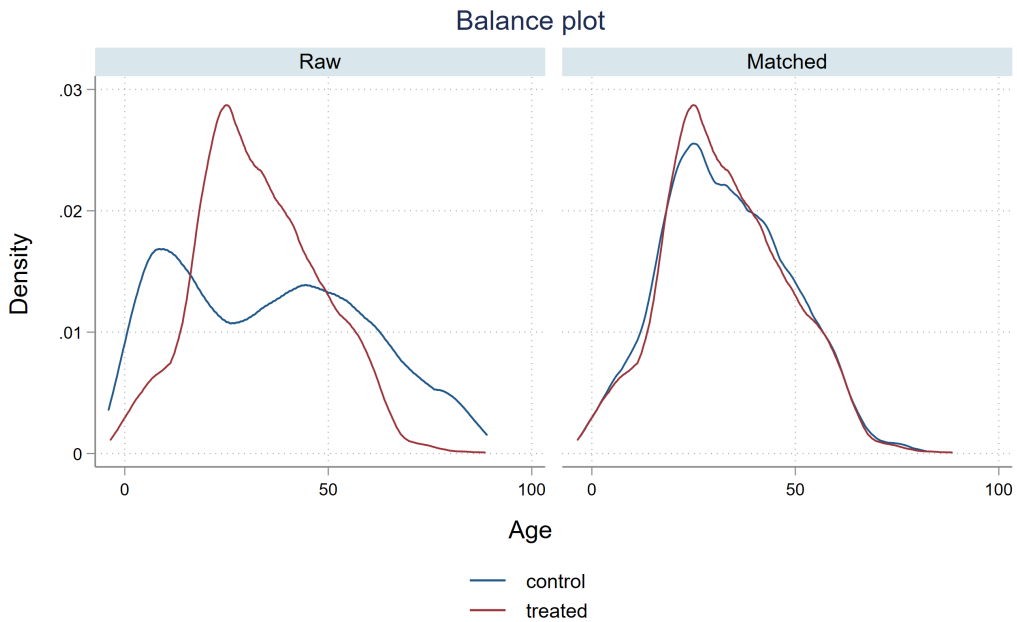
Stata's `tebalance box`

Can use `tebalance box` to get a fuller picture of the matched sample distributions:



Stata's `tebalance density`

Can use `tebalance density` to get a fuller picture of the matched sample distributions:



Checking covariate balance after psmatch2

If you use psmatch2 instead of `teffects psmatch`, can do covariate balance check using pstest:
`pstest age educ black hisp re74 re75`

```
. pstest age educ black hisp re74t re75t,both
```

Variable	Unmatched / Matched	Mean Treated	Mean Control	%bias	%reduct |bias|	t-test t	t-test p>|t|	V(T)/ V(C)
age	U	25.816	33.444	-82.3		-9.43	0.000	0.42*
	M	25.816	24.989	8.9	89.2	0.95	0.342	0.58*
education	U	10.346	12.04	-67.9		-7.92	0.000	0.48*
	M	10.346	10.811	-18.6	72.6	-1.95	0.053	0.62*
black	U	.84324	.09739	224.5		33.96	0.000	.
	M	.84324	.84865	-1.6	99.3	-0.14	0.886	.
hispanic	U	.05946	.06671	-3.0		-0.39	0.694	.
	M	.05946	.03784	8.9	-198.1	0.97	0.335	.
re74t	U	2.0956	14.746	-156.5		-16.63	0.000	0.22*
	M	2.0956	1.7488	4.3	97.3	0.79	0.433	1.96*
re75t	U	1.5321	14.38	-170.9		-17.24	0.000	0.10*
	M	1.5321	1.5778	-0.6	99.6	-0.14	0.891	1.03

* if variance ratio outside [0.75; 1.34] for U and [0.75; 1.34] for M

Sample	Ps R2	LR chi2	p>chi2	MeanBias	MedBias	B	R	%Var
Unmatched	0.463	961.39	0.000	117.5	119.4	266.1*	0.24*	100
Matched	0.013	6.66	0.354	7.2	6.6	27.0*	0.69	75

* if B>25%, R outside [0.5; 2]

Checking covariate balance after psmatch2

The column %bias above provides the standardized percent bias: the difference in sample means between the treated and untreated observations as a percentage of the square root of the average of the sample variances in the treated and untreated groups.

