

task-3 codsoft(DS)

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

```
df=pd.read_csv('/content/drive/MyDrive/codsodt1/IRIS.csv')
df.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

Next steps: [Generate code with df](#) [View recommended plots](#) [New interactive sheet](#)

```
df['species'],categories=pd.factorize(df['species'])
df.head()
```

	sepal_length	sepal_width	petal_length	petal_width	species
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

Next steps: [Generate code with df](#) [View recommended plots](#) [New interactive sheet](#)

```
df.describe
```

```
pandas.core.generic.NDFrame.describe
def describe(percentiles=None, include=None, exclude=None) -> NDFrameT

/usr/local/lib/python3.10/dist-packages/pandas/core/generic.py
Generate descriptive statistics.

Descriptive statistics include those that summarize the central
tendency, dispersion and shape of a
```

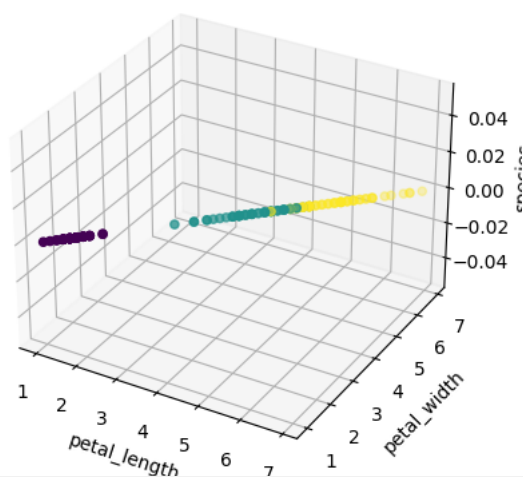
```
df.isna().sum()
```

```
sepal_length    0
sepal_width     0
petal_length    0
petal_width     0
species         0
dtype: int64
```

```
from mpl_toolkits.mplot3d import Axes3D
fig=plt.figure()
ax=fig.add_subplot(111,projection='3d')
ax.scatter(df.petal_length , df.petal_length, c=df.species)
ax.set_xlabel('petal_length')
ax.set_ylabel('petal_width')
ax.set_zlabel('species')
plt.title('3D Scatter Plot example')
plt.show()
```



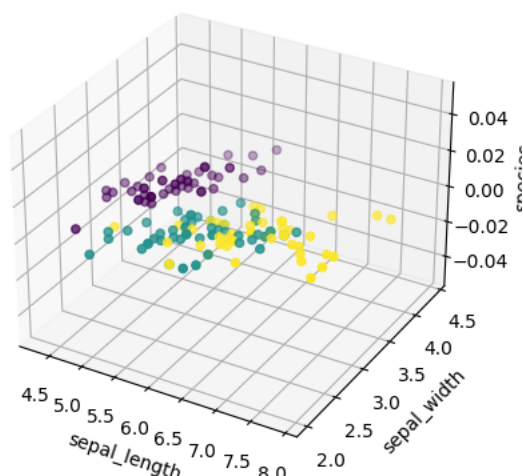
3D Scatter Plot example



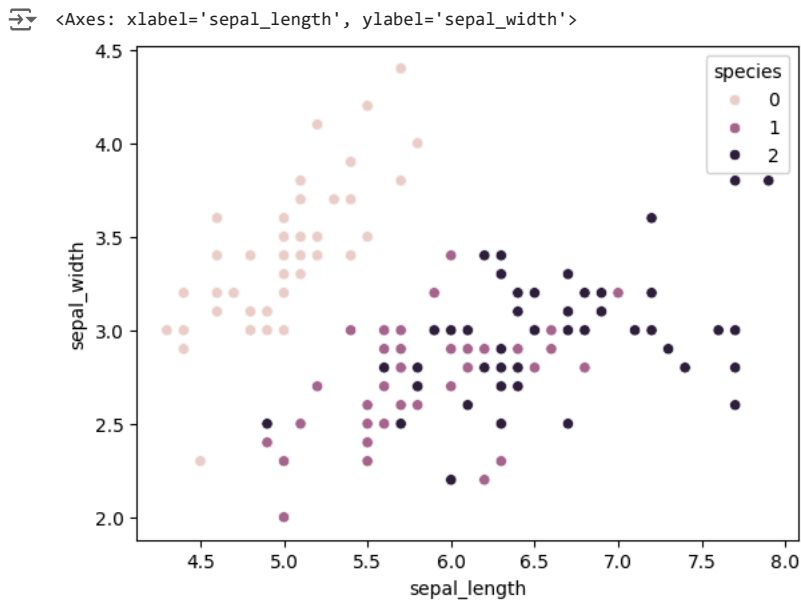
```
from mpl_toolkits.mplot3d import Axes3D
fig=plt.figure()
ax=fig.add_subplot(111,projection='3d')
ax.scatter(df.sepal_length , df.sepal_width, c=df.species)
ax.set_xlabel('sepal_length')
ax.set_ylabel('sepal_width')
ax.set_zlabel('species')
plt.title('3D Scatter Plot example')
plt.show()
```



3D Scatter Plot example



