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

1&2 Downloading & Loading Dataset

In [3]:
```
##Loading Dataset

df=pd.read_csv("penguins_size.csv")
df.head()
```

Out[3]:

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

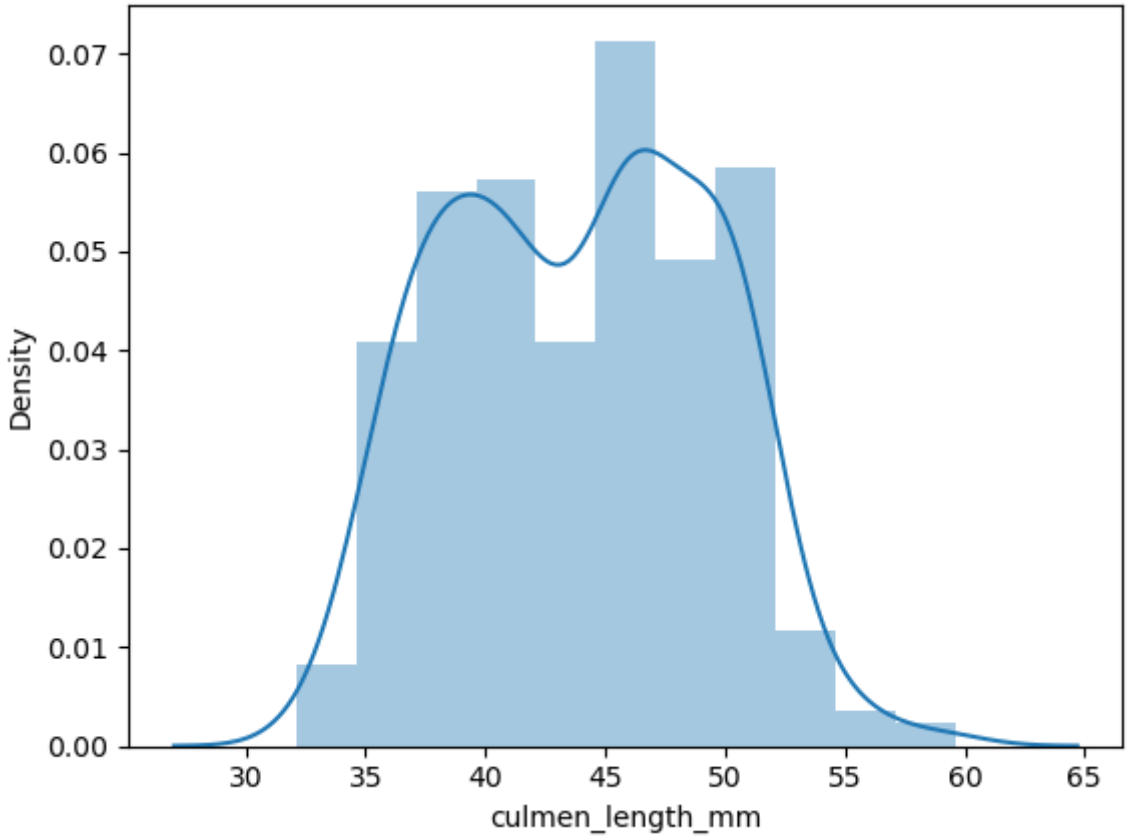
3. visualizations

3.1 Univariate Analysis

In [4]:
```
sns.distplot(df["culmen_length_mm"])
```

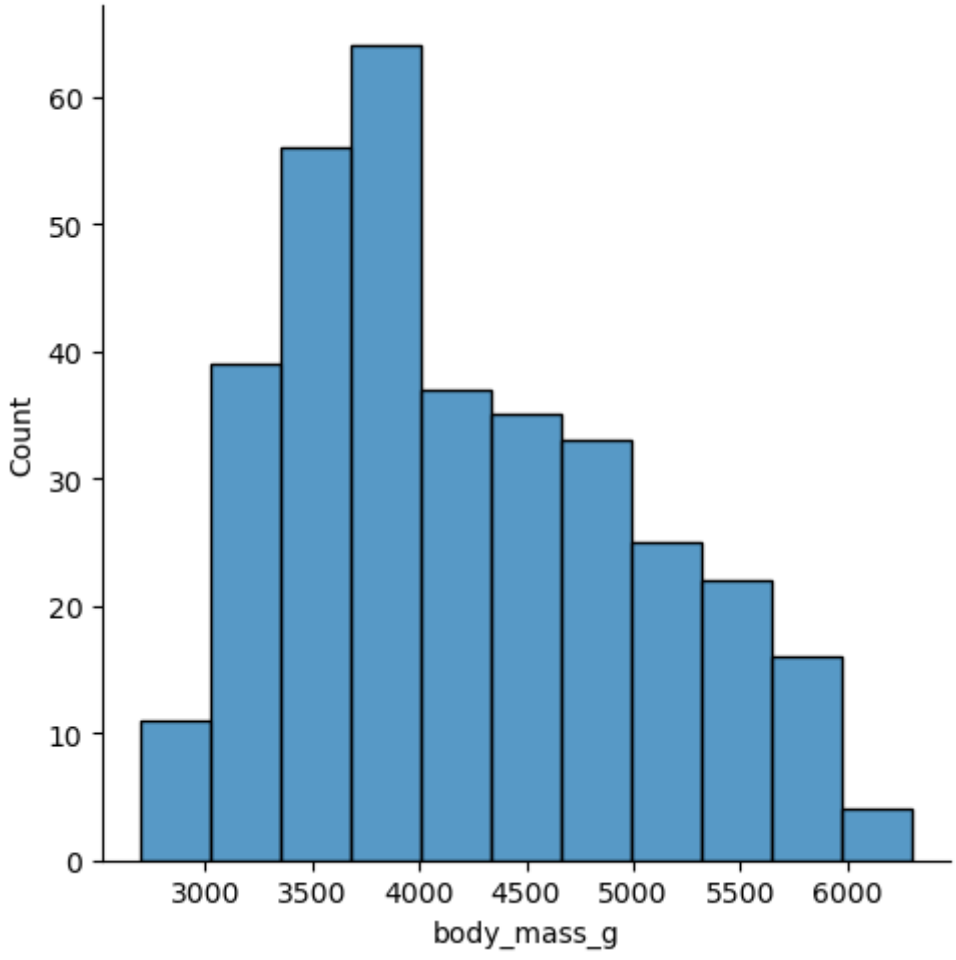
```
C:\Users\DELL\AppData\Local\Temp\ipykernel_12584\2669382467.py:1: UserWarning:

`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"])
```

