matching_lecture

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0.1 Introduction to Matching Methods for Causal Inference

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0.2 ## Introduction

- Useful for observational studies
- Sometimes better than simply using control variables.
- It's popular! (Since the 1970s, 93,700 articles uses matching method)

0.3 ## Regression v.s. Matching

Both methods assumes **Selection on Observables** - assume Potential outcomes (y_t, y_c) are independent of treatment after controlling for observed covariates x (Conditional Independence Assumption) - use a set of covariates to adjust the estimation

Both methods are **weight scheme**. Regression aims to minimize squared errors, so observations on the margins have more weight. Matching puts the emphasis on observations that have similar covariates.

Two methods can work together! (e.g. Regression with Propensity Score Matching)

0.4 ## Why matching

Reduce Model Dependence: - Does not rely on modeling assumptions of linear dependencies across the entire range of the control variables to do controlled comparisons. - Enhances apples to apples comparisons: Making sure the treated and untreated observations are balanced.

0.5 ## Matching Reduces Model Dependence

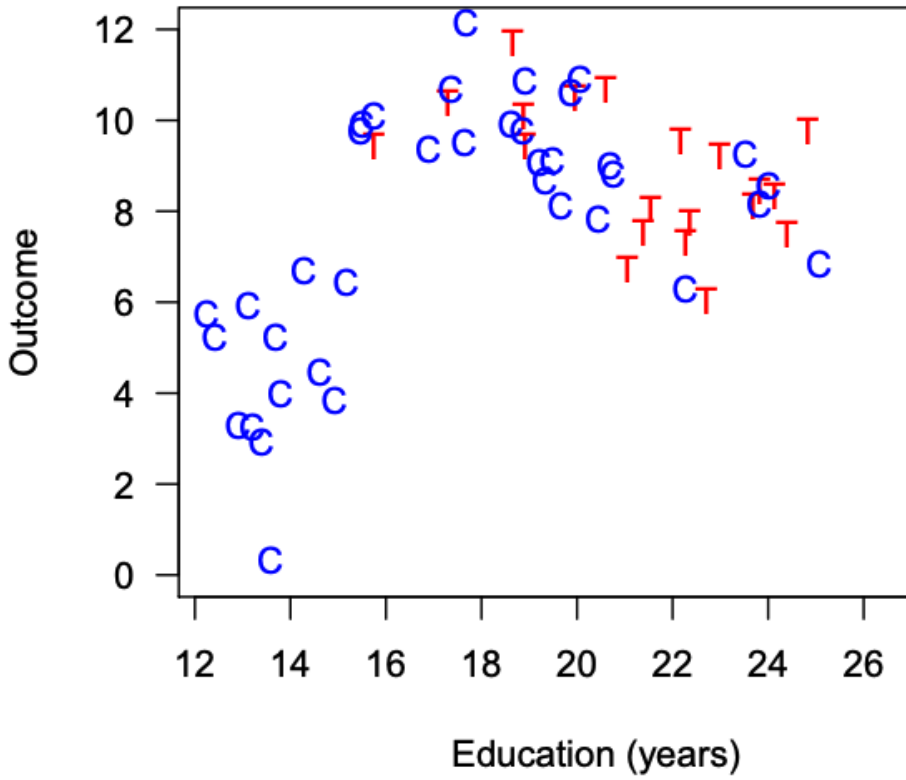


Figure from Ho, Imai, King, Stuart (2007)