$$\Delta_X = \frac{\bar{X}_1 - \bar{X}_0}{\sqrt{(s_0^2 + s_1^2)/2}}$$

Checking for balance after `teffects psmatch`

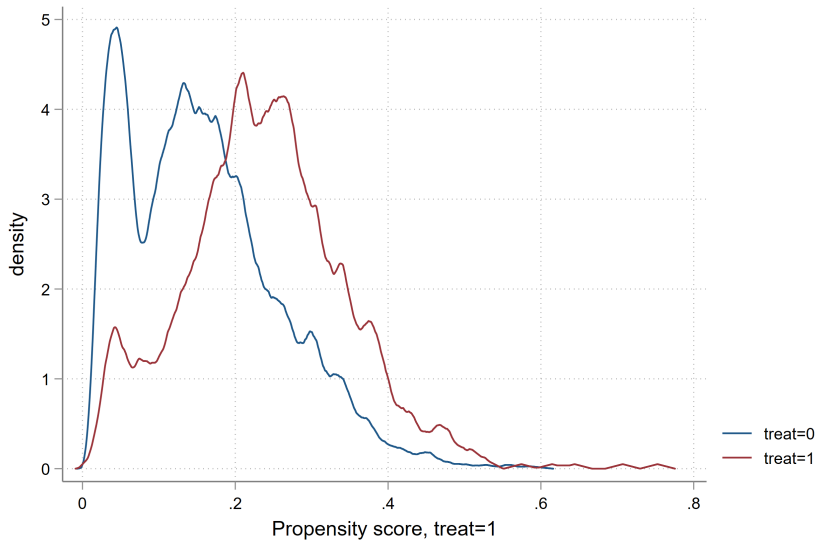
If matching on propensity scores, it makes sense that our matched samples should be balanced on these. Can save and inspect estimated propensity scores $\widehat{P(X)}$, to look for common support and balance.

- Can compare the maxima and minima of $\widehat{P(X)}$ for the two groups
- Can formally compare the density distributions for each

The command `teffects overlap` (following `teffects psmatch`) produces densities of propensity scores, although it uses the full sample rather than matched sample. Could save propensity scores and plot them yourself for matched sample.

Stata's `teffects overlap`

Can use `teffects overlap` to see overlapping distribution of propensity scores:



Note: need to specify which value of the treatment variable you are interested in the propensity of (option `ptlevel(1)`).

Checking for balance after propensity score matching

Dehejia & Wahba (2002): conditional on propensity score (binned for practicality), matching variables should not be related to treatment. If it is, may need to respecify model. (A "stratification test").

What to do when there is imbalance?

If matched samples are *not* sufficiently balanced, you may need to tweak your matching criteria or (in the case of propensity score matching) your propensity score model. In propensity score modeling, interaction terms, quadratic or higher-order terms, or additional (or fewer) covariates may help.

Practical advice on propensity score estimation

Choice of model:

- For binary treatment, whether one uses a logit, probit, or LPM model is probably not that consequential.
- For multiple treatments, the choice may be more important (see Caliendo & Kopeinig, 2008)

Covariate selection:

- Goal: choose X's such that the unconfoundedness holds—should promote covariate balance.
- Should be correlated with treatment (D) and the outcome Y.
- Selection should be based on theory and contextual knowledge.
- X should be measured *before* treatment, and not affected by it (or by the anticipation of treatment).
- X's should not be "too good" at predicting treatment—we are relying on common support.

In-class exercise

Using NSW data matched to CPS and PSID (Lalonde 1983 and others):

```
quietly teffects psmatch (re78) (treat age educ black hisp
re74 re75, probit), atet gen(mvar)
```

or

```
psmatch2 treat age educ black hisp re74 re75
```

- Estimates propensity scores (default for `psmatch2` is probit regression)
- Identifies nearest neighbor matches (default in `psmatch2` is matching with replacement).
- Use the option `ties` with `psmatch2` if you want to keep all matches with the same propensity score (the default in `teffects`).

In-class exercise

`psmatch2` will show you the probit estimates. Alternatively, could just use `probit` (or `logit`) command.

```
. psmatch2 treat age educ black hisp re74 re75

Probit regression                                 Number of obs     =     18,927
                                                  LR chi2(6)        =     861.45
                                                  Prob > chi2       =     0.0000
Log likelihood = -609.54681                       Pseudo R2         =     0.4140

------------------------------------------------------------------------------
       treat |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |  -.0171489   .0041262    -4.16   0.000    -.0252362   -.0090616
   education |  -.0301524    .015144    -1.99   0.046    -.0598342   -.0004707
       black |   1.589191   .0958607    16.58   0.000     1.401308    1.777075
    hispanic |   .6522818   .1525644     4.28   0.000      .353261    .9513026
        re74 |   -.000023   .0000105    -2.19   0.029    -.0000436   -2.40e-06
        re75 |   -.000082   .0000133    -6.14   0.000    -.0001081   -.0000558
       _cons |  -1.677663   .2261594    -7.42   0.000    -2.120927   -1.234399
------------------------------------------------------------------------------
Note: 346 failures and 0 successes completely determined.
```


