Matching and Re-weighting

When X differ...

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Recap: Potential outcomes and Identification

To identify treatment effects one could **just** compare potential outcomes in two states:

- with treatment
- without treatment

Mathematically, average treatment effects would be:

$$ATE = E(Y_i(1) - Y_i(0))$$

the problem: with real data, we are only able to see one outcome. The counter factual is not observed:

$$Y_i = Y_i(1) * D + Y_i(0) * (1 - D)$$

and simple differences may not capture ATE, because of selection bias and heterogeneity in effects.

Recap: Gold Standard - RCT

The easiest, but most expensive, way to deal with the problem is using **Randomized Control Trials**.

Effectively, you randomize Treatment, so that potential outcomes are independent of treatment:

$$Y(1), Y(0) \perp D$$

In other words, the distribution of potential outcomes is the same for those treated or untreated units.

$$E(Y, D = 1) = E(Y(1), D = 1) = E(Y(1), D = 0)$$
$$E(Y, D = 0) = E(Y(0), D = 1) = E(Y(0), D = 0)$$
$$ATT = E(Y, D = 1) - E(Y, D = 0)$$

But what if you can't Randomize

When unconditional fails

More often than not, specially if we didn't construct the data, it would be impossible to find that unconditional independence assumption holds.

For example, treatment (say having health insurance) may vary by age, gender, race, location, etc.

This is similar to the selection bias: Outcomes across treated and untreated groups will be different because:

- Composition: Characteristics of people among the treated could be different than those among the untreated For example, they could be older, more educated, mostly men, etc.
- Other factors: There could be factors we cannot control for, that also affect outcomes.

There is conditional

When unconditional independence assumption fails, we can call on Conditional independence assumption:

$$Y(1), Y(0) \perp D|X$$

In other words, If we can look into specific groups (given X), it may be possible to impose the Independence assumption.

This relaxes the independence condition, but assumes selection is due to observable characteristics only. (it still needs to be as good as randomized given X)

Implications:

$$E(Y|D = 1, X) = E(Y(1)|D = 1, X) = E(Y(1)|D = 0, X)$$
$$E(Y|D = 0, X) = E(Y(0)|D = 1, X) = E(Y(0)|D = 0, X)$$

Intuition

Matching is a methodology that falls within quasi-experimental designs. You cannot or could not decide the assignment rules, so now are using data as given.

The idea is to construct an artificial control and use it as a counter-factual, so that both treated and control groups "look similar" in terms of observables.

Once a group of synthetic controls has been constructed, treatment effects can be calculated for the whole population:

$$ATE(X) = E(Y|D = 1, X) - E(Y|D = 0, X)$$
$$ATE = \int ATE(X)dFx$$

How can we do this?

we just need to find observational twins!

Matching Twins

Figure 1: Matching on Observables

Subclassification or stratification

Consider the following dataset:

```
frause titanic, clear
expand freq
drop if freq==0
gen class1=class==1
tab survived class1 , nofreq col
```

```
<IPython.core.display.HTML object>
```

```
(Data downloaded from R base)
(8 zero counts ignored; observations not deleted)
(2,177 observations created)
(8 observations deleted)
```

```
           |        class1
  Survived |         0          1 |     Total
-----------+----------------------+----------
        No |     72.92      37.54 |     67.70
       Yes |     27.08      62.46 |     32.30
-----------+----------------------+----------
     Total |    100.00     100.00 |    100.00
```

If we assume full Independence assumption we would believe that being in first class increased chance of survival in 35.4%. but is that the case?

What if the composition of individuals differs across classes (women and children)

```
tab age class1, nofreq col
tab sex class1, nofreq col
```

```
           |        class1
       Age |         0          1 |     Total
-----------+----------------------+----------
     Child |      5.49       1.85 |      4.95
     Adult |     94.51      98.15 |     95.05
-----------+----------------------+----------
     Total |    100.00     100.00 |    100.00

           |        class1
       Sex |         0          1 |     Total
-----------+----------------------+----------
```

```
      Male |     82.68      55.38 |     78.65
    Female |     17.32      44.62 |     21.35
-----------+----------------------+----------
     Total |    100.00     100.00 |    100.00
```

