21BCI0075 GATIK GARG

September 13, 2023

#####1. penguins_size.csv is downloaded

#####2. Load the dataset into the tool.

```
[1]: import numpy as np
     import pandas as pd
```

```
[2]: df = pd.read_csv('/content/penguins_size.csv')
     df.head()
```

```
[2]:   species     island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  \
     0  Adelie  Torgersen              39.1             18.7              181.0
     1  Adelie  Torgersen              39.5             17.4              186.0
     2  Adelie  Torgersen              40.3             18.0              195.0
     3  Adelie  Torgersen               NaN              NaN                NaN
     4  Adelie  Torgersen              36.7             19.3              193.0

        body_mass_g     sex
     0       3750.0    MALE
     1       3800.0  FEMALE
     2       3250.0  FEMALE
     3          NaN     NaN
     4       3450.0  FEMALE
```

#####3.1. Perform Univariate Analysis

```
[3]: from matplotlib import rcParams
     import seaborn as sns
```

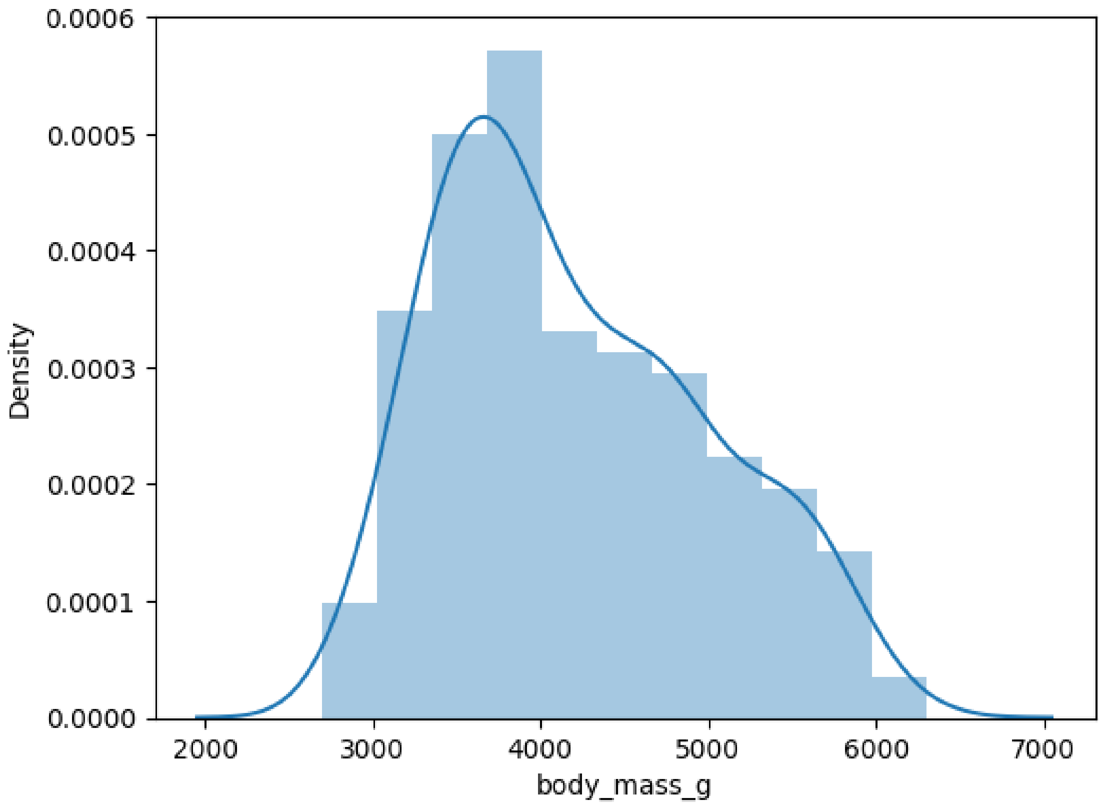
```
[4]: sns.distplot(df.body_mass_g)
```

```
<ipython-input-4-176964dae727>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
```

https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

```
sns.distplot(df.body_mass_g)
```

