Assignment 3

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Perform the below Tasks to complete the Assignment:-

Clustering the data and performing classification algorithms

- 1. Download the dataset: Dataset
- 2. Load the dataset into the tool.
- 3. Perform Below Visualizations.
 - Univariate Analysis
 - Bi- Variate Analysis
 - Multi-Variate Analysis
- 4. Perform descriptive statistics on the dataset.
- 5. Check for Missing values and deal with them.
- 6. Find the outliers and replace them outliers
- 7. Check the correlation of independent variables with the target
- 8. Check for Categorical columns and perform encoding.
- 9. Split the data into dependent and independent variables.
- 10. Scaling the data
- 11. Split the data into training and testing
- 12.check the training and testing data shape.

In [1]:

- 1 #importing required libraries
- 2 import pandas as pd
- 3 **import** numpy as np
- 4 import seaborn as sns
- 5 import matplotlib.pyplot as plt
- 6 **from** matplotlib **import** rcParams

Task 1 and 2: Dataset was Downloaded and then loaded

link of dataset: https://drive.google.com/file/d/1AvRp8hOK-O76WIFvPj_rk10fAZbt8nWH/view https://drive.google.com/file/d/1AvRp8hOK-O76WIFvPj_rk10fAZbt8nWH/view)

In [2]:

1 df=pd.read_csv("C:/Users/Charvi Upreti/Desktop/Assignments/Assignment 3/penguins_siz

Basic information

In [3]:

1 df.head().T

Out[3]:

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

```
In [4]:
```

```
df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 344 entries, 0 to 343
Data columns (total 7 columns):
    Column
                      Non-Null Count Dtype
                       -----
0
    species
                       344 non-null
                                      object
 1
    island
                       344 non-null
                                      object
 2
    culmen_length_mm
                                      float64
                       342 non-null
                       342 non-null
 3
    culmen_depth_mm
                                      float64
    flipper_length_mm 342 non-null
 4
                                      float64
 5
    body_mass_g
                       342 non-null
                                      float64
6
    sex
                       334 non-null
                                      object
dtypes: float64(4), object(3)
memory usage: 18.9+ KB
```

In [5]:

```
1 df['species'].value_counts()
```

Out[5]:

Adelie 152 Gentoo 124 Chinstrap 68

Name: species, dtype: int64

Task 3: Visualizations on initial dataset:-

**Visualizations are continued after dealing with missing values

In [6]:

```
1 rcParams['figure.figsize']=5,5
```

Univariate Analysis

In [7]:

```
#distribution of culmen_length
sns.distplot(df.culmen_length_mm)
plt.title('Distribution of Culmen Length in Millimeters')
plt.show()
```

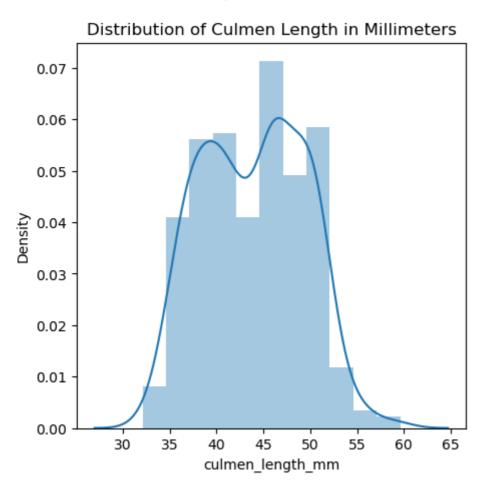
C:\Users\Charvi Upreti\AppData\Local\Temp\ipykernel_25624\2265130548.py:2:
UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.

