

Program Code: J620-002-4:2020

Program Name: FRONT-END SOFTWARE

DEVELOPMENT

Title: Exe12 - Confidence Intervals NHANES Exercise

Name: Phua Yan Han

IC Number: 050824070059

Date: 11/7/23

Introduction:

Conclusion:

Exercise 1: Confidence Intervals - NHANES

This exercise, we are going to practice on how to load data, clean/manipulate a dataset, and construct a confidence interval for the difference between two population proportions and means.

We will use the 2015-2016 wave of the NHANES data for our analysis.

For our population proportions, we will analyze the difference of proportion between female and male smokers. The column that specifies smoker and non-smoker is "SMQ020" in our dataset.

For our population means, we will analyze the difference of mean of body mass index within our female and male populations. The column that includes the body mass index value is "BMXBMI".

Additionally, the gender is specified in the column "RIAGENDR".

```
In [49]: import pandas as pd
import numpy as np
import matplotlib
matplotlib.use('Agg')
import seaborn as sns
%matplotlib inline
import matplotlib.pyplot as plt
import statsmodels.api as sm
In [50]: url = "../Data files/nhanes_2015_2016.csv"
da = pd.read_csv(url)
```

Out[50]:

da

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCITZI
0	83732	1.0	NaN	1.0	1	1	62	3	1.
1	83733	1.0	NaN	6.0	1	1	53	3	2.
2	83734	1.0	NaN	NaN	1	1	78	3	1.
3	83735	2.0	1.0	1.0	2	2	56	3	1.
4	83736	2.0	1.0	1.0	2	2	42	4	1.
5730	93695	2.0	2.0	NaN	1	2	76	3	1.
5731	93696	2.0	2.0	NaN	2	1	26	3	1.
5732	93697	1.0	NaN	1.0	1	2	80	3	1.
5733	93700	NaN	NaN	NaN	1	1	35	3	2.
5734	93702	1.0	NaN	2.0	2	2	24	3	1.
5735 rows × 28 columns									
<									>

Investigating and Cleaning Data

Create a new column named 'SMQ020x' and store data from column 'SMQ020' with following replacements:

- 1 to "Yes"
- 2 to "No"
- 7 to NaN
- 9 to NaN

```
In [51]: da['SMQ020x']=da['SMQ020']
         reset = {1: 'Yes',2: 'No',7:None,9:None}
         da = da.replace({'SMQ020x':reset})
         da['SMQ020x']
Out[51]: 0
                  Yes
         1
                  Yes
         2
                  Yes
         3
                   No
         4
                   No
         5730
                  Yes
         5731
                   No
         5732
                  Yes
         5733
                  Yes
         5734
                   No
         Name: SMQ020x, Length: 5735, dtype: object
```

Create a new column named 'RIAGENDRx' and store data from column 'RIAGENDR' with following replacements:

- 1 to "Male"
- 2 to "Female"

```
In [52]: da['RIAGENDRx']=da['RIAGENDR']
         reset = {1:'Male',2:'Female'}
         da = da.replace({'RIAGENDRx':reset})
         da['RIAGENDRx']
Out[52]: 0
                    Male
                    Male
         1
         2
                    Male
         3
                  Female
         4
                  Female
                   . . .
         5730
                  Female
         5731
                    Male
         5732
                  Female
         5733
                    Male
         5734
                  Female
         Name: RIAGENDRx, Length: 5735, dtype: object
```

In [53]: da

Out[53]:

	SEQN	ALQ101	ALQ110	ALQ130	SMQ020	RIAGENDR	RIDAGEYR	RIDRETH1	DMDCITZI
0	83732	1.0	NaN	1.0	1	1	62	3	1.
1	83733	1.0	NaN	6.0	1	1	53	3	2.
2	83734	1.0	NaN	NaN	1	1	78	3	1.
3	83735	2.0	1.0	1.0	2	2	56	3	1.
4	83736	2.0	1.0	1.0	2	2	42	4	1.
5730	93695	2.0	2.0	NaN	1	2	76	3	1.
5731	93696	2.0	2.0	NaN	2	1	26	3	1.
5732	93697	1.0	NaN	1.0	1	2	80	3	1.0
5733	93700	NaN	NaN	NaN	1	1	35	3	2.
5734	93702	1.0	NaN	2.0	2	2	24	3	1.
5735	5735 rows × 30 columns								
<									>

Drop all NAs from both SMQ020x & RIAGENDRx and store into a new dataframe named 'dx'. Plot the following crosstab using pd.crosstab library.

```
In [54]:  dx = da[da['SMQ020x'] !=None] 
pd.crosstab(dx['SMQ020x'],dx['RIAGENDRx'])
```

Out[54]:

RIAGENDRx	Female	Male	
SMQ020x			
No	2066	1340	
Yes	906	1413	

Replace dx['SMQ020x'] "Yes" to 1 and "No" to 0.

Out[55]:

	SMQ020x	RIAGENDRx
0	1.0	Male
1	1.0	Male
2	1.0	Male
3	0.0	Female
4	0.0	Female
5730	1.0	Female
5731	0.0	Male
5732	1.0	Female
5733	1.0	Male
5734	0.0	Female

5735 rows × 2 columns

Calculate the 'mean' and 'size' and store into a new dataframe called dz

```
In [56]: dz = dx[['SMQ020x','RIAGENDRx']].groupby('RIAGENDRx').agg(['mean','size'])
dz
```

Out[56]:

SMQ020x mean size RIAGENDRx 2976 Male 0.513258 2759

Constructing Confidence Intervals

Now that we have the population proportions of male and female smokers, we can begin to calculate confidence intervals. From lecture, we know that the equation is as follows:

Best Estimate ± Margin of Error

Where the *Best Estimate* is the **observed population proportion or mean** from the sample and the *Margin of Error* is the **t-multiplier**.

The equation to create a 95% confidence interval can also be shown as:

Population Proportion or Mean $\pm (t - multiplier * Standard Error)$

The Standard Error is calculated differenly for population proportion and mean:

 $Standard\ Error\ for\ Population\ Proportion = \sqrt{\frac{Population\ Proportion*(1-Popula)}{Number\ Of\ Observation}}$

$$Standard\ Error\ for\ Mean = \frac{Standard\ Deviation}{\sqrt{Number\ Of\ Observations}}$$

Lastly, the standard error for difference of population proportions and means is:

Standard Error for Difference of Two Population Proportions Or Means = $\sqrt{SE_I^2}$

Calculate the standard error for female

```
In [71]: import math
    p = dz['SMQ020x']['mean']['Female']
    n = dz['SMQ020x']['size']['Female']
    sef = math.sqrt(p*(1-p)/n)
    sef
```

Out[71]: 0.008438475404634192

Calculate the standard error for male

```
In [72]: p = dz['SMQ020x']['mean']['Male']
n = dz['SMQ020x']['size']['Male']
sem = math.sqrt((p*(1-p))/n)
sem
```

Out[72]: 0.009515714829783395

Calculate the difference between these two Standard Errors

```
In [59]: dse = math.sqrt(sef**2+sem**2)
dse
```

Out[59]: 1.0871506400747817

Calculate the confidence Interval

```
In [60]: ci = dz['SMQ020x']['mean']['Male']-dz['SMQ020x']['mean']['Female']
    x = ci-2*dse
    y = ci+2*dse
    print(x,y)
    print(dse)
```

-1.9658882385099279 2.382714321789199

1.0871506400747817

Difference of Two Population Means

Now we look into the differences between 2 population means

```
In [61]: | da["BMXBMI"].head()
Out[61]: 0
               27.8
               30.8
          1
               28.8
          2
          3
               42.4
               20.3
          4
          Name: BMXBMI, dtype: float64
In [62]: x = da[['BMXBMI','RIAGENDRx']].groupby('RIAGENDRx').agg(['mean','std','size'])
         Х
Out[62]:
                      BMXBMI
                               std
                      mean
                                        size
```

Calculate the Standard Error for Mean for both female and male

```
In [63]: s = x['BMXBMI']['std']['Female']
n = x['BMXBMI']['size']['Female']
semf = s/math.sqrt(n)
s = x['BMXBMI']['std']['Male']
n = x['BMXBMI']['size']['Male']
semm = s/math.sqrt(n)
print(semf,semm)
```

0.14212522940758335 0.11903715722332033

Female 29.939946 7.753319 2976

Male 28.778072 6.252568 2759

Calculate the difference between 2 Standard Error for Mean

RIAGENDRX

```
In [64]: dsem = math.sqrt(semf**2+semm**2)
dsem
```

Out[64]: 0.18538992862064455

The difference between two means for male and female

```
In [65]: dbm = math.sqrt(x['BMXBMI']['mean']['Female']**2+x['BMXBMI']['mean']['Male']**
dbm
```

Out[65]: 41.52803607359479

Calculate the confidence interval between two population means

```
In [66]: clpm = x['BMXBMI']['mean']['Female'] - x['BMXBMI']['mean']['Male']
y = clpm - 2*dsem
z = clpm + 2*dsem
print(y,z)
```

0.7910936830856763 1.5326533975682544