TASK 1 : Analyze a Real Dataset

- Goal: Perform basic data analysis and visualization. Example Tools: Python, Pandas, Matplotlib.

- Steps:

1. Load a dataset (e.g., Titanic dataset) using Pandas.
2. Analyze basic statistics (mean, median, etc.).
3. Visualize data (e.g., survival rates by gender) using Matplotlib.

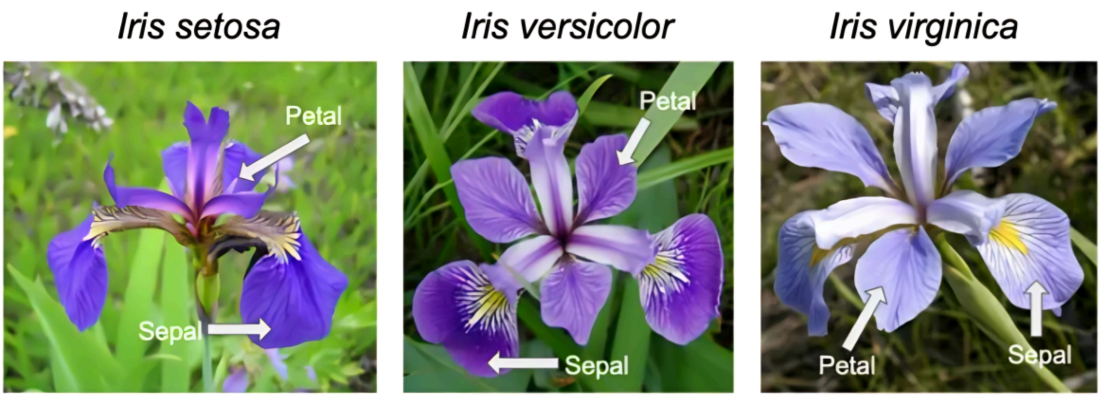
Analyzing The `Iris` Dataset

Importing Libraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
from IPython.display import Image
Image(filename='Iris Flowers Picture.png')
```

Out[2]:



About the Dataset

Description of the data:

- **Id**: Unique number for each row
- **SepalLengthCm**: Length of the sepal (in cm)
- **SepalWidthCm**: Width of the sepal (in cm)
- **PetalLengthCm**: Length of the petal (in cm)
- **PetalWidthCm**: Width of the petal (in cm)
- **Species**: Name of the species

In [3]:

```python
df_iris = pd.read_csv('Iris.csv')

print(30 * '-', 'Dataset', 30 * '-')
print(df_iris.head(5))
print('\n')


print(30 * '-', 'Info', 30 * '-')
print(df_iris.info())
print('\n')

print(30 * '-', 'Describe', 30 * '-')
print(df_iris.describe())
print('\n')

print(30 * '-', 'Null Values', 30 * '-')
print(df_iris.isna().sum())
print('Total Null Values: ', df_iris.isna().sum().sum())
print('\n')

print(30 * '-', 'Unique Values', 30 * '-')
for col in df_iris.columns:
    print(f"Column [{col}]: {df_iris[col].unique()}")
    print(f"Count of Unique Values: {df_iris[col].nunique()}\n\n")
```

```
------------------------------ Dataset ------------------------------
   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


------------------------------ Info ------------------------------
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 6 columns):
 #   Column         Non-Null Count  Dtype
---  ------         --------------  -----
 0   Id             150 non-null    int64
 1   SepalLengthCm  150 non-null    float64
 2   SepalWidthCm   150 non-null    float64
 3   PetalLengthCm  150 non-null    float64
 4   PetalWidthCm   150 non-null    float64
 5   Species        150 non-null    object
dtypes: float64(4), int64(1), object(1)
memory usage: 7.2+ KB
None


------------------------------ Describe ------------------------------
              Id  SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm
count  150.000000     150.000000    150.000000     150.000000    150.000000
mean    75.500000       5.843333      3.054000       3.758667      1.198667
std     43.445368       0.828066      0.433594       1.764420      0.763161
min      1.000000       4.300000      2.000000       1.000000      0.100000
25%     38.250000       5.100000      2.800000       1.600000      0.300000
50%     75.500000       5.800000      3.000000       4.350000      1.300000
75%    112.750000       6.400000      3.300000       5.100000      1.800000
max    150.000000       7.900000      4.400000       6.900000      2.500000


------------------------------ Null Values ------------------------------
Id               0
SepalLengthCm    0
SepalWidthCm     0
PetalLengthCm    0
PetalWidthCm     0
Species          0
dtype: int64
Total Null Values:  0


------------------------------ Unique Values ------------------------------
Column [Id]: [  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17
18
  19  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36
  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54
  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72
  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
  91  92  93  94  95  96  97  98  99 100 101 102 103 104 105 106 107 108
 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126
 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144
 145 146 147 148 149 150]
```

```
Count of Unique Values: 150


Column [SepalLengthCm]: [5.1 4.9 4.7 4.6 5.  5.4 4.4 4.8 4.3 5.8 5.7 5.2 5.5 4.5
5.3 7.  6.4 6.9
 6.5 6.3 6.6 5.9 6.  6.1 5.6 6.7 6.2 6.8 7.1 7.6 7.3 7.2 7.7 7.4 7.9]
Count of Unique Values: 35


Column [SepalWidthCm]: [3.5 3.  3.2 3.1 3.6 3.9 3.4 2.9 3.7 4.  4.4 3.8 3.3 4.1
4.2 2.3 2.8 2.4
 2.7 2.  2.2 2.5 2.6]
Count of Unique Values: 23


Column [PetalLengthCm]: [1.4 1.3 1.5 1.7 1.6 1.1 1.2 1.  1.9 4.7 4.5 4.9 4.  4.6
3.3 3.9 3.5 4.2
 3.6 4.4 4.1 4.8 4.3 5.  3.8 3.7 5.1 3.  6.  5.9 5.6 5.8 6.6 6.3 6.1 5.3
 5.5 6.7 6.9 5.7 6.4 5.4 5.2]
Count of Unique Values: 43


Column [PetalWidthCm]: [0.2 0.4 0.3 0.1 0.5 0.6 1.4 1.5 1.3 1.6 1.  1.1 1.8 1.2
1.7 2.5 1.9 2.1
 2.2 2.  2.4 2.3]
Count of Unique Values: 22