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

For a guide to updating your code to use the new functions, please see https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751 (https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751)

sns.distplot(df.culmen_length_mm)

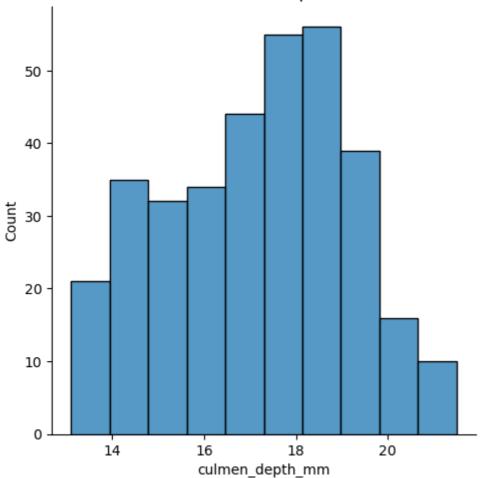


```
In [8]:
```

```
#distribution of culmen_depth
sns.displot(df.culmen_depth_mm)
plt.title('Distribution of Culmen Depth in Millimeters')
plt.show()
```

C:\Users\Charvi Upreti\anaconda3\lib\site-packages\seaborn\axisgrid.py:11
8: UserWarning: The figure layout has changed to tight
 self._figure.tight_layout(*args, **kwargs)

Distribution of Culmen Depth in Millimeters



```
In [9]:
```

```
1 df['flipper_length_mm'].nunique()
```

Out[9]:

55

In [10]:

```
1 list1=list(df['flipper_length_mm'].value_counts())
```

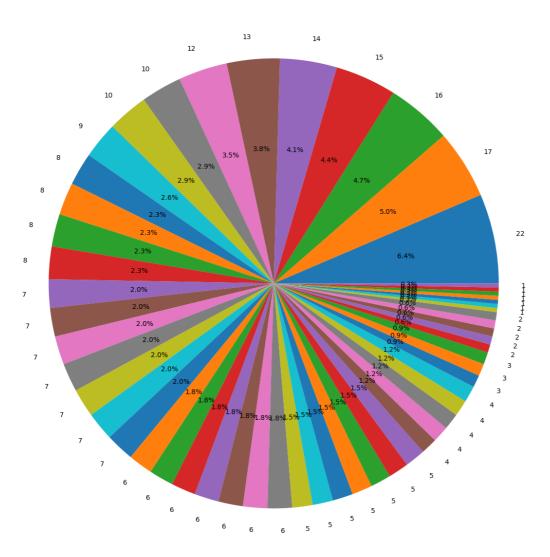
In [11]:

```
1 rcParams['figure.figsize']=15,15
```

In [12]:

```
plt.pie(df.flipper_length_mm.value_counts(),labels = list1,autopct ='%1.1f%%',)
plt.title('Flipper length in mm')
plt.show()
```

Flipper length in mm



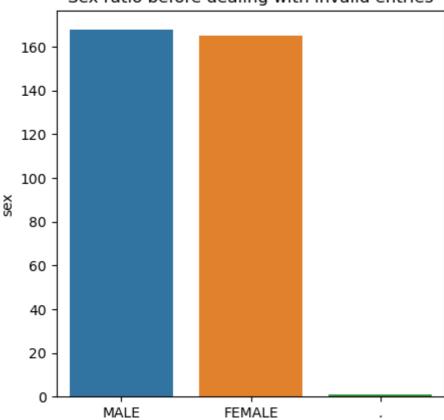
In [13]:

```
1 rcParams['figure.figsize']=5,5
```

In [14]:

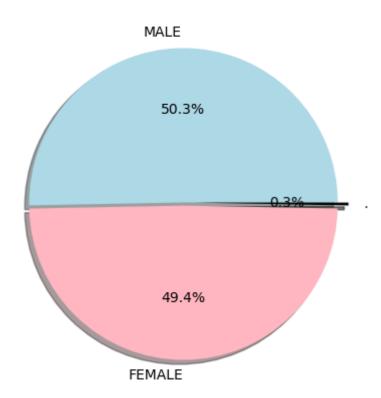
```
sns.barplot(x =df.sex.value_counts().index,y =df.sex.value_counts())
plt.title('Sex ratio before dealing with invalid entries')
# Done again after dealing with them later.
plt.show()
```

