lab08_student_version

November 3, 2021

1 Lab 8: Estimating Causal Effects Using Unconfoundedness

Welcome to the eighth DS102 lab!

The goals of this lab is to implement and better understand causal inference in observational studies using the unconfoundedness assumption.

The code you need to write is commented out with a message "TODO: fill in".

1.1 Collaboration Policy

Data science is a collaborative activity. While you may talk with others about the labs, we ask that you **write your solutions individually**. If you do discuss the assignments with others please **include their names** in the cell below.

1.2 Gradescope Submission

To submit this assignment, rerun the notebook from scratch (by selecting Kernel > Restart & Run all), and then print as a pdf (File > download as > pdf) and submit it to Gradescope.

This assignment should be completed and submitted before Wednesday November 3rd, 2021, at 11:59 PM PST.

1.3 Collaborators

Write the names of your collaborators in this cell.

`<Collaborator Name> <Collaborator e-mail>`

[1]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import statsmodels.api as sm
import seaborn as sns
import itertools


import hashlib

sns.set(style="dark")
plt.style.use("ggplot")
```

```
%matplotlib inline
```

2 Causal Inference Background and Review

In the last lab, you saw how we could use instrumental variables to identify a causal effect from observational study data. But in many cases, it may not be so easy to find a good instrumental variable. In this lab, we'll explore other ways to identify causal effects.

2.1 Potential Outcomes and Average Treatment Effect

In general, we can measure the causal effect of a binary treatment Z on an outcome Y by considering the potential outcomes $Y(0)$ and $Y(1)$. Recall that these are *potential* outcomes: they represent thought experiments about what would happen if the treatment was or wasn't applied. In the real world, we only ever get to observe one of them for any individual, depending on whether that unit received the treatment or not.

We defined the average treatment effect (ATE, represented by the Greek letter τ) as:

$$\tau = E[Y(1) - Y(0)]$$

This represents the causal effect of a treatment Z on an outcome Y. We saw that in general, we were unable to compute this without making assumptions. If our data come from a randomized experiment, then we saw that the difference in group means (SDO) was an unbiased estimate of the ATE:

$$\hat{\tau} = \underbrace{\frac{1}{n_1}\sum_{i:Z_i=1} Y_i}_{\text{mean of treatment group}} - \underbrace{\frac{1}{n_0}\sum_{i:Z_i=0} Y_i}_{\text{mean of control group}}$$

2.2 Independence and Unconfoundedness

Recall that in a randomized experiment, we make treatment decisions completely at random. This prevents the treatment from being confounded by any external factors. Unfortunately, in an observational study, we often must deal with confounders: variables that have a causal effect on both the treatment and the outcome. Mathematically, in a randomized experiment, we say that

$$Z_i \perp\!\!\!\perp \big(Y_i(0), Y_i(1)\big) \ \forall i$$

meaning that knowing any unit's treatment status doesn't give us any additional information about the distribution of their potential outcomes ("what-ifs"). For example, in a drug trial, because of randomization, the people who receive the drug have the same (distribution of) potential outcomes as the people who receive a placebo, since there are no systematic differences between the treatment and control groups.

In an observational study, this usually isn't true. For example, suppose we are interested in the effect of a job training program on income. People who receive the job training program might be poorer than people who don't, and so whether they receive the training or not, their incomes might be lower. In this case, the treatment variable (job training program) gives us information about both potential outcomes (income with the program, and income without the program), because of the confounding effect of socioeconomic status (and other variables which we'll explore in this lab).

Throughout this lab, we'll need to make the assumption of **unconfoundedness**, which says that the treatment and potential outcomes are *conditionally* independent given a set of known confounding variables X. Mathematically,

$$Z_i \perp\!\!\!\perp \big(Y_i(0), Y_i(1)\big) \mid X_i \; \forall i$$

If we make this assumption, we can use a few different approaches to estimate the average treatment effect.

3 Problem Setup and Data

For this lab, you'll be working with data from a job training program in the mid-1970s called the National Supported Work Demonstration. The data (and the results we'll reproduce) come from a famous 1986 paper by Robert LaLonde, Evaluating the Econometric Evaluations of Training Programs. Here's a description of the program from the original paper (emphasis added):

> The National Supported Work Demonstration (NSW) was a temporary employment program designed to help disadvantaged workers lacking basic job skills move into the labor market by giving them work experience and counseling in a sheltered environment. Unlike other federally sponsored employment and training programs, the NSW program **assigned qualified applicants to training positions randomly**. Those assigned to the treatment group received all the benefits of the NSW program, while those assigned to the control group were left to fend for themselves.

Here are a few more important excerpts from the paper, describing the participants and data collected (emphasis and links added):

> The MDRC admitted into the program AFDC women, ex-drug addicts, ex-criminal offenders, and high school dropouts of both sexes. For those assigned to the treatment group, the program guaranteed a job for 9 to 18 months, depending on the target group and site. The treatment group was divided into crews of three to five participants who worked together and met frequently with an NSW counselor to discuss grievances and performance…
>
> The type of work even varied within sites. In particular, **male and female participants frequently performed different sorts of work**. The female participants usually worked in service occupations, whereas the male participants tended to work in construction occupations.
>
> The MDRC collected earnings and demographic information from both the treatment and the control group at baseline and every nine months thereafter. MDRC also conducted up to four post-baseline interviews.

Our goal will be to estimate the causal effect of the training program on income. Specifically, we will compare the income of people in 1974, 1975 (before the training program) with their income in 1978 (after the program).

Just like LaLonde did, we'll start by evaluating the randomized experiment. Then, we'll look at what would happen if we didn't have a control group, and instead had to use data from an observational study.

4 Part I: Randomized Experiment

Let's begin by looking at the data from the NSW experiment. It contains the following columns: * `data_id`: always `NSW`, incidcating that the data are from the NSW randomized experiment * `treat`: binary variable indicating treatment (1 for job training, 0 for control) * `age`: age in years * `educ`: number of years of education * `black`: whether the worker was Black (1) or not (0). * `hisp`: whether the worker was Hispanic (1) or not (0). * `marr`: whether the worker was married (1) or not (0). * `nodegree`: whether the worker had a high school diploma (0) or not (1). * `re74`, `re75`: earnings in 1974 and 1975, before the program * `re78`: earnings in 1978, after the program. * `outcome`: difference in earnings from 1974 to 1978

[2]:
```python
nsw = pd.read_csv('nsw_dw.csv')
nsw
```

[2]:
```
    data_id  treat   age  educ  black  hisp  marr  nodegree       re74  \
0       NSW    1.0  37.0  11.0    1.0   0.0   1.0       1.0      0.000
1       NSW    1.0  22.0   9.0    0.0   1.0   0.0       1.0      0.000
2       NSW    1.0  30.0  12.0    1.0   0.0   0.0       0.0      0.000
3       NSW    1.0  27.0  11.0    1.0   0.0   0.0       1.0      0.000
4       NSW    1.0  33.0   8.0    1.0   0.0   0.0       1.0      0.000
..      …     …     …     …     …     …     …        …         …
440     NSW    0.0  21.0   9.0    1.0   0.0   0.0       1.0  31886.430
441     NSW    0.0  28.0  11.0    1.0   0.0   0.0       1.0  17491.450
442     NSW    0.0  29.0   9.0    0.0   1.0   0.0       1.0   9594.308
443     NSW    0.0  25.0   9.0    1.0   0.0   1.0       1.0  24731.620
444     NSW    0.0  22.0  10.0    0.0   0.0   1.0       1.0  25720.920

