2. Matching and weighting estimators

LPO 8852: Regression II

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Selection bias

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

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

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

- Randomization of D eliminates selection bias!
- Regression can help under very strong conditions about potential outcomes.

Matching and weighting

Matching and weighting estimators construct comparison groups that are *balanced* on a set of observable variables. There are lots of ways to do this:

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

Key assumption for causal interpretation: once we have conditioned on observables—by selecting matches, constructing weights, or stratifying—treatment assignment and potential outcomes are independent. This is the conditional independence assumption (CIA).

A note on weighted averages

What is a weighted average? Given a weight w_i 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: private vs. public colleges, revisited

This is a stylized version of the private college example in Lecture 1:

		Private			Public			
	Student	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: *Mastering Metrics* (2015). Shaded cell represents the student's chosen college, from those they were admitted to. Based on Dale & Krueger (2002).

Example 1

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 1

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 1

					All	Tall	Altered	Earnings
	Student	Ivy	Leafy	Smart	State	State	State	
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 1

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 students:

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

Another weighted average assigns weights to groups according to the number of *treated* students:

$$(-5,000) * (2/3) + (30,000) * (1/3) = \$6,666$$

Example 1

Weighted averages use the data more efficiently, and also generalize 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 1

Note in this example that neither the weighted nor unweighted average of groups A and B estimate the ATE or ATT for this population. 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 your data. Note: generalizing to groups A and B may still be interesting! It also may be the best you can do.

Example 1

Mastering Metrics explains 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). Groups C and D are excluded.

Using the Example 1 data, $\hat{\beta} = 10,000$. This is comparable to the averages found earlier, but is not identical to any of them. Regression effectively applies different weights. It estimates a **variance-weighted treatment effect**.

Example 1

The weighted averages in Example 1 can be characterized as:

- A **matching** approach: each treated case (private college attendee) is matched to one or more untreated case (public college attendee) with the same observable characteristic (application/admission group). Then the outcomes of the matched observations are compared.

- A **subclassification** approach: cases are stratified according to some observable characteristic (application/admission group), mean differences are calculated within each group, and then averaged across groups (e.g., weighting by the number of treated cases).

Identifying assumption: conditional on application/admissions group, potential outcomes are balanced across treated and untreated cases. Treatment assignment is "as good as random."

Example 2: 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:

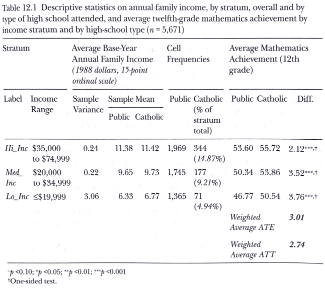


Table 12.1 Descriptive statistics on annual family income, by stratum, overall and by type of high school attended, and average twelfth-grade mathematics achievement by income stratum and by high-school type ($n = 5{,}671$)

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 2

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

The estimate of ATE (3.01) uses *total* cell sizes as weights; the estimate of ATT (2.74) uses counts of *treated* cases in each cell as weights. These estimates are smaller than the unconditional mean differences in math scores (3.895), suggesting an upward bias.

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

Identifying assumption: conditional on income (strata), enrollment in Catholic school is "as good as random" (!).

Example 2

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

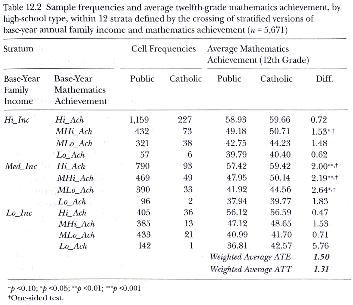


Table 12.2 Sample frequencies and average twelfth-grade mathematics achievement, by high-school type, within 12 strata defined by the crossing of stratified versions of base-year annual family income and mathematics achievement ($n = 5{,}671$)

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	$1.53^{*,\dagger}$
	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	$2.00^{**,\dagger}$
	MHi_Ach	469	49	47.95	50.14	$2.19^{**,\dagger}$
	MLo_Ach	390	33	41.92	44.56	$2.64^{*,\dagger}$
	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***

$^{\sim}p < 0.10$; $^{*}p < 0.05$; $^{**}p < 0.01$; $^{***}p < 0.001$
†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**.

