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Data Science & Business Analytics Internship

GRIP - The Spark Foundation

Task 2 : From the given ‘Iris’ dataset, predict the optimum number of clusters and represent it visually.

Machine learning can be of four types- Supervised, Unsupervised, Semi-supervised and Reinforcement learning. Unlike Supervised learning, Unsupervised learning has features measured for n observations but has no response, i.e., we have unlabeled training data. In this situation we cannot predict a response (as there is no response variable) and therefore we are left with the task of finding interesting patterns in the data. Some of the important unsupervised learning algorithms are - Clustering, Principal Component Analysis(PCA) and Association Rule learning. In this kernel we will explore Clustering and PCA

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

```
data=pd.read_csv('IRIS.csv')
```

```
data.head()
```

	sepal_length	sepal_width	petal_length	petal_width	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

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null    float64
 3   petal_width   150 non-null    float64
 4   species       150 non-null    object 
```

```
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

```
data.describe()
```

	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

```
data.duplicated().sum()
```

```
3
```

```
data.drop_duplicates(inplace=True)
```

```
data.duplicated().sum()
```

```
0
```

```
print('Data has {} number of rows and {} columns'.format(data.shape[0],data.shape[1]))
```

```
Data has 147 number of rows and 5 columns
```

```
print('The columns set in our dataset :',data.columns)
```

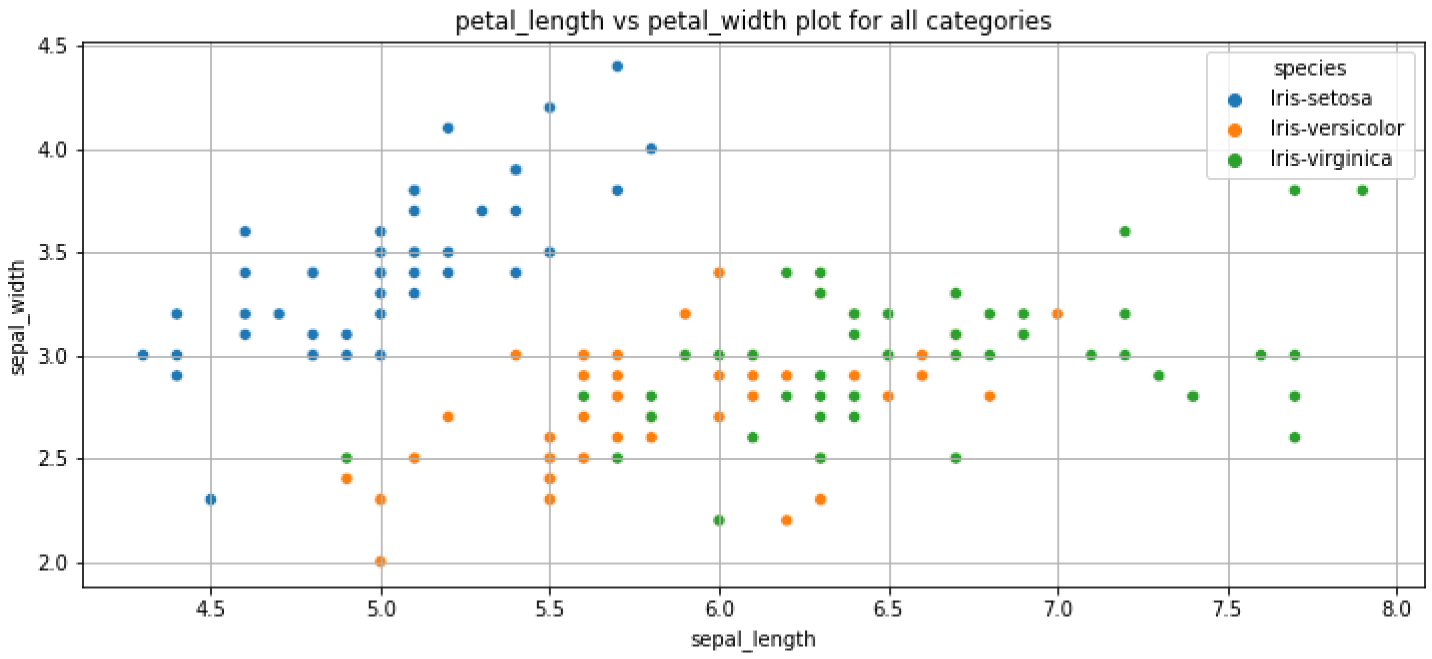
```
The columns set in our dataset : Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_w
       'species'],
      dtype='object')
```

```
#Frequency distribution of species
iris_tab=pd.crosstab(index=data['species'],columns='count')
iris_tab
```

col_0	count
species	
Iris-setosa	48
Iris-versicolor	50
Iris-virginica	49

Step 3 : Data Visualization

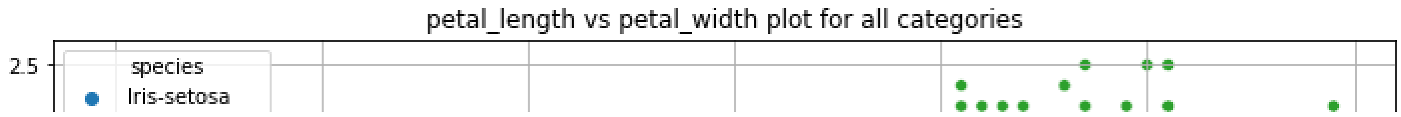
```
#numeric v/s numeric v/s categorical
plt.figure(figsize=(12,5))
sns.scatterplot(x='sepal_length',y='sepal_width',data=data,hue='species')
plt.title('sepal_length vs sepal_width plot for all categories')
plt.grid()
plt.show()
```



Observations:

- Here the plot indicates that Iris-Setosa forms a cluster that can be seperated from other categories based on sepal_length and sepal_width. While other 2 are mixed and cannot be seperated directly

```
#numeric v/s numeric v/s categorical
plt.figure(figsize=(12,5))
sns.scatterplot(x='petal_length',y='petal_width',data=data,hue='species')
plt.title('petal_length vs petal_width plot for all categories')
plt.grid()
plt.show()
```

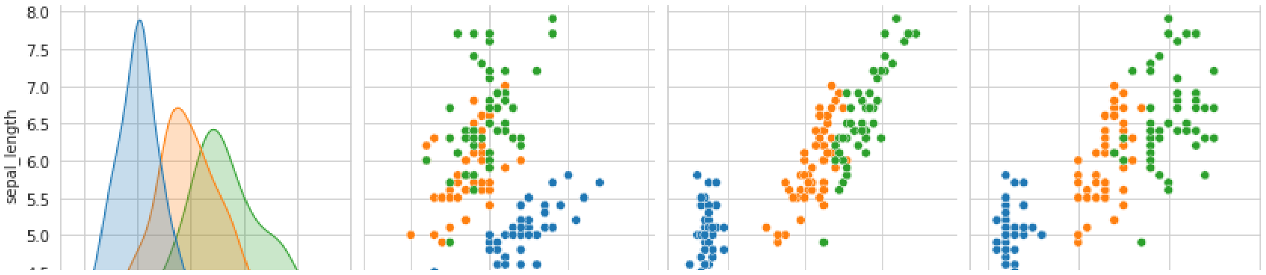


Observations:

