

Causal Inference Assignment

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April 2024

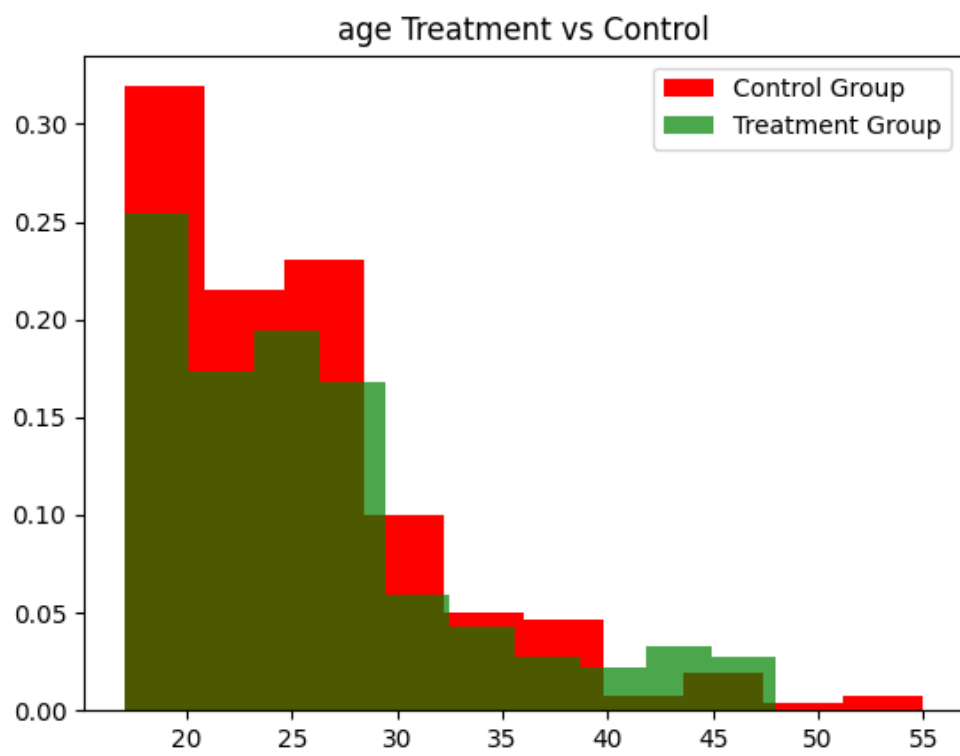
1 Q1

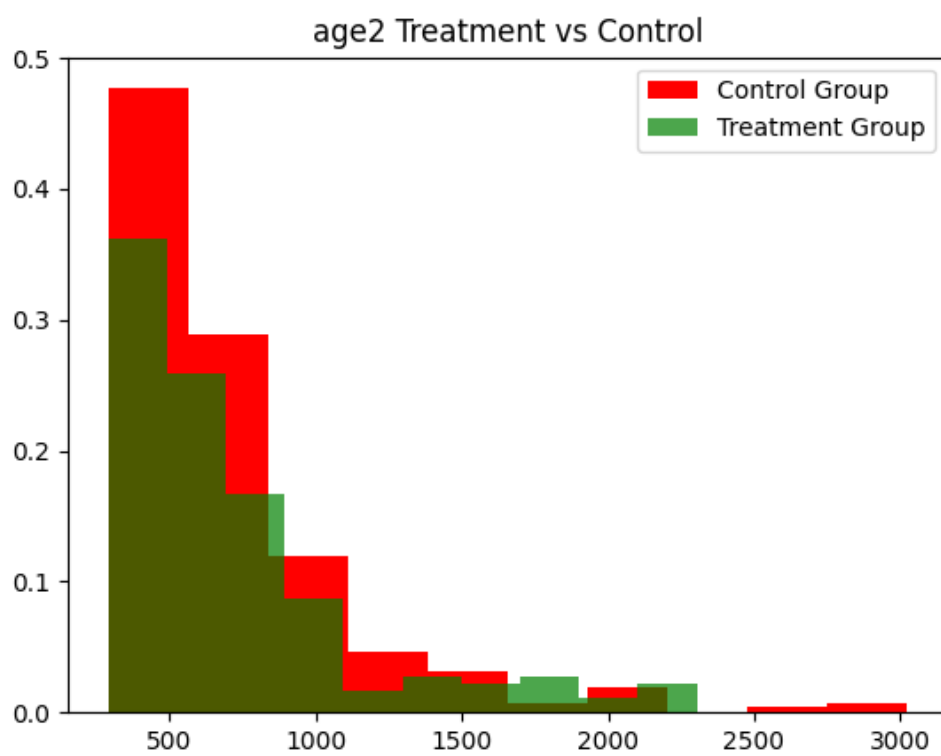
2 Q3

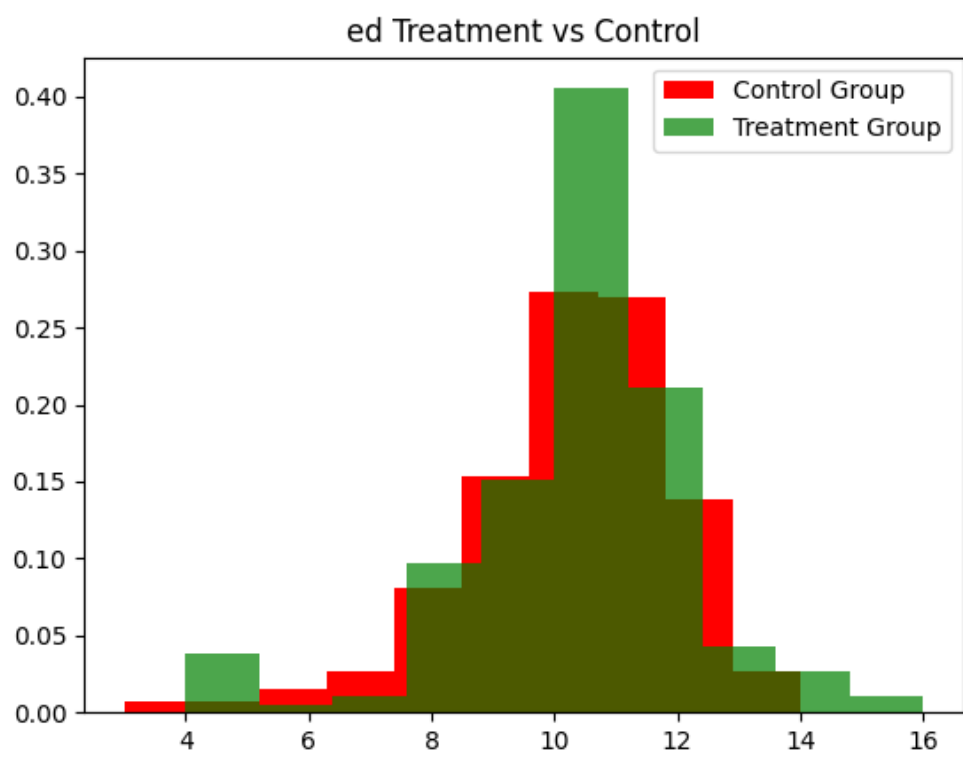
