Submission Date - 13.09.2023

ASSIGNMENT – 3

Artificial Intelligence & Machine Learning in collaboration with Google (Applied Data Science)

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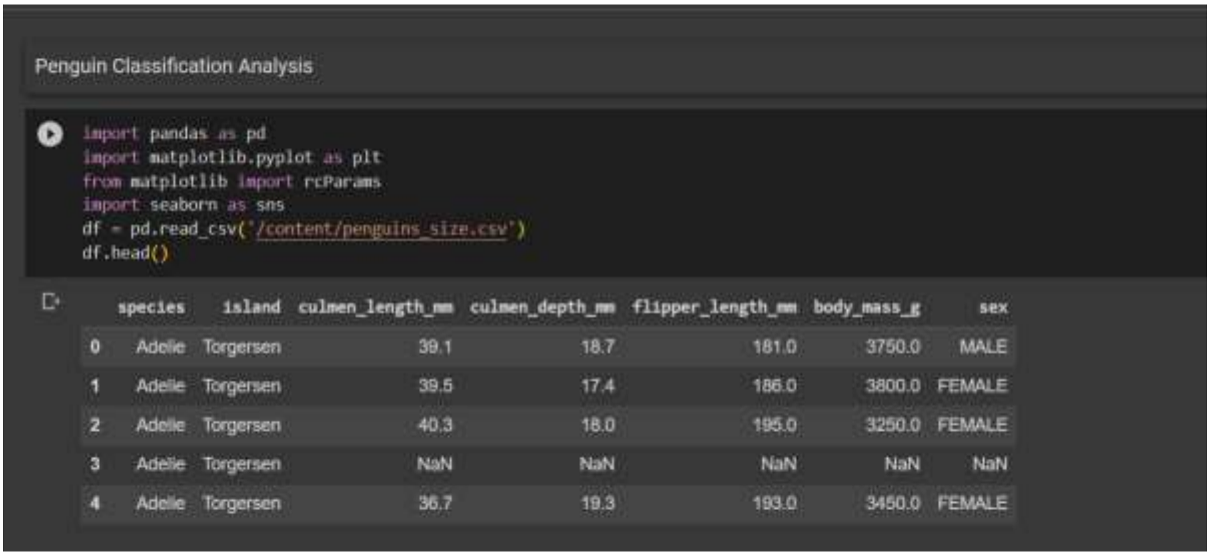
TASK

1. Download the dataset: Dataset

2. Load the dataset into the tool.



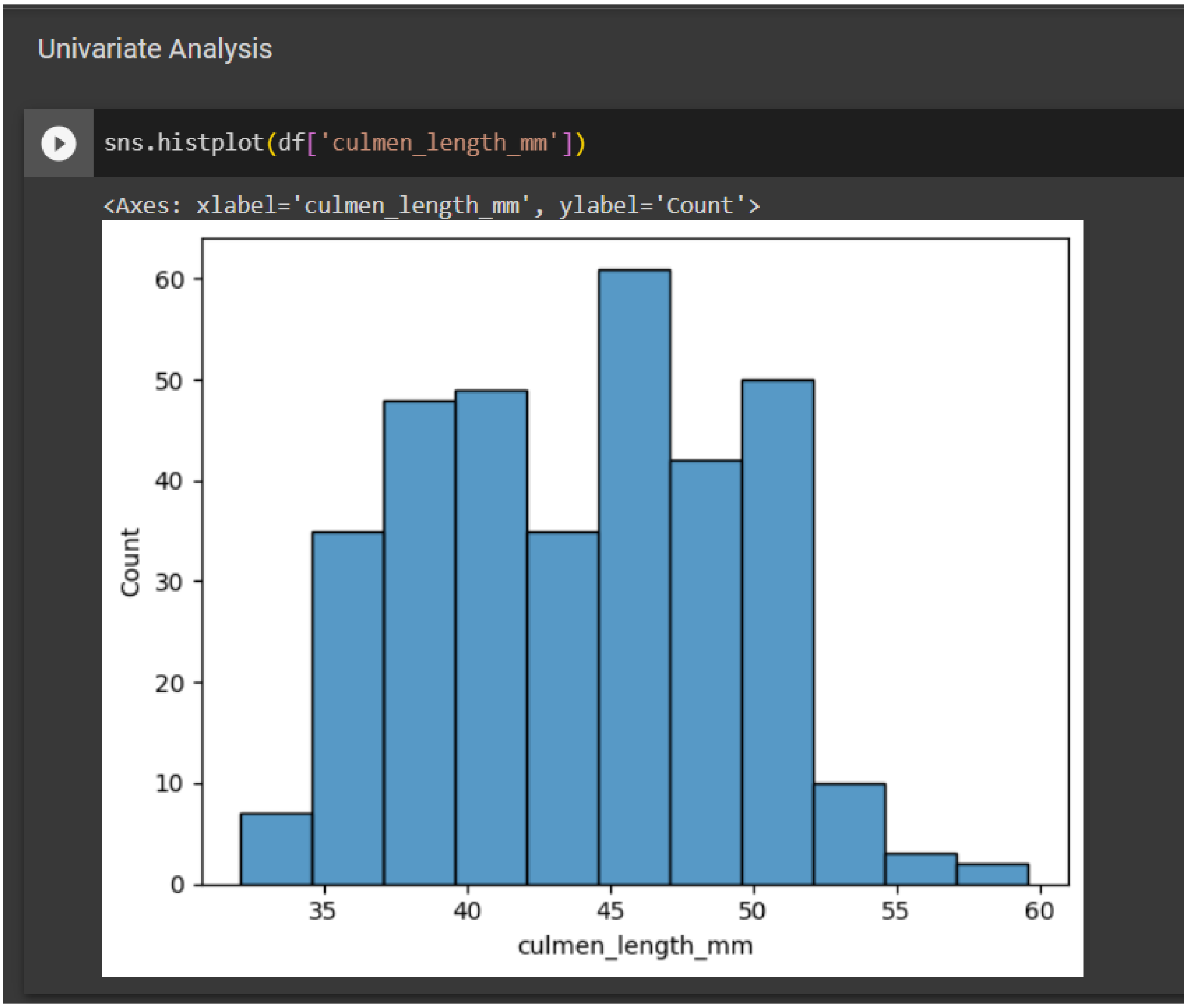
Penguin Classification Analysis

```
import pandas as pd
import matplotlib.pyplot as plt
from matplotlib import rcParams
import seaborn as sns
df = pd.read_csv('/content/penguins_size.csv')
df.head()
```

	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
3	Adelie	Torgersen	NaN	NaN	NaN	NaN	NaN
4	Adelie	Torgersen	36.7	19.3	193.0	3450.0	FEMALE

