

```

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import matplotlib.pyplot as plt
import seaborn as sns

iris=pd.read_csv('E:\DS&BDA\PR\iris.csv')

iris.head()

```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	1	5.1	3.5	1.4	0.2	Iris-setosa
1	2	4.9	3.0	1.4	0.2	Iris-setosa
2	3	4.7	3.2	1.3	0.2	Iris-setosa
3	4	4.6	3.1	1.5	0.2	Iris-setosa
4	5	5.0	3.6	1.4	0.2	Iris-setosa

```

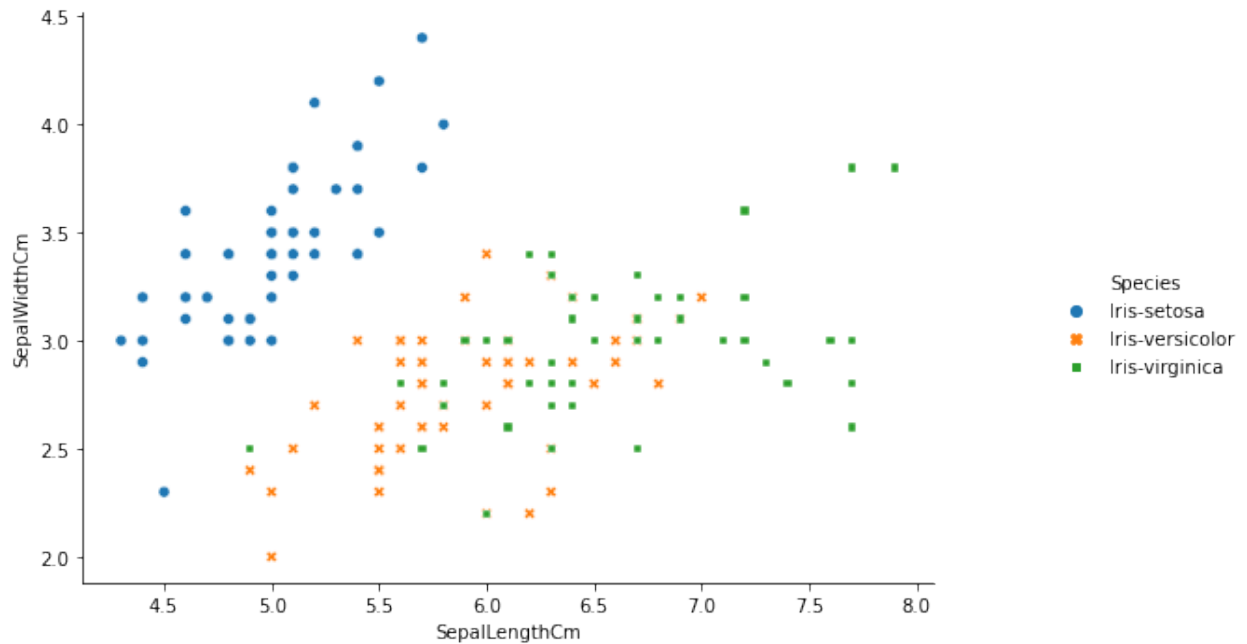
