Excercise 1

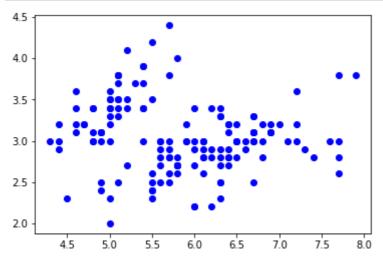
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats
from sklearn.decomposition import PCA
from sklearn.cluster import KMeans

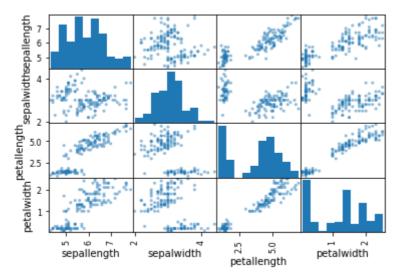
#Excercise 1

iris = pd.read_csv('iris_csv.csv')
length = iris['sepallength']
width = iris['sepalwidth']

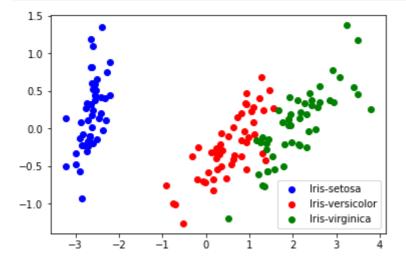
plt.plot(length, width, 'bo')
plt.show()

pd.plotting.scatter_matrix(iris)
```





```
In [123...
          #Excercise 2
          irisclass = iris['class']
          irisclass.to_numpy()
          irisnumbers = iris.drop(['class'], axis=1)
          pca = PCA(n\_components = 2)
          irispca = pca.fit_transform(irisnumbers)
          label_color = {'Iris-setosa' : 'blue', 'Iris-versicolor' : 'yellow', 'Iris-virginica
          setosa = irispca[irisclass == 'Iris-setosa']
          versicolor = irispca[irisclass == 'Iris-versicolor']
          virginica = irispca[irisclass == 'Iris-virginica']
          plt.scatter(setosa[:,0], setosa[:,1], color='blue', label="Iris-setosa")
          plt.scatter(versicolor[:,0], versicolor[:,1], color='red', label="Iris-versicolor")
          plt.scatter(virginica[:,0], virginica[:,1], color='green', label="Iris-virginica")
          plt.legend()
          plt.show()
```



Iris setosa is clearly distinct. There is some overlap between iris versicolor and iris virginica.

```
#Excercise 3
loadings = pd.DataFrame(pca.components_.T, index=irisnumbers.columns, columns=['1', print(loadings)
```

```
1 2
sepallength 0.361590 0.656540
sepalwidth -0.082269 0.729712
petallength 0.856572 -0.175767
petalwidth 0.358844 -0.074706
```

For component 1 the most important feature was petal length, while for component 2 it was sepal width followed by sepal ength.

```
iriscorrD = iris.corr(method = 'spearman')
pcadf = pd.DataFrame(irispca)
iriscorrP = pcadf.corr(method='spearman')

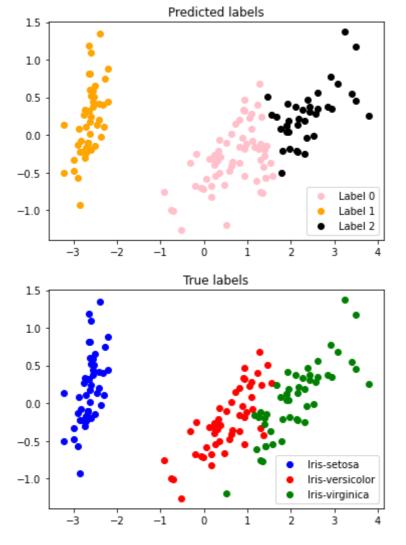
print(iriscorrD)
print(iriscorrP)

sepallength sepalwidth petallength petalwidth
sepallength 1.000000 -0.159457 0.881386 0.834421
sepallength 0.159457 1.000000 0.277511
```

sepallength 1.000000 -0.159457 0.881386 0.834421 sepalwidth -0.159457 1.000000 -0.303421 -0.277511 petallength 0.881386 -0.303421 1.000000 0.936003 petalwidth 0.834421 -0.277511 0.936003 1.000000 0 1 0 1.000000 0.141512 1.000000 0.141512 1.000000

Petal length + sepal length, petal width + sepal length, petal length + petal width

```
In [187...
          #Excercise 5
          kmeans = KMeans(n_clusters=3)
          clusters = kmeans.fit_predict(irisnumbers)
          label0 = irispca[clusters == 0]
          label1 = irispca[clusters == 1]
          label2 = irispca[clusters == 2]
          plt.scatter(label0[:,0], label0[:,1], color='pink', label="Label 0")
          plt.scatter(label1[:,0], label1[:,1], color='orange', label="Label 1")
          plt.scatter(label2[:,0], label2[:,1], color='black', label="Label 2")
          plt.title("Predicted labels")
          plt.legend()
          plt.show()
          plt.scatter(setosa[:,0], setosa[:,1], color='blue', label="Iris-setosa")
          plt.scatter(versicolor[:,0], versicolor[:,1], color='red', label="Iris-versicolor")
          plt.scatter(virginica[:,0], virginica[:,1], color='green', label="Iris-virginica")
          plt.title('True labels')
          plt.legend()
          plt.show()
```



The label 1 does correspond with Iris-setosa almost perfectly. The problem is with clusters of label 0 (mostly iris versicolor) and label 2 (iris virginica), which do differ a little bit.