Approaches to matching

There are many approaches to constructing matched comparison groups:

- Exact matching
- Coarsened exact matching
- Nearest neighbor/distance matching
- Propensity score matching

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.

Note: this could also be done for untreated observations to estimate ATU.

Nearest neighbor matching

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

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

$\widehat{ATT}$ is the same as the previous slide, but the matched case(s) used for $Y_{j(i)}$ are based on distance (e.g., nearest neighbor) criteria.

Euclidean and normalized Euclidean distance

Suppose you have a vector X of k variables for two units i and j. The Euclidean distance between X_i and X_j is:

$$||X_i - X_j|| = \sqrt{\sum_{m=1}^{k} (X_{mi} - X_{mj})^2}$$

These X_m variables are likely on different scales. The *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

Suppose you have a vector X of k variables for two units i and j. The Mahalanobis distance between X_i and X_j is:

$$d(X_i, X_j) = \sqrt{(X_i - X_j)' C^{-1} (X_i - X_j)}$$

Loosely, this is the sum of squared distances between values in X_i and X_j normalized 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.

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

The `teffects` manual from Stata is actually worth reading! See also my handout: *Stata commands for matching.*

Stata's `teffects nnmatch`

`teffects nnmatch` implements 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)`. Mahalanobis is the default.

There are lots of other options!

Matching: objectives

Again, there are lots of approaches to creating matched comparison groups. However, there are a few basic principles:

1. You are appealing to the **conditional independence** assumption. So choose matching variables that make this plausible.
2. Given a choice of X, you want to see **balance** in your matched comparison groups. Ideally, you want to see balance in the full distributions of X, not just the means.
3. You want **common support**: treated <u>and</u> untreated cases throughout your distribution of X.
4. You want **efficient** estimators (smaller standard errors). Use more of the data when possible, but there is a bias-efficiency tradeoff..

Staying honest with `teffects`

`teffects` will automatically give you a treatment effect estimate based on the procedure you request (e.g., `nnmatch`). The option `ate` or `atet` in the options will request the ATE or ATT, respectively.

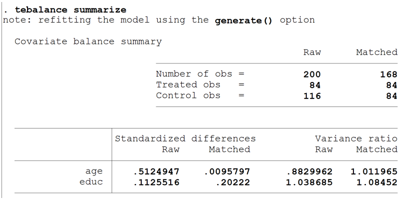
A word of caution: matching often involves multiple iterations to obtain better balance. It is <u>not</u> good practice to allow estimates of the treatment effect to guide your decisions about matching!!

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

Alternative commands like `psmatch2` can perform matching without requesting a treatment effect estimate.

Stata's tebalance summarize

Can use tebalance summarize following teffects nnmatch:

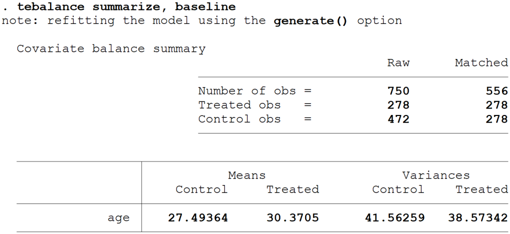


```
. tebalance summarize
note: refitting the model using the generate() option

  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 (pre-matching) differences in covariates in the original units.



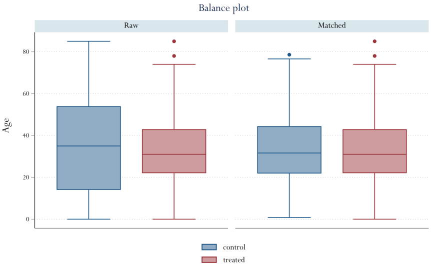
```
. tebalance summarize, baseline
note: refitting the model using the generate() option

  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`.

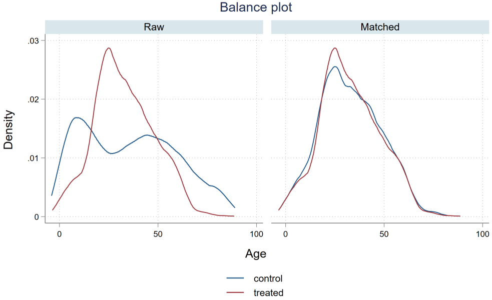
Stata's `tebalance box`

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:



In-class example 1

See do-file: *Lecture 2 matching with simulated data*. In this example, potential earnings (y) are affected by age and education. There is also a treatment (*treat*) that is positively related to age and education. This do-file illustrates:

- Exact matching on one variable (age)
- Exact matching on multiple variables (age and education)
- Nearest neighbor matching (Euclidean and Mahalanobis)
- Balance checking
- Capturing the observation numbers of nearest neighbors (and distance to these neighbors)

Refining nearest neighbor matches

There are a number of things you can do to control the number and quality of nearest neighbor matches:

- Choose a **caliper** or bandwidth for acceptable matches, in terms of distance. The option `caliper(#)` sets the max distance allowed.
- Can choose the number of nearest neighbors desired with `nneighbor(#)` option (the default is 1). Note ties are used.
- Can take all neighbors within a given caliper (**radius** matching) or *k* nearest neighbors subject to being within the caliper.
- Can perform matching with or without replacement. (`teffects nnmatch` is with replacement).

Refining nearest neighbor matches

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

Matching with replacement = "better" matches. But matching with replacement means fewer observations used in the estimator—the same observations may be used over and over again as nearest neighbors.

Abadie & Imbens (2011) bias correction

When the conditional independence assumption holds, the only source of bias when matching 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.

Post-matching predictions

After `teffects nnmatch` you can `predict` new variables that contain each unit's "potential outcomes" (`po`) and "treatment effect" (`te`). Obviously, we can't know these! These are imputed based on the matches.

- Need to specify which potential outcome condition you want (e.g., Y_{i0} or Y_{i1}). Let's call `po0` the potential outcome in the untreated state and `po1` the potential outcome in the treated state.
- For treated observations, `po0` is the mean outcome of their matched untreated observations. `te` is the difference between their actual y and this imputed counterfactual.
- For untreated observations, `po1` is the mean outcome of their matched treated observations. `te` is the difference between their actual y and this imputed counterfactual.

Using mahapick for Mahalanobis matching

FYI, an alternative command for identifying *k* nearest neighbors (with replacement) 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)
nummatches(#) genfile(filename) score
```

The *x1, x2, x3...* are the matching variables, *id* is the unique observation ID, *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. There are lots of other options. See also `mahascore` which gives you distance measures between all pairs.

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 an older command used for propensity score matching. (More on this later).