        re75        re78     outcome
0       0.00   9930.0460   9930.0460
1       0.00   3595.8940   3595.8940
2       0.00  24909.4500  24909.4500
3       0.00   7506.1460   7506.1460
4       0.00    289.7899    289.7899
..       …          …           …
440 12357.22      0.0000 -31886.4300
441 13371.25      0.0000 -17491.4500
442 16341.16  16900.3000   7305.9930
443 16946.63   7343.9640 -17387.6560
444 23031.98   5448.8010 -20272.1200

[445 rows x 12 columns]
```

In Part I, we assume the participants are randomly assigned to the treatment group, i.e attending the training program (`treat = 1`) and the control group, i.e. not attending the training program (`treat = 0`). Hence, we can compute the causal effect using the following expression:

$$\hat{\tau} = \underbrace{\frac{1}{n_1}\sum_{i:Z_i=1} Y_i}_{\text{mean of treatment group}} - \underbrace{\frac{1}{n_0}\sum_{i:Z_i=0} Y_i}_{\text{mean of control group}}$$

4.1 Question 1a Compute causal effect in randomized experiments

Complete the code below to output the causal effect of training program on participants' income using the expression above.

[3]:
```
# Question 1a, TODO here
causal_effect_nsw = np.mean(nsw.loc[nsw['treat'] == 1, 're78']) - np.mean(nsw.
↪loc[nsw['treat'] == 0, 're78']) # TODO
causal_effect_nsw
```

[3]:
```
1794.342404270271
```

[4]:
```
# Validation tests: Do not modify
assert np.abs(causal_effect_nsw - 1794.3424) < 0.1
print("Test passed!")
```

```
Test passed!
```

4.2 Question 1b Interpret the result

Based on your answer above, what is the causal effect of attending the training program on income? In other words, does attending the training program lead to higher income?

TODO: There is a large positive casual affect of attending the training program on income. So yes, attending the training program leads to higher income. This is because the `causal_effect_nsw` value is large, which means that the mean income of the treatment group is significantly higher than the mean income of the control group.

5 Part II: Using an Observational Study

Now, suppose instead that (like many programs) this hadn't been a randomized experiment. In that case, we would need to find a separate population to use as our "control group". LaLonde used the Current Population Survey (CPS), a publicly available dataset, as a control group. Let's now look at this data: for your convenience, it has the same columns as the NSW data above. Note that it's much larger!

[5]:
```
cps = pd.read_csv('cps.csv')
cps
```

[5]:
```
     data_id  treat  age  educ  black  hisp  marr  nodegree       re74  \
0        CPS      0   45    11      0     0     1         1  21516.670
1        CPS      0   21    14      0     0     0         0   3175.971
```

```
2           CPS      0    38     12       0      0      1         0  23039.020
3           CPS      0    48      6       0      0      1         1  24994.370
4           CPS      0    18      8       0      0      1         1   1669.295
…         …      …   …    …     …     …    …       …         …
15987       CPS      0    22     12       1      0      0         0   3975.352
15988       CPS      0    20     12       1      0      1         0   1445.939
15989       CPS      0    37     12       0      0      0         0   1733.951
15990       CPS      0    47      9       0      0      1         1  16914.350
15991       CPS      0    40     10       0      0      0         1  13628.660

            re75       re78     outcome
0      25243.550  25564.670   4048.0000
1       5852.565  13496.080  10320.1090
2      25130.760  25564.670   2525.6504
3      25243.550  25564.670    570.3008
4      10727.610   9860.869   8191.5740
…            …          …           …
15987   6801.435   2757.438  -1217.9141
15988  11832.240   6895.072   5449.1330
15989   1559.371   4221.865   2487.9140
15990  11384.660  13671.930  -3242.4200
15991  13144.550   7979.724  -5648.9360

[15992 rows x 12 columns]
```

For the rest of the lab, we'll work with a modified version of the data that doesn't have any randomized controls, only the ones from the general population. In the cell below, we creat a new dataframe called `obs` by concatenating the `cps` dataframe with rows of the `nsw` dataframe corresponding to the people who attended the training program.

Your answers to all remaining questions should only use the `obs` table, not the `nsw` table!*

[6]:
```
treated = nsw[nsw['treat'] == 1]
obs = pd.concat([treated, cps], ignore_index=True)
obs
```

[6]:
```
        data_id  treat   age  educ  black  hisp  marr  nodegree       re74  \
0           NSW    1.0  37.0  11.0    1.0   0.0   1.0       1.0      0.000
1           NSW    1.0  22.0   9.0    0.0   1.0   0.0       1.0      0.000
2           NSW    1.0  30.0  12.0    1.0   0.0   0.0       0.0      0.000
3           NSW    1.0  27.0  11.0    1.0   0.0   0.0       1.0      0.000
4           NSW    1.0  33.0   8.0    1.0   0.0   0.0       1.0      0.000
…         …    …    …    …    …    …    …     …        …         …
16172       CPS    0.0  22.0  12.0    1.0   0.0   0.0       0.0   3975.352
16173       CPS    0.0  20.0  12.0    1.0   0.0   1.0       0.0   1445.939
16174       CPS    0.0  37.0  12.0    0.0   0.0   0.0       0.0   1733.951
16175       CPS    0.0  47.0   9.0    0.0   0.0   1.0       1.0  16914.350
```

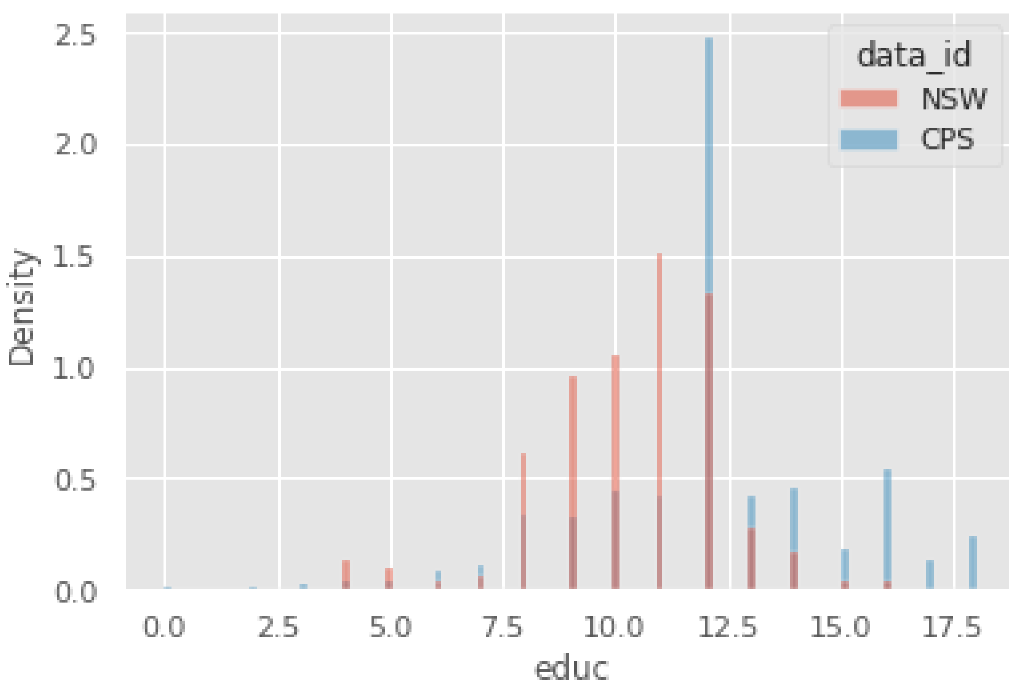
```
16176      CPS     0.0   40.0   10.0     0.0    0.0    0.0       1.0   13628.660

              re75        re78      outcome
0            0.000   9930.0460    9930.0460
1            0.000   3595.8940    3595.8940
2            0.000  24909.4500   24909.4500
3            0.000   7506.1460    7506.1460
4            0.000    289.7899     289.7899
…              …          …          …
16172     6801.435   2757.4380   -1217.9141
16173    11832.240   6895.0720    5449.1330
16174     1559.371   4221.8650    2487.9140
16175    11384.660  13671.9300   -3242.4200
16176    13144.550   7979.7240   -5648.9360

[16177 rows x 12 columns]
```

The following histogram compares the distribution of education between the NSW treatment group and the CPS group:

[7]:
```
sns.histplot(data=obs, x='educ', hue='data_id', stat='density',␣
↪common_norm=False);
```



5.1 Question 2a

Based on the histogram above, we can say that education is a confounding variable. How can you justify this claim? In other words, why is education a confounding variable?

Hint: What kind of association do you expect between education and income?

TODO: I expect a positive association between education and income. Hence, education is a confounding variable because it has a direct impact on the income.

5.2 Question 2b

As our first attempt to estimate the causal effect, we decide to try what we did in Question 1. In other words, we compute the Simple Difference in Observed group means (SDO) for this observational data.

Complete the code below to output compute the SDO using dataset `obs`.

Hint: The code is very similar to the code in question 1a.

[8]:
```
# Question 2b, TODO here
sdo = np.mean(obs.loc[obs['treat'] == 1, 're78']) - np.mean(obs.
 ↪loc[obs['treat'] == 0, 're78'])# TODO
sdo
```

[8]:
```
-8497.516142636992
```

[9]:
```
# Validation tests: Do not modify
assert np.abs(sdo + 8497.51614) < 0.1
print("Test passed!")
```

