

lab-session-8

September 17, 2024

Data Visualization with Matplotlib and Seaborn using Iris dataset

```
[35]: import seaborn as sns #import seaborn library
import matplotlib.pyplot as plt #import matplotlib library
import pandas as pd
```

PROGRAM 1:General Statistics Plot (Matplotlib or Seaborn):

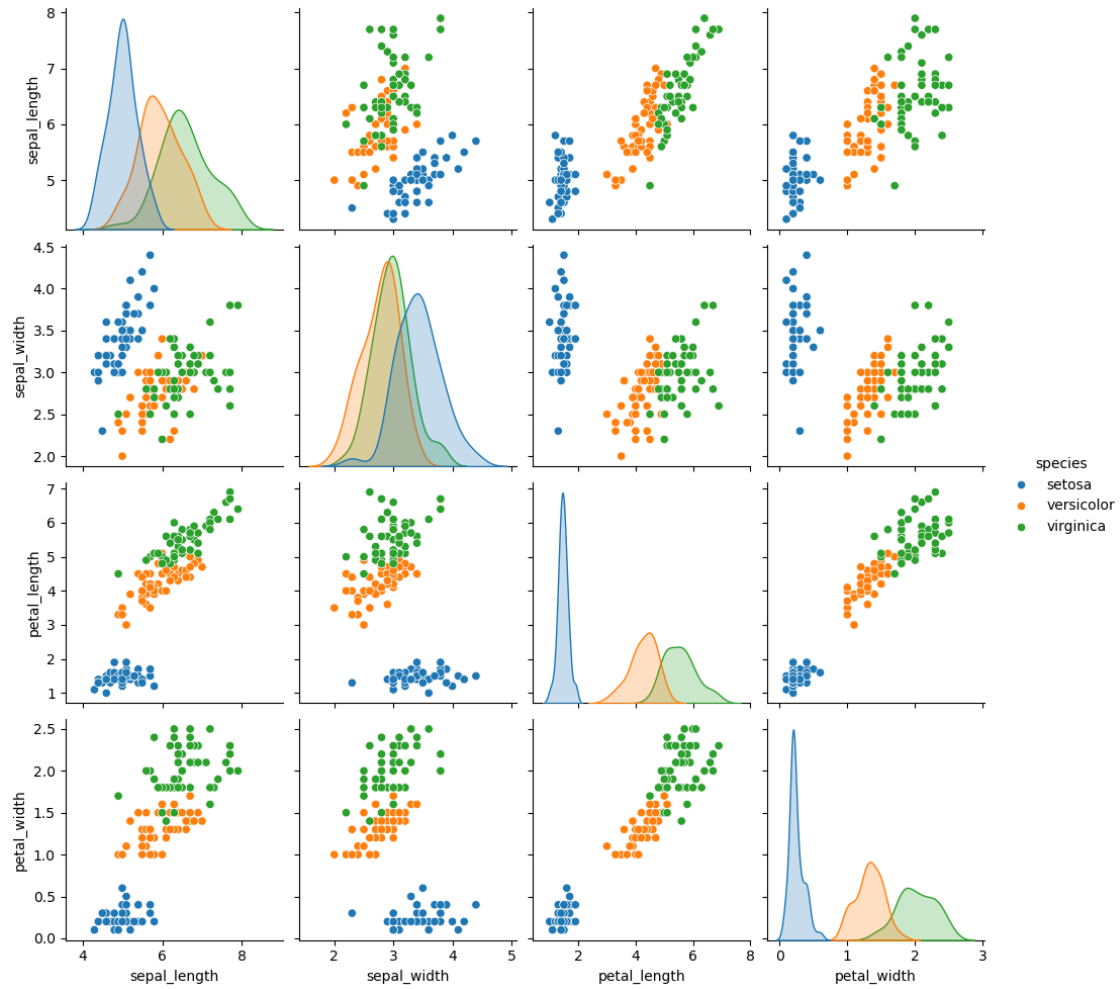
```
[27]: iris=sns.load_dataset('iris')#loading iris dataset using seaborn
```

```
[5]: species_counts=iris['species'].value_counts()
```

```
[36]: # Display statistical summary using describe()
print("Statistical Summary:")
print(iris.describe(include='all'))
sns.pairplot(iris, hue='species', height=2.5)
plt.show()
```