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



In [5]:
```
sns.displot(df["body_mass_g"])
```

Out[5]:
```
<seaborn.axisgrid.FacetGrid at 0x1f4bde12830>
```



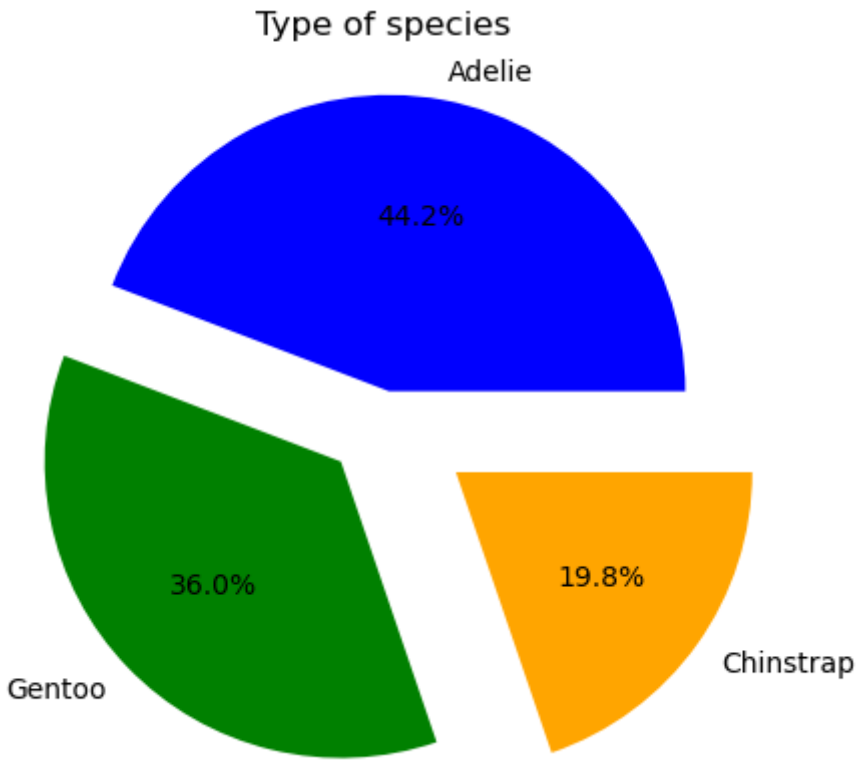
In [6]:
```
df["species"].unique()
```

Out[6]:
```
array(['Adelie', 'Chinstrap', 'Gentoo'], dtype=object)
```

In [7]:
```
df["species"].value_counts()
```

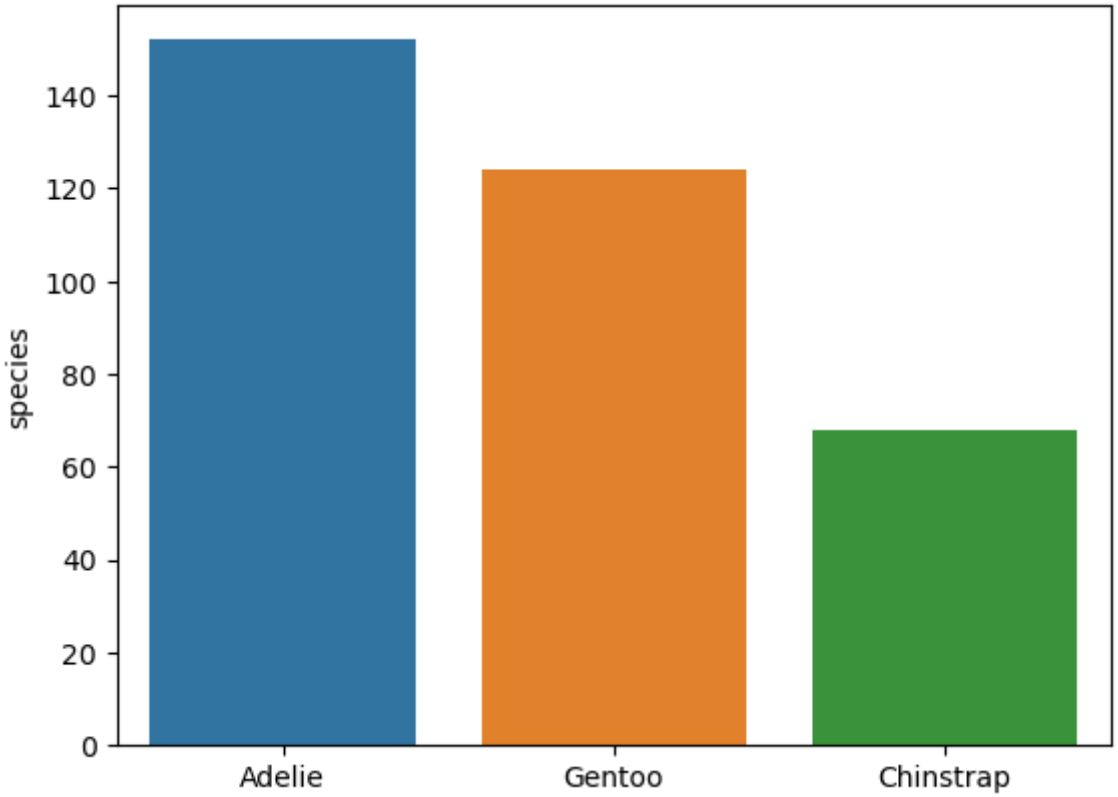
Out[7]:
```
Adelie       152
Gentoo       124
Chinstrap     68
Name: species, dtype: int64
```

