AdvStat-HW_PulkitGoyal

July 19, 2024

1 Imports

[1]:
```python
import math
```

[2]:
```python
import numpy as np

np.set_printoptions(suppress=True) # Suppress Scientific Notation for Printing
```

[3]:
```python
import pandas as pd
```

[4]:
```python
import matplotlib.pyplot as plt
```

[5]:
```python
import scipy.stats as st
```

[6]:
```python
import statsmodels.api as sm
import statsmodels.stats.power as sm_power
```

---

[7]:
```python
from IPython.display import display, HTML
```

<div class="alert alert-block alert-success">

</div>

[8]:
```python
def pprint(txt='', ltxt=None, alert='success'):
    display(HTML(f"""
        <div class='alert alert-block alert-{alert}'>
            {txt}
            {f'''/b/begin{{align*}}{ltxt}/b/end{{align*}}''' if ltxt else ''}
        </div>
    """.replace("/b/", "\\")))
```

Color Legend

```
Orange - <b>Given Info</b>
```

```
Blue - <b>Standard Result/Formula</b>
```

```
Green - <b>Solution</b>
```

```
Red - <b>My Questions</b>
```

2 Assignment 1

2.1 1.

$$n_m = 814 \qquad n_f = 854$$
$$\bar{x}_m = 177.7\,cm \qquad \bar{x}_f = 165.1\,cm$$
$$s_m^2 = 49.0\,cm^2 \qquad s_f^2 = 38.4\,cm^2$$

`b.`

$$Cohen's\ d = \frac{\bar{x}_1 - \bar{x}_2}{s} \quad s = \sqrt{\frac{(n_1-1).s_1^2 + (n_2-1).s_2^2}{n_1+n_2-2}} \tag{1}$$

`a.`

$$d = \frac{\bar{x}_m - \bar{x}_f}{s} = \frac{177.7 - 165.1}{s} = \frac{12.6}{s} \tag{2}$$
$$s = \sqrt{\frac{(n_m-1).s_m^2 + (n_f-1).s_f^2}{n_m+n_f-2}} \tag{3}$$
$$= \sqrt{\frac{(814-1)*49.0 + (854-1)*38.4}{814+854-2}} \tag{4}$$
$$= 6.601 \tag{5}$$
$$\tag{6}$$
$$\therefore d = \frac{12.6}{6.6} = 1.91 \tag{7}$$

`c.`

The effect size is large.

2.2 2.

For equal sample size and sample variance, the independent two-sample t-test t-statistic is related to the effct size by the following relationship.

$$t = d.\sqrt{\frac{n}{2}} \tag{8}$$

So, the t-value for the given conditions is $0.2 * \sqrt{\frac{72}{2}} = 1.2 > \alpha\ (0.05)$. Therefore, the effect is not significant.

2.3 3.

$$g_m = 8.66 \qquad g_f = 8.45$$
$$r = 0.47$$
$$s_m = 3.2 \qquad s_f = 2.8$$

$$d_{rm} = \frac{\bar{g}_m - \bar{g}_f}{s_z} = \frac{8.66 - 8.45}{s_z} = \frac{0.21}{s_z} \tag{9}$$
$$s_z = \sqrt{\frac{s_m^2 + s_f^2 - 2.r.s_m.s_f}{2.(1-r)}} \tag{10}$$
$$= \sqrt{\frac{3.2^2 + 2.8^2 - 2 * 0.47 * 3.2 * 2.8}{2 * (1 - 0.47)}} \tag{11}$$
$$= 3.018 \tag{12}$$
$$\tag{13}$$
$$\therefore d_{rm} = \frac{0.21}{3.018} = 0.696 \tag{14}$$

2.4 4

The variance explained can be captured partial eta-squared (η^2) measure, which is related to the f-statistic (f) in ANOVA as,

$$f^2 = \frac{\eta^2}{1-\eta^2} \tag{15}$$

$$\eta^2 = 0.1$$
$$1 - \beta = 0.9$$
$$\alpha = 0.05$$

$$\therefore f = \sqrt{\frac{0.1}{1-0.1}} = 0.333$$

a.

[9]:
```
nobs = math.ceil(sm_power.FTestAnovaPower().solve_power(effect_size=0.333,␣
    ↪alpha=0.05, power=0.9, k_groups=3))
pprint(ltxt=f"\\text{{Using power analyis, number of samples required for␣
    ↪effect size }} (f = 0.333) \\Rightarrow {nobs}")
```

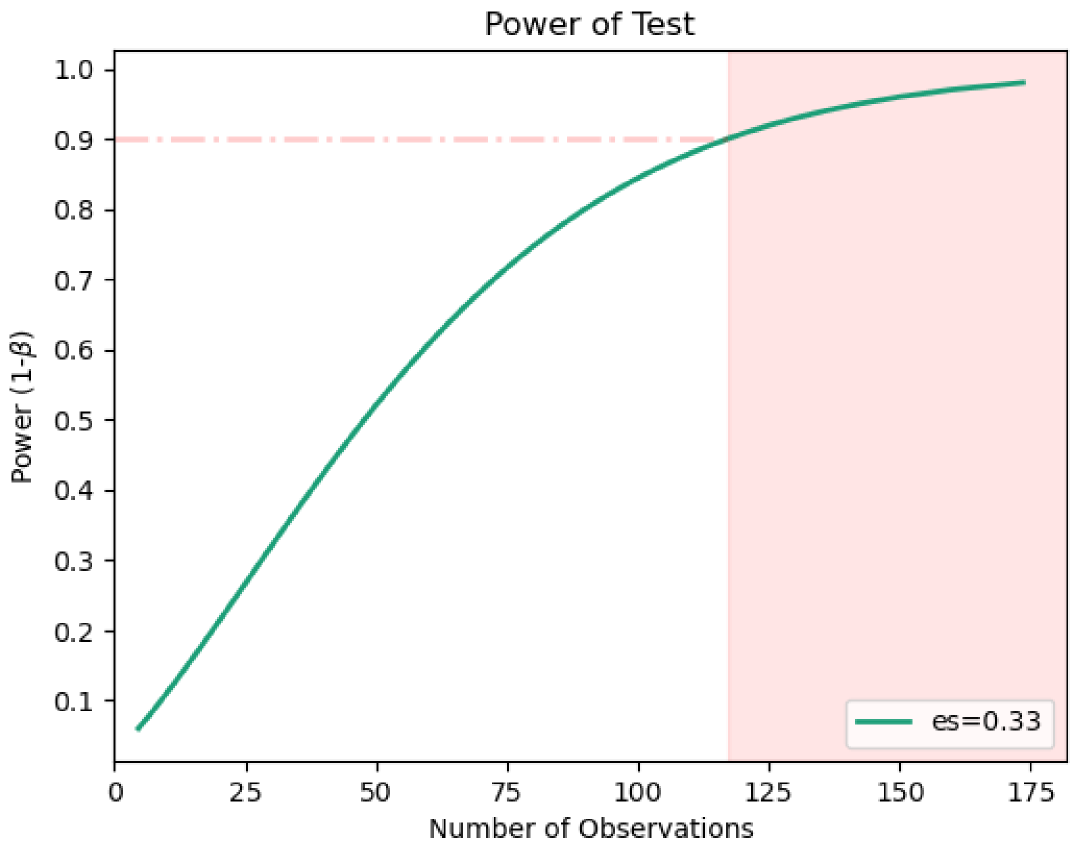
```
<IPython.core.display.HTML object>
```

b.

[10]:
```python
powers = np.arange(0.06, 0.99, 0.01)
nobss = np.array([float(sm_power.FTestAnovaPower().solve_power(effect_size=0.
↪333, alpha=0.05, power=power, k_groups=3)) for power in powers])
```

```
C:\Users\pulki\AppData\Local\Temp\ipykernel_17144\3694109675.py:2:
DeprecationWarning: Conversion of an array with ndim > 0 to a scalar is
deprecated, and will error in future. Ensure you extract a single element from
your array before performing this operation. (Deprecated NumPy 1.25.)
  nobss =
np.array([float(sm_power.FTestAnovaPower().solve_power(effect_size=0.333,
alpha=0.05, power=power, k_groups=3)) for power in powers])
```

[11]:
```python
sm_power.FTestAnovaPower().plot_power('nobs', nobs=nobss, effect_size=[0.333],␣
↪alpha=[0.05], k_groups=3)
plt.xlim([0, None])
# plt.xticks(np.append(plt.xticks()[0], math.ceil(nobss[np.isclose(powers, 0.
↪9)][0])))
plt.yticks(np.linspace(0, 1, 11))
plt.ylabel(r"Power (1-$\beta$)")
plt.axvspan(nobss[np.isclose(powers, 0.9)][0], plt.xticks()[0][-1], color='r',␣
↪alpha=0.1)
plt.hlines(0.9, 0, nobss[np.isclose(powers, 0.9)][0], color='r', ls='-.', lw=2,␣
↪alpha=0.2);
```



c.

```
[12]: nobs = math.ceil(sm_power.FTestAnovaPower().solve_power(effect_size=0.1,␣
        ↪alpha=0.05, power=0.9, k_groups=3))
      pprint(ltxt=f"\\text{{Using power analyis, number of samples required for␣
        ↪effect size }} (f = 0.1) \\Rightarrow {nobs}")
```

```
<IPython.core.display.HTML object>
```

2.5 5.

```
[13]: data = pd.read_csv('data/1/Table1.csv')
```

```
[14]: data.head()
```

```
[14]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2    SDGroup2  \
      0       1                 0    6.865663   93.243186    3.532821   92.849045
      1       2                 0  -19.103643   90.160491  -16.177325   88.983605
      2       3                 1  -15.747061  102.164439  -34.091446   93.417503
      3       4                 1    6.621659   83.492126   58.531006   89.420670
      4       5                 0  -12.783565  104.391452  -12.918734  113.932785

                p
      0  0.858232
      1  0.870582
      2  0.351061
      3  0.003420
      4  0.995077
```

```
[15]: alpha = 0.05
```

2.5.1 1. No Correction

```
[16]: c = 'n_c'
```

```
[17]: data[c] = data['p'] < alpha
```

Which items differ significantly using =0.05.?

```
[18]: data.loc[data[c]].sort_values('ItemNr', ignore_index=True)
```

```
[18]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2    SDGroup2  \
      0       4                 1    6.621659   83.492126   58.531006   89.420670
      1       7                 1    6.962812   96.066891  -35.132100   82.916984
      2       8                 1   -5.045829  105.239143   35.892766   99.306192
      3      15                 1   -9.250379  105.470703  -62.162545   99.005903
```

```
4       17                    1    5.176001  105.475429  -41.249891   79.441165
5       19                    1   -7.216715  126.894245   55.354562   99.668515
6       22                    1   10.473582  117.295995  -58.314360   99.941405
7       27                    1  -18.063857   90.477102   55.642084  102.978673
8       30                    1   16.420660  110.055172  -62.918949   98.684516
9       37                    0   33.910796   90.518823  -10.815471   90.254361

          p   n_c
0  0.003420  True
1  0.021014  True
2  0.048202  True
3  0.011169  True
4  0.014606  True
5  0.007259  True
6  0.002122  True
7  0.000249  True
8  0.000255  True
9  0.015074  True
```

How many items are false positives? Which items?

```
[19]: data.loc[data[c] & ~data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[19]:    ItemNr  PopulationEffect  MeanGroup1   SDGroup1  MeanGroup2   SDGroup2  \
      0      37                 0   33.910796  90.518823  -10.815471  90.254361

                p   n_c
      0  0.015074  True
```

How many items are false negatives? Which items?

```
[20]: data.loc[~data[c] & data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[20]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2   SDGroup2  \
      0       3                 1  -15.747061  102.164439  -34.091446  93.417503

                p    n_c
      0  0.351061  False
```

2.5.2 2. Bonferroni FWE Correction

```
[21]: c = 'bfwe_c'
```

```
[22]: data[c] = data['p'] < alpha/data.shape[0]
```

```
[23]: pprint(ltxt=f"\\alpha = {alpha/data.shape[0]:.5f}")
```

```
<IPython.core.display.HTML object>
```

Which items differ significantly using =0.05.?

```
[24]: data.loc[data[c]].sort_values('ItemNr', ignore_index=True)
```

```
[24]:    ItemNr  PopulationEffect  MeanGroup1   SDGroup1  MeanGroup2   SDGroup2  \
      0      27                 1  -18.063857  90.477102   55.642084 102.978673
      1      30                 1   16.420660 110.055172  -62.918949  98.684516

                p   n_c  bfwe_c
      0  0.000249  True    True
      1  0.000255  True    True
```

How many items are false positives? Which items?

```
[25]: data.loc[data[c] & ~data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[25]: Empty DataFrame
      Columns: [ItemNr, PopulationEffect, MeanGroup1, SDGroup1, MeanGroup2, SDGroup2,
      p, n_c, bfwe_c]
      Index: []
```

How many items are false negatives? Which items?

```
[26]: data.loc[~data[c] & data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[26]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2   SDGroup2  \
      0       3                 1  -15.747061  102.164439  -34.091446  93.417503
      1       4                 1    6.621659   83.492126   58.531006  89.420670
      2       7                 1    6.962812   96.066891  -35.132100  82.916984
      3       8                 1   -5.045829  105.239143   35.892766  99.306192
      4      15                 1   -9.250379  105.470703  -62.162545  99.005903
      5      17                 1    5.176001  105.475429  -41.249891  79.441165
      6      19                 1   -7.216715  126.894245   55.354562  99.668515
      7      22                 1   10.473582  117.295995  -58.314360  99.941405

                p    n_c  bfwe_c
      0  0.351061  False   False
      1  0.003420   True   False
      2  0.021014   True   False
      3  0.048202   True   False
      4  0.011169   True   False
      5  0.014606   True   False
      6  0.007259   True   False
      7  0.002122   True   False
```

2.5.3 3. Bonferroni-Holm FWE Correction

```
[27]: c = 'bhfwe_c'
```

```
[28]: data = data.sort_values('p', ignore_index=True) # Sort table in ascending order␣
       ↪of significances
      # Bonferroni-Holm iteration without EXIT
      data[c] = [h['p'] < alpha/(data.shape[0] - i) for i, h in data.iterrows()]
      # Account for the EXIT condition in separate step by carrying over a rejection␣
       ↪to the subsequent/following hypotheses
      data[c] = [h[c] & (data[c][i-1] if i else True) for i, h in data.iterrows()]
```

```
[29]: pprint(ltxt=f"\\alpha = {alpha/(data.shape[0] - data.loc[~data[c]].index[0]):.
       ↪5f}")
```

```
<IPython.core.display.HTML object>
```

Which items differ significantly using =0.05.?

```
[30]: data.loc[data[c]].sort_values('ItemNr', ignore_index=True)
```

```
[30]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2    SDGroup2  \
      0      27                 1  -18.063857   90.477102   55.642084  102.978673
      1      30                 1   16.420660  110.055172  -62.918949   98.684516

                p   n_c  bfwe_c  bhfwe_c
      0  0.000249  True    True     True
      1  0.000255  True    True     True
```

How many items are false positives? Which items?

```
[31]: data.loc[data[c] & ~data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[31]: Empty DataFrame
      Columns: [ItemNr, PopulationEffect, MeanGroup1, SDGroup1, MeanGroup2, SDGroup2,
      p, n_c, bfwe_c, bhfwe_c]
      Index: []
```

How many items are false negatives? Which items?

```
[32]: data.loc[~data[c] & data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

```
[32]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2   SDGroup2  \
      0       3                 1  -15.747061  102.164439  -34.091446  93.417503
      1       4                 1    6.621659   83.492126   58.531006  89.420670
      2       7                 1    6.962812   96.066891  -35.132100  82.916984
      3       8                 1   -5.045829  105.239143   35.892766  99.306192
      4      15                 1   -9.250379  105.470703  -62.162545  99.005903
```

```
5      17                   1    5.176001  105.475429  -41.249891  79.441165
6      19                   1   -7.216715  126.894245   55.354562  99.668515
7      22                   1   10.473582  117.295995  -58.314360  99.941405

          p    n_c  bfwe_c  bhfwe_c
0  0.351061  False   False    False
1  0.003420   True   False    False
2  0.021014   True   False    False
3  0.048202   True   False    False
4  0.011169   True   False    False
5  0.014606   True   False    False
6  0.007259   True   False    False
7  0.002122   True   False    False
```

2.5.4 4. Bonferroni-Hochberg FDR Correction

```
[33]: c = 'bhfdr_c'
```

```
[34]: # data = data.sort_values('p', ignore_index=True) # Sort table in ascending␣
       ↪order of significances
      # Bonferroni-Hochberg iteration
      data[c] = [h['p'] < alpha*(i+1)/data.shape[0] for i, h in data.iterrows()]
```

```
[35]: pprint(ltxt=f"\\alpha = {alpha*(data.loc[data[c]].index[-1]+2)/data.shape[0]:.
       ↪5f}")
```

```
<IPython.core.display.HTML object>
```

Which items differ significantly using =0.05.?

```
[36]: data.loc[data[c]].sort_values('ItemNr', ignore_index=True)
```

```
[36]:    ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2    SDGroup2  \
      0       4                 1    6.621659   83.492126   58.531006   89.420670
      1      22                 1   10.473582  117.295995  -58.314360   99.941405
      2      27                 1  -18.063857   90.477102   55.642084  102.978673
      3      30                 1   16.420660  110.055172  -62.918949   98.684516

                p   n_c  bfwe_c  bhfwe_c  bhfdr_c
      0  0.003420  True   False    False     True
      1  0.002122  True   False    False     True
      2  0.000249  True    True     True     True
      3  0.000255  True    True     True     True
```

How many items are false positives? Which items?

```
[37]: data.loc[data[c] & ~data['PopulationEffect']].sort_values('ItemNr',␣
       ↪ignore_index=True)
```

[37]:
```
Empty DataFrame
Columns: [ItemNr, PopulationEffect, MeanGroup1, SDGroup1, MeanGroup2, SDGroup2,
p, n_c, bfwe_c, bhfwe_c, bhfdr_c]
Index: []
```

How many items are false negatives? Which items?

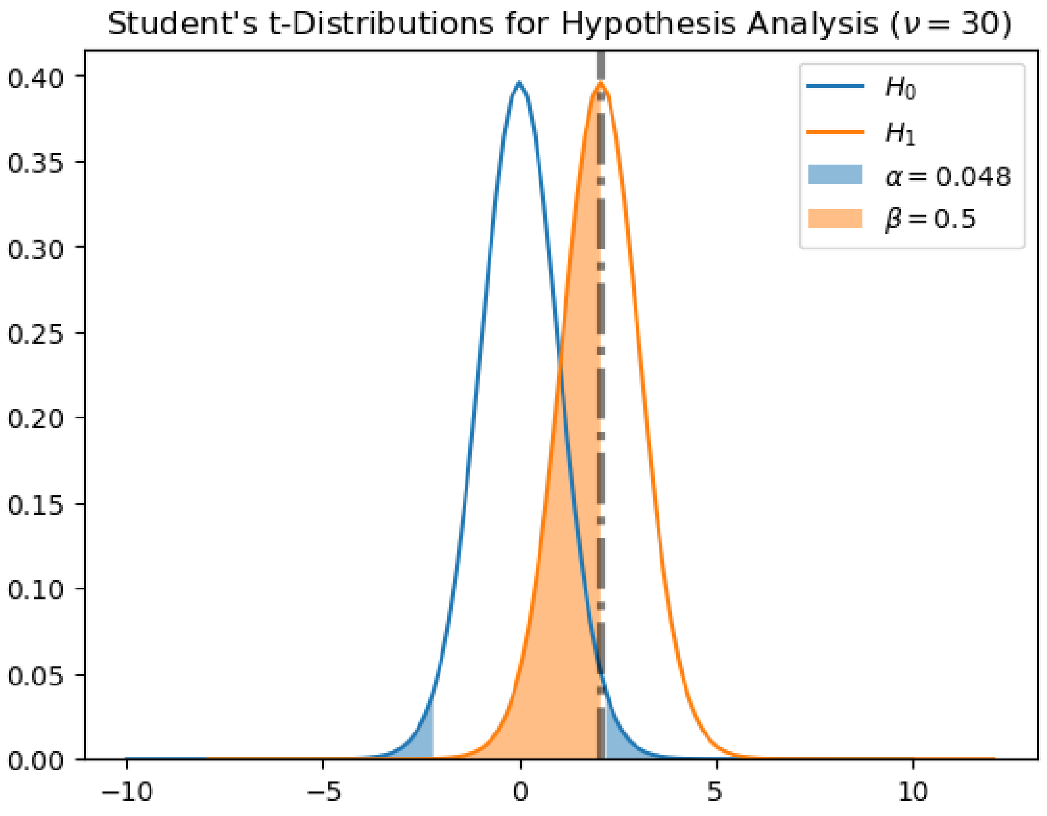
[38]:
```
data.loc[~data[c] & data['PopulationEffect']].sort_values('ItemNr',␣
↪ignore_index=True)
```

[38]:
```
   ItemNr  PopulationEffect  MeanGroup1    SDGroup1  MeanGroup2   SDGroup2  \
0       3                 1  -15.747061  102.164439  -34.091446  93.417503
1       7                 1    6.962812   96.066891  -35.132100  82.916984
2       8                 1   -5.045829  105.239143   35.892766  99.306192
3      15                 1   -9.250379  105.470703  -62.162545  99.005903
4      17                 1    5.176001  105.475429  -41.249891  79.441165
5      19                 1   -7.216715  126.894245   55.354562  99.668515

          p    n_c  bfwe_c  bhfwe_c  bhfdr_c
0  0.351061  False   False    False    False
1  0.021014   True   False    False    False
2  0.048202   True   False    False    False
3  0.011169   True   False    False    False
4  0.014606   True   False    False    False
5  0.007259   True   False    False    False
```

2.6 6.

$$\alpha = 0.048 \tag{16}$$

[39]:
```
alpha = 0.048

x = np.linspace(-10, 10, 1+100)
df = 30

y0 = st.t(df).pdf(x)
m = -st.t.ppf(alpha/2, df)

plt.plot(x, y0, label='$H_0$')
plt.plot(x+m, y0, label='$H_1$')

plt.ylim((0, None))

plt.fill_between(x, 0, y0, abs(x)>=m, alpha=0.5, label=rf'$\alpha = {alpha}$')
plt.fill_between(x+m, 0, y0, x<=0, alpha=0.5, label=r'$\beta = 0.5$')
plt.axvline(m, c='k', ls='-.', lw=3, alpha=0.5)
plt.title(rf"Student's t-Distributions for Hypothesis Analysis ($\nu = {df}$)")
plt.legend();
```



3 Assignment 2

3.1 1.

[40]:
```
data = pd.read_csv('data/2/Table1.csv')
```

[41]:
```
data.head()
```

[41]:
```
           y        cov  group
0  58.629443  11.298809      1
1  45.167029  11.094228      1
2  37.777554   8.434532      1
3  49.880216  14.434979      1
4  48.472039   4.347170      1
```

a.

[42]:
```
X = np.c_[np.ones(data.shape[0]), data['group'] - 1]
y = data['y'].to_numpy()
```

[43]:
```
# Alternative Hypothesis - H_1
beta_hat = np.linalg.inv(X.T @ X) @ X.T @ y
y_hat = X @ beta_hat
e_hat = y - y_hat
sse = e_hat @ e_hat
```

[44]:
```
pprint(ltxt=f"\\beta = {np.array2string(beta_hat, precision=5, separator=',')}")
pprint(ltxt=f"SSE = {sse:.5f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

---

[45]:
```
# Null Hypothesis - H_0
X_0 = np.ones(data.shape[0])[:, None]
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[46]:
```
pprint(ltxt=f"SSE_{{H_0}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[47]:
```
# Significance Test
pprint(ltxt=f"F = {(f := ((n:=len(y)) - (p:=X.shape[1]))/(r:=1) * (sse_0 - sse)/
  ↪sse):.5f}")
pprint(ltxt=f"p = {(pval := 1 - st.f.cdf(f, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

b.

[48]:
```
model = sm.OLS(y, X)
results = model.fit()
```

[49]:
```
results.summary()
```

[49]:

Dep. Variable:	y	**R-squared:**	0.163
Model:	OLS	**Adj. R-squared:**	0.149
Method:	Least Squares	**F-statistic:**	11.32
Date:	Fri, 19 Jul 2024	**Prob (F-statistic):**	0.00136
Time:	21:40:29	**Log-Likelihood:**	-231.50
No. Observations:	60	**AIC:**	467.0
Df Residuals:	58	**BIC:**	471.2
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
const	49.8847	2.129	23.427	0.000	45.622	54.147
x1	-10.1323	3.011	-3.365	0.001	-16.160	-4.104

Omnibus:	4.405	**Durbin-Watson:**	2.239
Prob(Omnibus):	0.111	**Jarque-Bera (JB):**	3.823
Skew:	0.616	**Prob(JB):**	0.148
Kurtosis:	3.109	**Cond. No.**	2.62

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

[50]:
```
pprint(ltxt=f"\\beta = {np.array2string(results.params, precision=5,␣
↪separator=',')}")
pprint(ltxt=f"SSE = {results.ssr:.5f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

[51]:
```
pprint(ltxt=f"\\text{{Degrees of Freedom}} = {int(results.df_model)},␣
↪{int(results.df_resid)}")
```

```
<IPython.core.display.HTML object>
```

[52]:
```
# Significance Test
pprint(ltxt=f"F = {results.fvalue:.5f}")
pprint(ltxt=f"p = {results.f_pvalue:.8f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

[53]:
```
# Other Effect Sizes
pprint(ltxt=f"R^2 = {results.rsquared:.5f}")
pprint(ltxt=f"R^2_{{adj}} = {results.rsquared_adj:.5f}")
# pprint(ltxt=f"Cohen's\ d = {results.tvalues/np.sqrt(len(X)):.5f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

[54]:
```
pprint(txt=f"""There {"isn't" if results.f_pvalue > 0.05 else "is"} a␣
↪significant effect of the drug $(p={results.f_pvalue:.8f}, F={results.fvalue:
↪.5f})$; it {("reduces" if results.params[1] < 0 else "increases") if results.
↪f_pvalue < 0.05 else "does not influence"} the time of the animals to find␣
↪the goal.""")
```

```
<IPython.core.display.HTML object>
```

c.

[55]:
```
X = np.c_[np.ones(data.shape[0]), data['cov']]
y = data['y'].to_numpy()
```

[56]:
```
# Alternative Hypothesis - H_1
beta_hat = np.linalg.inv(X.T @ X) @ X.T @ y
y_hat = X @ beta_hat
e_hat = y - y_hat
sse = e_hat @ e_hat
```

[57]:
```
pprint(ltxt=f"\\beta = {np.array2string(beta_hat, precision=5, separator=',')}")
pprint(ltxt=f"SSE = {sse:.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

---

[58]:
```
# Null Hypothesis - H_0
X_0 = np.ones(data.shape[0])[:, None]
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[59]:
```
pprint(ltxt=f"SSE_{{H_0}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[60]:
```
# Significance Test
pprint(ltxt=f"F = {(f := ((n:=len(y)) - (p:=X.shape[1]))/(r:=1) * (sse_0 - sse)/
↪sse):.5f}")
pprint(ltxt=f"p = {(pval := 1 - st.f.cdf(f, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

d.

[61]:
```
model = sm.OLS(y, X)
results = model.fit()
```

[62]:
```
results.summary()
```

[62]:

Dep. Variable:	y	**R-squared:**	0.429
Model:	OLS	**Adj. R-squared:**	0.419
Method:	Least Squares	**F-statistic:**	43.61
Date:	Fri, 19 Jul 2024	**Prob (F-statistic):**	1.35e-08
Time:	21:40:30	**Log-Likelihood:**	-220.03
No. Observations:	60	**AIC:**	444.1
Df Residuals:	58	**BIC:**	448.3
Df Model:	1		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
const	71.9826	4.297	16.751	0.000	63.381	80.584
x1	-1.9851	0.301	-6.604	0.000	-2.587	-1.383

Omnibus:	1.878	**Durbin-Watson:**	2.125
Prob(Omnibus):	0.391	**Jarque-Bera (JB):**	1.491
Skew:	0.386	**Prob(JB):**	0.475
Kurtosis:	3.008	**Cond. No.**	49.6

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

[63]:
```
pprint(ltxt=f"\\beta = {np.array2string(results.params, precision=5,␣
  ↪separator=',')}")
pprint(ltxt=f"SSE = {results.ssr:.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

[64]:
```
pprint(ltxt=f"\\text{{Degrees of Freedom}} = {int(results.df_model)},␣
  ↪{int(results.df_resid)}")
```

```
<IPython.core.display.HTML object>
```

[65]:
```
# Significance Test
pprint(ltxt=f"F = {results.fvalue:.5f}")
pprint(ltxt=f"p = {results.f_pvalue:.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

[66]:
```
# Other Effect Sizes
pprint(ltxt=f"R^2 = {results.rsquared:.5f}")
pprint(ltxt=f"R^2_{{adj}} = {results.rsquared_adj:.5f}")
# pprint(ltxt=f"Cohen's\ d = {results.tvalues/np.sqrt(len(X)):.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[67]: pprint(txt=f"""There {"isn't" if results.f_pvalue > 0.05 else "is"} a␣
      ↪significant effect of the speed of the animals $(p={results.f_pvalue:.8f},␣
      ↪F={results.fvalue:.5f})$; it {("reduces" if results.params[1] < 0 else␣
      ↪"increases") if results.f_pvalue < 0.05 else "does not influence"} the time␣
      ↪of the animals to find the goal.""")
```

```
<IPython.core.display.HTML object>
```

e.

```
[68]: X = np.c_[np.ones(data.shape[0]), data['group'] - 1, data['cov']]
      y = data['y'].to_numpy()
```

```
[69]: # Alternative Hypothesis - H_1
      beta_hat = np.linalg.inv(X.T @ X) @ X.T @ y
      y_hat = X @ beta_hat
      e_hat = y - y_hat
      sse = e_hat @ e_hat
```

```
[70]: pprint(ltxt=f"\\beta = {np.array2string(beta_hat, precision=5, separator=',')}")
      pprint(ltxt=f"SSE = {sse:.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[71]: # Null Hypothesis 1 - H_0_1
      X_0 = np.c_[np.ones(data.shape[0]), data['cov']]
      beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
      y_hat_0 = X_0 @ beta_hat_0
      e_hat_0 = y - y_hat_0
      sse_0 = e_hat_0 @ e_hat_0
```

```
[72]: pprint(ltxt=f"SSE_{{H_{{0_1}}}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

```
[73]: # Significance Test
      pprint(ltxt=f"F = {(f_1 := ((n:=len(y)) - (p:=X.shape[1]))/(r:=1) * (sse_0 -␣
      ↪sse)/sse):.5f}")
      pprint(ltxt=f"p = {(pval_1 := 1 - st.f.cdf(f_1, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[74]: # Null Hypothesis 2 - H_0_2
      X_0 = np.c_[np.ones(data.shape[0]), data['group'] - 1]
```

```
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[75]:
```
pprint(ltxt=f"SSE_{{H_{{0_2}}}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[76]:
```
# Significance Test
pprint(ltxt=f"F = {(f_2 := ((n:=len(y)) - (p:=X.shape[1]))/(r:=1) * (sse_0 -␣
↪sse)/sse):.5f}")
pprint(ltxt=f"p = {(pval_2 := 1 - st.f.cdf(f_2, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

f.
```

[77]:
```
model = sm.OLS(y, X)
results = model.fit()
```

[78]:
```
results.summary()
```

[78]:

Dep. Variable:	y	**R-squared:**	0.443
Model:	OLS	**Adj. R-squared:**	0.423
Method:	Least Squares	**F-statistic:**	22.62
Date:	Fri, 19 Jul 2024	**Prob (F-statistic):**	5.86e-08
Time:	21:40:30	**Log-Likelihood:**	-219.32
No. Observations:	60	**AIC:**	444.6
Df Residuals:	57	**BIC:**	450.9
Df Model:	2		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
const	75.0490	5.026	14.933	0.000	64.985	85.113
x1	4.2748	3.663	1.167	0.248	-3.061	11.610
x2	-2.3654	0.443	-5.343	0.000	-3.252	-1.479

Omnibus:	0.895	**Durbin-Watson:**	2.098
Prob(Omnibus):	0.639	**Jarque-Bera (JB):**	0.704
Skew:	0.263	**Prob(JB):**	0.703
Kurtosis:	2.936	**Cond. No.**	64.2

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

[79]:
```
pprint(ltxt=f"\\beta = {np.array2string(results.params, precision=5,␣
↪separator=',')}")
pprint(ltxt=f"SSE = {results.ssr:.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[80]: pprint(ltxt=f"\\text{{Degrees of Freedom}} = {int(results.df_model)},␣
        ↪{int(results.df_resid)}")
```

```
<IPython.core.display.HTML object>
```

```
[81]: # Significance Test
      pprint(ltxt=f"F = {results.fvalue:.5f}")
      pprint(ltxt=f"p = {results.f_pvalue:.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[82]: # Other Effect Sizes
      pprint(ltxt=f"R^2 = {results.rsquared:.5f}")
      pprint(ltxt=f"R^2_{{adj}} = {results.rsquared_adj:.5f}")
      # pprint(ltxt=f"Cohen's\ d = {results.tvalues/np.sqrt(len(X)):.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
[83]: pprint(txt=f"""There {"isn't" if pval_1 > 0.05 else "is"} a significant effect␣
        ↪of the drug $(p={pval_1:.8f}, F={f_1:.5f})$; it {("reduces" if results.
        ↪params[1] < 0 else "increases") if pval_1 < 0.05 else "does not influence"}␣
        ↪the time of the animals to find the goal.""")
      pprint(txt=f"""There {"isn't" if pval_2 > 0.05 else "is"} a significant effect␣
        ↪of the speed of the animals $(p={pval_2:.8f}, F={f_2:.5f})$; it {("reduces"␣
        ↪if results.params[2] < 0 else "increases") if pval_2 < 0.05 else "does not␣
        ↪influence"} the time of the animals to find the goal.""")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
Animals with higher running speeds can cover more distances in a shorter time and thus find the
The $\beta$ (slope) values give some insight for the above conclusions, i.e. it can be seen tha
```

3.2 2.

```
[84]: data = pd.read_csv('data/2/Table2.csv')
```

```
[85]: data.head()
```

```
[85]:             y  A  B
      0  124.118122  1  1
      1   79.961688  1  1
      2  101.762006  1  1
```

```
3   98.884491  1  1
4  113.239709  1  1
```

a.

[86]:
```python
# Dummy Coding
data['drug1'] = data['A']
data['drug1'].replace([1], 1, inplace=True)
data['drug1'].replace([2], 0, inplace=True)
data['drug1'].replace([3], -1, inplace=True)

data['drug2'] = data['A']
data['drug2'].replace([1], 0, inplace=True)
data['drug2'].replace([2], 1, inplace=True)
data['drug2'].replace([3], -1, inplace=True)
```

[87]:
```python
X = np.c_[np.ones(data.shape[0]), data['drug1'], data['drug2']]
y = data['y'].to_numpy()
```

[88]:
```python
# Alternative Hypothesis - H_1
beta_hat = np.linalg.inv(X.T @ X) @ X.T @ y
y_hat = X @ beta_hat
e_hat = y - y_hat
sse = e_hat @ e_hat
```

[89]:
```python
pprint(ltxt=f"\\beta = {np.array2string(beta_hat, precision=5, separator=',')}")
pprint(ltxt=f"SSE = {sse:.5f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

```
<b>MY QUESTION #1</b></br>
The second slope value above changes sign if I use effect coding instead of dummy coding! I ex
```

---

[90]:
```python
# Null Hypothesis 1 - H_0
X_0 = np.ones(data.shape[0])[:, None]
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[91]:
```python
pprint(ltxt=f"SSE_{{H_0}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[92]:
```python
# Significance Test
```

```
pprint(ltxt=f"F = {(f := ((n:=len(y)) - (p:=X.shape[1]))/(r:=2) * (sse_0 - sse)/
↪sse):.5f}")
pprint(ltxt=f"p = {(pval := 1 - st.f.cdf(f, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

[93]:
```
pprint(txt=f"""There {"isn't" if pval > 0.05 else "is"} a significant effect of␣
↪the drugs $(p={pval:.8f}, F={f:.5f})$; drug1 {("reduces" if beta_hat[1] < 0␣
↪else "increases") if pval < 0.05 else "does not influence"} intelligence and␣
↪drug2 {("reduces" if beta_hat[2] < 0 else "increases") if pval < 0.05 else␣
↪"does not influence"} intelligence.""")
```

```
<IPython.core.display.HTML object>
```

```
b.
```

```
<b>MY QUESTION #2</b></br>
I don't see why effect coding is "required" and why dummy coding cannot be used as long as inte
```

[94]:
```
# Interaction Coding (Dummy)
data['gender'] = data['B']
data['gender'].replace([1], -1, inplace=True)
data['gender'].replace([2], 1, inplace=True)

data['drug1_gender'] = data['drug1'] * data['gender']
data['drug2_gender'] = data['drug2'] * data['gender']
```

[95]:
```
X = np.c_[np.ones(data.shape[0]), data['drug1'], data['drug2'], data['gender'],␣
↪data['drug1_gender'], data['drug2_gender']]
y = data['y'].to_numpy()
```

[96]:
```
# Alternative Hypothesis - H_1
beta_hat = np.linalg.inv(X.T @ X) @ X.T @ y
y_hat = X @ beta_hat
e_hat = y - y_hat
sse = e_hat @ e_hat
```

[97]:
```
pprint(ltxt=f"\\beta = {np.array2string(beta_hat, precision=5, separator=',')}")
pprint(ltxt=f"SSE = {sse:.5f}")
```

```
<IPython.core.display.HTML object>
```

```
<IPython.core.display.HTML object>
```

---

[98]:
```
# Null Hypothesis 1 - H_0
X_0 = np.c_[np.ones(data.shape[0]), data['gender'], data['drug1_gender'],␣
↪data['drug2_gender']]
```

```
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[99]:
```
pprint(ltxt=f"SSE_{{H_{{0_1}}}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[100]:
```
# Significance Test
pprint(ltxt=f"F = {(f_1 := ((n:=len(y)) - (p:=X.shape[1]))/(r:=2) * (sse_0 -␣
    ↪sse)/sse):.5f}")
pprint(ltxt=f"p = {(pval_1 := 1 - st.f.cdf(f_1, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

---

[101]:
```
# Null Hypothesis 2 - H_0
X_0 = np.c_[np.ones(data.shape[0]), data['drug1'], data['drug2'],␣
    ↪data['drug1_gender'], data['drug2_gender']]
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[102]:
```
pprint(ltxt=f"SSE_{{H_{{0_2}}}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[103]:
```
# Significance Test
pprint(ltxt=f"F = {(f_2 := ((n:=len(y)) - (p:=X.shape[1]))/(r:=1) * (sse_0 -␣
    ↪sse)/sse):.5f}")
pprint(ltxt=f"p = {(pval_2 := 1 - st.f.cdf(f_2, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

---

[104]:
```
# Null Hypothesis 3 - H_0
X_0 = np.c_[np.ones(data.shape[0]), data['drug1'], data['drug2'],␣
    ↪data['gender']]
beta_hat_0 = np.linalg.inv(X_0.T @ X_0) @ X_0.T @ y
y_hat_0 = X_0 @ beta_hat_0
e_hat_0 = y - y_hat_0
sse_0 = e_hat_0 @ e_hat_0
```

[105]:
```
pprint(ltxt=f"SSE_{{H_{{0_3}}}} = {sse_0:.5f}")
```

```
<IPython.core.display.HTML object>
```

[106]:
```
# Significance Test
pprint(ltxt=f"F = {(f_3 := ((n:=len(y)) - (p:=X.shape[1]))/(r:=2) * (sse_0 -␣
↪sse)/sse):.5f}")
pprint(ltxt=f"p = {(pval_3 := 1 - st.f.cdf(f_3, dfn=r, dfd=n-p)):.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

[107]:
```
pprint(txt=f"""There {"isn't" if pval_1 > 0.05 else "is"} a significant effect␣
↪of the drugs $(p={pval_1:.8f}, F={f_1:.5f})$.""")
pprint(txt=f"""There {"isn't" if pval_2 > 0.05 else "is"} a significant effect␣
↪of gender $(p={pval_2:.8f}, F={f_2:.5f})$.""")
pprint(txt=f"""There {"isn't" if pval_3 > 0.05 else "is"} a significant effect␣
↪of the drug-gender interactions $(p={pval_3:.8f}, F={f_3:.5f})$.""")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

4 Assignment 3

4.1 1.

[108]:
```
data = pd.read_csv('data/3/Table1.csv')
```

[109]:
```
data.head()
```

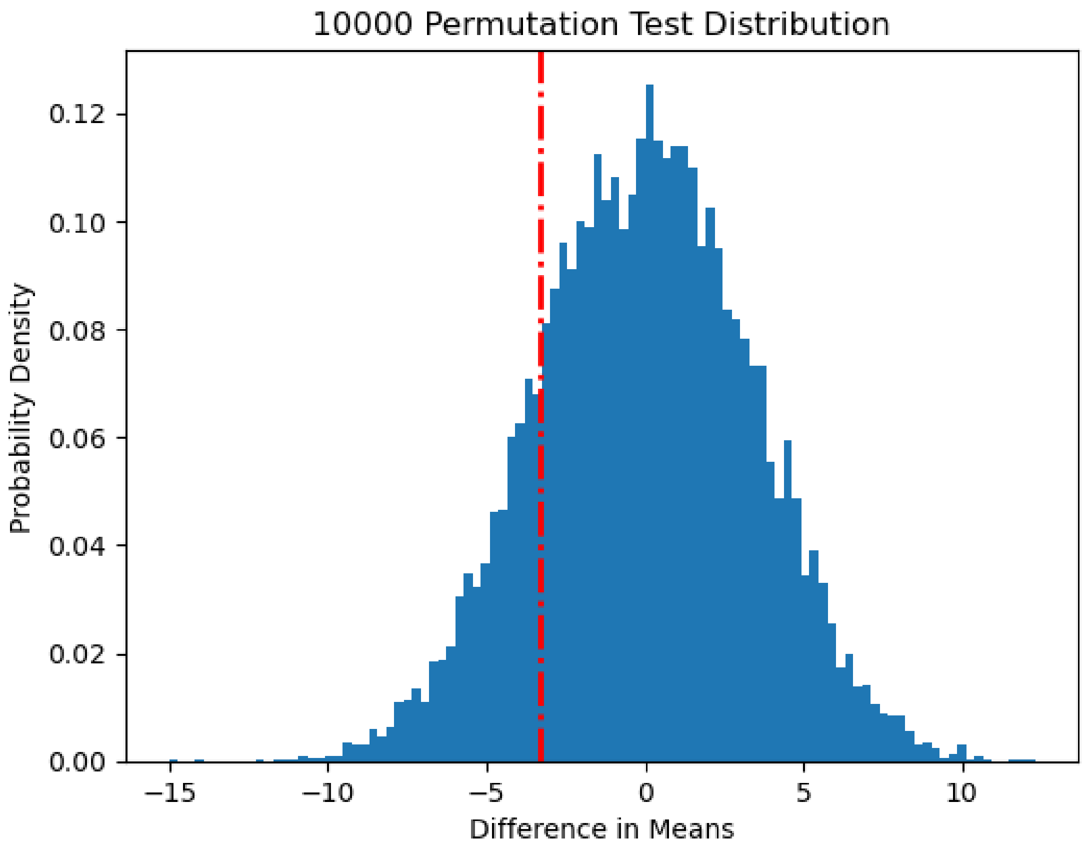
[109]:
```
      GroupA     GroupB
0  72.194926  75.628366
1  66.949193  65.292139
2  70.619039  68.209072
3  66.427349  71.732184
4  65.895107  67.537972
```

[110]:
```
# Significance test
t_stat, p_value = st.ttest_ind(data['GroupA'], data['GroupB'])
pprint("T-Test Result")
pprint(ltxt=f"t = {t_stat:.5f}")
pprint(ltxt=f"p = {p_value:.8f}")
```

```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>
```

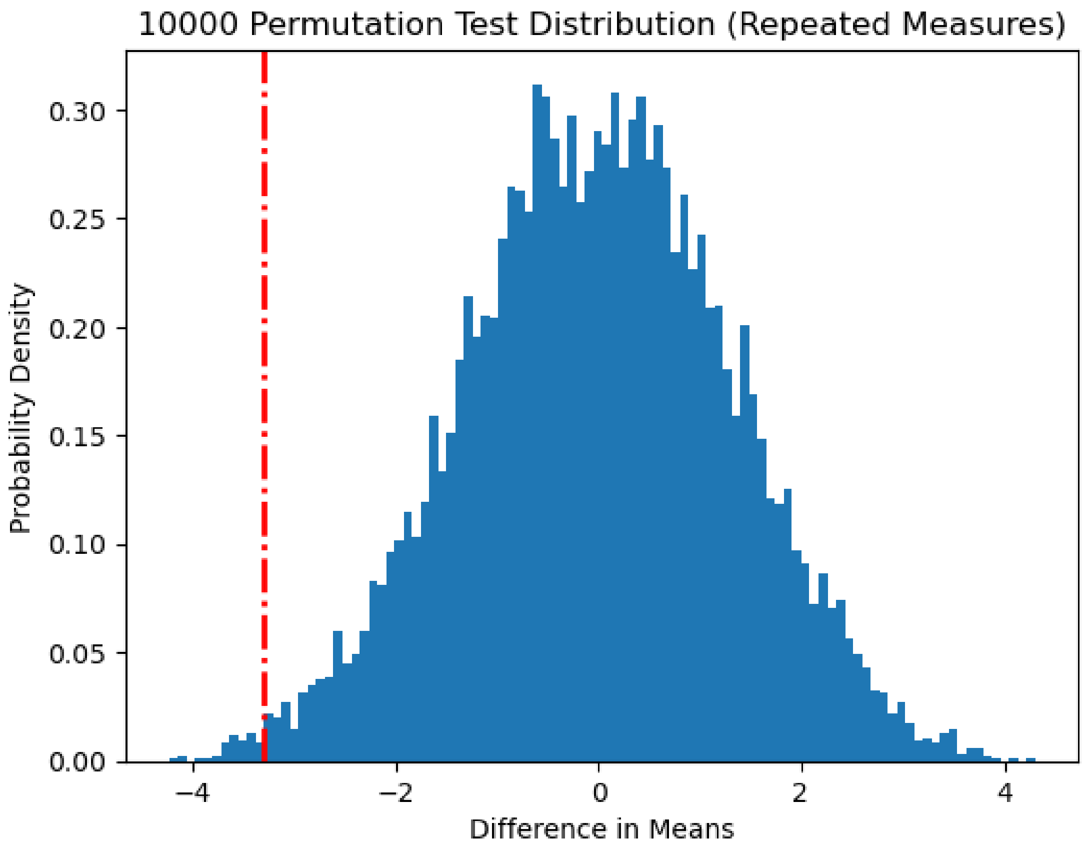
```
[111]: def permutation_test(groupA, groupB, num_permutations=10000, *,␣
        ↪repeated_measures=False, plot_dist=True, bins=100):
           if repeated_measures:
               assert len(groupA) == len(groupB), 'Both groups must have the same␣
        ↪number of samples for repeated measures.'

           observed_diff = np.mean(groupA) - np.mean(groupB)

           stacked = np.r_[groupA, groupB]
           distribution = []
           count = 0
           for _ in range(num_permutations):
               if repeated_measures:
                   signs = np.random.choice([-1, 1], size=len(groupA))
                   new_diff = np.r_[signs, -signs] @ stacked / len(groupA)
               else:
                   np.random.shuffle(stacked)
                   new_groupA = stacked[:len(groupA)]
                   new_groupB = stacked[len(groupA):]
                   new_diff = np.mean(new_groupA) - np.mean(new_groupB)

               distribution.append(new_diff)
               if abs(new_diff) >= abs(observed_diff):
                   count += 1

           if plot_dist:
               plt.hist(distribution, bins=bins, density=True)
               plt.axvline(observed_diff, c='r', ls='-.', lw=2)
               plt.title(f"{num_permutations} Permutation Test Distribution{'␣
        ↪(Repeated Measures)' if repeated_measures else ''}")
               plt.xlabel("Difference in Means")
               plt.ylabel("Probability Density")
               plt.show()

           return count / num_permutations
```

```
[112]: # Permutation test
       pprint("Permutation Test Result", f"p = {permutation_test(data['GroupA'],␣
        ↪data['GroupB']):.8f}")
```



```
<IPython.core.display.HTML object>
```

```
[113]: # Permutations test for repeated measures
       pprint("Permutation Test Result", f"p = {permutation_test(data['GroupA'],␣
        ↪data['GroupB'], repeated_measures=True):.8f}")
```



```
<IPython.core.display.HTML object>
```

4.2 2.

[114]:
```
data = pd.read_csv('data/3/Table2.csv')
```

[115]:
```
data.head()
```

[115]:
```
          x         y
0  0.026495 -0.641899
1  0.119065  1.036808
2 -0.457300  0.204774
3  0.066706 -0.182882
4  1.431809  2.034713
```

[116]:
```
def bootstrap_correlation(seriesA, seriesB, *, alpha=0.05, num_bootstrap=10000):
    assert len(seriesA) == len(seriesB), 'Both series must have the same number␣
↪of samples.'

    bootstrap_samples = []
    for _ in range(num_bootstrap):
        sample_indices = np.random.randint(0, len(seriesA), len(seriesA))
        sampleA, sampleB = seriesA[sample_indices], seriesB[sample_indices]
        sample_corr, _ = st.pearsonr(sampleA, sampleB)
        bootstrap_samples.append(sample_corr)

    return np.percentile(bootstrap_samples, [50 * alpha, 50 * (2 - alpha)])
```

[117]:
```
# Confidence interval using bootstrap
pprint(f"95% Confidence Interval = ${bootstrap_correlation(data['x'],␣
 ↪data['y'])}$.")
```

```
<IPython.core.display.HTML object>
```

[118]:
```
# Correlation and its significance
correlation, p_value = st.pearsonr(data['x'], data['y'])
pprint(f"""The correlation $(r={correlation:0.5f})$ {"isn't" if p_value > 0.05␣
 ↪else "is"} significantly different from zero $(p={p_value:.8f})$.""")
```

```
<IPython.core.display.HTML object>
```

4.3 3.

[119]:
```
data = pd.read_csv('data/3/Table3.csv')
```

[120]:
```
data.head()
```

[120]:
```
   Outcome  Clinic  Treatment
0     5.18       1          1
1     6.19       1          1
2     5.40       1          1
3     4.17       1          1
4     5.41       1          1
```

[121]:
```
X = np.c_[np.ones(data.shape[0]),
          data['Clinic'].replace([1, 2], [0, 1]),
          data['Treatment'].replace([1, 2], [0, 1]),
          data['Clinic'].replace([1, 2], [0, 1]) * data['Treatment'].
 ↪replace([1, 2], [0, 1])]
y = data['Outcome'].to_numpy()
```

[122]:
```
results = sm.OLS(y, X).fit()
results.summary()
```

[122]:

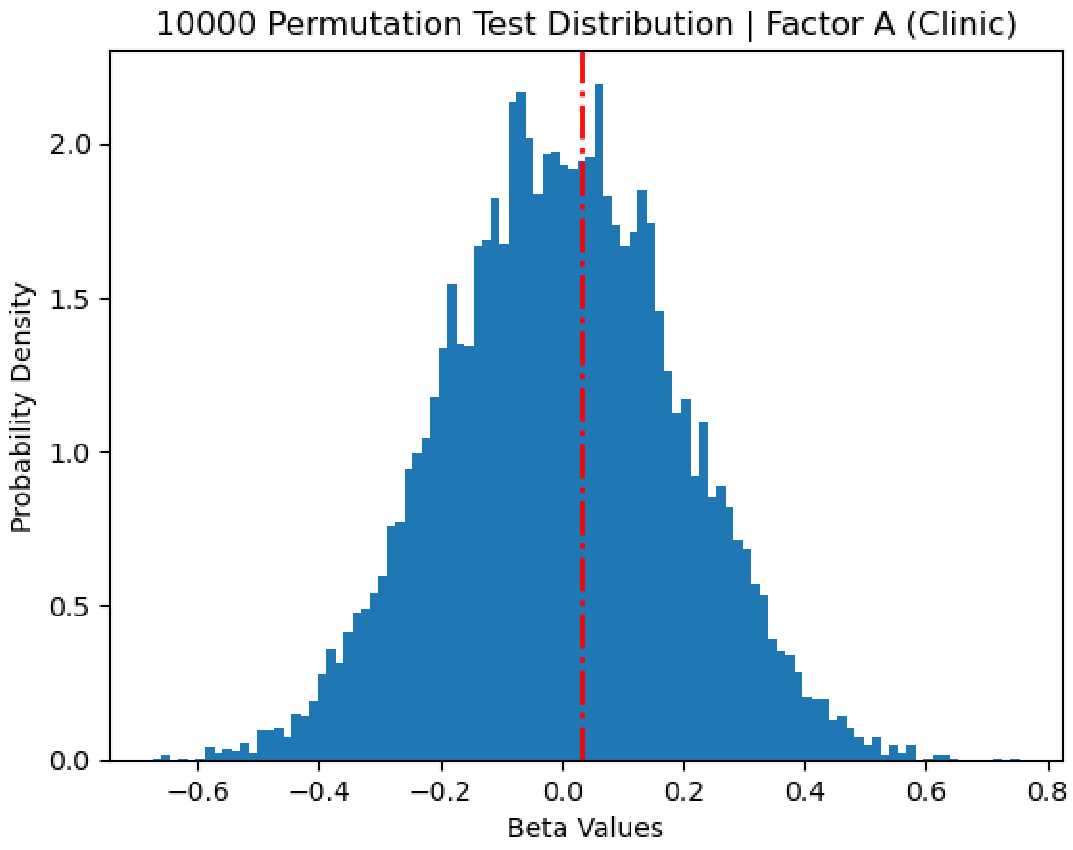
Dep. Variable:	y	**R-squared:**	0.087
Model:	OLS	**Adj. R-squared:**	0.064
Method:	Least Squares	**F-statistic:**	3.690
Date:	Fri, 19 Jul 2024	**Prob (F-statistic):**	0.0140
Time:	21:40:48	**Log-Likelihood:**	-174.58
No. Observations:	120	**AIC:**	357.2
Df Residuals:	116	**BIC:**	368.3
Df Model:	3		
Covariance Type:	nonrobust		

	coef	**std err**	**t**	**P> |t|**	**[0.025**	**0.975]**
const	5.0787	0.192	26.385	0.000	4.697	5.460
x1	0.0320	0.272	0.118	0.907	-0.507	0.571
x2	0.6023	0.272	2.213	0.029	0.063	1.141
x3	0.0677	0.385	0.176	0.861	-0.695	0.830

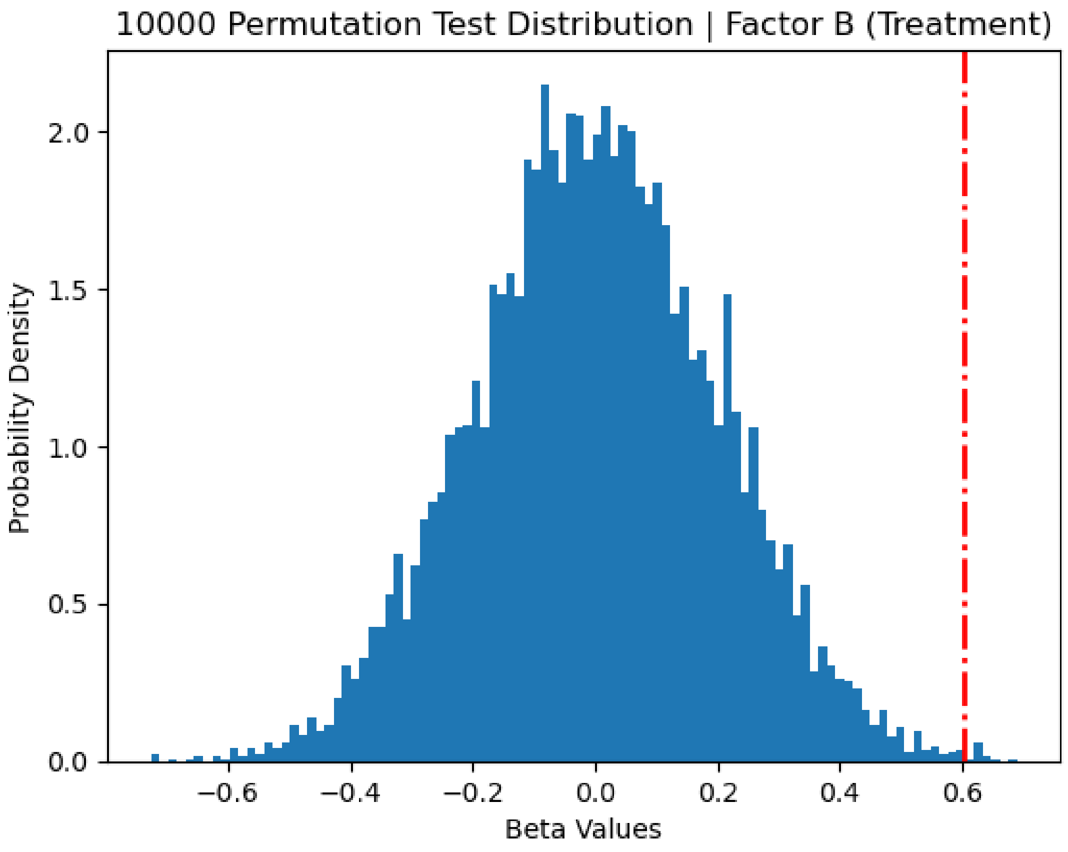
Omnibus:	2.175	**Durbin-Watson:**	2.266
Prob(Omnibus):	0.337	**Jarque-Bera (JB):**	1.556
Skew:	0.011	**Prob(JB):**	0.459
Kurtosis:	2.442	**Cond. No.**	6.85

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

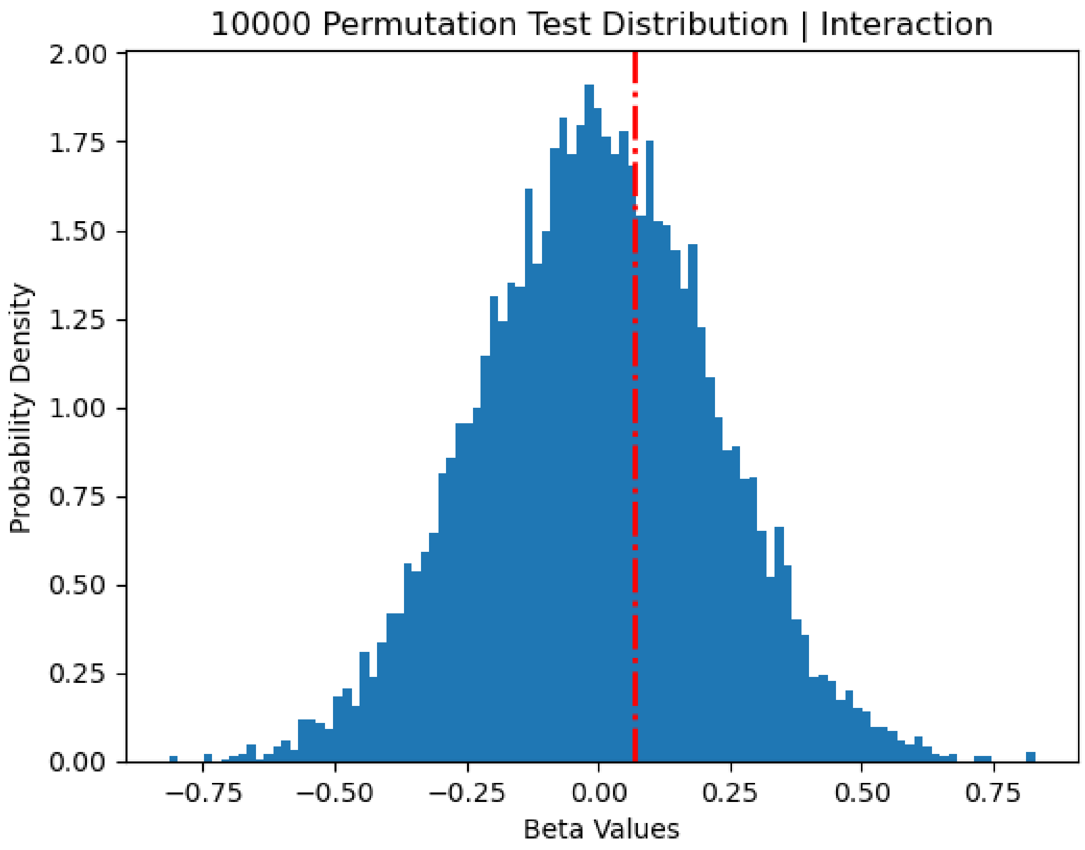
[123]:
```python
# Permutation Test
num_permutations = 10000

betas_original = results.params

for i, category in zip(range(1, X.shape[1]), ['Factor A (Clinic)', 'Factor B␣
 ↪(Treatment)', 'Interaction']):
    distribution = []
    count = 0

    for _ in range(num_permutations):
        X_perm = X.copy()
        np.random.shuffle(X_perm[:, i])
        results_perm = sm.OLS(y, X_perm).fit()
        beta_perm = results_perm.params[i]

        distribution.append(beta_perm)
        if abs(beta_perm) >= abs(betas_original[i]):
            count += 1

    plt.hist(distribution, bins=100, density=True)
    plt.axvline(betas_original[i], c='r', ls='-.', lw=2)
    plt.title(f"{num_permutations} Permutation Test Distribution | {category}")
    plt.xlabel("Beta Values")
    plt.ylabel("Probability Density")
    plt.show()

    pvalue = count / num_permutations
    pprint(f"""{category} {"doesn't have" if pvalue > 0.05 else "has"} a␣
↪significant effect $(p={pvalue:.8f})$ on the treatment outcome.""")
```



```
<IPython.core.display.HTML object>
```


10000 Permutation Test Distribution | Factor B (Treatment)
Probability Density
Beta Values
0.0
0.5
1.0
1.5
2.0
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6

```
<IPython.core.display.HTML object>
```


10000 Permutation Test Distribution | Interaction
Probability Density
Beta Values
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
−0.75
−0.50
−0.25
0.00
0.25
0.50
0.75

```
<IPython.core.display.HTML object>
```

```
[ ]:
```