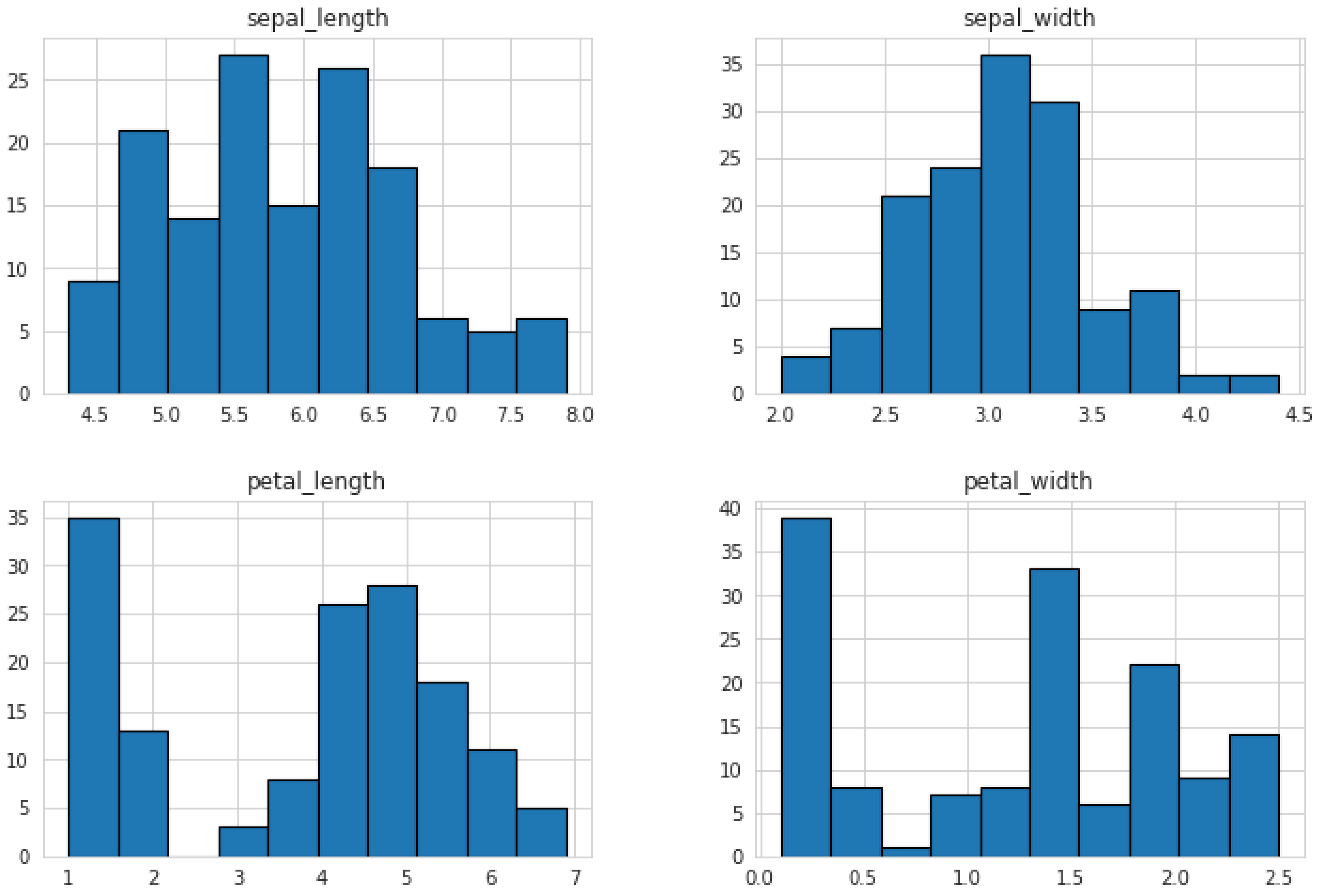
- Here also the plot indicates that Iris-Setosa forms a seperate cluster that can be extracted from other categories based on petal_length and petal_width. While other 2 can also be seperated .
- We can say that if the petal_length<2 and petal_width <0.95 the class is Setosa
- And if the petal_length is between (2.9 and 5) and petal_width is between (1 and 1.75) the class is Versicolor
- And if the petal_length is between (4.75 and 7) and petal_width is between (1.6 and 2.5) the class is Virginica

```
sns.set_style("whitegrid")
sns.pairplot(data,hue='species',size=3)
```

```
<seaborn.axisgrid.PairGrid at 0x7f077bfe4b70>
```



```
data.hist(edgecolor='black',linewidth=1.1,figsize=(12,8))
plt.show()
```

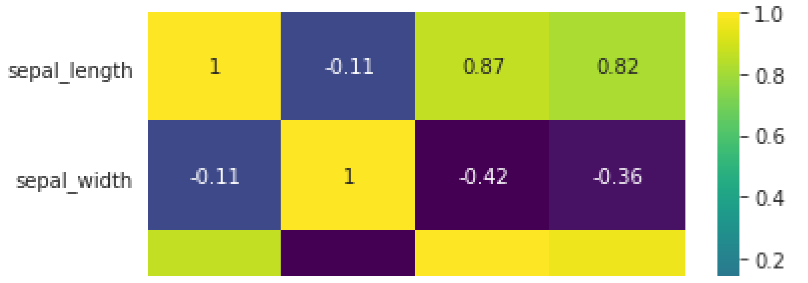


```
data.corr()
```

	sepal_length	sepal_width	petal_length	petal_width
sepal_length	1.000000	-0.109321	0.871305	0.817058
sepal_width	-0.109321	1.000000	-0.421057	-0.356376
petal_length	0.871305	-0.421057	1.000000	0.961883
petal_width	0.817058	-0.356376	0.961883	1.000000

