ICTE 6

February 23, 2023

```
[ ]: import numpy as np
     import pandas as pd
     import seaborn as sns
     from scipy import sparse
     from matplotlib import pyplot as plt
     from mpl_toolkits.mplot3d import Axes3D
     from sklearn.preprocessing import StandardScaler
     from sklearn.decomposition import PCA
     sns.set_style ('ticks')
```

0.1 Dataset Basics

```
[ ]: # Query 1

     # load iris data from csv to pandas dataframe
     iris = pd.read_csv('iris.csv')
     # iris_pd = pd.DataFrame(
     #     data = np.c_[iris['data'], iris['target']],
     #     columns= iris['feature_names'] + ['target']
     # )

     # print shape of data
     iris_shape = iris.shape
     print(f"Shape of the data is {iris_shape}.")

     # print type of data
     iris_type = type(iris)
     print(f"Type of the data is {iris_type}.")

     # print first 3 rows of data
     iris_head_3 = iris.head(3)
     print(f"First three rows of the data are as follows: \n{iris_head_3}.")
```

```
Shape of the data is (150, 5).
Type of the data is <class 'pandas.core.frame.DataFrame'>.
First three rows of the data are as follows:
   sepal.length  sepal.width  petal.length  petal.width variety
0           5.1          3.5           1.4          0.2  Setosa
```

```
1            4.9           3.0            1.4           0.2  Setosa
2            4.7           3.2            1.3           0.2  Setosa.
```

[ ]:
```python
# Query 2

# load iris data with scikit-learn
# iris = load_iris()

# print keys of data
iris_keys = iris.keys()
print(f"Keys of the data include {*iris_keys,}.")

# print number of rows-columns of data
print(f"Iris data has {iris_shape[0]} rows and {iris_shape[1]} columns.")

# print feature names of data
iris_feature_names = iris.columns  # +.values
print(f"Feature names of the data include {*iris_feature_names,}.")

# describe data with basic statistical details
iris_description = iris.describe()
```

```
Keys of the data include ('sepal.length', 'sepal.width', 'petal.length',
'petal.width', 'variety').
Iris data has 150 rows and 5 columns.
Feature names of the data include ('sepal.length', 'sepal.width',
'petal.length', 'petal.width', 'variety').
```

[ ]:
```python
# Query 3

# get number of observations
iris_observations = len(iris.index)
print(f"Data has {iris_observations} observations.")

# get number of missing values
iris_missing = pd.isna(iris).sum()
print(f"Data has {*iris_missing,} missing values in each column.")

# get number of NaN values
iris_nan = iris.isnull().sum().sum()
print(f"Data has {iris_nan} NaN values in total.")
```

```
Data has 150 observations.
Data has (0, 0, 0, 0, 0) missing values in each column.
Data has 0 NaN values in total.
```

[ ]:
```python
# Query 4
# create 2D array with ones on diagonal and zeros elsewhere
diag = np.eye(2)
print(f"The requested 2D array is \n{diag}.")

# convert to scipy sparse matrix
diag_sparse = sparse.csr_matrix(diag)
print(f"The requested matrix is \n{diag_sparse}.")
```

```
The requested 2D array is
[[1. 0.]
 [0. 1.]].
The requested matrix is
  (0, 0)        1.0
  (1, 1)        1.0.
```

[ ]:
```
# Query 5

# print description of data
print(f"Data can be described as follows: \n{iris_description}.")
```

```
Data can be described as follows:
       sepal.length  sepal.width  petal.length  petal.width
count    150.000000   150.000000    150.000000   150.000000
mean       5.843333     3.057333      3.758000     1.199333
std        0.828066     0.435866      1.765298     0.762238
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.
```

[ ]:
```
# Query 6

# get observations of species
iris_species = iris['variety'].value_counts()
print(f"Observations of each species amount to: \n{iris_species}.")
```

```
Observations of each species amount to:
Setosa        50
Versicolor    50
Virginica     50
Name: variety, dtype: int64.
```

[ ]:
```
# Query 7

# add and then drop the ID column
iris.insert(0, 'ID', range(1, len(iris) + 1))
iris_mod = iris.drop('ID', axis=1)
```

```
# print modified dataframe
print(f"The dataframe after adding the column is: \n{iris.head()}"
      f"\nAfter modification, it is: \n{iris_mod.head()}")
```

```
The dataframe after adding the column is:
   ID  sepal.length  sepal.width  petal.length  petal.width variety
0   1           5.1          3.5           1.4          0.2  Setosa
1   2           4.9          3.0           1.4          0.2  Setosa
2   3           4.7          3.2           1.3          0.2  Setosa
3   4           4.6          3.1           1.5          0.2  Setosa
4   5           5.0          3.6           1.4          0.2  Setosa
After modification, it is:
   sepal.length  sepal.width  petal.length  petal.width variety
0           5.1          3.5           1.4          0.2  Setosa
1           4.9          3.0           1.4          0.2  Setosa
2           4.7          3.2           1.3          0.2  Setosa
3           4.6          3.1           1.5          0.2  Setosa
4           5.0          3.6           1.4          0.2  Setosa
```

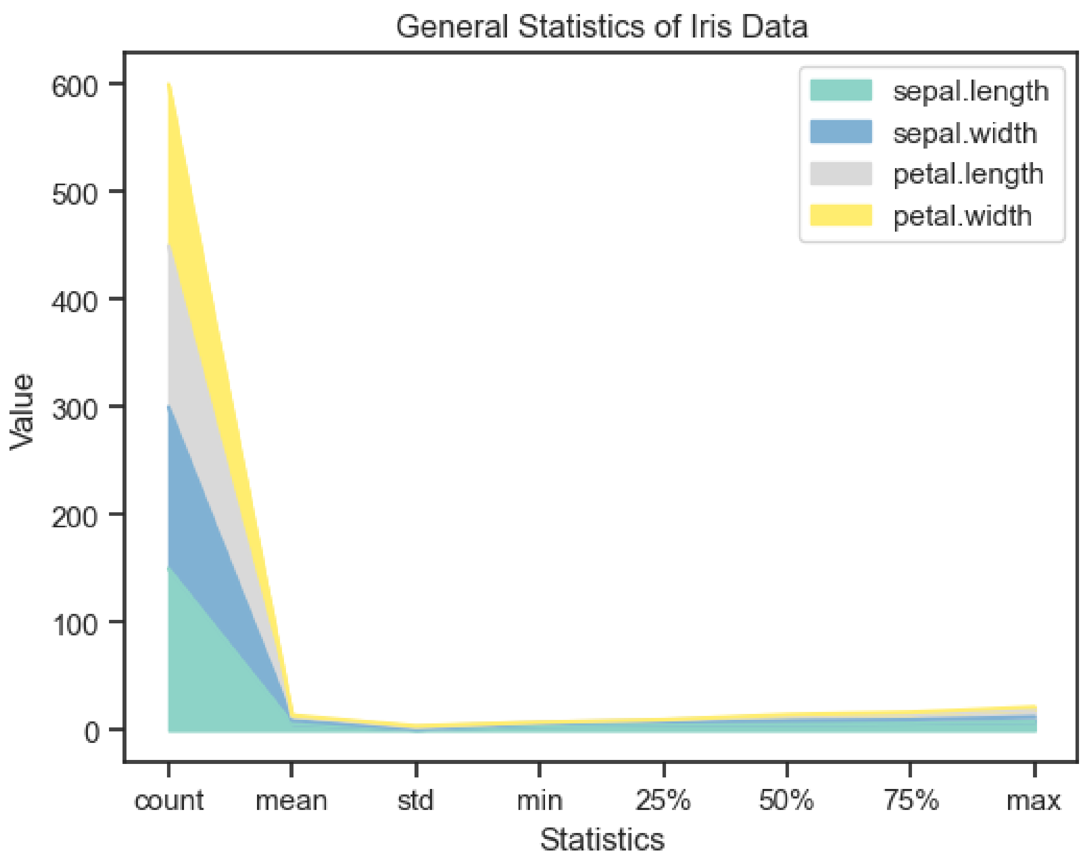
```
[ ]: # Query 8

     # access data with indices
     iris_iloc = iris.iloc[0:4, 1:5].values
     print(f"First four columns in first four rows accessed with indices are:␣
      ↪\n{iris_iloc}.")

     # access data with labels
     iris.set_index("ID", inplace=True)
     iris_loc = iris.loc[1:4, "sepal.length":"petal.width"].values
     print(f"First four columns in first four rows accessed with labels are:␣
      ↪\n{iris_loc}.")
```

```
First four columns in first four rows accessed with indices are:
[[5.1 3.5 1.4 0.2]
 [4.9 3.  1.4 0.2]
 [4.7 3.2 1.3 0.2]
 [4.6 3.1 1.5 0.2]].
First four columns in first four rows accessed with labels are:
[[5.1 3.5 1.4 0.2]
 [4.9 3.  1.4 0.2]
 [4.7 3.2 1.3 0.2]
 [4.6 3.1 1.5 0.2]].
```