In [8]:
```
plt.pie(df["species"].value_counts(),[0.1,0.2,0.3],labels=['Adelie','Gentoo','Chin
plt.title('Type of species')
plt.show()
```



In [9]:
```
sns.barplot(x =df["species"].value_counts().index,y =df["species"].value_counts()
```

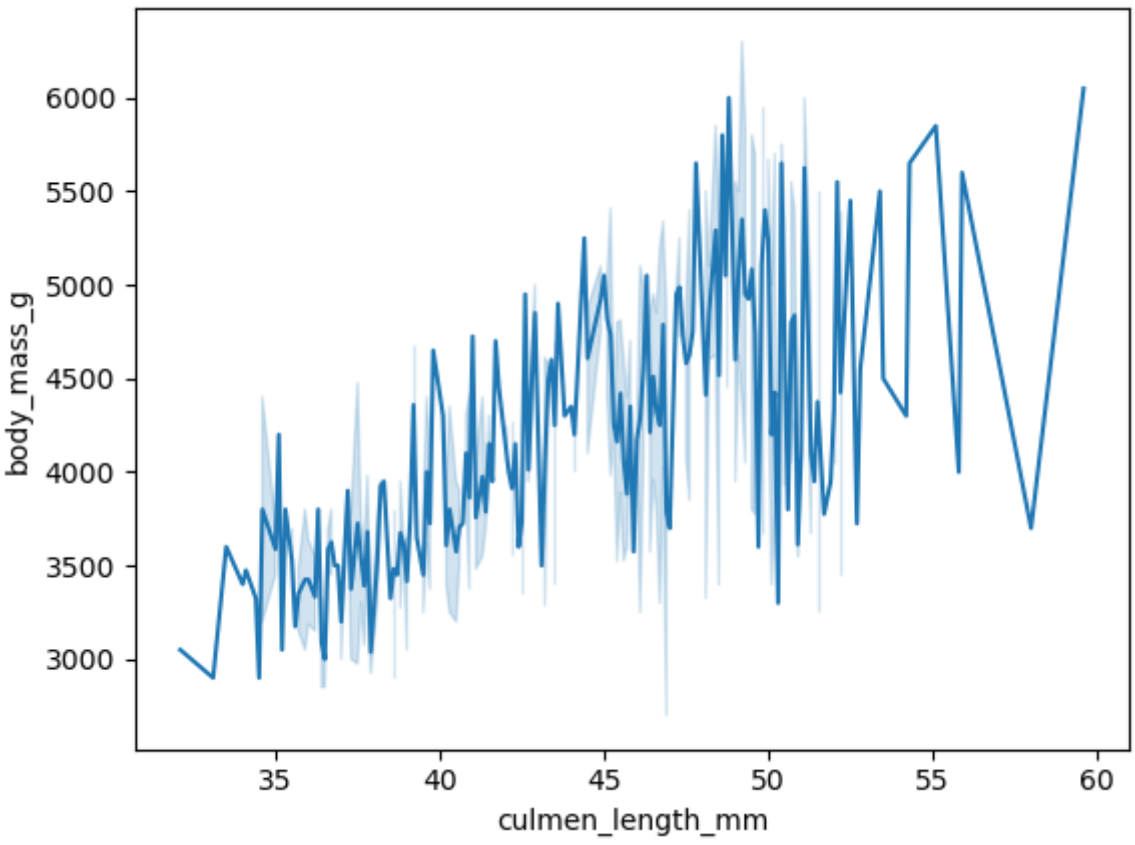
Out[9]:
```
<Axes: ylabel='species'>
```



