```
import numpy as np
import pandas as pd
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
sns.set(style="white", color_codes=True)
import warnings
warnings.filterwarnings("ignore")
%matplotlib inline
```

```
data = pd.read_csv('/content/Iris.csv')
data = data.drop('Id', axis=1)
data.head()
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa

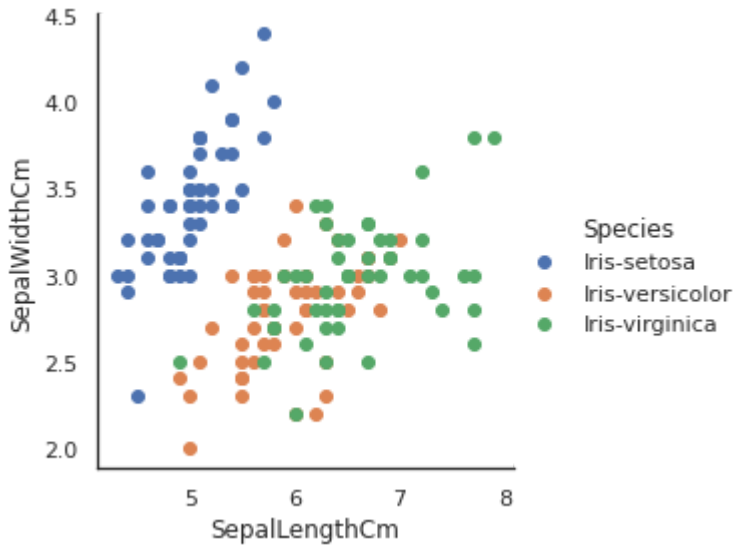
```
X = data.iloc[:,0:4]
y = data.iloc[:,-1]
print(X.sample(5))
print(y.sample(5))
```

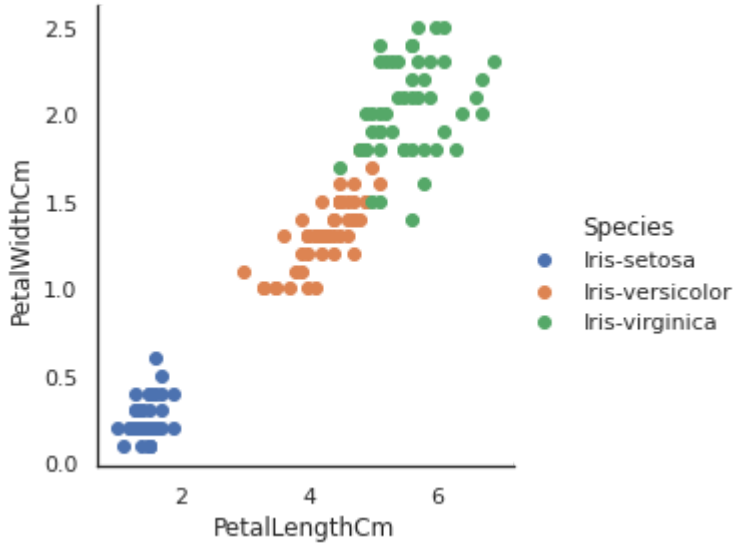
```
     SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm
29             4.7           3.2            1.6           0.2
140            6.7           3.1            5.6           2.4
116            6.5           3.0            5.5           1.8
118            7.7           2.6            6.9           2.3
109            7.2           3.6            6.1           2.5
108     Iris-virginica
61     Iris-versicolor
46         Iris-setosa
3          Iris-setosa
100     Iris-virginica
Name: Species, dtype: object
```

```
data["Species"].value_counts()
```

```
Iris-setosa        50
Iris-versicolor    50
Iris-virginica     50
Name: Species, dtype: int64
```

```
# use seaborn to make scatter plot showing species for each sample
sns.FacetGrid(data, hue="Species", size=4) \
   .map(plt.scatter, "SepalLengthCm", "SepalWidthCm") \
   .add_legend();
sns.FacetGrid(data, hue="Species", size=4) \
   .map(plt.scatter, "PetalLengthCm", "PetalWidthCm") \
   .add_legend();
```






```
from sklearn import preprocessing

scaler = preprocessing.StandardScaler()

scaler.fit(X)
X_scaled_array = scaler.transform(X)
X_scaled = pd.DataFrame(X_scaled_array, columns = X.columns)

X_scaled.sample(5)
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
15	-0.173674	3.114684	-1.284407	-1.050031
65	1.038005	0.106445	0.364699	0.264699
41	-1.627688	-1.744778	-1.398138	-1.181504
64	-0.294842	-0.356361	-0.090227	0.133226
39	-0.900681	0.800654	-1.284407	-1.312977

K-means clustering

```
from sklearn.cluster import KMeans

nclusters = 3
seed = 0

km = KMeans(n_clusters=nclusters, random_state=seed)
km.fit(X_scaled)

y_cluster_kmeans = km.predict(X_scaled)
y_cluster_kmeans
```

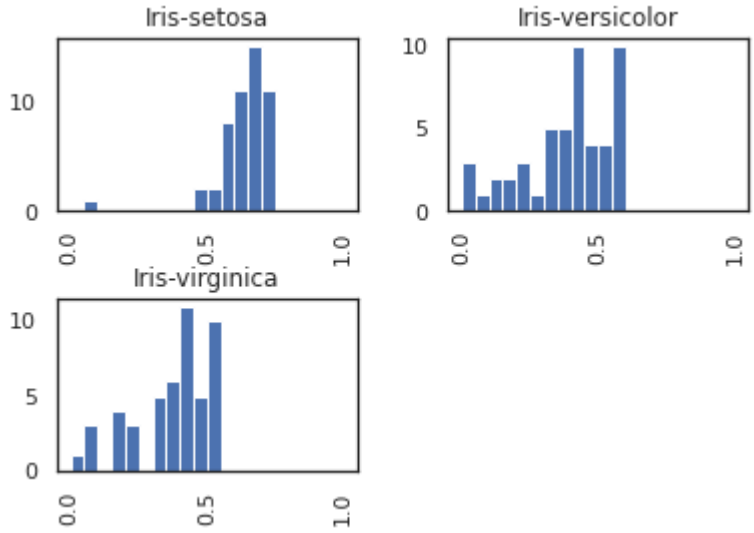
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 2, 2, 2, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 2,
       0, 0, 0, 0, 2, 0, 0, 0, 0, 2, 2, 2, 0, 0, 0, 0, 0, 0, 0, 2, 2, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 2, 2, 2, 2, 0, 2, 2, 2,
       2, 2, 2, 0, 0, 2, 2, 2, 2, 0, 2, 0, 2, 0, 2, 2, 0, 2, 2, 2, 2, 2,
       2, 0, 0, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 0], dtype=int32)
```

```
from sklearn import metrics
score = metrics.silhouette_score(X_scaled, y_cluster_kmeans)
score
```

```
0.4589717867018717
```

```
scores = metrics.silhouette_samples(X_scaled, y_cluster_kmeans)
sns.distplot(scores);
```


```
df_scores = pd.DataFrame()
df_scores['SilhouetteScore'] = scores
df_scores['Species'] = data['Species']
df_scores.hist(by='Species', column='SilhouetteScore', range=(0,1.0), bins=20);
```



PCA

```
from sklearn.decomposition import PCA

ndimensions = 2

pca = PCA(n_components=ndimensions, random_state=seed)
pca.fit(X_scaled)
X_pca_array = pca.transform(X_scaled)
X_pca = pd.DataFrame(X_pca_array, columns=['PC1','PC2']) # PC=principal component
X_pca.sample(5)
```

	PC1	PC2
26	-2.052063	0.266014
130	2.435497	0.246654
60	-0.124697	-2.658063
114	1.464062	-0.444148
14	-2.192292	1.889979

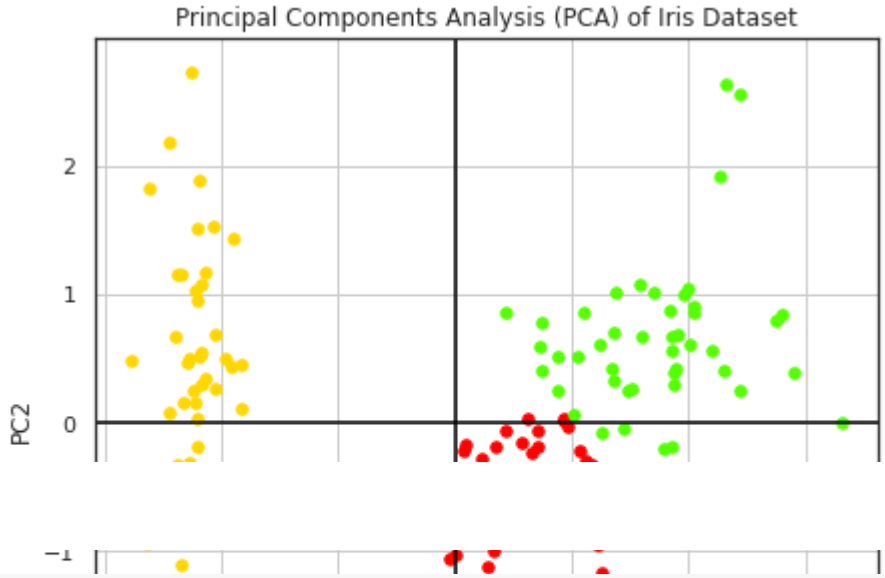
```
y_id_array = pd.Categorical(data['Species']).codes
#Categorical.from_array(data['Species']).codes

df_plot = X_pca.copy()
df_plot['ClusterKmeans'] = y_cluster_kmeans
df_plot['SpeciesId'] = y_id_array # also add actual labels so we can use it in later plots
df_plot.head(5)
```

	PC1	PC2	ClusterKmeans	SpeciesId
0	-2.264542	0.505704	1	0
1	-2.086426	-0.655405	1	0
2	-2.367950	-0.318477	1	0
3	-2.304197	-0.575368	1	0
4	-2.388777	0.674767	1	0

```
def plotData(df, groupby):
    "make a scatterplot of the first two principal components of the data, colored by the gro
    fig, ax = plt.subplots(figsize = (7,7))
    cmap = mpl.cm.get_cmap('prism')
    for i, cluster in df.groupby(groupby):
        cluster.plot(ax = ax,
                     kind = 'scatter',
                     x = 'PC1', y = 'PC2',
                     color = cmap(i/(nclusters-1)),
                     label = "%s %i" % (groupby, i),
                     s=30)
    ax.grid()
    ax.axhline(0, color='black')
    ax.axvline(0, color='black')
    ax.set_title("Principal Components Analysis (PCA) of Iris Dataset");
```

```
# plot the clusters each datapoint was assigned to
plotData(df_plot, 'ClusterKmeans')
```



GMM

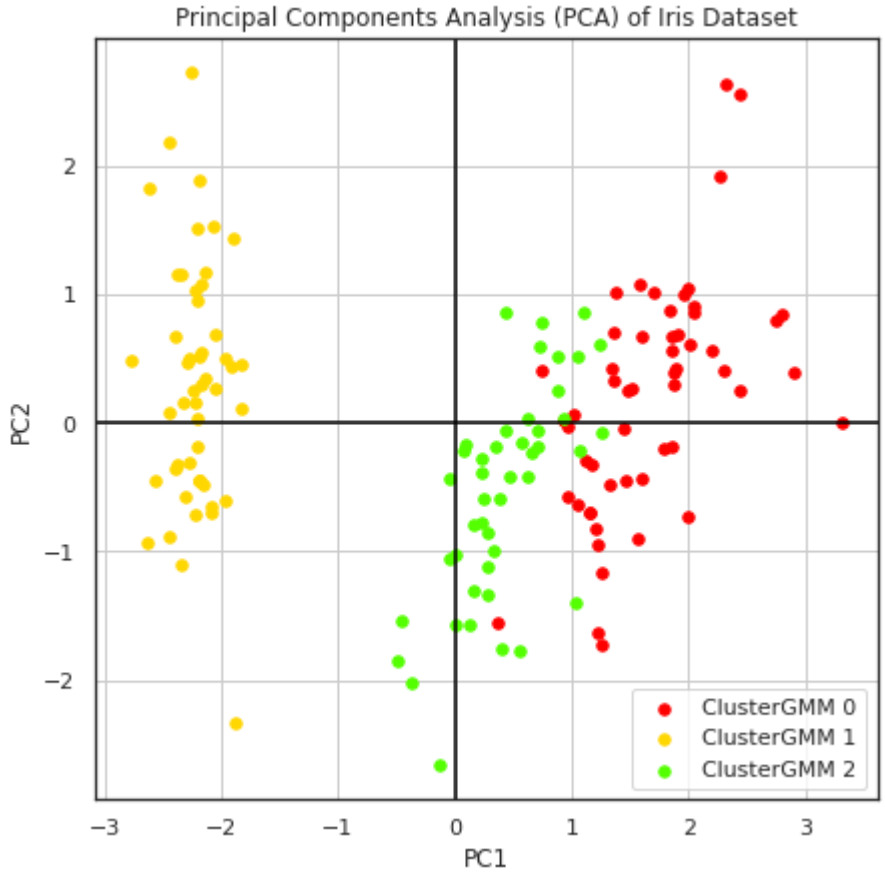
```
from sklearn.mixture import GaussianMixture

gmm = GaussianMixture(n_components=nclusters)
gmm.fit(X_scaled)

# predict the cluster for each data point
y_cluster_gmm = gmm.predict(X_scaled)
y_cluster_gmm
```

```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 0, 2, 0, 2, 0, 2, 2, 2, 2, 0, 2, 2, 2, 2, 2, 0, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0])
```

```
# add the GMM clusters to our data table and plot them
df_plot['ClusterGMM'] = y_cluster_gmm
plotData(df_plot, 'ClusterGMM')
```


Principal Components Analysis (PCA) of Iris Dataset
PC2
PC1
ClusterGMM 0
ClusterGMM 1
ClusterGMM 2
2
1
0
−1
−2
−3
−2
−1
0
1
2
3