2.1 a) Exploratory Data Analysis

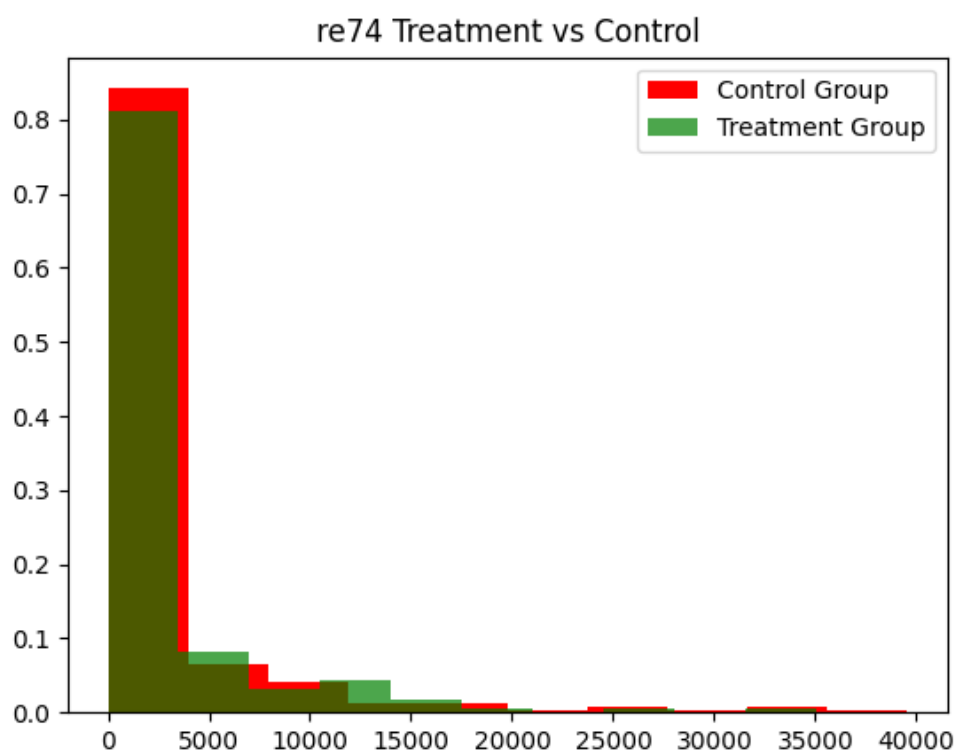
After exploratory data analysis we find that the data comes from the same distribution for both treatment and control groups for all variables.