```
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) introduced **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 (#), treatment(treat) showbreaks
```

The option (#) is the number of cutpoints for variable *x1*. For example, (#5) will use 5 equally-spaced cutpoints. This can be omitted and cem will automatically coarsen the data based on a binning algorithm.

Coarsened exact matching

cem performs the coarsening and matching and creates weights, but does not estimate the treatment effect. You can do this yourself using the weights created by cem (*cem_weights*):

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

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 result in a worse match on X_2.

Propensity scores

An alternative to matching on multiple variables is the **propensity score**. Think of the propensity score as a "one-number summary" capturing the relationship between a binary treatment and X: $Pr(D_i = 1|X_i)$. It is the **probability of treatment** for unit i given X_i.

The propensity score can be estimated using a logistic model:

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

where the log odds $P/(1 - P)$ is a linear function of X. Other options for estimating propensity scores include probit, machine learning methods like regularized regression, and boosted regression.

Propensity scores

Rosenbaum & Rubin (1983) showed that if potential outcomes Y_{0i}, Y_{1i} are independent of D conditional on X, then they are also independent of D conditional on the probability of treatment given X (the propensity score).

- 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: $Pr(D_i = 1|X_i)$
- Let $P(X)$ be shorthand for the propensity score $Pr(D_i = 1|X_i)$.

Propensity scores

The propensity score estimator for ATT can be written as:

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

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 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 (Examples 1 and 2)—is not feasible.

Thus, we can do other things with the propensity score, including nearest neighbor matching and weighted estimators. 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 video on Github). They argue that propensity scores should just be used for weighting.

Propensity scores

With nearest neighbor matching based on propensity scores, a common estimator of the ATT is:

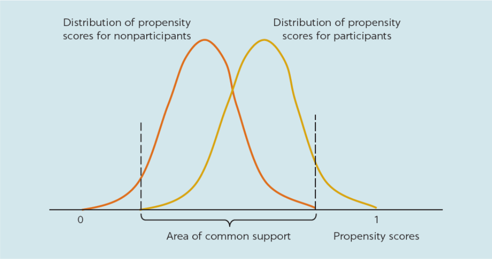
$$\widehat{ATT} = \frac{1}{N_T} \sum_{D_i=1} (Y_i - Y_{j(i)})$$

where $Y_{j(i)}$ represents the average Y for the matched case(s) for treated observation i.

- This sum would only be over the area of common support. It may be that some treated lack untreated cases with "similar" p-scores.
- One could also find matches for untreated cases and calculate $\widehat{ATU}$.
- Later: one can also assign more weight to neighbors that are "closer."

Propensity scores: common support

FIGURE 13.1 Propensity scores and the area of common support


Distribution of propensity scores for nonparticipants
Distribution of propensity scores for participants
0
1
Area of common support
Propensity scores

Source: Original figure for this publication.

Source: Glewwe & Todd chapter 13

Stata's `teffects psmatch`

`teffects psmatch` estimates propensity scores and can produce ATT and ATE using nearest neighbor matches.

`teffects psmatch` *(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` 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! Use `quietly` until you are ready.

Checking for balance after `teffects psmatch`

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

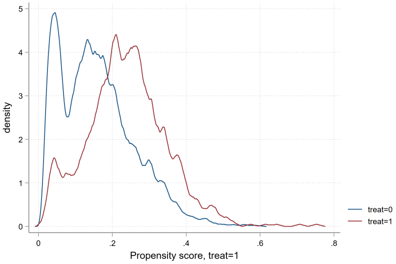
- Can compare the maxima and minima of $\widehat{P(X)}$ for the two groups
- Can compare the density distributions for each

The command `teffects overlap` (following `teffects psmatch`) produces densities of propensity scores, although it uses the *full sample* rather than the matched sample (not ideal). Could save propensity scores and plot them yourself for matched sample.

You can also check for balance on the covariates themselves (with `tebalance summarize`)

Stata's `teffects overlap`

`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)` if treatment=1).

Getting estimated propensity scores

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

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

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

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 t x , outcome(y) ate
```

t 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.

By default, `psmatch2` shows you the result of the propensity score model itself (logit or probit).

Using psmatch2 for propensity score matching

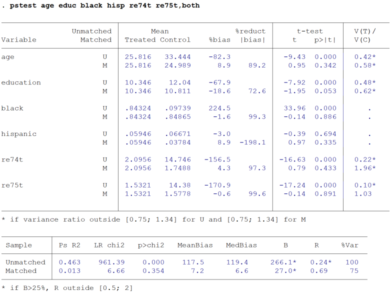
`psmatch2` creates several variables in your dataset: `_pscore`, `_treated`, `_support`, `_weight`, `_id`, `_n1`, `_nn`, `_pdif`

- `_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 covariate balance after psmatch2

If you use psmatch2 instead of teffects psmatch, can do covariate balance check using pstest:



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

----------------------------------------------------------------------------
                Unmatched |       Mean               %reduct |     t-test    |  V(T)/
Variable          Matched | Treated Control    %bias  |bias| |    t    p>|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]
```

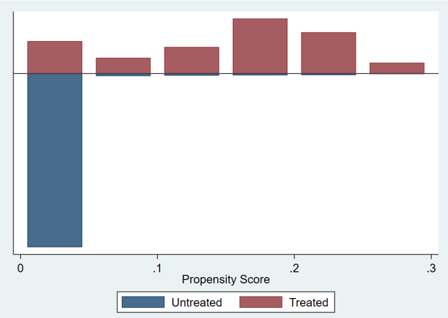
Checking covariate balance after psmatch2

The column %bias above provides the standardized difference: 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 common support after `psmatch2`

You can compare histograms of propensity scores for the treated and untreated observations using `psgraph` (uses *all* of the data, not just the matched sample)



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.

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 recommended in the weighted matched sample case (not selecting specific matches).

For now, just use default standard errors in `teffects` but don't take them as gospel.

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	Untreated	
	$(D = 1)$	$(D = 0)$	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): ATT

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

ATT: Weight the treated by 1 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 untreated cases with a high $P(X)$.

Inverse probability weighting (IPW): ATE

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

ATE: 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 $P(X)$.

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 `teffects 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).