Step-by-Step Guidelines for Propensity **Score Weighting** with Three or More Groups

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### Motivating example

- Case study: To estimate the relative causal effect of MET/CBT5 vs "usual care" vs SCY
  - Data from 3 SAMSHA CSAT discretionary grants

#### MET/CBT5

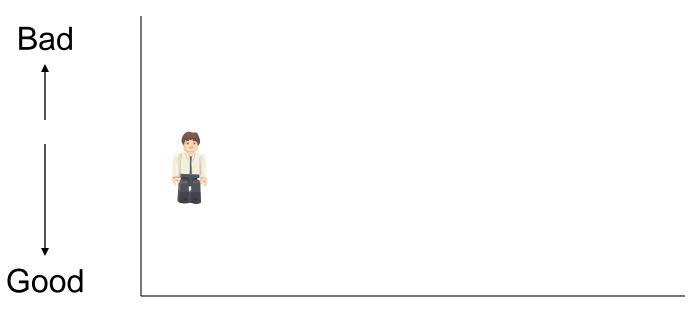
- Observational
- MET/CBT5 at 37 EAT sites
- N = 2459
- 2003/04 2007

#### "Usual Care"

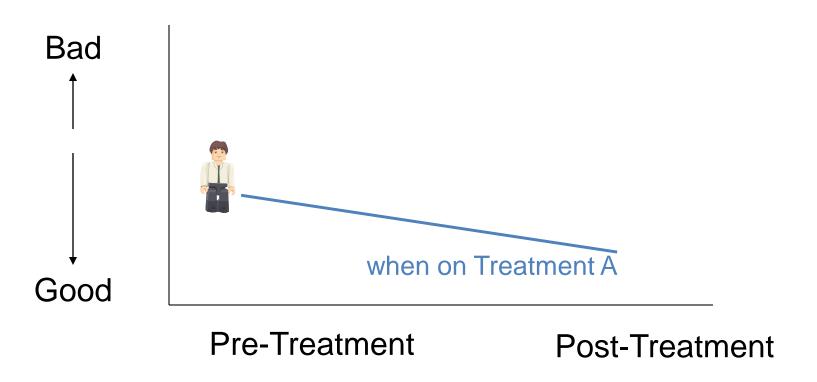
- Observational
- "Usual care" at 4 ATM sites
- N = 444
- 1998 1999

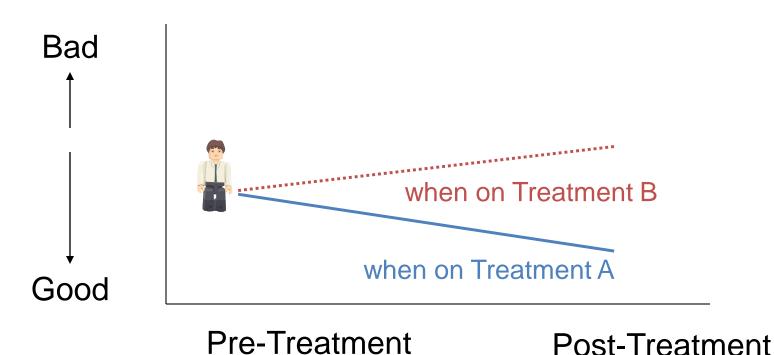
#### SCY

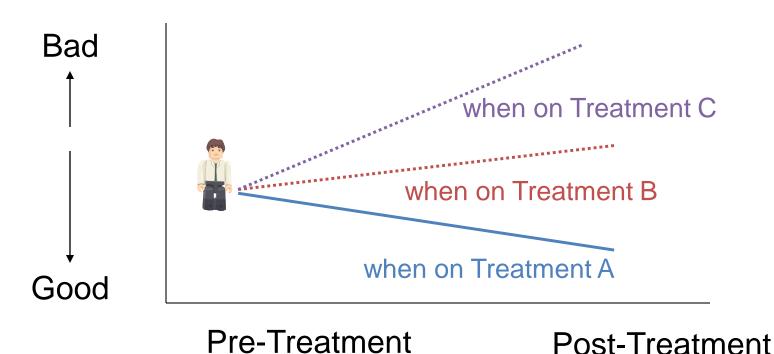
- Observational
- Community strengthening at 8 SCY sites
- N = 1351
- 2001 2002