Column [Species]: ['Iris-setosa' 'Iris-versicolor' 'Iris-virginica']
Count of Unique Values: 3
```

Exploratory Data Analysis (EDA)

--> We will drop the Column `Id` as it not needed in our EDA

In [4]:
```python
df_iris.drop(columns='Id', axis=1, inplace=True)
```

In [5]:
```python
df_iris.head(5)
```

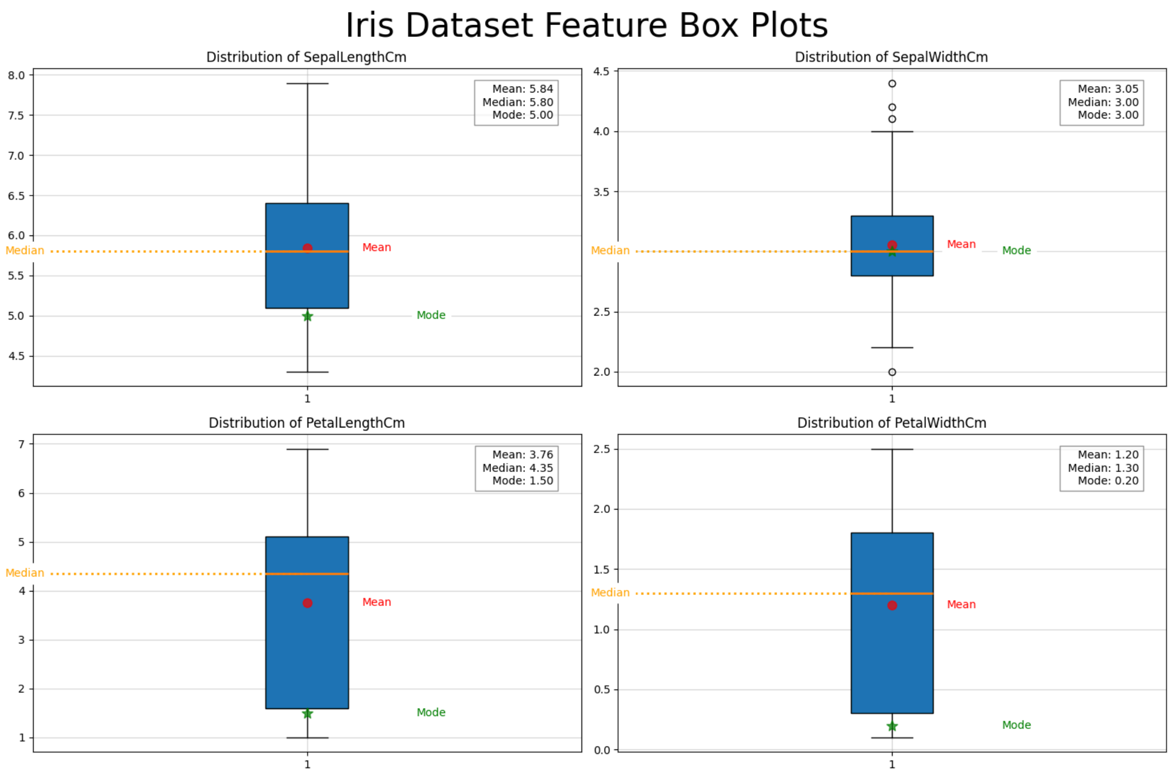
Out[5]:

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	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

Statistical Analysis

In [6]:

```python
def box_plt(df, ax, col):
    ax.boxplot(x=df[col], medianprops={'linewidth': 2}, showmeans=False, patch_a
    ax.set_title(f"Distribution of {col}")
    ax.grid(alpha=0.5)

    median = df[col].median()
    mean = df[col].mean()
    mode_val = df[col].mode()[0]

    # Statistical Value Box
    ax.text(0.95, 0.95, f"Mean: {mean:.2f}\n Median: {median:.2f}\nMode: {mode_v

    ax.axhline(median, color='orange', linestyle=':', linewidth=2, alpha=1, xmax
    ax.text(0.45, median, 'Median', ha='left', va='center', color='orange', back

    ax.plot(1, mean, 'ro', markersize=8, alpha=0.7) #Mean marker
    ax.text(1.1, mean, 'Mean', ha='left', va='center', color='red', backgroundcc

    ax.plot(1.0, mode_val, 'g*', markersize=10, alpha=0.7)  #Mode marker
    ax.text(1.2, mode_val, 'Mode', ha='left', va='center', color='green', backgr

fig = plt.figure(figsize=(15,10))
fig.suptitle("Iris Dataset Feature Box Plots", size=30)

for i in range(1, len(df_iris.columns)):
    ax = fig.add_subplot(2, 2, i)
    box_plt(df_iris, ax, df_iris.columns[i - 1])

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



Observations:

1. SepalLengthCm: Near-symmetric distribution (Mean ≈ Median), but the Mode (5.0) is slightly lower, indicating mild right-skew with clustering at smaller values.

2. SepalWidthCm: Perfect alignment of Mean, Median, and Mode (3.0) suggests symmetry, but outliers are present (visible in boxplot).

3. PetalLengthCm: Significant right-skew (Mean=3.76 < Median=4.35), with Mode (1.5) far left, implying most data clusters at lower values with a long right tail.

4. PetalWidthCm: No outliers detected; distribution appears unimodal but skewed (Mode=0.2 differs from Median=1.3).

Note:

1. if(Mean = Median = Mode), then Symmetric Data

2. if(Mean > Median > Mode), then Postively(Right) Skewed

3. if(Mean < Median < Mode), then Negatively(Left) Skewed

Skewness of Data

In [7]:
```
def get_skewness(df):
    print("Skewness in Dataset")
    for col in df.select_dtypes(include=['number']):

        #direction
        if df[col].skew() > 0:
            direction = "Skewed Right"
        elif df[col].skew() < 0:
            direction = "Skewed Left"
        else:
            direction = "Symmtrical Data"

        #magnitude
        if abs(df[col].skew()) > 1:
            magnitude='Highly'
        else:
            magnitude='Slightly'
        print(f"{col}: {df[col].skew():+.4f}, {magnitude} {direction}")

get_skewness(df_iris)
```