Sex ratio before dealing with invalid entries



In [15]:

```
counts = df['sex'].value_counts()
plt.figure()
plt.pie(counts, [0,0.02,0.07], shadow=True, labels=counts.index, autopct='%1.1f%%', col
plt.show()
```

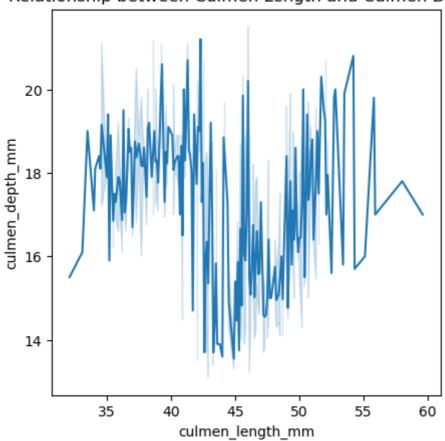


Bi - Variate Analysis

In [16]:

```
sns.lineplot(x = df.culmen_length_mm,y=df.culmen_depth_mm)
plt.title('Relationship between Culmen Length and Culmen Depth')
plt.show()
```

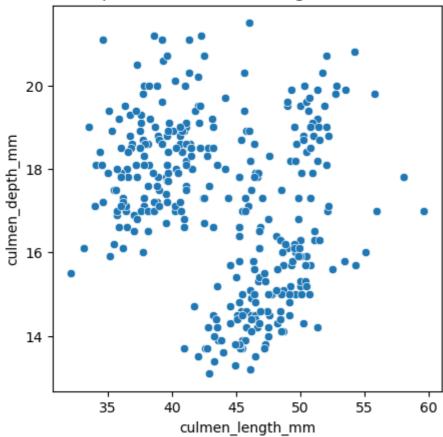
Relationship between Culmen Length and Culmen Depth



In [17]:

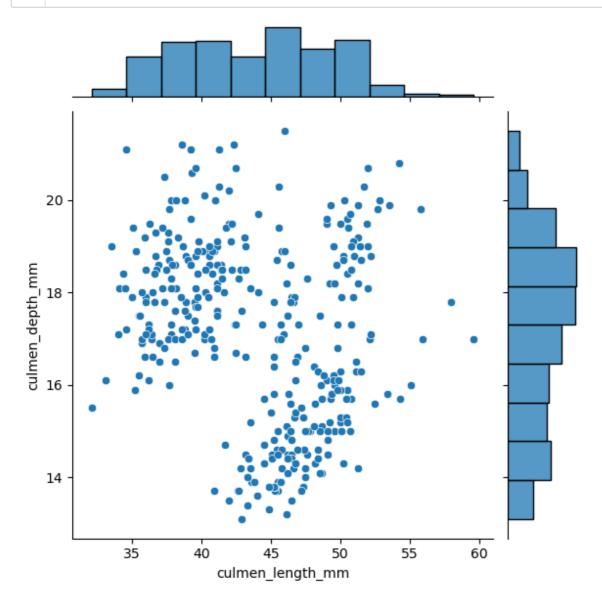
```
sns.scatterplot(x = df.culmen_length_mm,y=df.culmen_depth_mm)
plt.title('Relationship between Culmen Length and Culmen Depth')
plt.show()
```

Relationship between Culmen Length and Culmen Depth



In [18]:

```
sns.jointplot(x = df.culmen_length_mm,y=df.culmen_depth_mm)
plt.show()
```