0.6 ## Matching Reduces Model Dependence

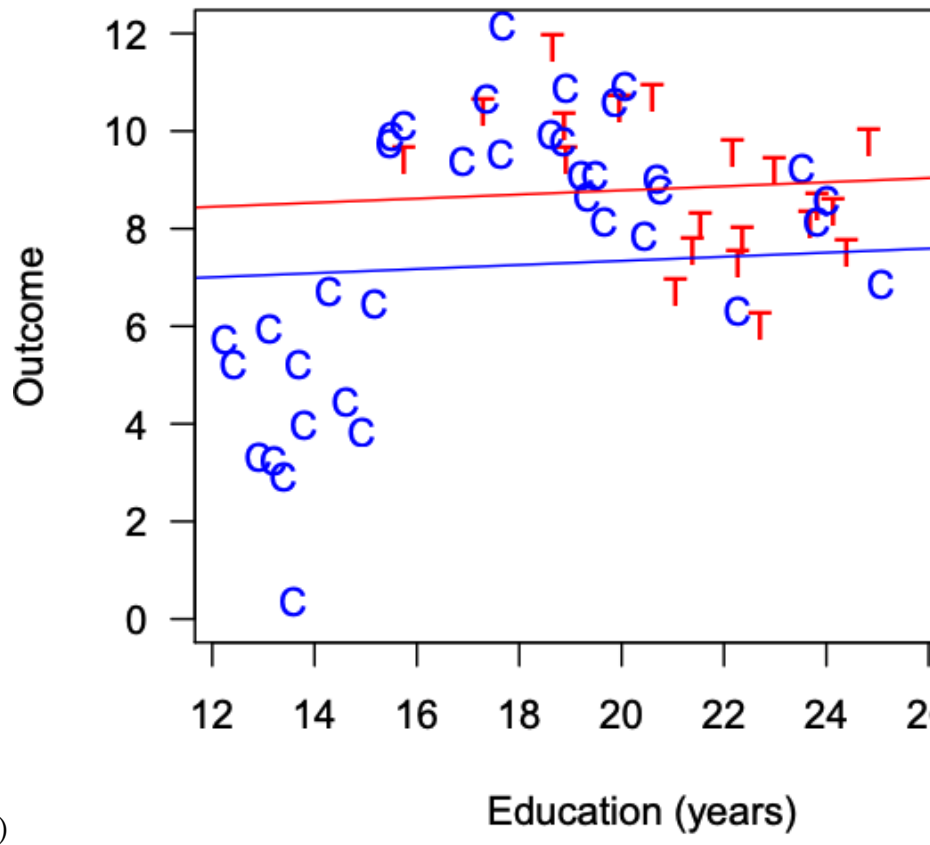


Figure from Ho, Imai, King, Stuart (2007)

0.7 ## Matching Reduces Model Dependence

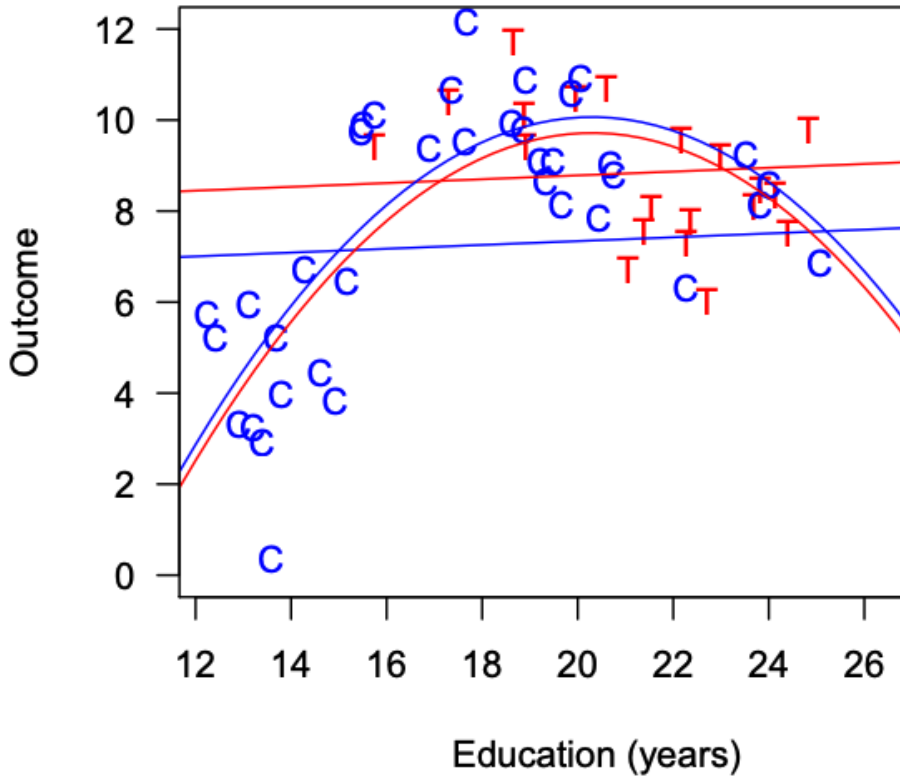


Figure from Ho, Imai, King, Stuart (2007)