iris['Species'].unique()

array(['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'],
      dtype=object)

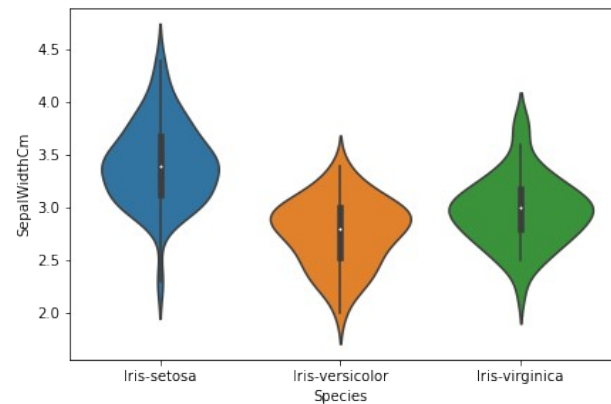
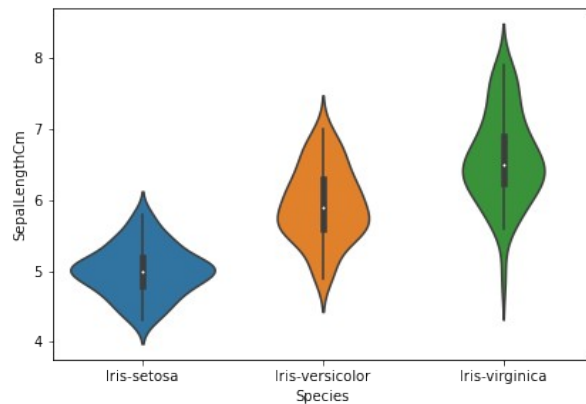
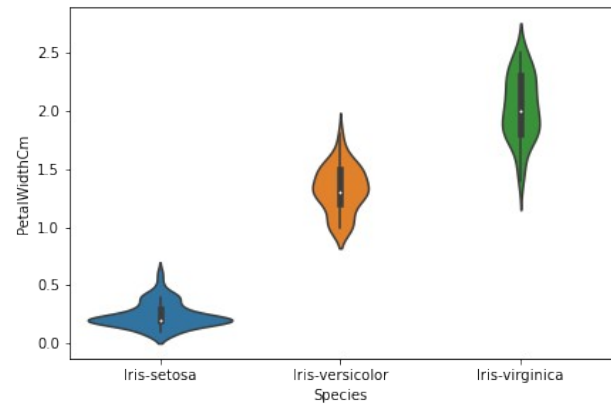
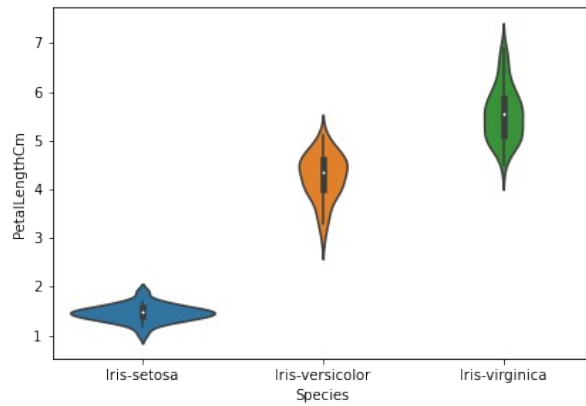
iris.drop(columns="Id",inplace=True)

g=sns.relplot(x='SepalLengthCm',y='SepalWidthCm',data=iris,hue='Species',style='Species')
g.fig.set_size_inches(10,5)
plt.show()