In-class exercise

Inspect the histograms of propensity scores for the treated and untreated observations: `psgraph` (uses *all* of the data, not just the matched sample)

In-class exercise

pstest age educ black hisp re74 re75

```
. pstest age educ black hisp re74t re75t,both
```

Variable	Unmatched / Matched	Mean Treated	Mean Control	%bias	%reduct |bias|	t-test t	t-test p>|t|	V(T)/ V(C)
age	U	25.816	33.444	-82.3		-9.43	0.000	0.42*
	M	25.816	24.989	8.9	89.2	0.95	0.342	0.58*
education	U	10.346	12.04	-67.9		-7.92	0.000	0.48*
	M	10.346	10.811	-18.6	72.6	-1.95	0.053	0.62*
black	U	.84324	.09739	224.5		33.96	0.000	.
	M	.84324	.84865	-1.6	99.3	-0.14	0.886	.
hispanic	U	.05946	.06671	-3.0		-0.39	0.694	.
	M	.05946	.03784	8.9	-198.1	0.97	0.335	.
re74t	U	2.0956	14.746	-156.5		-16.63	0.000	0.22*
	M	2.0956	1.7488	4.3	97.3	0.79	0.433	1.96*
re75t	U	1.5321	14.38	-170.9		-17.24	0.000	0.10*
	M	1.5321	1.5778	-0.6	99.6	-0.14	0.891	1.03

* if variance ratio outside [0.75; 1.34] for U and [0.75; 1.34] for M

Sample	Ps R2	LR chi2	p>chi2	MeanBias	MedBias	B	R	%Var
Unmatched	0.463	961.39	0.000	117.5	119.4	266.1*	0.24*	100
Matched	0.013	6.66	0.354	7.2	6.6	27.0*	0.69	75

* if B>25%, R outside [0.5; 2]

In-class exercise

psmatch2 treat age educ black hisp re74 re75, outcome(re78)

```
. psmatch2 treat age educ black hisp re74 re75, outcome(re78)

Probit regression                                 Number of obs     =     18,927
                                                  LR chi2(6)        =     861.45
                                                  Prob > chi2       =     0.0000
Log likelihood = -609.54681                       Pseudo R2         =     0.4140
```

treat	Coef	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.0171489	.0041262	-4.16	0.000	-.0252362	-.0090616
education	-.0301524	.015144	-1.99	0.046	-.0598342	-.0004707
black	1.589191	.0958607	16.58	0.000	1.401308	1.777075
hispanic	.6522818	.1525644	4.28	0.000	.353261	.9513026
re74	-.000023	.0000105	-2.19	0.029	-.0000436	-2.40e-06
re75	-.000082	.0000133	-6.14	0.000	-.0001081	-.0000558
_cons	-1.677663	.2261594	-7.42	0.000	-2.120927	-1.234399

, bin(20) fcolor(none) lcolor(red)) (histogram _pscore if treat==0 [fweight=_weight], bin(20) fcolor(none) lcolor(red))

Note: 346 failures and 0 successes completely determined.

Variable	Sample	Treated	Controls	Difference	S.E.	T-stat
re78	Unmatched	6349.1435	15594.9895	-9245.84596	803.597327	-11.51
	ATT	6349.1435	5528.42643	820.717073	829.853344	0.99

Note: S.E. does not take into account that the propensity score is estimated.

psmatch2: Treatment assignment	psmatch2: Common support On suppor	Total
Untreated	18,742	18,742
Treated	185	185
Total	18,927	18,927

Bias corrections

In this genre of estimators—in which the CIA is assumed to hold—the only source of bias comes from imbalance in the covariates (i.e., imperfect matches).

When there is imperfect matching, the treatment effect estimator is a combination of the "true" effect and differences in Y that are a byproduct of the imbalance in covariates.

Abadie & Imbens (2011) propose a consistent bias-corrected estimator. The idea here is that one can use OLS to estimate the relationship between Y and covariates X. The difference in (predicted) Y due to the differences in X (between the perfect and actual match) is used to adjust the treatment effect estimate. In `teffects`: use `biasadj(`*varnames*`)` option with *varnames* the list of continuous covariates.

On standard errors

The standard errors for matching and weighting estimators are complicated. Why?

- The matching procedure might involve multiple decision points, judgment calls—it's hard to think about these over repeated sampling.
- Propensity scores (and weights) have to be *estimated*, and some analysts may trim observations based on these.
- Bootstrapping for standard errors is an option—but only in the weighted matched sample case (not selecting specific matches).