3.2 Bivariate Analysis

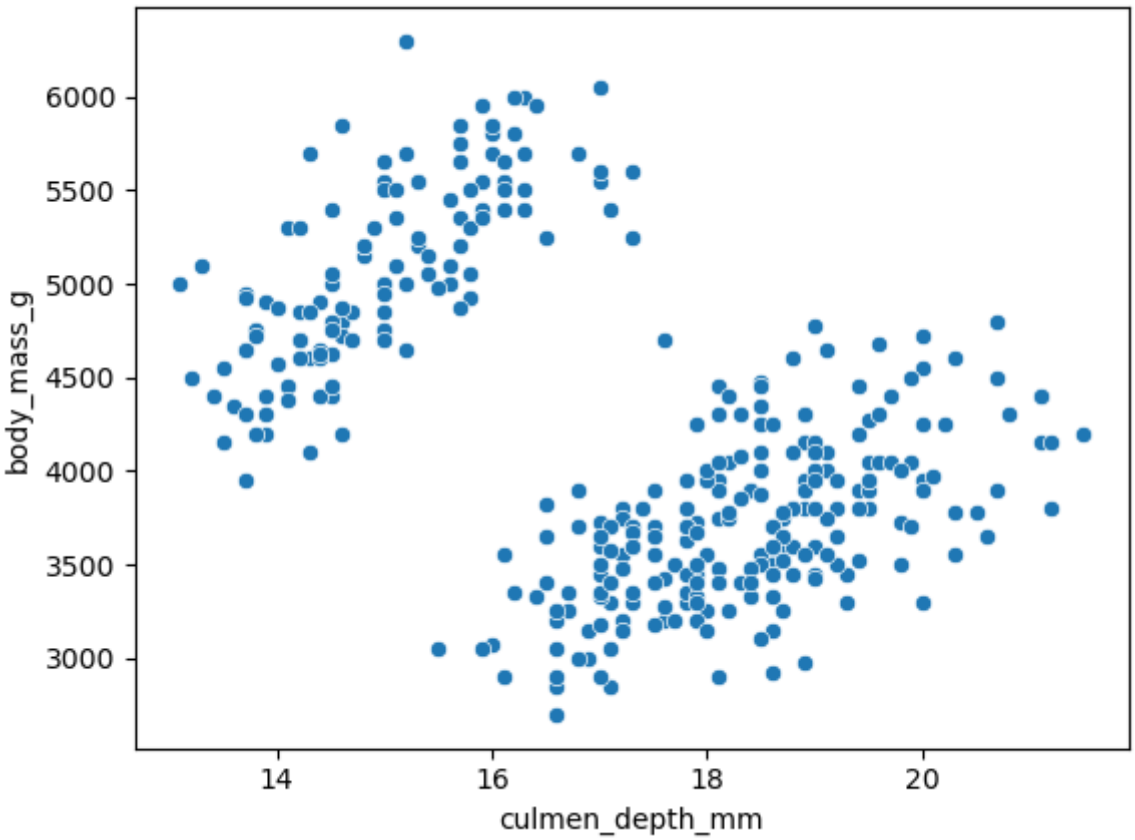
In [10]:
```
sns.lineplot(x = df["culmen_length_mm"],y=df["body_mass_g"])
```