```

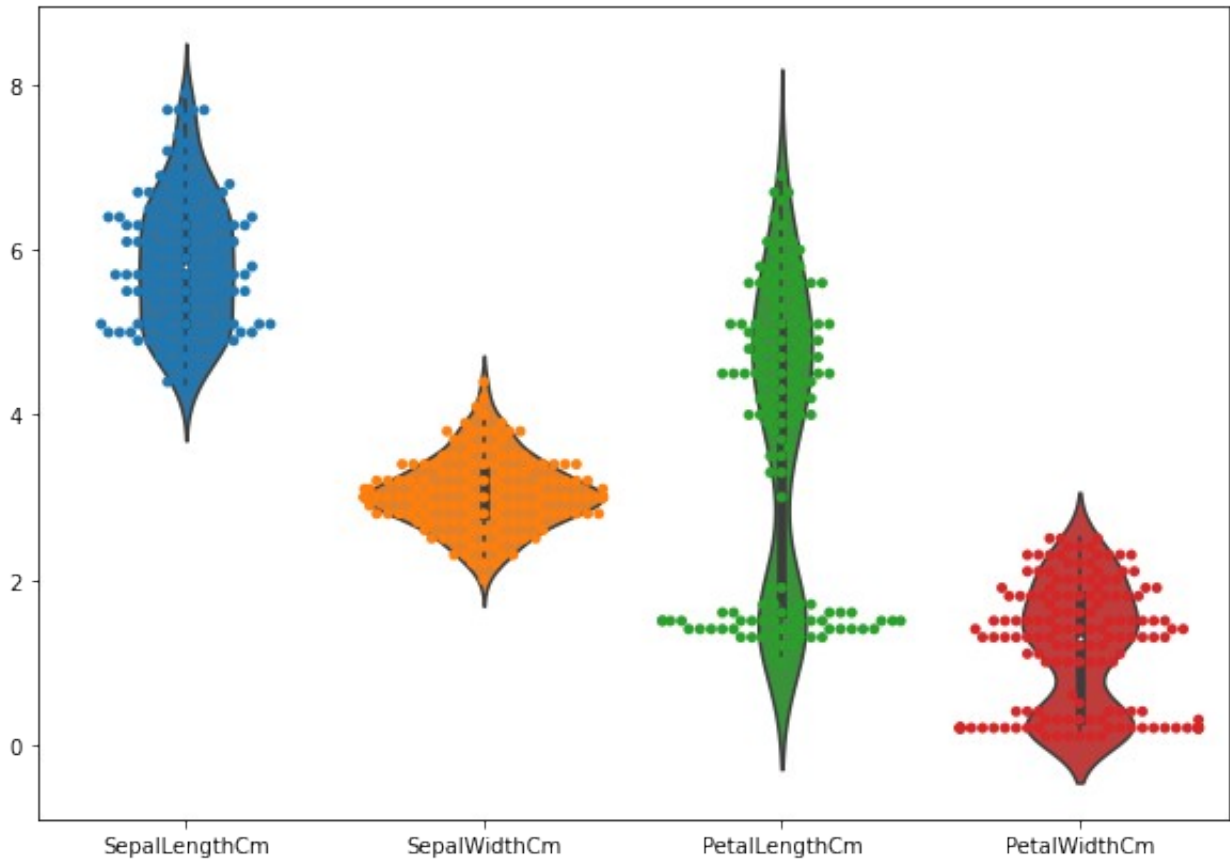


```
plt.figure(figsize=(15,10))
plt.subplot(2,2,1)
sns.violinplot(x='Species',y='PetalLengthCm',data=iris)
plt.subplot(2,2,2)
sns.violinplot(x='Species',y='PetalWidthCm',data=iris)
plt.subplot(2,2,3)
sns.violinplot(x='Species',y='SepalLengthCm',data=iris)
plt.subplot(2,2,4)
sns.violinplot(x='Species',y='SepalWidthCm',data=iris)
plt.show()
```



```
plt.subplots(figsize=(10,7))
sns.violinplot(data=iris)
sns.swarmplot( data=iris)
plt.show()
```

```
C:\Users\Vijay\anaconda3\lib\site-packages\seaborn\
categorical.py:1296: UserWarning: 9.3% of the points cannot be placed;
you may want to decrease the size of the markers or use stripplot.
  warnings.warn(msg, UserWarning)
```



```
iris.plot.area(y=['SepalLengthCm','SepalWidthCm','PetalLengthCm','PetalWidthCm'],alpha=0.4,figsize=(12, 6));
```

