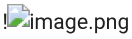
```
# import libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
%matplotlib inline


from google.colab import drive
drive.mount('/content/drive')


!


# read data set

df = pd.read_csv("/content/IRIS_FLOWER_CSV_FILE.csv")
df.head(5)
```

	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.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
```

```
df.shape
```

```
(150, 5)
```

```
df.describe()
```

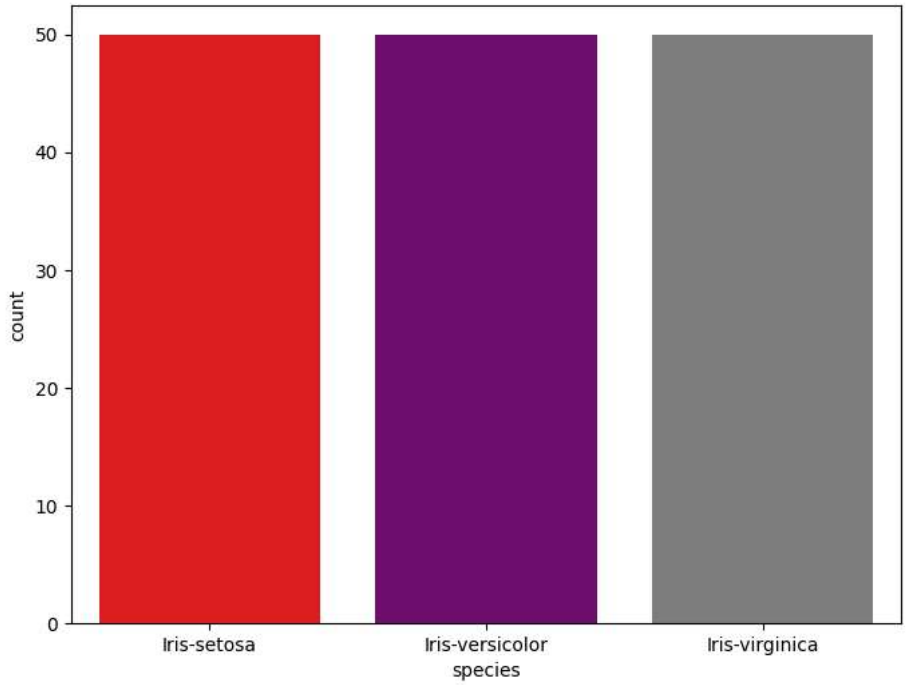
	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000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

```
# Checking the null values with their sum

df.isnull().sum()
```

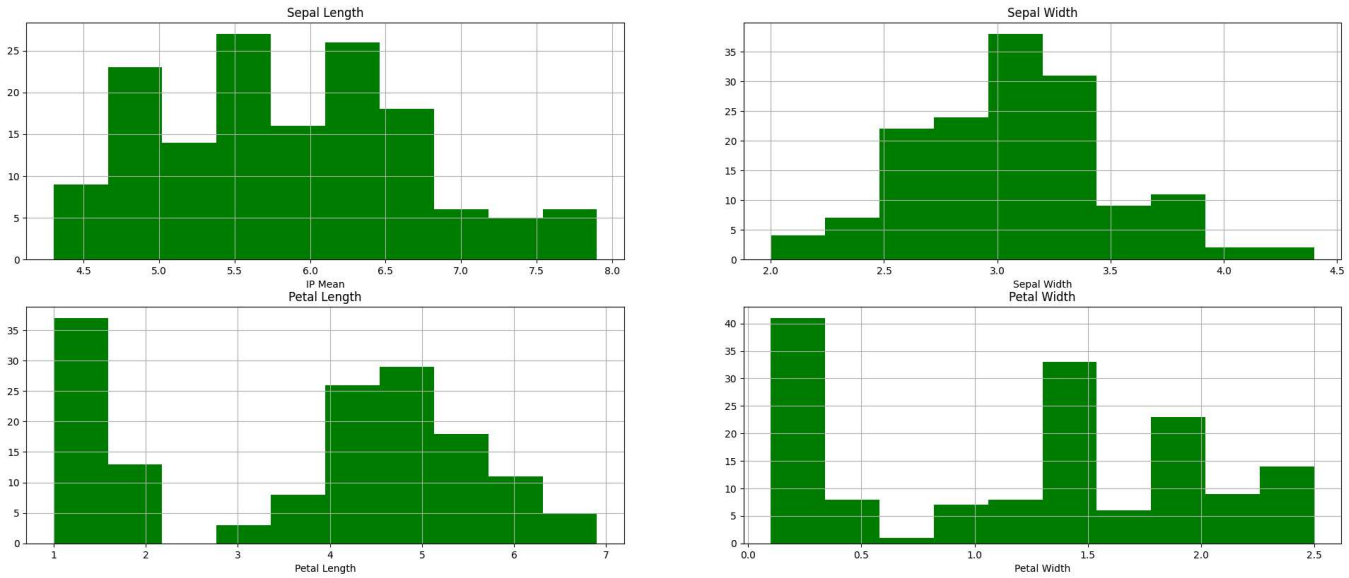
	0
sepal_length	0
sepal_width	0
petal_length	0
petal_width	0
species	0