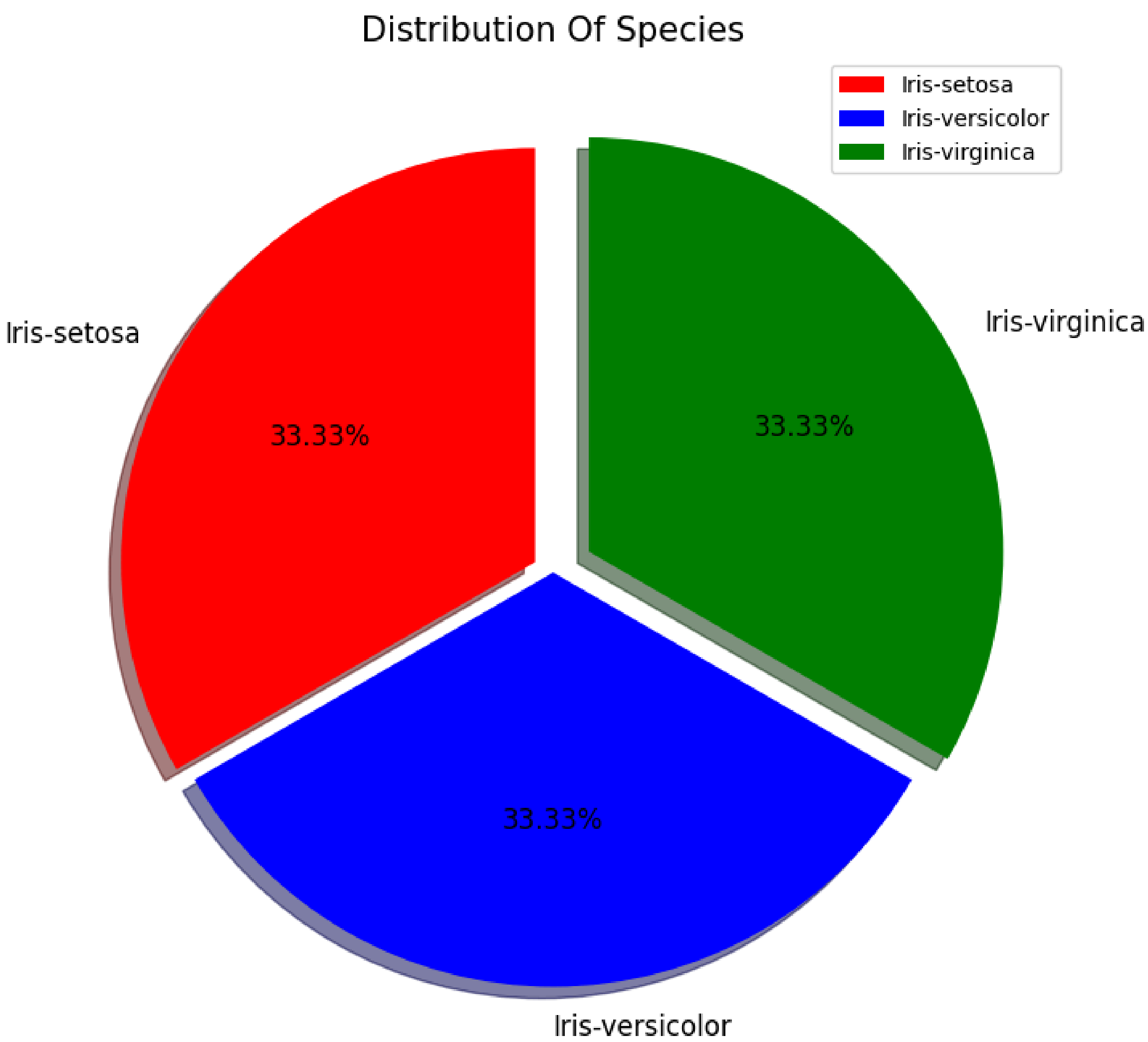
```
Skewness in Dataset
SepalLengthCm: +0.3149, Slightly Skewed Right
SepalWidthCm: +0.3341, Slightly Skewed Right
PetalLengthCm: -0.2745, Slightly Skewed Left
PetalWidthCm: -0.1050, Slightly Skewed Left
```

Distribution of Species

In [8]:
```
df_iris['Species'].value_counts()
```

Out[8]:
```
Species
Iris-setosa        50
Iris-versicolor    50
Iris-virginica     50
Name: count, dtype: int64
```

In [9]:
```
Species = df_iris['Species'].unique()

plt.figure(figsize=(10, 7))
plt.pie(x=df_iris['Species'].value_counts(), labels=Species, autopct='%.2f%%', e
plt.title("Distribution Of Species", fontsize=15)
plt.legend()
plt.tight_layout()
plt.show()
```



Observation: All classes are equally balanced

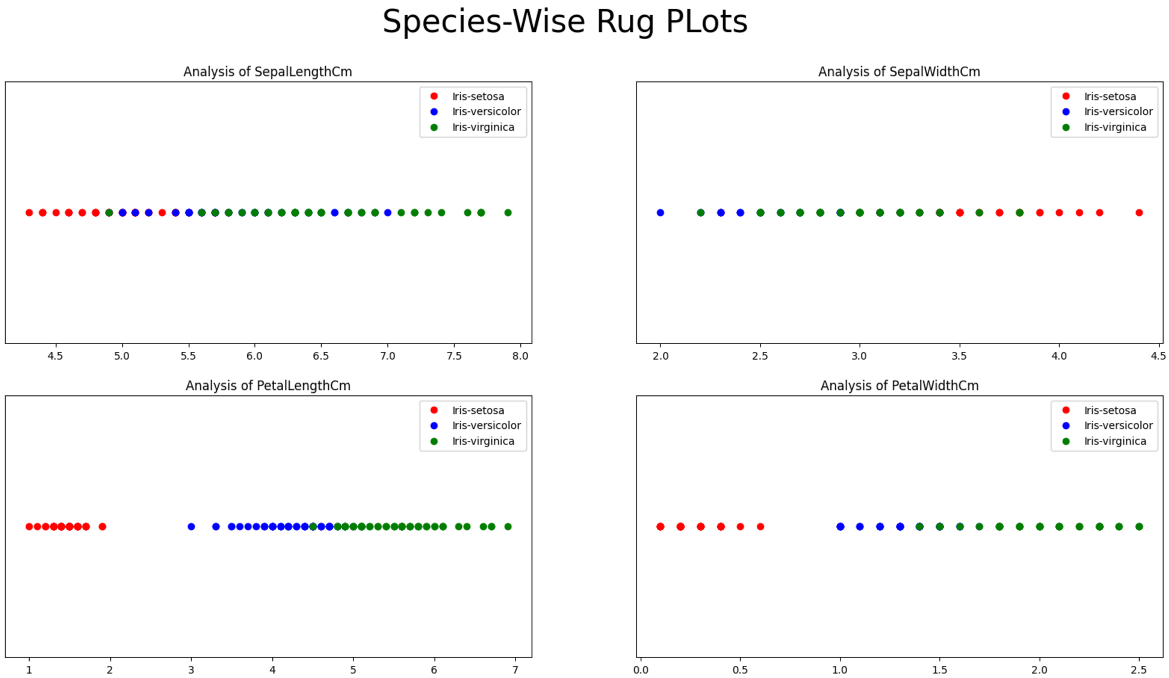
Species-Wise Analysis

In [10]:
```
(df_iris.Species.unique())
```

Out[10]:
```
array(['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'], dtype=object)
```

Rug Plots

In [11]:
```
fig = plt.figure(figsize=(20,10))
Types = df_iris['Species'].unique()

def rug_plot(df, ax, col):
    marker=['ro','bo','go']
    index = 0
    for Type in Types:
        ax.plot((df[df['Species'] == Type])[col], np.zeros_like((df[df['Species'
        index = index + 1

    ax.set_title(f"Analysis of {col}")
    ax.get_yaxis().set_visible(False)
    ax.legend()

fig.suptitle("Species-Wise Rug PLots", size=30)
for i in range(1, len(df_iris.columns)):
    ax = fig.add_subplot(2,2,i)
    rug_plot(df_iris, ax, df_iris.columns[i-1])


plt.show()
```



Observations:

- `SepalLengthCm` : Iris-setosa has the shortest sepals (≈ 4.3 – 4.8 cm) with one red outlier nudging 5.4 cm. Iris-versicolor occupies the middle band (5.0 – 5.5 cm). Iris-virginica shows the longest sepals, often ≥ 6 cm and approaching 8 cm.

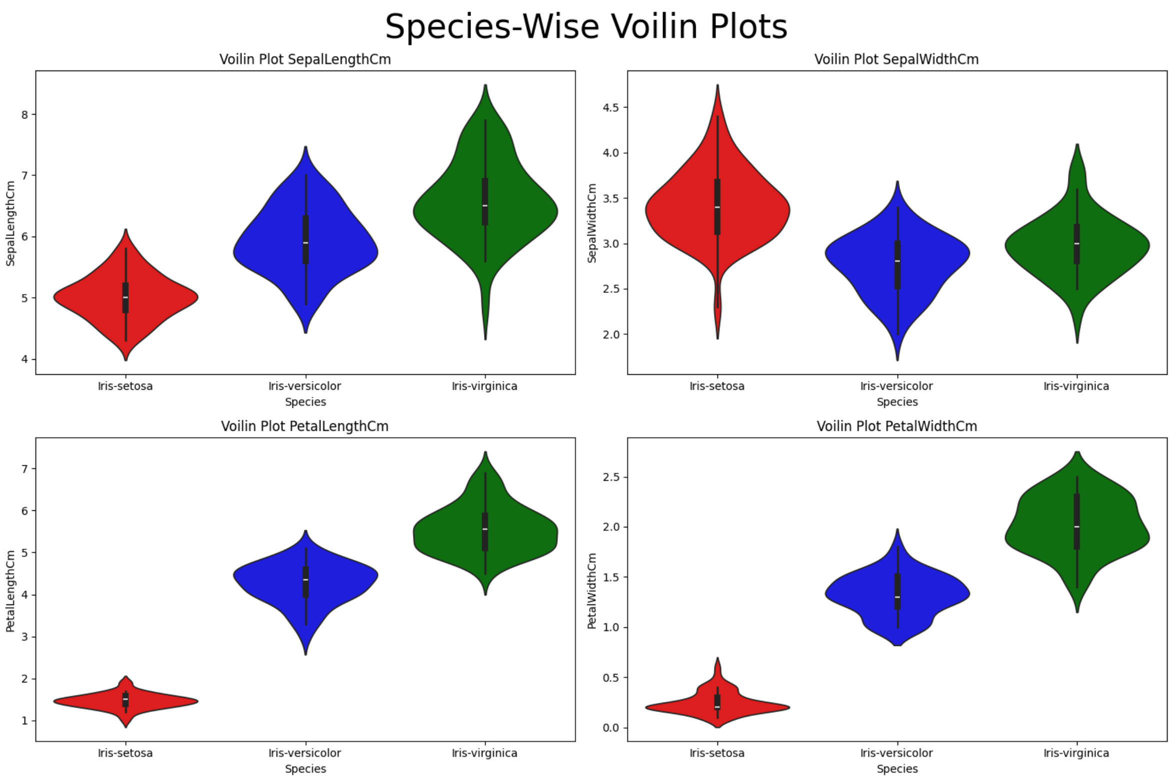
- `SepalWidthCm` : Iris-versicolor exhibits the narrowest sepals (≈ 2.0 – 2.4 cm). Widths ≥ 4 cm are seen only in Iris-setosa. In the 2.3 – 3.8 cm range lies Iris-virginica.

- `PetalLengthCm` : Iris-setosa petals never exceed 2 cm. Iris-versicolor petals cluster around 3 – 5 cm. Iris-virginica has the longest petals, generally ≥ 4.5 cm and stretching to ~7 cm.

- `PetalWidthCm` : Iris-setosa petals are the thinnest (≈ 0.1 – 0.6 cm). Iris-versicolor sits mid-range (≈ 1.0 – 1.3 cm). Iris-virginica boasts the widest petals, typically > 1.5 cm and up to ~2.5 cm.

Voilin Plots

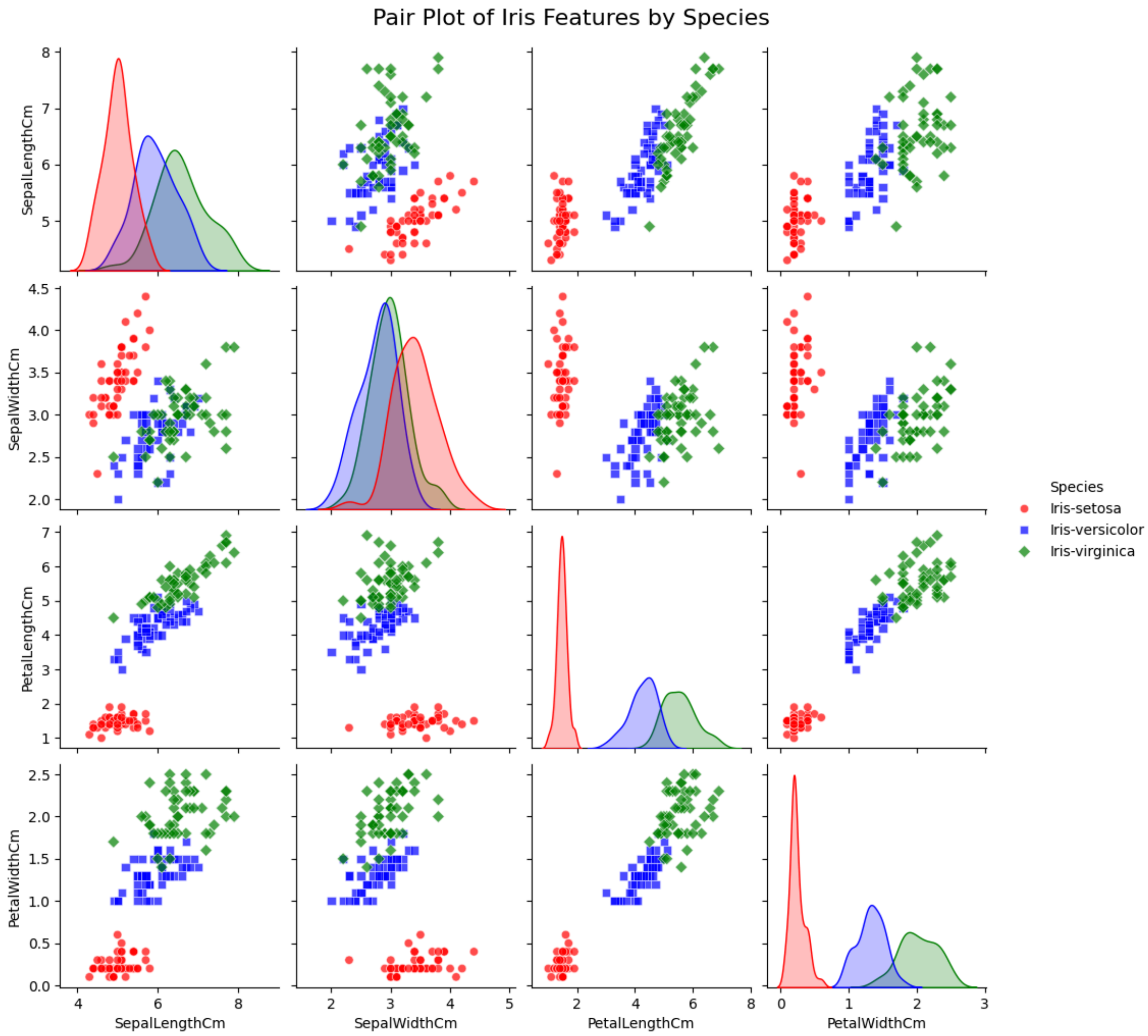
In [12]:
```
fig = plt.figure(figsize=(15,10))
Species = df_iris['Species'].unique()

def voilin_plot(df, ax, col):
    marker=['red', 'blue', 'green']
    sns.violinplot(data=df, x='Species', y=col, hue='Species', palette=marker, a

    plt.title(f"Voilin Plot {col}")

fig.suptitle("Species-Wise Voilin Plots", size=30)
for i in range(1, len(df_iris.columns)):
    ax = fig.add_subplot(2, 2, i)
    voilin_plot(df_iris, ax, df_iris.columns[i-1])

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



Pair PLot

In [13]:
```
plt.figure(figsize=(12, 10))
sns.pairplot(df_iris, hue='Species', palette=['red', 'blue', 'green'], markers=[
plt.suptitle('Pair Plot of Iris Features by Species', y=1.02, fontsize=16)
plt.show()
```

```
<Figure size 1200x1000 with 0 Axes>
```



`Analytical Interpretation of Pairplot`

- The pairplot provides a comprehensive view of pairwise relationships between the numerical features in the Iris dataset, segmented by species.

`Class Separability`

- Iris-setosa is linearly separable from the other two species in nearly all feature spaces, particularly when petal measurements are involved.
- Iris-versicolor and Iris-virginica exhibit partial overlap, especially in sepal dimensions, but show distinguishable clusters in petal-related feature spaces.

`Univariate Distributions (Diagonal)`

- The petal length and petal width features demonstrate distinct, unimodal distributions for each species, indicating high discriminative power.
- Sepal width shows considerable distributional overlap across classes, suggesting limited effectiveness for class separation in isolation.

`Bivariate Relationships (Off-diagonal)`

- PetalLength vs PetalWidth exhibits a strong positive correlation with minimal class overlap — a highly informative feature pair for classification models.

- PetalLength vs SepalLength also indicates a positive correlation with reasonable inter-species separation.
- SepalLength vs SepalWidth shows weaker class discrimination and should be deprioritized in feature selection for modeling tasks.

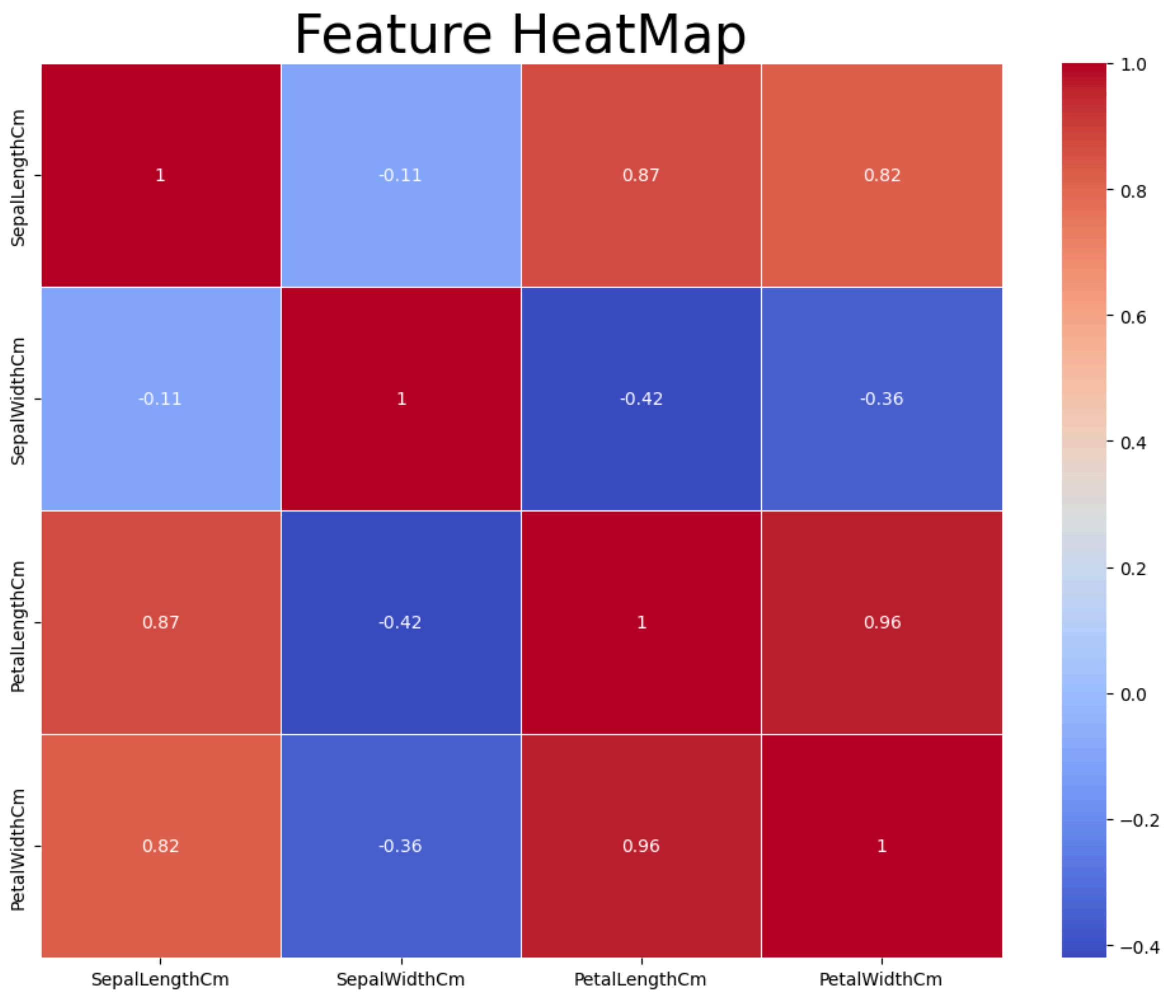
Describe Features By Species

In [14]:
```
for s in Species:
    df_temp = df_iris[df_iris['Species'] == s]
    print("\n" + (30*"-") + s.upper() + ("-"*30))
    print(df_temp.describe())
```

```
------------------------------IRIS-SETOSA------------------------------
       SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm
count       50.00000     50.000000      50.000000      50.00000
mean         5.00600      3.418000       1.464000       0.24400
std          0.35249      0.381024       0.173511       0.10721
min          4.30000      2.300000       1.000000       0.10000
25%          4.80000      3.125000       1.400000       0.20000
50%          5.00000      3.400000       1.500000       0.20000
75%          5.20000      3.675000       1.575000       0.30000
max          5.80000      4.400000       1.900000       0.60000

------------------------------IRIS-VERSICOLOR------------------------------
       SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm
count      50.000000     50.000000      50.000000     50.000000
mean        5.936000      2.770000       4.260000      1.326000
std         0.516171      0.313798       0.469911      0.197753
min         4.900000      2.000000       3.000000      1.000000
25%         5.600000      2.525000       4.000000      1.200000
50%         5.900000      2.800000       4.350000      1.300000
75%         6.300000      3.000000       4.600000      1.500000
max         7.000000      3.400000       5.100000      1.800000

------------------------------IRIS-VIRGINICA------------------------------
       SepalLengthCm  SepalWidthCm  PetalLengthCm  PetalWidthCm
count       50.00000     50.000000      50.000000      50.00000
mean         6.58800      2.974000       5.552000       2.02600
std          0.63588      0.322497       0.551895       0.27465
min          4.90000      2.200000       4.500000       1.40000
25%          6.22500      2.800000       5.100000       1.80000
50%          6.50000      3.000000       5.550000       2.00000
75%          6.90000      3.175000       5.875000       2.30000
max          7.90000      3.800000       6.900000       2.50000
```

Correlation Matrix

In [15]:
```
df_numeric = df_iris.select_dtypes(include=['number'])
plt.figure(figsize=(10, 8))

heatmap=sns.heatmap(data=df_numeric.corr(), annot=True, cmap='coolwarm', linewid

plt.title("Feature HeatMap", size=30)
plt.tight_layout()
plt.show()
```



Advanced Statistical Analysis

Normality Tests

Shapiro-Wilk Test For Normality Check

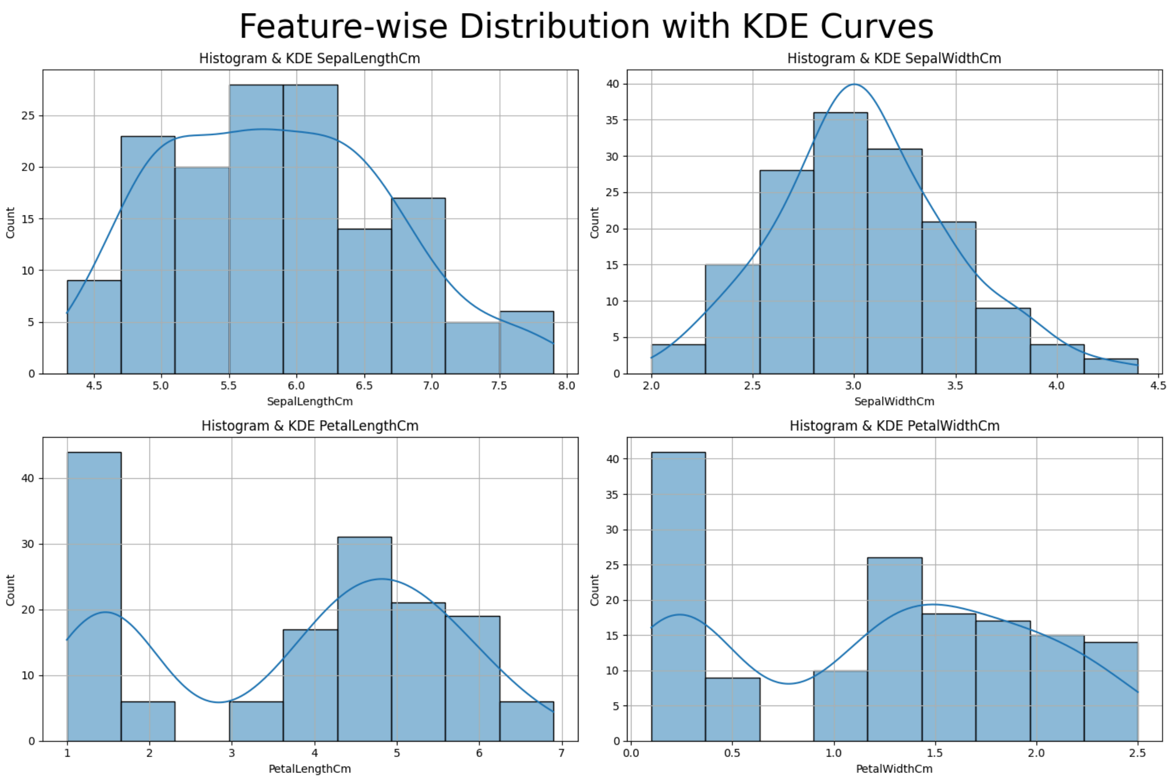
In [16]:
```
from scipy import stats
features = df_iris.columns[0:4]

print("NORMALITY TESTS (Shapiro-Wilk):")
print("-" * 40)
for feature in features:
    stat, p_value = stats.shapiro(df_iris[feature])
    print(f"{feature}: Statistic={stat:.4f}, p-value={p_value:.4f}")
    if p_value > 0.05:
        print(f"  → {feature} appears to be normally distributed") # Null Hypoth
    else:
        print(f"  → {feature} does not appear to be normally distributed") # Alt
```

```
NORMALITY TESTS (Shapiro-Wilk):
----------------------------------------
SepalLengthCm: Statistic=0.9761, p-value=0.0102
  → SepalLengthCm does not appear to be normally distributed
SepalWidthCm: Statistic=0.9838, p-value=0.0752
  → SepalWidthCm appears to be normally distributed
PetalLengthCm: Statistic=0.8764, p-value=0.0000
  → PetalLengthCm does not appear to be normally distributed
PetalWidthCm: Statistic=0.9026, p-value=0.0000
  → PetalWidthCm does not appear to be normally distributed
```

Histograms For Normality Check

In [17]:

```python
fig = plt.figure(figsize=(15, 10))

def draw_hist(df, col, ax):
    n = len(df[col])
    sns.histplot(x=df[col], ax=ax, kde=True, bins=int(np.ceil(np.log2(n) + 1)))
    plt.title(f"Histogram & KDE {col}")
    plt.grid()



for i in range(1, len(df_iris.columns)):
    ax = fig.add_subplot(2, 2, i)
    draw_hist(df_iris, features[i-1], ax)

plt.suptitle("Feature-wise Distribution with KDE Curves", size=30)
plt.tight_layout()
plt.show()
```



Outlier Detection

Note:

- IQR when not normal data
- Z_scores method when data is normally distributed

In [18]:
```
def outlier_IQR(df, col):
    Q1 = df[col].quantile(0.25)
    Q3 = df[col].quantile(0.75)
    IQR = Q3 - Q1

    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    outliers = df[(df[col] < lower_bound) | (df[col] > upper_bound)]
    return outliers

from scipy.stats import zscore
def outlier_Zscore(df, col):
    Zscores = stats.zscore(df[col])
    outliers = df[abs(Zscores) > 3]
    return outliers


print(f"{'='*10} IQR Method {'='*10}")
for col in features:
    outliers = outlier_IQR(df_iris, col)
    print(f"\n--> Column: {col} | Outliers Found: {len(outliers)}")
    if not outliers.empty:
        print(outliers[[col]])

print(f"\n\n\n{'='*10} Z-Score Method {'='*10}")
for col in features:
    outliers = outlier_Zscore(df_iris, col)
    print(f"\n--> Column: {col} | Outliers Found: {len(outliers)}")
    if not outliers.empty:
        print(outliers[[col]])
```

```
========== IQR Method ==========

--> Column: SepalLengthCm | Outliers Found: 0

--> Column: SepalWidthCm | Outliers Found: 4
    SepalWidthCm
15           4.4
32           4.1
33           4.2
60           2.0

--> Column: PetalLengthCm | Outliers Found: 0

--> Column: PetalWidthCm | Outliers Found: 0



========== Z-Score Method ==========

--> Column: SepalLengthCm | Outliers Found: 0

--> Column: SepalWidthCm | Outliers Found: 1
    SepalWidthCm
15           4.4

--> Column: PetalLengthCm | Outliers Found: 0

--> Column: PetalWidthCm | Outliers Found: 0
```

- Since `SepalWidthCm` follows a `normal distribution`, we go with the `Z-score` method for outlier detection.

ANOVA TESTS (Between Species)

In [19]:
```python
for feature in features:
    setosa = df_iris[df_iris['Species'] == 'Iris-setosa'][feature]
    versicolor = df_iris[df_iris['Species'] == 'Iris-versicolor'][feature]
    virginica = df_iris[df_iris['Species'] == 'Iris-virginica'][feature]

    f_stat, p_value = stats.f_oneway(setosa, versicolor, virginica)
    print(f"{feature}: F-statistic={f_stat:.4f}, p-value={p_value:.4f}")
    if p_value < 0.05:
        print(f"  → Significant difference between species for {feature}") # Alt
    else:
        print(f"  → No significant difference between species for {feature}") #
    print("-" * 40)
```

```
SepalLengthCm: F-statistic=119.2645, p-value=0.0000
  → Significant difference between species for SepalLengthCm
----------------------------------------
SepalWidthCm: F-statistic=47.3645, p-value=0.0000
  → Significant difference between species for SepalWidthCm
----------------------------------------
PetalLengthCm: F-statistic=1179.0343, p-value=0.0000
  → Significant difference between species for PetalLengthCm
----------------------------------------
PetalWidthCm: F-statistic=959.3244, p-value=0.0000
  → Significant difference between species for PetalWidthCm
----------------------------------------
```

📊 FINAL EDA SUMMARY & KEY INSIGHTS

---

1. Dataset Overview

- **Total Samples:** 150
- **Number of Features:** 4
- **Unique Species:** 3 (`Setosa` , `Versicolor` , `Virginica`)
- **Balanced Dataset:** Yes, all classes are equally represented

---

2. Key Correlations

The following feature pairs show strong correlation (|correlation| > 0.8):

- **PetalLength ↔ PetalWidth:** 0.962
- **SepalLength ↔ PetalLength:** 0.871
- **SepalLength ↔ PetalWidth:** 0.818

This indicates that petal-based features are strongly linearly related and may contribute redundantly.

---

3. Species Separability

- **Setosa** is the **most distinct** species — very easily separable from others.
- **Versicolor** and **Virginica** show **some overlap** but are still reasonably distinguishable.
- **Best Discriminating Features:**
  - `PetalLengthCm`
  - `PetalWidthCm`

---

4. Data Quality

- **No Missing Values**
- **Minimal Outliers** (1 in SepalWidth)
- **Good feature spread across all variables**

---

5. Recommendations for Modeling

- Use **all features** for classification tasks
- Petal features may be **most important for classification**

EDA COMPLETE — Ready for Machine Learning!

Task 2 : **Build a Simple Predictive Model**

`Goal:` Train a **Logistic Regression** model to predict binary outcomes. Example Tools: Python, scikit-learn.

`Steps:`

- Preprocess the dataset (handle missing values, encode categories).
- Split data into training and testing sets.
- Train and evaluate the model using scikit-learn

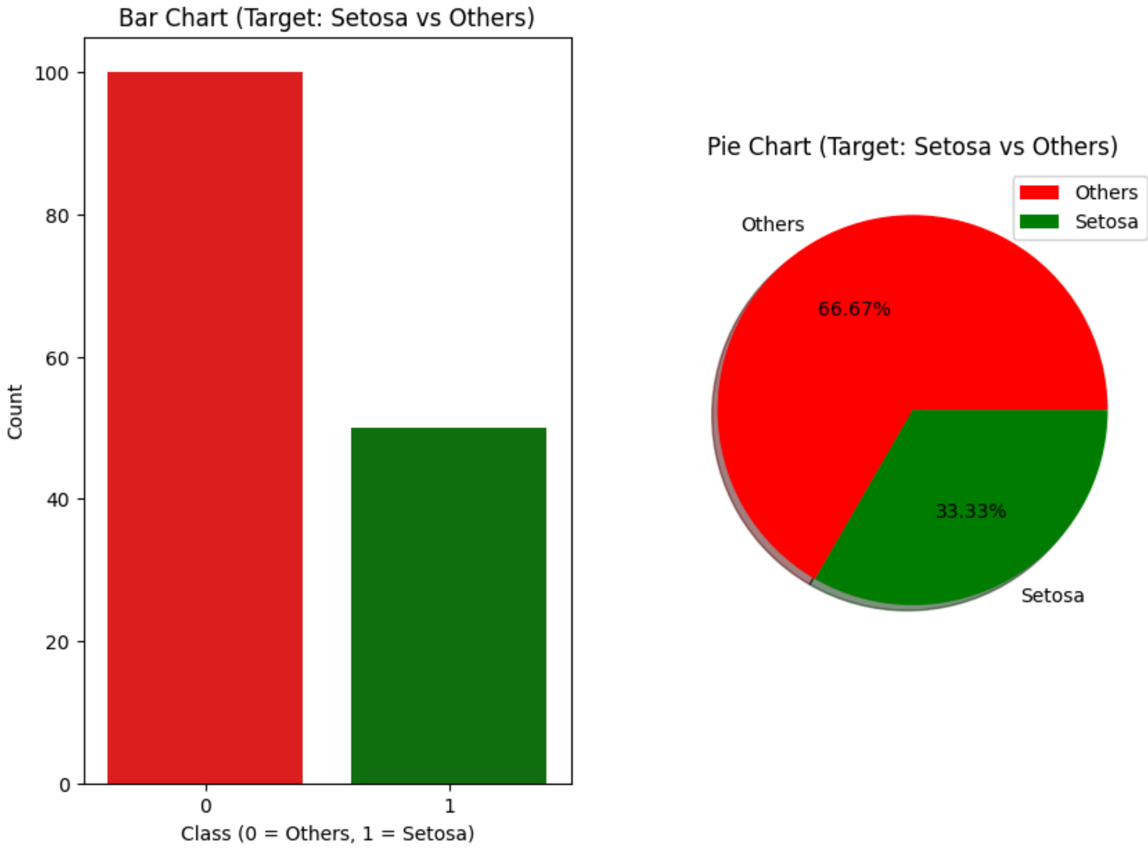
--> In order to complete the objective we will be creating a new column 'Target' that indicates the presence of our target species, in this case which is the `Iris-setosa`.

In [20]:
```
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report, confusion_mat


df = df_iris.copy()

# Encode target: 1 if Setosa, 0 otherwise
df['Target'] = df['Species'].apply(lambda x: 1 if x == 'Iris-setosa' else 0)

# using all features for prediction
X = df[['SepalLengthCm', 'SepalWidthCm', 'PetalLengthCm', 'PetalWidthCm']]
y = df['Target']
```

Class Distribution

In [21]:
```
fig = plt.figure(figsize=(10, 7))

fig.add_subplot(1,2,1)
sns.barplot(x=df['Target'].value_counts().index, y=df['Target'].value_counts().v
plt.title("Bar Chart (Target: Setosa vs Others)")
plt.xlabel("Class (0 = Others, 1 = Setosa)")
plt.ylabel("Count")


fig.add_subplot(1,2,2)
plt.pie(x=df['Target'].value_counts().values, labels=['Others', 'Setosa'], color
plt.title("Pie Chart (Target: Setosa vs Others)")


plt.legend()
plt.show()
```

```
C:\Users\sdnr1\AppData\Local\Temp\ipykernel_23732\178452276.py:4: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be removed in v
0.14.0. Assign the `x` variable to `hue` and set `legend=False` for the same effe
ct.

  sns.barplot(x=df['Target'].value_counts().index, y=df['Target'].value_counts().
values, palette=['red','green'])
```



In [22]:
```
# train-test split
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, stratify=y, random_state=42
)

# feature scaling
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
```

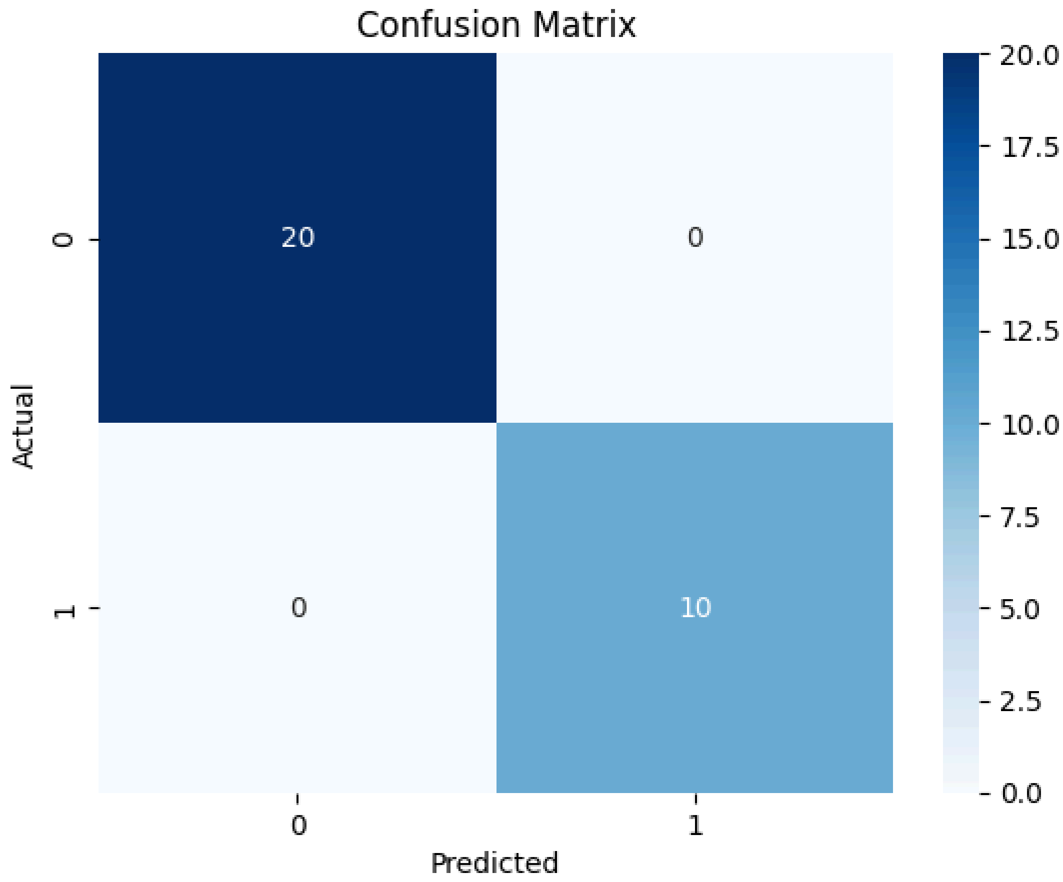
```
X_test_scaled = scaler.transform(X_test)

# model training
model = LogisticRegression()
model.fit(X_train_scaled, y_train)

# evaluation
y_pred = model.predict(X_test_scaled)
print("Train Accuracy:", model.score(X_train_scaled, y_train))
print("Test Accuracy :", model.score(X_test_scaled, y_test))
print("\nClassification Report:\n", classification_report(y_test, y_pred))
```

```
Train Accuracy: 1.0
Test Accuracy : 1.0

Classification Report:
               precision    recall  f1-score   support

           0       1.00      1.00      1.00        20
           1       1.00      1.00      1.00        10

    accuracy                           1.00        30
   macro avg       1.00      1.00      1.00        30
weighted avg       1.00      1.00      1.00        30
```

Confusion Matirx

In [23]:

```
cm = confusion_matrix(y_test, y_pred)
sns.heatmap(cm, annot=True, cmap='Blues', fmt='d')
plt.title("Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```



Cross Validation (5-fold)

In [24]:
```
X_scaled = scaler.fit_transform(X)
cv_scores = cross_val_score(model, X_scaled, y, cv=5)

print("Cross-Validation Accuracy Scores:", cv_scores)
print("Mean CV Accuracy:", cv_scores.mean())
```

```
Cross-Validation Accuracy Scores: [1. 1. 1. 1. 1.]
Mean CV Accuracy: 1.0
```

`Observations:`

- the model seems to be performing perfectly.
- However, this does not necessarily mean the model is memorizing the data (i.e., overfitting).
- This high performance was expected, as our EDA showed that the Iris-setosa species is clearly distinguishable from the other two.
- Therefore, the model achieves a perfect score largely due to the natural separability of the classes in the dataset, not due to overfitting.

In [25]:
```
import json

with open("Iris_EDA_Classification.ipynb", "r", encoding="utf-8") as f:
    notebook = json.load(f)

code_cells = [cell['source'] for cell in notebook['cells'] if cell['cell_type']
```

```
with open("extracted_code.py", "w", encoding="utf-8") as f:
    for i, code in enumerate(code_cells):
        f.write(f"# Cell {i+1}\n{''.join(code)}\n\n")
```