Statistical Summary:

	sepal_length	sepal_width	petal_length	petal_width	species
count	150.000000	150.000000	150.000000	150.000000	150
unique	NaN	NaN	NaN	NaN	3
top	NaN	NaN	NaN	NaN	setosa
freq	NaN	NaN	NaN	NaN	50
mean	5.843333	3.057333	3.758000	1.199333	NaN
std	0.828066	0.435866	1.765298	0.762238	NaN
min	4.300000	2.000000	1.000000	0.100000	NaN
25%	5.100000	2.800000	1.600000	0.300000	NaN
50%	5.800000	3.000000	4.350000	1.300000	NaN
75%	6.400000	3.300000	5.100000	1.800000	NaN
max	7.900000	4.400000	6.900000	2.500000	NaN



PROGRAM 2: Pie Plot for Species Frequency:

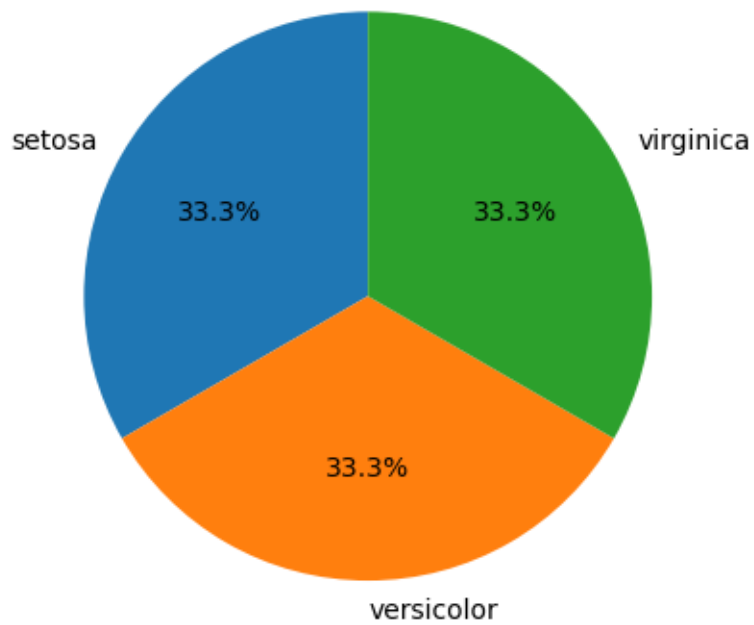
```
[37]: plt.figure(figsize=(8,6))
```

```
[37]: <Figure size 800x600 with 0 Axes>
```

```
<Figure size 800x600 with 0 Axes>
```

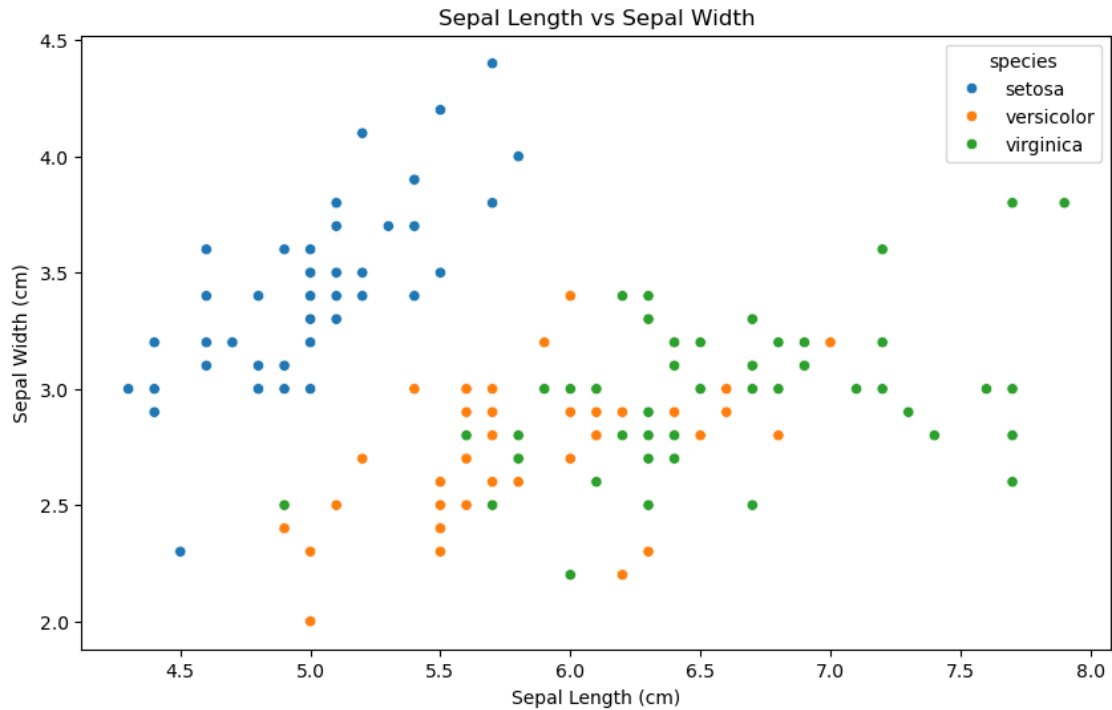
```
[16]: plt.pie(species_counts, labels=species_counts.index, autopct='%1.1f%%',startangle=90)
plt.title('Species Frequency in Iris Dataset')
plt.show()
```

