

MANOVA

1 - IRIS\ 2 - We are going to use the width and lngth columns as dependent variables.\ 3 - Besides, the species column is used as the indendent variable.\ 4 - MANOVA by the Statmodel library.

```
In [ ]: # import libraries
import seaborn as sns
import pandas as pd
import matplotlib.pyplot as plt
from statsmodels.multivariate.manova import MANOVA
```

```
In [ ]: # dataset load
df1= sns.load_dataset('iris')
df1.head()
```

```
Out[ ]:   sepal_length  sepal_width  petal_length  petal_width  species
0          5.1           3.5           1.4           0.2    setosa
1          4.9           3.0           1.4           0.2    setosa
2          4.7           3.2           1.3           0.2    setosa
3          4.6           3.1           1.5           0.2    setosa
4          5.0           3.6           1.4           0.2    setosa
```

```
In [ ]: df1.columns
```

```
Out[ ]: Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
              'species'],
              dtype='object')
```

```
In [ ]: # manova
mova = MANOVA.from_formula('sepal_length + sepal_width + petal_length + petal_width ~
print(mova.mv_test())
```

Multivariate linear model

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Intercept	Value	Num DF	Den DF	F Value	Pr > F	

Wilks' lambda	0.0170	4.0000	144.0000	2086.7720	0.0000	
Pillai's trace	0.9830	4.0000	144.0000	2086.7720	0.0000	
Hotelling-Lawley trace	57.9659	4.0000	144.0000	2086.7720	0.0000	
Roy's greatest root	57.9659	4.0000	144.0000	2086.7720	0.0000	

species	Value	Num DF	Den DF	F Value	Pr > F	

Wilks' lambda	0.0234	8.0000	288.0000	199.1453	0.0000	
Pillai's trace	1.1919	8.0000	290.0000	53.4665	0.0000	
Hotelling-Lawley trace	32.4773	8.0000	203.4024	582.1970	0.0000	
Roy's greatest root	32.1919	4.0000	145.0000	1166.9574	0.0000	
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1 The p-value to consider in this case is that of Wilk's lambda, relative to the output variable specie we can see, even in this case it is significant.