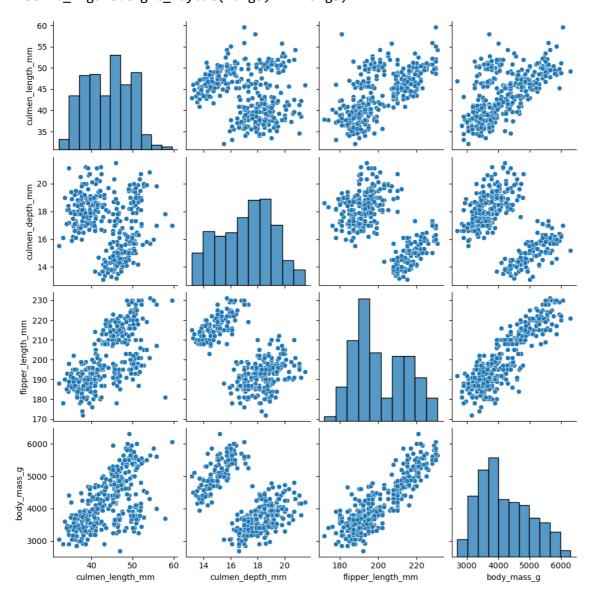


Multi-Variate Analysis

In [19]:

```
sns.pairplot(df)
plt.show()
```

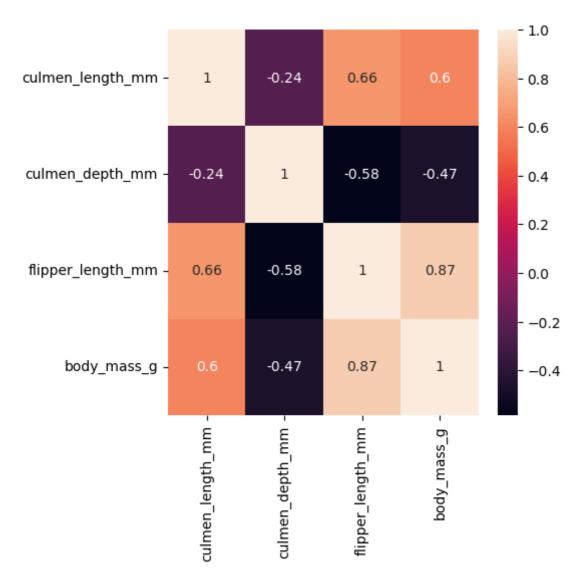
C:\Users\Charvi Upreti\anaconda3\lib\site-packages\seaborn\axisgrid.py:11
8: UserWarning: The figure layout has changed to tight
 self._figure.tight_layout(*args, **kwargs)



In [20]:

1 sns.heatmap(df.corr(),annot=True)

Out[20]:



Task 4: Descriptive statistice on the dataset

```
In [21]:
```

```
1 df.describe()
```

Out[21]:

| | 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 |

Task 5: Checking missing values and dealing with them

```
In [22]:
```

```
1 df.isnull().sum()

Out[22]:

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 [23]:
```

```
1 df.sex.value_counts()
```

Out[23]:

MALE 168 FEMALE 165 . 1

Name: sex, dtype: int64

In [24]:

```
1 df['sex'] = df['sex'].replace(".", df['sex'].mode()[0])
```

```
In [25]:
 1 df.sex.value_counts()
Out[25]:
MALE
          169
FEMALE
          165
Name: sex, dtype: int64
In [26]:
   df['sex'] = df['sex'].fillna(df['sex'].mode()[0])
In [27]:
   df.sex.value_counts()
Out[27]:
MALE
          179
FEMALE
          165
Name: sex, dtype: int64
In [28]:
 1 | df=df.fillna(df.median())
C:\Users\Charvi Upreti\AppData\Local\Temp\ipykernel_25624\308181716.py:1:
FutureWarning: Dropping of nuisance columns in DataFrame reductions (with
'numeric_only=None') is deprecated; in a future version this will raise Ty
peError. Select only valid columns before calling the reduction.
  df=df.fillna(df.median())
In [29]:
   df.isna().sum()
Out[29]:
species
                     0
island
                     0
culmen_length_mm
                     0
                     0
culmen_depth_mm
flipper_length_mm
                     0
                     0
body_mass_g
                     0
sex
dtype: int64
```

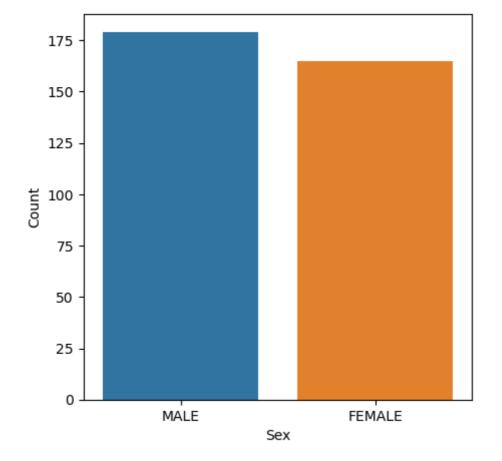
```
In [30]:
```

```
df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 344 entries, 0 to 343
Data columns (total 7 columns):
    Column
                       Non-Null Count Dtype
                       -----
 0
    species
                       344 non-null
                                       object
 1
    island
                       344 non-null
                                       object
 2
    culmen_length_mm
                                       float64
                       344 non-null
 3
    culmen_depth_mm
                       344 non-null
                                       float64
    flipper_length_mm 344 non-null
 4
                                       float64
 5
    body_mass_g
                       344 non-null
                                       float64
 6
                       344 non-null
                                       object
    sex
dtypes: float64(4), object(3)
memory usage: 18.9+ KB
```

Task 3 (Continued): Some visualizations done after dealing with missing / invalid values

In [31]:

```
1 sns.barplot(x =df.sex.value_counts().index,y =df.sex.value_counts())
2 # Done after dealing with invalid/missing entries.
3 plt.xlabel('Sex')
4 plt.ylabel('Count')
5 plt.show()
```



In [32]:

```
1 sns.distplot(df.culmen_length_mm)
2 plt.show()
```

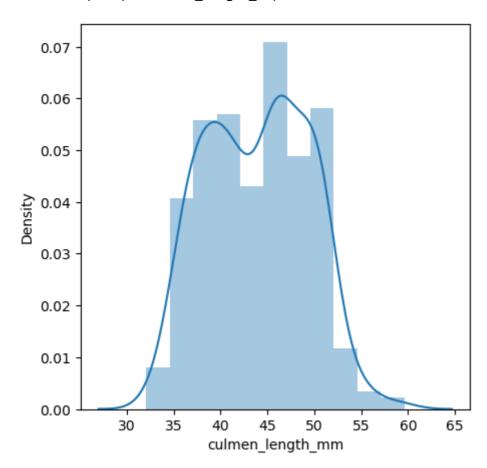
C:\Users\Charvi Upreti\AppData\Local\Temp\ipykernel_25624\1383932245.py:1:
UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.

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

For a guide to updating your code to use the new functions, please see https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751 (https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751)

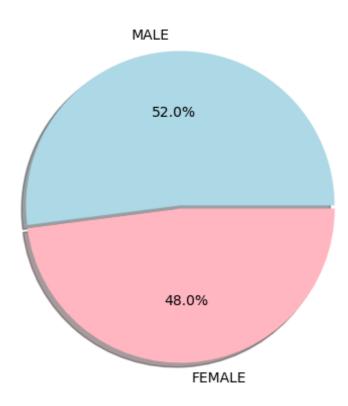
sns.distplot(df.culmen_length_mm)



Univariate

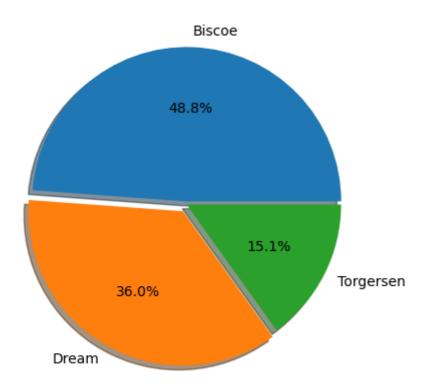
In [33]:

```
counts = df['sex'].value_counts()
plt.figure()
plt.pie(counts, [0.02,0], shadow=True, labels=counts.index, autopct='%1.1f%%', colors=[
plt.show()
```