```
plt.figure(figsize=(8, 6))
colors = ['red', 'purple', 'gray']
sns.countplot(x='species', data=df, palette=colors)

plt.show()
```

```
<ipython-input-12-8b658e6ba159>:3: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v0.14.0. Assign the `x` variable to `hue` and set `le

  sns.countplot(x='species', data=df, palette=colors)
```



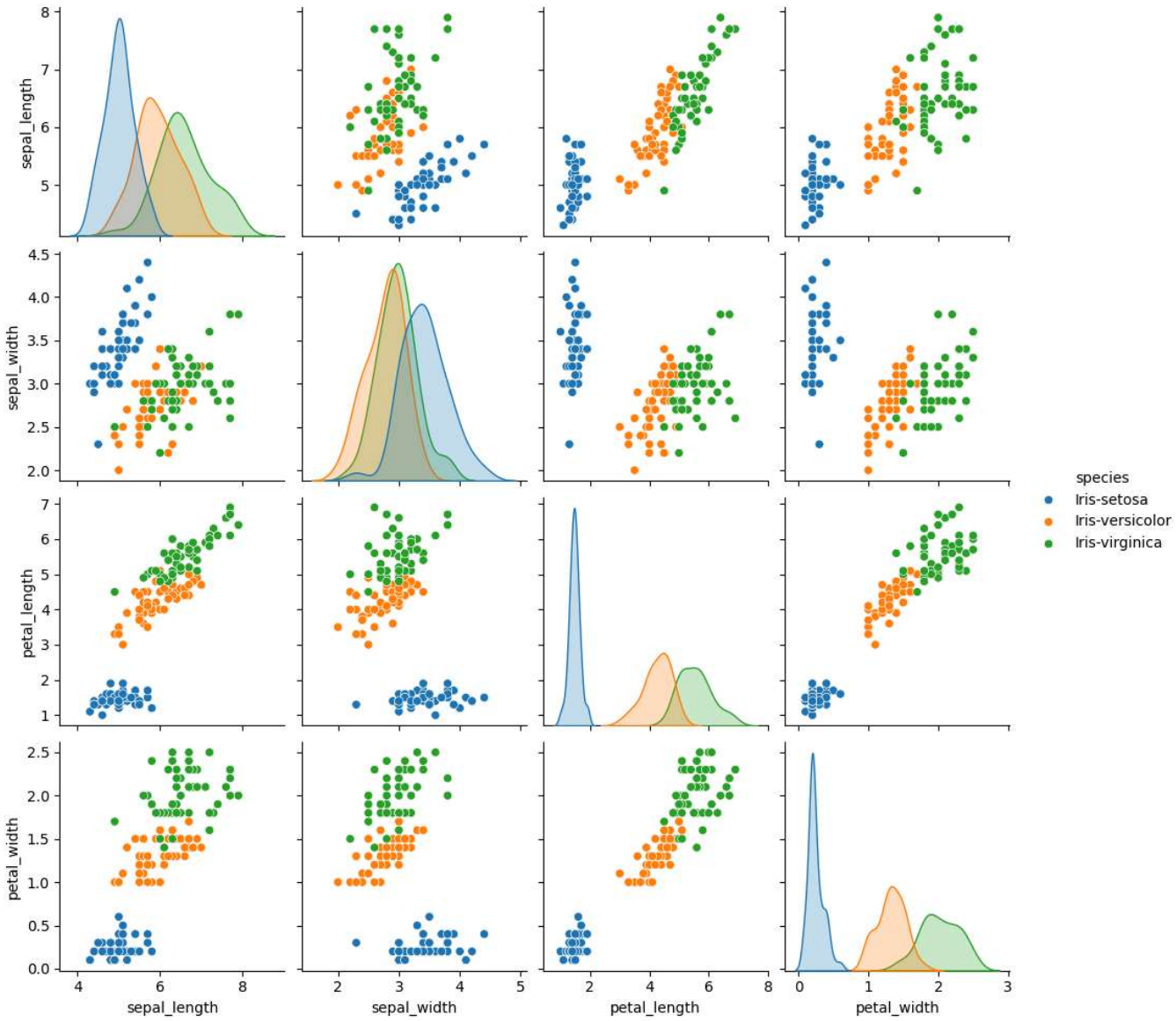

```
plt.figure(figsize=(24, 20))

# Subplot 1
plt.subplot(4, 2, 1)
fig = df['sepal_length'].hist(bins=10, color='green')  # Set the color to green
fig.set_xlabel('IP Mean')
fig.set_title('Sepal Length')

# Subplot 2
plt.subplot(4, 2, 2)
fig = df['sepal_width'].hist(bins=10, color='green')
fig.set_xlabel('Sepal Width')
fig.set_title('Sepal Width')

# Subplot 3
plt.subplot(4, 2, 3)
fig = df['petal_length'].hist(bins=10, color='green')
fig.set_xlabel('Petal Length')
fig.set_title('Petal Length')

# Subplot 4
plt.subplot(4, 2, 4)
fig = df['petal_width'].hist(bins=10, color='green')
fig.set_xlabel('Petal Width')
fig.set_title('Petal Width')

plt.show()
```



Start coding or generate with AI.

```
sns.pairplot(df,hue='species')
```

```
<seaborn.axisgrid.PairGrid at 0x7c4fb8c7d840>
```



Start coding or generate with AI.

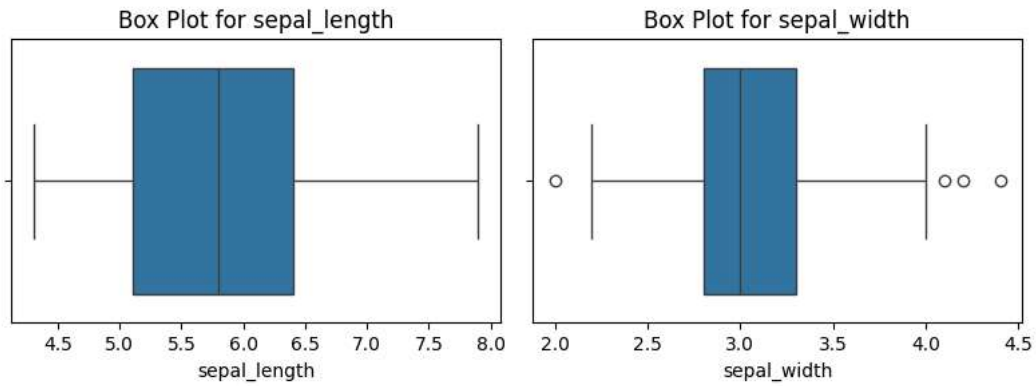
```
df['width_zscore']=(df.sepal_width-df.sepal_width.mean())/df.sepal_width.std()
df.head()
```

	sepal_length	sepal_width	petal_length	petal_width	species	width_zscore
0	5.1	3.5	1.4	0.2	Iris-setosa	1.028611
1	4.9	3.0	1.4	0.2	Iris-setosa	-0.124540
2	4.7	3.2	1.3	0.2	Iris-setosa	0.336720
3	4.6	3.1	1.5	0.2	Iris-setosa	0.106090
4	5.0	3.6	1.4	0.2	Iris-setosa	1.259242

Next steps: Generate code with df | View recommended plots | New interactive sheet

```
columns_to_plot = ['sepal_length', 'sepal_width', 'petal_length', 'petal_width']

# Create subplots using a for loop
plt.figure(figsize=(8, 6))
for i, column in enumerate(columns_to_plot, start=1):
    plt.subplot(2, 2, i)
    sns.boxplot(x=df[column])
    plt.title(f'Box Plot for {column}')
```

```
plt.tight_layout()
plt.show()
```




```
# Now we will check all the outliers in these 4 columns
data_1 = df[['sepal_length','sepal_width','petal_length','petal_width']]

# Creating a new dataframe
data_1 = pd.DataFrame(data_1)

# Calculate mean and standard deviation for all columns
means = data_1.mean()
stds = data_1.std()

# Calculate Z-scores for all columns
z_scores = (df - means) / stds

# Set a threshold for Z-score to identify outliers
threshold = 3  # You can adjust this threshold based on your preference

# Identify rows where any column has an outlier
outliers = (z_scores.abs() > threshold).any(axis=1)

# Display rows with outliers
print("Rows with outliers:")
print(data_1[outliers])
```

```
Rows with outliers:
    sepal_length  sepal_width  petal_length  petal_width
15           5.7          4.4           1.5          0.4
```

```
df_no_outliers = data_1[~outliers]

# Display the DataFrame without outliers
print("DataFrame without outliers:")
print(df_no_outliers.head(5))
```

```
DataFrame without outliers:
   sepal_length  sepal_width  petal_length  petal_width
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
```