```
sns.scatterplot(data=df,x='sepal_length',y='sepal_width',hue='species')
```



```
k_rng=range(1,10)
sse=[]
for k in k_rng:
    km=KMeans(n_clusters=k)
    km.fit(df[['petal_length', 'petal_width']])
    sse.append(km.inertia_)
```

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 1 in the future. Please set `n_init` to the desired value.

warnings.warn(

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 1 in the future. Please set `n_init` to the desired value.

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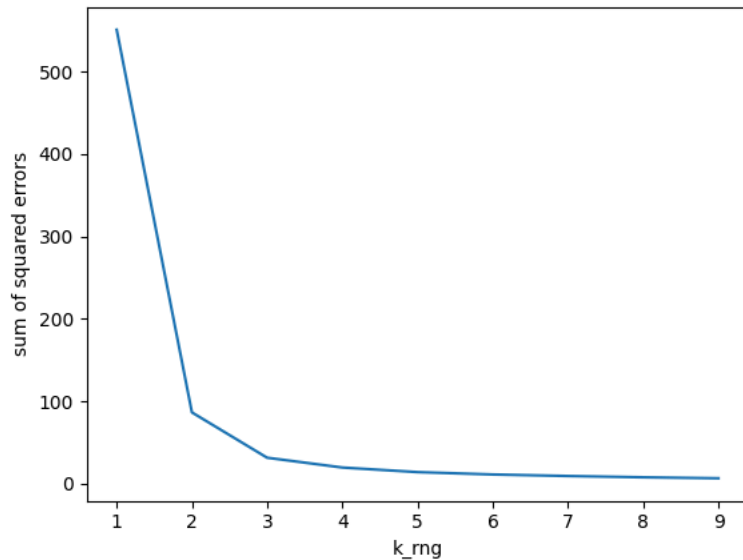
warnings.warn(

sse

```
[550.6434666666669,
 86.40394533571003,
 31.38775897435897,
 19.499400899685114,
 13.933308757908755,
 11.056639971910453,
 9.21026673204751,
 7.640593062579722,
 6.472894541406307]
```

```
plt.xlabel('k_rng')
plt.ylabel('sum of squared errors')
plt.plot(k_rng,sse)
```

```
→ [matplotlib.lines.Line2D at 0x7e9328d2a320]
```



APPLYING KMEAN ALGORITHM

```
km=KMeans(n_clusters=3,random_state=0,)  
y_predicted=km.fit_predict(df[['petal_length','petal_width']])  
y_predicted
```

```

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 1 in the future. This will affect the results of the fit method when random initialization is used.
  warnings.warn(
array([[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, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
        2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2,
        2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1,
        1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1,
        1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)

```

```
df['cluster']=y_predicted
df.head(150)
```

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

150 rows x 6 columns

Next steps:

Generate code with df

☐ View recommended plots

[New interactive sheet](#)

ACCURACY MEASURE

```
from sklearn.metrics import confusion_matrix
cm=confusion_matrix(df['species'],df['cluster'])
cm
```

```
array([[50,  0,  0],
       [ 0,  2, 48],
       [ 0, 46,  4]])
```

```
true_labels=df.species
predicted_labels=df.cluster
```

```
cm=confusion_matrix(true_labels,predicted_labels)
class_labels=['setosa','versicolor','virginica']
```

```
#plot confusion matrix
plt.imshow(cm,interpolation='nearest',cmap=plt.cm.Blues)
plt.title('Confusion Matrix')
plt.colorbar()
tick_marks=np.arange(len(class_labels))
plt.xticks(tick_marks,class_labels,rotation=45)
plt.yticks(tick_marks,class_labels)
```

```
#fill matrix with values
for i in range(len(class_labels)):
    for j in range(len(class_labels)):
        plt.text(j,i,cm[i,j],horizontalalignment='center',color='white')
```

```
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.show()
```