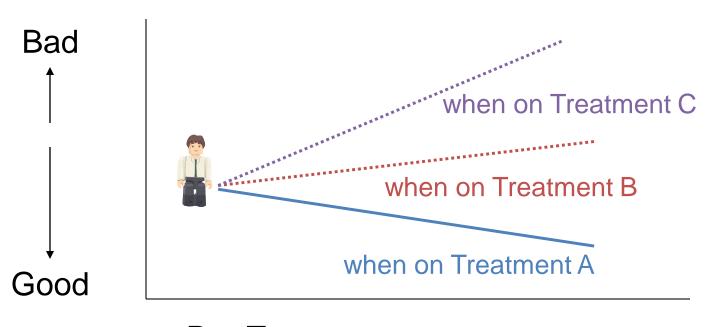


**Pre-Treatment** 









Pre-Treatment

Post-Treatment

Now even more potential outcomes/counterfactuals and more treatment effects that might be of interest

## Expand potential outcomes for *J* treatments

- J potential outcomes for each study participant
  - Potential outcome after receiving treatment  $1, \dots J = Y_1, \dots, Y_J$
- $Y_1, ..., Y_J$  exist for all individuals in the population regardless of the treatment they actually received
- Still only one of these outcomes observed for each participant

#### Primary types of causal effects

- Average treatment effect in the population (ATE)
  - Answers the question:
    - What is the relative effectiveness of all the treatments on average in the population?
  - $-E(Y_1-Y_2), E(Y_1-Y_3), ..., E(Y_1-Y_J), E(Y_2-Y_3), etc.$
- Average treatment effect in the treated population (ATT)
  - Answers the question:
    - How would those who received a particular treatment have done had they received any of the other treatments?
  - $-E(Y_1-Y_2|Z=1), E(Y_1-Y_3|Z=1), ..., E(Y_1-Y_1|Z=1)$

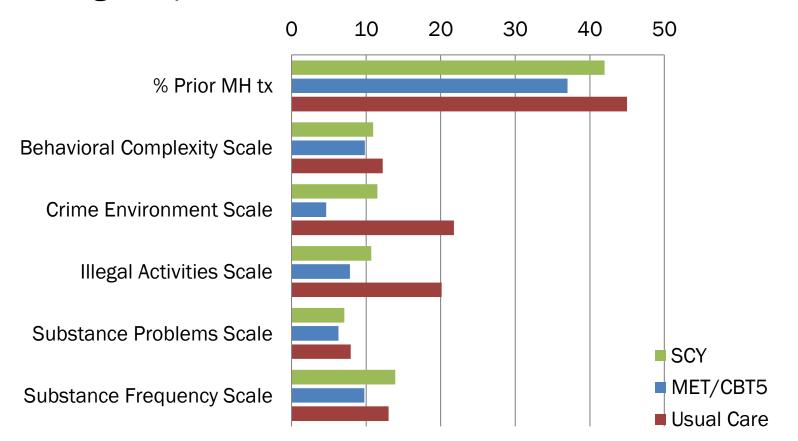
# Primary types of causal effects: case study

- Average treatment effect in the population (ATE)
  - Answers the question:
    - What is the relative effectiveness of MET/CBT5, usual care, and SCY on average in the population?
  - $-E(Y_1-Y_2), E(Y_1-Y_3), ..., E(Y_1-Y_J), E(Y_2-Y_3), etc.$
- Average treatment effect in the treated population (ATT)
  - Answers the question:
    - How would youth like those who received usual care have done had they received MET/CBT5 or SCY?

$$-E(Y_1-Y_2|Z=1), E(Y_1-Y_3|Z=1), ..., E(Y_1-Y_2|Z=1)$$

## Biggest challenge to causal estimation is selection effects

 Selection occurs when the people getting the treatments being compared differ



# Propensity scores with more than 2 groups

- Let Z denote the categorical treatment assignment measure (values = 1, ..., J)
- Propensity score is an individual's probability of receiving one of the treatments given pretreatment characteristics
  - $-p_{j}(X) = \Pr(Z = j|X)$
- Propensity scores still have balancing property
  - All needed to control for pretreatment differences between the groups
  - Assumes no unobserved differences between groups and overlap (strong ignorability)

# Weighting with more than 2 groups

#### For ATE:

- weight individuals in each sample by the inverse probability of receiving the treatment they received
- For an individual receiving treatment j, the weight equals  $1/p_j(X)$

#### For ATT:

- weight individuals in each sample by the ratio of the probability receiving the target treatment to the probability of receiving the treatment they received
- For an individual receiving treatment j and where target treatment equals  $j^*$ , the weight equals  $p_{j^*}(X)/p_i(X)$

#### STEP-BY-STEP GUIDELINES

#### Four Key Steps

- 1) Choose the primary treatment effect of interest (ATEs or ATTs)
- 2) Estimate propensity score (ps) weights
- 3) Evaluate the quality of the ps weights
- 4) Estimate the treatment effects

# Step 1: Choose the primary treatment effect (ATE or ATT)

- Today, we chose to focus on estimating ATE
- Why?
  - We want to know how well each treatment is doing in general
  - Thus, the policy question we want to address is:

What are the relative causal treatment effects of MET/CBT5, SCY, and usual care on average for youth in our population?