Choosing specific matches versus weighting

All of the techniques illustrated thus far involve identifying specific matches:

- Exact matching: each treated (untreated) case is matched to one or more untreated (treated) cases with the same X.
- Nearest neighbor matching: each treated (untreated) case is matched to one or more untreated (treated) cases with the *closest* X.
- Propensity score matching: each treated (untreated) case is matched to one or more untreated (treated) cases with the *closest* $\widehat{P(X)}$.

The matched sample is used to calculate the ATE/ATT.

Where do *weights* come in? So far, only to account for multiple matches (e.g., 1 treated observation may be matched to 10 neighbors, so each of the 10 get 1/10 weight). Data are "pruned" if they aren't matched.

Inverse probability weighting (IPW)

Inverse probability weighting uses all of the data, reweighting observations to create desired balance. Weights use the propensity scores:

$$w_{ATT} = D_i + (1 - D_i)\frac{\widehat{P(X)}}{1 - \widehat{P(X)}}$$

$$w_{ATE} = \frac{D_i}{\widehat{P(X)}} + \frac{(1 - D_i)}{1 - \widehat{P(X)}}$$

Inverse probability weighting (IPW)

Intuition using a simple example:

	Treated ($D = 1$)	Untreated ($D = 0$)	P(D|X)
X=1	1	9	0.1
X=0	4	1	0.8

1 confounding covariate X, where the probability of treatment varies with X (0.1 for $X = 1$ and 0.8 for $X = 0$).

For the $X = 1$ group, treatment is rare.
For the $X = 0$ group, treatment is common.

Inverse probability weighting (IPW)

	Treated ($D = 1$)	Untreated ($D = 0$)	P(D|X)
X=1	1	9	0.1
X=0	4	1	0.8

Goal: for a given X, construct weights for the treated and untreated so that their "effective sample sizes" are equal.

For ATT, choose weights so the untreated "look like" the treated. For ATE, choose weights so that both groups "look like" the full sample.

Inverse probability weighting (IPW)

	Treated	Untreated	P(D|X)	IPW Treated	IPW Untreated
X=1	1	9	0.1	10.00	1.11
X=0	4	5	0.8	1.25	5.00

ATT: Weight the treated by $1/P(X)$ and the untreated by $1/(1 - P(X))$. Within each X (and thus, $P(X)$), the effective sample size is the same.

IPWs give more weight to treated cases with a low $P(X)$ and untreated cases with a high $P(X)$. This is essentially what we did in Example 1 to balance by gender.

Inverse probability weighting (IPW)

Note: IPW estimators become unstable when there is low overlap (cases with very low probability of treatment). Re: these observations get extremely high weight when using inverse probability.

Stata's `teffects ipw`

`teffects ipw` can estimate ATT and ATE using inverse probability weighting. Propensity scores (probability of treatment) are used in the weights. The syntax is very similar to `psmatch`:

`teffects ipw` *(y) (t x, tmodel), options*

y is the outcome, *x* are the covariates, and *t* is the treatment indicator. *tmodel* is the type of propensity score model you would like to estimate (e.g., logit, probit). In the options can specify `ate`, `atet`, or the potential outcome means `po`.

Stata's `teffects ipw`

After estimating the propensity score model using `teffects ipw`, one should do a check for common support with `teffects overlap`.

Trimming observations is an option if there are cases outside the common support, or that have very low or high propensities for treatment. (Treated cases with very low propensities and untreated cases with very high propensities will get large weights).

Matching vs. regression

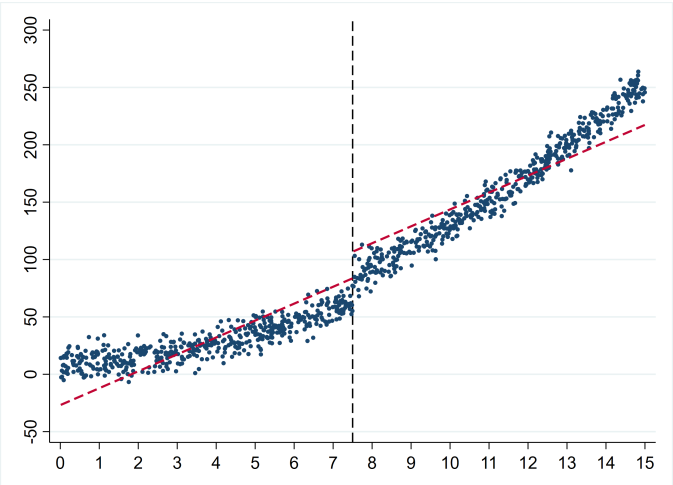
If potential outcomes are independent of treatment conditional on X, why not just estimate a regression controlling for X?