```
# Merging the data without outliers on the index basis
merged_df = pd.merge(df_no_outliers, df, left_index=True, right_index=True)
merged_df.head(5)
```

	sepal_length_x	sepal_width_x	petal_length_x	petal_width_x	sepal_length_y	sepal_width_y	petal_length_y	petal_width_y	speci
0	5.1	3.5	1.4	0.2	5.1	3.5	1.4	0.2	Ir seto
1	4.9	3.0	1.4	0.2	4.9	3.0	1.4	0.2	Ir seto
2	4.7	3.2	1.3	0.2	4.7	3.2	1.3	0.2	Ir seto
3	4.6	3.1	1.5	0.2	4.6	3.1	1.5	0.2	Ir seto
4	5.0	3.6	1.4	0.2	5.0	3.6	1.4	0.2	Ir seto

Next steps: Generate code with merged_df View recommended plots New interactive sheet

```
# Now we will remove Duplicate Columns
merged_df = merged_df[['sepal_length_x','sepal_width_x','petal_length_x','petal_width_x','species']]

# Removing _x and replacing it in first 4 columns to make column easy to read
merged_df.columns = merged_df.columns.str.replace('_x', '')

# Creating a dataframe without any outliers
df = merged_df.copy()

# Finnaly we have the data without Outliers
df.head(5)
```

	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

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image.png

```
# Splitting the features and targets

x=df[['sepal_length','sepal_width','petal_length','petal_width']]
y=df['species']

x.head()
```

	sepal_length	sepal_width	petal_length	petal_width
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

Next steps: Generate code with x View recommended plots New interactive sheet

```
y.head()
```

	species
0	Iris-setosa
1	Iris-setosa
2	Iris-setosa
3	Iris-setosa
4	Iris-setosa

```
### Importing the dependencies
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.metrics import accuracy_score
from sklearn.model_selection import GridSearchCV


### Machine Learning models Libraries:
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import KFold,cross_val_score
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression


x_train,x_test,y_train,y_test = train_test_split(x,y,test_size=0.2,random_state=3)


print(x.shape,x_train.shape,x_test.shape)
```

```
(149, 4) (119, 4) (30, 4)
```

Accuracy Score

```
models = [LogisticRegression(max_iter=1000),DecisionTreeClassifier(),RandomForestClassifier(),KNeighborsClassifier()]


def compare_models_train_test():
    for model in models:
        model.fit(x_train,y_train)
        y_predicted = model.predict(x_test)
        accuracy = accuracy_score(y_test,y_predicted)
        print("Accuracy of the ",model,"=",accuracy)
        print("="*100)


compare_models_train_test()
```

```
Accuracy of the  LogisticRegression(max_iter=1000) = 0.9666666666666667
====================================================================================================
Accuracy of the  DecisionTreeClassifier() = 0.9333333333333333
====================================================================================================
Accuracy of the  RandomForestClassifier() = 0.9
====================================================================================================
Accuracy of the  KNeighborsClassifier() = 0.9666666666666667
====================================================================================================
```

Cross Validation

```
models = [LogisticRegression(max_iter=1000),DecisionTreeClassifier(),RandomForestClassifier(),KNeighborsClassifier()]


def compare_models_cv():
    for model in models:
        cv_score =cross_val_score(model,x,y,cv=5)
        mean_accuracy = sum(cv_score)/len(cv_score)
        mean_accuracy= mean_accuracy*100
        mean_accuracy = round(mean_accuracy,2)
        print("cv_score of the",model,"=",cv_score)
        print("mean_accuracy % of the",model,"=",mean_accuracy,"%")
        print("="*100)


compare_models_cv()
```

```
cv_score of the LogisticRegression(max_iter=1000) = [0.96666667 1.         0.93333333 0.96666667 1.        ]
mean_accuracy % of the LogisticRegression(max_iter=1000) = 97.33 %
```

```
==========================================================================================================
cv_score of the DecisionTreeClassifier() = [0.96666667 0.96666667 0.9        0.96666667 1.        ]
mean_accuracy % of the DecisionTreeClassifier() = 96.0 %
==========================================================================================================
cv_score of the RandomForestClassifier() = [0.96666667 0.96666667 0.93333333 0.96666667 1.        ]
mean_accuracy % of the RandomForestClassifier() = 96.67 %
==========================================================================================================
cv_score of the KNeighborsClassifier() = [0.96666667 1.         0.93333333 0.96666667 1.        ]
mean_accuracy % of the KNeighborsClassifier() = 97.33 %
==========================================================================================================
```

```
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, roc_auc_score
```

```
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, roc_auc_score
```