3. Perform Below Visualizations.

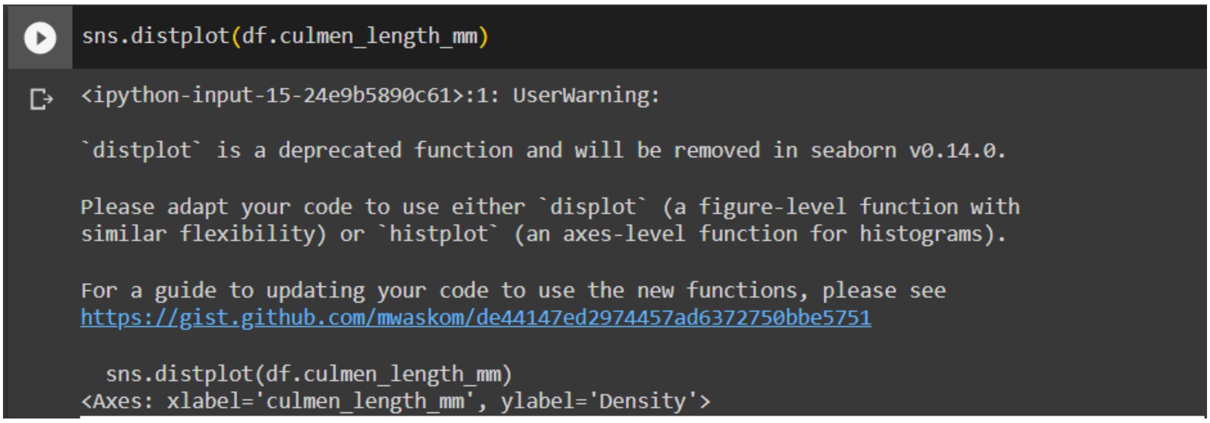
- Univariate Analysis



Univariate Analysis

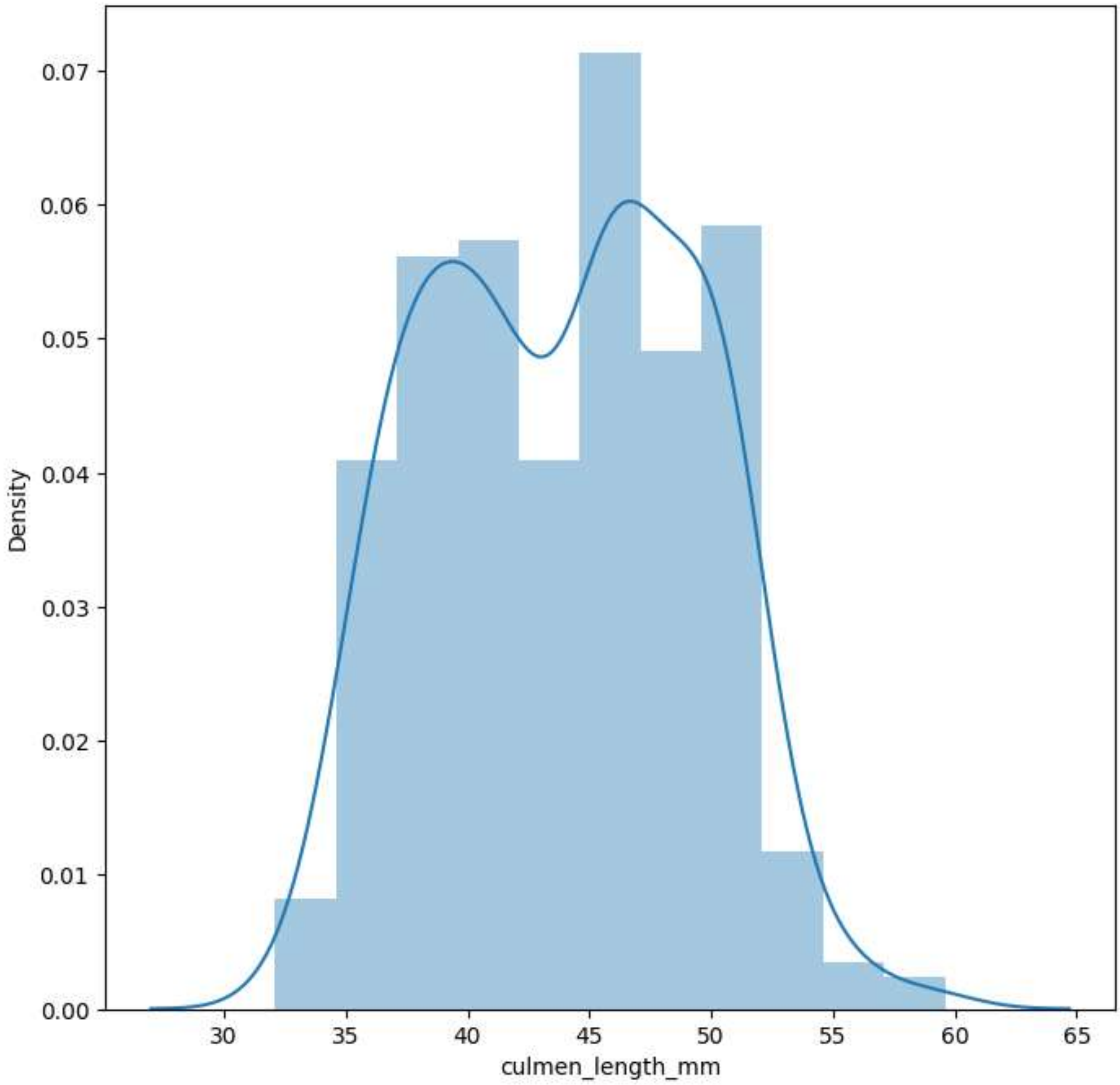
```
sns.histplot(df['culmen_length_mm'])
```

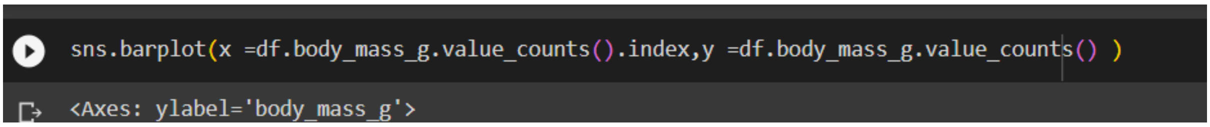
```
<Axes: xlabel='culmen_length_mm', ylabel='Count'>
```



```
sns.distplot(df.culmen_length_mm)
```

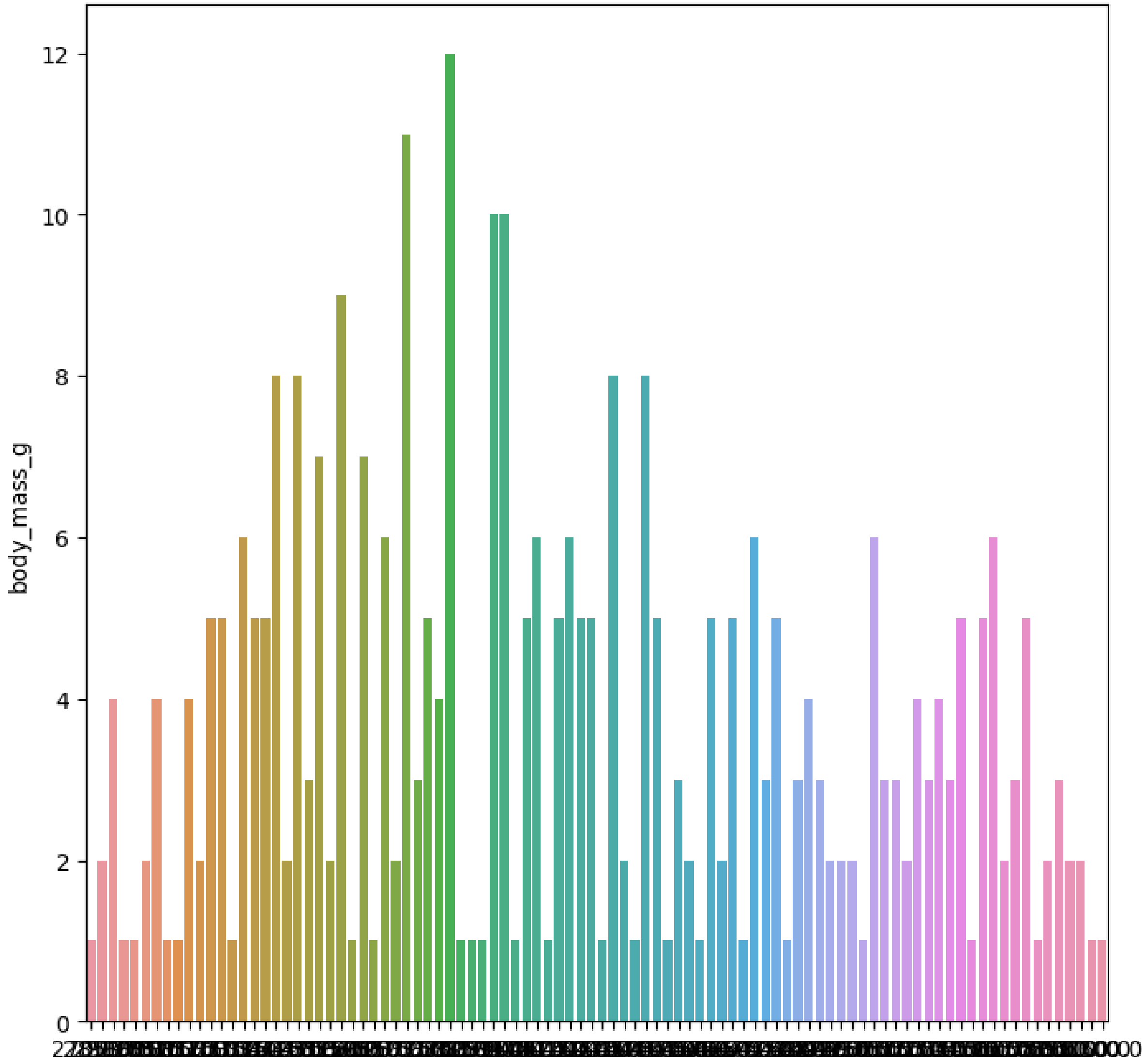
```
<ipython-input-15-24e9b5890c61>:1: UserWarning:

`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.culmen_length_mm)
<Axes: xlabel='culmen_length_mm', ylabel='Density'>
```



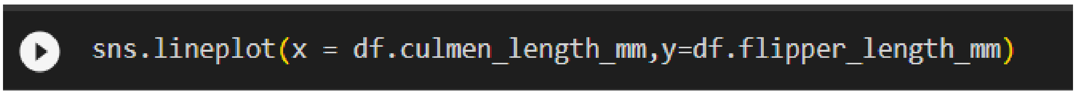


```
sns.barplot(x =df.body_mass_g.value_counts().index,y =df.body_mass_g.value_counts() )
```

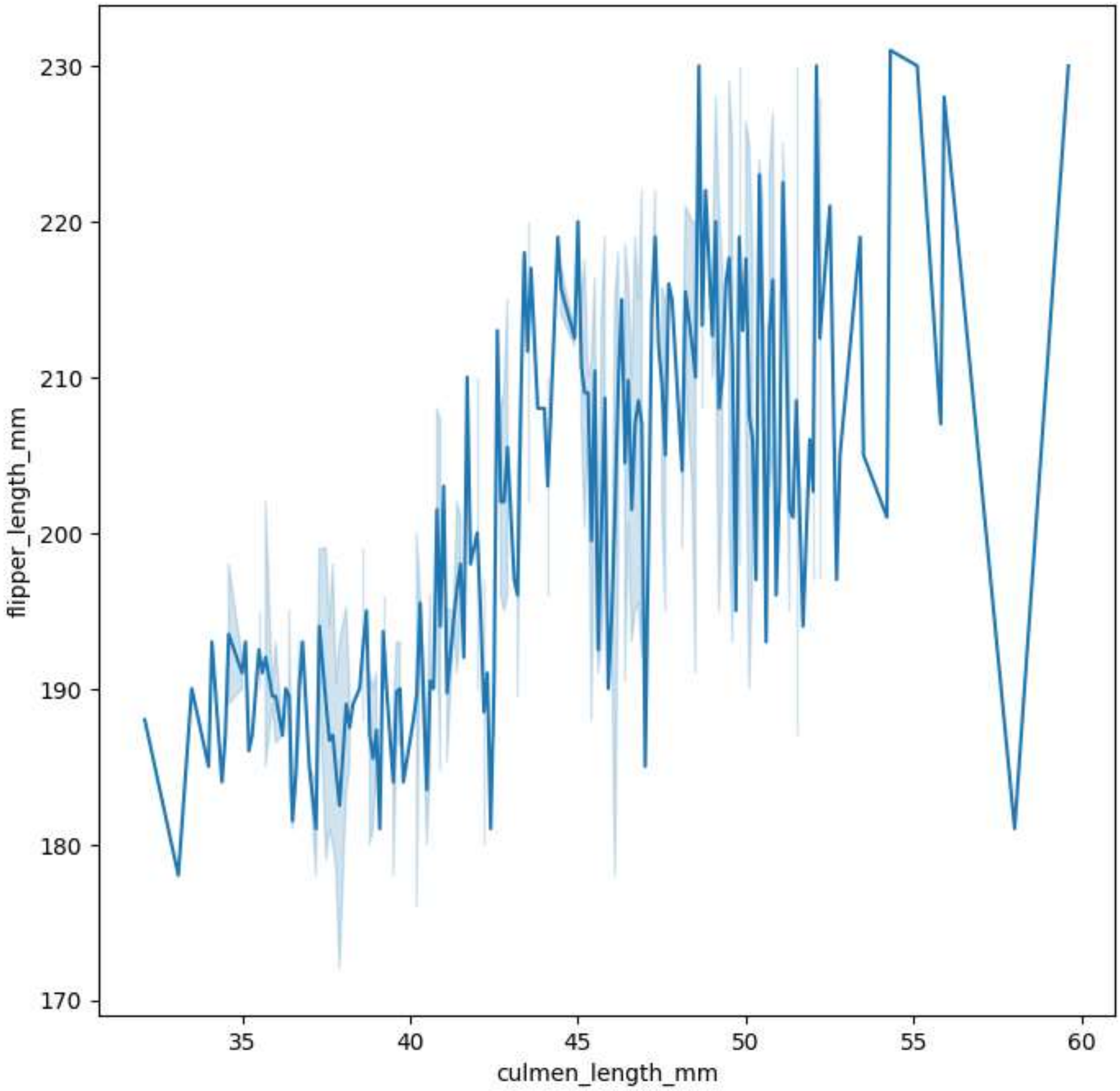
```
<Axes: ylabel='body_mass_g'>
```

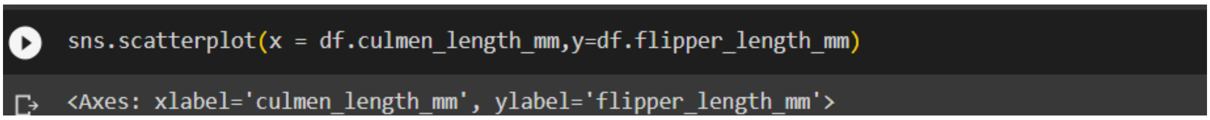


- ## Bi- Variate Analysis



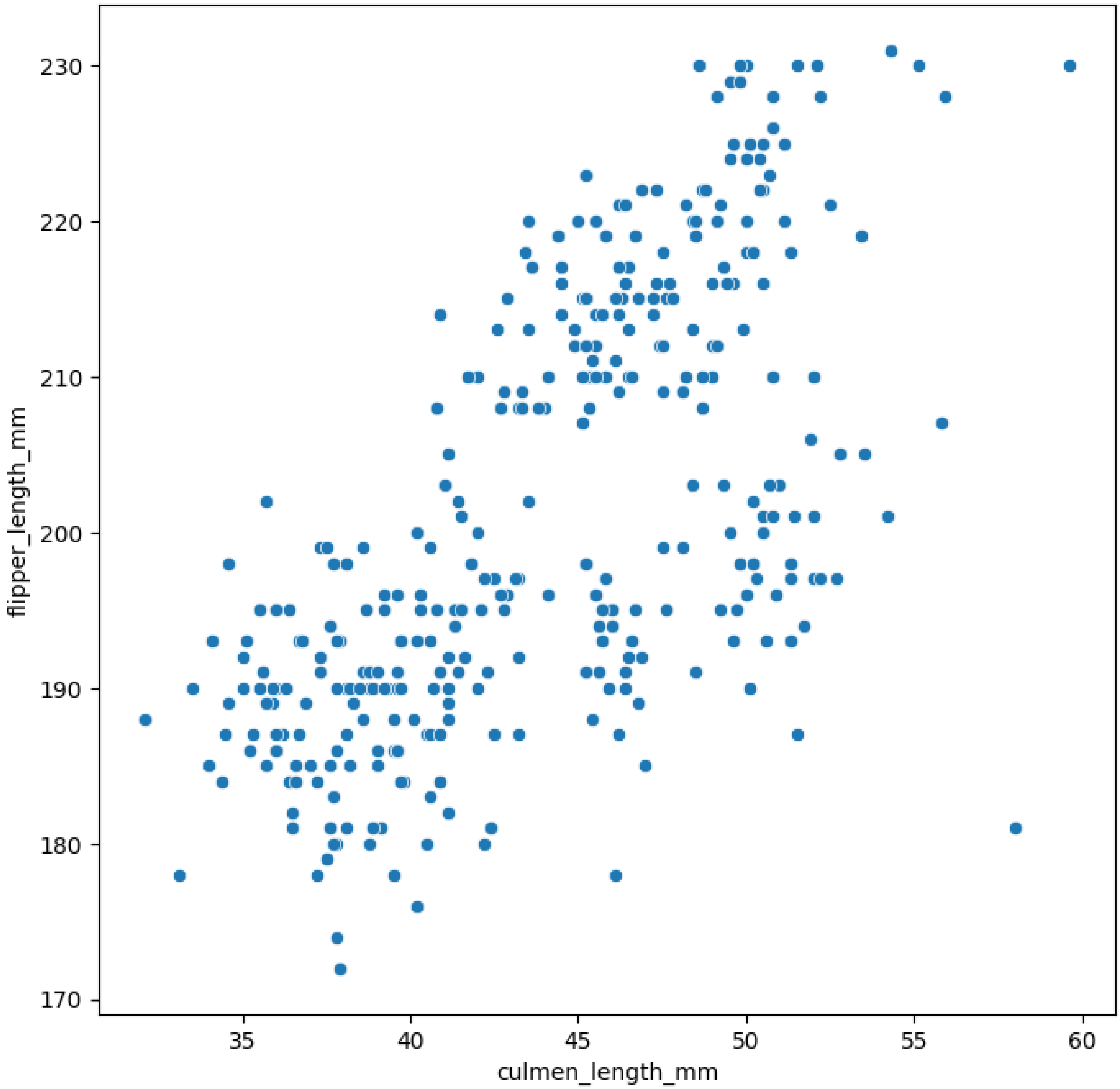
```
sns.lineplot(x = df.culmen_length_mm,y=df.flipper_length_mm)
```

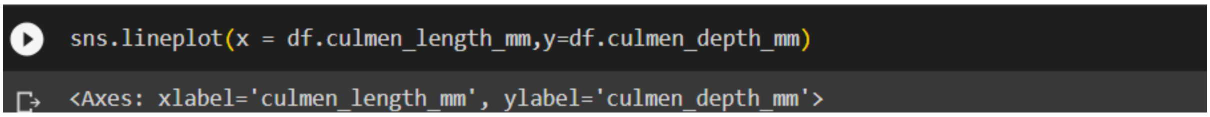




```
sns.scatterplot(x = df.culmen_length_mm,y=df.flipper_length_mm)
```

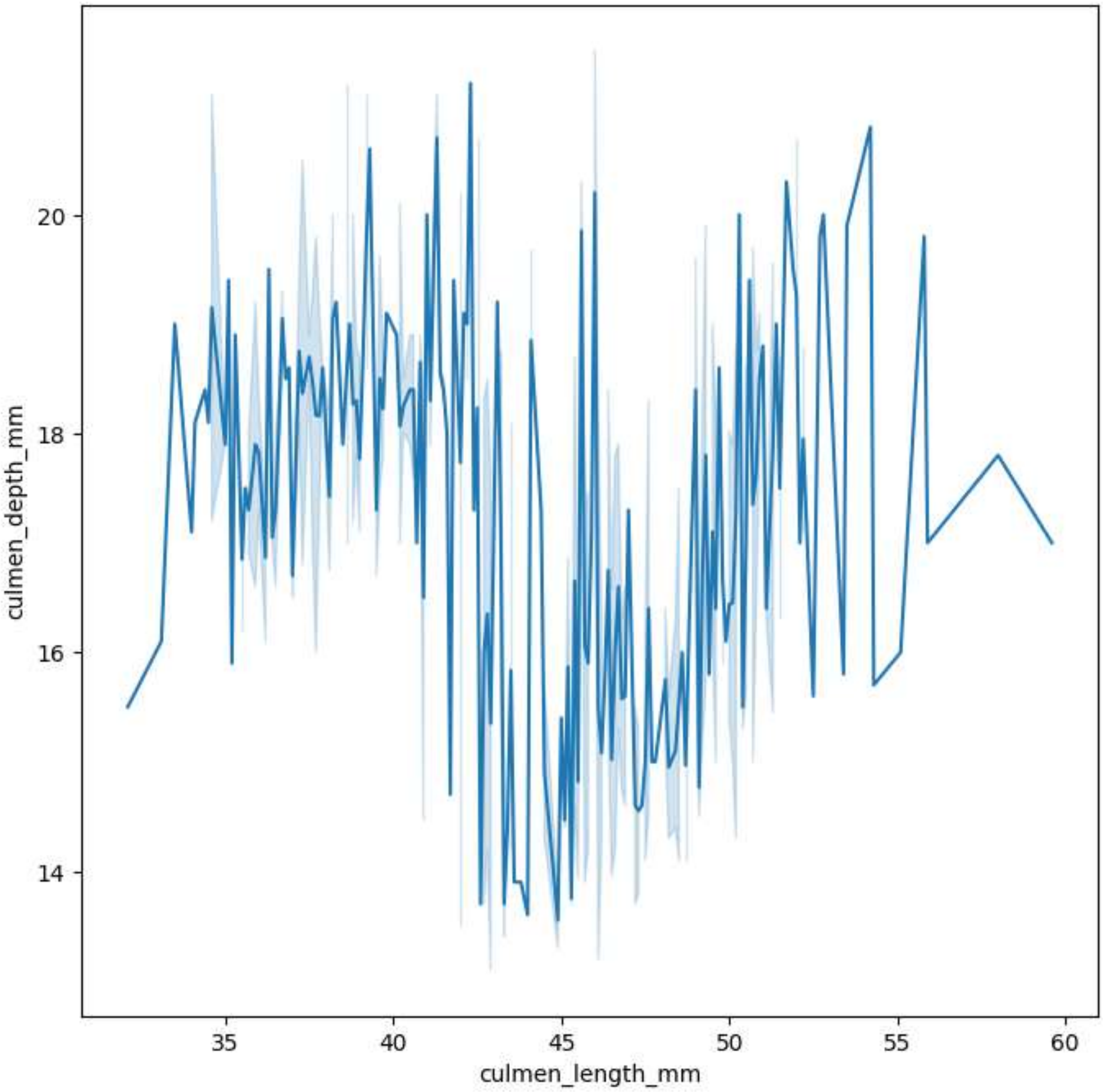
```
<Axes: xlabel='culmen_length_mm', ylabel='flipper_length_mm'>
```



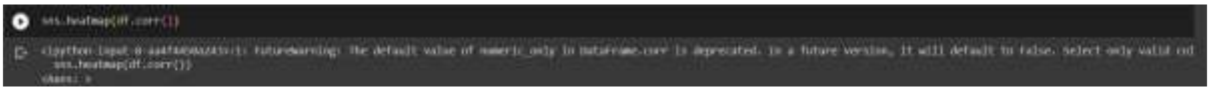


```
sns.lineplot(x = df.culmen_length_mm,y=df.culmen_depth_mm)
```

```
<Axes: xlabel='culmen_length_mm', ylabel='culmen_depth_mm'>
```

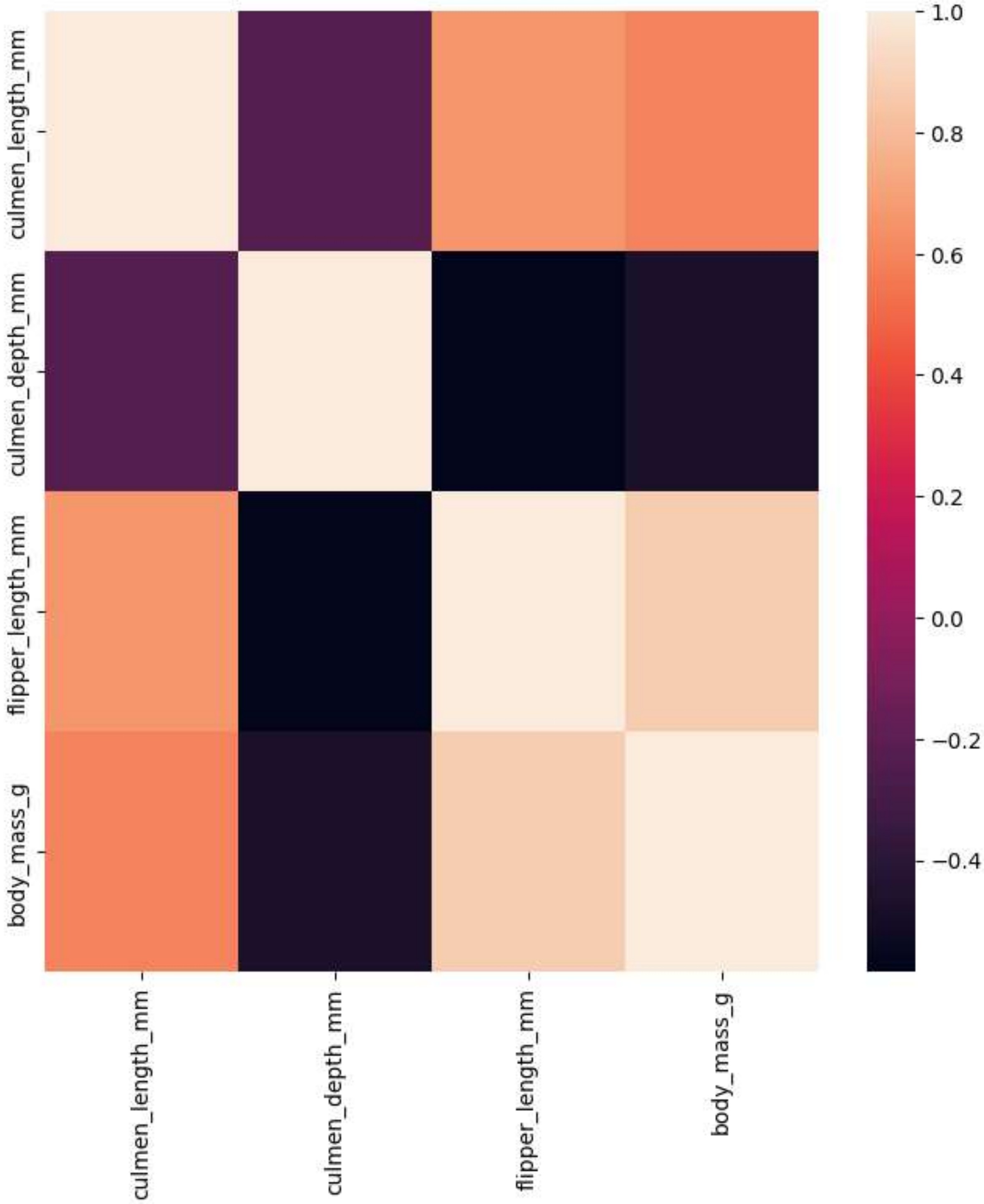


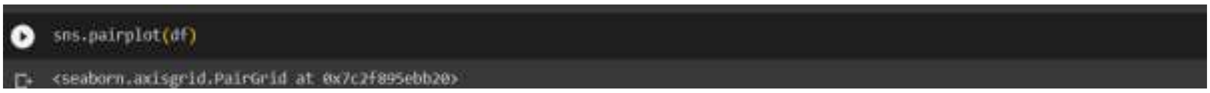
- ## Multi-Variate Analysis



```
sns.heatmap(df.corr())
```

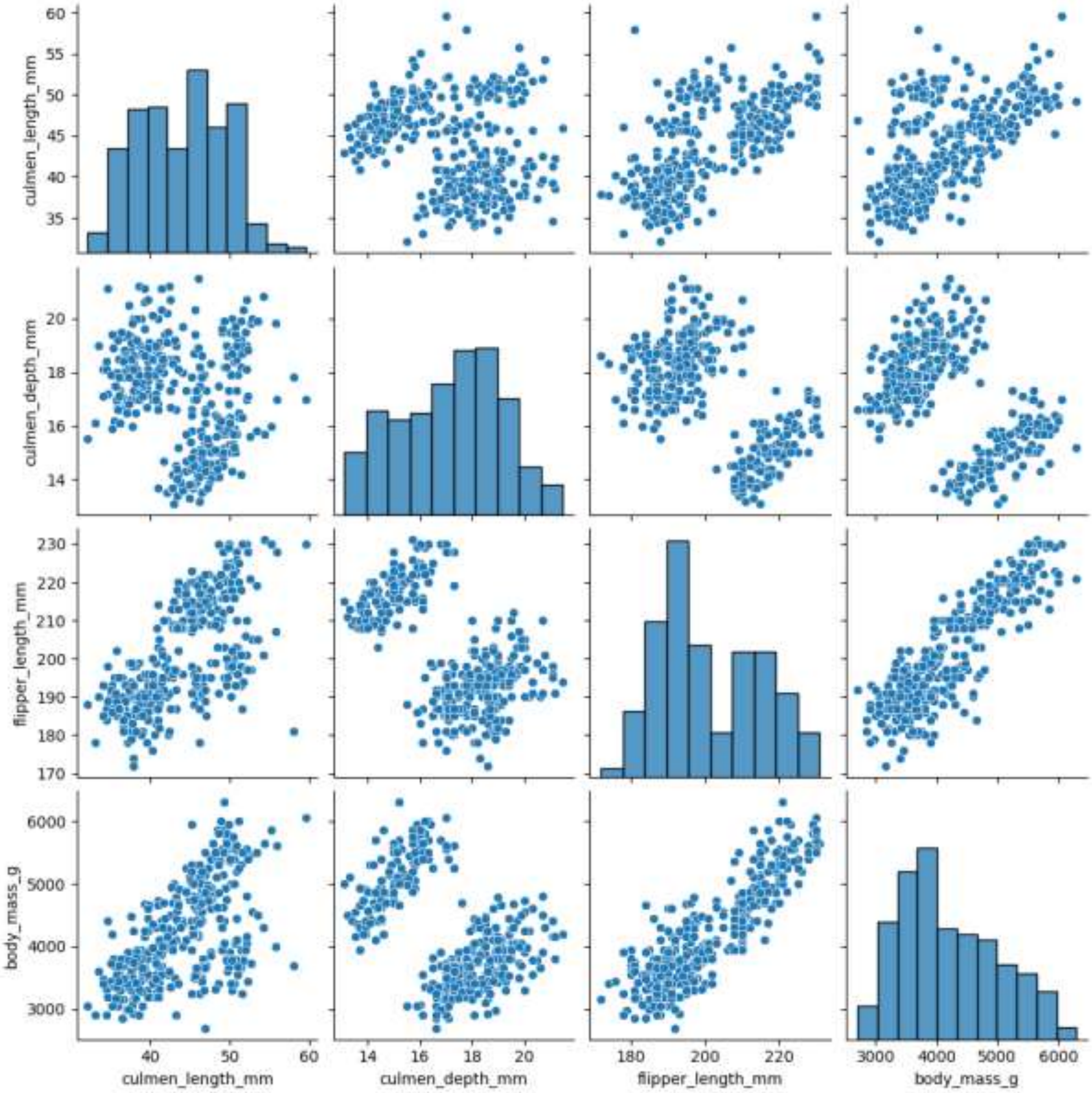
```
<ipython-input-8-[illegible]>:1: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid col
  sns.heatmap(df.corr())
<Axes: >
```



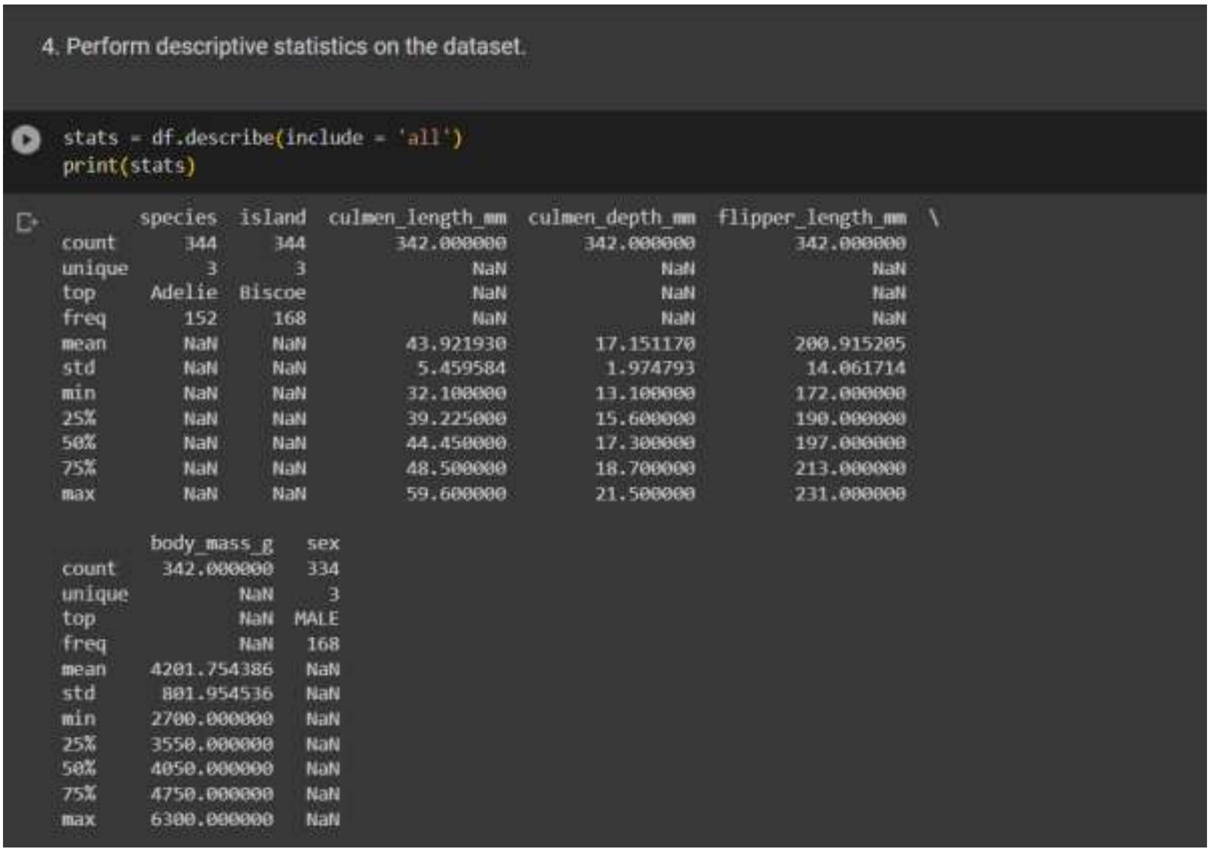


```
sns.pairplot(df)
```

```
<seaborn.axisgrid.PairGrid at 0x7c2f895ebb20>
```



4. Perform descriptive statistics on the dataset

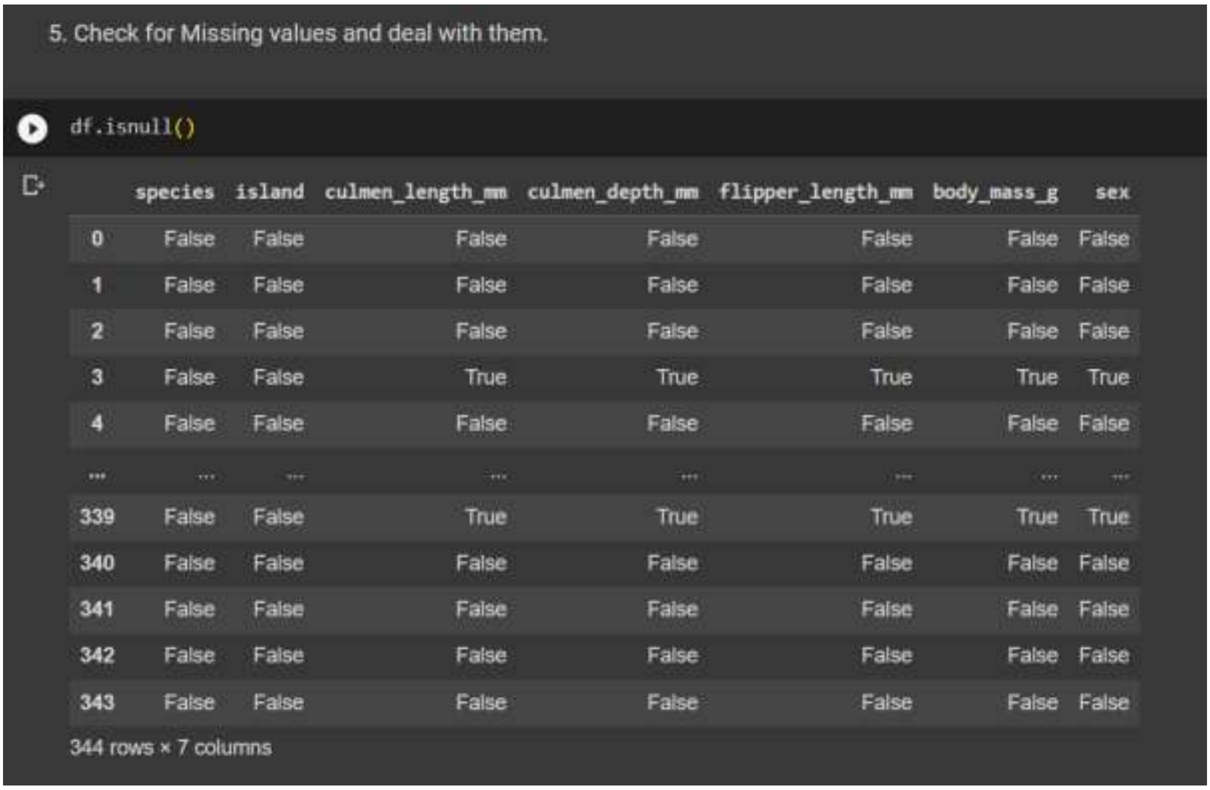


4. Perform descriptive statistics on the dataset.

```
stats = df.describe(include = 'all')
print(stats)
```

```
        species  island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  \
count       344     344        342.000000       342.000000         342.000000
unique        3       3               NaN              NaN                NaN
top      Adelie  Biscoe               NaN              NaN                NaN
freq        152     168               NaN              NaN                NaN
mean        NaN     NaN         43.921930        17.151170         200.915205
std         NaN     NaN          5.459584         1.974793          14.061714
min         NaN     NaN         32.100000        13.100000         172.000000
25%         NaN     NaN         39.225000        15.600000         190.000000
50%         NaN     NaN         44.450000        17.300000         197.000000
75%         NaN     NaN         48.500000        18.700000         213.000000
max         NaN     NaN         59.600000        21.500000         231.000000

        body_mass_g   sex
count    342.000000   334
unique          NaN     3
top             NaN  MALE
freq            NaN   168
mean    4201.754386   NaN
std      801.954536   NaN
min     2700.000000   NaN
25%     3550.000000   NaN
50%     4050.000000   NaN
75%     4750.000000   NaN
max     6300.000000   NaN
```

5. Check for Missing values and deal with them.

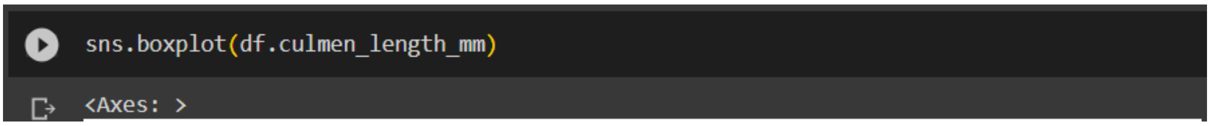


5. Check for Missing values and deal with them.

```
df.isnull()
```

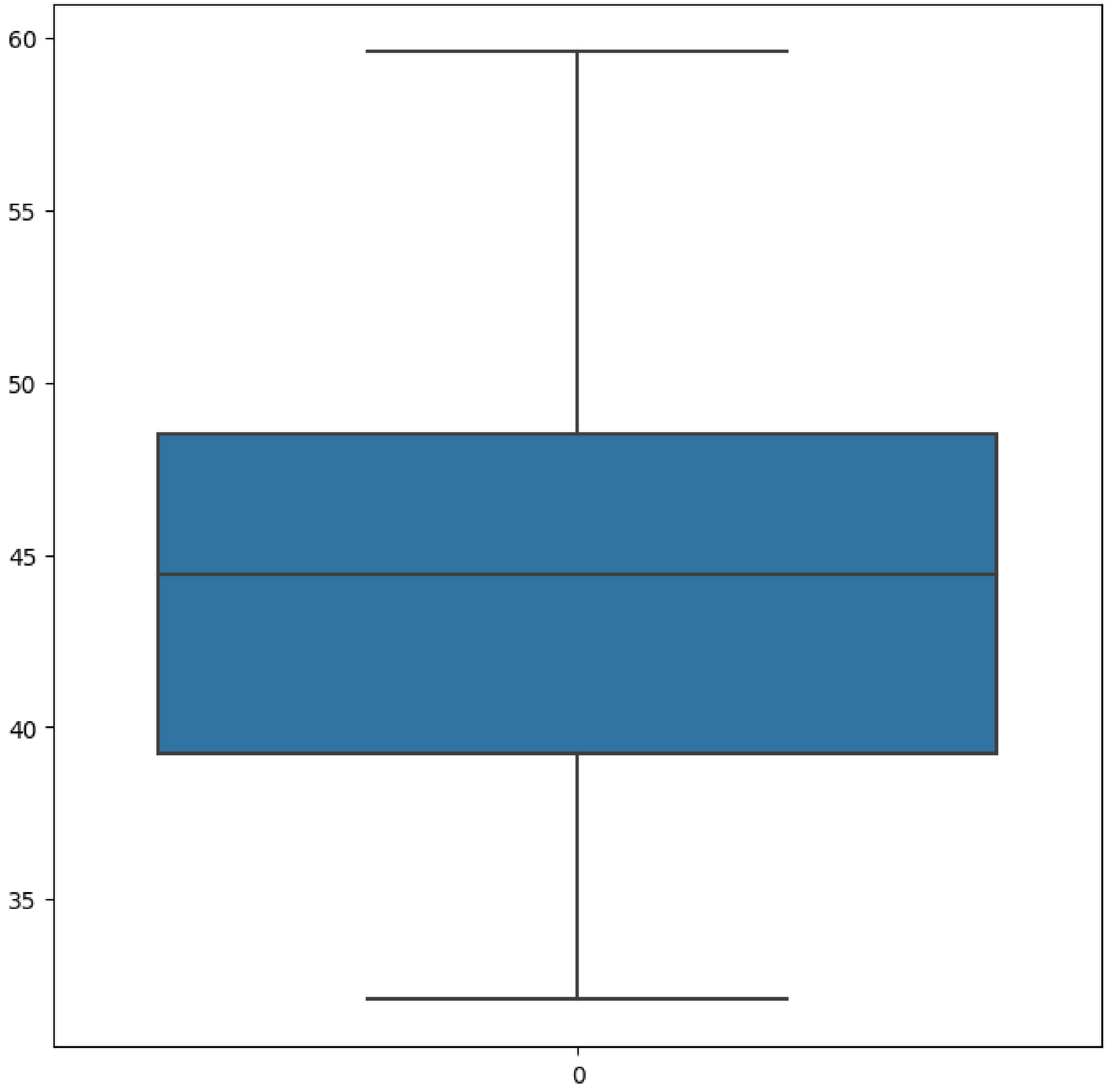
```
     species  island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  body_mass_g    sex
0      False   False             False            False              False        False  False
1      False   False             False            False              False        False  False
2      False   False             False            False              False        False  False
3      False   False              True             True               True         True   True
4      False   False             False            False              False        False  False
...      ...     ...               ...              ...                ...          ...    ...
339    False   False              True             True               True         True   True
340    False   False             False            False              False        False  False
341    False   False             False            False              False        False  False
342    False   False             False            False              False        False  False
343    False   False             False            False              False        False  False
344 rows × 7 columns
```

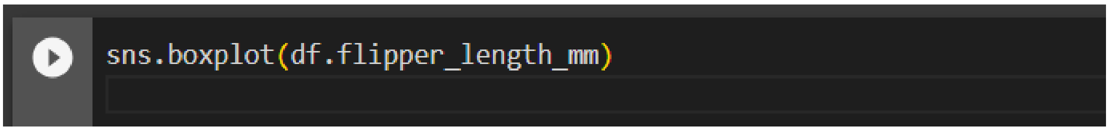
6. Find the outliers and replace them outliers.



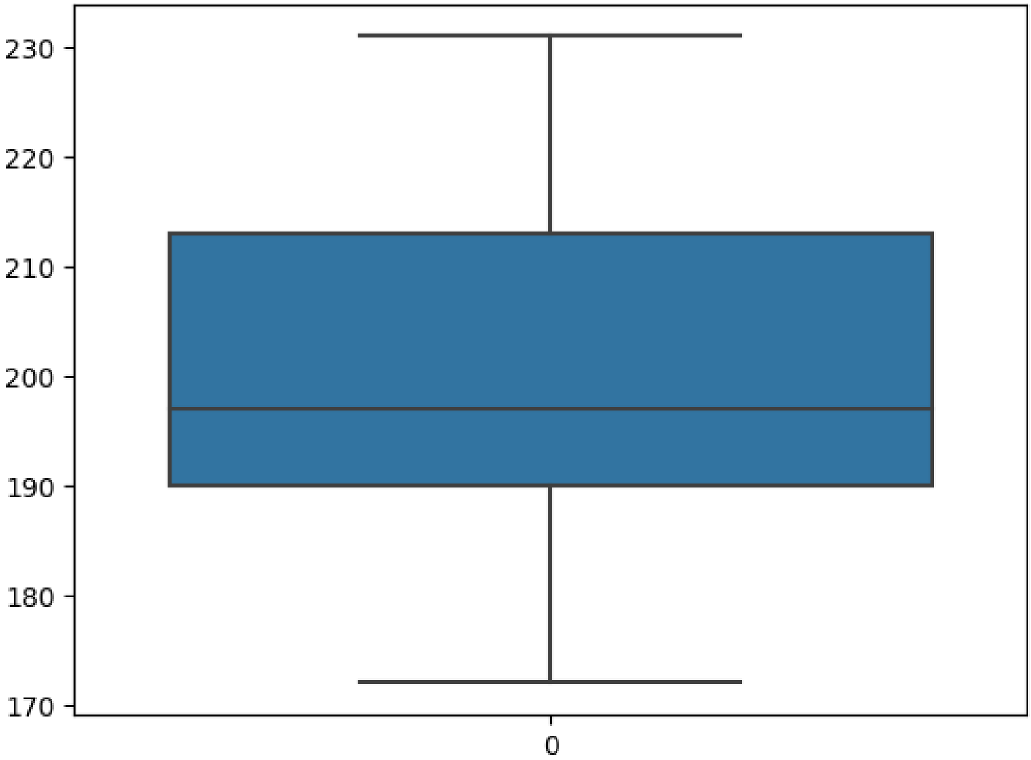
```
sns.boxplot(df.culmen_length_mm)
```

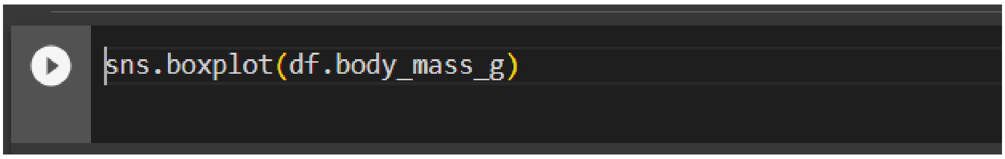
```
<Axes: >
```



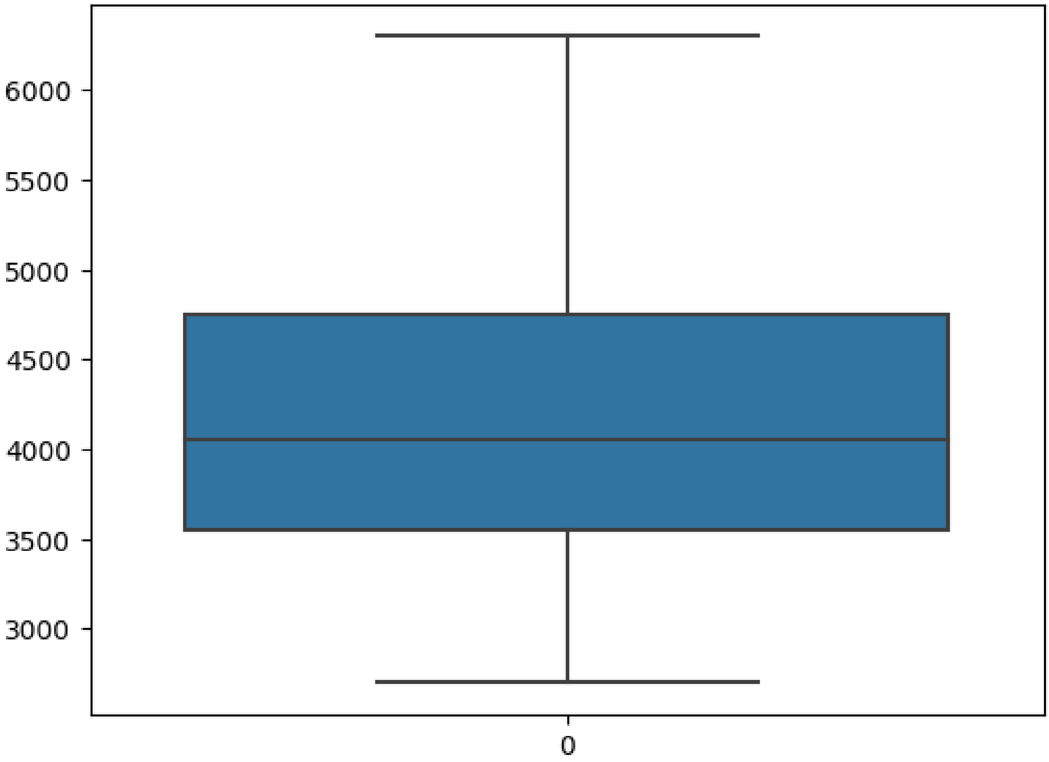


```
sns.boxplot(df.flipper_length_mm)
```

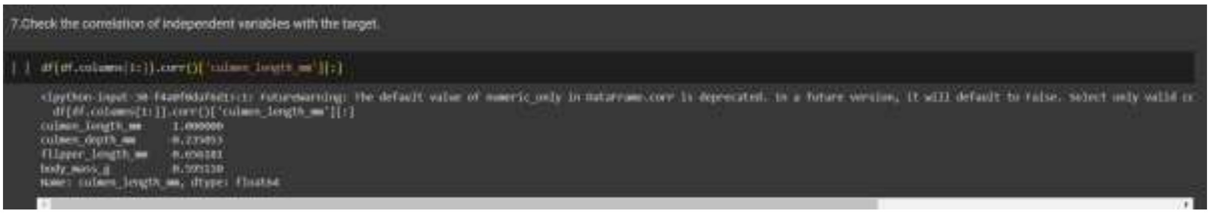




```
sns.boxplot(df.body_mass_g)
```



7.Check the correlation of independent variables with the target.

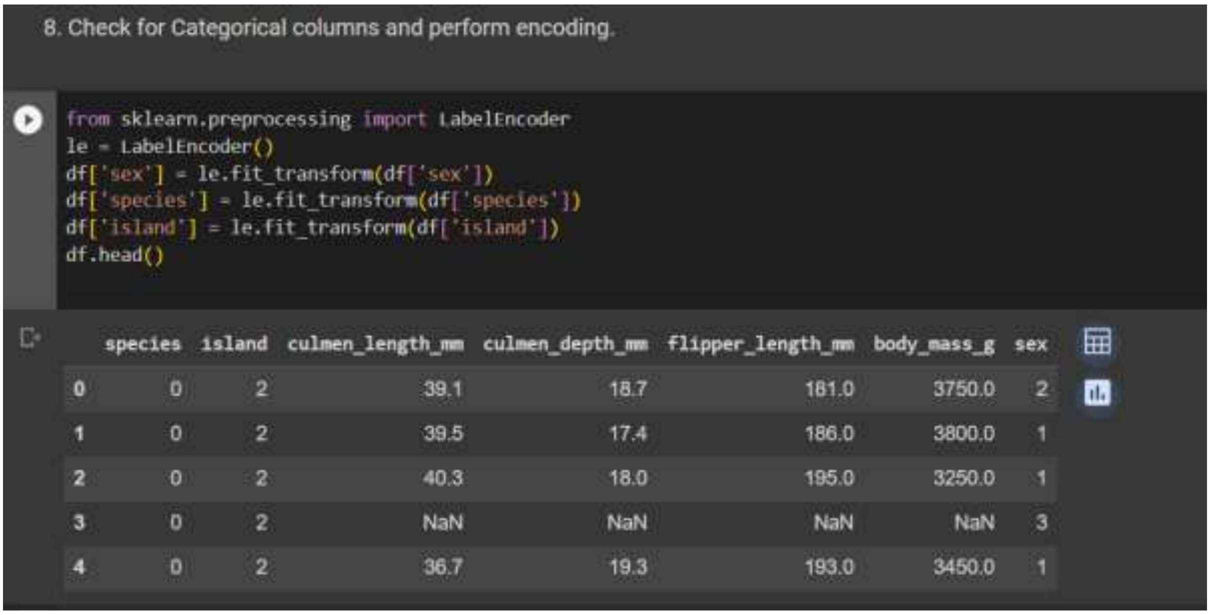


7.Check the correlation of independent variables with the target.

```
[ ] df[df.columns[1:]].corr()['culmen_length_mm'][:]
```

```
<ipython-input-30-f4a0f0daf6d1>: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 co
  df[df.columns[1:]].corr()['culmen_length_mm'][:]
culmen_length_mm     1.000000
culmen_depth_mm      0.235053
flipper_length_mm    0.656181
body_mass_g          0.595110
Name: culmen_length_mm, dtype: float64
```

8. Check for Categorical columns and perform encoding.

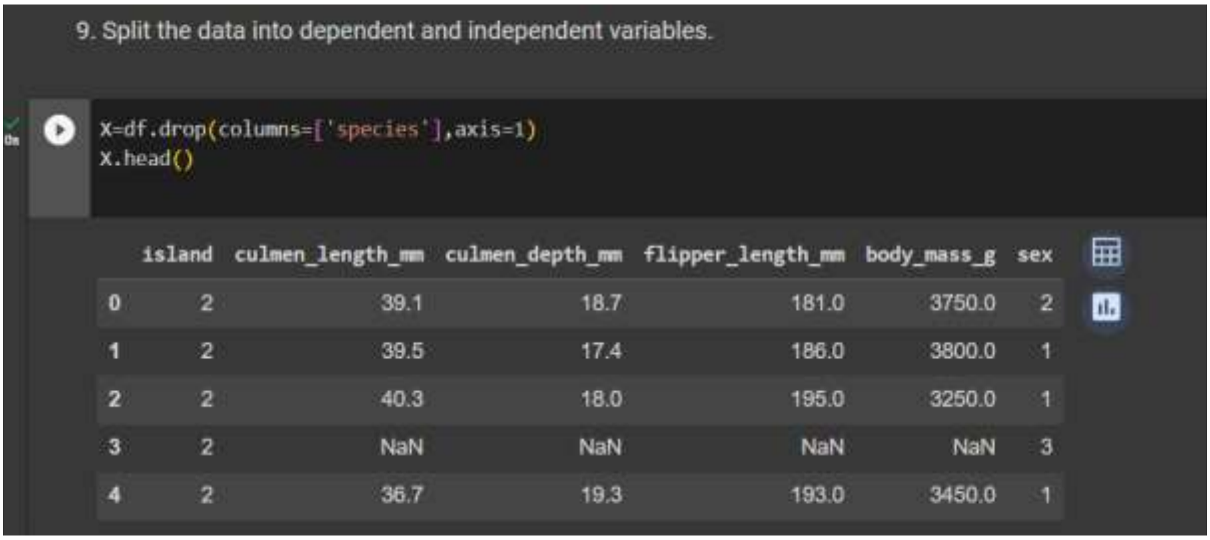


8. Check for Categorical columns and perform encoding.

```python
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()
```

```
   species  island  culmen_length_mm  culmen_depth_mm  flipper_length_mm  body_mass_g  sex
0        0       2              39.1             18.7              181.0       3750.0    2
1        0       2              39.5             17.4              186.0       3800.0    1
2        0       2              40.3             18.0              195.0       3250.0    1
3        0       2               NaN              NaN                NaN          NaN    3
4        0       2              36.7             19.3              193.0       3450.0    1
```

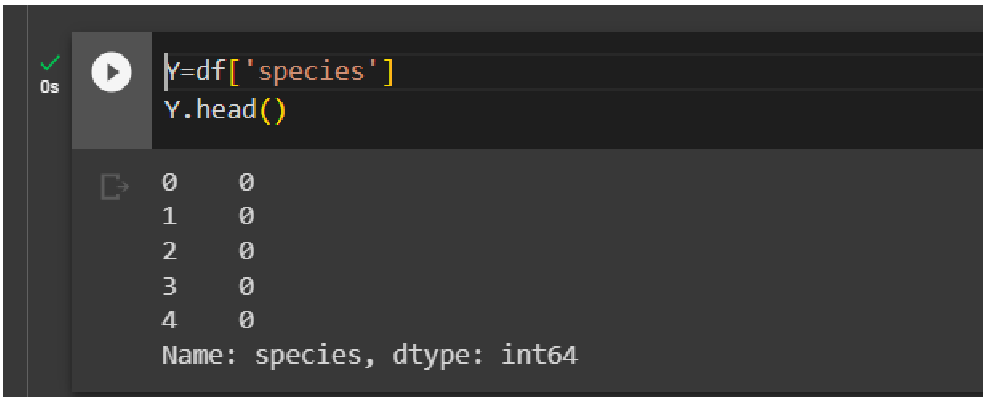
9. Split the data into dependent and independent variables.



9. Split the data into dependent and independent variables.

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

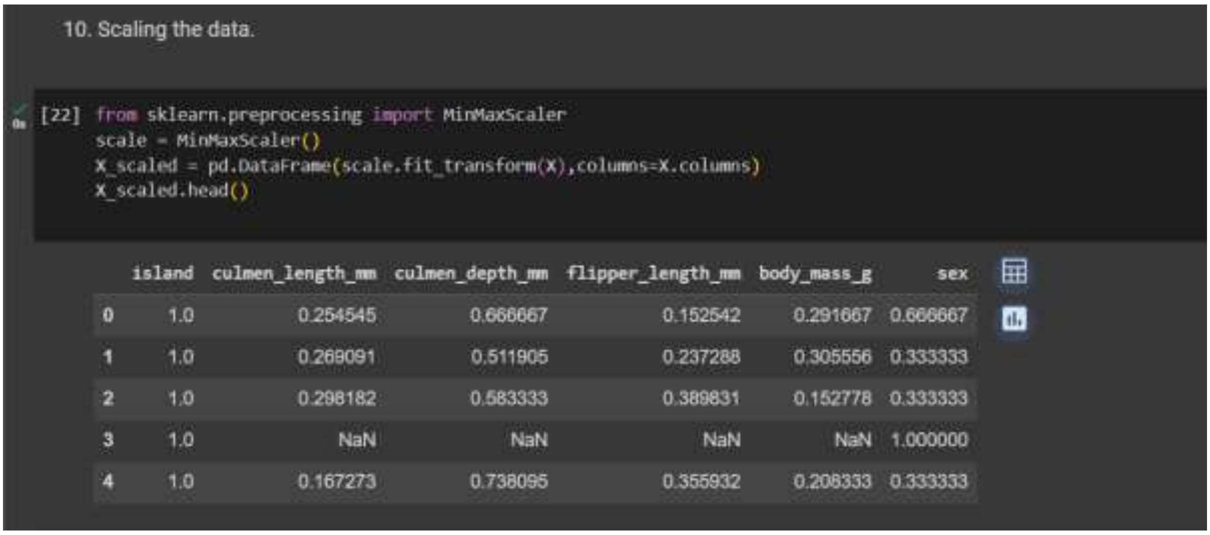
	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
0	2	39.1	18.7	181.0	3750.0	2
1	2	39.5	17.4	186.0	3800.0	1
2	2	40.3	18.0	195.0	3250.0	1
3	2	NaN	NaN	NaN	NaN	3
4	2	36.7	19.3	193.0	3450.0	1



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

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

10. Scaling the data

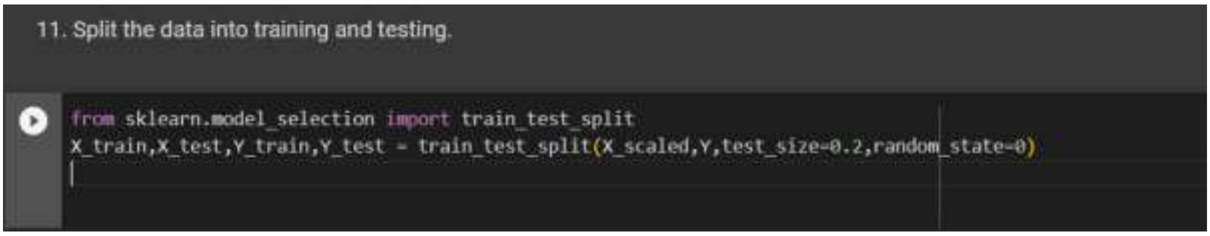


10. Scaling the data.

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

	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
0	1.0	0.254545	0.666667	0.152542	0.291667	0.666667
1	1.0	0.269091	0.511905	0.237288	0.305556	0.333333
2	1.0	0.298182	0.583333	0.389831	0.152778	0.333333
3	1.0	NaN	NaN	NaN	NaN	1.000000
4	1.0	0.167273	0.738095	0.355932	0.208333	0.333333

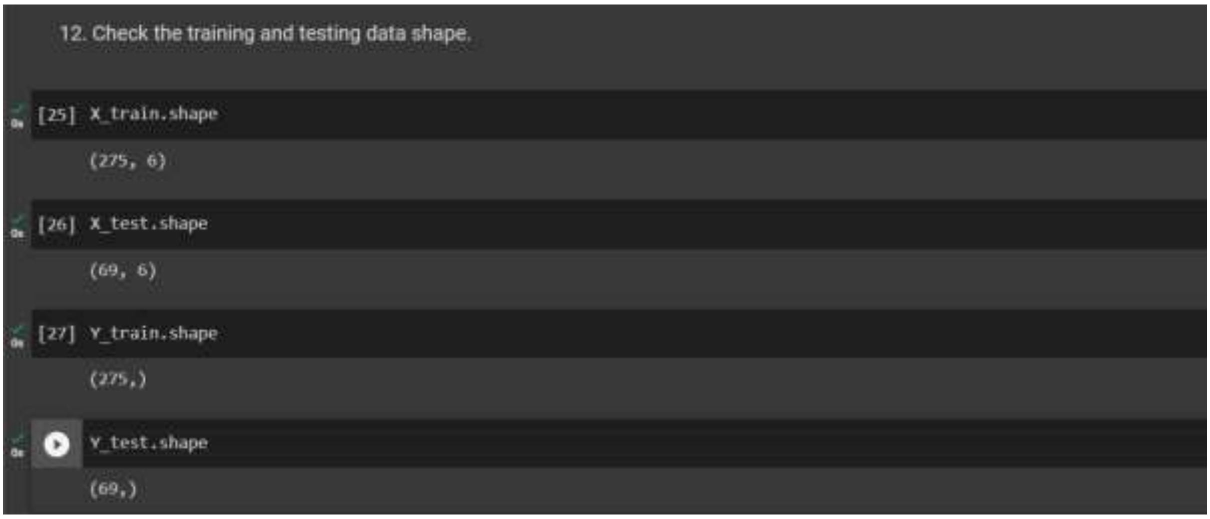
11. Split the data into training and testing.



11. Split the data into training and testing.

```
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.



12. Check the training and testing data shape.

```
[25] X_train.shape

(275, 6)

[26] X_test.shape

(69, 6)

[27] Y_train.shape

(275,)

Y_test.shape

(69,)
```