- Matching does not require assumptions about functional form for the outcome model (e.g., a linear relationship between Y and X).
- Regression runs the risk of extrapolating onto a space where there is little common support.
- Matching focuses our attention on balance and the degree of common support.
- Can estimate treatment effects for different groups.

That said, matching or weighting using propensity scores "shifts the problem to the task of estimating the propensity score." If the model for the propensity score is poor, the propensity score matching estimator will be biased.

Matching vs. regression

By making strong functional form assumptions, one can use regression to estimate treatment effects even when there is little overlap in X between the treated and untreated cases. But getting the functional form wrong can lead to poor inferences. We'll see this later with regression discontinuity:



Matching vs. regression

See also Murnane & Willett ch. 12 on the differences between matching strategies and regression (pp. 304-ff).

Additional resources

- Guo & Fraser (2015) textbook: all things propensity scores.
- See Caliendo & Kopeinig (2008) for practical guidance on propensity score matching.
- See Imbens (2015) for guidance on matching and subclassificaion.
- There are many studies comparing impact estimates from randomized experiments to those using matching methods. E.g., Wilde & Hollister, 2007 using Tennessee STAR experiment; Dehejia & Wahba (1999, 2002); Smith & Todd (2005); Agodini & Dynarski (2004); Diaz & Handa (2006); Michalopoulos, Bloom & Hill (2004)

Imbens (2015)

Useful guidance from Imbens (2015) on matching methods, with examples.

- Cases in which OLS estimators are likely to be especially problematic for estimating causal effects with non-experimental data
- Two recommended methods: (1) subclassification and regression; or (2) matching
- Trimming and other pre-processing steps to improve balance
- Supplementary analyses for assessing plausibility of conditional independence assumption

A key takeaway: "there are no, and will not be, general results implying that in general some estimators are superior to all others"

Imbens (2015) on OLS

Imbens provides an example illustrating why and when OLS can be problematic. Key takeaway points:

1. The OLS regression aims to provide the average of the potential control outcomes for the treated
2. Functional form assumptions can matter a lot: extrapolation and misspecification
3. This is especially true when the distribution of covariates differs between the treated and untreated cases
4. Extreme values can have a large influence on the OLS estimates: "regression models are not fundamentally robust to the substantial differences between treatment and control groups"

Imbens (2015) on analytic methods

Stages:

1. **Design stage**: trimming the full sample and balancing on covariates
2. **Supplementary analysis stage**: assessing balance
3. **Analysis stage**: estimating treatment effect

Important: the outcome data are not used until the last stage.

Imbens (2015) advice

- **Normalized differences**: for assessing balance, use *normalized differences in mean covariates*. In Stata, this is the "% bias" in `pstest`. This is preferable to t-tests of significant differences.
- **Propensity score**: Imbens uses logit, but notes the choice of probit or logit matters more when there are cases with pscores close to 0 or 1
  - "the propensity score plays a mechanical role in balancing the covariates ... In choosing a specification, there is therefore little role for theoretical substantive arguments. We are mainly looking for a specification that leads to an accurate approximation to the conditional expectation."
  - There is no harm in specification searches at this stage
  - Interactions and non-linearities are often important
  - There are data-driven algorithms for selecting covariates (e.g., stepwise approach of Imbens & Rubin, 2015; lasso methods)

Imbens (2015) advice

- **Propensity score**
  - "However, the point is again not to find a single method for estimating the propensity score that will outperform all others. Rather, the goal is to find a reasonable method for estimating the propensity score that will, in combination with the subsequent adjustment methods, lead to estimates for the treatment effects of interest that are similar to those based on other reasonable methods for estimating the propensity score"
  - Stepwise approach of Imbens & Rubin: first choose a set of predictors that will be in the model, regardless of other decisions (e.g., lagged measures of the outcome). Then determined a threshold for inclusion of other linear and quadratic terms. Finally, successively add predictors and compare to this threshold.

Imbens (2015) on analytic methods

- **Blocking method**: one recommended estimator uses the propensity score to block (or subclassify) observations and then use regression within blocks.
  - Partition the range of the propensity score into J intervals
  - Within each interval, estimate a linear regression with some covariates (all or a subset of those thought to be most important)
  - The J estimates of the treatment effects are then combined into one overall effect
  - 5 blocks is common, but Imbens & Rubin (2015) propose an algorithm for selecting this
- **Matching method**: with replacement. Rather than using propensity scores, they use the Mahalanobis distance metric: