MANOVA

- IRIS
- We are going to use the width and length columns as depedent variabbles.
- Besides, the species column is used as the independent variable.
- MANOVA by the Statsmodel library.

```
In [ ]:
        # import librarires
        import pandas as pd
        import seaborn as sns
        import matplotlib.pyplot as plt
        from statsmodels.multivariate.manova import MANOVA
In [ ]:
        # Load the dataset
        phool = sns.load_dataset('iris')
        phool.head()
        sepal_length sepal_width petal_length petal_width species
Out[ ]:
       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
                5.0
                          3.6
                                     1.4
                                              0.2 setosa
In [ ]:
        phool.columns
Out[ ]: Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
              species'],
             dtype='object')
In [ ]:
        # Apply MANOVA
        manova_phool = MANOVA.from_formula('sepal_length + sepal_width + petal_length + petal_
        print(manova_phool.mv_test())
                        Multivariate linear model
       ______
                        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
        ______
                            Value Num DF Den DF F Value Pr > F
              species
                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
       -----
```

How to read MANOVA.\ The p-value to consider in this case is that of Wilk's lambda, relative
to output variable (Species). As we can see even in this case it is significant

ASSIGNMENTS

1. How to save the results in a tabulated format or a picture?

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2 How to interpret Manaya?

Solutions to ASSIGNMENTS

1. How to save the results in a tabulated format or a picture?

```
In [ ]:     x = pd.DataFrame((manova_phool.mv_test().results['species']['stat']))
     x
```

Out[]:		Value	Num DF	Den DF	F Value	Pr > F
	Wilks' lambda	0.023439	8	288.0	199.145344	0.0
	Pillai's trace	1.191899	8.0	290.0	53.466489	0.0
	Hotelling-Lawley trace	32.47732	8	203.40239	582.197018	0.0
	Roy's greatest root	32.191929	4	145	1166.957433	0.0

2. How to interpret Manova?

- F Value This is the F statistic for the given predictor and test statistic.
- Num DF This is the number of degrees of freedom in the model.
- Den DF This is the number of degrees of freedom associated with the model errors. Note
 that there are instances in MANOVA when the degrees of freedom may be a non-integer
 (here, the DF associated with Hotelling-Lawley Trace is a non-integer) because these degrees
 of freedom are calculated using the mean squared errors, which are often non-integers.
- Pr > F This is the p-value associated with the F statistic of a given effect and test statistic. The null hypothesis that a given predictor has no effect on either of the outcomes is evaluated with regard to this p-value. For a given alpha level, if the p-value is less than alpha, the null hypothesis is rejected. If not, then we fail to reject the null hypothesis. In this example, we reject the null hypothesis that group has no effect on useful, difficulty or importance scores at alpha level .05 because the p-values are all less than .05.

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