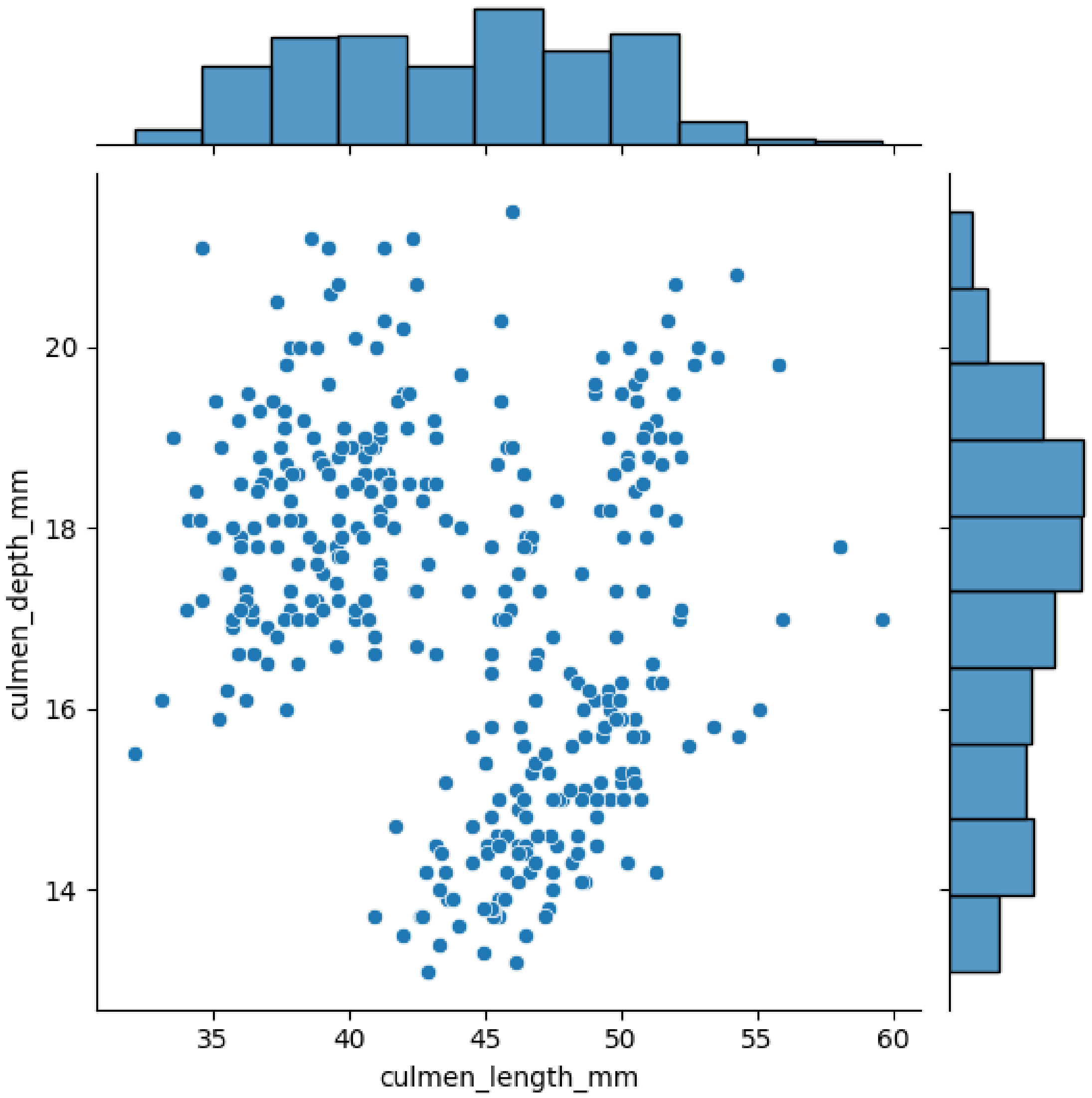
```
[4]: <Axes: xlabel='body_mass_g', ylabel='Density'>
```



#####3.2. Perform Bivariate Analysis

```
[5]: sns.jointplot(x='culmen_length_mm',y='culmen_depth_mm',data=df)
```

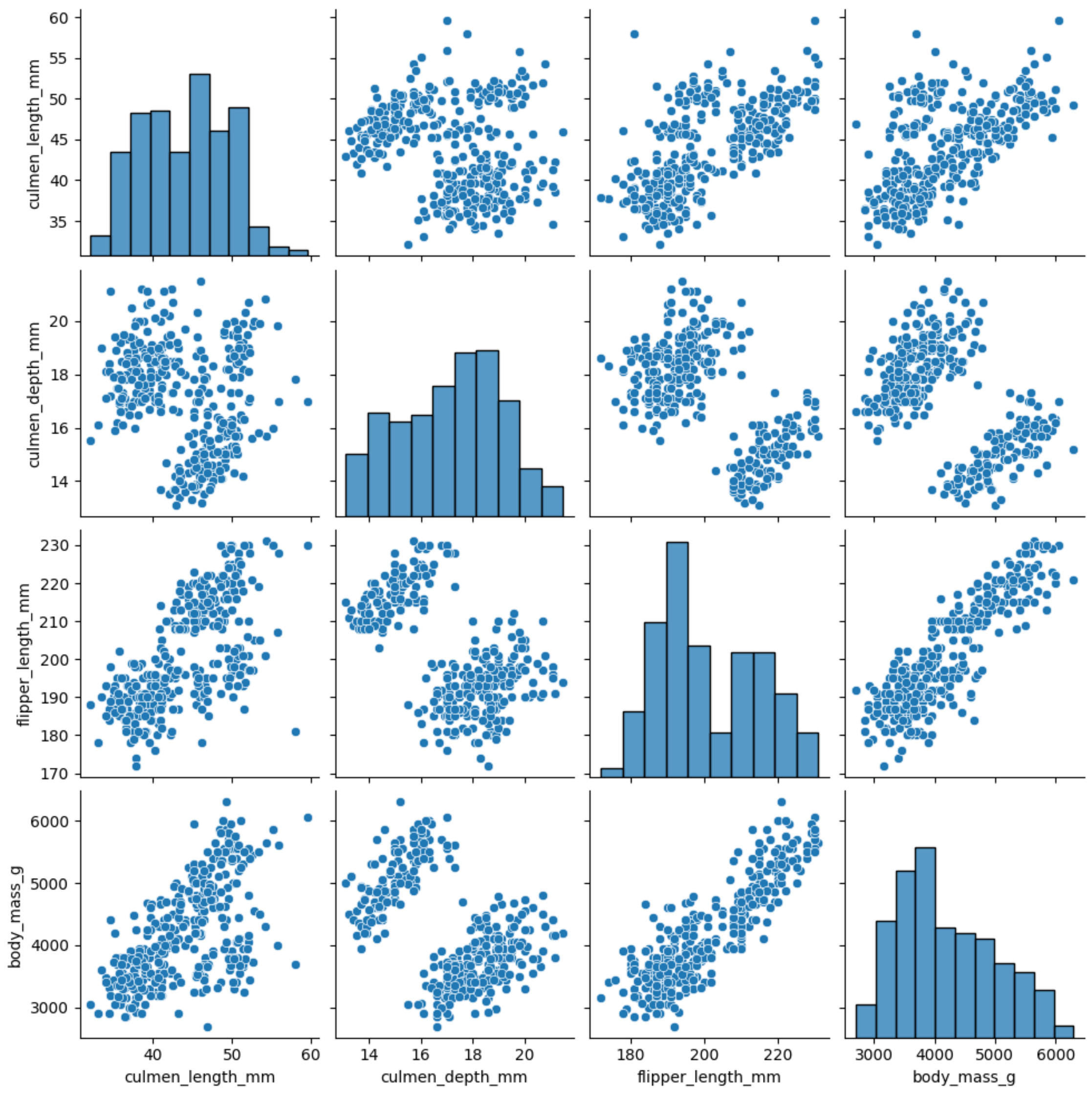
```
[5]: <seaborn.axisgrid.JointGrid at 0x7c313325c6a0>
```



#####3.3. Perform Multi-Variate Analysis

[6]:
```
sns.pairplot(df)
```

[6]:
```
<seaborn.axisgrid.PairGrid at 0x7c31298f71f0>
```



#####4. Perform descriptive statistics on the dataset.

[7]:
```
df.describe()
```

[7]:
```
       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
```

#####5. Check for Missing values and deal with them.

[8]:
```
df.isnull().any() #Checking is there any null values in our dataset
```

[8]:
```
species               False
island                False
culmen_length_mm       True
culmen_depth_mm        True
flipper_length_mm      True
body_mass_g            True
sex                    True
dtype: bool
```

[9]:
```
df.isnull().sum()
```

[9]:
```
species                0
island                 0
culmen_length_mm       2
culmen_depth_mm        2
flipper_length_mm      2
body_mass_g            2
sex                   10
dtype: int64
```

[25]:
```
# Code to replace null values in numerical columns with MEDIAN
df['culmen_length_mm'].fillna(df['culmen_length_mm'].median(),inplace=True)
df['culmen_depth_mm'].fillna(df['culmen_depth_mm'].median(),inplace=True)
df['flipper_length_mm'].fillna(df['flipper_length_mm'].median(),inplace=True)
df['body_mass_g'].fillna(df['body_mass_g'].median(),inplace=True)

# Code to replace null values in categorical column with MODE
df['sex'].fillna(df['sex'].mode().iloc[0],inplace=True)
```

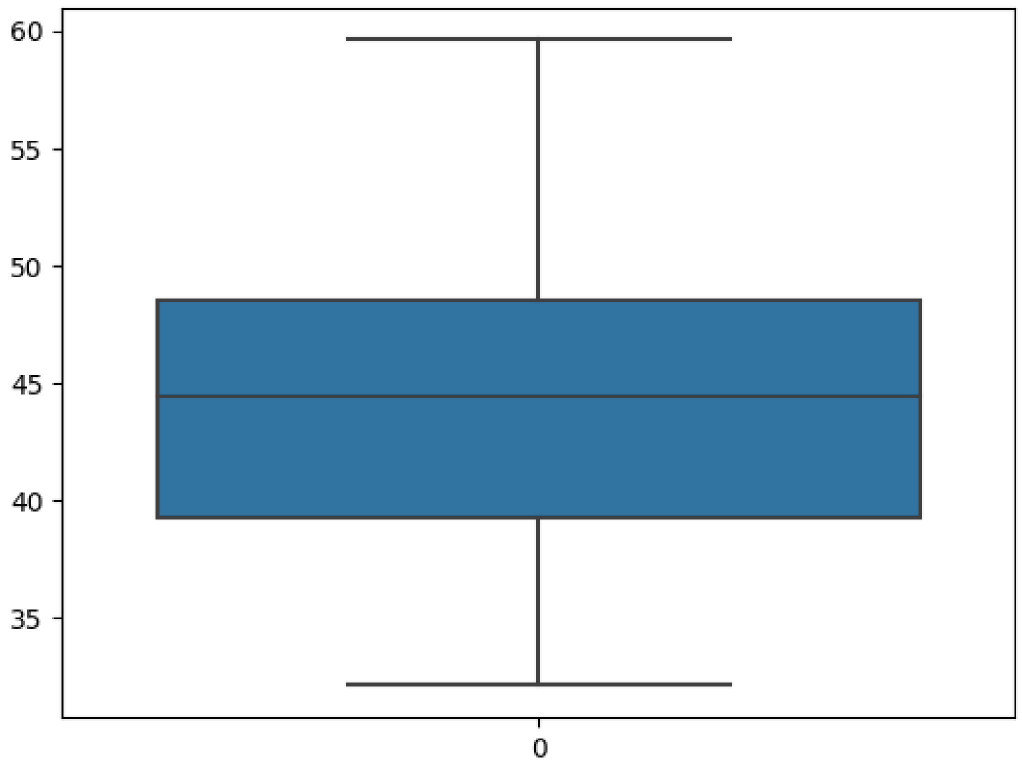
[26]:
```
# Now all null values are replaced with median and mode and dealt properly.

df.isnull().any()
```

[26]:
```
species               False
island                False
culmen_length_mm      False
culmen_depth_mm       False
flipper_length_mm     False
body_mass_g           False
sex                   False
dtype: bool
```

#####6. Find the outliers and replace the outliers

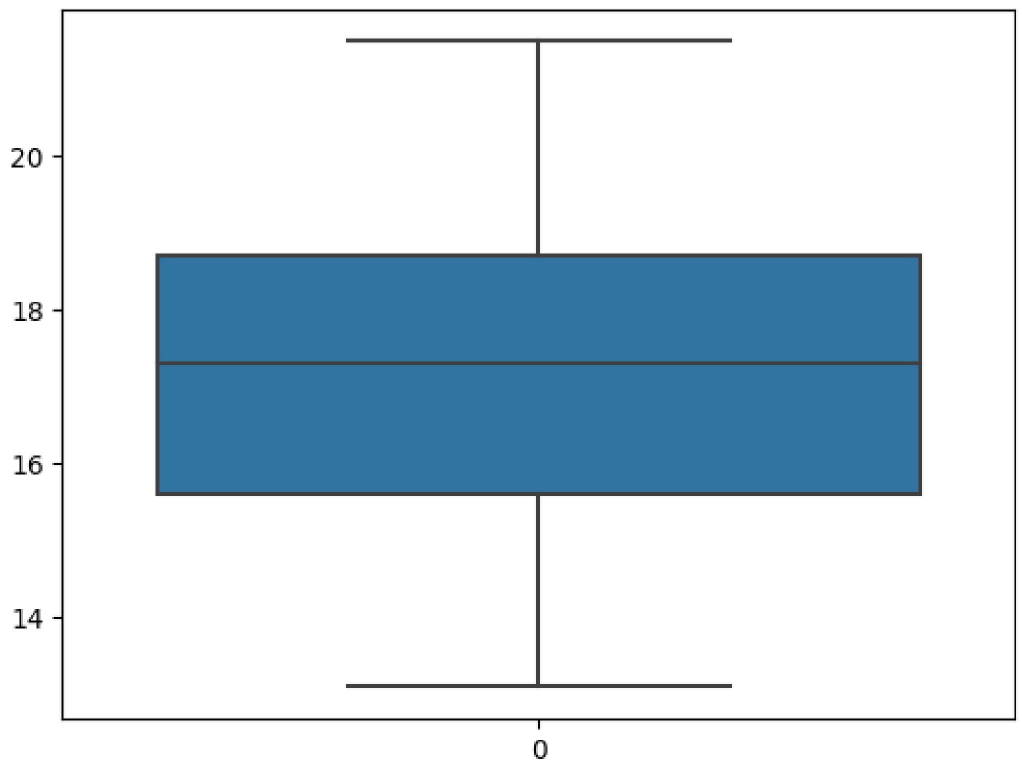
[29]:
```
sns.boxplot(df.culmen_length_mm)
```

[29]:
```
<Axes: >
```



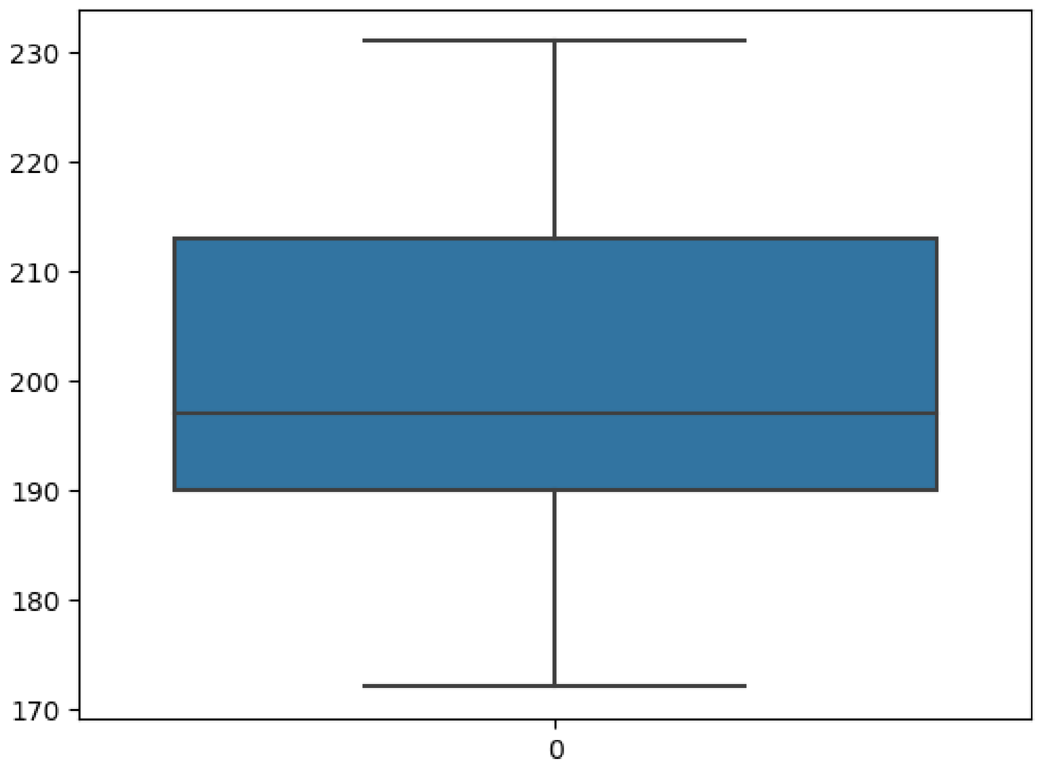
[30]:
```
sns.boxplot(df.culmen_depth_mm)
```

[30]:
```
<Axes: >
```



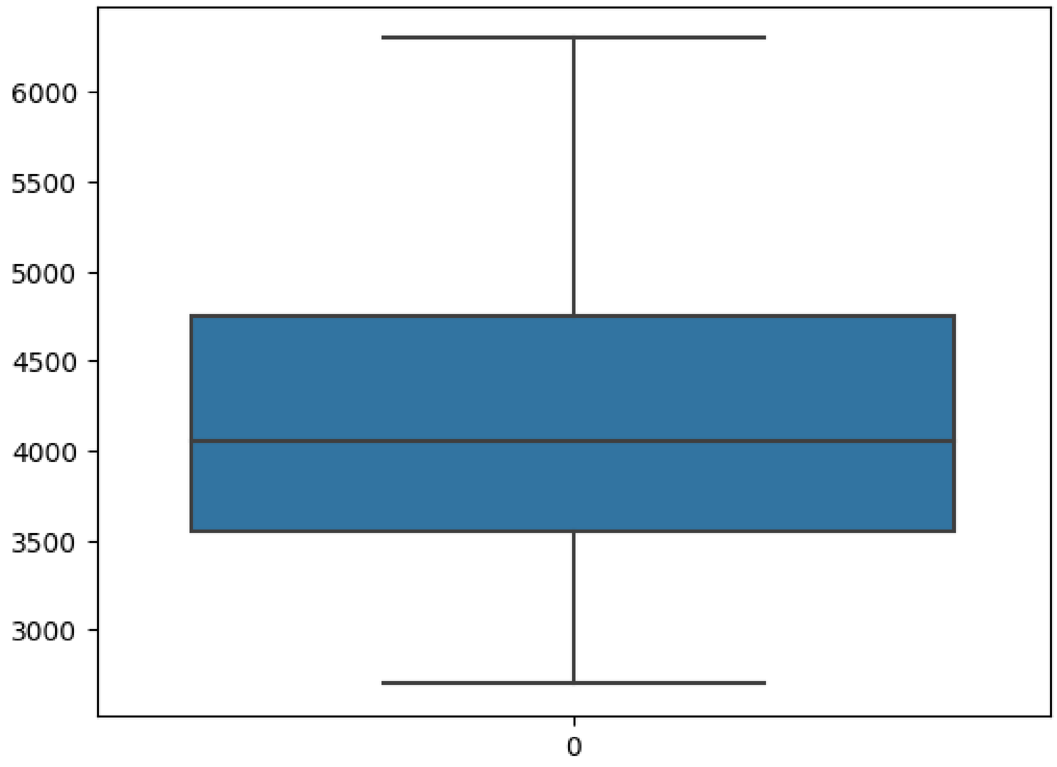
```
[31]: sns.boxplot(df.flipper_length_mm)
```

```
[31]: <Axes: >
```



[32]:
```
sns.boxplot(df.body_mass_g)
```

[32]:
```
<Axes: >
```



######Hence there are no outliers in the dataset.

#####7. Check for Categorical columns and perform encoding.

[37]:
```
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
df['sex'] = le.fit_transform(df['sex'])
df['species'] = le.fit_transform(df['species'])
df['island'] = le.fit_transform(df['island'])
df.head()
```

[37]:
```
   species  island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  \
0        0       2             39.10             18.7              181.0
1        0       2             39.50             17.4              186.0
2        0       2             40.30             18.0              195.0
3        0       2             44.45             17.3              197.0
4        0       2             36.70             19.3              193.0

   body_mass_g  sex
0       3750.0    2
1       3800.0    1
2       3250.0    1
3       4050.0    2
```

```
4       3450.0    1
```

#####8. Check the correlation of independent variables with the target (TARGET IS SPECIES and remaining are independent)

```
[38]: df.corr().species.sort_values(ascending=False)
```

```
[38]: species              1.000000
      flipper_length_mm    0.850819
      body_mass_g          0.747547
      culmen_length_mm     0.728706
      sex                 -0.003823
      island              -0.635659
      culmen_depth_mm     -0.741282
      Name: species, dtype: float64
```

#####9. Split the data into dependent and independent variables

```
[40]: X=df.drop(columns=['species'],axis=1)
      X.head()
```

```
[40]:    island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  body_mass_g  \
      0       2             39.10             18.7              181.0       3750.0
      1       2             39.50             17.4              186.0       3800.0
      2       2             40.30             18.0              195.0       3250.0
      3       2             44.45             17.3              197.0       4050.0
      4       2             36.70             19.3              193.0       3450.0

         sex
      0    2
      1    1
      2    1
      3    2
      4    1
```

```
[41]: Y=df['species']
      Y.head()
```

```
[41]: 0    0
      1    0
      2    0
      3    0
      4    0
      Name: species, dtype: int64
```

#####10. Scaling the data

[42]:
```
from sklearn.preprocessing import MinMaxScaler
scale = MinMaxScaler()
X_scaled = pd.DataFrame(scale.fit_transform(X),columns=X.columns)
X_scaled.head()
```

[42]:
```
   island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  body_mass_g  \
0     1.0          0.254545         0.666667           0.152542     0.291667
1     1.0          0.269091         0.511905           0.237288     0.305556
2     1.0          0.298182         0.583333           0.389831     0.152778
3     1.0          0.449091         0.500000           0.423729     0.375000
4     1.0          0.167273         0.738095           0.355932     0.208333

   sex
0  1.0
1  0.5
2  0.5
3  1.0
4  0.5
```

#####11. Split the data into training and testing

[48]:
```
from sklearn.model_selection import train_test_split
X_train,X_test,Y_train,Y_test = train_test_split(X_scaled,Y,test_size=0.
 ↪2,random_state=0)
```

#####12. Check the training and testing data shape.

[49]:
```
X_train.shape
```

[49]:
```
(275, 6)
```

[50]:
```
X_test.shape
```

[50]:
```
(69, 6)
```

[51]:
```
Y_train.shape
```

[51]:
```
(275,)
```

[52]:
```
Y_test.shape
```

[52]:
```
(69,)
```

#The End!!!