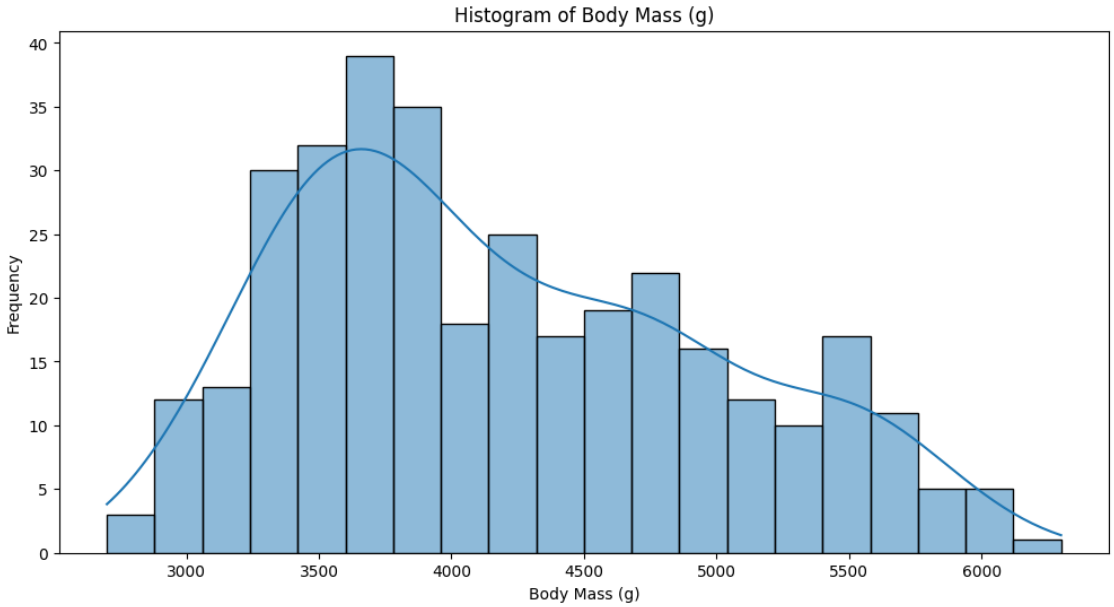
untitled1-1

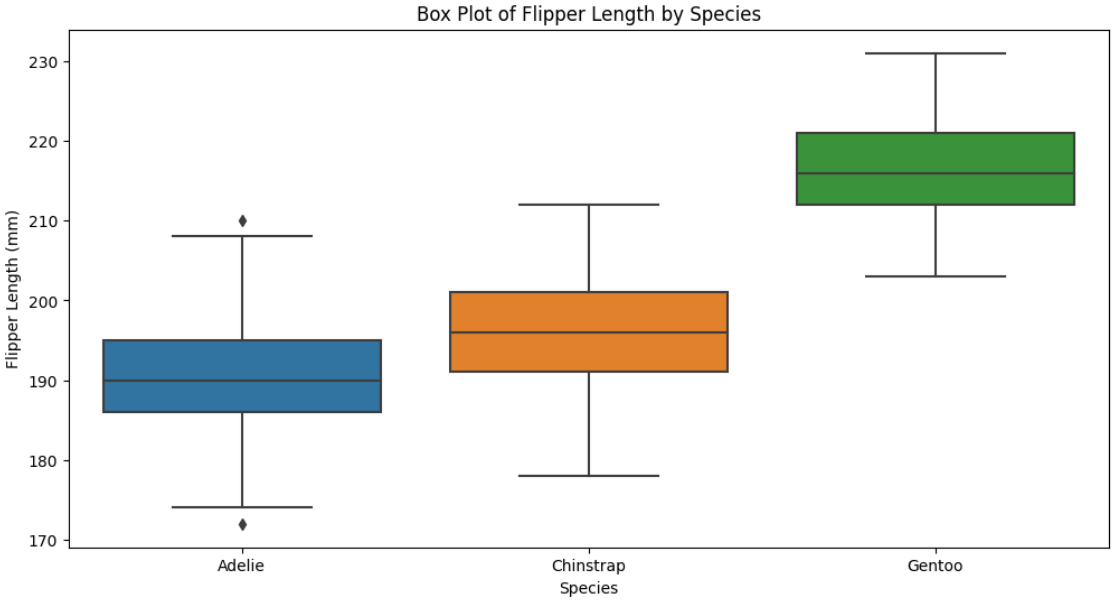
September 19, 2023

[28]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, accuracy_score,␣
↪confusion_matrix
```

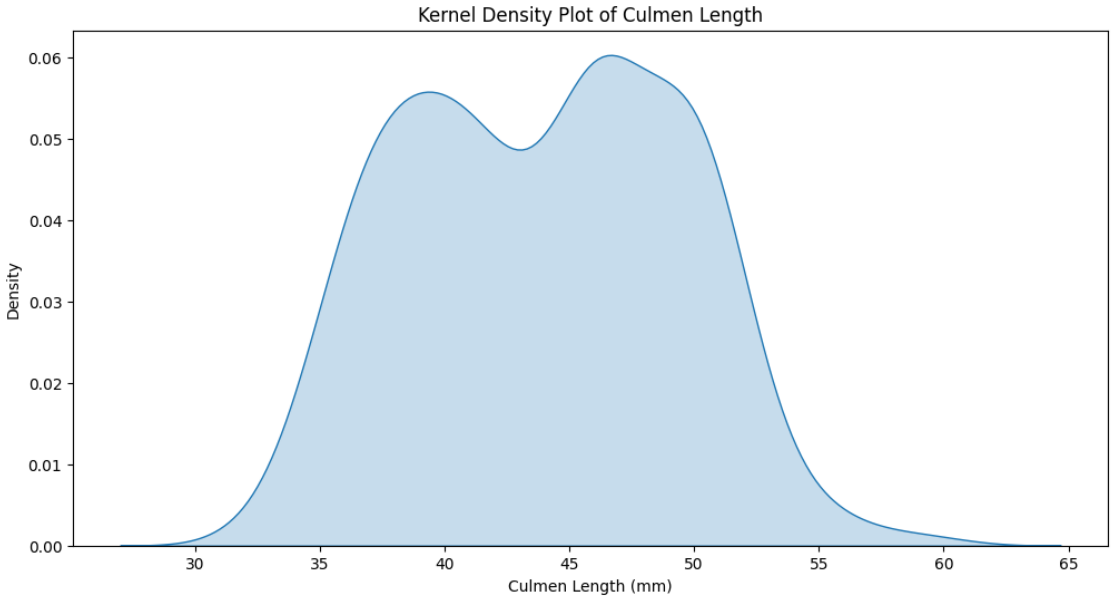
[29]:
```
file_path = "/content/penguins_size.csv"
df = pd.read_csv(file_path)
```

[35]:
```
# Univariate analysisis
# Plot 1: Histogram of Body Mass
plt.figure(figsize=(12, 6))
sns.histplot(df['body_mass_g'], bins=20, kde=True)
plt.title('Histogram of Body Mass (g)')
plt.xlabel('Body Mass (g)')
plt.ylabel('Frequency')
plt.show()

# Plot 2: Box Plot of Flipper Length
plt.figure(figsize=(12, 6))
sns.boxplot(x='species', y='flipper_length_mm', data=df)
plt.title('Box Plot of Flipper Length by Species')
plt.xlabel('Species')
plt.ylabel('Flipper Length (mm)')
plt.show()

# Plot 3: Kernel Density Plot of Culmen Length
plt.figure(figsize=(12, 6))
sns.kdeplot(df['culmen_length_mm'], shade=True)
plt.title('Kernel Density Plot of Culmen Length')
plt.xlabel('Culmen Length (mm)')
plt.show()
```

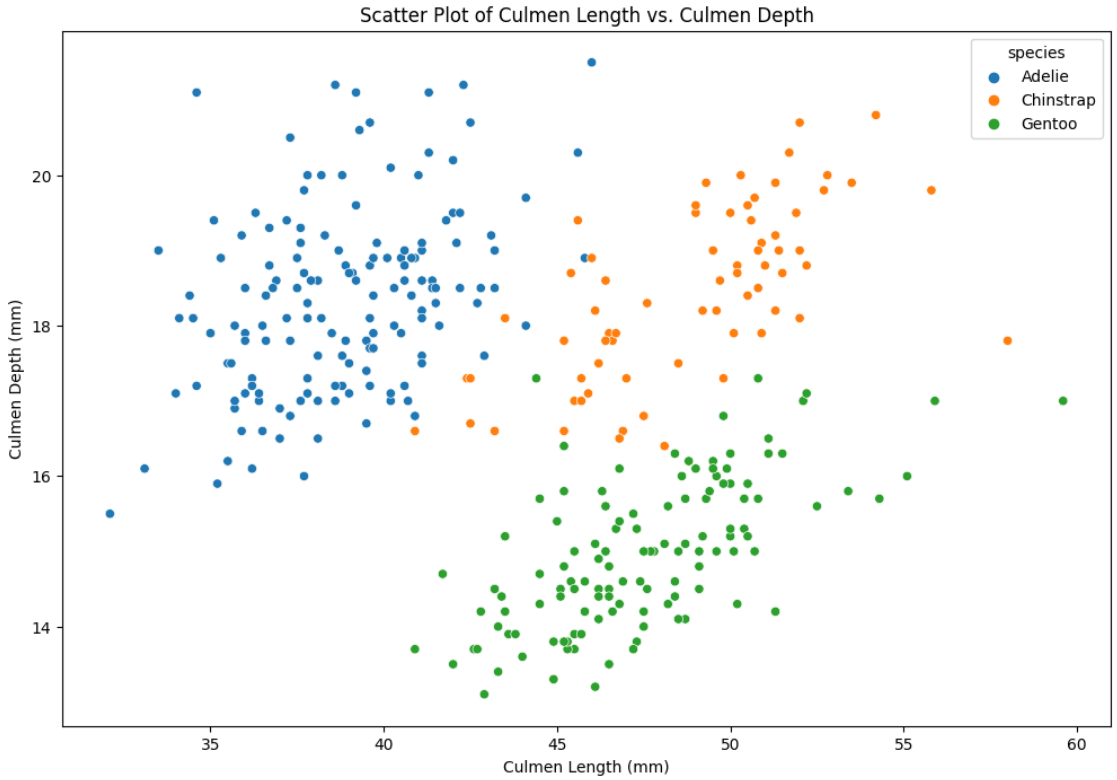


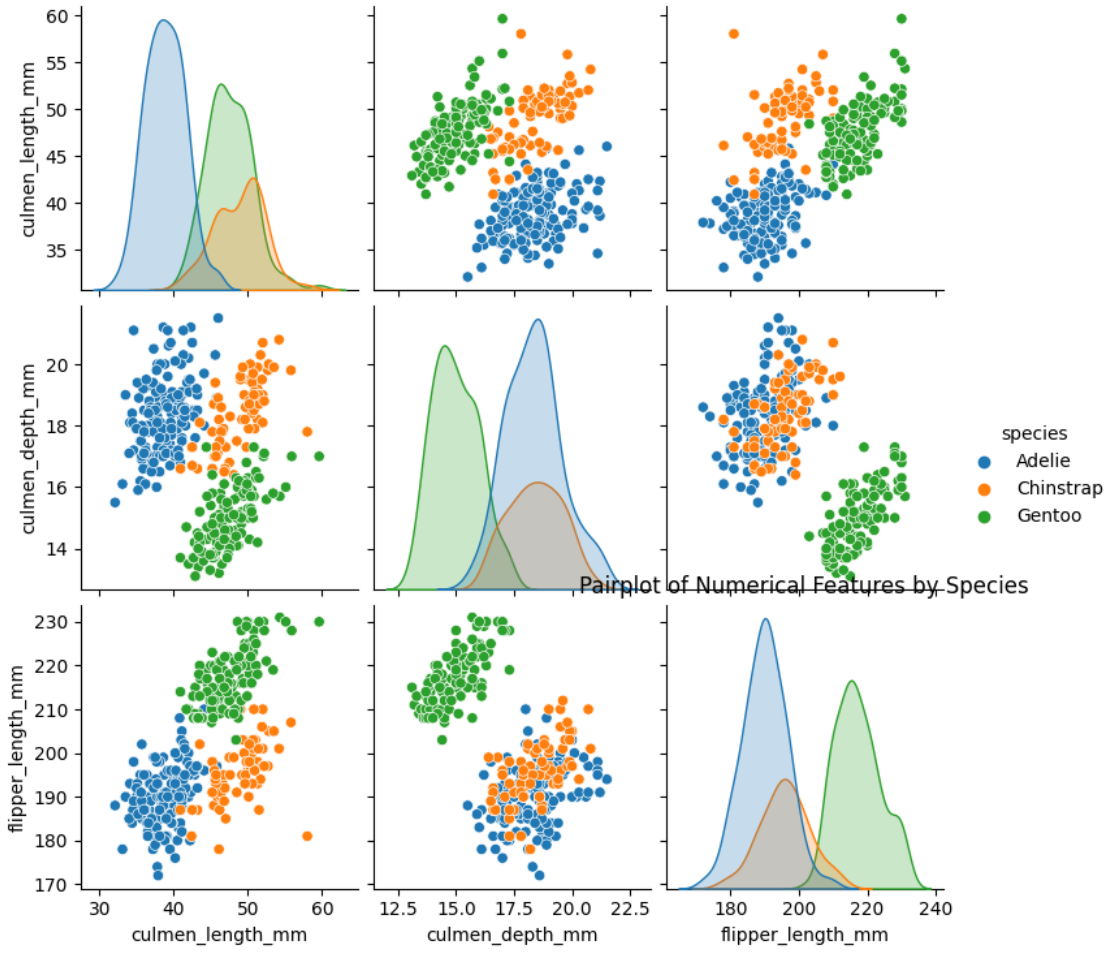



```
<ipython-input-35-ca6a13648d13>:20: FutureWarning:


`shade` is now deprecated in favor of `fill`; setting `fill=True`.
This will become an error in seaborn v0.14.0; please update your code.
```

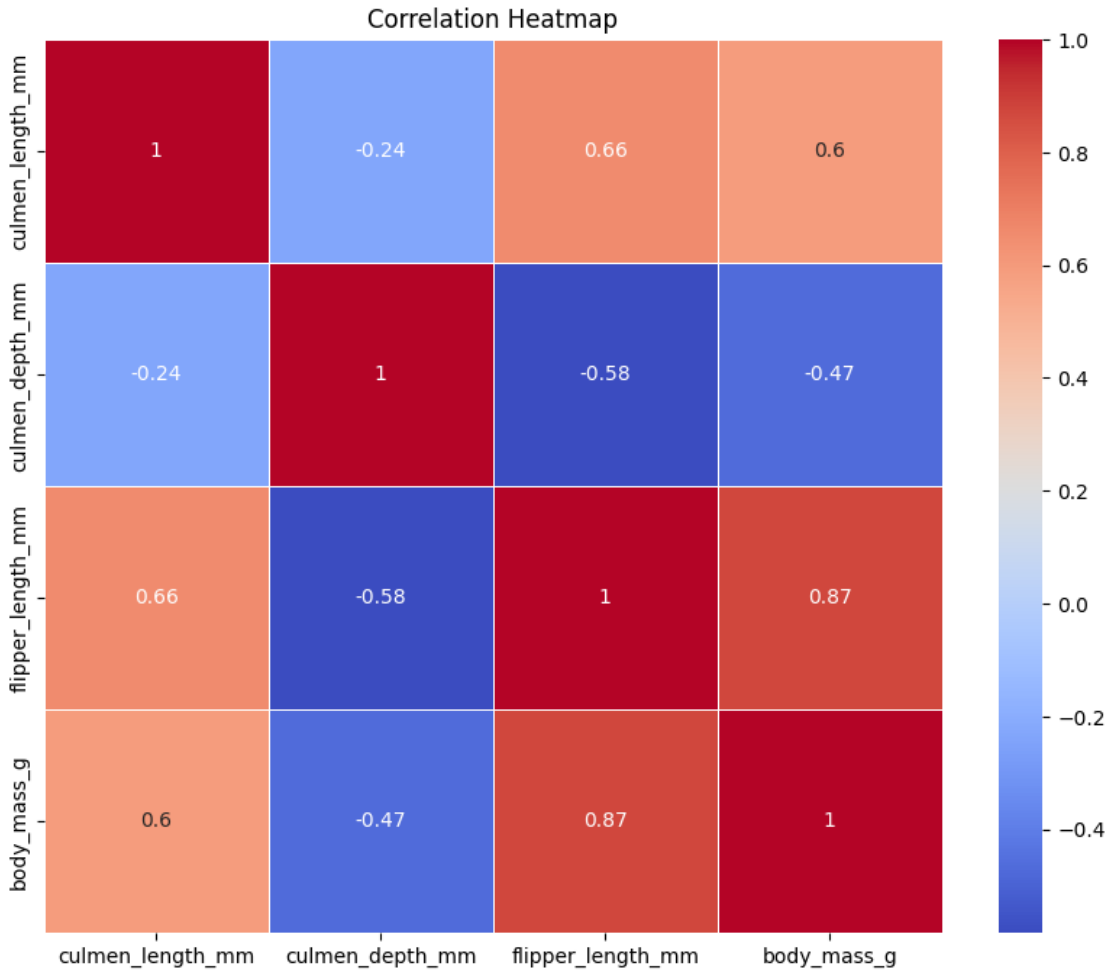


[36]:
```
# Bivariate Analysis
# Plot 1: Scatter Plot of Culmen Length vs. Culmen Depth
plt.figure(figsize=(12, 8))
sns.scatterplot(x='culmen_length_mm', y='culmen_depth_mm', hue='species',␣
 ↪data=df)
plt.title('Scatter Plot of Culmen Length vs. Culmen Depth')
plt.xlabel('Culmen Length (mm)')
plt.ylabel('Culmen Depth (mm)')
plt.show()

# Plot 2: Pairplot of Numerical Features
sns.pairplot(df, hue='species', vars=['culmen_length_mm', 'culmen_depth_mm',␣
 ↪'flipper_length_mm'])
plt.title('Pairplot of Numerical Features by Species')
plt.show()

# Plot 3: Heatmap of Correlation Matrix
correlation_matrix = df.corr()
plt.figure(figsize=(10, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', linewidths=.5)
plt.title('Correlation Heatmap')
plt.show()
```


Scatter Plot of Culmen Length vs. Culmen Depth
species
Adelie
Chinstrap
Gentoo
Culmen Depth (mm)
Culmen Length (mm)
20
18
16
14
35
40
45
50
55
60

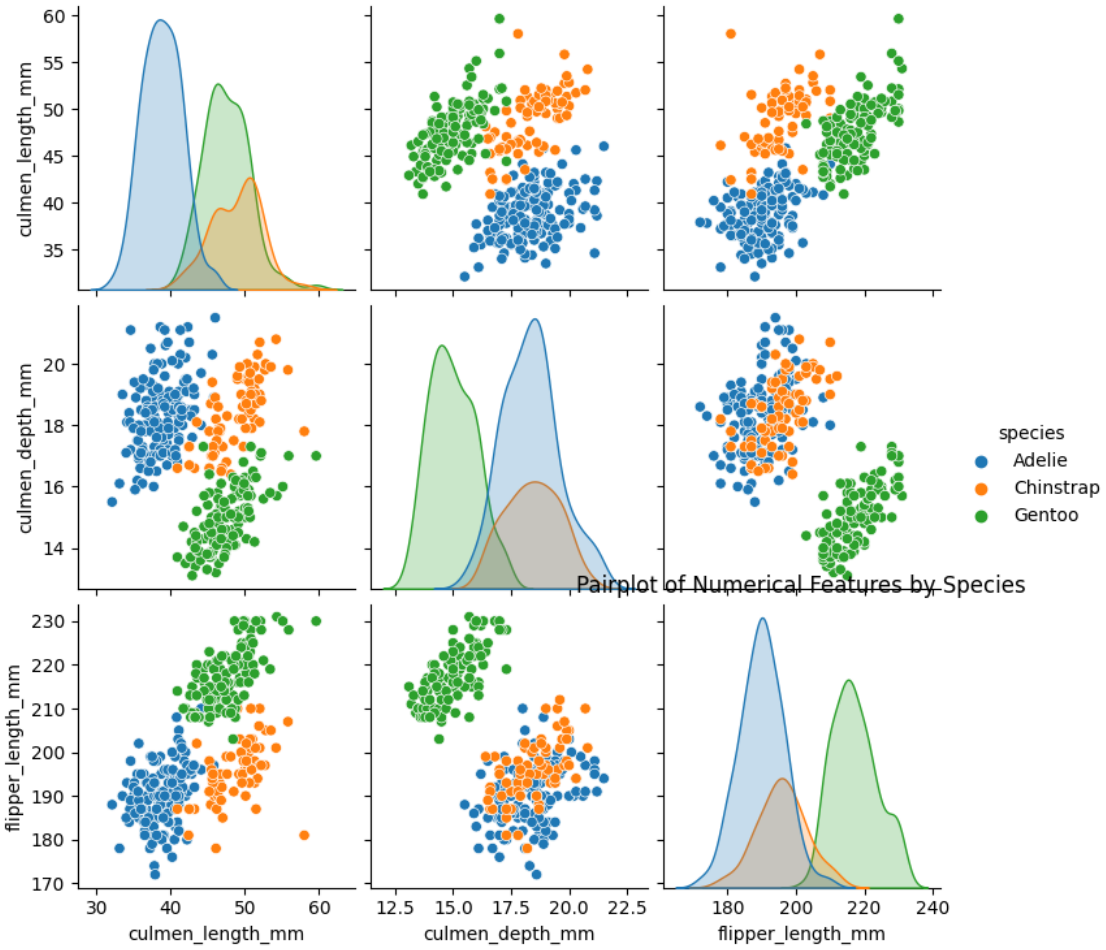



```
<ipython-input-36-4ef9336d90b1>:16: FutureWarning:

The default value of numeric_only in DataFrame.corr is deprecated. In a future
version, it will default to False. Select only valid columns or specify the
value of numeric_only to silence this warning.
```

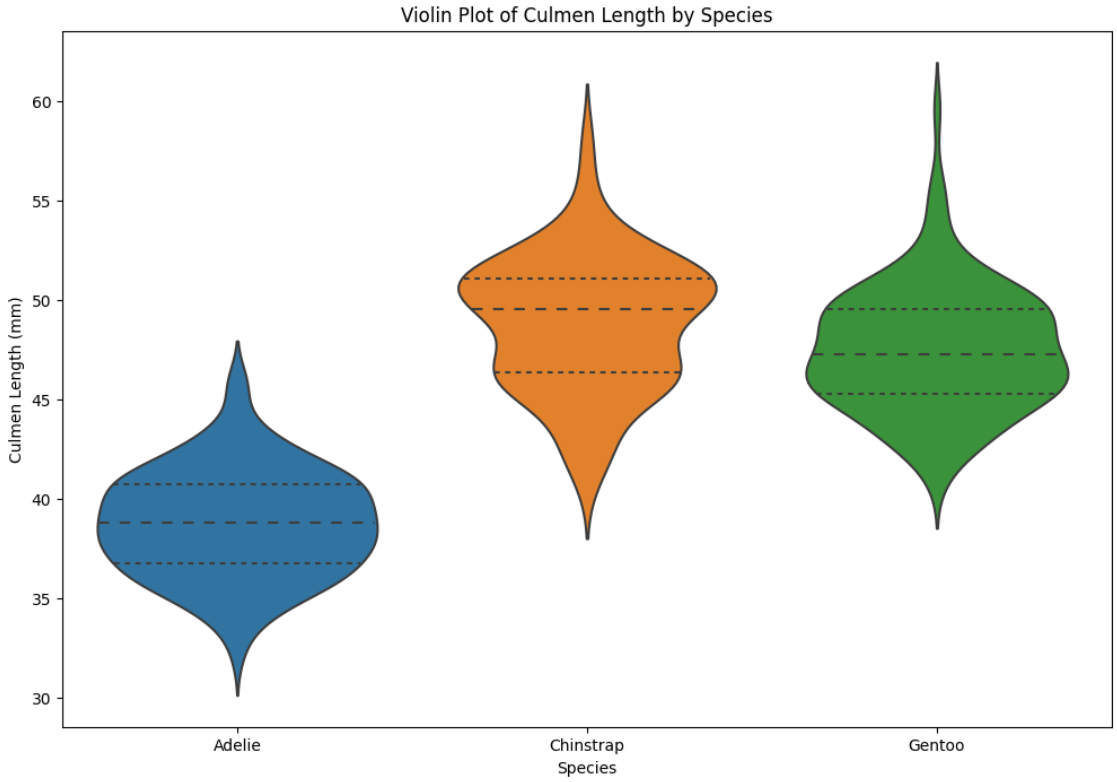


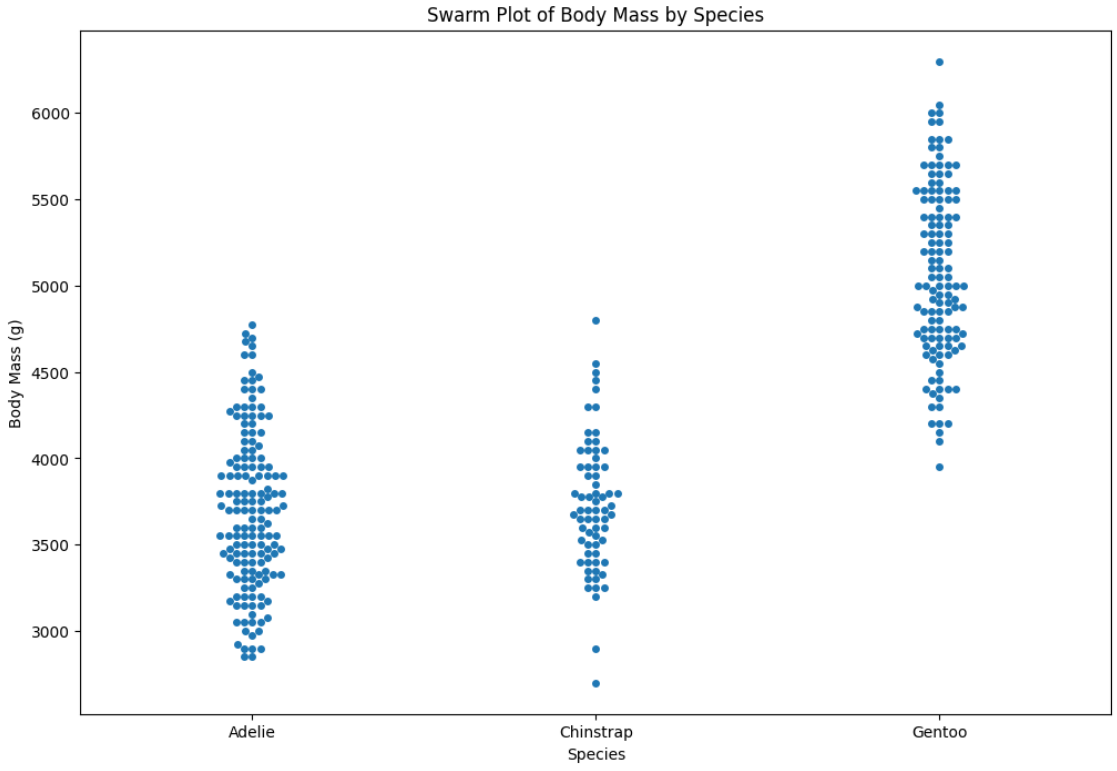
[41]:
```
# Multivariate Analysis
# Plot 1: Pairplot of Numerical Features
sns.pairplot(df, hue='species', vars=['culmen_length_mm', 'culmen_depth_mm',␣
 ↪'flipper_length_mm'])
plt.title('Pairplot of Numerical Features by Species')
plt.show()

# Plot 2: Violin Plot of Numerical Features by Species
plt.figure(figsize=(12, 8))
sns.violinplot(x='species', y='culmen_length_mm', data=df, inner='quart')
plt.title('Violin Plot of Culmen Length by Species')
plt.xlabel('Species')
plt.ylabel('Culmen Length (mm)')
plt.show()

# Plot 3: Swarm Plot
```

```
plt.figure(figsize=(12, 8))
sns.swarmplot(x='species', y='body_mass_g', data=df)
plt.title('Swarm Plot of Body Mass by Species')
plt.xlabel('Species')
plt.ylabel('Body Mass (g)')
plt.show()
```



Pairplot of Numerical Features by Species


Violin Plot of Culmen Length by Species
Culmen Length (mm)
60
55
50
45
40
35
30
Adelie
Chinstrap
Gentoo
Species


Swarm Plot of Body Mass by Species
Body Mass (g)
6000
5500
5000
4500
4000
3500
3000
Adelie
Chinstrap
Gentoo
Species

[42]:
```
#Descriptive Statistics
descriptive_stats = df.describe()
print(descriptive_stats)
```

```
       culmen_length_mm  culmen_depth_mm  flipper_length_mm  body_mass_g
count        342.000000       342.000000         342.000000   342.000000
mean          43.921930        17.151170         200.915205  4201.754386
std            5.459584         1.974793          14.061714   801.954536
min           32.100000        13.100000         172.000000  2700.000000
25%           39.225000        15.600000         190.000000  3550.000000
50%           44.450000        17.300000         197.000000  4050.000000
75%           48.500000        18.700000         213.000000  4750.000000
max           59.600000        21.500000         231.000000  6300.000000
```

[44]:
```
missing_values = df.isnull().sum()
print("Missing Values:\n", missing_values)
```

```
Missing Values:
 species               0
island                0
culmen_length_mm      2
culmen_depth_mm       2
flipper_length_mm     2
body_mass_g           2
sex                  10
dtype: int64
```

[45]:
```
df.dropna(inplace=True)
```

[51]:
```
df['culmen_length_mm'].fillna(df['culmen_length_mm'].mean(), inplace=True)
df['culmen_depth_mm'].fillna(df['culmen_depth_mm'].mean(), inplace=True)
df['flipper_length_mm'].fillna(df['flipper_length_mm'].mean(), inplace=True)
df['body_mass_g'].fillna(df['body_mass_g'].mean(), inplace=True)
```

[47]:
```
df['sex'].fillna(df['sex'].mode()[0], inplace=True)
```

[53]:
```
df['culmen_length_mm'].ffill(inplace=True)  # Forward fill
df['culmen_length_mm'].bfill(inplace=True)  # Backward fill
df['culmen_depth_mm'].ffill(inplace=True)  # Forward fill
df['culmen_depth_mm'].bfill(inplace=True)  # Backward fill
df['flipper_length_mm'].ffill(inplace=True)  # Forward fill
df['flipper_length_mm'].bfill(inplace=True)  # Backward fill
df['body_mass_g'].ffill(inplace=True)  # Forward fill
df['body_mass_g'].bfill(inplace=True)  # Backward fill
df['sex'].ffill(inplace=True)  # Forward fill
```

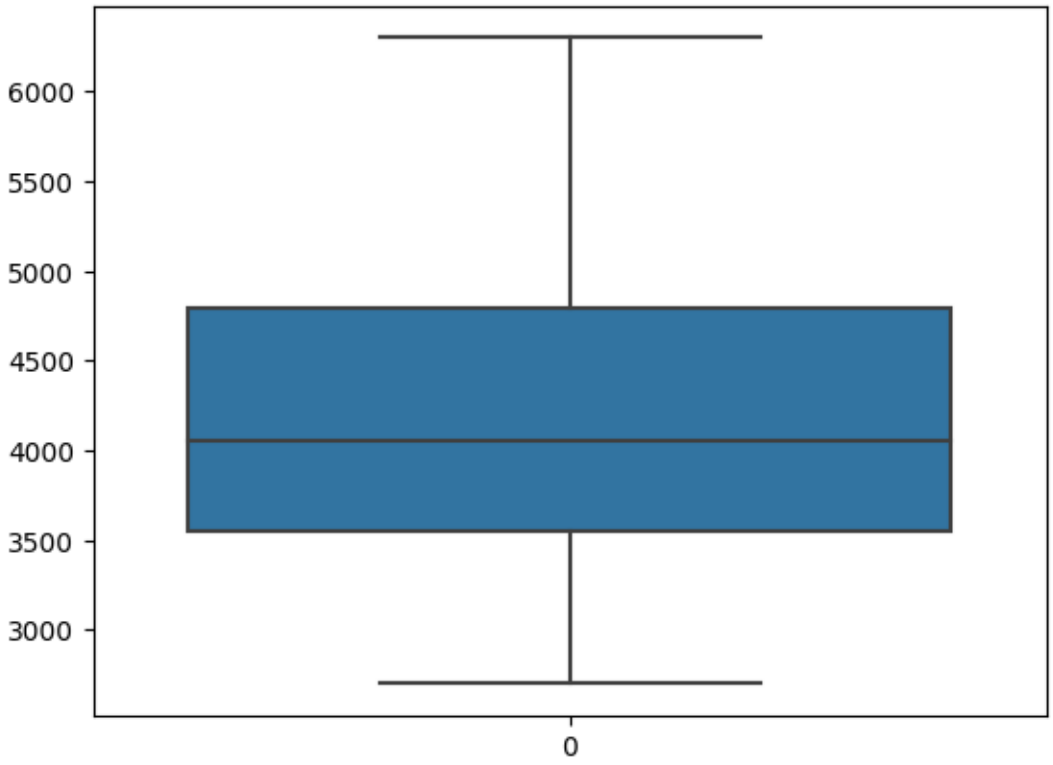
```
df['sex'].bfill(inplace=True)  # Backward fill
```

[55]:
```
df.isnull().sum()
```

[55]:
```
species              0
island               0
culmen_length_mm     0
culmen_depth_mm      0
flipper_length_mm    0
body_mass_g          0
sex                  0
dtype: int64
```

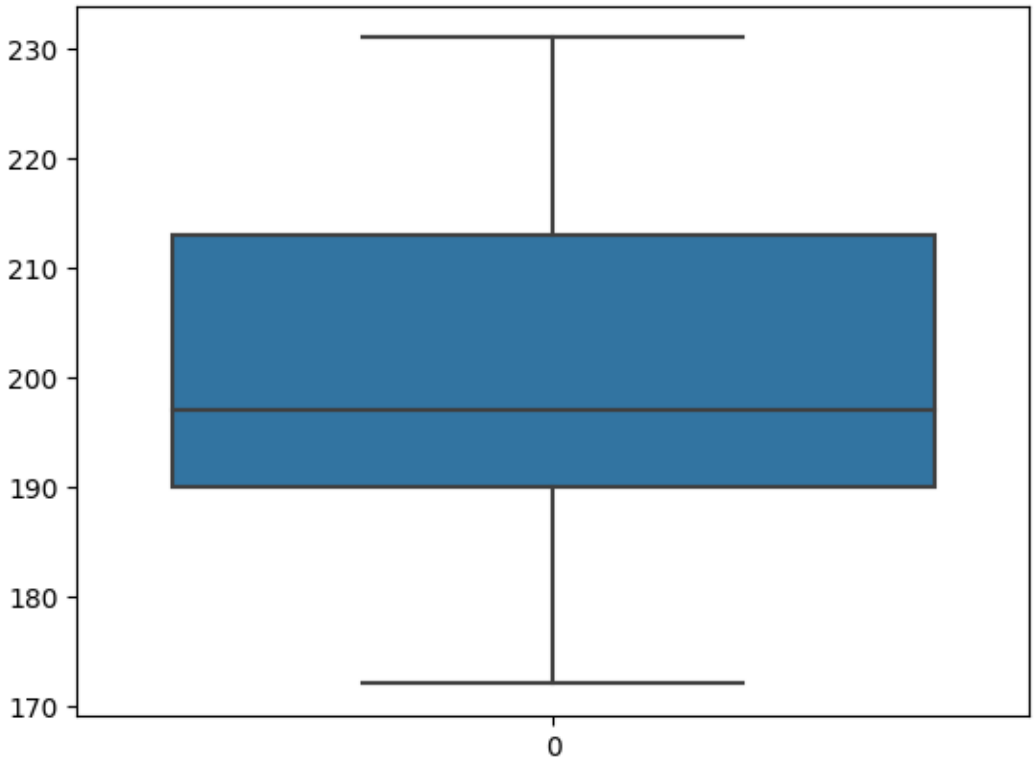
[63]:
```
#checking ouliers
sns.boxplot(df.body_mass_g)
```

[63]:
```
<Axes: >
```



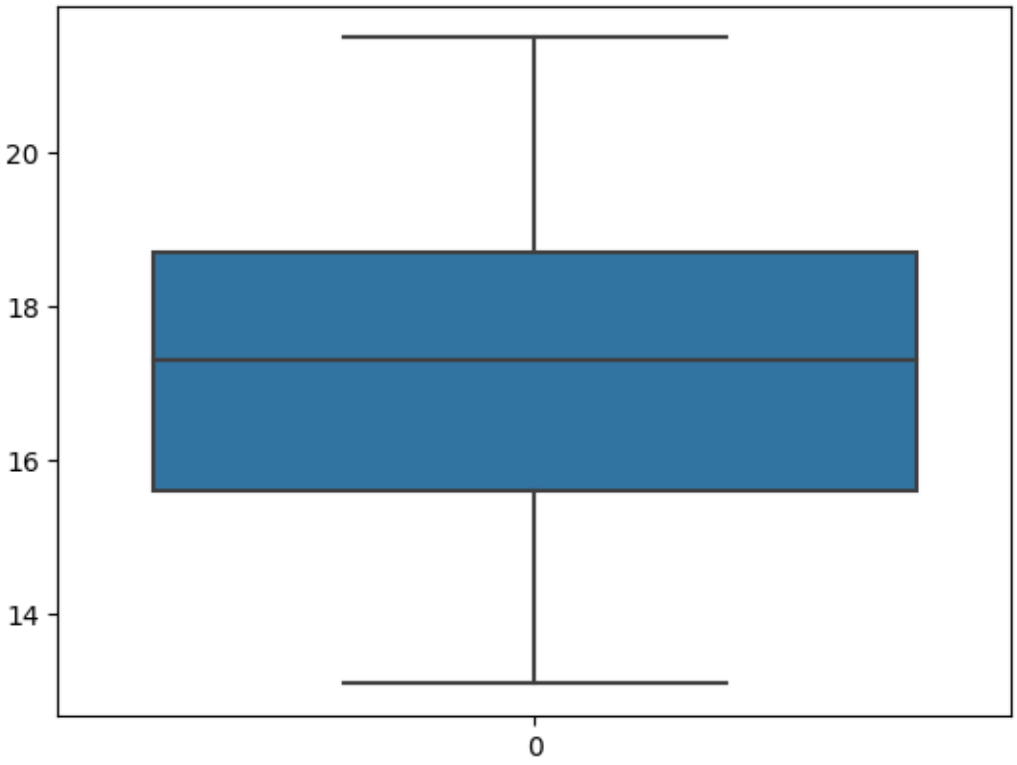
[64]:
```
sns.boxplot(df.flipper_length_mm)
```

[64]:
```
<Axes: >
```



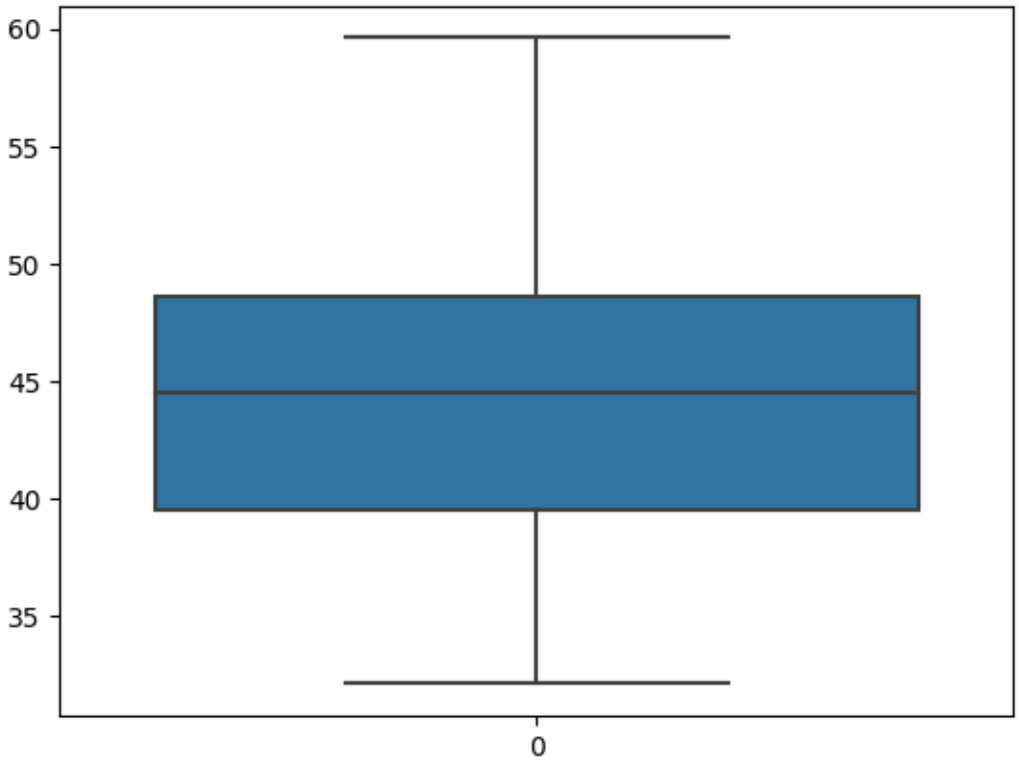
[65]:
```
sns.boxplot(df.culmen_depth_mm)
```

[65]: <Axes: >



[66]:
```
sns.boxplot(df.culmen_length_mm)
```

[66]: <Axes: >



[67]:
```
#no outliers
```

[71]:
```
# Check the correlation of independent variables with the target
df.corr()
```

```
<ipython-input-71-11907088e578>:2: FutureWarning:

The default value of numeric_only in DataFrame.corr is deprecated. In a future
version, it will default to False. Select only valid columns or specify the
value of numeric_only to silence this warning.
```

[71]:

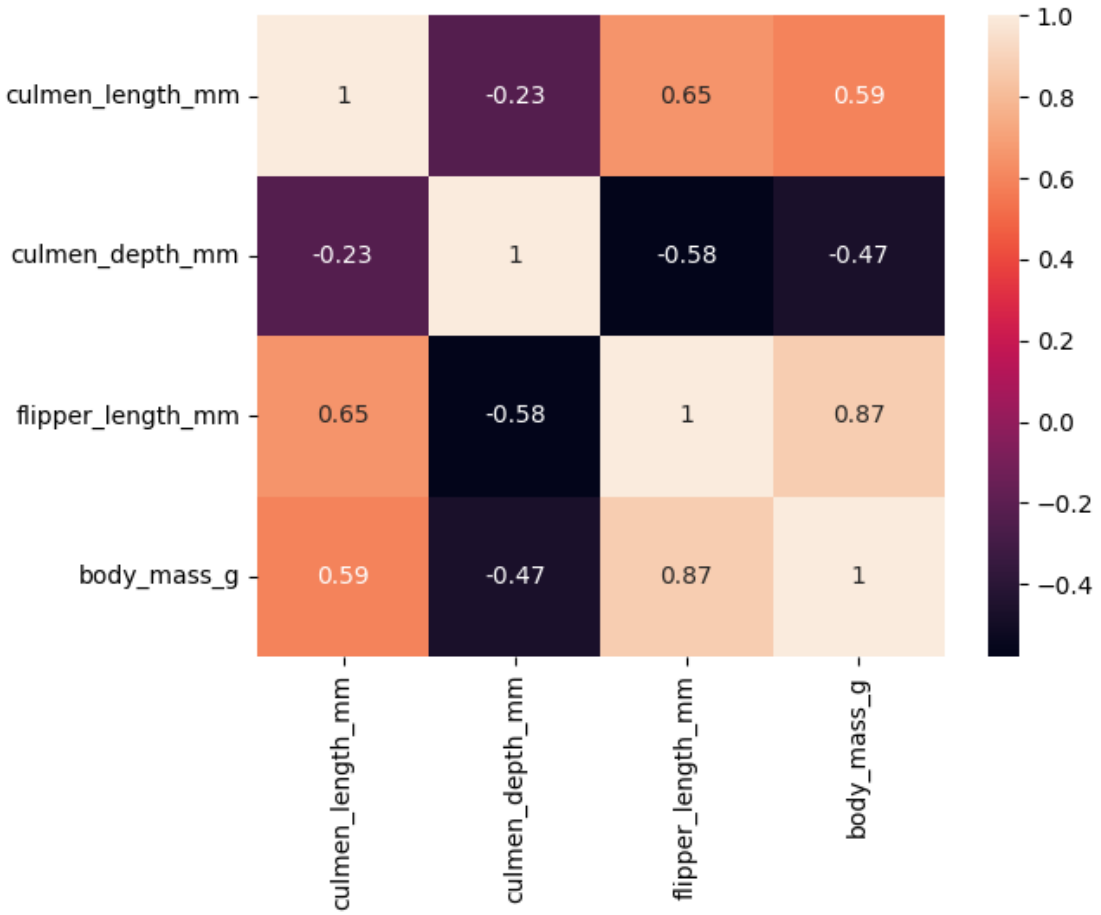
	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
culmen_length_mm	1.000000	-0.228640	0.652126	0.589066
culmen_depth_mm	-0.228640	1.000000	-0.578730	-0.472987
flipper_length_mm	0.652126	-0.578730	1.000000	0.873211
body_mass_g	0.589066	-0.472987	0.873211	

```
body_mass_g            1.000000
```

[72]:
```
sns.heatmap(df.corr(),annot=True)
```

```
<ipython-input-72-8df7bcac526d>:1: FutureWarning:

The default value of numeric_only in DataFrame.corr is deprecated. In a future
version, it will default to False. Select only valid columns or specify the
value of numeric_only to silence this warning.
```

[72]: <Axes: >



[75]:
```
df.corr().body_mass_g.sort_values(ascending=False)
```

```
<ipython-input-75-94e77a915008>:1: FutureWarning:

The default value of numeric_only in DataFrame.corr is deprecated. In a future
version, it will default to False. Select only valid columns or specify the
```

```
value of numeric_only to silence this warning.
```

[75]:
```
body_mass_g          1.000000
flipper_length_mm    0.873211
culmen_length_mm     0.589066
culmen_depth_mm     -0.472987
Name: body_mass_g, dtype: float64
```

[76]:
```
df.head()
```

[76]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
0	Adelie	Torgersen	39.1	18.7	181.0	3750.0	MALE
1	Adelie	Torgersen	39.5	17.4	186.0	3800.0	FEMALE
2	Adelie	Torgersen	40.3	18.0	195.0	3250.0	FEMALE
4	Adelie	Torgersen	36.7	19.3	193.0	3450.0	FEMALE
5	Adelie	Torgersen	39.3	20.6	190.0	3650.0	MALE

[77]:
```
# 8. Check for Categorical columns and perform encoding
categorical_cols = df.select_dtypes(include=['object']).columns
le = LabelEncoder()
df[categorical_cols] = df[categorical_cols].apply(le.fit_transform)
```

[78]:
```
X = df.drop(columns=['species'])
y = df['species']
```

[79]:
```
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)
```

[80]:
```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2,␣
↪random_state=42)
```

[81]:
```
# Check the training and testing data shape
print("X_train shape:", X_train.shape)
print("X_test shape:", X_test.shape)
print("y_train shape:", y_train.shape)
print("y_test shape:", y_test.shape)
```

```
X_train shape: (267, 6)
X_test shape: (67, 6)
```

```
y_train shape: (267,)
y_test shape: (67,)
```

[ ]: