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January 31, 2022

1 Hypothesis Testing - Cumulative Lab

1.1 Introduction

In this cumulative lab, you will use pandas to clean up a dataset and perform some EDA, then perform statistical tests and interpret their results in order to answer some business questions.

1.2 Objectives

You will be able to:

- Practice using a data dictionary
- Practice using pandas to prepare data for statistical analysis
- Practice identifying an appropriate statistical test for a given question
- Practice defining the null and alternative hypotheses
- Practice executing statistical tests and interpreting their results

link to github is:

`https://github.com/miladshiraniUCB/dsc-hypothesis-testing-lab`

1.3 Your Task: Analyzing Health Trends

Photo by Kelly Sikkema on Unsplash

1.3.1 Business Understanding

Flatiron Health Insurance (FHI) is a growing private healthcare insurance provider founded on the premise that using data and analytics can improve the health insurance industry by providing better care and offerings to its patients. Every year, the Center for Disease Control (CDC) conducts surveys to understand the latest demographic, health, and fitness trends. You have been tasked with analyzing the recently published results of the 2017-2018 survey and providing your recommendations back to the Chief Analytics Officer and Chief Marketing Officer. You have been assigned the task of taking a first look at the data and beginning to answer several key questions:

1. How does health status, represented by average number of days with bad physical health in the past month (`PHYSHLTH`), differ by state?

2. Digging deeper into the data, what are some factors that impact health (demographics, behaviors, etc.)?

1.3.2 Data Understanding

To get you started, the IT department formatted the data set into a tab delimited text file for only NY, NJ, and CT (FHI's primary markets) called `case_study.csv`.

There is also a PDF data dictionary called `data_dictionary.pdf`, which explains the meanings of the features and codes contained in this dataset.

Both files are located in the `data/` directory of this repository.

Prior to each statistical test, you will need to perform some data preparation, which could include:

- Filtering out rows with irrelevant values
- Transforming data from codes into human-readable values
- Binning data to transform it from numeric to categorical
- Creating new columns based on queries of the values in other columns

For steps 2-5, you will need to select and execute an appropriate statistical test. Recall these tests we have learned so far:

1. Chi-squared test: used for comparing a categorical feature against a categorical feature, to determine whether they are independent
2. t-test: used for comparing two categories of a numeric feature, to determine whether their means are the same across categories
3. ANOVA: used for comparing more than two categories of a numeric feature, to determine whether their means are the same across categories

1.3.3 Requirements

1. Prepare `PHYSHLTH` Data for Analysis Using the data dictionary, ensure that you understand the meaning of the `PHYSHLTH` column. Then clean the data so that only valid records of `PHYSHLTH` remain.

2. Describe the Distribution of Health Status by State Does health status (`PHYSHLTH`) differ by state (`STATE_`)? If so, by how much, and is it statistically significant?

3. Describe the Relationship between Health Status and Home Ownership Status Does health status (`PHYSHLTH`) differ between home owners and renters (`RENTHOM1`)? If so, by how much, and is it statistically significant?

4. Describe the Relationship between Chronic Sickness and Nicotine Use Does chronic sickness (`PHYSHLTH >= 15`) differ based on nicotine use (various columns)? If so, by how much, and is it statistically significant?

5. Choose Your Own Question Thinking about the business case, what is another question that might be useful to answer? Perform all analysis steps to answer this question.

1.4 1. Prepare `PHYSHLTH` Data for Analysis

In the cells below, we include the relevant imports and load the data into a dataframe called `df`:

[210]:
```
# Run this cell without changes
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
```

```
%matplotlib inline
```

[211]:
```
# Run this cell without changes
df = pd.read_csv("data/case_study.csv", index_col=0, low_memory=False)
df
```

[211]:
```
        _STATE  FMONTH    IDATE  IMONTH  IDAY  IYEAR  DISPCODE       SEQNO  \
49938      9.0     5.0  5172017       5    17   2017    1200.0  2017000001
49939      9.0     2.0  2142017       2    14   2017    1200.0  2017000002
49940      9.0     1.0  1292017       1    29   2017    1200.0  2017000003
49941      9.0     7.0  9112017       9    11   2017    1200.0  2017000004
49942      9.0     5.0  7182017       7    18   2017    1200.0  2017000005
…         …    …     …      …    …    …        …          …
303774    36.0     5.0  5152017       5    15   2017    1200.0  2017012245
303775    36.0     6.0  6252017       6    25   2017    1200.0  2017012246
303776    36.0     7.0  7212017       7    21   2017    1200.0  2017012247
303777    36.0     7.0  7202017       7    20   2017    1200.0  2017012248
303778    36.0     7.0  7252017       7    25   2017    1200.0  2017012249

                _PSU  CTELENM1  …  _PA300R2  _PA30021  _PASTRNG  _PAREC1  \
49938   2.017000e+09       NaN  …       2.0       2.0       2.0      4.0
49939   2.017000e+09       NaN  …       1.0       1.0       1.0      1.0
49940   2.017000e+09       NaN  …       3.0       2.0       1.0      3.0
49941   2.017000e+09       NaN  …       2.0       2.0       2.0      2.0
49942   2.017000e+09       NaN  …       2.0       2.0       1.0      1.0
…              …       …  …        …       …       …       …
303774  2.017012e+09       NaN  …       3.0       2.0       2.0      4.0
303775  2.017012e+09       NaN  …       2.0       2.0       2.0      4.0
303776  2.017012e+09       NaN  …       2.0       2.0       2.0      4.0
303777  2.017012e+09       NaN  …       9.0       9.0       9.0      9.0
303778  2.017012e+09       NaN  …       3.0       2.0       2.0      4.0

        _PASTAE1  _RFSEAT2  _RFSEAT3  _FLSHOT6  _PNEUMO2  _AIDTST3
49938        2.0       1.0       1.0       NaN       NaN       1.0
49939        1.0       2.0       2.0       NaN       NaN       2.0
49940        2.0       1.0       1.0       NaN       NaN       2.0
49941        2.0       1.0       1.0       NaN       NaN       1.0
49942        1.0       1.0       1.0       NaN       NaN       2.0
…            …       …       …       …       …       …
303774       2.0       1.0       1.0       NaN       NaN       1.0
303775       2.0       1.0       1.0       NaN       NaN       1.0
303776       2.0       1.0       1.0       NaN       NaN       1.0
303777       9.0       9.0       9.0       9.0       9.0       9.0
303778       2.0       1.0       1.0       NaN       NaN       1.0

[34545 rows x 358 columns]
```