Out[10]:
```
<Axes: xlabel='culmen_length_mm', ylabel='body_mass_g'>
```



In [11]:
```
sns.scatterplot(x=df["culmen_depth_mm"],y=df["body_mass_g"])
```

Out[11]:
```
<Axes: xlabel='culmen_depth_mm', ylabel='body_mass_g'>
```

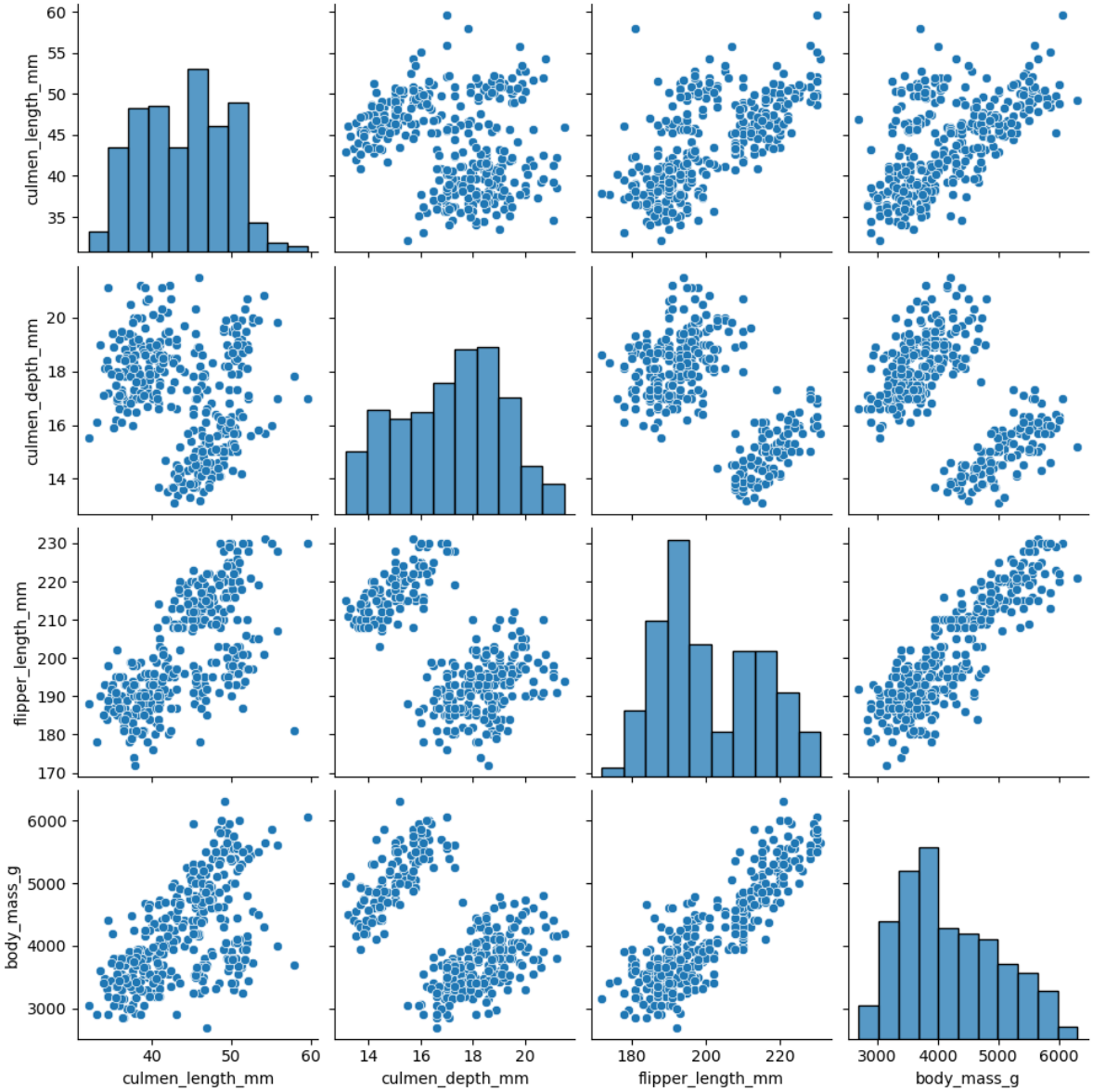


3.3 Multivariate Analysis

In [12]:
```
plt.figure(figsize=(4,4))
sns.pairplot(df)
```

Out[12]:
```
<seaborn.axisgrid.PairGrid at 0x1f4c20c8970>
```

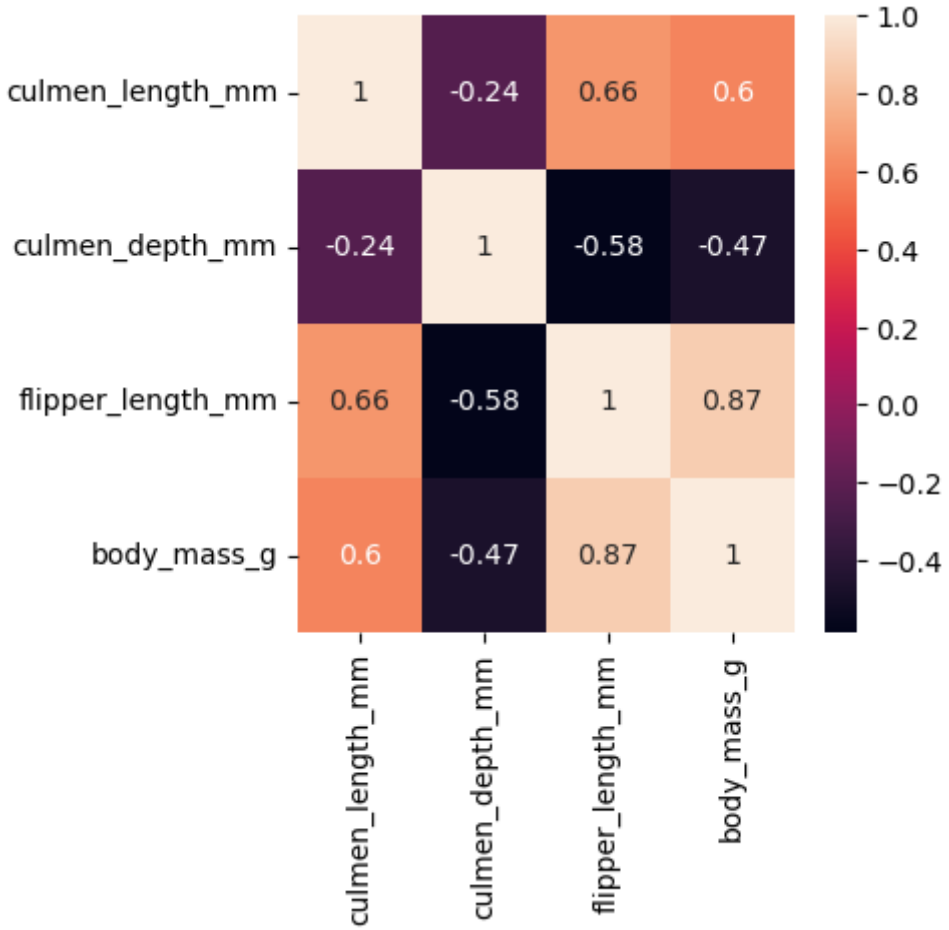
```
<Figure size 400x400 with 0 Axes>
```



In [13]:
```
plt.figure(figsize=(4,4))
sns.heatmap(df.corr(),annot=True)
```

```
C:\Users\DELL\AppData\Local\Temp\ipykernel_12584\3789453644.py:2: FutureWarning: T
he default value of numeric_only in DataFrame.corr is deprecated. In a future vers
ion, it will default to False. Select only valid columns or specify the value of n
umeric_only to silence this warning.
  sns.heatmap(df.corr(),annot=True)
```

Out[13]:
```
<Axes: >
```



4. descriptive statistics

In [14]:
```
##descriptive statistics
df.describe()
```

Out[14]:

	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. Handling Missing Values

In [15]:
```
##checking missing values
df.isnull().any()
```

Out[15]:
```
species              False
island               False
culmen_length_mm      True
culmen_depth_mm       True
flipper_length_mm     True
body_mass_g           True
sex                   True
dtype: bool
```

In [16]:
```
df.isnull().sum()
```

Out[16]:
```
species              0
island               0
culmen_length_mm     2
culmen_depth_mm      2
flipper_length_mm    2
body_mass_g          2
sex                 10
dtype: int64
```

In [17]:
```
#handling null values of numerical parameters using 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)
```

In [18]:
```
#handling null values of categorical parameters using mode()
df["sex"].mode()
```

Out[18]:
```
0    MALE
Name: sex, dtype: object
```

In [19]:
```
df["sex"].fillna("MALE",inplace=True)
```

In [20]:
```
df.isnull().sum()
```

Out[20]:
```
species              0
island               0
culmen_length_mm     0
culmen_depth_mm      0
flipper_length_mm    0
body_mass_g          0
sex                  0
dtype: int64
```

6. Outlier detection

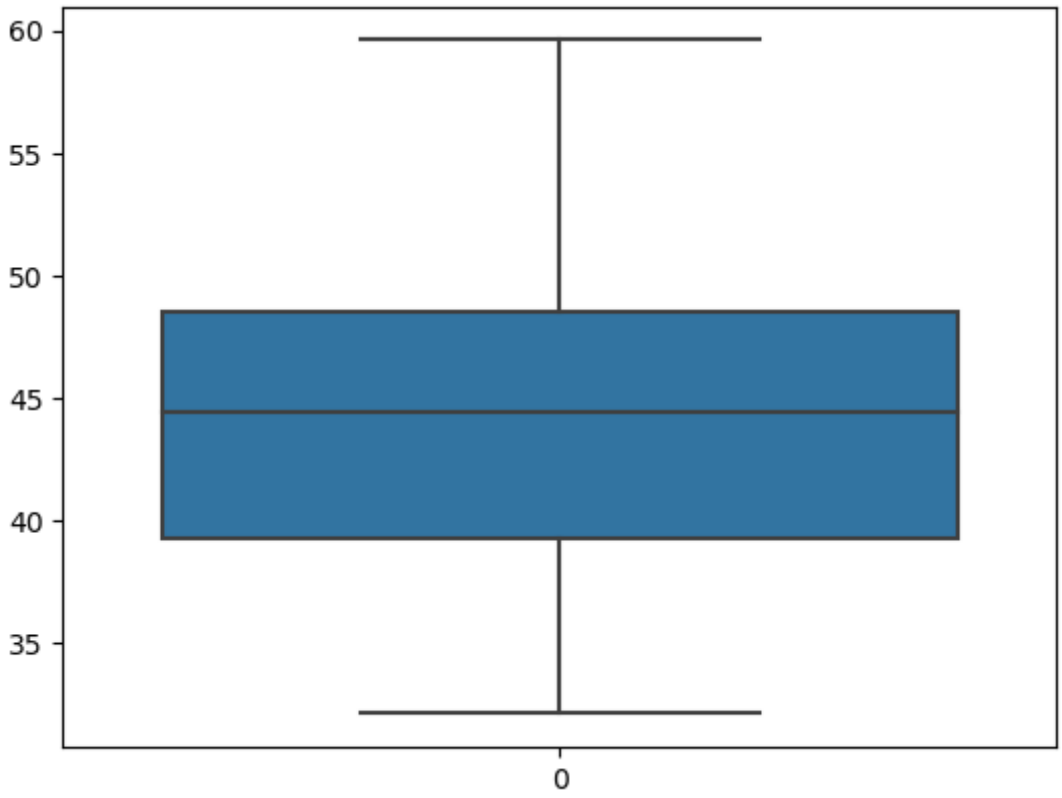
In [21]:
```
df.head()
```

Out[21]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	
0	Adelie	Torgersen	39.10	18.7	181.0	3750.0	
1	Adelie	Torgersen	39.50	17.4	186.0	3800.0	FE
2	Adelie	Torgersen	40.30	18.0	195.0	3250.0	FE
3	Adelie	Torgersen	44.45	17.3	197.0	4050.0	
4	Adelie	Torgersen	36.70	19.3	193.0	3450.0	FE

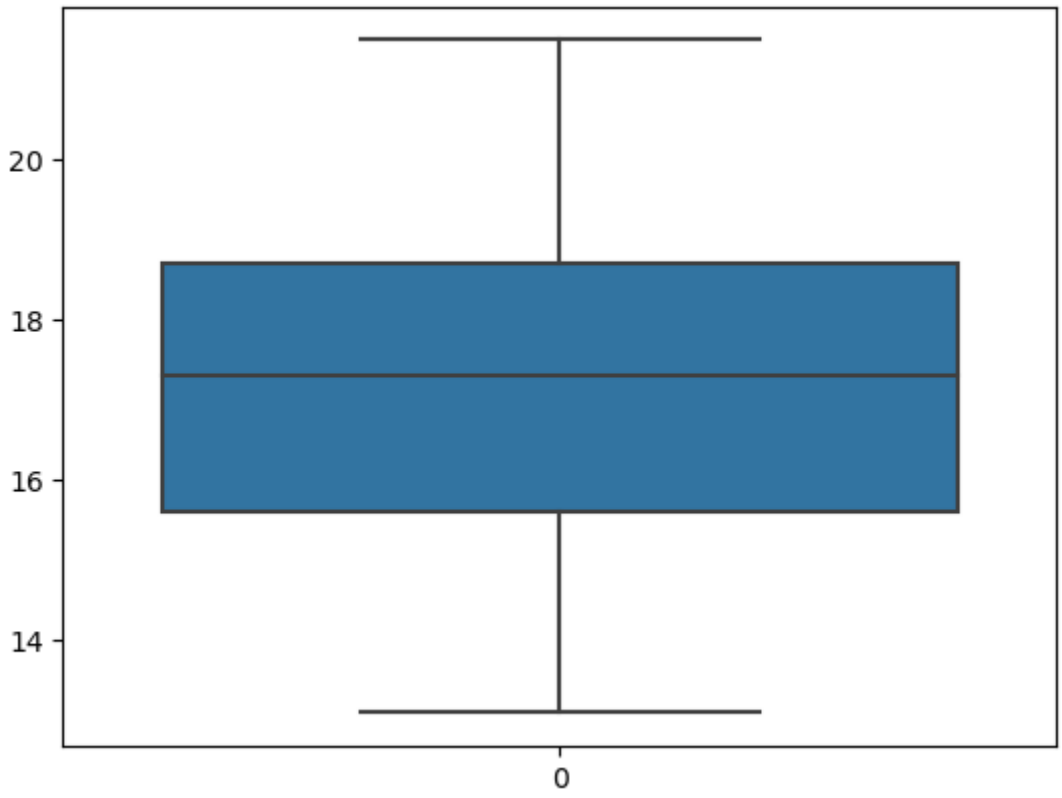
In [22]:
```
sns.boxplot(df["culmen_length_mm"])
```

Out[22]: <Axes: >



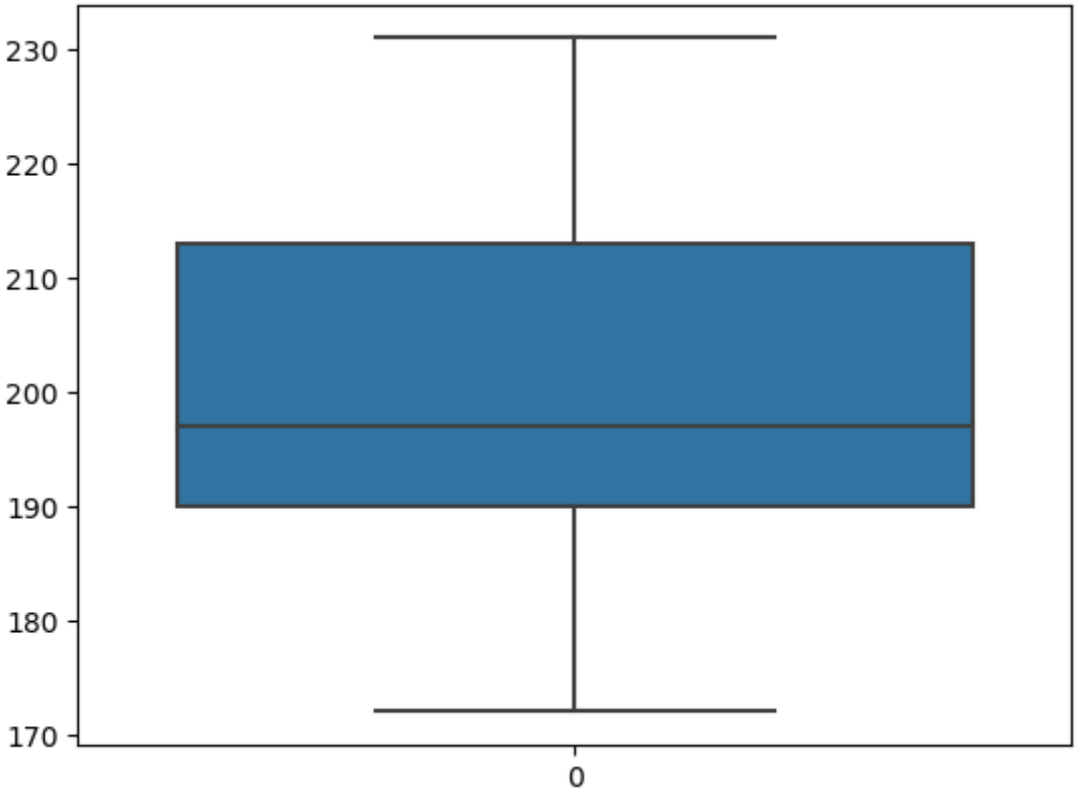
In [23]:
```
sns.boxplot(df["culmen_depth_mm"])
```

Out[23]: <Axes: >



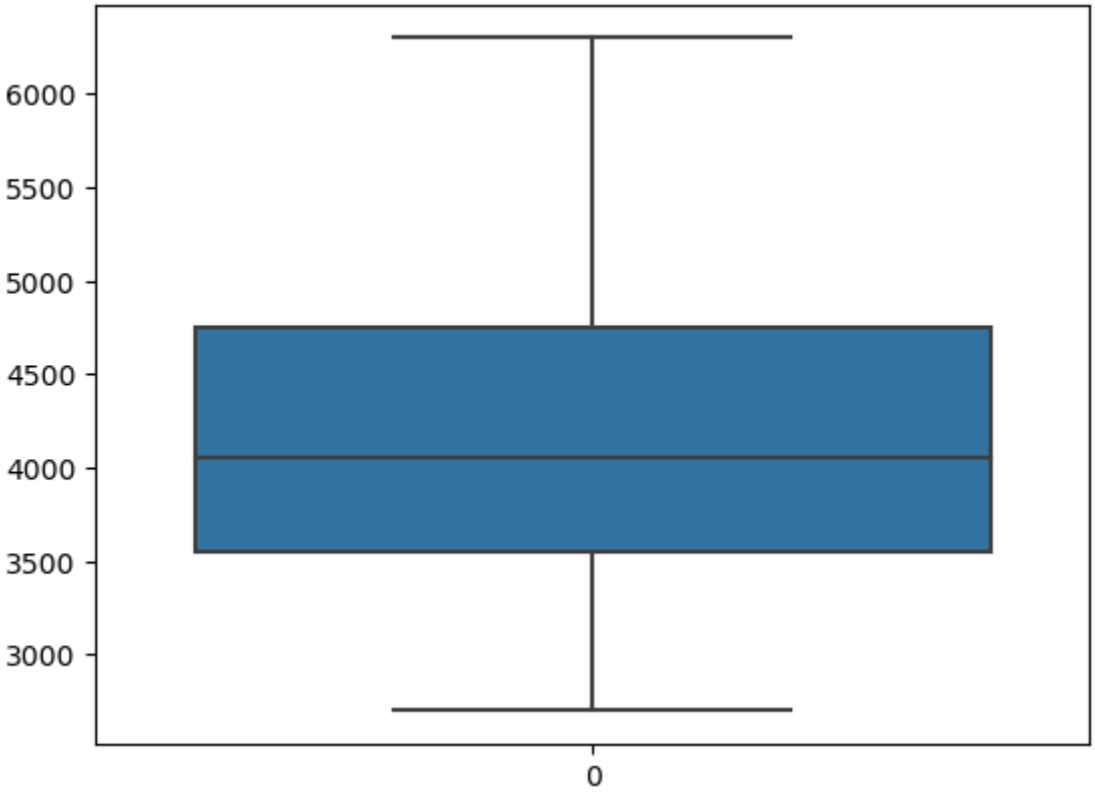
In [24]:
```
sns.boxplot(df["flipper_length_mm"])
```

Out[24]: <Axes: >



In [25]:
```
sns.boxplot(df["body_mass_g"])
```

Out[25]: <Axes: >



In [26]:
```
## no outlier's has been detected in any of the patrameters of
##culmen_length_mm      culmen_depth_mm flipper_length_mm       body_mass_g
```

7. Indentifying Correlation

In [27]:
```
df.corr()
```

```
C:\Users\DELL\AppData\Local\Temp\ipykernel_12584\1134722465.py:1: FutureWarning: T
he default value of numeric_only in DataFrame.corr is deprecated. In a future vers
ion, it will default to False. Select only valid columns or specify the value of n
umeric_only to silence this warning.
  df.corr()
```

Out[27]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
culmen_length_mm	1.000000	-0.235000	0.655858	0.594925
culmen_depth_mm	-0.235000	1.000000	-0.583832	-0.471942
flipper_length_mm	0.655858	-0.583832	1.000000	0.871221
body_mass_g	0.594925	-0.471942	0.871221	1.000000

8. Encoding

In [28]:
```
df.head()
```

Out[28]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	
0	Adelie	Torgersen	39.10	18.7	181.0	3750.0	
1	Adelie	Torgersen	39.50	17.4	186.0	3800.0	FE
2	Adelie	Torgersen	40.30	18.0	195.0	3250.0	FE
3	Adelie	Torgersen	44.45	17.3	197.0	4050.0	
4	Adelie	Torgersen	36.70	19.3	193.0	3450.0	FE

In [29]:
```
#perform encoding for the categorical columns i.e., species,island,sex
#label encoder is used to encode the categorical columns to convert into numerical
```

In [30]:
```
#importing LabelEncoder from sklearn
from sklearn.preprocessing import LabelEncoder
le=LabelEncoder()
```

In [31]:
```
df["species"]=le.fit_transform(df['species'])
df["island"]=le.fit_transform(df['island'])
df["sex"]=le.fit_transform(df['sex'])
```

In [32]:
```
df.head()
```

Out[32]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
0	0	2	39.10	18.7	181.0	3750.0	2
1	0	2	39.50	17.4	186.0	3800.0	1
2	0	2	40.30	18.0	195.0	3250.0	1
3	0	2	44.45	17.3	197.0	4050.0	2
4	0	2	36.70	19.3	193.0	3450.0	1

9. X&Y Split

In [33]:
```
X=df.drop(columns=["body_mass_g"],axis=1)
X.head()
```

Out[33]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	sex
0	0	2	39.10	18.7	181.0	2
1	0	2	39.50	17.4	186.0	1
2	0	2	40.30	18.0	195.0	1
3	0	2	44.45	17.3	197.0	2
4	0	2	36.70	19.3	193.0	1

In [34]:
```
Y=df["body_mass_g"]
Y.head()
```

Out[34]:
```
0    3750.0
1    3800.0
2    3250.0
3    4050.0
4    3450.0
Name: body_mass_g, dtype: float64
```

10. Scaling the data

In [35]:
```
from sklearn.preprocessing import MinMaxScaler
scale=MinMaxScaler()
```

In [36]:
```
X_scaled=pd.DataFrame(scale.fit_transform(X),columns=X.columns)
```

In [37]:
```
X_scaled.head()
```

Out[37]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	sex
0	0.0	1.0	0.254545	0.666667	0.152542	1.0
1	0.0	1.0	0.269091	0.511905	0.237288	0.5
2	0.0	1.0	0.298182	0.583333	0.389831	0.5
3	0.0	1.0	0.449091	0.500000	0.423729	1.0
4	0.0	1.0	0.167273	0.738095	0.355932	0.5

11. Spliting Training & Testing Data

In [38]:
```
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_sta
```

12. Checking Training & Testing data shape

In [39]:
```
x_train.shape
```

Out[39]:
```
(275, 6)
```

In [40]:
```
y_train.shape
```

Out[40]:
```
(275,)
```

In [41]:
```
x_test.shape
```

Out[41]:
```
(69, 6)
```

In [42]:
```
y_test.shape
```

Out[42]:
```
(69,)
```

In [ ]:
```

```