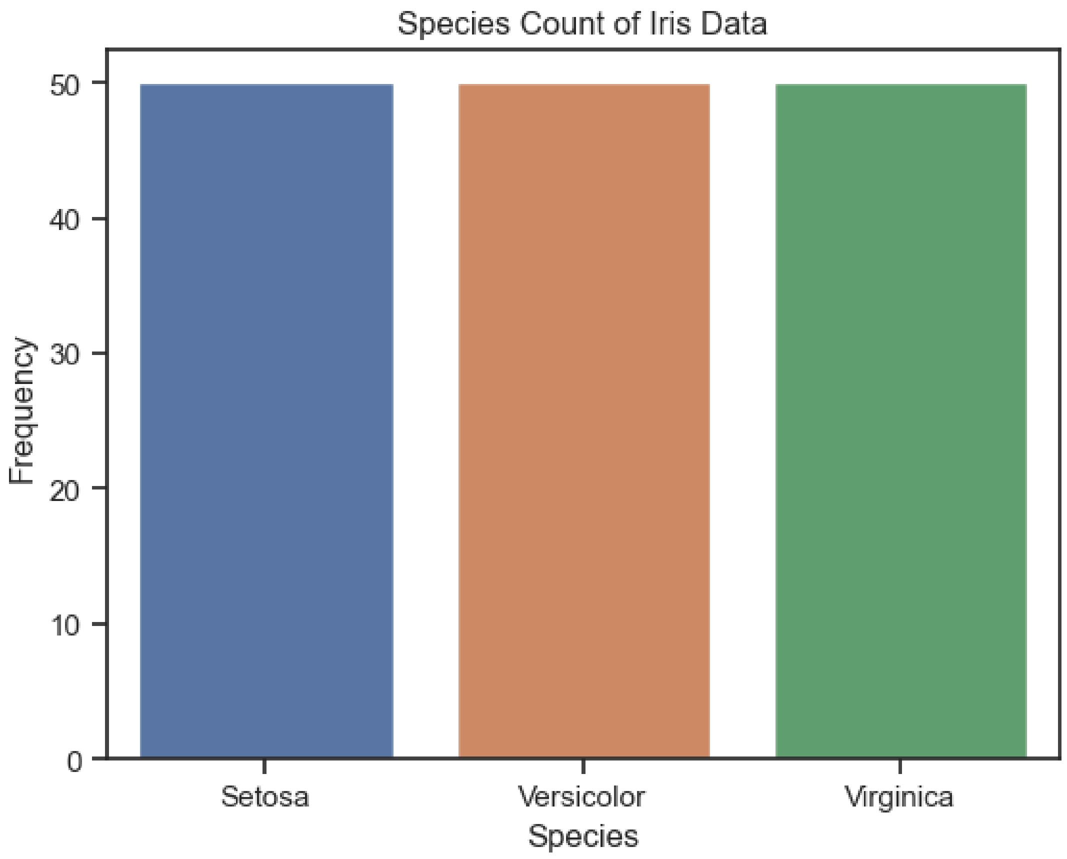
0.2 Dataset Visualization

```
[ ]: # Query 1

     # create plot of description
     iris_description.plot(kind='area', colormap='Set3')

     plt.xlabel("Statistics")
     plt.ylabel("Value")
     plt.title("General Statistics of Iris Data")
```

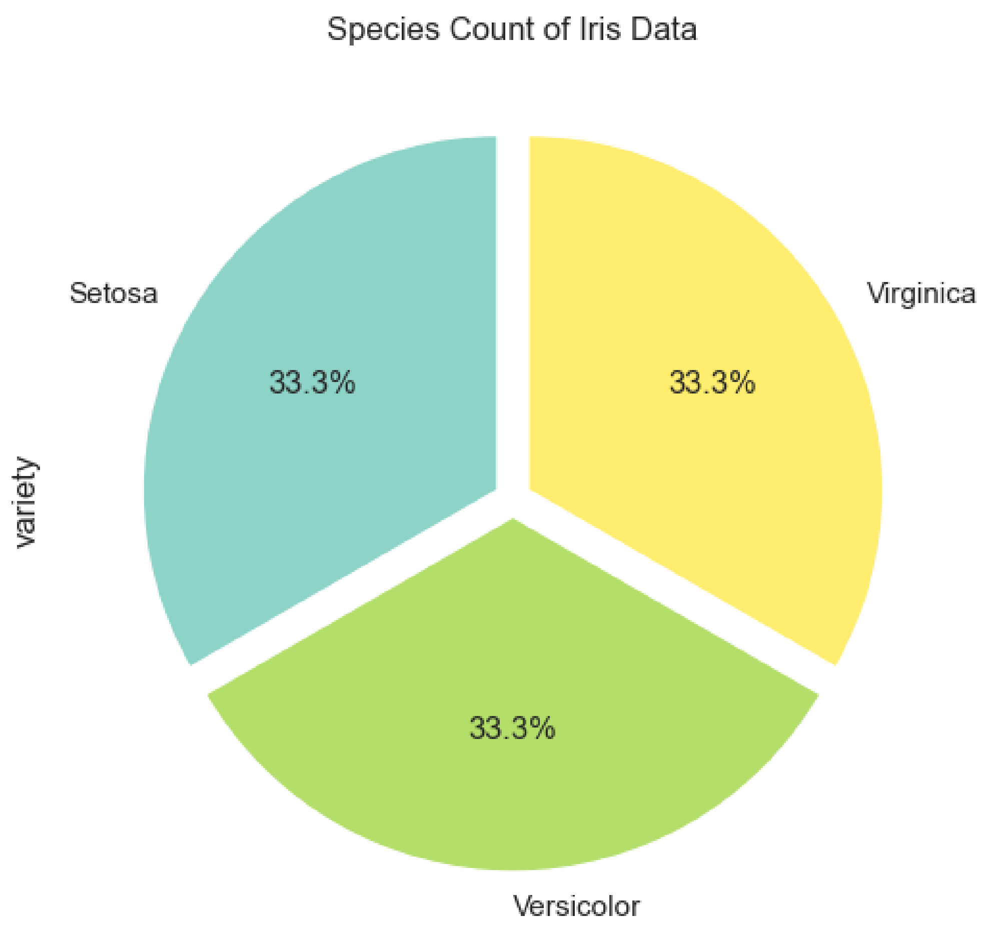
```
[ ]: Text(0.5, 1.0, 'General Statistics of Iris Data')
```



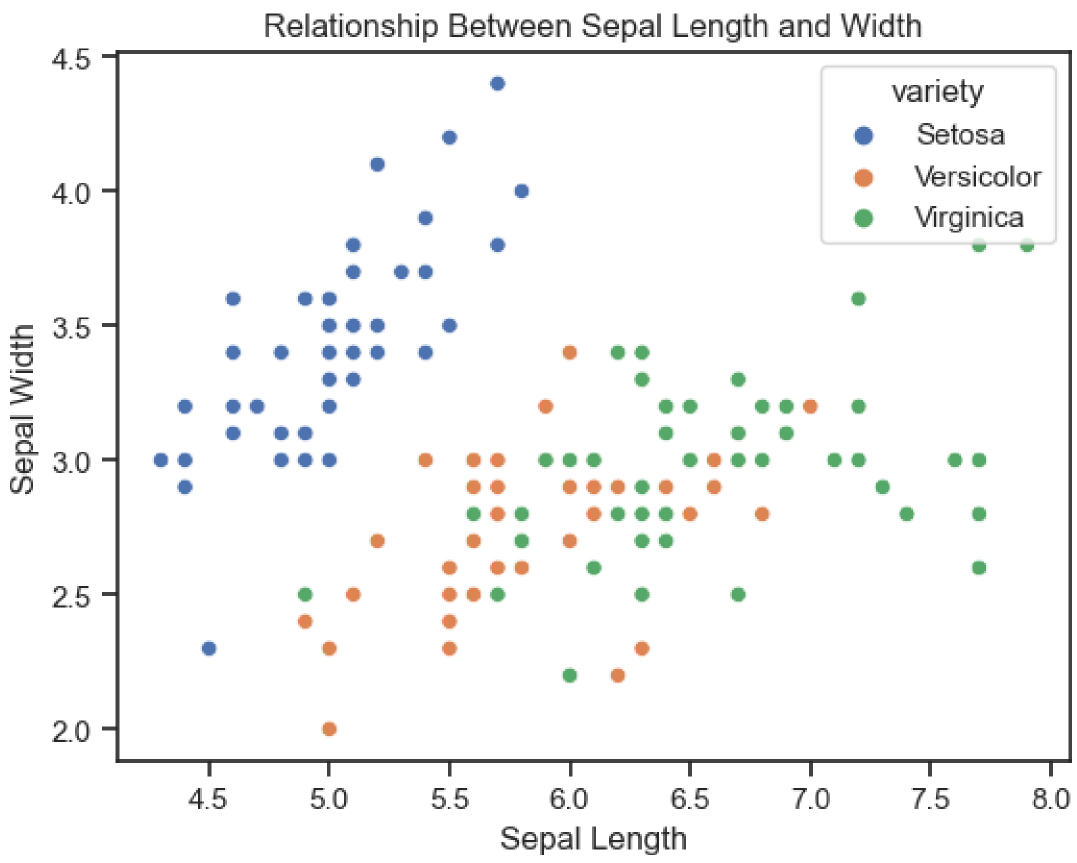
```
[ ]: # Query 2

     # create plot of frequency
     bar = sns.countplot(
         data=iris, x='variety'
     ).set(
         xlabel='Species', ylabel='Frequency',
         title='Species Count of Iris Data'
     )
     # iris_species.plot(kind='bar', figsize=(12, 8), color=['orange', 'green',␣
     ↪'blue'], rot=0)
```



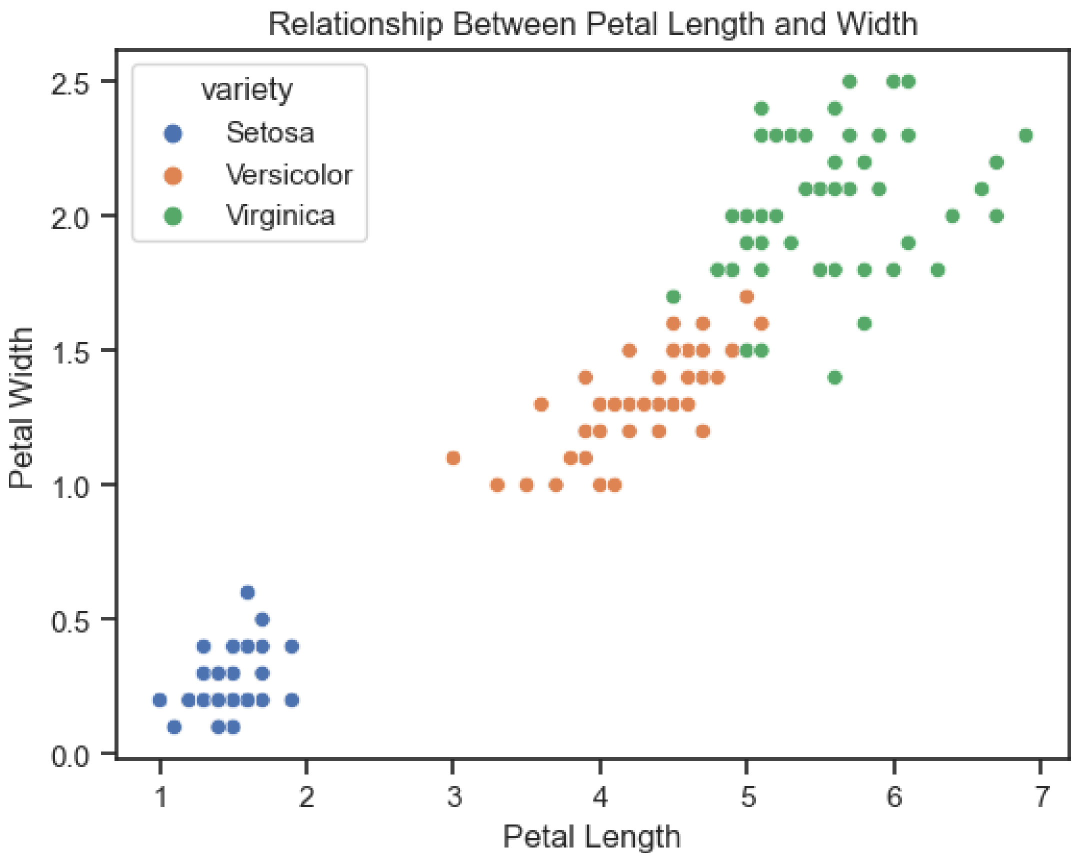
[ ]:
```
# Query 3

# create pie plot of species frequency
pie = iris_species.plot(
    kind='pie', figsize=(10, 6), colormap='Set3',
    explode=[0.05, 0.05, 0.05], autopct='%.1f%%', startangle=90
).set(
    title='Species Count of Iris Data'
)
```



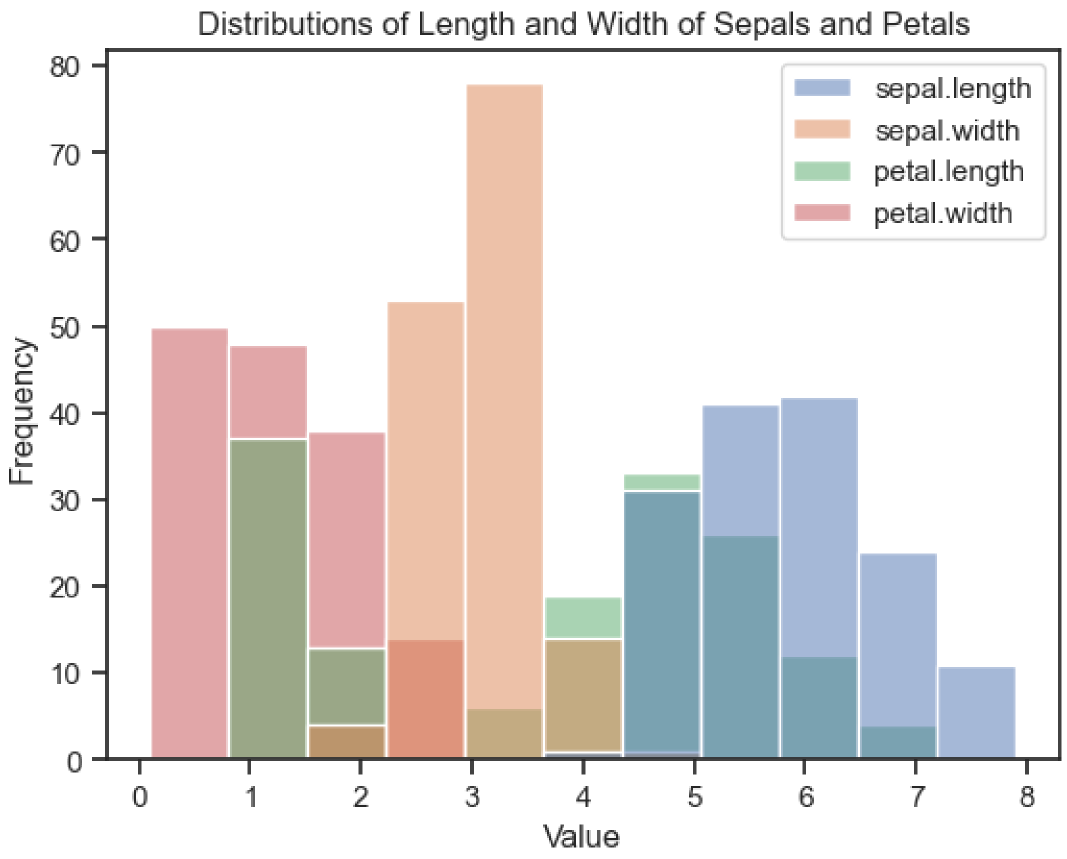
```
[ ]: # Query 4

     # create scatter plot of sepal length-width
     scat_sep = sns.scatterplot(
         data=iris, x='sepal.length', y='sepal.width', hue='variety'
     ).set(
         xlabel='Sepal Length', ylabel='Sepal Width',
         title='Relationship Between Sepal Length and Width'
     )
```

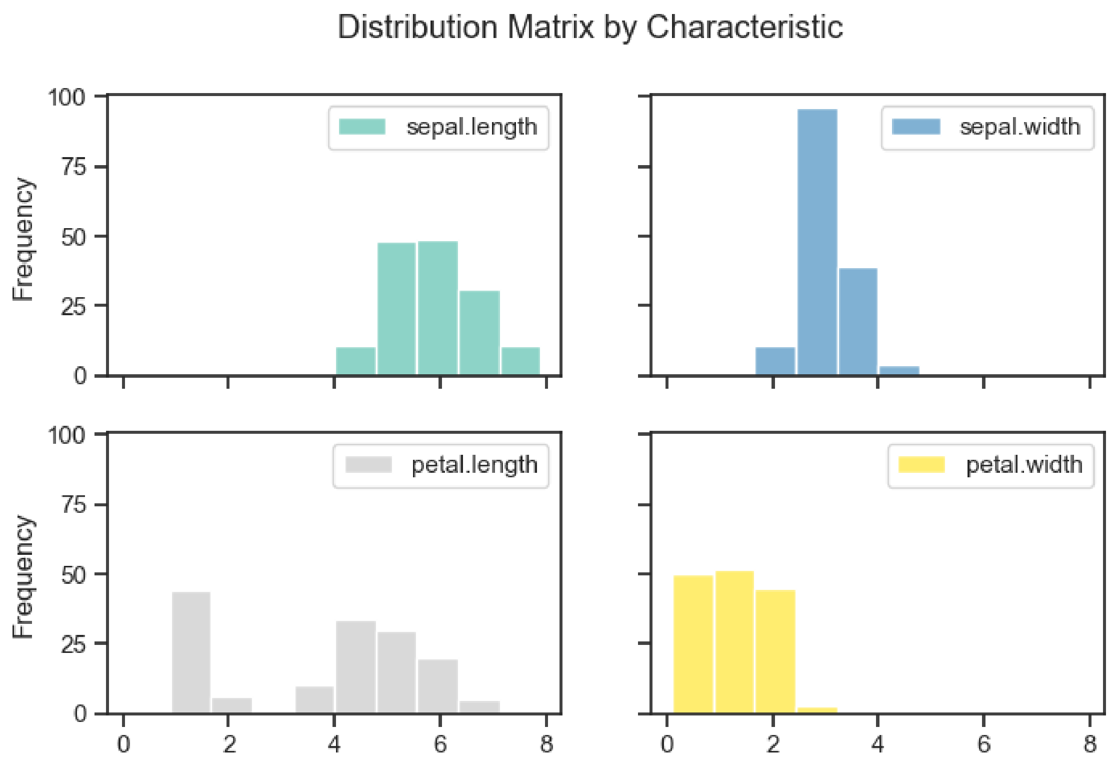


```
[ ]: # Query 5

     # create scatter plot of petal length-width
     scat_pet = sns.scatterplot(
         data=iris, x='petal.length', y='petal.width', hue='variety'
     ).set(
         xlabel='Petal Length', ylabel='Petal Width',
         title='Relationship Between Petal Length and Width'
     )
```