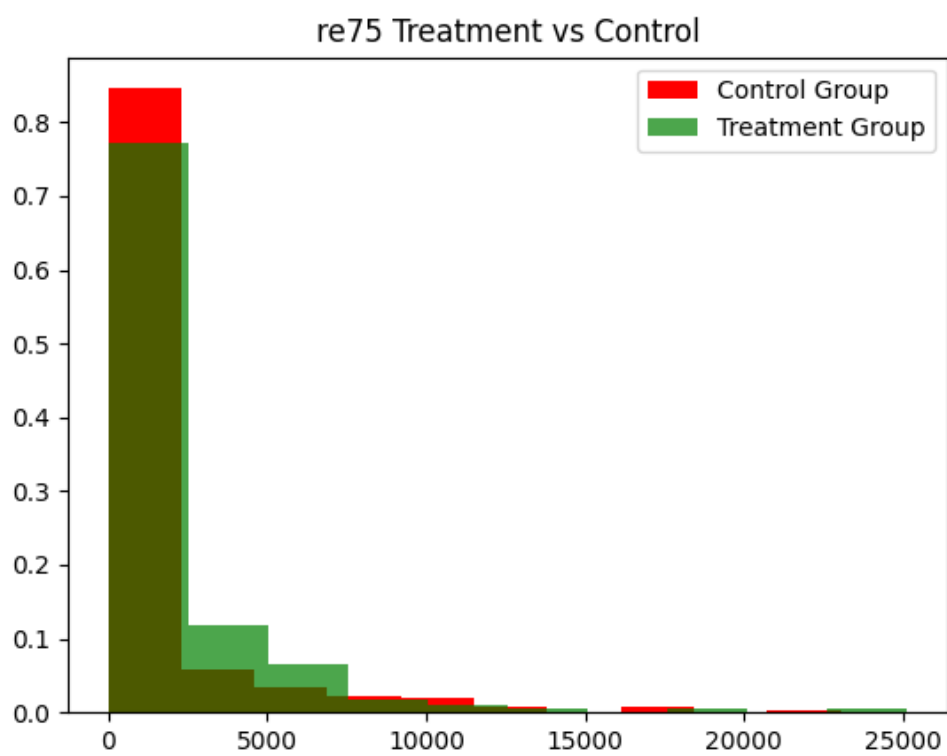
To do this we first plot the probability distributions of the columns in the form of a histogram and overlap the histogram for each columns for treatment and control groups.











As we can see for all of the variable the distributions look similar. Now we use statistical tests to estimate the difference between these.

2.1.1 Continuous Variables

For continuous variables we use the students t-test to see if the means of the distributions are significantly different or not.

Here is what we obtain:

Column age has T-statistic value = 1.116614928783765 with p-value = 0.2647642688056856
Hence we cannot say that the distributions are different with significance (<0.05)

Column re74 has T-statistic value = -0.022175136958298255 with p-value = 0.9823182350488567
Hence we cannot say that the distributions are different with significance (<0.05)

Column re75 has T-statistic value = 0.8746214935780514 with p-value = 0.3822538041052975
Hence we cannot say that the distributions are different with significance (<0.05)

Column age2 has T-statistic value = 0.9694696864328992 with p-value = 0.3328398944498051
Hence we cannot say that the distributions are different with significance (<0.05)

Column ed has T-statistic value = 1.4958255190965968 with p-value = 0.13541116716943868
Hence we cannot say that the distributions are different with significance (<0.05)

2.1.2 Binary Variables

For binary variables we use the chi-square test to check if the categorical distributions are significantly different.