There were fewer children, but more women in first class. Perhaps that explains the difference in survival rates

A better approach would be to look into the survival probabilities stratifying the data:

```
gen surv=survived==2
bysort age sex class1:egen sr_mean=mean(survived==2)
table (age sex) (class1), stat(mean surv) nototal
```

```
------------------------------------
             |         class1
             |         0          1
-------------+----------------------
Age          |
  Child      |
    Sex      |
      Male   |  .4067797          1
      Female |  .6136364          1
  Adult      |
    Sex      |
      Male   |  .1883378   .3257143
      Female |  .6263345   .9722222
------------------------------------
```

So even within each group, the survival probability is larger in first class. What about Average?

```
bysort age sex:egen sr_mean_class1=max(sr_mean*(class1==1))
bysort age sex:egen sr_mean_class0=max(sr_mean*(class1==0))
gen teff = sr_mean_class1-sr_mean_class0
sum teff if class1==1 // ATT
sum teff if class1==0 // ATU
sum teff  // ATE
```

```
    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
        teff |        325    .2375421    .1125033   .1373765   .5932204

    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
        teff |      1,876    .1887847    .1089261   .1373765   .5932204

    Variable |        Obs        Mean    Std. dev.       Min        Max
-------------+---------------------------------------------------------
        teff |      2,201    .1959842    .1107948   .1373765   .5932204
```

What did we do?

The procedure above is a simple stratification approach, aka matching, to analyze the true impact of the treatment (being a 1st class passenger).

1. Stratified the sample in groups by age and gender.
    - Identify the shares of each group by class1
2. Predict probability of survival per strata and class1
3. Obtain the Strata level Effects
4. Aggregate as needed.
    - Here, we could estimate ATE, ATT or ATU!

Where could things go wrong?

Overlapping

The procedure describe above works well whenever there is data overlapping.

- For every combination of X, you see data on the control and treated group $0 < P(D|X) < 1$

When this fails, you wont be able to estimate ATE's, although ATT's or ATU's might still be possible:

- for ATT: $P(D|X) < 1$
- for ATU: $0 < P(D|X)$

For example:

```
frause hhprice, clear
keep price rooms type_h
tab rooms type_h
```

```
           |    =0 if house, =1
 Number of |       TownHouse
     rooms |         0          1 |     Total
-----------+----------------------+----------
         1 |        37         72 |       109
         2 |     1,134        751 |     1,885
         3 |     4,634        648 |     5,282
         4 |     2,465        115 |     2,580
         5 |       465          2 |       467
         6 |        46          0 |        46
         7 |         7          0 |         7
-----------+----------------------+----------
     Total |     8,788      1,588 |    10,376
```

Would not be able to estimate ATE nor ATU. Only ATT for townhouses.

Curse of dimensionality

There is a second problem in terms of stratification. How would we deal with Multiple dimensions? Would it be possible to find "twins" for every observation?

The answer is, probably no. Too many groups to track, to many micro cells to make use of:

```
frause oaxaca, clear
drop if lnwage==.
egen strata=group(educ isco)
bysort strata:egen flag=mean(female)
list educ isco female if (flag==0 | flag==1) & educ == 10, sep(0)
```

```
(Excerpt from the Swiss Labor Market Survey 1998)
(213 observations deleted)

      +----------------------+
      | educ   isco   female |
```

```
     |----------------------|
158. |   10      1        0 |
159. |   10      1        0 |
197. |   10      7        0 |
198. |   10      7        0 |
199. |   10      9        1 |
200. |   10      9        1 |
     +----------------------+
```

Alternative: Matching as a weighted

The problem of curse of dimensional states that as the number of desired characteristics to match increase, fewer "twins" will be available in the data. At the end…no one will be like you!

The alternative, is to look into People that are sufficiently close so they can be used for matching.

$$ATT_i = Y_i - \sum_{j \in C} w(x_j, x_i) Y_j$$

$$ATT = \frac{1}{N_T} \sum (ATT_i)$$

$$ATT = E(Y|D=1) - E_i \left(\sum_{j \in C} w(x_j, x_i) Y_j \Big| D = 0 \right)$$

Depending how $w(.)$ is defined, we would be facing different kinds of matching estimators.