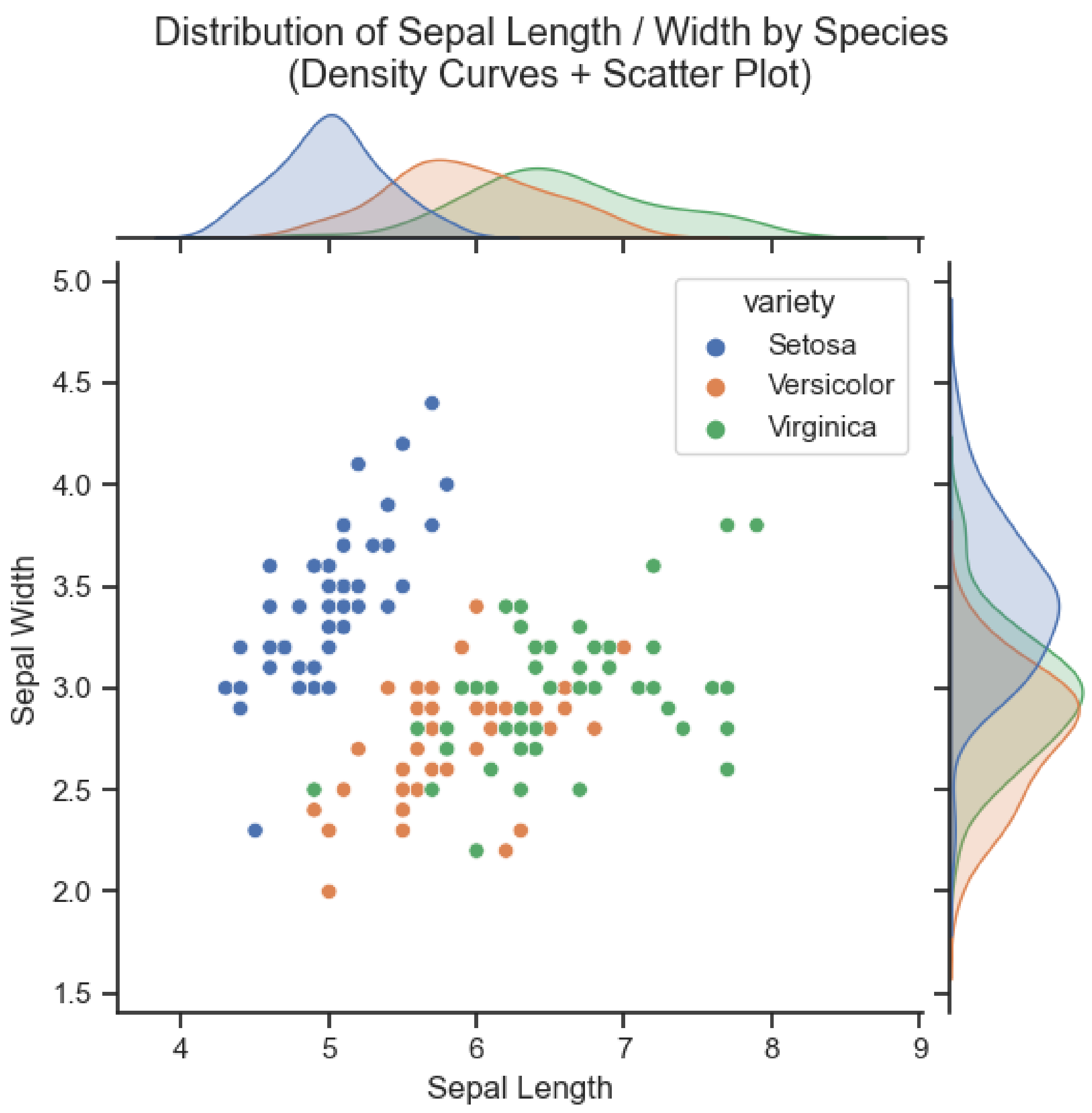


```
[ ]: # Query 6

     # create combined histogram plot of lengths and widths
     hist = sns.histplot(
         data=iris
     ).set(
         xlabel='Value', ylabel='Frequency',
         title='Distributions of Length and Width of Sepals and Petals'
     )

     # create histogram matrix plots of lengths and widths
     hist_matrix = iris_mod.plot(
         kind='hist', subplots=True, figsize=(8, 5),
         layout=[2, 2], colormap='Set3', edgecolor='white',
         sharex=True, sharey=True,
         xlabel='Value', ylabel='Frequency',
         title='Distribution Matrix by Characteristic')
```

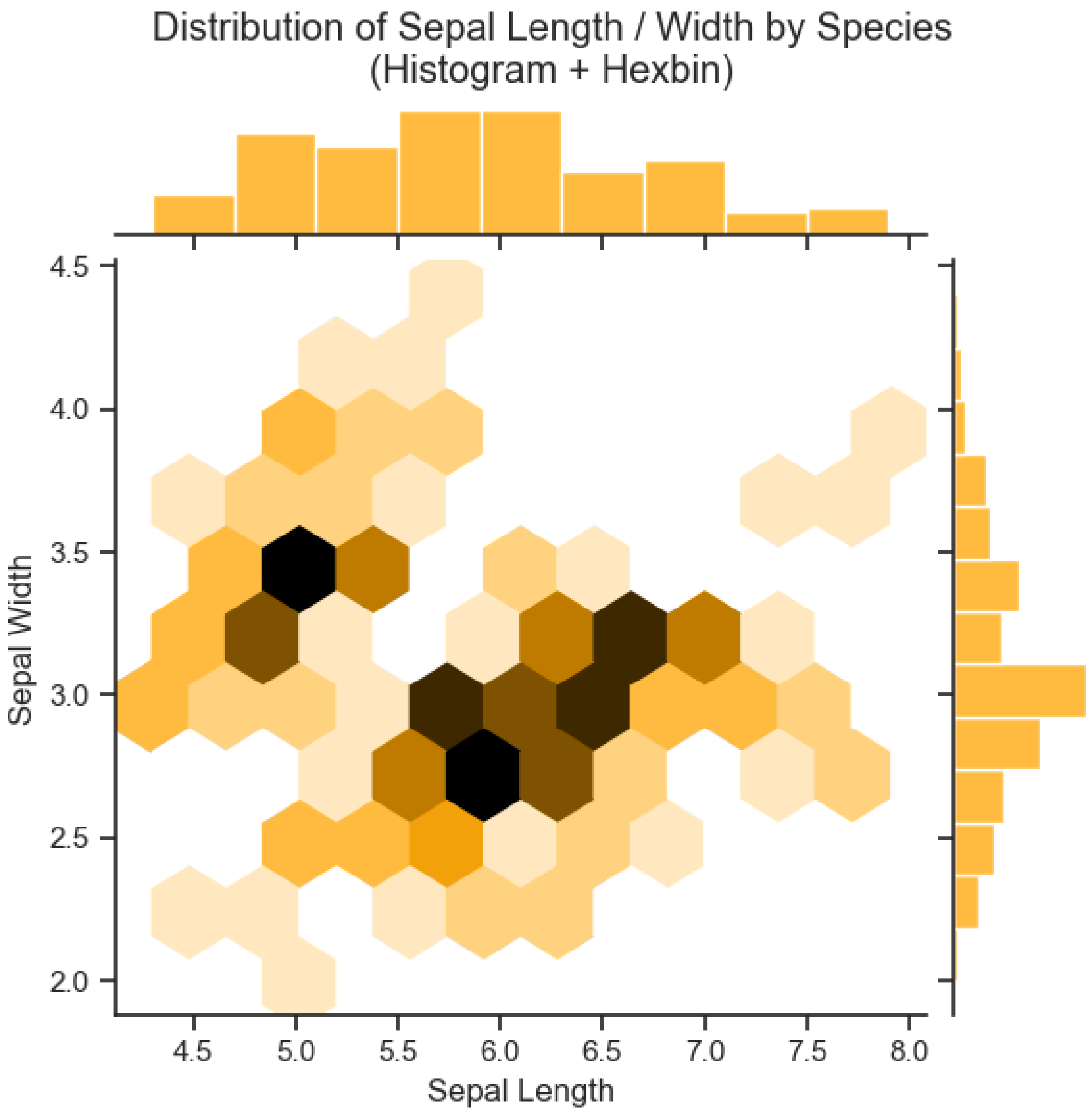

Distributions of Length and Width of Sepals and Petals
sepal.length
sepal.width
petal.length
petal.width
Frequency
Value
0
10
20
30
40
50
60
70
80
0
1
2
3
4
5
6
7
8



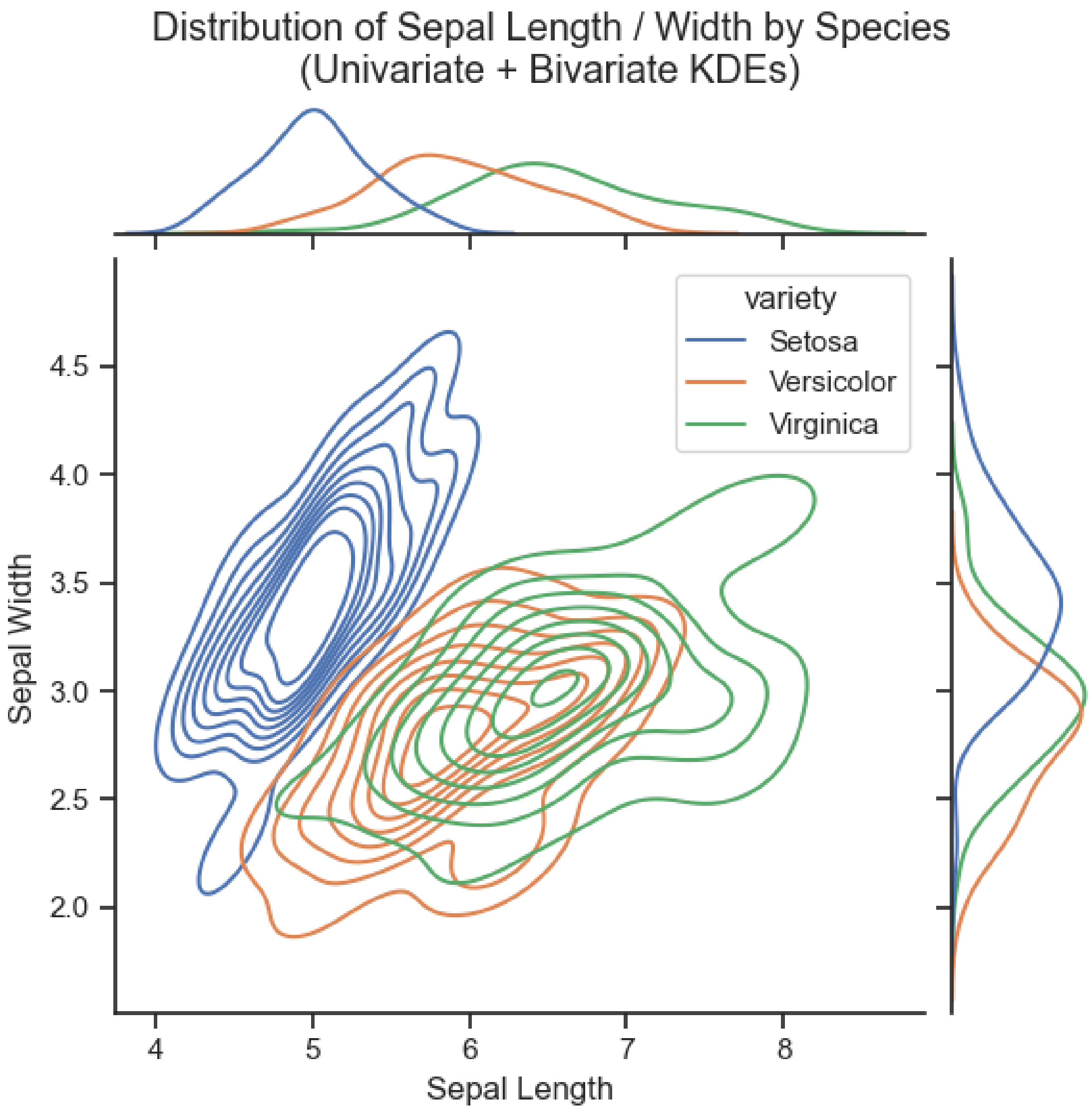
```
[ ]: # Query 7

     # create joint plot of sepal length and width
     joint_scat = sns.jointplot(
         data=iris, x='sepal.length', y='sepal.width', hue='variety'
     )

     joint_scat.set_axis_labels('Sepal Length', 'Sepal Width')
     joint_scat.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                             '(Density Curves + Scatter Plot)')
     joint_scat.fig.subplots_adjust(top=0.9)
```



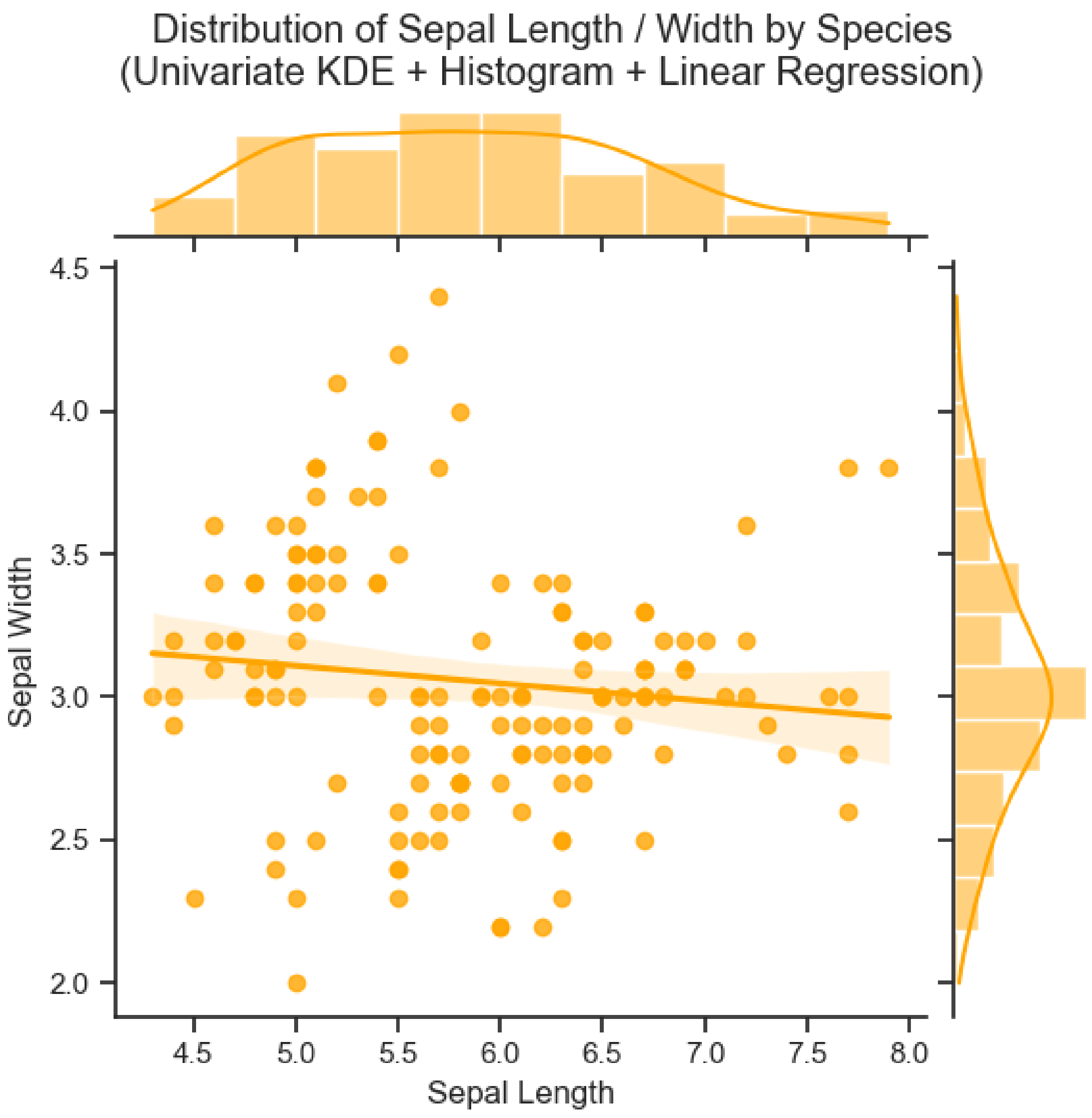
```
[ ]: # Query 8

     # create joint plot of sepal length and width
     joint_hex = sns.jointplot(
         data=iris, x='sepal.length', y='sepal.width', kind='hex', color='orange'
     )

     joint_hex.set_axis_labels('Sepal Length', 'Sepal Width')
     joint_hex.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                            '(Histogram + Hexbin)')
     joint_hex.fig.subplots_adjust(top=0.9)
```



```
[ ]: # Query 9

     # create joint plot of sepal length and width
     joint_kde_hue = sns.jointplot(
         data=iris, x='sepal.length', y='sepal.width', kind='kde', hue='variety'
     )

     joint_kde_hue.set_axis_labels('Sepal Length', 'Sepal Width')
     joint_kde_hue.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                                '(Univariate + Bivariate KDEs)')
     joint_kde_hue.fig.subplots_adjust(top=0.9)
```