Here is what we obtain:

Column black as chi-sq value = 0.10662384969179997 with p-value = 0.7440210684680046
Hence we cannot say that the distributions are different with significance (<0.05)

Column hisp as chi-sq value = 2.5705628867929904 with p-value = 0.10886898726859187
Hence we cannot say that the distributions are different with significance (<0.05)

Column married as chi-sq value = 0.7277914114738451 with p-value = 0.39360001605637096
Hence we cannot say that the distributions are different with significance (<0.05)

Column nodeg as chi-sq value = 9.41953941767863 with p-value = 0.0021468543756801464
Hence the distributions are the same with significance (<0.05)

2.2 b) Regression Analysis

Next we perform linear regression on both the NSW dataset and the CPS dataset, predicting the Earnings in 1978 (re78) based on all the other variables.

Here were the results:

Model Coefs for NSW linear regression model:

```
{'treat': 1675.86237707045,
'age': 141.7305740712043,
'ed': 385.0161271012323,
'black': -2155.6413034136403,
'hisp': 187.26272427409285,
'married': -184.89434030167712,
'nodeg': -55.544821817317654,
're74': 0.08147524244690274,
're75': 0.05081520903056003,
'age2': -1.4353216616441316,
'intercept': -307.01194195694006}
```

Model coefs for CPS linear regression model:

```
{'treat': 0.0,
'age': -252.04850736152875,
'ed': 166.5983024477533,
'black': -773.8794130598889,
'hisp': -168.2285611161221,
'married': 244.1442902105978,
'nodeg': 330.6765477182316,
're74': 0.2988692873561547,
're75': 0.46995885500493273,
'age2': 2.0408054257313957,
'intercept': 7908.362295098289}
```

2.3 c) Matching through Propensity Score

2.3.1 Calculate Propensity Score

We perform logistic regression, with treatment variable as the dependent variable and all the other columns, other than re78 as the predictors since re78 is an effect of treatment variable.

Here is the logitic model we obtain for calculating the Propensity score:

Model Coefs for propensity score model:

```
{'age': -0.021718495698239637,
'ed': -0.013541674687343404,
```

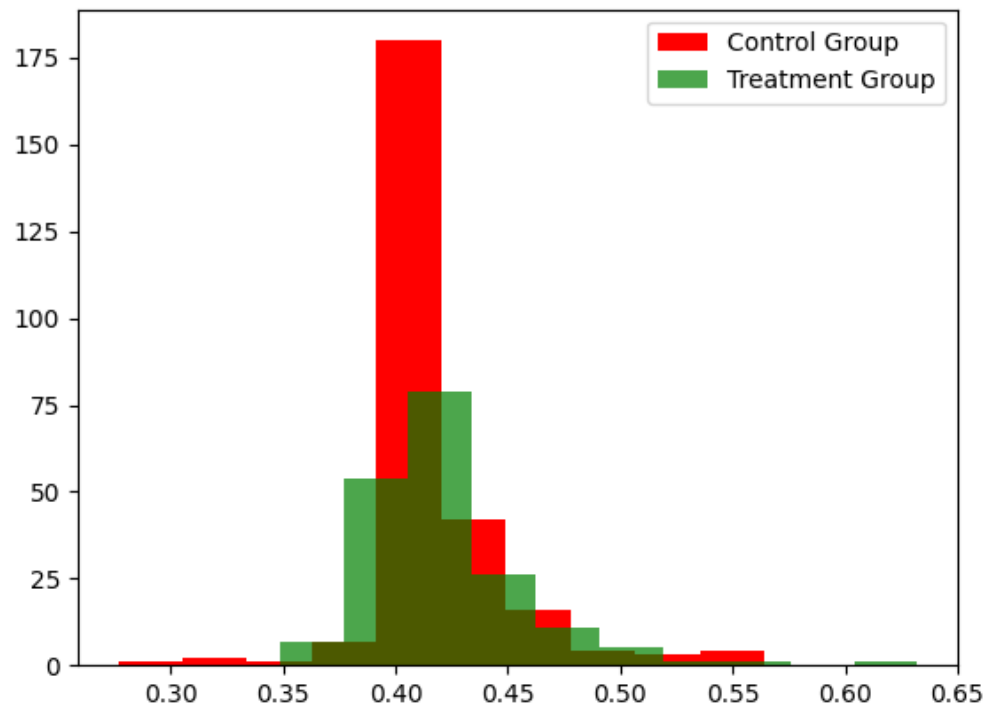


```
'black': -0.0010854880038832747,  
'hisp': -0.0008041072459307032,  
'married': 0.00020745846105355112,  
'nodeg': -0.0029588755215886027,  
're74': -1.8443713277604196e-05,  
're75': 4.548966676852774e-05,  
'age2': 0.0004956004644433062,  
'intercept': -0.0016417668379095835}
```

2.3.2 Matching Method

First we plot the propensity scores of the treatment group and control group on a histogram to compare there values.