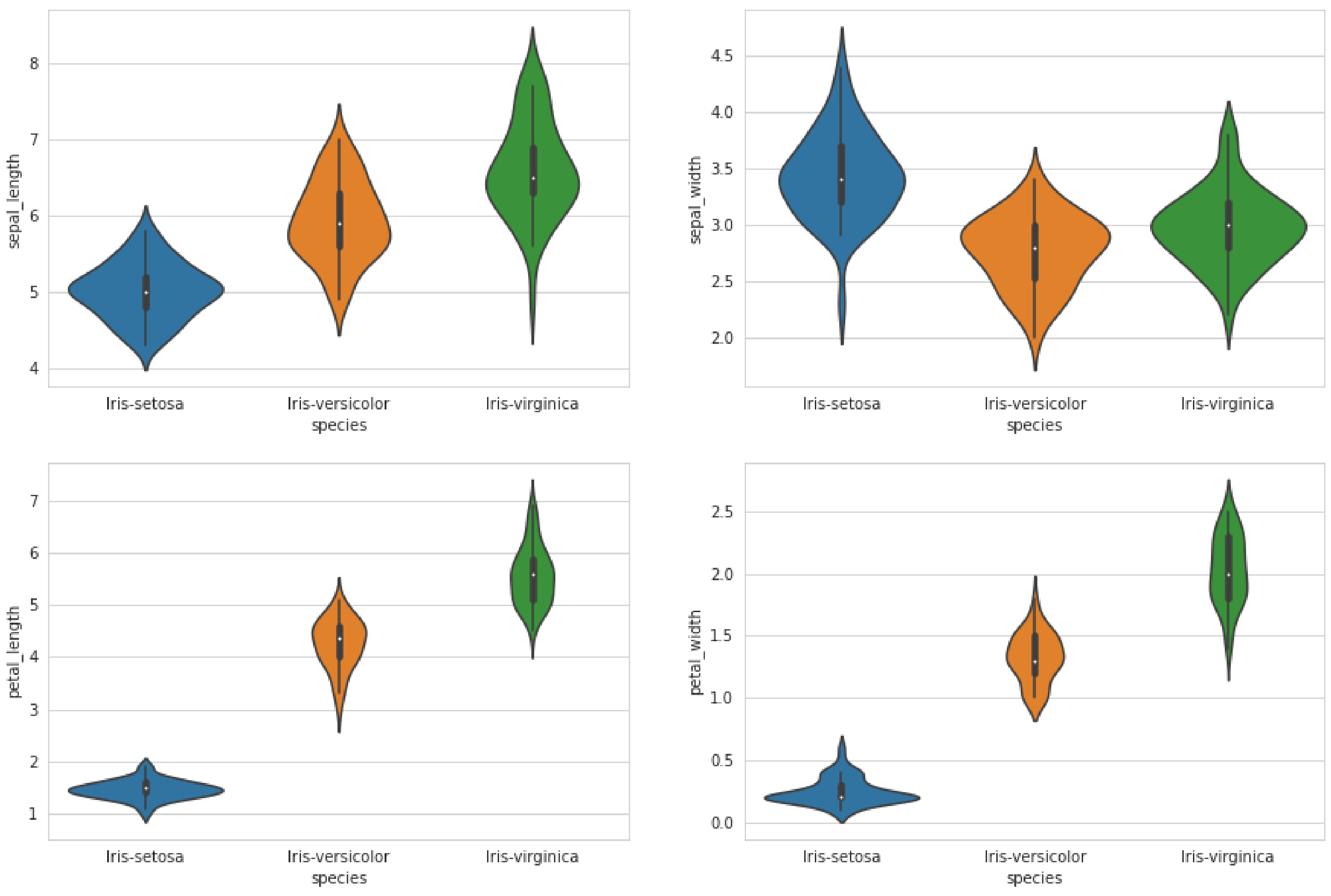
```
sns.heatmap(data.corr(),annot=True,fmt='.2g',cmap='viridis')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f07775d8898>
```



- petal_length is higly correlated with sepal_length and petal_width and vice-versa.
- sepal_width is not correlated with any feature it can be useful in seperating features

```
plt.figure(figsize=(15,10))
plt.subplot(2,2,1)
sns.violinplot(x='species',y='sepal_length',data=data)
plt.subplot(2,2,2)
sns.violinplot(x='species',y='sepal_width',data=data)
plt.subplot(2,2,3)
sns.violinplot(x='species',y='petal_length',data=data)
plt.subplot(2,2,4)
sns.violinplot(x='species',y='petal_width',data=data)
plt.show()
```



- The violinplot shows density of the length and width in the species. The thinner part denotes that

K-Means Clustering

- K-Mean is a centroid-based algorithm, or a distance-based algorithm, where we calculate the distances to assign a point to a cluster. In K-Means, each cluster is associated with a centroid.

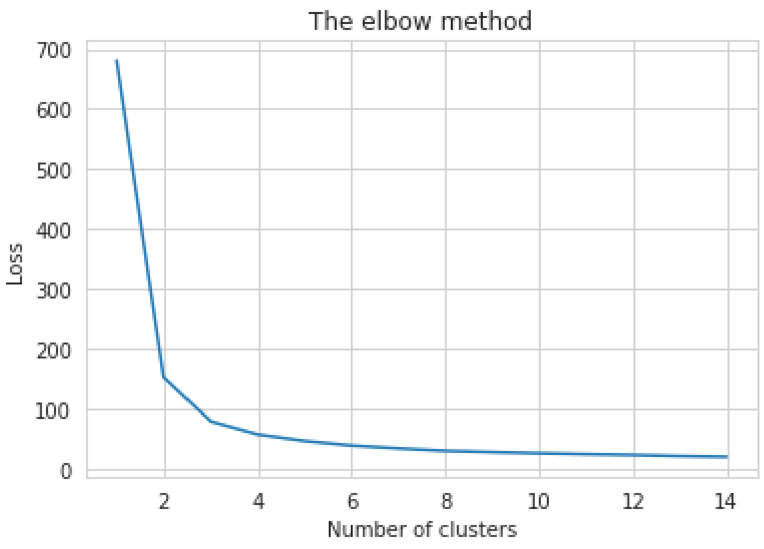
How to Implementing K-Means Clustering ?