Our main column of interest is called PHYSHLTH. We display summary statistics and plot a distribution below:

[212]:
```python
# Run this cell without changes
df['PHYSHLTH'].describe()
```

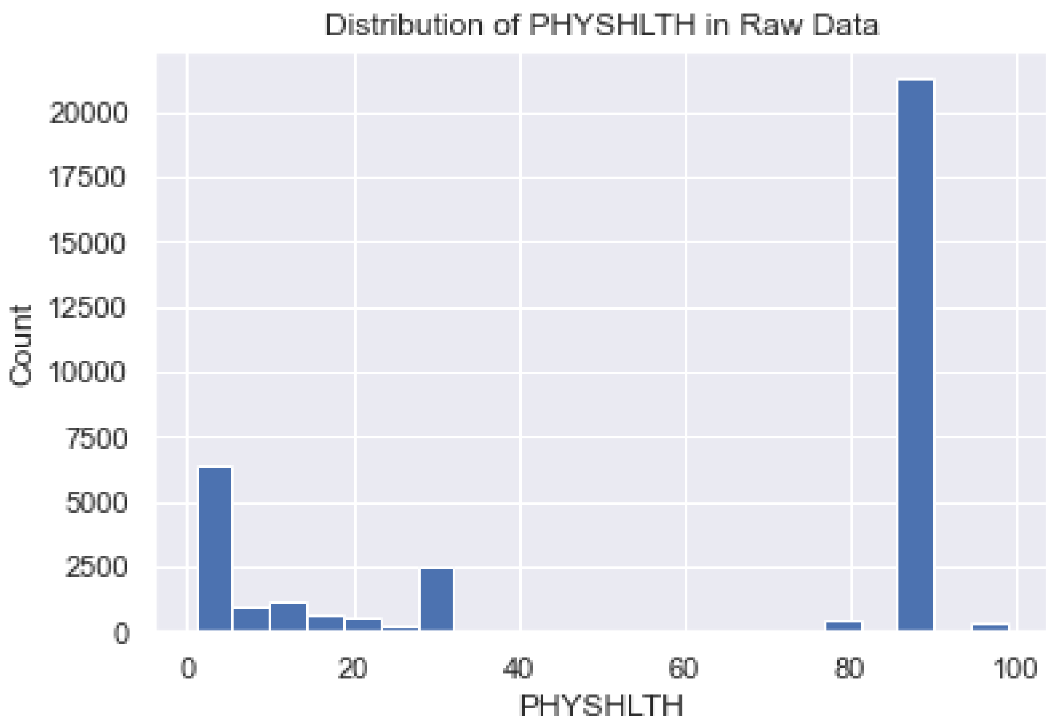
[212]:
```
count    34545.000000
mean        60.213403
std         37.504566
min          1.000000
25%         15.000000
50%         88.000000
75%         88.000000
max         99.000000
Name: PHYSHLTH, dtype: float64
```

[213]:
```python
df['PHYSHLTH'].value_counts().sort_values(ascending = False)
```

[213]:
```
88.0    21296
30.0     2438
2.0      1993
1.0      1538
3.0      1187
5.0      1092
10.0      751
7.0       641
15.0      640
4.0       622
77.0      493
20.0      402
14.0      326
99.0      305
6.0       187
25.0      159
8.0        99
21.0       70
12.0       69
28.0       57
29.0       35
27.0       22
18.0       19
16.0       16
17.0       15
9.0        15
22.0       12
13.0       10
19.0       10
11.0        8
```

```
26.0        7
24.0        7
23.0        4
Name: PHYSHLTH, dtype: int64
```

[214]:
```python
# Run this cell without changes
fig, ax = plt.subplots()
ax.hist(df["PHYSHLTH"], bins="auto")
ax.set_xlabel("PHYSHLTH")
ax.set_ylabel("Count")
ax.set_title("Distribution of PHYSHLTH in Raw Data");
```



This feature is supposed to represent the number of days with bad physical health out of the past 30 days. Do you see anything wrong with what is displayed above? Explain.

[215]:
```python
# Replace None with appropriate text
"""
Since each month has around 30 days, the values more than 30 should have
different meaning than hte number of days in a month. By checking the PDF␣
↪provided
in the folder Data we find that
`df["PHYSHLTH"] = 88` represents `None` value
`df["PHYSHLTH"] = 77` represents `Don't know/Not sure` value
`df["PHYSHLTH"] = 99` represents `Refused` value
```

```
"""
```

[215]:

```
'\nSince each month has around 30 days, the values more than 30 should have
\ndifferent meaning than hte number of days in a month. By checking the PDF
provided\nin the folder Data we find that\n`df["PHYSHLTH"] = 88` represents
`None` value\n`df["PHYSHLTH"] = 77` represents `Don't know/Not sure`
value\n`df["PHYSHLTH"] = 99` represents `Refused` value\n'
```

Look in the data dictionary, page 17, to understand what is happening with these values. Then edit the cell below so:

- The records where the `PHYSHLTH` value label is `None` are converted to 0
- The records where the `PHYSHLTH` value label is `Number of days` are kept as-is
- All other records are dropped (i.e. records with `Don't know/Not sure`, `Refused`, and `Not asked or Missing` value labels for `PHYSHLTH` are dropped)

[216]:

```
# Your code here
df.loc[df["PHYSHLTH"] == 88, "PHYSHLTH"] = 0

df = df[(df["PHYSHLTH"] != 77) & (df["PHYSHLTH"] != 99)].copy()
# df.drop(index = to_drop, axis = 1,inplace = True)

## From GitHub Solution

# # Code 88 means None, replace it with 0
# df.loc[df["PHYSHLTH"]==88, "PHYSHLTH"] = 0

# # Now, only keep records where PHYSHLTH is <= 30
# # (making a copy to avoid future SettingWithCopyWarning messages)
# df = df[df["PHYSHLTH"] <= 30].copy()

# df
```

Run the code below to ensure you have the correct, cleaned dataframe:

[217]:

```
# Run this cell without changes

# We should have fewer rows, the same number of columns
assert df.shape == (33747, 358)

# The maximum value in this column should now be 30
assert df["PHYSHLTH"].max() == 30.0
```

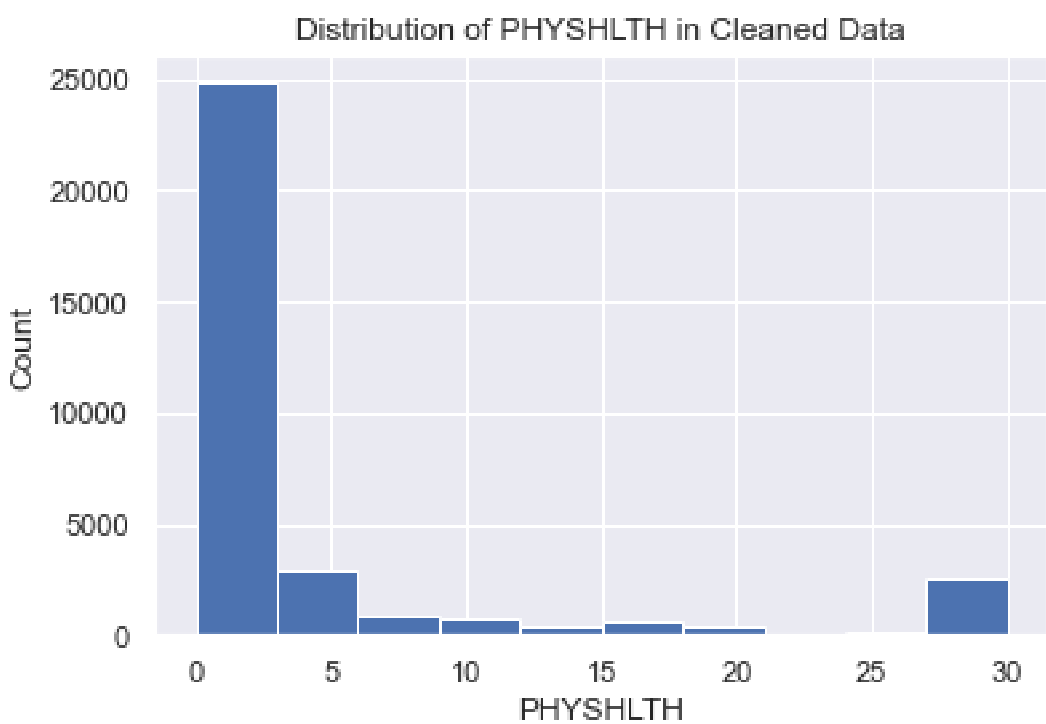
Now we can look at the same descriptive information on our cleaned data:

[218]:

```
# Run this cell without changes
df['PHYSHLTH'].describe()
```

[218]:
```
count    33747.000000
mean         4.085341
std          8.513293
min          0.000000
25%          0.000000
50%          0.000000
75%          3.000000
max         30.000000
Name: PHYSHLTH, dtype: float64
```

[219]:
```
# Run this cell without changes
fig, ax = plt.subplots()
ax.hist(df["PHYSHLTH"])
ax.set_xlabel("PHYSHLTH")
ax.set_ylabel("Count")
ax.set_title("Distribution of PHYSHLTH in Cleaned Data");
```



That looks a lot more reasonable. Let's move on to the next step.

1.5 2. Describe the Distribution of Health Status by State

As mentioned previously, this dataset only includes data from three states.

[220]:
```python
# Run this cell without changes
df["_STATE"].value_counts()
```

[220]:
```
36.0    11876
34.0    11458
9.0     10413
Name: _STATE, dtype: int64
```

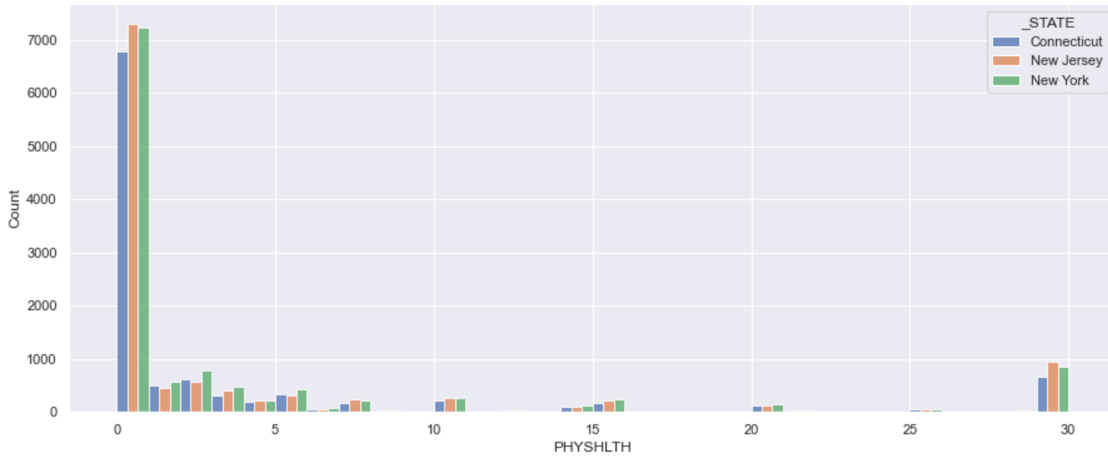
Look in the data dictionary, pages 2-3, to determine which states map onto which codes. Then replace the numbers with strings representing the state names.

[221]:
```python
# Your code here
df.loc[df["_STATE"] == 9 , "_STATE"] = "Connecticut"
df.loc[df["_STATE"] == 34, "_STATE"] = "New Jersey"
df.loc[df["_STATE"] == 36, "_STATE"] = "New York"

### From GitHub

# df["_STATE"].replace({36: "New York", 34: "New Jersey", 9: "Connecticut"},
#                        inplace=True)
# df
```

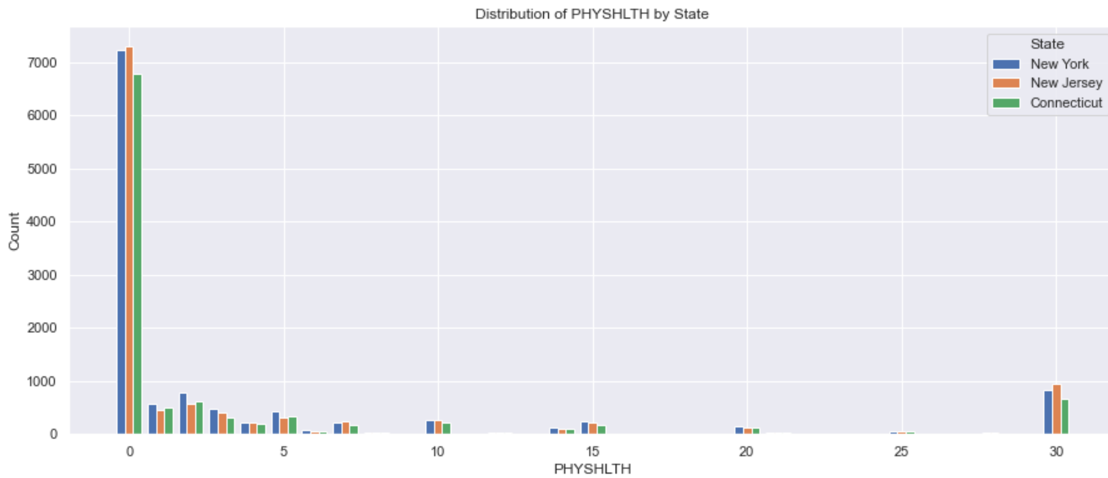
Below, we check the values:

[223]:
```python
# Run this cell without changes

# Shape should be the same
assert df.shape == (33747, 358)

# Values in state column should be changed
assert sorted(list(df["_STATE"].value_counts().index)) == ['Connecticut', 'New␣
↪Jersey', 'New York']
```

[227]:
```python
# Your code here

sns.set(rc={"figure.figsize":(15, 6)})
sns.histplot(data =  df[["_STATE", "PHYSHLTH"]], x = "PHYSHLTH",
             hue = "_STATE", multiple = "dodge", # stat = "density",
             binwidth = 1);
```



[228]:
```python
# Run this cell without changes

ny = df.loc[df["_STATE"] == "New York", "PHYSHLTH"]
nj = df.loc[df["_STATE"] == "New Jersey", "PHYSHLTH"]
ct = df.loc[df["_STATE"] == "Connecticut", "PHYSHLTH"]

fig, ax = plt.subplots(figsize=(15, 6))

ax.hist(
    x=[ny, nj, ct],
    label=["New York", "New Jersey", "Connecticut"],
    bins=range(32),
    align="left"
)

ax.set_xlabel("PHYSHLTH")
ax.set_ylabel("Count")
ax.set_title("Distribution of PHYSHLTH by State")

ax.legend(title="State");
```



Looking at the plot above, does the distribution seem to differ by state?

(Just answer based on a visual inspection; we will do the statistical assessment next.)

[229]:
```
# Replace None with appropriate text
"""
It seems that there is not differences between these states
"""
```

[229]: `'\nIt seems that there is not differences between these states\n'`

For the statistical test, we will be comparing the *means* of `PHYSHLTH` across states, as a representation of the overall distribution. In other words, when operationalizing the question **does `PHYSHLTH` differ by state?** we want to answer that in terms of the mean `PHYSHLTH`.

Let's look at those means:

[230]:
```
# Run this cell without changes
df.groupby("_STATE")["PHYSHLTH"].mean()
```

[230]:
```
_STATE
Connecticut    3.688562
New Jersey     4.380957
New York       4.148030
Name: PHYSHLTH, dtype: float64
```

You likely noted that the overall distribution looked about the same, but these means are different. We have a range from Connecticut with about 3.7 days of bad health to New Jersey with about 4.4 days. But is that difference statistically significant?

Identify which of the statistical tests you have learned is the most appropriate for this question, and why. Make sure you mention what kinds of variables are being compared (numeric and categorical), and how many categories there are.

[305]:
```python
# Replace None with appropriate text
"""
I would use ANOVA test since we want to see if these means are really different
from one another or not
"""

#### From GitHub

"""
ANOVA is the most appropriate technique since we are trying to determine
whether there is a difference in PHYSHLTH (a numeric feature) across 3
categories. If we only had 2 categories, a t-test would be appropriate,
but we want to use ANOVA because there are 3
"""
```

[305]:
```
'\nANOVA is the most appropriate technique since we are trying to
determine\nwhether there is a difference in PHYSHLTH (a numeric feature) across
3\ncategories. If we only had 2 categories, a t-test would be appropriate,\nbut
we want to use ANOVA because there are 3\n'
```

Now, identify the null and alternative hypotheses:

[232]:
```python
# Replace None with appropriate text
"""
Null Hypothesis: there are no differeces between PHYSHLTH means in these states
Alternative Hypothesis: these states have different PHYSHLTH means
"""

### From GitHub

"""
Null hypothesis: the means of PHYSHLTH are the same across states

Alternative hypothesis: the means of PHYSHLTH are not the same across states
"""
```

[232]:
```
'\nNull hypothesis: the means of PHYSHLTH are the same across
states\n\nAlternative hypothesis: the means of PHYSHLTH are not the same across
states\n'
```

In the cell below, we set up and execute the statistical test for you. If this doesn't match your previous answer about which test to perform, look at the solution branch to understand why this is the appropriate test.

[233]:
```python
# Run this cell without changes
import statsmodels.api as sm
from statsmodels.formula.api import ols
```

```
formula = 'PHYSHLTH ~ C(_STATE)'
lm = ols(formula, df).fit()
sm.stats.anova_lm(lm)
```

[233]:

	df	sum_sq	mean_sq	F	PR(>F)
C(_STATE)	2.0	2.687322e+03	1343.660882	18.558645	8.800607e-09
Residual	33744.0	2.443093e+06	72.400809	NaN	NaN

Interpret the results of this statistical test below. What is the calculated p-value? Were we able to reject the null hypothesis at an alpha of 0.05? What does this say about how `PHYSHLTH` varies by state? What recommendations would you make to the business?

[234]:

```
# Replace None with appropriate text
"""
P_value is much less that alpha = 0.05 and we can reject the null hypothesis
at the significant level of 95%
"""

### From GitHub

"""
Yes, we were able to reject the null hypothesis. The p-value,
identified here as PR(>F) for the _STATE category, is much
smaller than 0.05.

This means that even though the overall distribution seemed
similar across states, and the means are all around 3-4 days
per month, with this sample size we can say that there is a
statistically significant difference between them.

Based on this information, we might recommend to the business
that they investigate further why people in Connecticut have
the best health and why people in New Jersey have the worst
health out of these states.
"""
```

[234]:

```
'\nYes, we were able to reject the null hypothesis. The p-value,\nidentified
here as PR(>F) for the _STATE category, is much\nsmaller than 0.05.\n\nThis
means that even though the overall distribution seemed\nsimilar across states,
and the means are all around 3-4 days\nper month, with this sample size we can
say that there is a \nstatistically significant difference between
them.\n\nBased on this information, we might recommend to the business\nthat
they investigate further why people in Connecticut have\nthe best health and why
people in New Jersey have the worst\nhealth out of these states.\n'
```

With that section wrapped up, let's move on to the next step.

1.6 3. Describe the Relationship between Health Status and Home Ownership Status

This time, we want to categorize respondents by demographic information: specifically, we'll look at whether or not they own their home.

Once again, this will require some data preparation. The variable of interest is contained in the `RENTHOM1` column. Currently the values look like this:

[235]:
```
# Run this cell without changes
df["RENTHOM1"].value_counts()
```

[235]:
```
1.0    21690
2.0    10244
3.0     1526
9.0      194
7.0       93
Name: RENTHOM1, dtype: int64
```

In the cell below, modify `df` so that we have dropped all records where the `RENTHOM1` value label is neither `Own` nor `Rent`, and we have replaced the numeric codes with `Own` and `Rent` respectively. You can find more information about codes on page 33 of the data dictionary.

[236]:
```
# Your code here
df.loc[df["RENTHOM1"] == 1, "RENTHOM1"] = "Own"
df.loc[df["RENTHOM1"] == 2, "RENTHOM1"] = "Rent"

df = df.loc[(df["RENTHOM1"] == "Own") | (df["RENTHOM1"] == "Rent")].copy()
# df[df["RENTHOM1"].isin(["Own", "Rent"])].copy()
```

[237]:
```
# Run this cell without changes
df["RENTHOM1"].value_counts()
```

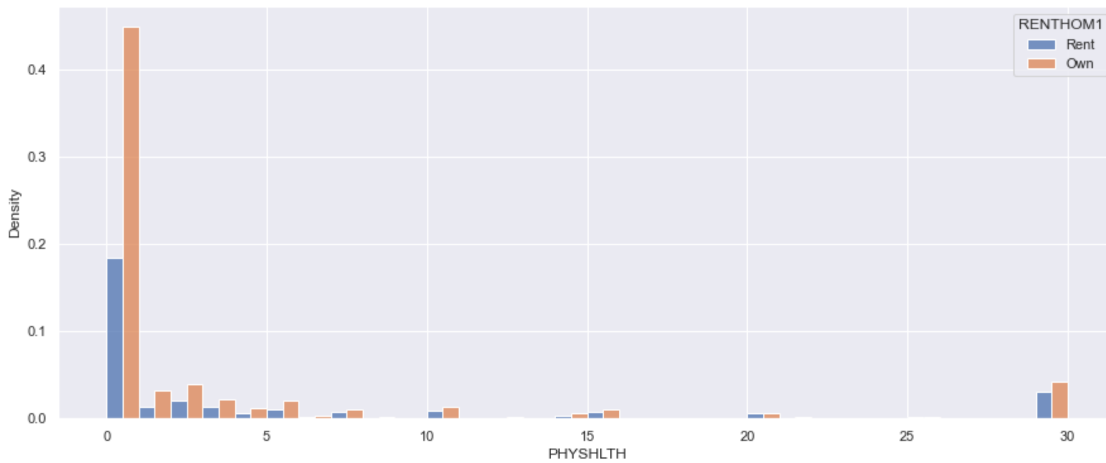
[237]:
```
Own     21690
Rent    10244
Name: RENTHOM1, dtype: int64
```

Below, we check that this was done correctly:

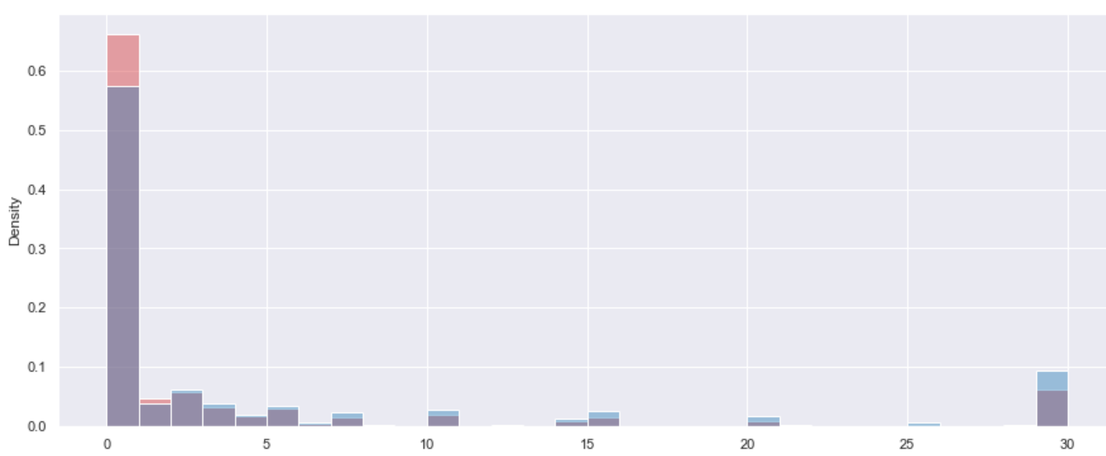
[238]:
```
# Run this cell without changes

# Number of rows should be smaller again
assert df.shape == (31934, 358)

# Only two values should be present in this column
assert sorted(list(df["RENTHOM1"].value_counts().index)) == ['Own', 'Rent']
```

Now, similar to the previous step, create a plot that shows the distribution of `PHYSHLTH` for those who own vs. rent their homes, including appropriate axis labels and legend. Because there is more of an imbalance of categories this time (more than twice as many owners as renters, compared to nearly-even numbers from New York, New Jersey, and Connecticut), make sure you add the argument **density=True**, so that the y-axis shows the density (proportion) rather than the count.

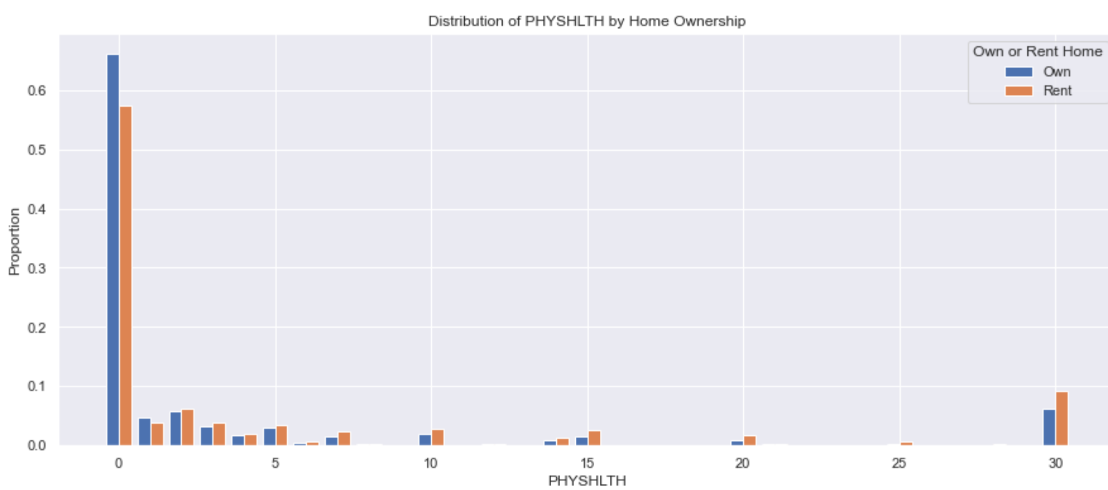
[245]:
```
# Your code here
own = df[df["RENTHOM1"] == "Own"]
rent = df[df["RENTHOM1"] == "Rent"]

sns.histplot(data =  df[["RENTHOM1", "PHYSHLTH"]], x = "PHYSHLTH",
            hue = "RENTHOM1", multiple = "dodge", stat = "density",
            binwidth = 1);
```



[246]:
```
own = df.loc[df["RENTHOM1"] == "Own", "PHYSHLTH"]
rent = df.loc[df["RENTHOM1"] == "Rent", "PHYSHLTH"]
sns.histplot(own, binwidth = 1, color = "tab:red", stat = "density",
             alpha = 0.4);
sns.histplot(rent, binwidth = 1, color = "tab:blue", stat = "density",
             alpha = 0.4);
```



[247]:
```python
### From gitHub

own = df.loc[df["RENTHOM1"] == "Own", "PHYSHLTH"]
rent = df.loc[df["RENTHOM1"] == "Rent", "PHYSHLTH"]

fig, ax = plt.subplots(figsize=(15, 6))

ax.hist(
    x=[own, rent],
    label=["Own", "Rent"],
    bins=range(32),
    align="left",
    density=True
)

ax.set_xlabel("PHYSHLTH")
ax.set_ylabel("Proportion")
ax.set_title("Distribution of PHYSHLTH by Home Ownership")

ax.legend(title="Own or Rent Home");
```



Then run this code to find the averages:

[248]:
```python
# Run this cell without changes
df.groupby("RENTHOM1")["PHYSHLTH"].mean()
```

[248]:
```
RENTHOM1
Own     3.531213
```

```
Rent    5.197970
Name: PHYSHLTH, dtype: float64
```

Now, interpret the plot and averages. Does it seem like there a difference in the number of unhealthy days between those who rent their homes and those who own their homes? How does this compare to the distributions by state?

[ ]:
```python
# Replace None with appropriate text
"""
It seems that there is a difference between the means
"""

## From GitHub

"""
While the overall distribution is fairly similar again, there is
a clearer difference between renters and owners. Home owners are
more likely to report 0 unhealthy days than renters are, whereas
renters are more likely to report all other numbers of unhealthy
days.

The difference in means is also larger: about 3.5 vs. about 5.2
unhealthy days per month.
"""

"""
Here we choose a t-test since we are comparing a numeric feature
(PHYSHLTH) vs. a categorical feature (RENTHOM1), and the categorical
feature contains only two categories.

Null hypothesis: there is no difference in mean unhealthy days per
month between homeowners and renters

Alternative hypothesis: renters have more mean unhealthy days per
month than homeowners

Because we set the alternative hypothesis to be "more" and not just
that the means are not the same, this is a one-tailed t-test and we
need to divide the result of the t-test from SciPy in half
"""
```

Now, choose and execute an appropriate statistical test. Make sure you describe why you chose the test, the null and alternative hypotheses, and what the result of the test means.

[257]:
```python
# Your code here (create additional cells as needed)

import scipy.stats as stats
```

```
results = stats.ttest_ind(own, rent, equal_var = False)
pval = results.pvalue / 2
print("p value is: ", pval)
```

```
p value is:  5.394649320817826e-54
```

1.7 4. Describe the Relationship between Chronic Sickness and Nicotine Use

Once again, this will require some preparation before we can run the statistical test. Create a new column `NICOTINE_USE` with 1 representing someone who uses or has used nicotine in some form, and 0 representing someone who hasn't.

We define nicotine use as:

- Answered `Yes` to the `SMOKE100` question (*Have you smoked at least 100 cigarettes in your entire life?*, page 43), OR
- Answered `Every day` or `Some days` to the `USENOW3` question (*Do you currently use chewing tobacco, snuff, or snus every day, some days, or not at all?*, page 46), OR
- Answered `Yes` to the `ECIGARET` question (*Have you ever used an e-cigarette or other electronic vaping product, even just one time, in your entire life?*, page 46)

If a record matches one or more of the above criteria, `NICOTINE_USE` should be 1. Otherwise, `NICOTINE_USE` should be 0. Go ahead and keep all of the "Don't know" or "Refused" answers as 0.

[289]:
```
# Your code here

df["NICOTINE_USE"] = 0
df["NICOTINE_USE_2"] = 0

df.loc[df["SMOKE100"] == 1, "NICOTINE_USE"] = 1
df.loc[(df["USENOW3"] == 1) | (df["USENOW3"] == 1), "NICOTINE_USE"] = 1
df.loc[df["ECIGARET"] == 1, "NICOTINE_USE"] = 1
# df.loc[df["SMOKE100"] == 1, "NICOTINE_USE"] = 1

conditions = (
                (df["SMOKE100"] == 1) |
                (df["USENOW3"]  == 1) |
                (df["USENOW3"]  == 1) |
                (df["ECIGARET"] == 1)
             )
df.loc[conditions, "NICOTINE_USE_2"] = 1

# Look at the distribution of values
print(df["NICOTINE_USE"].value_counts(normalize=True))
print(df["NICOTINE_USE_2"].value_counts(normalize=True))
```

```
0    0.566763
1    0.433237
Name: NICOTINE_USE, dtype: float64
0    0.566763
```

```
1    0.433237
Name: NICOTINE_USE_2, dtype: float64
```

[291]:
```
### From GitHub

# Set everything to 0 initially
df["NICOTINE_USE"] = 0

# Make a mask to select the relevant values
# (this separate variable is not necessary
# but helps with readability)
mask = (
    # Has smoked at least 100 cigarettes
    (df["SMOKE100"] == 1) |
    # Uses chewing tobacco/snuff/snus every day or some days
    (df["USENOW3"] == 1) |
    (df["USENOW3"] == 2) |
    # Has smoked an e-cigarette
    (df["ECIGARET"] == 1)
)

# Set values to 1 where the mask condition is true
df.loc[mask, "NICOTINE_USE"] = 1

# Look at the distribution of values
df["NICOTINE_USE"].value_counts(normalize=True)
```

[291]:
```
0    0.563036
1    0.436964
Name: NICOTINE_USE, dtype: float64
```

This time, let's treat health status as a categorical variable. We'll say that a "chronically sick" person is a person who reports that their physical health was not good for 15 or more out of the past 30 days. (This is a simplification but it will work for this analysis.)

In the cell below, create a new column of `df` called `CHRONIC`, which is 0 for records where `PHYSHLTH` is less than 15, and 1 for records where `PHYSHLTH` is 15 or more.

[290]:
```
# Your code here
df["CHRONIC"] = 1

conditions = df["PHYSHLTH"] < 15
df.loc[conditions, "CHRONIC"] = 0
# View the distribution of the newly-created column
df["CHRONIC"].value_counts()
```

[290]:
```
0    28246
1     3688
```

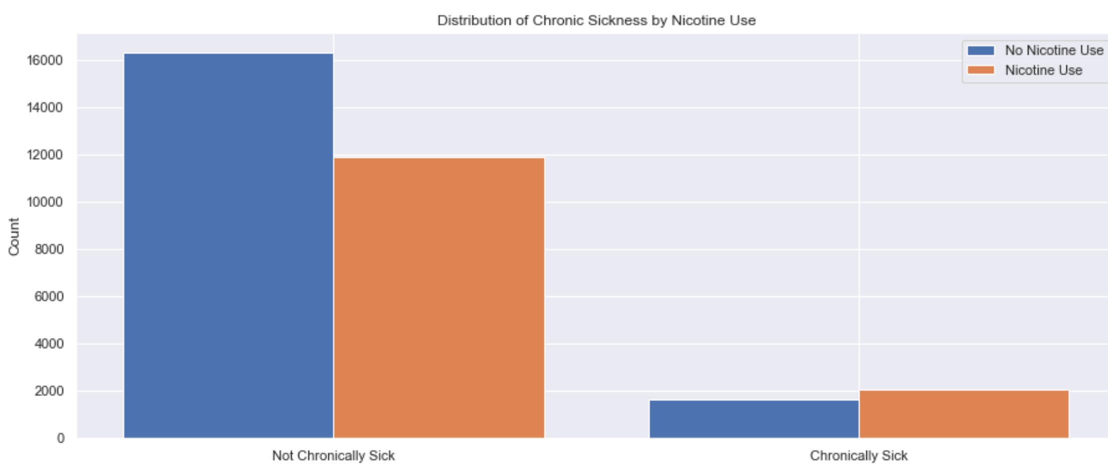
```
Name: CHRONIC, dtype: int64
```

Now we can view the crosstabs for these two categorical variables, as well as display their distributions:

[292]:
```python
# Run this cell without changes
contingency_table = pd.crosstab(index=df["CHRONIC"], columns=df["NICOTINE_USE"])
contingency_table
```

[292]:
```
NICOTINE_USE      0      1
CHRONIC
0             16332  11914
1              1648   2040
```

[295]:
```python
# Run this cell without changes

no_nicotine_use = df.loc[df["NICOTINE_USE"] == 0, "CHRONIC"]
nicotine_use = df.loc[df["NICOTINE_USE"] == 1, "CHRONIC"]

fig, ax = plt.subplots()

ax.hist(
    x=[no_nicotine_use, nicotine_use],
    label=["No Nicotine Use", "Nicotine Use"],
    bins=[0,1,2],
    align="left"
)

ax.set_ylabel("Count")
ax.set_xticks([0,1])
ax.set_xticklabels(["Not Chronically Sick", "Chronically Sick"])
ax.set_title("Distribution of Chronic Sickness by Nicotine Use")

ax.legend();
```



Once again, it appears that there is a difference in health outcomes between these categories. In the cell below, select an appropriate statistical test, describe the null and alternative hypotheses, execute the test, and interpret the result.

[306]:
```python
# Your code here (create additional cells as needed)

### From GitHub

"""
Here we are comparing two categorical features, each with two
categories. A chi-squared test is appropriate for this, since
it compares proportions to expected proportions.

Null hypothesis: chronic sickness and nicotine use are
independent, i.e. that the proportion of people reporting
chronic sickness does not differ based on whether or not
the person has used nicotine

Alternative hypothesis: chronic sickness and nicotine use are
not independent
"""

# Reusing the contingency_table created above

chi2, p, dof, expected = stats.chi2_contingency(contingency_table)

print("chi-squared p-value:", p)

results_table = pd.concat([pd.DataFrame(expected), contingency_table])
results_table.columns.name = "NICOTINE_USE"

results_table.index = ["0 (expected)", "1 (expected)", "0 (actual)", "1␣
↪(actual)"]
results_table.index.name = "CHRONIC"
results_table
```

```
chi-squared p-value: 1.4525226945056695e-51
```

[306]:

NICOTINE_USE	0	1
CHRONIC		
0 (expected)	15903.522265	12342.477735
1 (expected)	2076.477735	1611.522265
0 (actual)	16332.000000	11914.000000
1 (actual)	1648.000000	2040.000000

[307]:
```python
### From GitHub

"""
Interpreting the result above, we can reject the null hypothesis
because we have a p-value much smaller than 0.05. In other words,
this finding is consistent with a statistically significant
relationship between nicotine use and incidence of chronic
sickness.

We can interpret the results table like this:

If nicotine use made no difference in chronic sickness, we would
expect to see about 2076 people who did not use nicotine and had
chronic sickness, and about 1611 people who did use nicotine and
had chronic sickness. The first category is larger because over
half (~56%) of people stated no nicotine use.

Instead what we found was that 1648 people who did not use
nicotine and had chronic sickness, and 2040 people who did use
nicotine and had chronic sickness. Thus even though people who
used nicotine formed the smaller group, they represented the
majority of those with chronic sickness.

Of course, this does not prove a causal link. It is possible that
people who were already experiencing a large number of unhealthy
days actually started using nicotine to treat their symptoms. But
this seems to demonstrate that there is an important link between
nicotine use and not only long-term health issues, but also
short-term health status within the past 30 days.
"""
```

[307]:
```
'\nInterpreting the result above, we can reject the null hypothesis\nbecause we
have a p-value much smaller than 0.05. In other words,\nthis finding is
consistent with a statistically significant\nrelationship between nicotine use
and incidence of chronic\nsickness.\n\nWe can interpret the results table like
this:\n\nIf nicotine use made no difference in chronic sickness, we
would\nexpect to see about 2076 people who did not use nicotine and had\nchronic
sickness, and about 1611 people who did use nicotine and\nhad chronic sickness.
The first category is larger because over\nhalf (~56%) of people stated no
nicotine use.\n\nInstead what we found was that 1648 people who did not
use\nnicotine and had chronic sickness, and 2040 people who did use\nnicotine
and had chronic sickness. Thus even though people who\nused nicotine formed the
smaller group, they represented the \nmajority of those with chronic
sickness.\n\nOf course, this does not prove a causal link. It is possible
that\npeople who were already experiencing a large number of unhealthy\ndays
actually started using nicotine to treat their symptoms. But\nthis seems to
demonstrate that there is an important link between\nnicotine use and not only
```

```
long-term health issues, but also\nshort-term health status within the past 30
days.\n'
```

[321]:
```
## Let's see if we can perform ANOVA test

formula = 'CHRONIC ~ NICOTINE_USE'
lm = ols(formula, df).fit()
sm.stats.anova_lm(lm)
```

[321]:

	df	sum_sq	mean_sq	F	PR(>F)
NICOTINE_USE	1.0	23.367994	23.367994	230.396186	7.415216e-52
Residual	31932.0	3238.711545	0.101425	NaN	NaN

1.8 5. Choose Your Own Question

Now that you have investigated physical health and chronic sickness and their relationships with state, home ownership, and nicotine use, you will conduct a similar investigation with variables of your choosing.

Select an independent variable based on looking at the information in the data dictionary, and perform any additional transformations needed to use it in an analysis. Then set up, execute, and interpret a statistical test that addresses the relationship between that independent variable and `PHYSHLTH`.

(There is no solution branch for this question, and feel free to move on if you have already spent more than 1.5 hours on this lab.)

[ ]:
```
# Your code here (create additional cells as needed)
```

1.9 Conclusion

Congratulations, another cumulative lab down! In this lab you practiced reading a data dictionary, performing various data transformations with pandas, and executing statistical tests to address business questions.