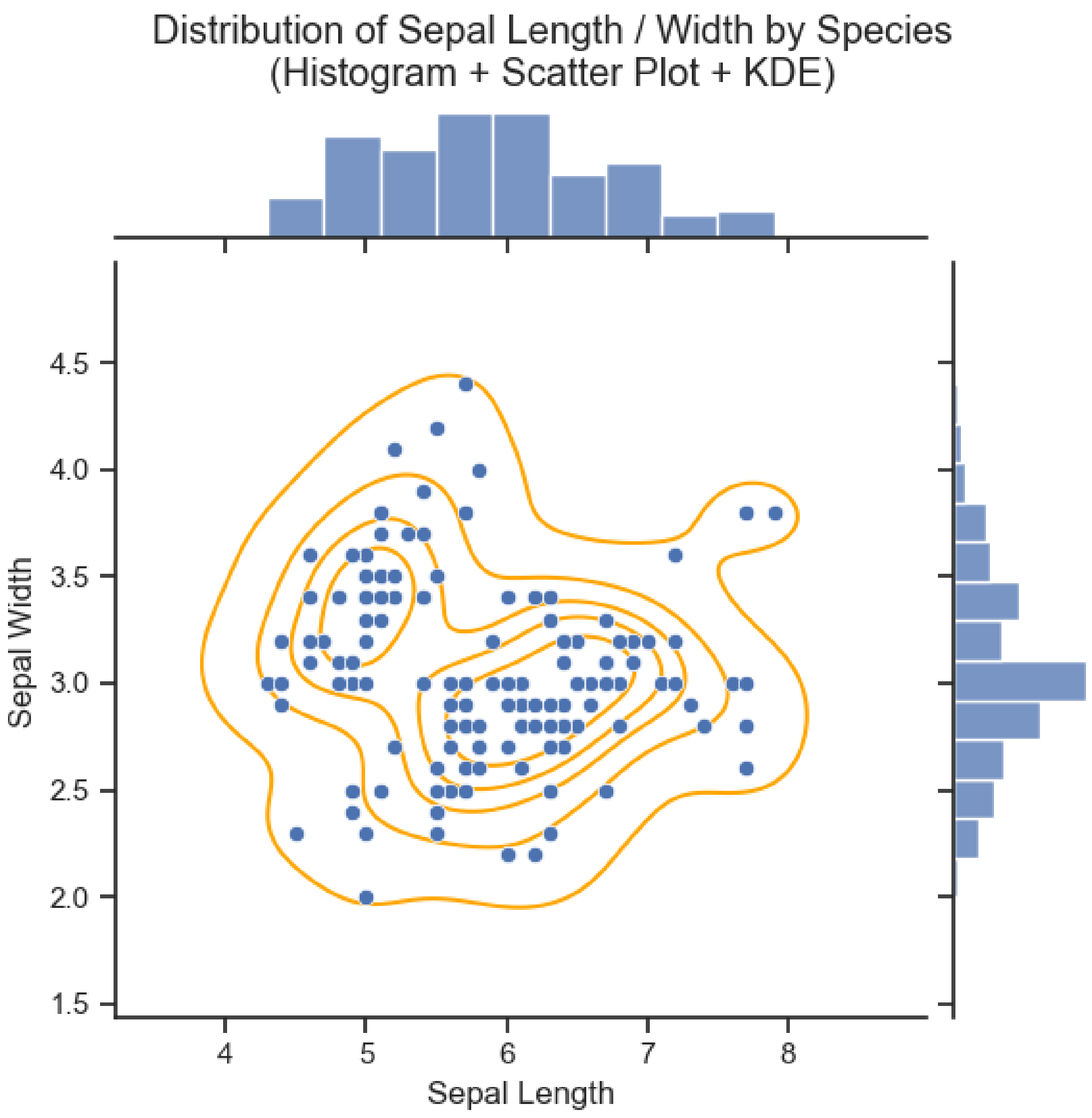


```
[ ]: # Query 10

     # create joint plot of sepal length and width
     joint_reg = sns.jointplot(data=iris, x='sepal.length', y='sepal.width',␣
      ↪kind='reg', color='orange')

     joint_reg.set_axis_labels('Sepal Length', 'Sepal Width')
     joint_reg.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                            '(Univariate KDE + Histogram + Linear Regression)')
     joint_reg.fig.subplots_adjust(top=0.9)
```



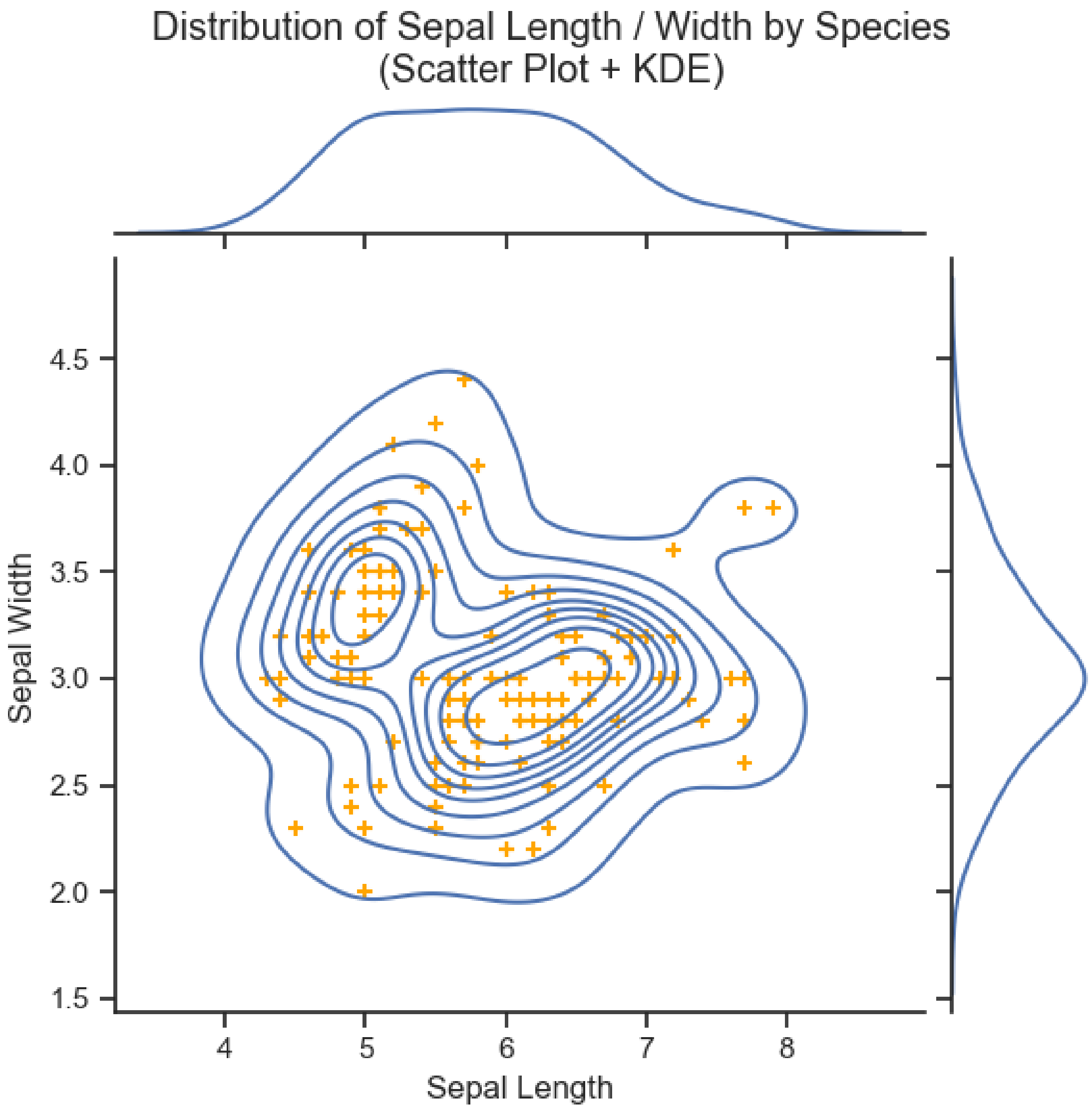
```
[ ]: # Query 11

     # create scatterplot of sepal length and width
     joint_scat = sns.jointplot(data=iris, x='sepal.length', y='sepal.width')

     # add kdeplot player to scatterplot
     joint_scat.plot_joint(sns.kdeplot, color='orange', zorder=0, levels=6)

     # plot characteristics
     joint_scat.set_axis_labels('Sepal Length', 'Sepal Width')
     joint_scat.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                             '(Histogram + Scatter Plot + KDE)')
```

```
joint_scat.fig.subplots_adjust(top=0.9)
```



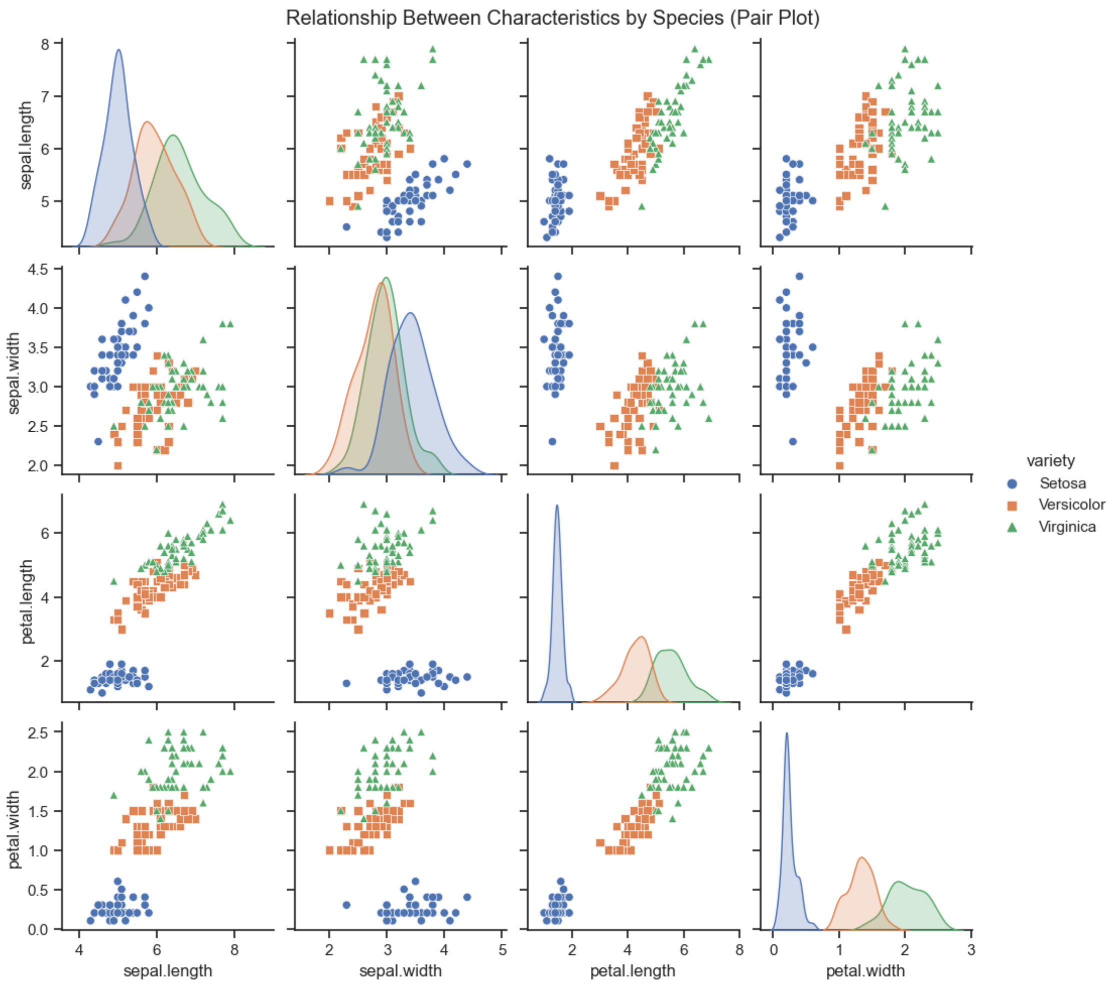
[ ]:
```
# Query 12

# create kdeplot of sepal length and width
joint_kde = sns.jointplot(data=iris, x='sepal.length', y='sepal.width',␣
 ↪kind='kde')

# add scatterplot player to kdeplot
joint_kde.plot_joint(sns.scatterplot, color='orange', marker='+', linewidth=1.5)

# plot characteristics
```

```
joint_kde.set_axis_labels('Sepal Length', 'Sepal Width')
joint_kde.fig.suptitle('Distribution of Sepal Length / Width by Species\n'
                       '(Scatter Plot + KDE)')
joint_kde.fig.subplots_adjust(top=0.9)
```



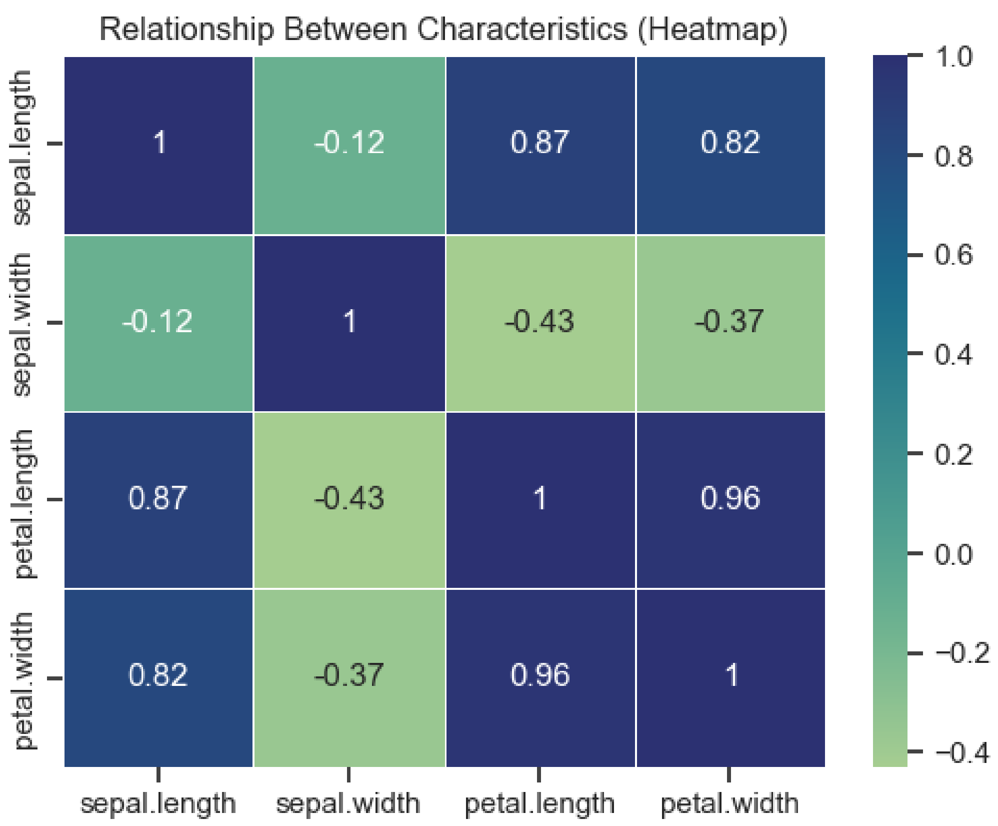
```
[ ]: # Query 13

     # create pairplot of data
     pair = sns.pairplot(
         data=iris, hue='variety', markers=["o", "s", "^"]
     )
```

```
pair.fig.suptitle('Relationship Between Characteristics by Species (Pair Plot)')
pair.fig.subplots_adjust(top=0.95)
```



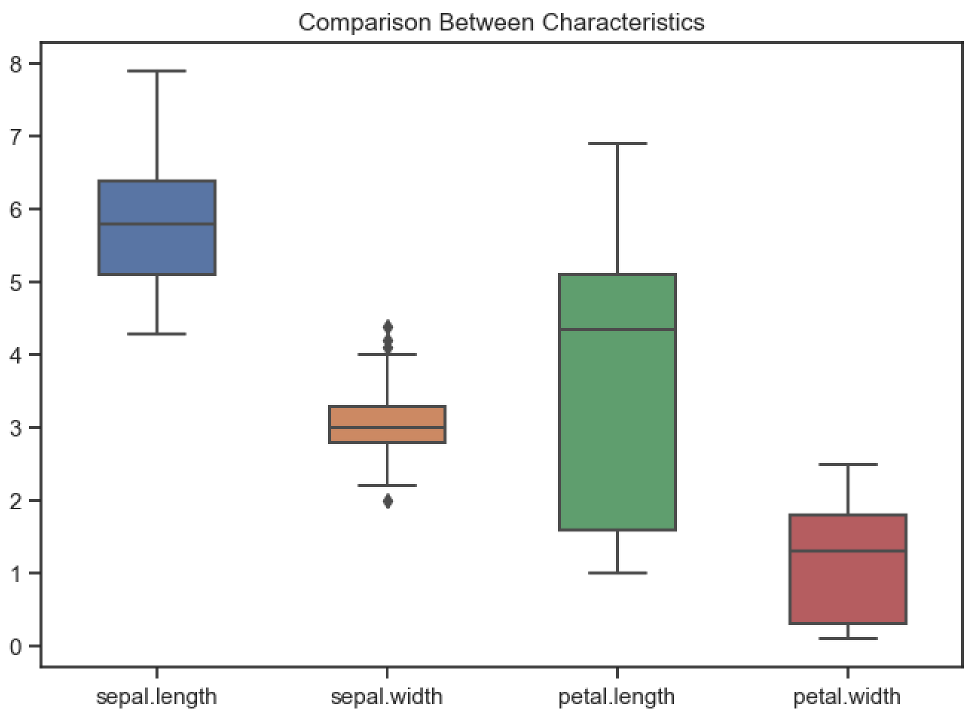
[ ]:
```
# Query 14

# find correlation between variables of data
correlation = iris.iloc[:, 0:4].corr()

# create heatmap of correlation
heat = sns.heatmap(
    correlation, annot=True, linewidth=.5, cmap="crest"
)

plt.title('Relationship Between Characteristics (Heatmap)')
```

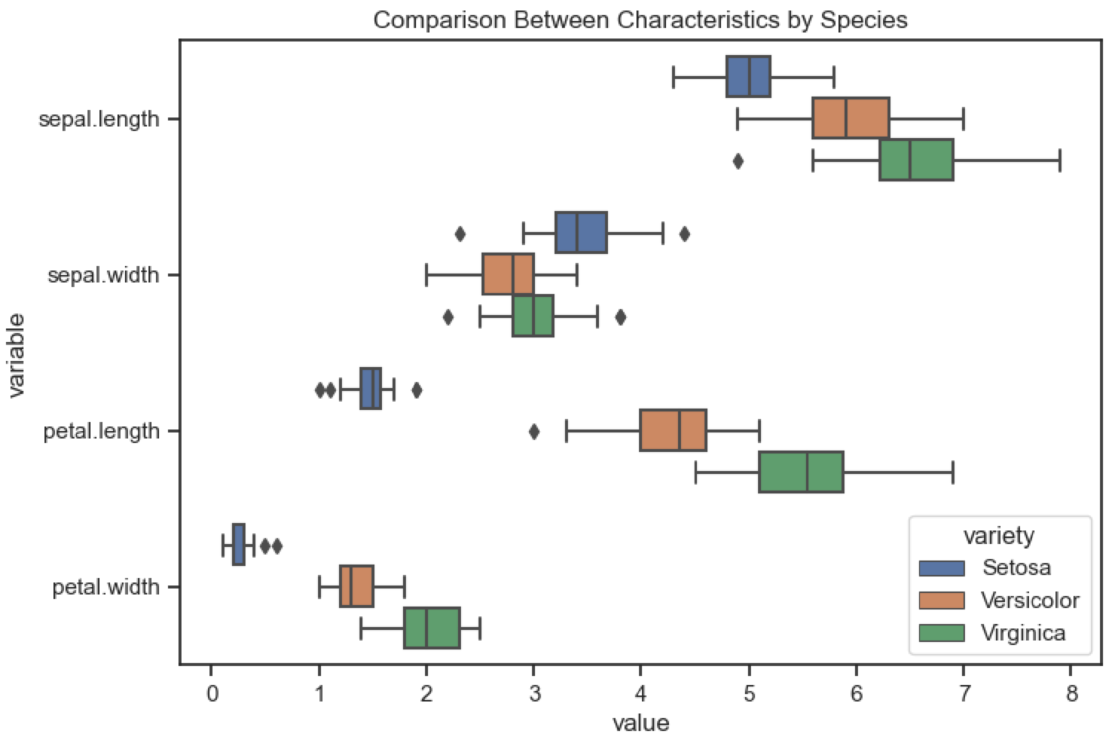
[ ]:
```
Text(0.5, 1.0, 'Relationship Between Characteristics (Heatmap)')
```



```
[ ]: # Query 15

     # create two subplots
     fig, axes = plt.subplots(2, 1, figsize=(8, 12))

     # create box plot of data
     box = sns.boxplot(
         ax=axes[0], data=iris, width=0.5
     )

     # create box plot with melted data
     iris_long = iris.melt(id_vars=['variety'])
     box_hue = sns.boxplot(
         ax=axes[1], data=iris_long, x='value', y='variable', hue='variety'
     )

     box.set_title('Comparison Between Characteristics')
     box_hue.set_title('Comparison Between Characteristics by Species')
```

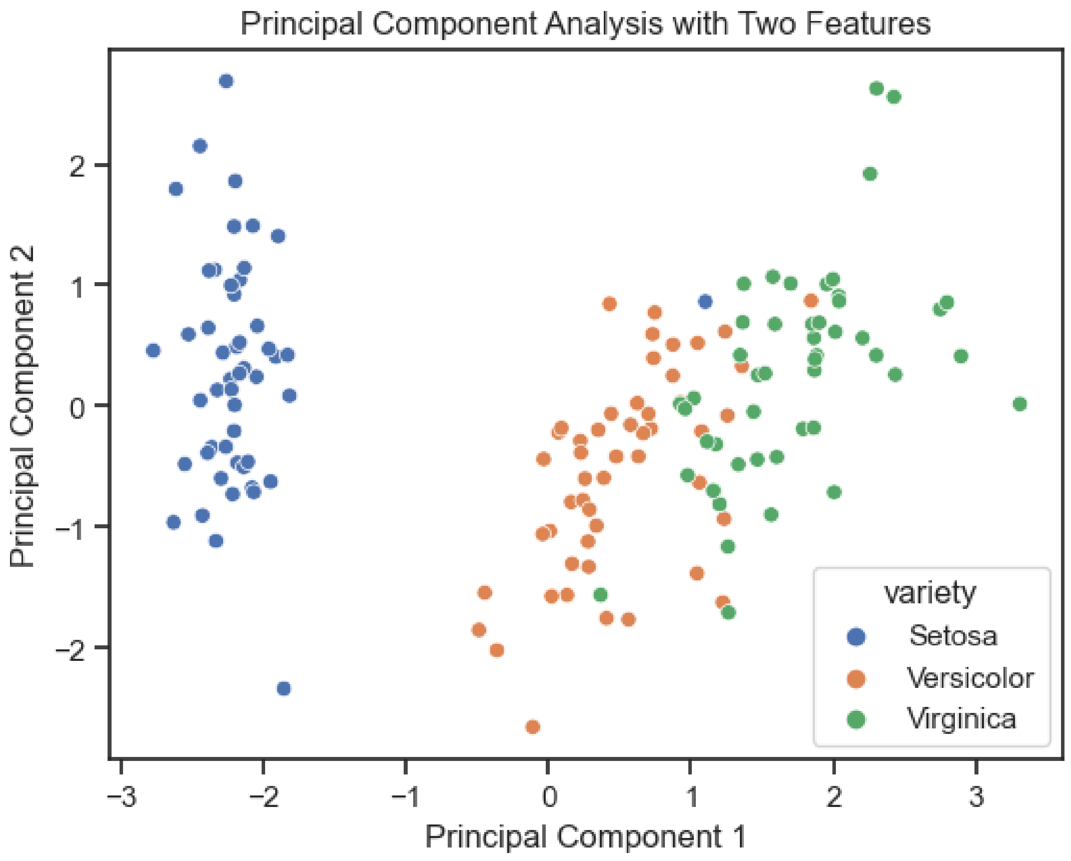
```
[ ]: Text(0.5, 1.0, 'Comparison Between Characteristics by Species')
```


Comparison Between Characteristics
8
7
6
5
4
3
2
1
0
sepal.length
sepal.width
petal.length
petal.width


Comparison Between Characteristics by Species
sepal.length
sepal.width
petal.length
petal.width
variable
0
1
2
3
4
5
6
7
8
value
variety
Setosa
Versicolor
Virginica

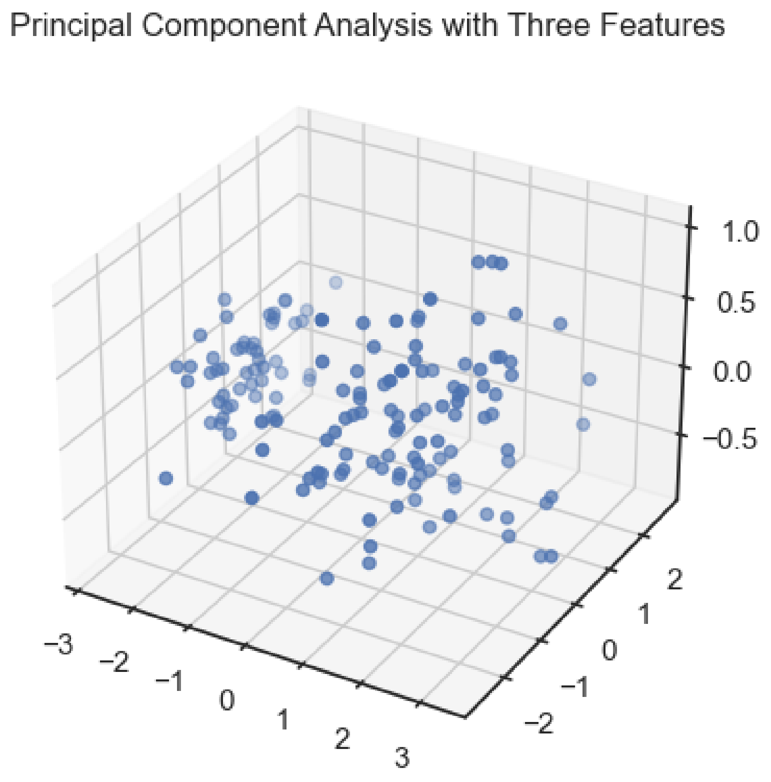
[ ]:
```
# Query 16
# scale feature coefs
features = iris[['sepal.length', 'sepal.width', 'petal.length', 'petal.width']]
scaled_features = StandardScaler().fit_transform(features)

# reduce to two principal components
pca_2 = PCA(n_components=2)
pc_2 = pca_2.fit_transform(scaled_features)
pca2_df = pd.DataFrame(
    data=pc_2, columns=['pca1', 'pca2']
)

# create scatter plot of PCA with two features
pca_2_scat = sns.scatterplot(
    x=pca2_df.pca1, y=pca2_df.pca2, hue=iris.variety
).set(
    xlabel='Principal Component 1', ylabel='Principal Component 2',
    title='Principal Component Analysis with Two Features'
)

"""https://medium.com/swlh/an-intuitive-approach-to-pca-fc4d05c14c19"""
```

```
[ ]: 'https://medium.com/swlh/an-intuitive-approach-to-pca-fc4d05c14c19'
```



```
[ ]: # Query 16-2

     # reduce to three principal components
     pca_3 = PCA(n_components=3)
     pc_3 = pca_3.fit_transform(scaled_features)
     pca3_df = pd.DataFrame(
         data=pc_3, columns=['pca1', 'pca2', 'pca3']
     )

     # create 3D scatter plot of PCA with three features
     fig = plt.figure()
     ax = fig.add_subplot(projection='3d')
     pca_3_scat = ax.scatter(
         pca3_df.pca1, pca3_df.pca2, pca3_df.pca3
     )

     plt.title('Principal Component Analysis with Three Features')
```

```
[ ]: Text(0.5, 0.92, 'Principal Component Analysis with Three Features')
```


Principal Component Analysis with Three Features