Species Frequency in Iris Dataset



PROGRAM 3:Relationship Between Sepal Length and Width:

```
[17]: plt.figure(figsize=(10, 6))
sns.scatterplot(x='sepal_length', y='sepal_width', hue='species', data=iris)
plt.title('Sepal Length vs Sepal Width')
plt.xlabel('Sepal Length (cm)')
plt.ylabel('Sepal Width (cm)')
plt.show()
```



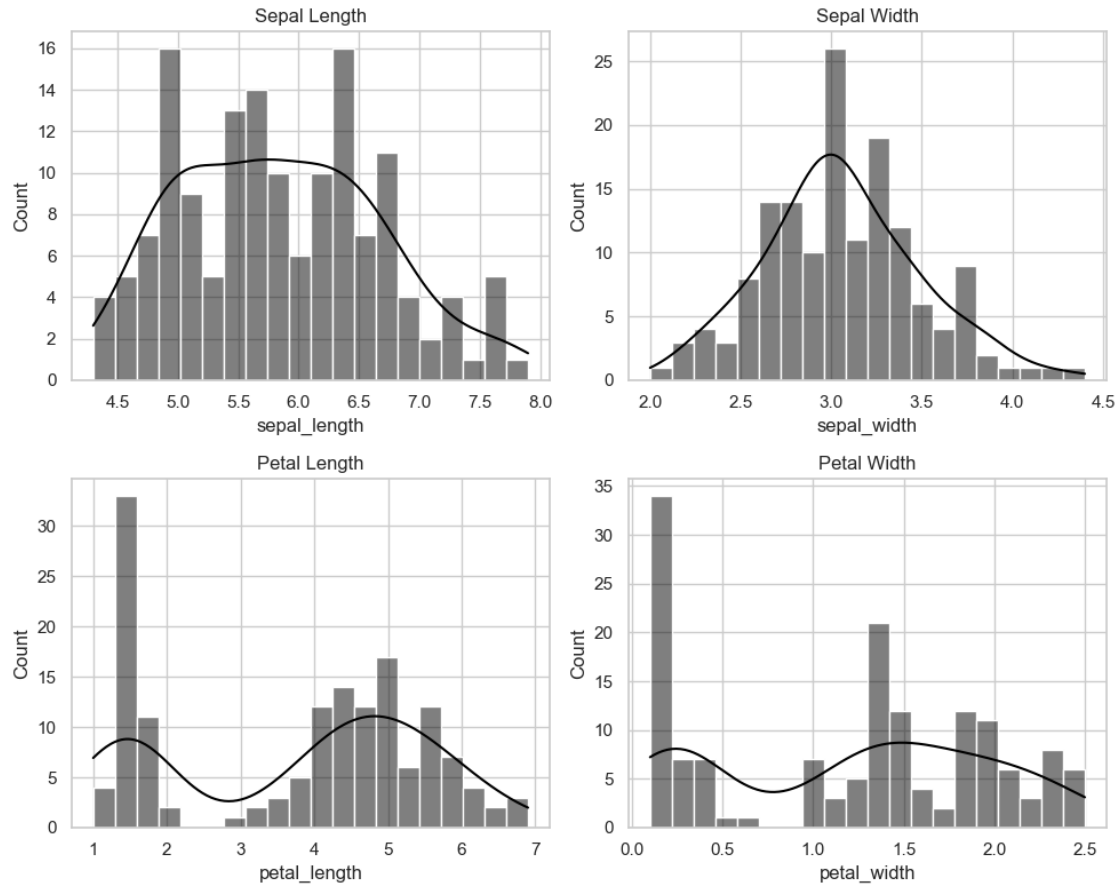
PROGRAM 4: Distribution of Sepal and Petal Features:

```
[52]: # Define features and titles
features = ['sepal_length', 'sepal_width', 'petal_length', 'petal_width']
titles = ['Sepal Length', 'Sepal Width', 'Petal Length', 'Petal Width']

# Create a figure with subplots for each feature
fig, axes = plt.subplots(2, 2, figsize=(10, 8))

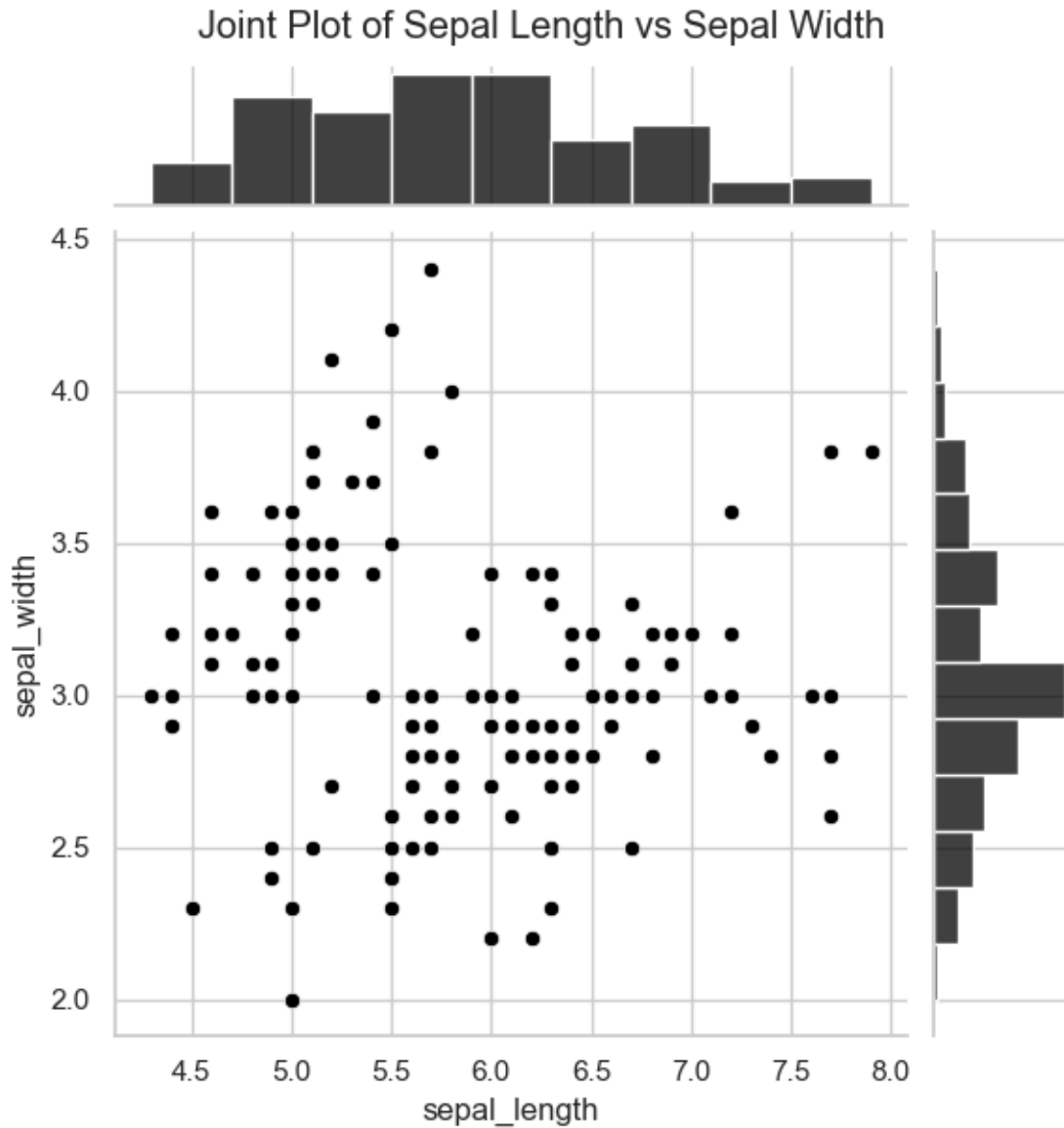
# Plot histograms with KDE for each feature
for ax, feature, title in zip(axes.flat, features, titles):
    sns.histplot(iris[feature], kde=True, bins=20, ax=ax, color='black')
    ax.set_title(title)

# Adjust layout and show plot
plt.tight_layout()
plt.show()
```



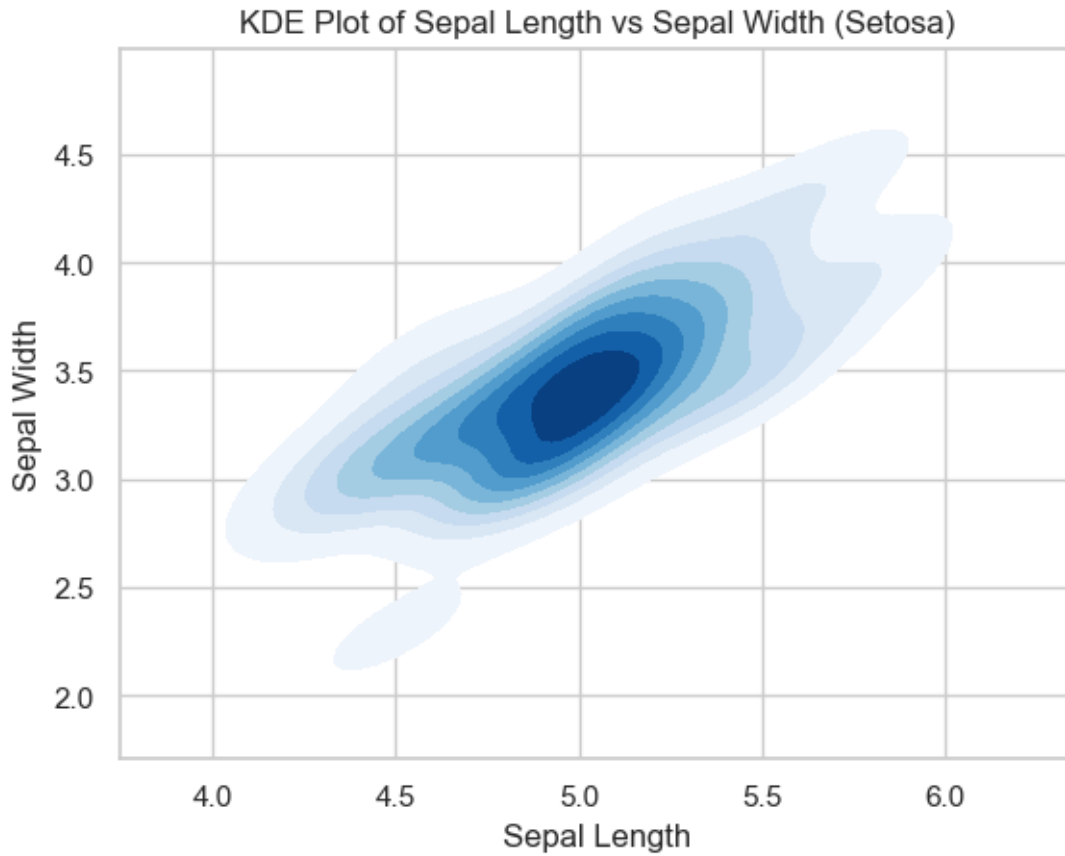
PROGRAM 5: Jointplot of Sepal Length vs Sepal Width:

```
[53]: #Create a joint plot for Sepal Length vs Sepal Width
sns.jointplot(data=iris, x='sepal_length', y='sepal_width', kind='scatter',
             color='black')
# Add title to the plot
plt.suptitle('Joint Plot of Sepal Length vs Sepal Width', y=1.02)
# Show the plot
plt.show()
```



PROGRAM 6: KDE Plot for Setosa Species (Sepal Length vs Sepal Width)

```
[62]: setosa = iris[iris['species'] == 'setosa']
# Create a KDE plot for Sepal Length vs Sepal Width
sns.kdeplot(data=setosa, x='sepal_length', y='sepal_width', fill=True,
            cmap='Blues')
# Add title and labels
plt.title('KDE Plot of Sepal Length vs Sepal Width (Setosa)')
plt.xlabel('Sepal Length')
plt.ylabel('Sepal Width')
# Show the plot
plt.show()
```



PROGRAM 7:KDE Plot for Setosa Species (Petal Length vs Petal Width):

```
[64]: setosa = iris[iris['species'] == 'setosa']
# Create a KDE plot for Petal Length vs Petal Width
sns.kdeplot(data=setosa, x='petal_length', y='petal_width', fill=True,
            cmap='Greens')
# Add title and labels
plt.title('KDE Plot of Petal Length vs Petal Width (Setosa)')
plt.xlabel('Petal Length')
plt.ylabel('Petal Width')
# Show the plot
plt.show()
```