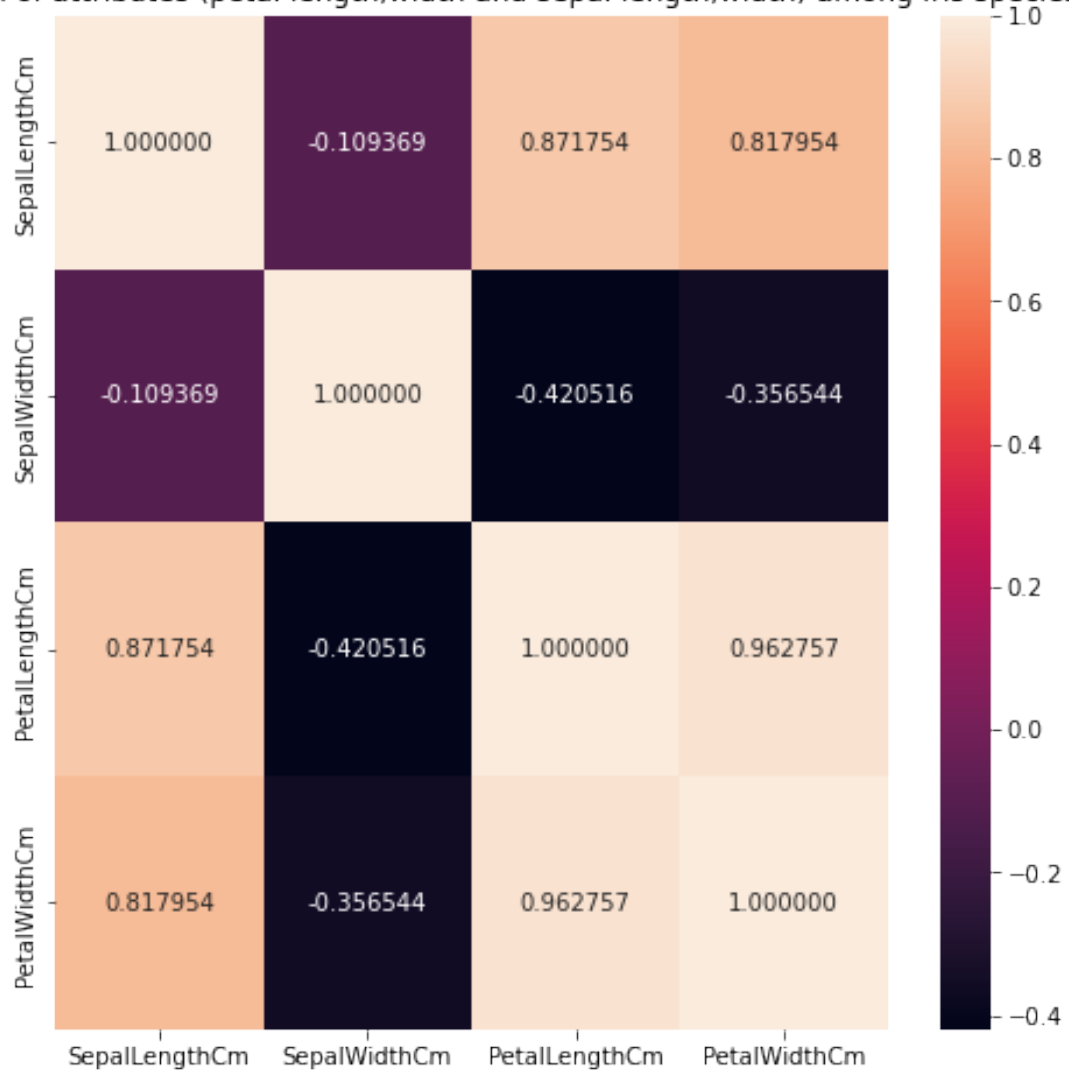


```
iris.corr()
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm
PetalWidthCm			
SepalLengthCm	1.000000	-0.109369	0.871754
0.817954			
SepalWidthCm	-0.109369	1.000000	-0.420516
0.356544			
PetalLengthCm	0.871754	-0.420516	1.000000
0.962757			
PetalWidthCm	0.817954	-0.356544	0.962757
1.000000			

```
plt.subplots(figsize = (8,8))
sns.heatmap(iris.corr(),annot=True,fmt="f").set_title("Corelation of
attributes (petal length,width and sepal length,width) among Iris
species")
plt.show()
```

Corelation of attributes (petal length,width and sepal length,width) among Iris species



```
X=iris.iloc[:,0:4].values
y=iris.iloc[:,4].values

from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
y = le.fit_transform(y)

#Metrics
from sklearn.metrics import make_scorer,
accuracy_score,precision_score
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from sklearn.metrics import
accuracy_score ,precision_score,recall_score,f1_score
```

```

#Model Select
from sklearn.naive_bayes import GaussianNB

#Train and Test split
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.3,random_state=0)

gaussian = GaussianNB()
gaussian.fit(X_train, y_train)
Y_pred = gaussian.predict(X_test)
accuracy_nb=round(accuracy_score(y_test,Y_pred)* 100, 2)
acc_gaussian = round(gaussian.score(X_train, y_train) * 100, 2)

cm = confusion_matrix(y_test, Y_pred)
accuracy = accuracy_score(y_test,Y_pred)
precision =precision_score(y_test, Y_pred,average='micro')
recall = recall_score(y_test, Y_pred,average='micro')
f1 = f1_score(y_test,Y_pred,average='micro')
print('Confusion matrix for Naive Bayes\n',cm)
print('accuracy_Naive Bayes: %.3f' %accuracy)
print('precision_Naive Bayes: %.3f' %precision)
print('recall_Naive Bayes: %.3f' %recall)
print('f1-score_Naive Bayes : %.3f' %f1)

Confusion matrix for Naive Bayes
[[16  0  0]
 [ 0 18  0]
 [ 0  0 11]]
accuracy_Naive Bayes: 1.000
precision_Naive Bayes: 1.000
recall_Naive Bayes: 1.000
f1-score_Naive Bayes : 1.000

```