0.8 ## Matching Reduces Model Dependence

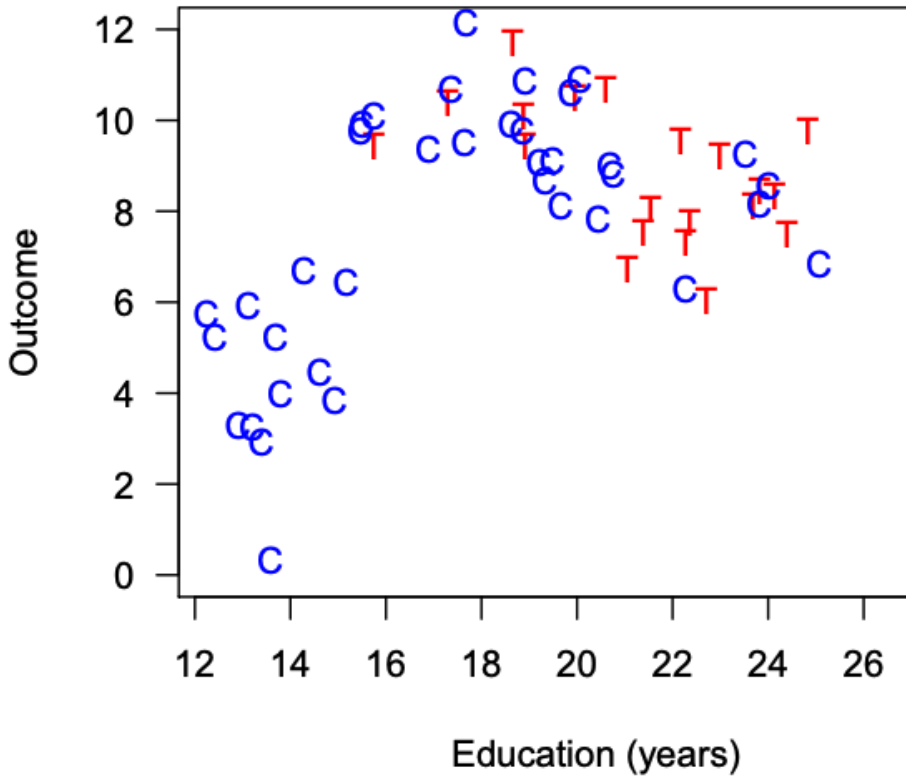


Figure from Ho, Imai, King, Stuart (2007)