- Choose the number of clusters k
- Select k random points from the data as centroids
- Assign all the points to the closest cluster centroid
- Recompute the centroids of newly formed clusters
- Repeat steps 3 and 4

[ ] ↳ *2 cells hidden*

Using the elbow method to determine the optimal number of clusters for k-means clustering

```
plt.plot(range(1,15),loss)
plt.title('The elbow method')
plt.xlabel('Number of clusters')
plt.ylabel('Loss')
plt.show()
```



The bend in the curve is at 3.

```
kmeans=KMeans(n_clusters=3,random_state=95,n_jobs=-1)
kmeans.fit(x)
y_kmeans = kmeans.fit_predict(x)
```

```
y_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, 1, 1, 1, 1, 0, 0, 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, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 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, 0, 2, 2, 2, 2,
            2, 0, 2, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 0], dtype=int32)
```

```
kmeans.cluster_centers_
```

```
     array([[5.9016129 , 2.7483871 , 4.39354839, 1.43387097],
            [5.006     , 3.418     , 1.464     , 0.244     ],
            [6.85      , 3.07368421, 5.74210526, 2.07105263]])
```

```
#Visualising the clusters
plt.figure(figsize=(15,10))
plt.scatter(x[y_kmeans == 0, 0], x[y_kmeans == 0, 1], s = 100, c = 'purple', label = 'Iris-setosa')
plt.scatter(x[y_kmeans==1,0],x[y_kmeans==1,1],s=100,c='orange',label='Iris-versicolour')
plt.scatter(x[y_kmeans==2,0],x[y_kmeans==2,1],s=100,c='green',label='Iris-virginica')

#Plotting the centroids of the clusters
plt.scatter(kmeans.cluster_centers_[:,0],kmeans.cluster_centers_[:,1],s=100,c='red',label='Centroids
plt.legend()
plt.show()
```

```
---------------------------------------------------------------------------
TypeError                                 Traceback (most recent call last)
<ipython-input-97-2e192c0872cd> in <module>()
      1 #Visualising the clusters
      2 plt.figure(figsize=(15,10))
----> 3 plt.scatter(x[y_kmeans == 0, 0], x[y_kmeans == 0, 1], s = 100, c = 'purple', label =
```

Prediction

```
data['predicted']=y_kmeans
```

```
    /usr/local/lib/python3.6/dist-packages/pandas/core/indexes/base.py in get_loc(self, key,
```

```
data
```

	sepal_length	sepal_width	petal_length	petal_width	species	predicted
0	5.1	3.5	1.4	0.2	Iris-setosa	1
1	4.9	3.0	1.4	0.2	Iris-setosa	1
2	4.7	3.2	1.3	0.2	Iris-setosa	1
3	4.6	3.1	1.5	0.2	Iris-setosa	1
4	5.0	3.6	1.4	0.2	Iris-setosa	1
...	...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	Iris-virginica	2
146	6.3	2.5	5.0	1.9	Iris-virginica	0
147	6.5	3.0	5.2	2.0	Iris-virginica	2
148	6.2	3.4	5.4	2.3	Iris-virginica	2
149	5.9	3.0	5.1	1.8	Iris-virginica	0

150 rows × 6 columns

```
       False, False, False,  True, False, False, False,  True, False,
```

```
centroids=kmeans.cluster_centers_
centroids
```

```
array([[5.9016129 , 2.7483871 , 4.39354839, 1.43387097],
       [5.006     , 3.418     , 1.464     , 0.244     ],
       [6.85      , 3.07368421, 5.74210526, 2.07105263]])
```

```
df=data.copy()
df["species"]=df["species"].map({'Iris-versicolor':0,'Iris-setosa':1,'Iris-virginica':2}).astype(int
df['predicted']=y_kmeans
df
```

	sepal_length	sepal_width	petal_length	petal_width	species	predicted
0	5.1	3.5	1.4	0.2	1	1
1	4.9	3.0	1.4	0.2	1	1
2	4.7	3.2	1.3	0.2	1	1
3	4.6	3.1	1.5	0.2	1	1
4	5.0	3.6	1.4	0.2	1	1
...	...	...	...	...	...	...

```
from sklearn.metrics import confusion_matrix
confusion_matrix(df['species'],y_kmeans)
```

```
     array([[48,  0,  2],
            [ 0, 50,  0],
            [14,  0, 36]])
```

