```
import pandas as pd
import scipy.stats as stats
import matplotlib.pyplot as plt
import seaborn as sns
data = pd.read csv('iris.txt')
print(data)
     sepal_length sepal_width petal_length petal_width
species
              5.1
                            3.5
                                          1.4
                                                       0.2
                                                                Iris-
setosa
              4.9
                            3.0
                                          1.4
                                                       0.2
                                                                Iris-
setosa
              4.7
                            3.2
                                          1.3
                                                       0.2
                                                                Iris-
2
setosa
                                                       0.2
              4.6
                            3.1
                                          1.5
                                                                Iris-
setosa
              5.0
                            3.6
                                          1.4
                                                       0.2
                                                                Iris-
setosa
                                                        . . .
. .
              6.7
                            3.0
                                          5.2
                                                       2.3 Iris-
145
virginica
              6.3
                            2.5
                                          5.0
                                                       1.9 Iris-
146
virginica
              6.5
147
                            3.0
                                          5.2
                                                       2.0 Iris-
virginica
              6.2
148
                            3.4
                                          5.4
                                                       2.3 Iris-
virginica
149
              5.9
                            3.0
                                          5.1
                                                       1.8 Iris-
virginica
[150 rows x 5 columns]
setosa = data[data['species'] == 'Iris-setosa']['sepal_width']
virginica = data[data['species'] == 'Iris-virginica']['sepal width']
print(f'Value of stosa is {setosa}')
print(f'Value of virginica is {virginica}')
Value of stosa is 0 3.5
      3.0
1
2
      3.2
3
      3.1
4
      3.6
5
      3.9
6
      3.4
7
      3.4
8
      2.9
9
      3.1
```

```
10
      3.7
11
      3.4
      3.0
12
13
      3.0
14
      4.0
15
      4.4
      3.9
16
17
      3.5
18
      3.8
19
      3.8
20
      3.4
21
      3.7
22
      3.6
23
      3.3
24
      3.4
25
      3.0
26
      3.4
27
      3.5
28
      3.4
29
      3.2
30
      3.1
31
      3.4
32
      4.1
33
      4.2
34
      3.1
35
      3.2
36
      3.5
37
      3.1
38
      3.0
39
      3.4
      3.5
40
41
      2.3
42
      3.2
43
      3.5
44
      3.8
45
      3.0
46
      3.8
47
      3.2
48
      3.7
49
      3.3
Name: sepal_width, dtype: float64
Value of virginica is 100 3.3
101
       2.7
102
       3.0
103
       2.9
       3.0
104
105
       3.0
106
       2.5
107
       2.9
```

```
108
       2.5
109
       3.6
110
       3.2
       2.7
111
       3.0
112
113
       2.5
114
       2.8
115
       3.2
116
       3.0
117
       3.8
118
       2.6
       2.2
119
120
       3.2
121
       2.8
122
       2.8
123
       2.7
       3.3
124
       3.2
125
126
       2.8
127
       3.0
128
       2.8
129
       3.0
130
       2.8
131
       3.8
132
       2.8
133
       2.8
134
       2.6
135
       3.0
136
       3.4
137
       3.1
138
       3.0
139
       3.1
140
       3.1
141
       3.1
142
       2.7
       3.2
143
144
       3.3
145
       3.0
146
       2.5
147
       3.0
148
       3.4
149
       3.0
Name: sepal_width, dtype: float64
```

Checkign normality using shapiro wilk test

```
shapiro_setosa, p_setosa = stats.shapiro(setosa)
print(f'Value of p_setosa is {p_setosa}')
```

```
shapiro_virginica, p_virginica = stats.shapiro(virginica)
print(f'Value of shapiro_virginica is {p_virginica}')

Value of p_setosa is 0.20465666067562632
Value of shapiro_virginica is 0.18089604109069918
```

Checking variance

```
levene test, levene p = stats.levene(setosa, virginica)
print(f'Value of levene p is {levene p}')
Value of levene p is 0.30632327568956713
t stat, p value = stats.ttest ind(setosa, virginica, equal var=True)
print("Shapiro-Wilk Test for Normality (Setosa):", shapiro_setosa)
print("Shapiro-Wilk Test for Normality (Virginica):",
shapiro virginica)
print("Levene's Test for Equal Variances:", levene test)
print("Two-sample t-test p-value:", p value)
Shapiro-Wilk Test for Normality (Setosa):
ShapiroResult(statistic=0.9686918964570316,
pvalue=0.20465666067562632)
Shapiro-Wilk Test for Normality (Virginica):
ShapiroResult(statistic=0.9673905311257006,
pvalue=0.18089604109069918)
Levene's Test for Equal Variances:
LeveneResult(statistic=1.0574747096290729, pvalue=0.30632327568956713)
Two-sample t-test p-value: 8.916634067006443e-09
```

F-Test for Comparing Variances

```
f_stat = setosa.var() / virginica.var()
dfn = len(setosa) - 1
dfd = len(virginica) - 1
f_p_value = 1 - stats.f.cdf(f_stat, dfn, dfd)

print("F-statistic for Variance Comparison:", f_stat)
print("F-test p-value:", f_p_value)

F-statistic for Variance Comparison: 1.3959028295592788
F-test p-value: 0.12327029558510993
```