0.9 ## Matching Reduces Model Dependence

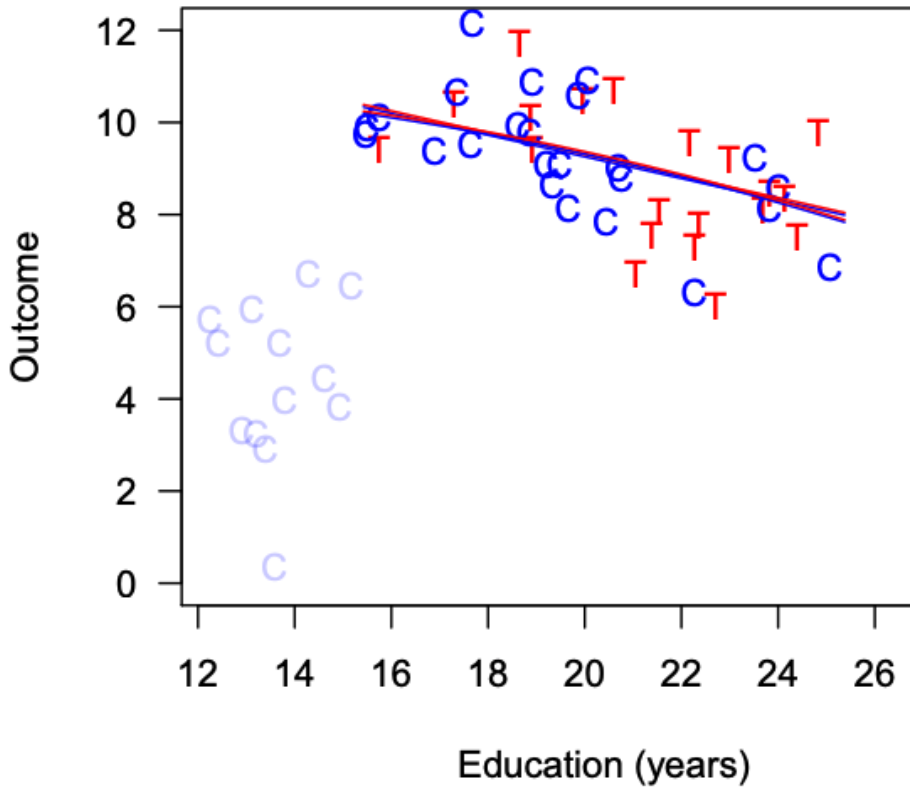
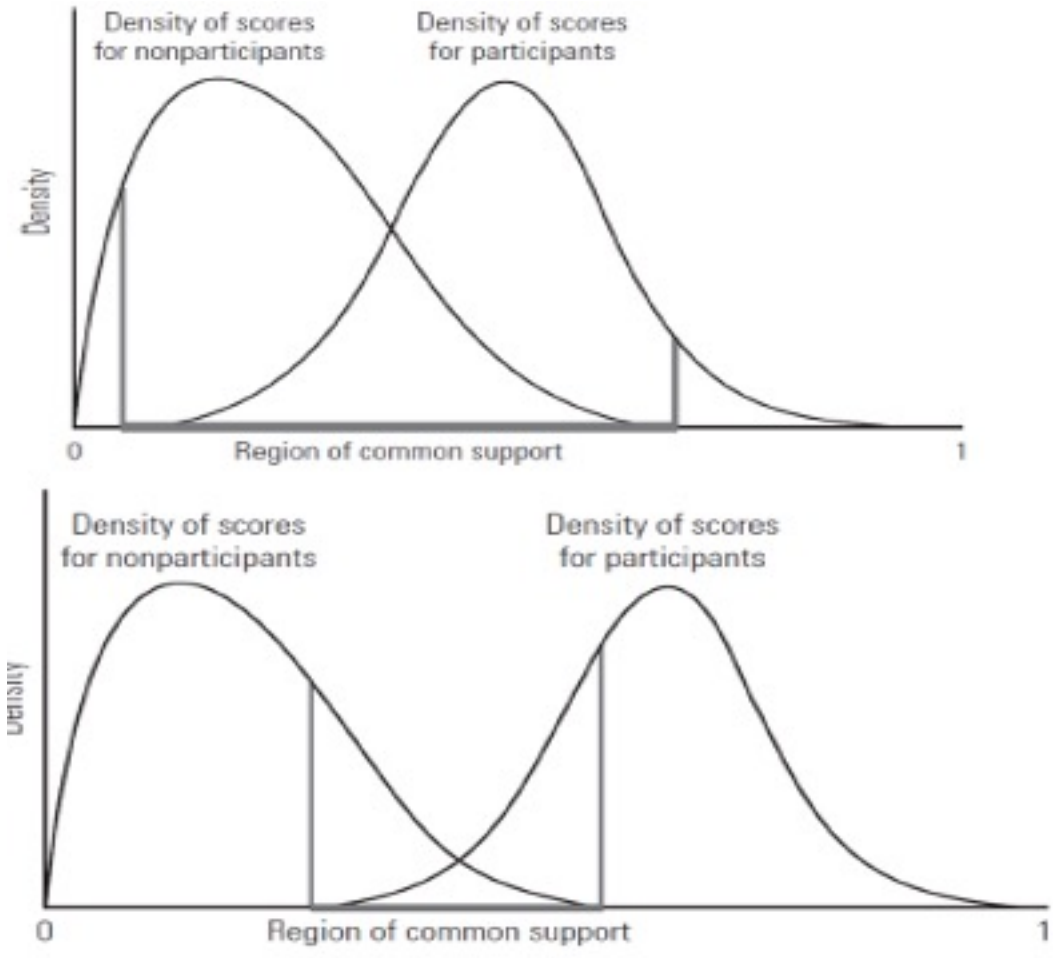


Figure from Ho, Imai, King, Stuart (2007)

0.10 ## Matching & Common Support

- Common support ensures the treated have the control with "close" P(x)
- Lack of common support appears in tails of distributions
- Larger sample of eligible nonparticipants helps matching
- Poor common support can induce bias in matching estimator
  - E.g., if no matches may drop nonrandom subset of participants

0.11 Matching & Common Support



0.12 ## When Matching

- usually used in observational studies
- treatment and control groups are imbalanced
- a lot of covariates may be correlated with Y and D
- pre-process the data before running regression
- as a robustness check