Types of Matching

Matching on covariates

The first decision to take is whether one should find matches based on covariates, or based on scores (propensity scores).

Using covariates implies that will aim to find the closest "twin" possible, based on multiple dimensions:

$$Eclidean = d(x_i, x_j) = \sqrt{(x_i - x_j)'(x_i - x_j)}$$

$$WEclidean = d(x_i, x_j) = \sqrt{(x_i - x_j)' W (x_i - x_j)}$$

$$Maha = d(x_i, x_j) = \sqrt{(x_i - x_j)' S^{-1} (x_i - x_j)}$$

Distance measures are used to identify the closest matches to a given observation, and thus the weight assigned to that observation.

Has the advantage of looking at individuals who are indeed close to each other, but becomes more difficult as the dimensionality of X's increase. (you will not find close matches)

Matching on Scores

A second approach is to match individuals based on some summary index that condenses the information in X into a single scalar $h(x)$, reducing the dimensionality problem fron K to 1.

Few candidates:

- Propensity Score: $P(D|X)$ based on a logit/probit/binomial model. Most common approach!
- Predicted Mean: $X\beta$ if there is information on outcome to be predicted
- PCA: Using Principal components to reduce dimensionality before Matching

Since there is only 1 dimension to consider, multiple distance measures are possible:

- nearest neighbors, kernel weight matching, radious matching.

But one has to be careful with the approach. King and Nielsen (2019) Argue about the risks of PSM

1 vs K matching; With and without replacement

Two additional questions remain regarding matching. How many "twins" to use, and if twins will be obtained with/without replacement.

- Fewer matches reduce bias (choosing only the closest observation), but increase variance.
- More matches increase bias, but reduce variance. (because of less optimal matches)
- with replacement: control units may be used more than once. This will improve matching quality reducing bias. But by using the same units multiple times, it will increase variance.
- without replacement: Control units are used once, potentially reducing matching quality, but reducing variance. It will be order dependent.

see Caliendo and Kopeing (2008)

What about SE? and Statistical inference?

Well….this is one of the few cases where Bootstrapping WON'T work!

Standard errors are more cumbersome. So we will just rely on software results

Other considerations

Once you have chosen your matching method, find your "statistical twins", and estimate your differences you are done! (or are you)

Not yet…common practice: Evaluate the balance of your data

> Matching aims to reduce or eliminate differences in characteristics between treatment and control units. Thus, one should evaluate the differences (before and after match) of your characteristis

1. Check for overlapping condition.

- either variable by variable or with pscore

2. Assess Matching Quality: Have differences across groups vanished?

- Check Standardized differences $\frac{\mu_1 - \mu_2}{\sqrt{0.5*(V_1+V_2)}}$
- t-tests
- PR2 of regression with matched data

Implementation

In `Stata`, there are at least two approaches that can be used for matching:

- `psmatch2` (from ssc)
- `teffects` (Official `Stata` command)

We will use this to answer a simple question:

> What is the impact of Traing Jobs on Earnings?

Example

This file contains information on experimental and observed data for the analysis of training on earnings program:

```
use https://friosavila.github.io/playingwithstata/drdid/lalonde.dta, clear
keep if year==1978
drop if dwincl==0
label define sample 1 "exper"  2 "CPS" 3 "PSID"
label values sample sample
tab sample treated,m
```

```
(19,204 observations deleted)
(277 observations deleted)

           |            treated
    sample |         0          1          . |     Total
-----------+---------------------------------+----------
     exper |       260        185          0 |       445
       CPS |         0          0     15,992 |    15,992
      PSID |         0          0      2,490 |     2,490
-----------+---------------------------------+----------
     Total |       260        185     18,482 |    18,927
```

First Experimental design - RCT

```
reg re treated
tabstat age educ black married nodegree , by(treated)
logit treated age educ black hisp married nodegree
```

```
      Source |       SS           df       MS      Number of obs   =       445
-------------+----------------------------------   F(1, 443)       =      8.04
       Model |   348013183         1   348013183   Prob > F        =    0.0048
    Residual |  1.9178e+10       443  43290369.3   R-squared       =    0.0178
-------------+----------------------------------   Adj R-squared   =    0.0156
       Total |  1.9526e+10       444  43976681.9   Root MSE        =    6579.5

------------------------------------------------------------------------------
          re | Coefficient  Std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
```

```
     treated |   1794.342   632.8534     2.84   0.005     550.5745     3038.11
       _cons |   4554.801   408.0459    11.16   0.000     3752.855    5356.747
------------------------------------------------------------------------------

Summary statistics: Mean
Group variable: treated

 treated |       age      educ     black   married  nodegree
---------+--------------------------------------------------
       0 |  25.05385  10.08846  .8269231  .1538462  .8346154
       1 |  25.81622  10.34595  .8432432  .1891892  .7081081
---------+--------------------------------------------------
   Total |  25.37079  10.19551  .8337079  .1685393  .7820225
------------------------------------------------------------

Iteration 0:  Log likelihood =     -302.1
Iteration 1:  Log likelihood = -294.72908
Iteration 2:  Log likelihood = -294.71464
Iteration 3:  Log likelihood = -294.71464

Logistic regression                                     Number of obs =    445
                                                        LR chi2(6)    =  14.77
                                                        Prob > chi2   = 0.0221
Log likelihood = -294.71464                             Pseudo R2     = 0.0244

------------------------------------------------------------------------------
     treated | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
         age |   .0059171   .0142668     0.41   0.678    -.0220452    .0338794
        educ |  -.0639597    .071354    -0.90   0.370     -.203811    .0758916
       black |  -.2543689   .3639735    -0.70   0.485    -.9677438    .4590061
        hisp |  -.8291587   .5042305    -1.64   0.100    -1.817432     .159115
     married |   .2342415   .2661824     0.88   0.379    -.2874665    .7559495
    nodegree |  -.8385524   .3093833    -2.71   0.007    -1.444933   -.2321722
       _cons |   1.053028   1.047384     1.01   0.315    -.9998064    3.105862
------------------------------------------------------------------------------
```

Then using PScore Matching CPS

```
keep if treated == 1 | sample ==2
replace treated=0 if treated==.
reg re treated
tabstat age educ black hisp married nodegree , by(treated)
```

```
(2,750 observations deleted)
(15,992 real changes made)

      Source |       SS           df       MS      Number of obs   =    16,177
-------------+----------------------------------   F(1, 16175)     =    142.43
       Model |  1.3206e+10         1  1.3206e+10   Prob > F        =    0.0000
    Residual |  1.4997e+12    16,175  92717515.8   R-squared       =    0.0087
-------------+----------------------------------   Adj R-squared   =    0.0087
       Total |  1.5129e+12    16,176  93528158.4   Root MSE        =      9629

------------------------------------------------------------------------------
          re | Coefficient  Std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
     treated |  -8497.516   712.0207   -11.93   0.000    -9893.156   -7101.877
       _cons |   14846.66   76.14292   194.98   0.000     14697.41    14995.91
------------------------------------------------------------------------------

Summary statistics: Mean
Group variable: treated

 treated |       age      educ     black      hisp   married  nodegree
---------+--------------------------------------------------------------
       0 |  33.22524  12.02751  .0735368   .072036  .7117309  .2958354
       1 |  25.81622  10.34595  .8432432  .0594595  .1891892  .7081081
---------+--------------------------------------------------------------
   Total |  33.14051  12.00828  .0823391  .0718922  .7057551  .3005502
------------------------------------------------------------------------
```

We need to do trimming

```
bysort educ black hisp married:egen n11=sum(treated==1)
bysort age  black hisp married:egen n22=sum(treated==1)
drop if n11==0 | n22 ==0
```

```
tabstat age educ black hisp married nodegree , by(treated)
reg re treated
```

```
(13,536 observations deleted)

Summary statistics: Mean
Group variable: treated

 treated |       age      educ     black      hisp   married  nodegree
---------+--------------------------------------------------------------
       0 |  24.24145  11.69788   .252443  .0260586  .3346906  .2569218
       1 |  25.81622  10.34595  .8432432  .0594595  .1891892  .7081081
---------+--------------------------------------------------------------
   Total |  24.35176  11.60318  .2938281  .0283983  .3244983  .2885271
------------------------------------------------------------------------

      Source |       SS           df       MS      Number of obs   =     2,641
-------------+----------------------------------   F(1, 2639)      =     73.89
       Model |  5.7607e+09         1  5.7607e+09   Prob > F        =    0.0000
    Residual |  2.0575e+11     2,639  77964783.1   R-squared       =    0.0272
-------------+----------------------------------   Adj R-squared   =    0.0269
       Total |  2.1151e+11     2,640  80117339.3   Root MSE        =    8829.8

------------------------------------------------------------------------------
          re | Coefficient  Std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
     treated |  -5786.584   673.1834    -8.60   0.000    -7106.605   -4466.564
       _cons |   12135.73   178.1702    68.11   0.000     11786.36     12485.1
------------------------------------------------------------------------------
```

Lets do some matching

```
teffects nnmatch (re age educ black   married nodegree  ) (treated)
tebalance summarize
teffects nnmatch (re age educ black   married nodegree  ) (treated), nn(2)
tebalance summarize
teffects psmatch (re) (treated age educ black   married nodegree  )
tebalance summarize
```

```
teffects psmatch (re) (treated age educ black   married nodegree  ) ,  nn(2)
tebalance summarize
```

```
Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : nearest-neighbor matching     Matches: requested =          1
Outcome model  : matching                                  min =          1
Distance metric: Mahalanobis                               max =        138
------------------------------------------------------------------------------
             |               AI robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |  -3685.665   1188.666    -3.10   0.002    -6015.407   -1355.923
------------------------------------------------------------------------------
(refitting the model using the generate() option)

Covariate balance summary

                        Raw      Matched
-----------------------------------------
Number of obs =       2,641        5,282
Treated obs   =         185        2,641
Control obs   =       2,456        2,641
-----------------------------------------

-------------------------------------------------------------------
                |Standardized differences          Variance ratio
                |        Raw     Matched           Raw    Matched
----------------+--------------------------------------------------
            age |   .2342346    -.015417      1.305844   .8410946
           educ |  -.7684118   -.0812288      1.881909   .8598207
          black |   1.473105           0      .7039609          1
        married |  -.3351313   -.0008087      .6923501    .999393
       nodegree |   1.010393           0      1.088086          1
-------------------------------------------------------------------

Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : nearest-neighbor matching     Matches: requested =          2
Outcome model  : matching                                  min =          2
Distance metric: Mahalanobis                               max =        138
```

```
------------------------------------------------------------------------------
             |               AI robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |  -5166.888   1107.653    -4.66   0.000    -7337.848   -2995.929
------------------------------------------------------------------------------
(refitting the model using the generate() option)

Covariate balance summary

                          Raw      Matched
-----------------------------------------
Number of obs =         2,641        5,282
Treated obs   =           185        2,641
Control obs   =         2,456        2,641
-----------------------------------------

-------------------------------------------------------------
                |Standardized differences          Variance ratio
                |        Raw     Matched           Raw    Matched
----------------+--------------------------------------------
            age |   .2342346   -.0209048      1.305844   .7345997
           educ |  -.7684118   -.0385284      1.881909   .8978301
          black |   1.473105    .0074673      .7039609   1.006716
        married |  -.3351313    -.004586      .6923501   .9965432
       nodegree |   1.010393    .0016705      1.088086   1.001557
-------------------------------------------------------------

Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : propensity-score matching     Matches: requested =          1
Outcome model  : matching                                  min =          1
Treatment model: logit                                     max =        138
------------------------------------------------------------------------------
             |               AI robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |  -4278.549   1135.847    -3.77   0.000    -6504.768   -2052.331
------------------------------------------------------------------------------
(refitting the model using the generate() option)
```

```
Covariate balance summary

                          Raw      Matched
-----------------------------------------
Number of obs =         2,641        5,282
Treated obs   =           185        2,641
Control obs   =         2,456        2,641
-----------------------------------------

------------------------------------------------------------------
                |Standardized differences          Variance ratio
                |        Raw     Matched           Raw    Matched
----------------+-------------------------------------------------
            age |   .2342346    .0014058      1.305844   .9313458
           educ |  -.7684118   -.1308249      1.881909   .9665937
          black |   1.473105   -.0926638      .7039609     .90999
        married |  -.3351313   -.0973289      .6923501   .9197524
       nodegree |   1.010393    .0821105      1.088086    1.07103
------------------------------------------------------------------

Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : propensity-score matching     Matches: requested =          2
Outcome model  : matching                                  min =          2
Treatment model: logit                                     max =        138
------------------------------------------------------------------------------
             |               AI robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |  -4380.078   1158.019    -3.78   0.000    -6649.754   -2110.403
------------------------------------------------------------------------------
(refitting the model using the generate() option)

Covariate balance summary

                          Raw      Matched
-----------------------------------------
Number of obs =         2,641        5,282
Treated obs   =           185        2,641
Control obs   =         2,456        2,641
-----------------------------------------
```

```
-------------------------------------------------------------
                |Standardized differences          Variance ratio
                |        Raw     Matched           Raw    Matched
----------------+--------------------------------------------
            age |   .2342346     -.06133      1.305844   .8834346
           educ |  -.7684118   -.1321518      1.881909   1.021302
          black |   1.473105   -.0698339      .7039609    .933348
        married |  -.3351313   -.0414439      .6923501   .9674741
       nodegree |   1.010393    .0939209      1.088086   1.080951
-------------------------------------------------------------
```

A missing variable? Earnings in previous year. May capture information of Need to do treatment (selection)

```
tabstat age educ black hisp married nodegree re74, by(treated)
gen dre = re-re74
teffects nnmatch (dre age educ black   married nodegree  ) (treated)

teffects nnmatch (dre age educ black   married nodegree  ) (treated), nn(2)

teffects psmatch (dre) (treated age educ black   married nodegree  )

teffects psmatch (dre) (treated age educ black   married nodegree  ) ,  nn(2)
```

```
Summary statistics: Mean
Group variable: treated

 treated |       age      educ     black      hisp   married  nodegree
---------+------------------------------------------------------------
       0 |  24.24145  11.69788   .252443  .0260586  .3346906  .2569218
       1 |  25.81622  10.34595  .8432432  .0594595  .1891892  .7081081
---------+------------------------------------------------------------
   Total |  24.35176  11.60318  .2938281  .0283983  .3244983  .2885271
-------------------------------------------------------------------------

 treated |      re74
---------+----------
```

```
       0 |  9347.406
       1 |  2095.574
---------+----------
   Total |  8839.421
--------------------
```

```
Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : nearest-neighbor matching     Matches: requested =          1
Outcome model  : matching                                  min =          1
Distance metric: Mahalanobis                               max =        138
------------------------------------------------------------------------------
             |               AI robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |   2616.653   1803.172     1.45   0.147    -917.4997    6150.806
------------------------------------------------------------------------------
```

```
Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : nearest-neighbor matching     Matches: requested =          2
Outcome model  : matching                                  min =          2
Distance metric: Mahalanobis                               max =        138
------------------------------------------------------------------------------
             |               AI robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |   730.2925    1674.91     0.44   0.663     -2552.47    4013.055
------------------------------------------------------------------------------
```

```
Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : propensity-score matching     Matches: requested =          1
Outcome model  : matching                                  min =          1
Treatment model: logit                                     max =        138
------------------------------------------------------------------------------
             |               AI robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |   2162.311    1740.12     1.24   0.214    -1248.262    5572.884
```

```
------------------------------------------------------------------------------

Treatment-effects estimation                   Number of obs      =      2,641
Estimator      : propensity-score matching     Matches: requested =          2
Outcome model  : matching                                      min =          2
Treatment model: logit                                         max =        138
------------------------------------------------------------------------------
             |               AI robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |    1833.03   1739.496     1.05   0.292    -1576.318    5242.379
------------------------------------------------------------------------------
```

In this case, Matching alone could not get the right answer. Who were the most likely to "go to the training?"

So instead we change the question: How much the change in earnings compare across groups.

Wait: What about Reweighting?

An alternative method to Matching is to do Re-weighting.

We have seen this!