### Step 2: Estimate the ps weights

- Only 1 command needed for this step
- Multiple treatment command in TWANG currently available in R and SAS
  - Stata available in Fall 2015

use import delimited "C:\Data\subdata.csv", clear

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) ///
objpath(C:\MyProjects\TWANG ) ///
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)
```

```
Stata
                                           trtvar is the
                                           treatment
                                           indicator; it must
                                           have 3 or more
                                           values and it
                                           must be a factor
mnps trtvar
                                           in R
age female i.race4g sfs sps sds ias ces eps
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) ///
objpath(C:\MyProjects\TWANG) ///
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)
save C:\MyProjects\TWANG\subdata_wgts)
```

**Specifies list of** 

pretreatment

covariates to balance on *mnps* trtvar /// age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx /// ntrees(5000) /// stopmethod(es.max) /// estimand(ATE) /// rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) /// objpath(C:\MyProjects\TWANG) /// plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf) save C:\MyProjects\TWANG\subdata\_wgts)

Stata Add i. before **Specifies list of** categorical pretreatment variables like covariates race to balance on *mnps* trtvar /// age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx /// ntrees(5000) /// stopmethod(es.max) /// estimand(ATE) /// rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) /// objpath(C:\MyProjects\TWANG) /// plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)

save C:\MyProjects\TWANG\subdata\_wgts)

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) /4/
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) ///
objpath(C:\MyProjects\TWANC) ///
                                     Specifies the
plotname(C:\MyProjects\TWANG\Mul
                                     maximum
                                     number of
save C:\MyProjects\TWANG\subda
                                     iterations used
                                     by GBM. Should
                                     be large (5000 to
                                     10000)
```

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) / //
                                               Specifies the
estimand(ATE) ///
                                               criteria for
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) //
                                              choosing the
                                               optimal number
objpath(C:\MyProjects\TWANG) ///
                                              of iterations.
plotname(C:\MyProjects\TWANG \MultiTwangA
                                               Available choices
                                               include mean or
save C:\MyProjects\TWANG\subdata_wgts)
                                              max ES and
                                               mean or max KS
                                               statistics
```

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) //
estimand(C:\Program Files\R\R-3.0.1\bin interest (ATT or
objpath(C:\MyProjects\TWANG) ///
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)

save C:\MyProjects\TWANG\subdata_wgts)
```

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) / **
objpath(C:\MyProjects\TWANG) ///
                                                     Specifies
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)
                                                     the R
                                                     executable
save C:\MyProjects\TWANG\subdata_wgts)
                                                     by name
                                                     and path
```

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe)///
objpath(C:\MyProjects\TWANG) ///
                                                   Specifies
plotname(C:\MyProjects\TWANG\MultiTyangATE.pdf)
                                                   folder
                                                   where
save C:\MyProjects\TWANG\subdata_wgts)
                                                   outputted
                                                   data will
                                                   go
```

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe)///
objpath(C:\MyProjects\TWANG)///
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)
                                                       Specifies
                                                       name of
save C:\MyProjects\TWANG\subdata_wgts)
                                                       file where
```

7

diagnostic

plots will

go

use import delimited "C:\Data\subdata.csv", clear

```
mnps trtvar ///
age female i.race4g sfs sps sds ias ces eps imds bcs prmhtx ///
ntrees(5000) ///
stopmethod(es.max) ///
estimand(ATE) ///
rcmd(C:\Program Files\R\R-3.0.1\bin\R.exe) ///
objpath(C:\MyProjects\TWANG)///
plotname(C:\MyProjects\TWANG \MultiTwangATE.pdf)_
save C:\MyProjects\TWANG\subdata_wgts)
```

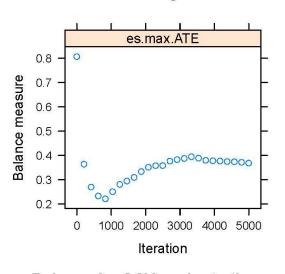
**Specifies** name of outputted dataset with ps weights

# Step 3: Evaluate the quality of the ps weights

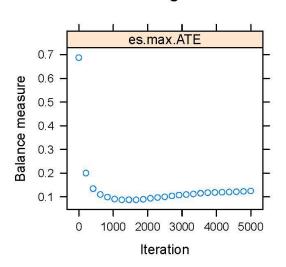
- Key issues that should be checked
  - Convergence = did the algorithm run long enough
  - Balance = how well matched the groups look after weighting
  - Overlap = whether there is evidence that the distributions of the pretreatment covariates in the groups line up well

### Step 3: Checking convergence

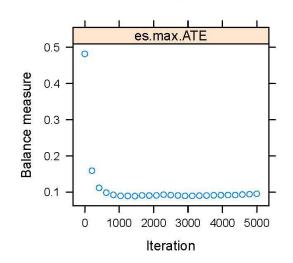
#### Balance for ATM against others



#### **Balance for EAT against others**



#### Balance for SCY against others



Note:

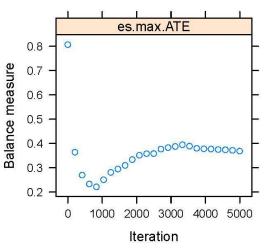
ATM = Usual care group

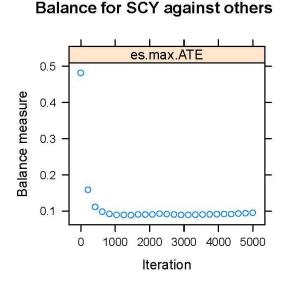
EAT = MET/CBT5 group

SCY = 3<sup>rd</sup> treatment grp

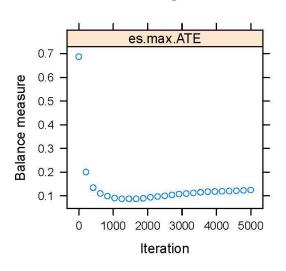
### Step 3: Checking convergence

#### Balance for ATM against others





#### Balance for EAT against others



There are three convergence plots because there are three GBM fits

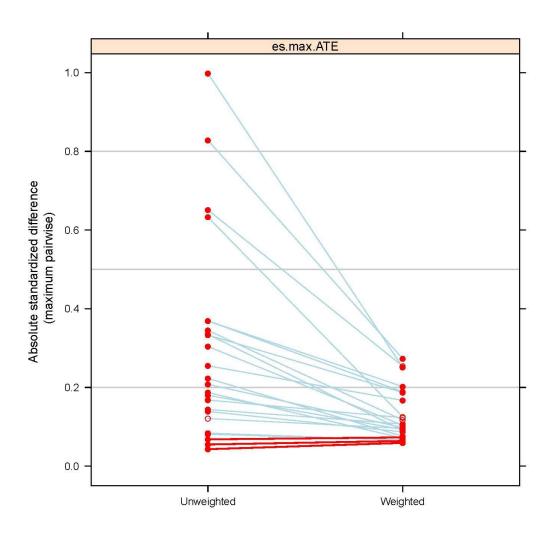
#### Step 3: Checking balance

- What does balance mean for more than 2 groups?
  - For ATE: All possible pairs of treatment conditions are balanced
  - For ATT: J-1 groups each balance with the target group of interest
- Multiple pairwise sets of balance metrics can be difficult to navigate if there are more than a 3 or 4 treatments, especially for ATE
  - There are J choose 2 pairs for ATE and J-1 for ATT
- Summarize over all pairs using the maximum of each pairwise balance metric for each covariate and then the maximum or mean across covariates
  - For p-values use the minimum

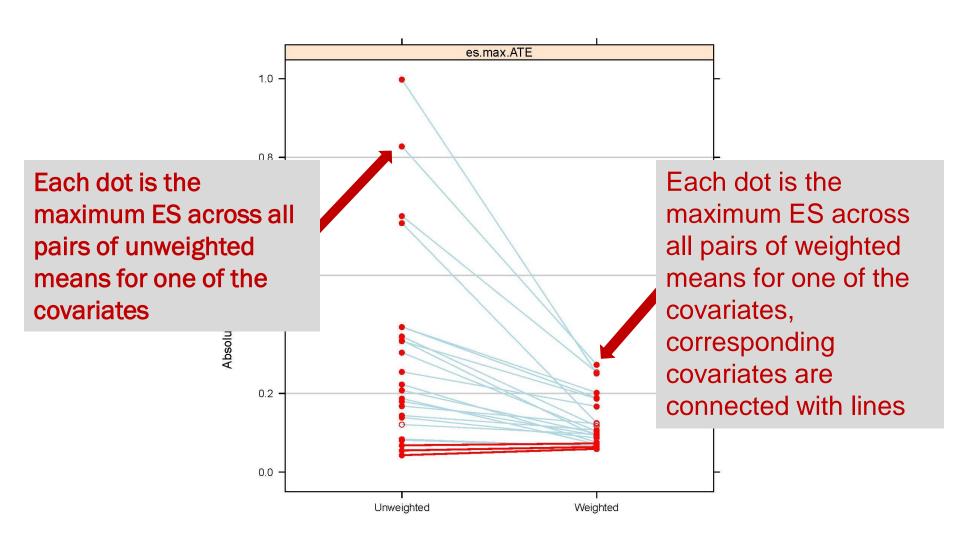
#### Step 3: Checking balance

- For more than 2 treatment groups, it is recommended to check balance across groups first and then to dive in if there appears to be a problem
- Summary measures one can use to assess balance in that first sweep
  - Maximum of the pairwise ES (or ASMDs)
  - Maximum of the pairwise KS or correspondingly the minimum of the pairwise KS statistic p-values
  - Also could use p-values from ANOVA's or joint F-tests to test if the means of the groups are different

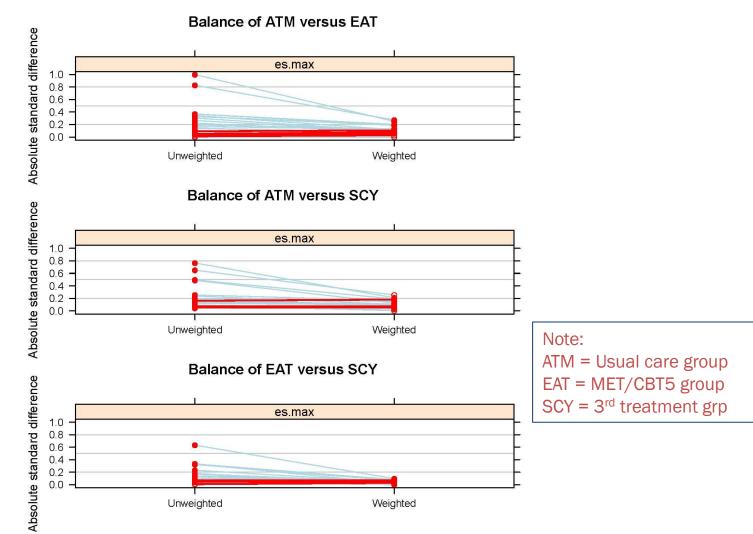
# Step 3: Checking balance graphically – Maximum ES plot



## Step 3: Checking balance graphically – Maximum ES plot



# Step 3: Checking balance graphically – Pairwise ES plots



### Stata Code for ES plots

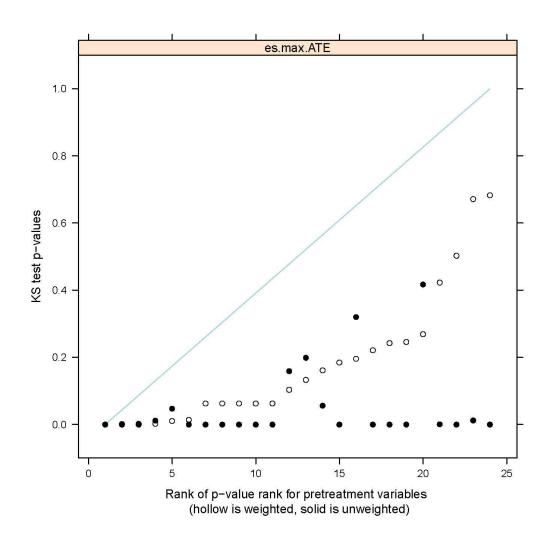
#### Maximum plot

mnplot, plotname(mnps\_example\_plot\_es\_max.pdf) plots(3)

#### Pairwise plots

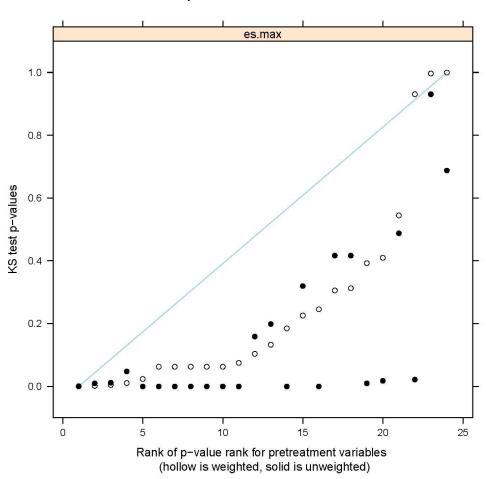
mnplot, plotname(mnps\_example\_plot\_es\_pairwise.pdf) ///
plots(3) nopairwisemax figurerows(3)

## Step 3: Checking balance graphically – Minimum KS p-values plot



# Step 3: Checking balance graphically – Pairwise KS plots





### Stata Code for KS plots

#### Maximum plot

```
mnplot, plotname(mnps_example_plot_ks_max.pdf) ///
plots(5)
```

#### Pairwise plots

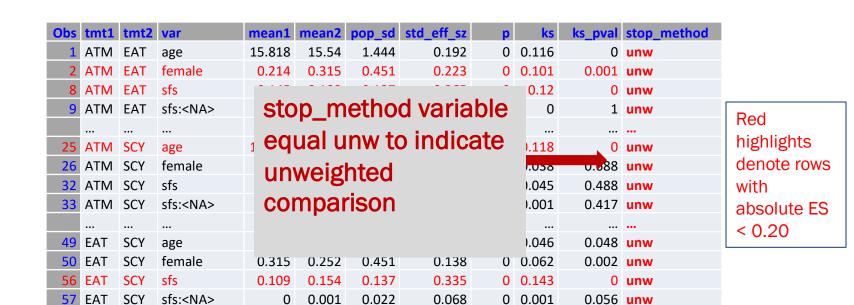
```
mnplot, plotname(mnps_example_plot_ks_pairwise.pdf) ///
plots(5) nopairwisemax ///
multipage singleplot(2)
```

# Step 3: Checking balance with tables: Unweighted pairwise balance table

Obs	tmt1	tmt2	var	mean1	mean2	pop sd	std eff sz	р	ks	ks_pval	stop_method
1	ATM	EAT	age	15.818	15.54	1.444	0.192	0	0.116	0	unw
2	ATM	EAT	female	0.214	0.315	0.451	0.223	0	0.101	0.001	unw
8	ATM	EAT	sfs	0.145	0.109	0.137	0.265	0	0.12	0	unw
9	ATM	EAT	sfs: <na></na>	0	0	0.022	0	1	0	1	unw
25	ATM	SCY	age	15.818	15.45	1.444	0.255	0	0.118	0	unw
26	ATM	SCY	female	0.214	0.252	0.451	0.085	0.092	0.038	0.688	unw
32	ATM	SCY	sfs	0.145	0.154	0.137	0.07	0.235	0.045	0.488	unw
33	ATM	SCY	sfs: <na></na>	0	0.001	0.022	0.068	0	0.001	0.417	unw
											***
49	EAT	SCY	age	15.54	15.45	1.444	0.062	0.057	0.046	0.048	unw
50	EAT	SCY	female	0.315	0.252	0.451	0.138	0	0.062	0.002	unw
56	EAT	SCY	sfs	0.109	0.154	0.137	0.335	0	0.143	0	unw
57	EAT	SCY	sfs: <na></na>	0	0.001	0.022	0.068	0	0.001	0.056	unw

Red highlights denote rows with absolute ES < 0.20

### Unweighted pairwise balance table for AOP example



### Unweighted pairwise balance table for AOP example

Obs	tmt1	tmt2	var	mean1	mean2	pop_sd	std_eff_sz	р	ks	ks_pval	stop_method
1	ATM	EAT	age	15.818	15.54	1.444	0.192	0	0.116	0	unw
2	<b>ATM</b>	<b>EAT</b>	female	0.214	0.315	0.451	0.223	0	0.101	0.001	unw
8	<b>ATM</b>	<b>EAT</b>	sfs 💮	0.145	0.109	0.137	0.265	0	0.12	0	unw
9	<b>ATM</b>	<b>EAT</b>	sfs: <na></na>	0	0	0.022	0	1	0	1	unw
						aa dr	oun of				
25	<b>ATM</b>	SCY	age	15.818		ie gr	oup of			0	unw
26	<b>ATM</b>	SCY	female	0.214	O CC	mna	risons	for		0.688	unw
32	<b>ATM</b>	SCY	sfs	U.2 .U				_		0.488	unw
33	<b>ATM</b>	SCY	sfs: <na></na>	0	o <b>e</b> a	ach g	roup o	t		0.417	unw
					tre	eatm	onte .				•••
49	<b>EAT</b>	SCY	age	1 04	1	<del>s</del> aum	CIILO			0.048	unw
50	EAT	SCY	female	0.315	0.252	0.451	0.138	0	0.062	0.002	unw
56	EAT	SCY	sfs	0.109	0.154	0.137	0.335	0	0.143	0	unw
57	EAT	SCY	sfs: <na></na>	0	0.001	0.022	0.068	0	0.001	0.056	unw

Red highlights denote rows with absolute ES < 0.20

# Step 3: Checking balance with tables: Weighted pairwise balance table

Obs	tmt1	tmt2	var	mean1	mean2	pop_sd	std_eff_sz	р	ks	ks_pval	stop_method
73	ATM	EAT	age	15.736	15.547	1.444	0.131	0.069	0.077	0.364	es.max
74	ATM	EAT	female	0.267	0.302	0.451	0.076	0.356	0.034	0.994	es.max
80	ATM	EAT	sfs	0.135	0.123	0.137	0.091	0.257	0.069	0.503	es.max
81	ATM	EAT	sfs: <na></na>	0	0	0.022	0	1	0	1	es.max
97	ATM	SCY	age	15.736	15.495	1.444	0.167	0.025	0.088	0.246	es.max
98	ATM	SCY	female	0.267	0.269	0.451	0.004	0.965	0.002	1	es.max
104	ATM	SCY	sfs	0.135	0.125	0.137	0.073	0.373	0.068	0.544	es.max
105	ATM	SCY	sfs: <na></na>	0	0.002	0.022	0.073	0	0.002	0.306	es.max
											•••
121	EAT	SCY	age	15.547	15.495	1.444	0.036	0.31	0.025	0.742	es.max
122	EAT	SCY	female	0.302	0.269	0.451	0.073	0.053	0.033	0.424	es.max
128	EAT	SCY	Sfs	0.123	0.125	0.137	0.018	0.605	0.019	0.957	es.max
129	EAT	SCY	sfs: <na></na>	0	0.002	0.022	0.073	0	0.002	0.162	es.max

Red highlights denote rows with absolute ES < 0.20

### Step 3: Checking balance with tables: Unweighted covariate balance table

#### Balance table: unw

Obsvar	max_std_ eff_sz	min_p	max_ks	min_ks_pval	stop_method
1 age	0.255	0	0.118	0	unw
2 female	0.223	0	0.101	0.001	unw
3 race4g:1	0.651	0	0.324	0	unw
4 race4g:2	0.633	0	0.235	0	unw
5 race4g:3	0.345	0	0.144	0	unw
6 race4g:4	0.208	0	0.076	0	unw
7 race4g: <na></na>	0.139	0	0.002	0	unw
8 sfs	0.335	0	0.143	0	unw
9 sfs: <na></na>	0.068	0	0.001	0.056	unw
10 sps	0.369	0	0.141	0	unw
11 sps: <na></na>	0.043	0	0.001	0.417	unw
12 sds	0.333	0	0.147	0	unw
13 sds: <na></na>	0.18	0	0.015	0	unw
14 ias	0.998	0	0.485	0	unw
15 ias: <na></na>	0.144	0	0.014	0.012	unw
16 ces	0.828	0	0.262	0	unw
17 eps	0.369	0	0.186	0	unw
18 eps: <na></na>	0.081	0	0.004	0.199	unw
19 imds	0.187	0	0.081	0	unw
20 imds: <na></na>	0.055	0	0.002	0.32	unw
21 bcs	0.304	0	0.177	0	unw
22 bcs: <na></na>	0.084	0	0.004	0.159	unw
23 prmhtx	0.168	0.001	0.082	0.012	unw
24 prmhtx: <na></na>	0.121	0.051	0.011	0.047	unw

Red highlights denote rows with absolute ES < 0.20

### Step 3: Checking balance with tables: Weighted covariate balance table

#### Balance table: es.max

Obsvar	max_std_ eff_sz	min_p	max_ks	min_ks_pval	stop_method
25 age	0.167	0.025	0.088	0.246	es.max
26 female	0.076	0.053	0.034	0.424	es.max
27 race4g:1	0.254	0.063	0.126	0.063	es.max
28 race4g:2	0.125	0.063	0.046	0.063	es.max
29 race4g:3	0.117	0.063	0.049	0.063	es.max
30 race4g:4	0.098	0.063	0.036	0.063	es.max
31 race4g: <na></na>	0.087	0.063	0.001	0.063	es.max
32 sfs	0.091	0.257	0.069	0.503	es.max
33 sfs: <na></na>	0.073	0	0.002	0.162	es.max
34 sps	0.189	0.044	0.085	0.243	es.max
35 sps: <na></na>	0.059	0	0.002	0.269	es.max
36 sds	0.187	0.053	0.087	0.221	es.max
37 sds: <na></na>	0.093	0	0.008	0.002	es.max
38 ias	0.251	0.004	0.176	0	es.max
39 ias: <na></na>	0.107	0	0.01	0.002	es.max
40 ces	0.273	0	0.154	0.002	es.max
41 eps	0.202	0.012	0.132	0.014	es.max
42 eps: <na></na>	0.067	0	0.003	0.133	es.max
43 imds	0.071	0.242	0.046	0.68	es.max
44 imds: <na></na>	0.064	0	0.003	0.196	es.max
45 bcs	0.104	0.233	0.094	0.184	es.max
46 bcs: <na></na>	0.066	0	0.003	0.104	es.max
47 prmhtx	0.123	0.153	0.06	0.672	es.max
48 prmhtx: <na></na>	0.096	0.035	0.009	0.011	es.max

Red highlights denote rows with absolute ES < 0.20

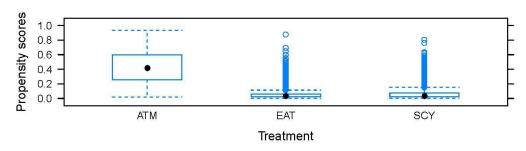
# Step 3: Checking balance with tables

Stata code for previous 2 tables

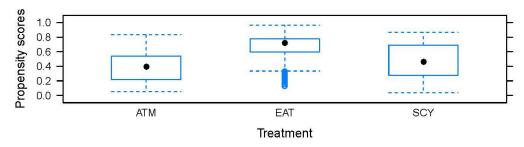
**balance**, unweighted weighted collapseto(covariate)

### Step 3: Checking overlap

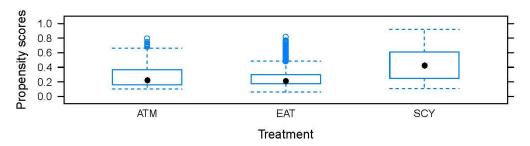
#### ATM propensity scores by Tx group



#### EAT propensity scores by Tx group



SCY propensity scores by Tx group



# Step 4: Estimate the treatment effect

#### **Stata Code:**

use C:\MyProjects\TWANG \subdata\_wgts, clear
endcode trtvar, generate(trtvar2)
svyset [pweight=esmaxate]

fvset base 1 trtvar2

svy: regress sfs8p12 i.trtvar2

**Estimated Regression Coefficients** 

		6. 1.15		D. 111
Parameter	Estimate	Standard Error	t Value	Pr >  t
Intercept	0.111	0.013	8.81	<.0001
metcbt5	-0.039	0.013	-3	0.0027
scy	-0.036	0.013	-2.72	0.0065

# Step 4: Estimate the treatment effect (cont.)

#### **Stata Code:**

use C:\MyProjects\TWANG \subdata\_wgts, clear
endcode trtvar, generate(trtvar2)

svyset [pweight=esmaxate]

**fvset** base 1 trtvar2

svy: regress sfs8p12 i.trtvar2

#### **Estimated Regression Coefficients**

		Standard		
Parameter	Estimate	Error	t Value	<b>Pr &gt;  t </b>
Intercept	0.111	0.013	8.81	<.0001
metcbt5	-0.039	0.013	-3	0.0027
scy	-0.036	0.013	-2.72	0.0065

Results show that youth would have fared better had they received either MET/CBT5 or SCY vs "usual care"

# Comparison with unweighted treatment effect

#### **Stata Code:**

regress sfs8p12 i.trtvar2

### Parameter Estimates Parameter Standard

			Standard		
<b>Parameter</b>	DF	<b>Estimate</b>	Error	t Value	Pr >  t
Intercept	1	0.114	0.006	19.83	<.0001
metcbt5	1	-0.047	0.006	-7.52	<.0001
scy	1	-0.038	0.007	-5.65	<.0001

# Comparison with unweighted treatment effect

#### **Stata Code:**

regress sfs8p12 i.trtvar2

### Parameter Estimates Parameter Standard

			Standard		
<b>Parameter</b>	DF	<b>Estimate</b>	Error	t Value	Pr >  t
Intercept	1	0.114	0.006	19.83	<.0001
metcbt5	1	-0.047	0.006	-7.52	<.0001
scy	1	-0.038	0.007	-5.65	<.0001

Similar evidence, though magnitude of the effect for MET/CBT5 vs usual care changes the most, likely because greatest pretreatment differences between MET/CBT5 and usual care

# Step 4: Doubly robust estimation Adding in covariates with lingering imbalances

#### **Stata Code:**

use C:\MyProjects\TWANG \subdata\_wgts, clear
endcode trtvar, generate(trtvar2)
svyset [pweight=esmaxate]
fvset base 1 trtvar2
svy: regress sfs8p12 i.trtvar2 ces eps ias i.race4g

#### **Estimated Regression Coefficients**

		Standard		
Parameter	<b>Estimate</b>	Error	t Value	Pr >  t
Intercept	0.072	0.015	4.83	<.0001
metcbt5	-0.032	0.014	-2.38	0.0173
scy	-0.030	0.014	-2.22	0.0262
ces	-0.003	0.014	-0.25	0.8042
eps	0.048	0.020	2.35	0.0190
ias	0.128	0.027	4.79	<.0001
race4g 1	0.012	0.007	1.65	0.0993
race4g 2	-0.008	0.008	-0.99	0.3200
race4g 3	0.021	0.011	2.00	0.0451
race4g 4	0.000	0.000		

### Conclusions

- Propensity score weights improved balance on observed pretreatment covariates
- Greatest changes in treatment effect estimate comparing MET/CBT5 vs usual care
  - Likely because group of youth were more dissimilar than SCY vs usual care
- Doubly robust model which controlled for lingering imbalances provides our most robust inferences concerning causal effects





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