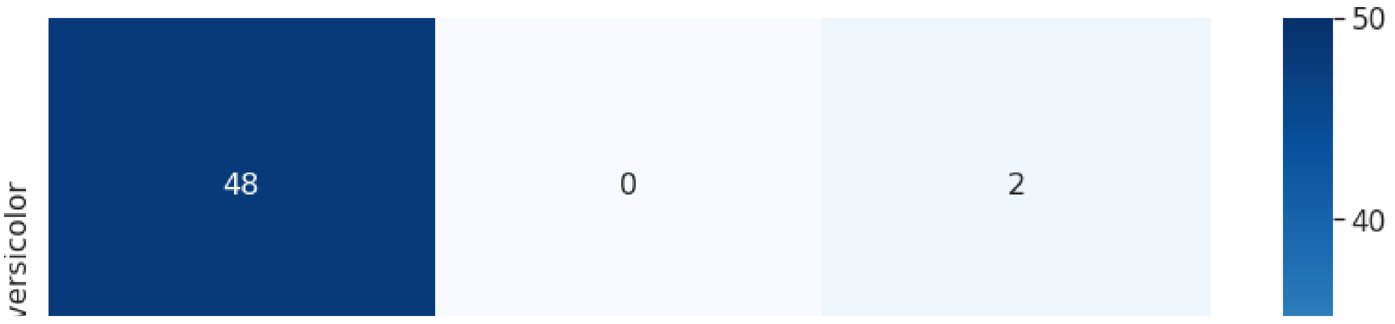
149	5.9	3.0	5.1	1.8	2	0

```
import scikitplot as skplt
true_labels = ["Iris-versicolor", "Iris-setosa", "Iris-virginica"]
pred_labels = ["Iris-versicolor", "Iris-setosa", "Iris-virginica"]

y_true=df['species']

data = confusion_matrix(y_true,y_kmeans)
df_cm = pd.DataFrame(data, columns=np.unique(y_true), index = np.unique(y_true))
df_cm.index.name = 'Actual'
df_cm.columns.name = 'Predicted'
plt.figure(figsize = (14,10))
sns.set(font_scale=1.4)

sns.heatmap(df_cm, cmap="Blues",xticklabels=true_labels,yticklabels=true_labels, annot=True,annot_kw
<matplotlib.axes._subplots.AxesSubplot at 0x7f077763c828>
```



From the confusion matrix we can see that out of all 50 data of class Iris-versicolor 48 are correctly predicted whereas 2 are wrongly predicted as Iris-virginica. For 50 data of Iris-setosa all are correctly predicted. And for 50 data of Iris-virginica 36 are correctly predicted whereas 14 are wrongly predicted as Iris-versicolor.

```
data["predicted"]=data["predicted"].map({0:'Iris-versicolor',1:'Iris-setosa',2:'Iris-virginica'})
data.head()
```

	sepal_length	sepal_width	petal_length	petal_width	species	predicted
0	5.1	3.5	1.4	0.2	Iris-setosa	NaN
1	4.9	3.0	1.4	0.2	Iris-setosa	NaN
2	4.7	3.2	1.3	0.2	Iris-setosa	NaN
3	4.6	3.1	1.5	0.2	Iris-setosa	NaN
4	5.0	3.6	1.4	0.2	Iris-setosa	NaN

Predicted

```
data.tail()
```

	sepal_length	sepal_width	petal_length	petal_width	species	predicted
145	6.7	3.0	5.2	2.3	Iris-virginica	Iris-virginica
146	6.3	2.5	5.0	1.9	Iris-virginica	Iris-versicolor
147	6.5	3.0	5.2	2.0	Iris-virginica	Iris-virginica
148	6.2	3.4	5.4	2.3	Iris-virginica	Iris-virginica
149	5.9	3.0	5.1	1.8	Iris-virginica	Iris-versicolor

```
#
```

