Step-by-Step Guidelines for Propensity Score Weighting with Two Groups

Beth Ann Griffin
Daniel McCaffrey
Four key steps

1) Choose the primary treatment effect of interest (ATE or ATT)
2) Estimate propensity score (ps) weights
3) Evaluate the quality of the ps weights
4) Estimate the treatment effect
Case study

**Aim:** To estimate the causal effect of MET/CBT5 versus “usual care”

- Data from 2 SAMSHA CSAT discretionary grants

**MET/CBT5**
- Longitudinal, observational
- 37 sites from EAT study
- \( N = 2459 \)
- 2003/04 - 2007

**“Usual Care”**
- Longitudinal, observational
- 4 sites from ATM study
- \( N = 444 \)
- 1998-1999
Case study

- **Aim:** To estimate the causal effect of MET/CBT5 versus “usual care”
  - Data from 2 SAMSHA CSAT discretionary grants

**MET/CBT5**
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- Longitudinal, observational
- 4 sites from ATM study
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- 1998-1999

All youth assessed with the GAIN at baseline, 6 months, and 12 months
Selection exists: Various meaningful ways in which the groups differ
Step 1: Choose the primary treatment effect (ATE or ATT)

- Today, we chose to focus on estimating ATT
- Why?
  - Youth in the community are different from those targeted to receive MET/CBT5 in the EAT study
  - Thus, the policy question we want to address is How would youth like those receiving “usual care” in the community have fared had they received MET/CBT5?
Step 2: Estimate the ps weights

• Only 1 command needed for this step

• Binary treatment command in TWANG currently available in R, SAS and STATA
Command to estimate ps weights in SAS

%ps(treatvar=atm,
    vars=age female race4g sfs sps sds ias ces eps
        imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata_twogrp,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATT,
    output_dataset=subdata_twogrp_att_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=binary_twang_att.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
%ps(treatvar=atm, 
vars=age female race4g sfs sps sds idm dsd imds bcs prmhtx, 
class = race4g, 
dataset=sasin.subdata_twogrp, 
tag=5000, 
stopmethod=es.max, 
estimand = ATT, 
output_dataset=subdata_twogrp_att_wgts, 
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe, 
plotname=binary_twang_att.pdf, 
objpath=C:\Users\bethg\Documents\TWANG\SAS work);
Command to estimate ps weights in SAS

```r
%ps(treatvar=atm,
    vars=age female race4g sfs sps sds ias ces eps
     imds bcs pmh
    class = race4g,
    dataset=sasin.subdata_twogrp,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATT,
    output_dataset=subdata_twogrp_att_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=binary_twang_att.pdf,
    objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```
Command to estimate ps weights in SAS

```sas
%ps(treatvar=atm,
     vars=age female race4g sfs sps sds ias ces eps
        imds bcs prmhtx,
     class = race4g,
     dataset=sasin.subdata_twogrp,
     ntrees=5000,
     stopmethod=es.max,
     estimand = ATT,
     output_dataset=subdata_twogrp_att_wgts,
     Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
     plotname=binary_twang_att.pdf,
     objpath=C:\Users\bethg\Documents\TWANG\SAS work);
```

Specifies which pretreatment variables are categorical.
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_twogrp,
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    stopmethod=es.max,
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vars=age female race4g sfs sps sds ias ces eps
imds bcs prmhtx,
class = race4g,
dataset=sasin.subdata_twogrp,
ntrees=5000, \(\textbf{\textcolor{red}{Stop Method}}\),
stopmethod=es.max,
estimand = ATT,
output_dataset=subdata_twogrp_att_wgts,
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
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Command to estimate ps weights in SAS

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vars=age female race4g sfs sps sds ias ces eps imds bcs prmhtx,
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estimand = ATT,
output_dataset=subdata_twogrp_att;
Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
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objpath=C:\Users\bethg\Documents\TWANG\SAS work);

Specifies the criteria for choosing the optimal number of iterations. Available choices include mean or max ES and mean or max KS statistics
%ps(treatvar=atm, 
    vars=age female race4g sfs sps sds ias ces eps 
    imds bcs prmhtx, 
    class = race4g, 
    dataset=sasin.subdata_twogrp, 
    ntrees=5000, 
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\%

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vars=age female race4g sfs sps sds ias ces eps
     imds bcs prmhtx,
\texttt{class = race4g,}
\texttt{dataset=sasin.subdata_twogrp,}
\texttt{ntrees=5000,}
\texttt{stopmethod=es.max,}
\texttt{estimand = ATT,}
\texttt{output_dataset=subdata_twogrp_att_wgts,}
\texttt{Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,}
\texttt{plotname=binary_twang_att.pdf,}
\texttt{objpath=C:\Users\bethg\Documents\TWANG\SAS work);}

\textbf{Specifies name of outputted dataset with ps weights}
Command to estimate ps weights in SAS

%ps(treatvar=atm,
    vars=age female race4g sfs sps sds ias ces eps imds bcs prmhtx,
    class = race4g,
    dataset=sasin.subdata_twogrp,
    ntrees=5000,
    stopmethod=es.max,
    estimand = ATT,
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    dataset=sasin.subdata_twogrp,
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    stopmethod=es.max,
    estimand = ATT,
    output_dataset=subdata_twogrp_att_wgts,
    Rcmd=C:\Program Files\R\R-3.0.1\bin\R.exe,
    plotname=binary_twang_att.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 two groups look after weighting
  – **Overlap** = whether there is evidence that the distributions of the pretreatment covariates in the two groups line up well
Step 3: Checking convergence

Bad Convergence

Good Convergence
Step 3: Checking balance

• TWANG has numerous diagnostics for assessing balance
Step 3: Checking balance with tables
### Step 3: Checking balance with tables

**Unweighted balance table**

<table>
<thead>
<tr>
<th>Obs</th>
<th>row_name</th>
<th>tx_mn</th>
<th>tx_sd</th>
<th>ct_mn</th>
<th>ct_sd</th>
<th>std_eff_sz</th>
<th>stat</th>
<th>p</th>
<th>ks</th>
<th>ks_pval</th>
<th>table_name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>unw.age</td>
<td>15.82</td>
<td>1.09</td>
<td>15.54</td>
<td>1.57</td>
<td>0.26</td>
<td>4.59</td>
<td>0.00</td>
<td>0.12</td>
<td>0.00</td>
<td>unw</td>
</tr>
<tr>
<td>2</td>
<td>unw.female</td>
<td>0.21</td>
<td>0.41</td>
<td>0.32</td>
<td>0.47</td>
<td>-0.25</td>
<td>-4.67</td>
<td>0.00</td>
<td>0.10</td>
<td>0.00</td>
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<td>0.08</td>
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<td>0.00</td>
<td>0.05</td>
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<td>.</td>
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<td>0.00</td>
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<td>0.00</td>
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<td>0.14</td>
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<td>0.09</td>
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<td>0.37</td>
<td>7.27</td>
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<td>0.19</td>
<td>0.00</td>
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<tr>
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<td>-0.04</td>
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<td>-0.04</td>
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</tbody>
</table>
## Step 3: Checking balance with tables

### Unweighted balance table

**Balance table: unw**

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<tr>
<td>1</td>
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<td>4.27</td>
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Red highlights denote rows with absolute ES < 0.20
### Step 3: Checking balance with tables

**Weighted balance table**

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</table>

Red highlights denote rows with absolute ES < 0.20.
Step 3: Checking balance graphically
Step 3: Checking balance graphically
ES plot
Step 3: Checking balance graphically

ES plot

Want as many dots as possible to go below 0.20 after weighting
Step 3: Checking balance graphically

KS plot

Plot 5 (ks): K-S P-values of Group Distns of Covariates

KS test p-values vs. Rank of p-value rank for pretreatment variables
(hollow is weighted, solid is unweighted)
Step 3: Checking balance graphically

KS plot

Plot 5 (ks): K–S P–values of Group Distns of Covariates

Solid dots = unweighted p-values. Note many less than 0.05
Step 3: Checking balance graphically

KS plot

Open dots = weighted p-values. Note getting larger and moving towards the diagonal line.

Solid dots = unweighted p-values. Note many less than 0.05.
Step 3: Checking overlap
Note: We haven’t even begun to talk about the outcome yet
- Steps 1 to 3 do not involve any outcomes
- We first focus on dealing with selection/pre-treatment group differences
- Then, if we do a good job, we will move to outcome analyses
Step 4: Estimate the treatment effect

- Estimate as difference in propensity score weighted means between the two groups of interest
  - Since we are using weights, we need to adjust our standard errors for the weighting
  - Analogous to fitting regression models with survey data with survey weights
Step 4: Estimate the treatment effect

• Estimate as difference in propensity score weighted means between the two groups of interest
  – Since we are using weights, we need to adjust our standard errors for the weighting
  – Analogous to fitting regression models with survey data with survey weights

We can use survey analysis commands in any software to estimate treatment effects
Step 4: Estimate the treatment effect (cont.)

SAS Code:

```sas
proc surveyreg data=subdata_twogrp_att_wgts;
model sfs8p12 = metcbt5;
weight es_max_att;
run;
```

**PS Weighted Regression Coefficients**

| Parameter     | Estimate | Standard Error | t Value | Pr > |t| |
|---------------|----------|----------------|---------|------|---|
| Intercept     | 0.114    | 0.007          | 17.13   | <.0001 |
| metcbt5       | -0.020   | 0.009          | -2.17   | 0.0304 |
Step 4: Estimate the treatment effect (cont.)

SAS Code:

```
proc surveyreg data=subdata_twogrp_att_wgts;
model sfs8p12 = metcbt5;
weight es_max_att;
run;
```

**PS Weighted Regression Coefficients**

| Parameter | Estimate | Standard Error | t Value | Pr > |t| |
|-----------|----------|----------------|---------|------|---|
| Intercept | 0.114    | 0.007          | 17.13   | <.0001 |
| metcbt5   | -0.020   | 0.009          | -2.17   | 0.0304 |

Results show that youth like those in “usual care” would have fared better had they received MET/CBT5
Comparison with unweighted treatment effect

SAS Code:

```sas
proc reg data=subdata_twogrp_att_wgts;
model sfs8p12 = metcbt5;
run;
```

Unweighted Parameter Estimates

| Variable | DF | Parameter Estimate | Standard Error | t Value | Pr > |t| |
|----------|----|--------------------|----------------|---------|-------|-------|
| Intercept | 1 | 0.114              | 0.006          | 20.07   | <.0001|
| metcbt5  | 1 | -0.047             | 0.006          | -7.61   | <.0001|
Comparison with unweighted treatment effect

SAS Code:

```sas
proc reg data=subdata_twogrp_att_wgts_atm;
model sfs8p12 = metcbt5;
run;
```

**Unweighted Parameter Estimates**

| Variable | DF | Parameter Estimate | Standard Error | t Value | Pr > |t| |
|----------|----|--------------------|----------------|---------|------|---|
| Intercept| 1  | 0.114              | 0.006          | 20.07   | <.0001|
| metcbt5  | 1  | -0.047             | 0.006          | -7.61   | <.0001|

- Also shows significant evidence that youth in “usual care” have higher substance use frequency at 12-months than those in MET/CBT5
- Magnitude of the effect unweighted is double (-0.02 vs -0.047)
Step 4: Doubly robust estimation

• “Doubly robust” estimation is the preferred route for estimating causal treatment effects
  – Combines fitting a propensity score weighted regression model with the inclusion of additional pretreatment control covariates
  – As long as one piece is right (either the multivariate outcome model or the propensity score model), obtain consistent treatment effect estimates
Step 4: Doubly robust estimation: Adding in covariates with lingering imbalances

SAS Code:

```sas
proc surveyreg data=subdata_twogrp_att_wgts;
  model sfs8p12 = metcbt5 ces;
  weight es_max_att;
run;
```

*PS Weighted Regression Coefficients*

| Parameter | Estimate | Standard Error | t Value | Pr > |t| |
|-----------|----------|----------------|---------|------|---|
| Intercept | 0.119    | 0.008          | 15.2    | <.0001 |
| metcbt5   | -0.022   | 0.010          | -2.28   | 0.0227 |
| ces       | -0.019   | 0.016          | -1.18   | 0.2363 |
Conclusions

• Use of propensity score weighting reduced bias in our treatment effect estimate
  – Greatly improved balance on observed pretreatment covariates
  – Magnitude of change went from 0.40 effect size difference to 0.20 effect size difference

• Use of propensity score weighting helped us produce more robust estimates of how youth like those in usual care would have fared had they received MET/CBT5
Please note this video is part of a three-part series. We encourage viewers to watch all three segments.
Please check out our website

http://www.rand.org/statistics/twang.html

**Toolkit for Weighting and Analysis of Nonequivalent Groups (TWANG)**

The Toolkit for Weighting and Analysis of Nonequivalent Groups, or **TWANG**, contains a set of functions to support causal modeling of observational data through the estimation and evaluation of propensity score weights. The TWANG package was first developed in 2004 by RAND researchers for the R statistical computing language and environment. The R version of the package contains functions for creating high-quality propensity score weights which can be used to estimate treatment effects with two or more treatment groups.

In 2014, TWANG macros were developed for SAS to support the use of these tools without requiring researchers and analysts to learn R. At this time, the SAS TWANG macros can support estimation of propensity scores and their associated weights for comparisons involving two treatment groups. SAS macros will be made available shortly for handling the case of three or more treatment groups.

**History**
Please check out our website

http://www.rand.org/statistics/twang.html

Click on “Stay Informed” to keep up-to-date on tools available
Acknowledgements

• This work has been generously supported by NIDA grant 1R01DA034065

• Our colleagues

  Daniel Almirall          Rajeev Ramchand
  Craig Martin             Lisa Jaycox
  James Gazis              Natalia Weil
  Andrew Morral            Greg Ridgeway
Data acknowledgements

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