Your control group has a distribution $g(x)$ and your treatment $f(x)$. We can use some weighting factors $h(x)$ that reshapes $g(x) \rightarrow \hat{f}(x)$.

How? Using Propensity scores

Why does it work? Just as matching, your goal is to compare distributions of outcomes, forcing differences in observed characteristics to be the same.

IPW, does this by reweighting the distribution! (rather than matching)

Inverse Probability Weighting:IPW

s1: Estimate Pscore

$$p(D = 1|X) = F(X\beta)$$

S2: Estimate IPW

For ATT: $W(D=1,x)=1$ & $W(D=0,X)=\frac{\hat{p}(x)}{1-\hat{p}(x)}$

For ATU: $W(D=0,x)=1$ & $W(D=1,X)=\frac{1-\hat{p}(x)}{\hat{p}(x)}$

For ATE: $W(D=0,x)=\frac{1}{1-\hat{p}(x)}$ & $W(D=1,X)=\frac{1}{\hat{p}(x)}$

s3: Estimate Treatment effect:

$$TE=\sum_{i\in D=1} w_i^s(1)Y_i-\sum_{i\in D=0} w_i^s(0)Y_i$$

Even Better: Go DR!

An interesting advantage of IPW approach is that you can gain efficiency using Doubly Robust Methods. Namely, instead of comparing outcomes directly, you could compare predicted outcomes!

$$ATT=\frac{1}{N_t}\sum(Y_1-X'\hat{\beta}_w^0)$$
$$ATU=\frac{1}{N_c}\sum(X'\hat{\beta}_w^1-Y_0)$$
$$ATE=\frac{1}{N}\sum(X'\hat{\beta}_w^1-X'\hat{\beta}_w^0)$$

where $\hat{\beta}_w^k$ can be modeled using weighted least squares

Comparing to Matching

```
teffects ipw (re) (treated age educ black   married nodegree) , iter(3) nolog
teffects ipwra (re age educ black   married nodegree) (treated age educ black married nodegre
teffects ipw (dre) (treated age educ black   married nodegree), iter(3) nolog
teffects ipwra (dre age educ black   married nodegree) (treated age educ black   married node
```

```
Treatment-effects estimation                    Number of obs     =      2,641
Estimator      : inverse-probability weights
Outcome model  : weighted mean
Treatment model: logit
------------------------------------------------------------------------------
             |               Robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
```

```
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |  -4833.352   1088.667    -4.44   0.000    -6967.101   -2699.603
-------------+----------------------------------------------------------------
POmean       |
     treated |
           0 |   11979.19   179.1903    66.85   0.000     11627.99     12330.4
------------------------------------------------------------------------------

Treatment-effects estimation                    Number of obs     =      2,641
Estimator      : IPW regression adjustment
Outcome model  : linear
Treatment model: logit
------------------------------------------------------------------------------
             |               Robust
          re | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |   -4835.38   1012.598    -4.78   0.000    -6820.036   -2850.724
-------------+----------------------------------------------------------------
POmean       |
     treated |
           0 |   11976.52   179.0958    66.87   0.000     11625.49    12327.54
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Treatment-effects estimation                    Number of obs     =      2,641
Estimator      : inverse-probability weights
Outcome model  : weighted mean
Treatment model: logit
------------------------------------------------------------------------------
             |               Robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |    1475.71   1792.427     0.82   0.410    -2037.382    4988.802
-------------+----------------------------------------------------------------
POmean       |
     treated |
```

```
          0  |   2746.475   161.2845    17.03   0.000     2430.363    3062.587
------------------------------------------------------------------------------
Warning: Convergence not achieved.

Treatment-effects estimation                    Number of obs     =      2,641
Estimator      : IPW regression adjustment
Outcome model  : linear
Treatment model: logit
------------------------------------------------------------------------------
             |               Robust
         dre | Coefficient  std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
ATE          |
     treated |
   (1 vs 0)  |   1286.605   1516.493     0.85   0.396    -1685.666    4258.875
-------------+----------------------------------------------------------------
POmean       |
     treated |
          0  |   2754.756   161.4406    17.06   0.000     2438.338    3071.173
------------------------------------------------------------------------------
Warning: Convergence not achieved.
```

Next: Regression Discontinuity