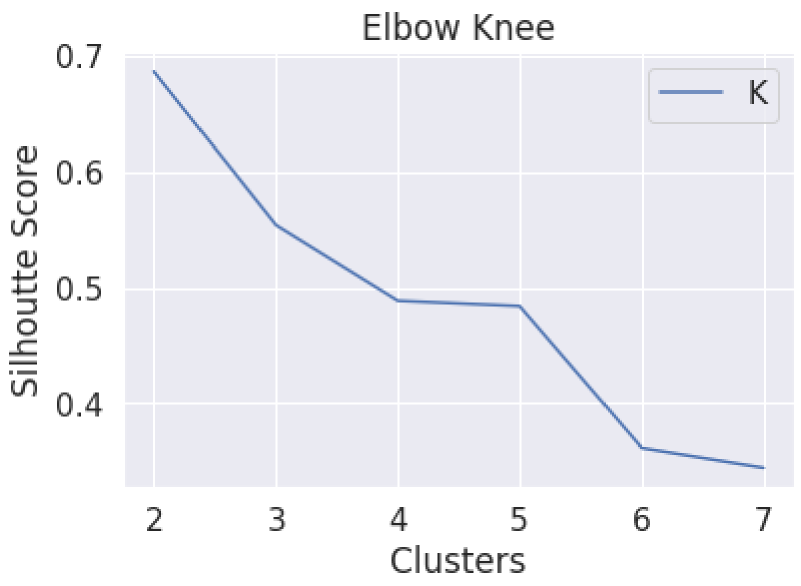
Double-click (or enter) to edit

```
%%time
from sklearn.cluster import AgglomerativeClustering
from sklearn.metrics import silhouette_score
scores = []
for i in range(2,8):
   print(f'Starting Cluster #{i}')
   aggl_cluster=AgglomerativeClustering(n_clusters=i)
   aggl_cluster.fit(x)
   scores.append(silhouette_score(x,aggl_cluster.labels_,random_state=25))
```

```
Starting Cluster #2
Starting Cluster #3
Starting Cluster #4
Starting Cluster #5
Starting Cluster #6
Starting Cluster #7
CPU times: user 40.6 ms, sys: 27.1 ms, total: 67.7 ms
Wall time: 48.2 ms
```

```
# plot k vs Silhoutte Score

plt.plot(range(2,8), scores)
plt.xlabel('Clusters')
plt.ylabel('Silhoutte Score')
plt.title('Elbow Knee')
plt.legend('Knee')
plt.show()
```



```
aggl_cluster = AgglomerativeClustering(n_clusters=3)
aggl_cluster.fit(x)
```

```
AgglomerativeClustering(affinity='euclidean', compute_full_tree='auto',
                        connectivity=None, distance_threshold=None,
                        linkage='ward', memory=None, n_clusters=3)
```

```
aggl_cluster.labels_
```

```
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, 1, 1, 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, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 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, 0, 2, 2, 2, 2,
       2, 0, 0, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 2, 0, 2, 2, 0])
```

```
# Collect data points from each cluster
clusters_set = {i: np.where(aggl_cluster.labels_ == i)[0] for i in range(aggl_cluster.n_clusters)}
```

```
clusters_set
```

```
{0: array([ 50,  51,  52,  53,  54,  55,  56,  57,  58,  59,  60,  61,  62,
         63,  64,  65,  66,  67,  68,  69,  70,  71,  72,  73,  74,  75,
         76,  78,  79,  80,  81,  82,  83,  84,  85,  86,  87,  88,  89,
         90,  91,  92,  93,  94,  95,  96,  97,  98,  99, 101, 106, 113,
        114, 119, 121, 123, 126, 127, 133, 134, 138, 142, 146, 149]),
 1: array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12, 13, 14, 15, 16,
        17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,
        34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49]),
 2: array([ 77, 100, 102, 103, 104, 105, 107, 108, 109, 110, 111, 112, 115,
        116, 117, 118, 120, 122, 124, 125, 128, 129, 130, 131, 132, 135,
        136, 137, 139, 140, 141, 143, 144, 145, 147, 148])}
```

```
agg_pred=aggl_cluster.fit_predict(x)
```

```
df1=data.copy()
df1["species"]=df1["species"].map({'Iris-versicolor':0,'Iris-setosa':1,'Iris-virginica':2}).astype(i
df1['predicted']=agg_pred
df1
```

	sepal_length	sepal_width	petal_length	petal_width	species	predicted
0	5.1	3.5	1.4	0.2	1	1
1	4.9	3.0	1.4	0.2	1	1
2	4.7	3.2	1.3	0.2	1	1
3	4.6	3.1	1.5	0.2	1	1
4	5.0	3.6	1.4	0.2	1	1
...	...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	2	2
146	6.3	2.5	5.0	1.9	2	0
147	6.5	3.0	5.2	2.0	2	2
148	6.2	3.4	5.4	2.3	2	2
149	5.9	3.0	5.1	1.8	2	0

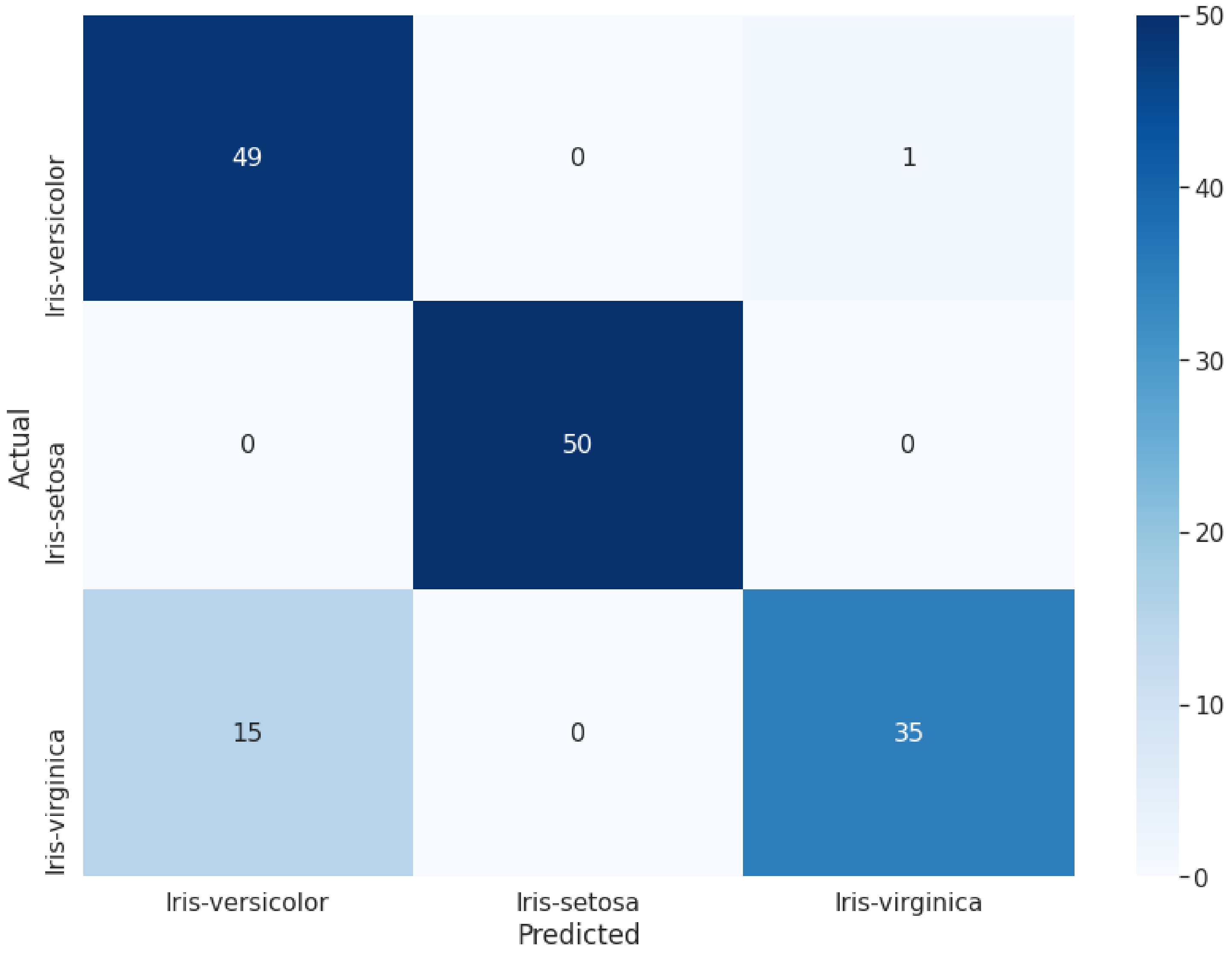
150 rows × 6 columns

```
import scikitplot as skplt
true_labels = ["Iris-versicolor", "Iris-setosa", "Iris-virginica"]
pred_labels = ["Iris-versicolor", "Iris-setosa", "Iris-virginica"]

y_true=df1['species']

data = confusion_matrix(y_true,agg_pred)
df_cm = pd.DataFrame(data, columns=np.unique(y_true), index = np.unique(y_true))
df_cm.index.name = 'Actual'
df_cm.columns.name = 'Predicted'
plt.figure(figsize = (14,10))
sns.set(font_scale=1.4)

sns.heatmap(df_cm, cmap="Blues",xticklabels=true_labels,yticklabels=true_labels, annot=True,annot_kw
<matplotlib.axes._subplots.AxesSubplot at 0x7f076f501668>
```



From the confusion matrix we can see that out of all 50 data of class Iris-versicolor 49 are correctly predicted whereas 2 are wrongly predicted as Iris-virginica. For 50 data of Iris-setosa all are wcorrectly predicted. And for 50 data of Iris-virginica 35 are correctly predicted whereas 15 are wrongly predicted as Iris-versicolor.