0.13 ## Steps of Matching

0.13.1 Defining closeness I: Variables to Include

Defining "closeness": the distance measure used to determine whether an individual is a good match for another

- Be liberal in terms of including variables that may be associated with treatment assignment & outcomes
- In small sample, select variables without using the observed outcomes, but based on the previous research

- DO NOT include post-treatment variables

0.13.2 Defining closeness II: Metric of Closeness

- Exact
- Mahalanobis
- Propensity Score

0.13.3 Matching Methods

Implement a matching method, given that measure of closeness

- Nearest neighbor matching
- Subclassification, Full Matching, and Weighting

0.13.4 Assessing Common Support

- show distributions of propensity scores of treat&control groups
- substantial overlap of the propensity score distributions in the two groups

0.13.5 Matching Diagnostics

Assess the quality of the resulting matched samples

- diagnose the quality of the matching through an assessment of **covariate balance**
- **covariate balance** is defined as similarity of empirical distributions of the full set of covariates in the matched treated and control groups
- **Numerical diagnostics** (e.g. standardized difference in means): difference in means of each covariate, divided by the standard deviation in the full treated group: $\frac{X_t - X_c}{\sigma_t}$
- Graphical diagnostics

0.13.6 Analysis of the outcome

Analyze of the outcome and estimation of the treatment effect

- **Matching** and **Regression** have been shown to work best in combination
- After k:1 matching
  - do same analysis as what did with original data, but using the matched data instead, e.g. regression
  - weight needs to be incorporated
- After subclassification or full matching

0.14 Propentiy Score Matching Example

We practise the matching method by replicating the prominent paper on job training. The 'lalonde.dta' consists of the real earnings in the year 1978 (the response), a treatment indicator, and a number of demographic variables (controls). Here are the variable definitions.

- age: age in years.

- educ: years of schooling.
- black: indicator variable for blacks.
- hisp: indicator variable for Hispanics.
- married: indicator variable for martial status.
- nodegr: indicator variable for high school diploma.
- re74: real earnings in 1974.
- re75: real earnings in 1975.
- re78: real earnings in 1978.
- treat: an indicator variable for treatment status.

The original paper is here: Robert Lalonde, "Evaluating the Econometric Evaluations of Training Programs", American Economic Review, Vol. 76, pp. 604-620

[41]:
```
# load packages
# now pymatch only works with older versions of pandas, please make sure you␣
↪have a version older than 0.23.4
# If not, try this to downgrade pandas: pip install pandas==0.23.4
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from pymatch.Matcher import Matcher
%matplotlib inline
```

[42]:
```
lalonde = pd.read_stata("lalonde.dta")
lalonde.head()
```

[42]:
```
   treated  age  education  black  married  nodegree          re74  \
0      1.0   33         12      0        1         0      0.000000
1      1.0   20         12      0        1         0   8644.156250
2      0.0   39         12      1        1         0  19785.320312
3      1.0   49          8      0        1         1   9714.596680
4      0.0   26          8      0        1         1  37211.757812

           re75          re78  hispanic  u74  u75              q1
0      0.000000  12418.070312         0  1.0  1.0        disagree
1   8644.156250  11656.505859         0  0.0  0.0  strongly agree
2   6608.137207    499.257202         0  0.0  0.0         neutral
3   7285.947754  16717.121094         0  0.0  0.0      no opinion
4  36941.265625  30247.500000         0  0.0  0.0      no opinion
```

[43]:
```
lalonde.groupby("treated").mean()
```

[43]:
```
               age  education     black   married  nodegree         re74  \
treated
0.0      24.447059  10.188235  0.800000  0.157647  0.814118  3672.485151
1.0      24.626263  10.380471  0.801347  0.168350  0.730640  3570.998967

                re75         re78  hispanic       u74       u75
```

```
treated
0.0      3026.682738  5090.048201  0.112941  0.461176  0.418824
1.0      3066.098189  5976.352012  0.094276  0.441077  0.373737
```

0.15 Data Prepreation

load the `lalonde.dta`, show the raw mean difference in earning between the control group and the treated group.

[44]:
```
data = lalonde[["treated","age","education", "black",␣
 ↪"married","nodegree","hispanic","re74","re75","re78"]]
data.head()
```

[44]:

	treated	age	education	black	married	nodegree	hispanic	re74	re75	re78
0	1.0	33	12	0	1	0	0	0.000000	0.000000	12418.070312
1	1.0	20	12	0	1	0	0	8644.156250	8644.156250	11656.505859
2	0.0	39	12	1	1	0	0	19785.320312	6608.137207	499.257202
3	1.0	49	8	0	1	1	0	9714.596680	7285.947754	16717.121094
4	0.0	26	8	0	1	1	0	37211.757812	36941.265625	30247.500000

[45]:
```
treatment = data[data.treated == 1]
control = data[data.treated == 0]
```

0.16 Fit Propensity Score Model(s)

First we initialize the Matcher object:

- `Matcher` shows the formula used to fit logistic regression model(s) and the number of records in the majority/minority class.
- we use the covariates on the right side of the equation to estimate the probability of being treated (treated = 1).
- Any covariates passed to the (optional) exclude parameter will be ignored from the model fitting process. This parameter is particularly useful for unique identifiers like a userid.

[46]:
```
m = Matcher(control, treatment, yvar="treated", exclude=["re78"])
```

```
Formula:
treated ~ age+black+education+hispanic+married+nodegree+re74+re75
n majority: 425
n minority: 297
```

- The model shows an **imbalance** in our data. The majority group (control group) having more observations than the minority group (treatment group). We account for this by setting `balance=True` in `Matcher.fit_scores()`.
- This tells `Matcher()` to sample from the majority group when fitting the logistic regression model(s) so that the groups are of equal size.
- When undersampling this way, it is highly recommended that nmodels is explicitly assigned to a integer much larger than 1. This ensures that more of the majority group is contributing to the generation of propensity scores.
- The value of this integer should depend on the severity of the imbalance: here we use nmodels=100.

[47]:
```
np.random.seed(2020)
m.fit_scores(balance=True, nmodels=100)
```

```
Fitting Models on Balanced Samples: 100\100
Average Accuracy: 55.53%
```

- The average accuracy of our 100 models is 55.31%, suggesting that there's separability within our data and justifiying the need for the matching procedure.
- We don't pay **too much** attention to the estimates of logistic models
- We are interested in **the predicted value of the model** (propensity score of each observation).

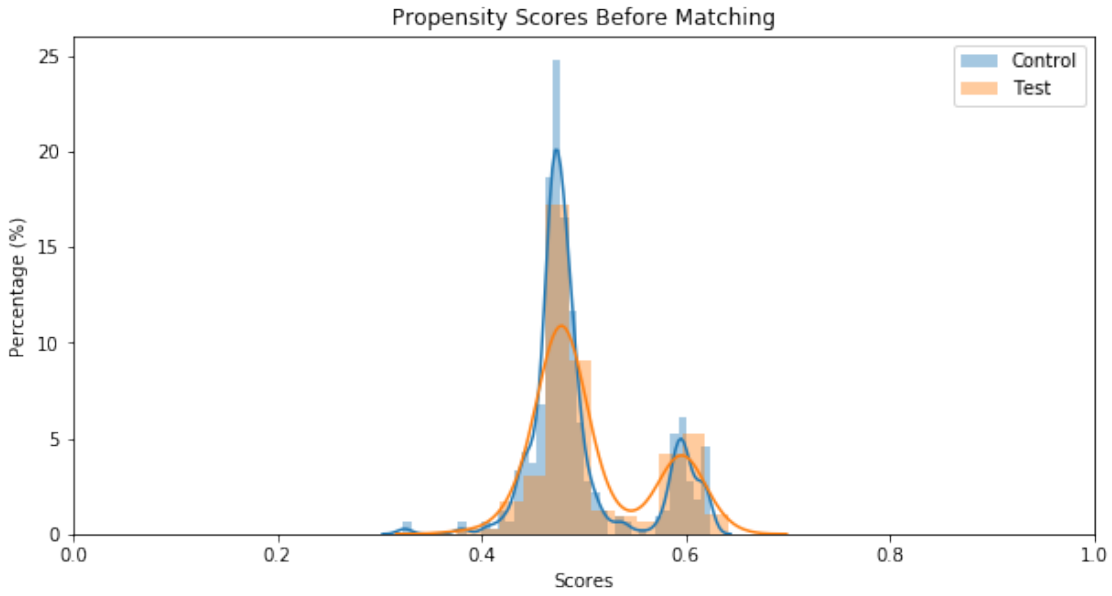
0.16.1 Assign a propensity score to each record in the dataset

[48]:
```
m.predict_scores()
```

0.17 Evaluating Common Support

We can view the distributions using `m.plot_score()`. It shows that the test and control have good common support.

[49]:
```
m.plot_scores()
```



0.17.1 K:1 Matching

Then we match one observation from the majority group to each record in the minority group with **replacement**. It means a single majority record can be matched to multiple minority records.

`Matcher` assigns a unique record_id to each record in the test and control groups so this can be addressed after matching. If subsequent modeling is planned, one might consider weighting models using a weight vector of 1/f for each record, f being an observation's frequency in the matched dataset. Thankfully Matcher can handle all of this for you :).

[50]:
```
m.match(method="min", nmatches=1) # you can also tune the threshold
```

The matching result is shown as follows: the bulk of our matched-majority-group observation occur only once, 38 occur twice, ... etc.

[51]:
```
m.record_frequency()
```

[51]:

	freq	n_records
0	1	422
1	2	38
2	3	21
3	4	7
4	5	1

We can preemptively generate a weight vector using `Matcher.assign_weight_vector()`

[52]:
```
m.assign_weight_vector()
```

0.17.2 Matched Data

Let's take a look at our matched data!

Note that in addition to the weight vector, Matcher has also assigned a match_id to each record indicating our (in this cased) paired matches since we use nmatches=1. We can verify that matched records have scores within 0.0001 of each other.

[53]:
```
matched = m.matched_data.sort_values("match_id")
matched.head(10)
```

[53]:

	record_id	weight	age	black	education	hispanic	married	nodegree	re74	re75	re78	treated	scores	match_id
8	12	0.250000	18	0	12	0	0	0	735.205078	735.205078	2502.525879	0	0.623146	0
297	425	1.000000	33	0	12	0	1	0	0.000000	0.000000	12418.070312	1	0.636166	0
9	12	0.250000	18	0	12	0	0	0	735.205078	735.205078	2502.525879	0	0.623146	1
298	426	1.000000	20	0	12	0	1	0	8644.156250	8644.156250	11656.505859	1	0.641232	1
106	152	0.250000	19	1	9	0	1	1	0.000000	0.000000	16658.250000	0	0.503781	2
299	427	1.000000	49	0	8	0	1	1	9714.596680	7285.947754	16717.121094	1	0.504047	2
170	216	0.333333	19	1	12	0	0	0	8417.000000	2814.195068	1720.906982	0	0.571606	3
300	428	1.000000	33	1	12	0	1	0	20279.949219	10941.349609	15952.599609	1	0.565150	3
93	131	1.000000	25	1	10	0	1	1	0.000000	0.000000	0.000000	0	0.494722	4
301	429	1.000000	35	1	9	0	1	1	13602.429688	13830.639648	12803.969727	1	0.494733	4

0.17.3 Assess Matched Data

[54]:
```
matched.groupby("treated").mean()
```

[54]:

treated	record_id	weight	age	black	education	hispanic	married	nodegree	re74	re75	re78	scores
0	203.814815	0.646465	24.292929	0.774411	10.313131	0.111111	0.148148	0.73064	3510.692041	3039.423917	5429.345977	0.506961
1	573.000000	1.000000	24.626263	0.801347	10.380471	0.094276	0.168350	0.73064	3570.998967	3066.098189	5976.352012	0.507069

```
          match_id
treated
0            148.0
1            148.0
```

[55]:
```
# standardized mean difference
def stmean(x):
    x_t = matched[x][matched.treated == 1].mean()
    x_c = matched[x][matched.treated == 0].mean()
    sd_t = matched[x][matched.treated == 1].std()
    stdmean =  (x_t-x_c)/sd_t
    print(stdmean)

covariates = ["age","education", "black",␣
 ↪"married","nodegree","hispanic","re74","re75"]
for x in covariates:
    stmean(x)
```

```
0.049852505643968814
0.03704661050257367
0.06739739852585085
0.053899582655417604
0.0
-0.05751517950116839
0.010446133396393737
0.005471770201405774
```

0.17.4 Regression with the Matched Data

According to Ho, Imai, King, and Stuart (2007), we can use regression to fit the model.

[56]:
```
# load regression package
import statsmodels.formula.api as smf
import statsmodels.api as sm

weight = matched["weight"].values
smf.wls('re78 ~treated',matched, weights = weight ).fit().summary()
```

[56]:
```
<class 'statsmodels.iolib.summary.Summary'>
"""
                            WLS Regression Results
==============================================================================
Dep. Variable:                   re78   R-squared:                       0.002
Model:                            WLS   Adj. R-squared:                  0.001
Method:                 Least Squares   F-statistic:                     1.419
Date:                Mon, 24 Feb 2020   Prob (F-statistic):              0.234
```

```
Time:                        11:12:02   Log-Likelihood:                -6085.8
No. Observations:                 594   AIC:                         1.218e+04
Df Residuals:                     592   BIC:                         1.218e+04
Df Model:                           1
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept   5323.2134    427.232     12.460      0.000    4484.138    6162.288
treated      653.1386    548.201      1.191      0.234    -423.517    1729.795
==============================================================================
Omnibus:                      394.296   Durbin-Watson:                   1.933
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             6572.060
Skew:                           2.678   Prob(JB):                         0.00
Kurtosis:                      18.390   Cond. No.                         2.95
==============================================================================

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
"""
```

[57]:
```
# regression with unmatached data
smf.ols('re78 ~treated',lalonde ).fit().summary()
```

[57]:
```
<class 'statsmodels.iolib.summary.Summary'>
"""
                            OLS Regression Results
==============================================================================
Dep. Variable:                   re78   R-squared:                       0.005
Model:                            OLS   Adj. R-squared:                  0.003
Method:                 Least Squares   F-statistic:                     3.525
Date:                Mon, 24 Feb 2020   Prob (F-statistic):             0.0609
Time:                        11:12:03   Log-Likelihood:                -7333.1
No. Observations:                 722   AIC:                         1.467e+04
Df Residuals:                     720   BIC:                         1.468e+04
Df Model:                           1
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept   5090.0482    302.783     16.811      0.000    4495.606    5684.491
treated      886.3038    472.086      1.877      0.061     -40.526    1813.134
==============================================================================
Omnibus:                      384.449   Durbin-Watson:                   2.072
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             3767.288
Skew:                           2.195   Prob(JB):                         0.00
```

```
Kurtosis:                       13.294   Cond. No.                         2.46
==============================================================================

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
"""
```

[58]:
```
# you could also add covariates into the regression
smf.wls('re78 ~treated + age+ education + black+ married + nodegree + hispanic +␣
 ↪re74 + re75', matched, weights =weight ).fit().summary()
```

[58]:
```
<class 'statsmodels.iolib.summary.Summary'>
"""
                            WLS Regression Results
==============================================================================
Dep. Variable:                   re78   R-squared:                       0.029
Model:                            WLS   Adj. R-squared:                  0.014
Method:                 Least Squares   F-statistic:                     1.925
Date:                Mon, 24 Feb 2020   Prob (F-statistic):             0.0460
Time:                        11:12:04   Log-Likelihood:                -6077.8
No. Observations:                 594   AIC:                         1.218e+04
Df Residuals:                     584   BIC:                         1.222e+04
Df Model:                           9
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept    367.5721   2940.969      0.125      0.901   -5408.592    6143.736
treated      606.3762    546.507      1.110      0.268    -466.983    1679.735
age           29.9408     40.656      0.736      0.462     -49.909     109.790
education    398.9888    200.406      1.991      0.047       5.384     792.594
black       -261.3799    864.816     -0.302      0.763   -1959.908    1437.148
married      774.7219    765.501      1.012      0.312    -728.749    2278.193
nodegree    -189.5796    834.935     -0.227      0.820   -1829.420    1450.261
hispanic     858.3063   1164.786      0.737      0.461   -1429.373    3145.986
re74          -0.0135      0.096     -0.140      0.889      -0.202       0.176
re75           0.1005      0.113      0.892      0.373      -0.121       0.322
==============================================================================
Omnibus:                      397.540   Durbin-Watson:                   1.931
Prob(Omnibus):                  0.000   Jarque-Bera (JB):             7054.114
Skew:                           2.685   Prob(JB):                         0.00
Kurtosis:                      19.006   Cond. No.                     1.03e+05
==============================================================================

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
```

```
specified.
[2] The condition number is large, 1.03e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
"""
```

[ ]: