

```
In [1]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn import datasets
import plotly.express as px
from sklearn.decomposition import PCA
from pylab import *
import pylab as pl
%matplotlib inline
import seaborn as sns
from itertools import cycle
from sklearn.preprocessing import StandardScaler

In [2]: #import iris dataset from sklearn
iris = datasets.load_iris()

In [3]: #features in the iris dataset
iris.feature_names

Out[3]: ['sepal length (cm)',
'sepal width (cm)',
'petal length (cm)',
'petal width (cm)']

In [4]: #target in the iris dataset
iris.target_names

Out[4]: array(['setosa', 'versicolor', 'virginica'], dtype='<U10')

In [5]: #update X,y from iris dataset
X = iris.data
y = iris.target

In [6]: #create dataframe using X,y
df = pd.DataFrame(X,columns=iris.feature_names)

#check header of the created dataframe
df.head()
```

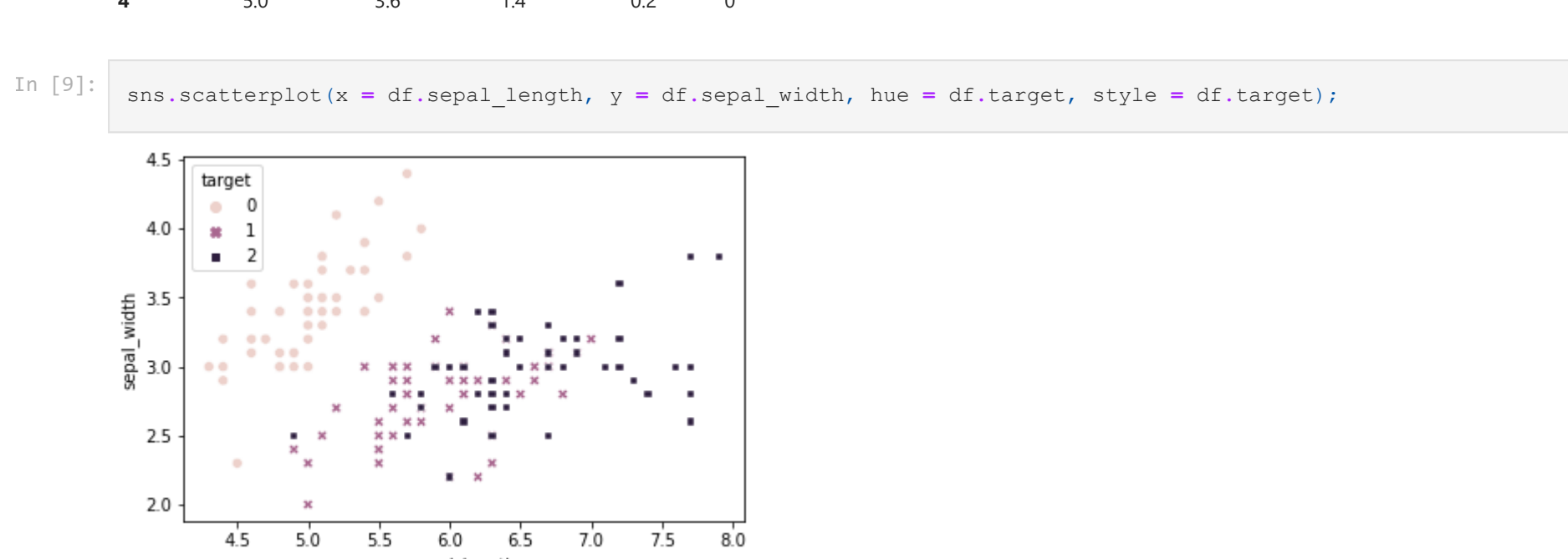
	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

```
In [7]: #append target into dataframe
df['target'] = iris.target

In [8]: df.columns=['sepal_length', 'sepal_width', 'petal_lenth', 'petal_width', 'target']
df.head()

Out[8]:
```

	sepal_length	sepal_width	petal_lenth	petal_width	target
0	5.1	3.5	1.4	0.2	0
1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0



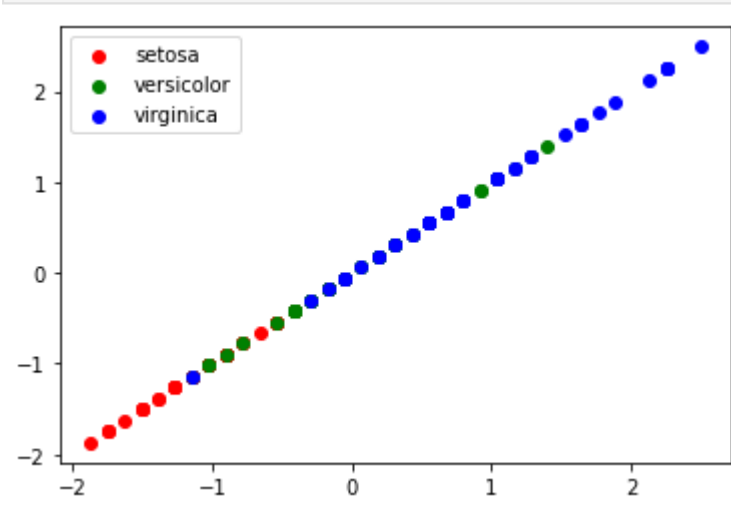
Standardize the Data

```
In [10]: x_temp = df.iloc[:, 0:4].values
y_temp = df.target.values

x_temp = StandardScaler().fit_transform(x_temp)
```

2D representation of the data

```
In [11]: colors = cycle('rgb')
target_ids = range(len(iris.target_names))
pl.figure()
for i, c, label in zip(target_ids, colors, iris.target_names):
    pl.scatter(x_temp[iris.target == i, 0], x_temp[iris.target == i, 1],
              c=c, label=label)
pl.legend()
pl.show()
```



The three different types of Iris are still clustered pretty well.

Compute the Eigenvectors and Eigenvalues

```
In [12]: covariance_matrix = np.cov(x_temp.T)
print("Covariance matrix:\n", covariance_matrix)

Covariance matrix:
[[ 1.00671141 -0.11835884  0.87760447  0.82343066]
 [-0.11835884  1.00671141 -0.43131554 -0.36858315]
 [ 0.87760447 -0.43131554  1.00671141  0.96932762]
 [ 0.82343066 -0.36858315  0.96932762  1.00671141]]

In [13]: eigen_values, eigen_vectors = np.linalg.eig(covariance_matrix)
print("Eigenvectors:\n", eigen_vectors, "\n")
print("Eigenvalues:\n", eigen_values)

Eigenvectors:
[[ 0.52106591 -0.37741762 -0.71956635  0.26128628]
 [-0.26934744 -0.92329566  0.24438178 -0.12350962]
 [ 0.5804131  -0.02449161  0.14212637 -0.80144925]
 [ 0.56485654 -0.06694199  0.63427274  0.52359713]]

Eigenvalues:
[2.93808505 0.9201649  0.14774182 0.02085386]
```

PCA for transformation into 2D data and visualization

```
In [14]: #Apply PCA to transform iris dataset into 2D for visuallization
pca2 = PCA(n_components=2)
principalComponents2 = pca2.fit_transform(X)
principalDf2 = pd.DataFrame(data = principalComponents2, columns = ['principal component 1', 'principal component 2'])
finalDf2 = pd.concat([principalDf2, df[['target']]], axis = 1)
finalDf2.head(5)

Out[14]:
```

	principal component 1	principal component 2	target
0	-2.684126	0.319397	0
1	-2.714142	-0.177001	0
2	-2.888991	-0.144949	0
3	-2.745343	-0.318299	0
4	-2.728717	0.326755	0

```
In [15]: #check the statistical values of the model transformed from 4D to 2D
print(f"components_ in the data transformed to 2D : \n{pca2.components_}\n")
print(f"explained_variance_ in the data transformed to 2D : \n{pca2.explained_variance_}\n")
print(f"score in the data transformed to 2D : \n{pca2.score(X)}")

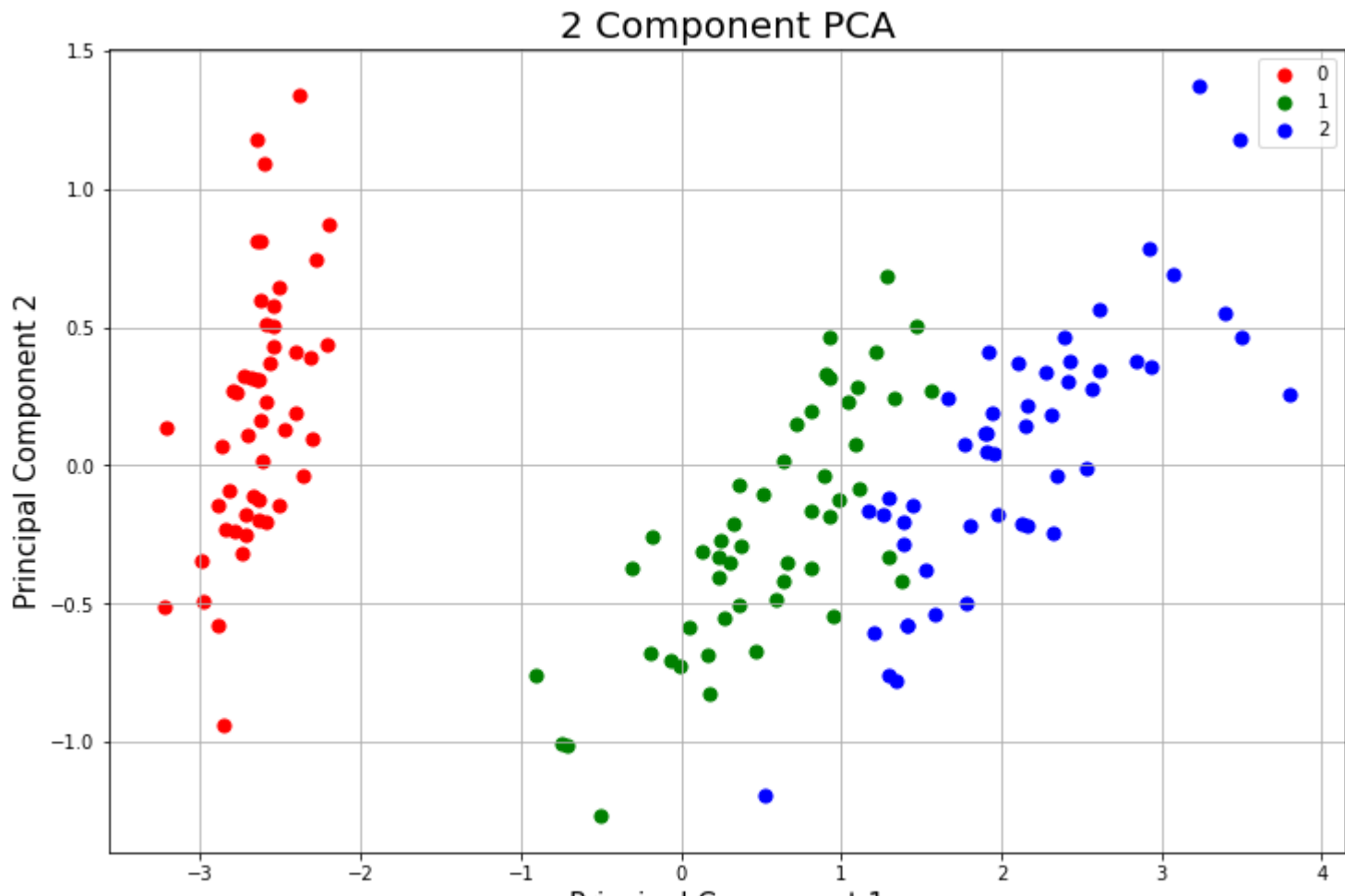
components_ in the data transformed to 2D :
[[ 0.36138659 -0.08452251  0.85667061  0.3582892 ]
 [ 0.65658877  0.73016143 -0.17337266 -0.07548102]]

explained_variance_ in the data transformed to 2D :
[4.22824171 0.24267075]

score in the data transformed to 2D :
-2.699796510675664
```

```
In [16]: #Visualize the data into 2D
fig = plt.figure(figsize = (12,8))
ax = fig.add_subplot(1,1,1)
ax.set_xlabel('Principal Component 1', fontsize = 15)
ax.set_ylabel('Principal Component 2', fontsize = 15)
ax.set_title('2 Component PCA', fontsize = 20)

#targets = ['Iris-setosa', 'Iris-versicolor', 'Iris-virginica']
targets = [0,1,2]
colors = ['r', 'g', 'b']
for target, color in zip(targets,colors):
    indicesToKeep = finalDf2['target'] == target
    ax.scatter(finalDf2.loc[indicesToKeep, 'principal component 1'],
              finalDf2.loc[indicesToKeep, 'principal component 2'],
              c = color
              , s = 50)
ax.legend(targets)
ax.grid()
```



```
In [17]: #Apply PCA to transform iris dataset into 2D for visuallization
pca2 = PCA(n_components=3)
principalComponents2 = pca2.fit_transform(X)
principalDf2 = pd.DataFrame(data = principalComponents2, columns = ['principal component 1', 'principal component 2', 'principal component 3'])
finalDf2 = pd.concat([principalDf2, df[['target']]], axis = 1)
finalDf2.head(5)

Out[17]:
```

	principal component 1	principal component 2	principal component 2	target
0	-2.684126	0.319397	-0.027915	0
1	-2.714142	-0.177001	-0.210464	0
2	-2.888991	-0.144949	0.017900	0
3	-2.745343	-0.318299	0.031559	0
4	-2.728717	0.326755	0.090079	0

```
In [18]: #check the statistical values of the model transformed from 4D to 2D
print(f"components_ in the data transformed to 2D : \n{pca2.components_}\n")
print(f"explained_variance_ in the data transformed to 2D : \n{pca2.explained_variance_}\n")
print(f"score in the data transformed to 2D : \n{pca2.score(X)}")

components_ in the data transformed to 2D :
[[ 0.36138659 -0.08452251  0.85667061  0.3582892 ]
 [ 0.65658877  0.73016143 -0.17337266 -0.07548102]
 [-0.58202985  0.59791083  0.07623608  0.54583143]]

explained_variance_ in the data transformed to 2D :
[4.22824171 0.24267075 0.0782095 ]

score in the data transformed to 2D :
-2.5328088437833913
```

```
In [19]: fig = px.scatter_3d(
    principalComponents2, x=0, y=1, z=2, color=df['target'],
    labels={'0': 'PC 1', '1': 'PC 2', '2': 'PC 3'})
fig.show()
```



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