```
Test passed!
```

You should have found a negative result. This is because of confounding: even though the actual effect of the program is positive (as we saw from the randomized experiment), the treatment group and our CPS group are very different. In particular, individuals in the treatment group face many disadvantages that cause their earnings to be lower, and also cause them to be more likely to end up in the treatment group.

6 Part III: Unconfoundedness Techniques

6.1 Technique 1. Outcome Regression

Suppose the provided variables (age, years of education, Black/Hispanic race, marriage, and diploma) are the only confounders in this problem. In that case, we can make the unconfoundedness assumption, where X represents the collection of all 6 confounding variables listed above.

Suppose we fit a linear model of the following form:

Earnings $= \tau * Z + a*$age $+ b*$years of education $+ c*$isBlack $+ d*$isHispanic $+ e*$isMarried $+ f*$hasDiploma.

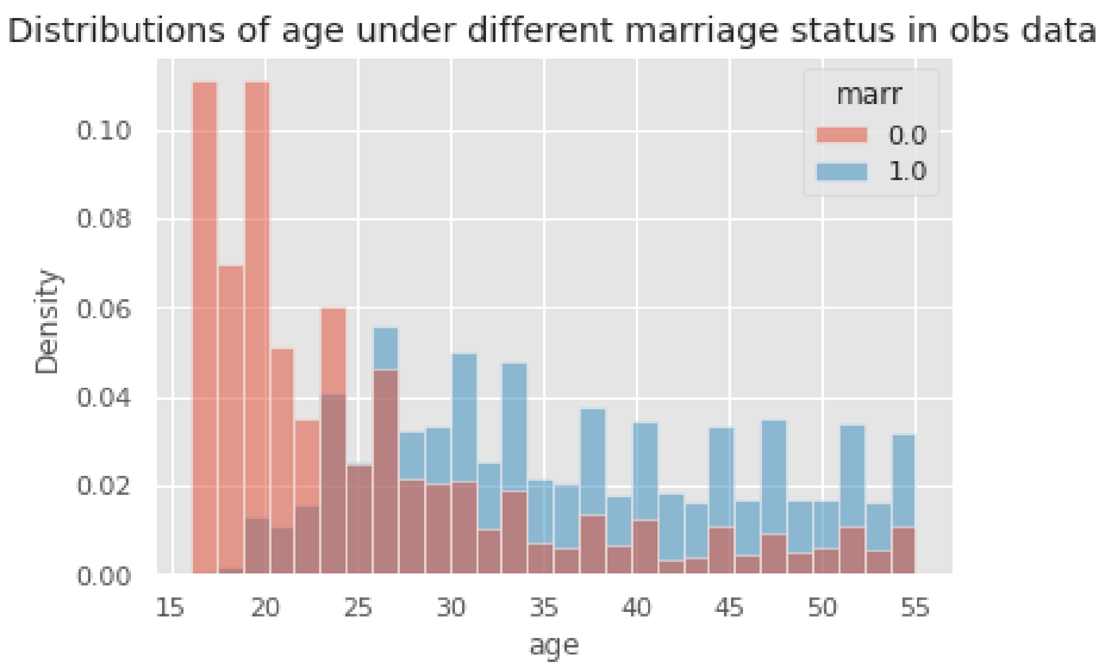
We saw in lecture that if we make two assumptions, then the estimated coefficient of treament from OLS, $\hat{\tau}$, will be an unbiased estimate of the ATE. The two assumptions are:

1. Assume unconfoundedness (described above).
2. Assume this linear model correctly describes the interaction between the variables.

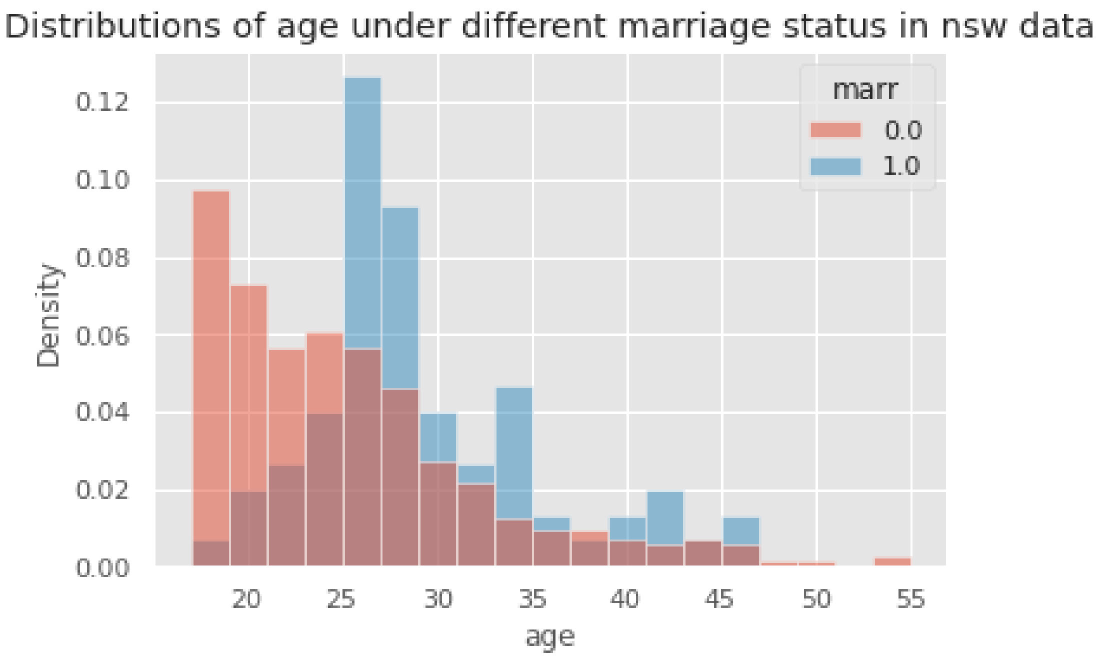
We'll take assumption 1 for granted for now. Assumption 2, however, is much more questionable: it's not clear that the confounding variables would all have a linear effect on earnings. Much worse than that, though, is the fact that the linear model above does not model any interactions between the variables. In particular, it assumes that the effect of each confounder is the same for both treatment and control. This is probably unrealistic.

For example, married individuals in the CPS sample might have more financial stability (since they may wait for financial stability to get married), which might not be true in the NSW sample (where individuals have much lower financial stability overall). But, the model above only uses one coefficient, e, for the effect of marriage on income, regardless of whether an individual is from the treatment or control. See the histograms below.

[10]:
```
sns.histplot(data=obs, x='age', hue='marr', stat='density', common_norm=False);
plt.title("Distributions of age under different marriage status in obs data");
```



[11]:
```
sns.histplot(data=nsw, x='age', hue='marr', stat='density', common_norm=False);
plt.title("Distributions of age under different marriage status in nsw data");
```



Neverthless, let's try to fit a linear model and see how well it performs. The code below are taken from previous labs.

[12]:
```
# No TODOs here: Just examine the code
def fit_OLS_model(df, target_variable, explanatory_variables, intercept =␣
↪False):
    """
    Fits an OLS model from data.

    Inputs:
        df: pandas DataFrame
        target_variable: string, name of the target variable
        explanatory_variables: list of strings, names of the explanatory␣
↪variables
        intercept: bool, if True add intercept term
    Outputs:
        fitted_model: model containing OLS regression results
    """

    target = df[target_variable]
    inputs = df[explanatory_variables]
    if intercept:
        inputs = sm.add_constant(inputs)

    fitted_model = sm.OLS(target, inputs).fit()
```

```
    return(fitted_model)

def mean_squared_error(true_vals, predicted_vals):
    """
    Return the mean squared error

    Inputs:
        true_vals: array of true labels
        predicted_vals: array labels predicted from the data
    Output:
        float, mean squared error of the predicted values
    """
    return np.mean((true_vals - predicted_vals) ** 2)
```

As a reminder, in previous labs, we used it like this: `fit_OLS_model(student_data, 'NumBooks', ['ReadathonDuration', 'Income'])`

6.2 Question 3a

Complete the code below by using the functions above to fit a model to predict 1978 income from the treatment and the confounding variables.

[13]:
```
# Question 3a, TODO here
linear_model = fit_OLS_model(obs, 're78', ['treat','age', 'educ', 'black',␣
 ↪'hisp', 'marr', 'nodegree'], intercept=False)  # TODO
#print(linear_model.summary())
```

[14]:
```
# Compute the mean square error of the values predicted by model. No need to␣
 ↪modify here,
predicted = linear_model.predict(obs[['treat', 'age', 'educ', 'black', 'hisp',␣
 ↪'marr', 'nodegree']]).values
err = mean_squared_error(obs['re78'].values, predicted)
err
```

[14]: 84944525.405008

[15]:
```
# Validation tests: Do not modify
assert np.abs(err - 84944525) < 100
print("Test passed!")
```

```
Test passed!
```

6.3 Question 3b

Explain, in your own words, why linear regression produces a very incorrect result for this question.

Hint: we've mostly answered this question for you above; you just have to understand and explain in your own words here.

TODO: If we pick OLS as a regression model, then we assume that the relationship between variables is linear. In this case, the relationship between variables is not linear which is why it produces a very incorrect result.

6.4 Technique 2: Matching

We have seen above that a simple linear regression model is not ideal. Now, we consider a technique introduced in lecture called matching.

Consider two individuals, one treated and one untreated, with the exact same values of all confounding variables X. Here's an example of someone from the NSW study and someone from the CPS data with the exact same set of confounding variables:

[16]:
```
nsw.iloc[50:51, :]
```

[16]:
```
   data_id  treat   age  educ  black  hisp  marr  nodegree  re74  re75  re78  \
50     NSW    1.0  28.0   8.0    1.0   0.0   0.0       1.0   0.0   0.0   0.0

    outcome
50      0.0
```

[17]:
```
cps.iloc[2363:2364, :]
```

[17]:
```
     data_id  treat  age  educ  black  hisp  marr  nodegree     re74  \
2363     CPS      0   28     8      1     0     0         1  15286.2

          re75  re78  outcome
2363  3863.516   0.0 -15286.2
```

If we assume unconfoundedness, then for these two people, there should be no other variables that have an effect on both the treatment and the outcome. So, by subtracting their outcomes, we should be able to estimate the causal effect of the job training program for this particular X (specifically, 28-year old, unmarried, Black, non-Hispanic people without high school diplomas who've completed 8 years of schooling).

If we do this for every possible set of values for the confounders X, then we can take all of them and compute the expectation (weighting each by the probability of seeing that corresponding value of X). Empirically, this corresponds to just taking the average of all the data points.

Here is the matching algorithm in English:

1. For each treated row:
    - Find all untreated rows that have the exact same values of all confounders.
    - Take those untreated rows and average their outcome
    - Subtract the average above from the treated row's outcome
2. For each *untreated* row:
    - Find all *treated* rows that have the exact same values of all confounders.
    - Take those *treated* rows and average their outcome
    - Subtract the *untreated* row's outcome from the average above

3. Average all the results from steps 1 and 2.

6.5 Question 3c

Explain why this exact maching algorithm will not work for the dataset provided.

Hint: What if there are no matches for a person?

TODO: If there are no matches for a person, the algorithm just won't do anything. There are no "untreated/treated rows that have the exact same values of all confounders". In this case, it is unlikely that treatment, age, educ, black, hisp, marr, nodegree are all the same. It will be hard to find exact matches.

There are solutions such as approximate matching which matches people if they have similar features (not necessarily identical), but we'll instead turn to using propensity scores instead.

6.6 Technique 3: Inverse Propensity Weighting

Recall the definition of the propensity score: it is the probability that a unit was treated, conditioned on a particular set of confounders x:

$$e(x) = P(Z = 1|X = x)$$

We've already seen that for this dataset, we can't use the simple difference in observed group means (SDO) to estimate the causal ATE. In this section, we'll try inverse propensity weighting instead.

The simplest and most common way to compute propensity scores is using logistic regression: you'll get practice with this on HW4. In particular, in this example, we would use the `treat` column as our target variable and the confounders as our predictors.

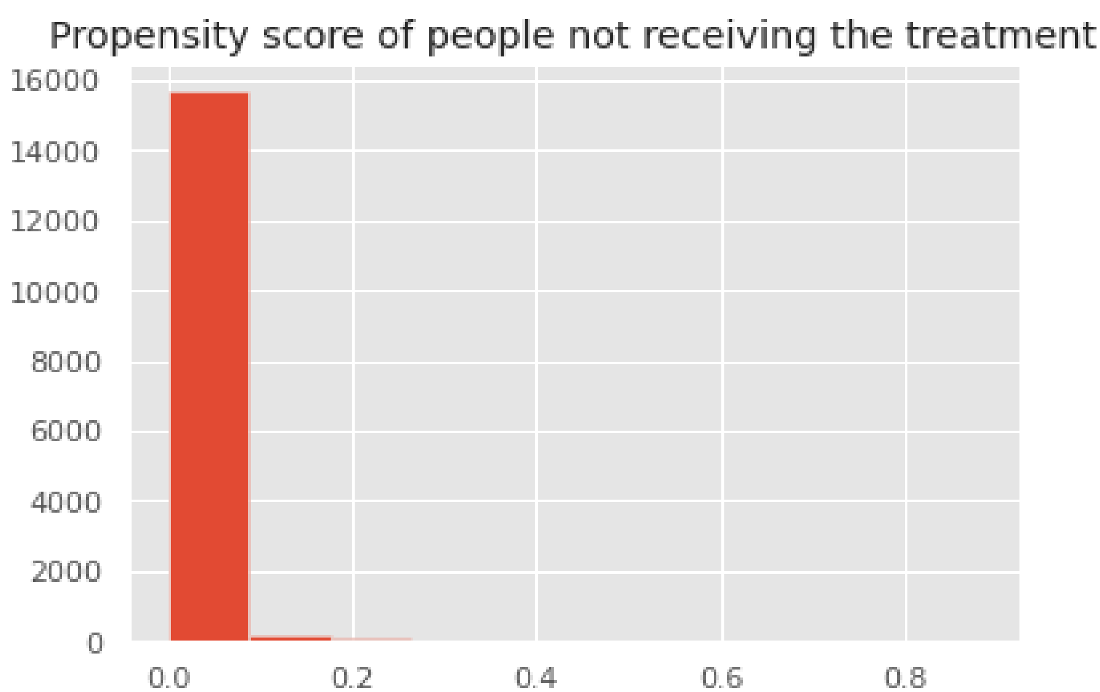
In this lab, we have computed the propensity scores for you using a slightly more complex model that also includes income before the program (`re74`) and includes some nonlinear interactions.

[18]:
```
# Import obs data with propensity scores computed
obs_prop = pd.read_csv('obs_with_propensity_scores.csv')
obs_prop.drop('Unnamed: 0', axis = 1, inplace = True)
```

Examine the following histogram of propensity scores, grouped by dataset:

[19]:
```
plt.hist(obs_prop[obs_prop['treat'] == 1]['pscore']);
plt.title("Propensity score of people receiving the treatment");
```

[20]:
```
plt.hist(obs_prop[obs_prop['treat'] == 0]['pscore']);
plt.title("Propensity score of people not receiving the treatment");
```



6.7 Question 3d

Explain why the two histograms are so different.

Hint: Think about the characteristics of the people participating in the training program (see Problem Setup and Data section).

TODO: For people who got the treatment, there were a lot of confounders e.g. recovering addicts, ex-criminal offenders, and high school dropouts. However, in the control group, these confounders did not exist. Since there are more confounders for the treatment group, there is a higher chance that a unit received treatment given the confounders (i.e., a higher propensity score).

6.8 Question 3e

We could use the propensity scores for a number of things, including matching (as described in Discussion 7), but in this lab we'll focus on inverse propensity weighting (IPW). Recall from lecture that the IPW estimator of the ATE is:

$$\hat{\tau}_{IPW} = \underbrace{\frac{1}{n_1}\sum_{i:Z_i=1}\frac{Y_i}{e(X_i)}}_{\text{weighted mean of treated rows}} - \underbrace{\frac{1}{n_0}\sum_{i:Z_i=0}\frac{Y_i}{1-e(X_i)}}_{\text{weighted mean of untreated rows}}$$

Note that the weights are different for the two groups. Intuitively, the weights decrease the importance of points that have a high probability of being in the group that they're in.

For example, consider two individuals from the CPS data: person A, who looks very different from the treatment (NSW) population, and person B, who looks much more similar to the treatment (NSW) population. Person A's propensity score will be much closer to 1, and so the denominator $1 - e(X_A)$ will be small, increasing our weight of their outcome. On the other hand, person B's propensity score will be closer to 0, decreasing our weight of their outcome. This way, we give less weight to person B, who doesn't look like someone from the treatment group anyway.

Complete the cell below to compute the IPW estimate for the ATE.

[21]:
```
# Question 3e, TODO here
p_score_treatment = obs_prop[obs_prop['treat'] == 1]['pscore']
p_score_control = 1 - obs_prop[obs_prop['treat'] == 0]['pscore']

treat_y = obs_prop[obs_prop['treat'] == 1]['re78']
control_y = obs_prop[obs_prop['treat'] == 0]['re78']

treated_mean = np.mean(treat_y/p_score_treatment)
control_mean = np.mean(control_y/p_score_control)

ipw_estimate = treated_mean - control_mean # TODO (You might need several lines)
ipw_estimate
```

[21]: 248589.3473843762

[22]:
```
# Validation tests: Do not modify
assert np.abs(ipw_estimate - 248589) < 1000
print("Test passed!")
```

```
Test passed!
```

6.9 Question 3f

You might find a surprisingly large result in 3e. Recent work in IPW suggests that a good rule of thumb is to only include points with propensity scores between 0.1 and 0.9

In the cell below, remove any data points with propensity scores that are too low or too high, and repeat the computation in 3e.

[23]:
```
# Question 3f, TODO here
cleaned_obs_prop = obs_prop[obs_prop['pscore'].between(0.1, 0.9)] # TODO
p_score_treatment = cleaned_obs_prop[cleaned_obs_prop['treat'] == 1]['pscore']
p_score_control = 1 - cleaned_obs_prop[cleaned_obs_prop['treat'] == 0]['pscore']

treat_y = cleaned_obs_prop[cleaned_obs_prop['treat'] == 1]['re78']
control_y = cleaned_obs_prop[cleaned_obs_prop['treat'] == 0]['re78']

treated_mean = np.mean(treat_y/p_score_treatment)
control_mean = np.mean(control_y/p_score_control) # TODO
ipw_estimate =  treated_mean - control_mean # TODO
ipw_estimate
```

[23]: 9298.639890330083

[24]:
```
# Validation tests: Do not modify
assert np.abs(ipw_estimate - 9298) < 100
print("Test passed!")
```

```
Test passed!
```

This estimate is much closer to the true causal effect we obtained from the randomized experiment in part I, even if it is quite a bit larger.

6.10 Question 3g

Now let's interpret the result of IPW. Fill in the blanks below with the appropriate phrases:

If we assume that _____, *then the estimated effect of the program using IPW is that the program causes people to earn _____* *more than they would have.*

TODO: Your answer here

Blank 1: the treatment and potential outcomes are conditionally independent given a set of known confounding variables X (unconfoundedness)

Blank 2: $9298

6.11 Question 3h

Give at least one reason why the IPW estimate doesn't match the true estimate, using what you know about the assumptons we've made.

Hint: there is more than one right answer.

TODO: In reality, we might not have data for all our variables. This means that we might not know or have access to all our confounding variables X, which breaks the unconfoundedness assumption that IPW uses.

[25]:
```
import matplotlib.image as mpimg
img = mpimg.imread('baby_duckling.jpg')
imgplot = plt.imshow(img)
imgplot.axes.get_xaxis().set_visible(False)
imgplot.axes.get_yaxis().set_visible(False)
print("Yay, you've made it to the end of Lab 8!")
plt.show()
```

```
Yay, you've made it to the end of Lab 8!
```

[ ]:
```
```