Here is the plot:



So we can see that they do have a common support ranging from around 0.35 to 0.50.

Now we figure out the matchings between the control and treatment group. Since we are to match every treatment point to one control point and repetition is allowed.

We follow the following algorithm:

1. Choose point in treatment data
2. Get its propensity score
3. Iterate over all points in control group, and using a distance metric find the point in control whose propensity score is closest to the point in treatment
4. Match this control point to the choosen treatment point
5. Choose the next point in treatment
6. Repeat untill all points in treatment have a match

To perform this 1 nearest neibour approach we use the following distance metric:

$$d_{PS} = (\log(\frac{\hat{\pi}_1}{1 - \hat{\pi}_1}) - \log(\frac{\hat{\pi}_2}{1 - \hat{\pi}_2}))^2$$

Here are the matchings that we obtained:

Dictionary of matches: {0: 403, 1: 187, 2: 260, 3: 253, 4: 405, 5: 187, 6: 265, 7: 278, 8: 374, 9: 317, 10: 287, 11: 387, 12: 316, 13: 223, 14: 254, 15: 322, 16: 279, 17: 185, 18: 396, 19: 310, 20: 234, 21: 306, 22: 406, 23: 233, 24: 326, 25: 292, 26: 203, 27: 223, 28: 327, 29: 233, 30: 327, 31: 435, 32: 270, 33: 217, 34: 252, 35: 406, 36: 227, 37: 265, 38: 443, 39: 201, 40: 265, 41: 222, 42: 317, 43: 276, 44: 224, 45: 270, 46: 317, 47: 343, 48: 227, 49: 265, 50: 389, 51: 315, 52: 320, 53: 252, 54: 222, 55: 327, 56: 232, 57: 434, 58: 406, 59: 366, 60: 317, 61: 254, 62: 216, 63: 253, 64: 424, 65: 196, 66: 253, 67: 380, 68: 443, 69: 234, 70: 266, 71: 189, 72: 298, 73: 252, 74: 408, 75: 198, 76: 265, 77: 187, 78: 406, 79: 251, 80: 252, 81: 310, 82: 424, 83: 279, 84: 207, 85: 425, 86: 315, 87: 225, 88: 382, 89: 208, 90: 315, 91: 327, 92: 203, 93: 265, 94: 281, 95: 299, 96: 188, 97: 436, 98: 219, 99: 197, 100: 201, check python code for more values.

2.3.3 New dataset and Analysis

Based on the matching, we create a new dataset where only those points in control group are included which are matched to some value in the treatment group.

But it turns out in our analysis, all the control points were matched to some point in the treatment group, since the control group is smaller than the treatment group. So we obtain exactly the same dataset.

Yet we perform regression analysis on it again and obtain the following model:

Model Coefs for new NSW linear regression model:

```
{'treat': 1675.86237707045,  
'age': 141.7305740712043,  
'ed': 385.0161271012323,  
'black': -2155.6413034136403,  
'hisp': 187.26272427409285,  
'married': -184.89434030167712,  
'nodeg': -55.544821817317654,  
're74': 0.08147524244690274,  
're75': 0.05081520903056003,  
'age2': -1.4353216616441316,  
'intercept': -307.01194195694006}
```

Which is exactly the same as our previous model:

Model Coefs for NSW linear regression model:

```
{'treat': 1675.86237707045,  
'age': 141.7305740712043,  
'ed': 385.0161271012323,  
'black': -2155.6413034136403,  
'hisp': 187.26272427409285,  
'married': -184.89434030167712,  
'nodeg': -55.544821817317654,  
're74': 0.08147524244690274,  
're75': 0.05081520903056003,  
'age2': -1.4353216616441316,  
'intercept': -307.01194195694006}
```

Click [here](#) to see the python implementation on github.

I have also attached the whole code as a zip file for your convenience.