## 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

<table>
<thead>
<tr>
<th>MET/CBT5</th>
<th>“Usual Care”</th>
<th>SCY</th>
</tr>
</thead>
<tbody>
<tr>
<td>- Observational</td>
<td>- Observational</td>
<td>- Observational</td>
</tr>
<tr>
<td>- MET/CBT5 at 37 EAT sites</td>
<td>- “Usual care” at 4 ATM sites</td>
<td>- Community strengthening at 8 SCY sites</td>
</tr>
<tr>
<td>- N = 2459</td>
<td>- N = 444</td>
<td>- N = 1351</td>
</tr>
</tbody>
</table>
How do we get a causal effect estimate?
How do we get a causal effect estimate?

When on Treatment A
How do we get a causal effect estimate?

- **Pre-Treatment**: When on Treatment A
- **Post-Treatment**: When on Treatment B

Y-axis: Good to Bad

Graph showing the change in outcomes before and after treatment, comparing Treatment A and Treatment B.
How do we get a causal effect estimate?
How do we get a causal effect estimate?

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 $1, \ldots, J = Y_1, \ldots, Y_J$

• $Y_1, \ldots, Y_J$ 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?*
    
    – $E(Y_1 - Y_2 | Z=1), E(Y_1 - Y_3 | Z=1), ..., E(Y_1 - Y_J | Z=1)$
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?
    – $E(Y_1 - Y_2|Z=1), E(Y_1 - Y_3|Z=1), ..., E(Y_1 - Y_J|Z=1)$
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 $p_{↓j↑^*}(X)/p_j(X)$
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
Command to estimate ps weights in SAS

```sas
%mnps(treatvar=trtvar,
    vars=age female race4g sfs sps sds ias ces eps
    imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```
%mnps(treatvar=trtvar, vars=age female race4g sfs sps sds imds bcs prmhtx, class = race4g, dataset=sasin.subdata, ntrees=5000, stopmethod=es.max, estimand = ATE, treatatt = NULL, output_dataset=subdata_wgts, Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe, plotname=multi_twang_ate.pdf, objpath=C:\Users\bethg\Documents\TWANG\SAS work);
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plotname=multi_twang_ate.pdf,
objpath=C:\Users\bethg\Documents\TWANG\SAS work);
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vars=age female race4g sfs sps sds ias ces eps
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dataset=sasin.subdata,
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stopmethod=es.max,
estimand = ATE,
treatatt = NULL,
output_dataset=subdata_wgts,
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
plotname=multi_twang_ate.pdf,
objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Command to estimate ps weights in SAS

```plaintext
%mnps(treatvar=trtvar,
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    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```

Specifies name of dataset
%mnps(treatvar=trtvar,
   vars=age female race4g sfs sps sds ias ces eps
   imds bcs prmhtx,
   class = race4g,
   dataset=sasin.subdata,
   ntrees=5000,    
   stopmethod=es.max,
   estimand = ATE,
   treatatt = NULL,
   output_dataset=subdata_wgts,
   Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
   plotname=multi_twang_ate.pdf,
   objpath=C:\Users\bethg\Documents\TWANG\SAS work);

Specifies the maximum number of iterations used by GBM. Should be large (5000 to 10000)
Command to estimate ps weights in SAS

\%mnps(treatvar=trtvar,
    vars=age female race4g sfs sps sds ias ces eps
        imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
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    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Command to estimate ps weights in SAS

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%mnps(treatvar=trtvar,
    vars=age female race4g sfs sps sds ias ces eps
        imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
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    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```

Specifies primary estimand of interest (ATT or ATE)
Command to estimate ps weights in SAS

```sas
%mnpstreatvar=trtvar,
   vars=age female race4g sfs sps sds ias ces eps
   imds bcs prmhtx,
   class = race4g,
   dataset=sasin.subdata,
   ntrees=5000,
   stopmethod=es.max,
   estimand = ATE,
   treatatt = NULL,
   output_dataset=subdata_wgts,
   Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
   plotname=multi_twang_ate.pdf,
   objpath=C:\Users\bethg\Documents\TWANG\SAS work); 
```

Specifies which treatment condition is considered “the treated” for estimating ATTs
Command to estimate ps weights in SAS

```
%mnps(treatvar=trtvar,
    vars=age female race4g sfs sps sds ias ces eps
         imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```

Specifies name of outputted dataset with ps weights
%mnps(treatvar=trtvar,
   vars=age female race4g sfs sps sds ias ces eps
   imds bcs prmhtx,
   class = race4g,
   dataset=sasin.subdata,
   ntrees=5000,
   stopmethod=es.max,
   estimand = ATE,
   treatatt = NULL,
   output_dataset=subdata_wgts,
   Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
   plotname=multi_twang_ate.pdf,
   objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Command to estimate ps weights in SAS

%mnps(treatvar=trtvar,
    vars=age female race4g sfs sps sds ias ces eps
    imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Command to estimate ps weights in SAS

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    vars=age female race4g sfs sps sds ias ces eps
        imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATE,
    treatatt = NULL,
    output_dataset=subdata_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=multi_twang_ate.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
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 measure

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0

1000 2000 3000 4000 5000

Balance for SCY against others

Balance measure

0.5
0.4
0.3
0.2
0.1
0

1000 2000 3000 4000 5000

Balance for EAT against others

Balance measure

0.7
0.6
0.5
0.4
0.3
0.2
0.1
0

1000 2000 3000 4000 5000

Note:
ATM = Usual care group
EAT = MET/CBT5 group
Step 3: Checking convergence

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

Each dot is the maximum ES across all pairs of unweighted means for one of the covariates

Each dot is the maximum ES across all pairs of weighted means for one of the covariates, corresponding covariates are connected with lines
Step 3: Checking balance graphically – Pairwise ES plots

Balance of ATM versus EAT

Balance of ATM versus SCY

Balance of EAT versus SCY

Note:
ATM = Usual care group
EAT = MET/CBT5 group
Sas Code for ES plots

**Maximum plot**

```sas
%mnplot(inputobj=mnps.RData, plotname=mnps_example_plot_es_max.pdf, plotformat=pdf, plots=3, pairwisemax=TRUE, Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe, objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```

**Pairwise plots**

```sas
%mnplot(inputobj=mnps.RData, plotname=mnps_example_plot_es_pairwise.pdf, plotformat=pdf, plots=3, pairwisemax=FALSE, figurerows=3, Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe, objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```
Step 3: Checking balance graphically
– Minimum KS p-values plot
Step 3: Checking balance graphically – Pairwise KS plots
Sas Code for KS plots

Maximum plot

%%%mnplot(inputobj=mnps.RData,
plotname=mnps_example_plot_ks_max.pdf,
plotformat=pdf,
plots=5,
pairwisemax=TRUE,
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
objpath=C:\Users\bethg\Documents\TWANG\SAS work);

Pairwise plots

%%%mnplot(inputobj=mnps.RData,
plotname=mnps_example_plot_ks_pairwise.pdf,
plotformat=pdf,
plots=5,
pairwisemax=FALSE,
multipage=TRUE,
singleplot=2,
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Step 3: Checking balance with tables: Unweighted pairwise balance table

<table>
<thead>
<tr>
<th>Obs</th>
<th>tmt1</th>
<th>tmt2</th>
<th>var</th>
<th>mean1</th>
<th>mean2</th>
<th>pop_sd</th>
<th>std_eff_sz</th>
<th>p</th>
<th>ks</th>
<th>ks_pval</th>
<th>stop_method</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ATM</td>
<td>EAT</td>
<td>age</td>
<td>15.818</td>
<td>15.54</td>
<td>1.444</td>
<td>0.192</td>
<td>0</td>
<td>0.116</td>
<td>0</td>
<td>unw</td>
</tr>
<tr>
<td>2</td>
<td>ATM</td>
<td>EAT</td>
<td>female</td>
<td>0.214</td>
<td>0.315</td>
<td>0.451</td>
<td>0.223</td>
<td>0</td>
<td>0.101</td>
<td>0.001</td>
<td>unw</td>
</tr>
<tr>
<td>8</td>
<td>ATM</td>
<td>EAT</td>
<td>sfs</td>
<td>0.145</td>
<td>0.109</td>
<td>0.137</td>
<td>0.265</td>
<td>0</td>
<td>0.12</td>
<td>0</td>
<td>unw</td>
</tr>
<tr>
<td>9</td>
<td>ATM</td>
<td>EAT</td>
<td>sfs:&lt;NA&gt;</td>
<td>0</td>
<td>0</td>
<td>0.022</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>unw</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
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<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>25</td>
<td>ATM</td>
<td>SCY</td>
<td>age</td>
<td>15.818</td>
<td>15.45</td>
<td>1.444</td>
<td>0.255</td>
<td>0</td>
<td>0.118</td>
<td>0</td>
<td>unw</td>
</tr>
<tr>
<td>26</td>
<td>ATM</td>
<td>SCY</td>
<td>female</td>
<td>0.214</td>
<td>0.252</td>
<td>0.451</td>
<td>0.085</td>
<td>0.092</td>
<td>0.038</td>
<td>0.688</td>
<td>unw</td>
</tr>
<tr>
<td>32</td>
<td>ATM</td>
<td>SCY</td>
<td>sfs</td>
<td>0.145</td>
<td>0.154</td>
<td>0.137</td>
<td>0.07</td>
<td>0.235</td>
<td>0.045</td>
<td>0.488</td>
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<tr>
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<td>ATM</td>
<td>SCY</td>
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<td>0.001</td>
<td>0.417</td>
<td>unw</td>
</tr>
<tr>
<td>...</td>
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<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>49</td>
<td>EAT</td>
<td>SCY</td>
<td>age</td>
<td>15.54</td>
<td>15.45</td>
<td>1.444</td>
<td>0.062</td>
<td>0.057</td>
<td>0.046</td>
<td>0.048</td>
<td>unw</td>
</tr>
<tr>
<td>50</td>
<td>EAT</td>
<td>SCY</td>
<td>female</td>
<td>0.315</td>
<td>0.252</td>
<td>0.451</td>
<td>0.138</td>
<td>0</td>
<td>0.062</td>
<td>0.002</td>
<td>unw</td>
</tr>
<tr>
<td>56</td>
<td>EAT</td>
<td>SCY</td>
<td>sfs</td>
<td>0.109</td>
<td>0.154</td>
<td>0.137</td>
<td>0.335</td>
<td>0</td>
<td>0.143</td>
<td>0</td>
<td>unw</td>
</tr>
<tr>
<td>57</td>
<td>EAT</td>
<td>SCY</td>
<td>sfs:&lt;NA&gt;</td>
<td>0</td>
<td>0.001</td>
<td>0.022</td>
<td>0.068</td>
<td>0</td>
<td>0.001</td>
<td>0.056</td>
<td>unw</td>
</tr>
</tbody>
</table>

Note: ATM = Usual care group; EAT = MET/CBT5 group

Red highlights denote rows with absolute ES < 0.20
### Unweighted pairwise balance table for AOP example

<table>
<thead>
<tr>
<th>Obs</th>
<th>tmt1</th>
<th>tmt2</th>
<th>var</th>
<th>mean1</th>
<th>mean2</th>
<th>pop_sd</th>
<th>std_eff_sz</th>
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<td>0.101</td>
<td>0</td>
<td>0</td>
<td>unw</td>
</tr>
<tr>
<td>8</td>
<td>ATM</td>
<td>EAT</td>
<td>sfs</td>
<td>0.145</td>
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Stop_method variable: equal unw to indicate unweighted comparison. Red highlights denote rows with absolute ES < 0.20.

Note: ATM = Usual care group; EAT = MET/CBT5 group
## Unweighted pairwise balance table for AOP example

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<th>mean2</th>
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</tbody>
</table>

**Note:** ATM = Usual care group; EAT = MET/CBT5 group

Red highlights denote rows with absolute ES < 0.20

**One group of comparisons for each group of treatments**
## Step 3: Checking balance with tables: Weighted pairwise balance table

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<tr>
<th>Obs</th>
<th>tmt1</th>
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<th>mean2</th>
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</table>

Red highlights denote rows with absolute ES < 0.20

Note: ATM = Usual care group; EAT = MET/CBT5 group
### Step 3: Checking balance with tables: Unweighted covariate balance table

**Balance table: unw**

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Red highlights denote rows with absolute ES < 0.20
Step 3: Checking balance with tables: Weighted covariate balance table

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<td>26 female</td>
<td>0.076</td>
<td>0.053</td>
<td>0.034</td>
<td>0.424</td>
<td>es.ma</td>
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<tr>
<td>40 ces</td>
<td>0.273</td>
<td>0</td>
<td>0.154</td>
<td>0.002</td>
<td>es.ma</td>
</tr>
<tr>
<td>41 eps</td>
<td>0.202</td>
<td>0.012</td>
<td>0.132</td>
<td>0.014</td>
<td>es.ma</td>
</tr>
<tr>
<td>42 eps: &lt;NA&gt;</td>
<td>0.067</td>
<td>0</td>
<td>0.003</td>
<td>0.133</td>
<td>es.ma</td>
</tr>
<tr>
<td>43 imds</td>
<td>0.071</td>
<td>0.242</td>
<td>0.046</td>
<td>0.68</td>
<td>es.ma</td>
</tr>
<tr>
<td>44 imds: &lt;NA&gt;</td>
<td>0.064</td>
<td>0</td>
<td>0.003</td>
<td>0.196</td>
<td>es.ma</td>
</tr>
<tr>
<td>45 bcs</td>
<td>0.104</td>
<td>0.233</td>
<td>0.094</td>
<td>0.184</td>
<td>es.ma</td>
</tr>
<tr>
<td>46 bcs: &lt;NA&gt;</td>
<td>0.066</td>
<td>0</td>
<td>0.003</td>
<td>0.104</td>
<td>es.ma</td>
</tr>
<tr>
<td>47 prmhtx</td>
<td>0.123</td>
<td>0.153</td>
<td>0.06</td>
<td>0.672</td>
<td>es.ma</td>
</tr>
<tr>
<td>48 prmhtx: &lt;NA&gt;</td>
<td>0.096</td>
<td>0.035</td>
<td>0.009</td>
<td>0.011</td>
<td>es.ma</td>
</tr>
</tbody>
</table>

Red highlights denote rows with absolute ES < 0.20
Step 3: Checking balance with tables

SAS code for previous 2 tables

```sas
%mnbaltable(inputobj=mnps.RData,
collapseto=covariate,
Rcmd=C:\Program Files\R\R-3.0.1\bin\x64\R.exe,
objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```
Step 3: Checking balance with tables – Using es_cutoff

**Balance table: es.max**

<table>
<thead>
<tr>
<th>Obstmt1</th>
<th>tmt2</th>
<th>var</th>
<th>mean1</th>
<th>mean2</th>
<th>pop_sd</th>
<th>std_eff_sz</th>
<th>p</th>
<th>ks</th>
<th>ks_pval</th>
<th>stop_method</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATM</td>
<td>EAT</td>
<td>ias</td>
<td>0.137</td>
<td>0.103</td>
<td>0.137</td>
<td>0.251</td>
<td>0.004</td>
<td>0.176</td>
<td>0</td>
<td>es.max</td>
</tr>
<tr>
<td>ATM</td>
<td>EAT</td>
<td>ces</td>
<td>0.139</td>
<td>0.076</td>
<td>0.23</td>
<td>0.273</td>
<td>0</td>
<td>0.154</td>
<td>0.002</td>
<td>es.max</td>
</tr>
<tr>
<td>ATM</td>
<td>EAT</td>
<td>eps</td>
<td>0.257</td>
<td>0.218</td>
<td>0.193</td>
<td>0.202</td>
<td>0.012</td>
<td>0.132</td>
<td>0.014</td>
<td>es.max</td>
</tr>
<tr>
<td>ATM</td>
<td>SCY</td>
<td>race4g:1</td>
<td>0.577</td>
<td>0.45</td>
<td>0.498</td>
<td>0.254</td>
<td>0.063</td>
<td>0.126</td>
<td>0.063</td>
<td>es.max</td>
</tr>
<tr>
<td>ATM</td>
<td>SCY</td>
<td>ias</td>
<td>0.137</td>
<td>0.108</td>
<td>0.137</td>
<td>0.21</td>
<td>0.016</td>
<td>0.174</td>
<td>0.001</td>
<td>es.max</td>
</tr>
</tbody>
</table>

Note: ATM = Usual care group; EAT = MET/CBT5 group

**SAS Code:**

```sas
%mnbaltable(inputobj=mnps.RData,
   es_cutoff=.2,
   ks_cutoff=,
   p_cutoff=,
   ks_p_cutoff=,
   Rcmd=C:\Program Files\R\R-3.0.1\bin\x64\R.exe,
   objpath=C:\Users\bethg\Documents\TWANG\Sas work);
```
Step 3: Checking overlap

Note: ATM = Usual care group; EAT = MET/CBT5 group
Step 4: Estimate the treatment effect (cont.)

**SAS Code:**

```
proc surveyreg data=subdata_wgts;
  model sfs8p12 = metcbt5 scy;
  weight es_max_ate;
run;
```

**Estimated Regression Coefficients**

| 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.)

**SAS Code:**

```
proc surveyreg data=subdata_wgts;
model sfs8p12 = metcbt5 scy;
weight es_max_ate;
run;
```

| 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 |

Results show that youth would have fared better had they received either MET/CBT5 or SCY vs “usual care”
Comparison with unweighted treatment effect

SAS Code:

```
proc reg data=sasin.subdata;
model sfs8p12 = metcbt5 scy;
run;
```

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>0.114</td>
<td>0.006</td>
<td>19.83</td>
<td>&lt;.0001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>metcbt5</td>
<td>1</td>
<td>-0.047</td>
<td>0.006</td>
<td>-7.52</td>
<td>&lt;.0001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scy</td>
<td>1</td>
<td>-0.038</td>
<td>0.007</td>
<td>-5.65</td>
<td>&lt;.0001</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Comparison with unweighted treatment effect

**SAS Code:**

```sas
proc reg data=sasin.subdata;
model sfs8p12 = metcbt5 scy;
run;
```

| Parameter | DF | Estimate | Standard 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

SAS Code:

```sas
proc surveyreg data=subdata_wgts;
class race4g;
model sfs8p12 = metcbt5 scy ces eps ias race4g/solution;
weight es_max_ate;
where race4g ne "NA";
run;
```

| Parameter | Estimate | Standard 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
Please note this video is part of a three-part series. We encourage viewers to watch all three segments.
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  James Gazis                   Natalia Weil
  Andrew Morral                 Greg Ridgeway
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