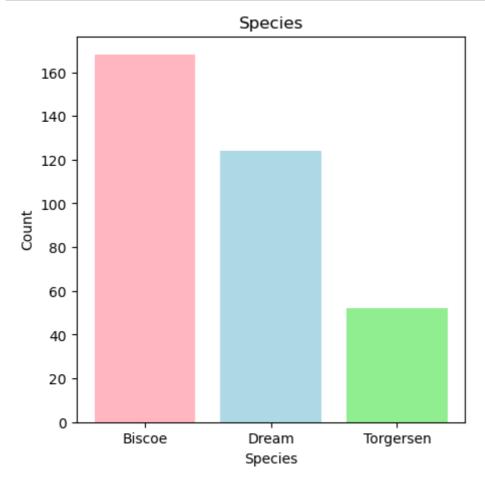
In [34]:

```
counts = df['island'].value_counts()
plt.figure()
plt.pie(counts, [0.02,0.05,0],shadow=True,labels=counts.index, autopct='%1.1f%%')
plt.show()
```



In [35]:

```
plt.bar(counts.index, counts, color=['lightpink', 'lightblue', 'lightgreen'])
plt.xlabel('Species')
plt.ylabel('Count')
plt.title('Species')
plt.show()
```



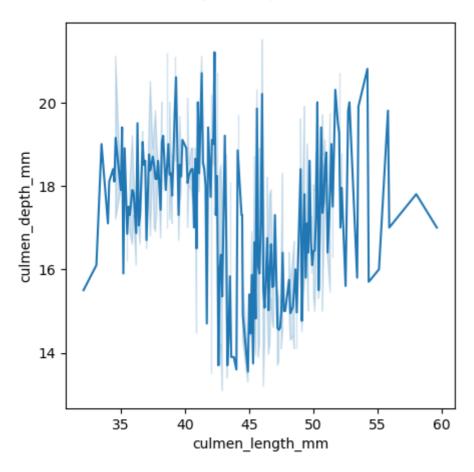
Bi - Variate Analysis

In [36]:

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

Out[36]:

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

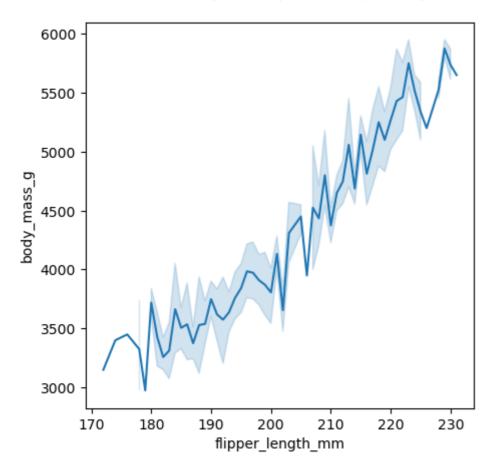


In [37]:

1 sns.lineplot(x = df.flipper_length_mm,y=df.body_mass_g)

Out[37]:

<Axes: xlabel='flipper_length_mm', ylabel='body_mass_g'>

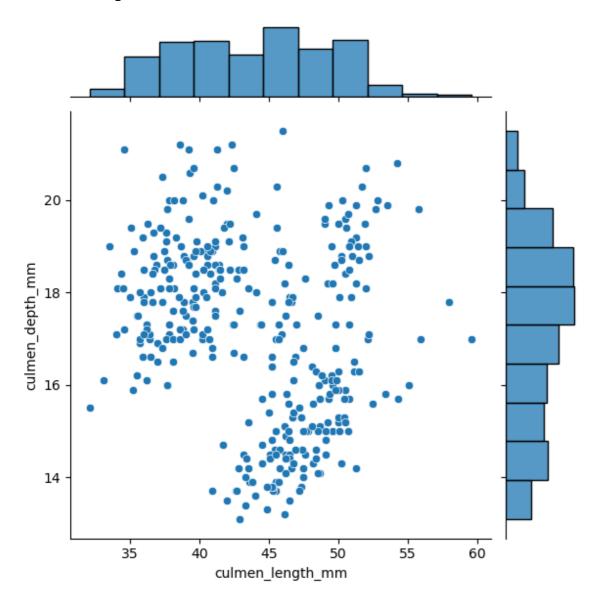


In [38]:

sns.jointplot(x = df.culmen_length_mm,y=df.culmen_depth_mm)

Out[38]:

<seaborn.axisgrid.JointGrid at 0x25f80359940>

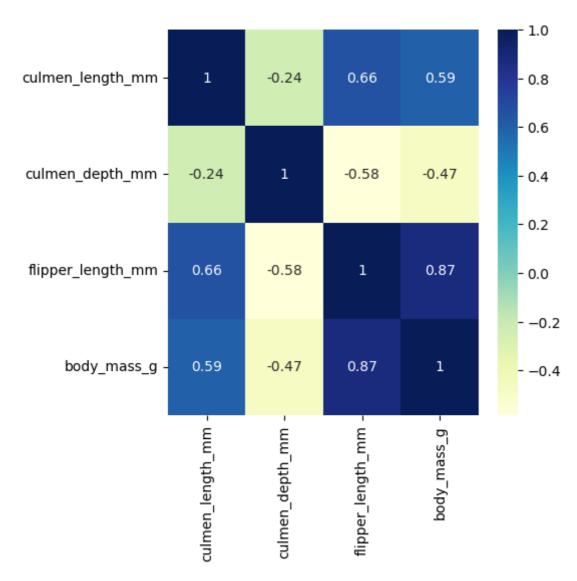


Multi-Variate Analysis

```
In [39]:
```

sns.heatmap(df.corr(),annot=True,cmap="YlGnBu")

Out[39]:

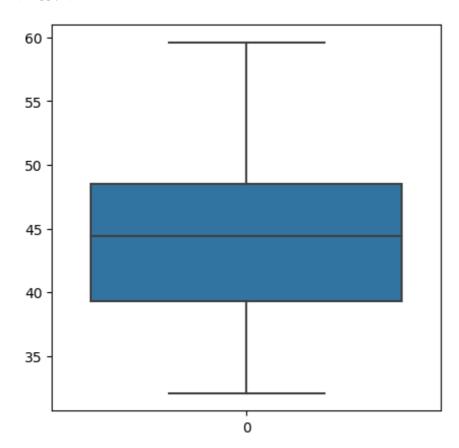


Task 6: Finding and replacing outliers

In [40]:

```
1 sns.boxplot(df.culmen_length_mm)
2 #### seems like no outliers
```

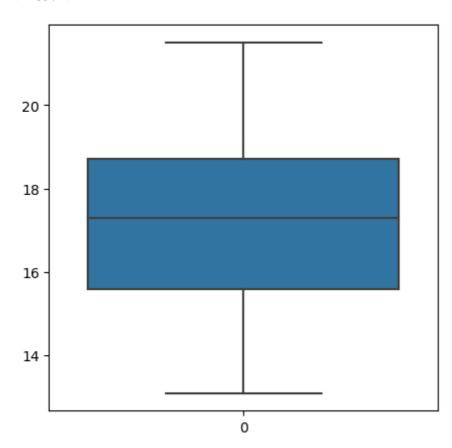
Out[40]:



In [41]:

```
sns.boxplot(df.culmen_depth_mm)
#### seems like no outliers
```

Out[41]:

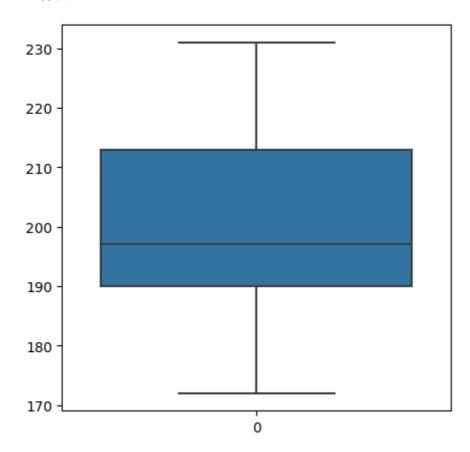


In [42]:

```
1 sns.boxplot(df.flipper_length_mm)
2 #### seems like no outliers
```

Out[42]:

<Axes: >



Outliers not present, but trying removal on culmen_length_mm by replacement with median

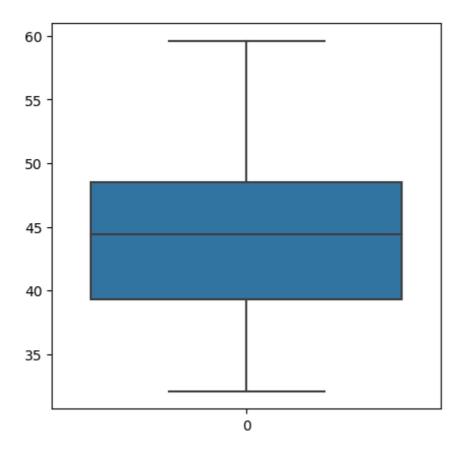
In [43]:

```
q1 = df.culmen_length_mm.quantile(0.25)
 2 q3 = df.culmen_length_mm.quantile(0.75)
   print("Before: ")
 4 print(q1)
 5
   print(q3)
 6 IQR = q3-q1
 7
   upper_limit = q3+1.5*IQR
   df['culmen_length_mm'] = np.where(df['culmen_length_mm']>upper_limit,30,df['culmen_l
 9
   sns.boxplot(df['culmen_length_mm'])
10
   plt.show()
q1 = df.culmen_length_mm.quantile(0.25) #Q1
   q3 = df.culmen_length_mm.quantile(0.75) #Q3
13
   print("After: ")
14 | print(q1)
15 print(q3)
   print("No change as no outliers present.")
```

Before:

39.275

48.5



After:

39.275

48.5

No change as no outliers present.

Task 8: Checking for categorical columns and performing encoding.

In [44]: 1 df.info() <class 'pandas.core.frame.DataFrame'> RangeIndex: 344 entries, 0 to 343 Data columns (total 7 columns): Column Non-Null Count Dtype -----0 species 344 non-null object 1 island 344 non-null object 2 culmen_length_mm float64 344 non-null 344 non-null float64 3 culmen_depth_mm flipper_length_mm 344 non-null 4 float64 5 body_mass_g 344 non-null float64 6 344 non-null object sex dtypes: float64(4), object(3) memory usage: 18.9+ KB In [45]: 1 **from** sklearn.preprocessing **import** LabelEncoder 2 le=LabelEncoder() 3 | df['island']=le.fit_transform(df['island']) 4 df['sex']=le.fit_transform(df['sex']) 5 #Species is target variable hence we did not encode it

Task 7: Checking correlation of independent variables with the target

```
In [46]:
1 df.corr()
```

Out[46]:

| | island | culmen_length_mm | culmen_depth_mm | flipper_length_mm | bo |
|-------------------|-----------|------------------|-----------------|-------------------|----|
| island | 1.000000 | -0.351189 | 0.567701 | -0.562957 | |
| culmen_length_mm | -0.351189 | 1.000000 | -0.235000 | 0.655858 | |
| culmen_depth_mm | 0.567701 | -0.235000 | 1.000000 | -0.583832 | |
| flipper_length_mm | -0.562957 | 0.655858 | -0.583832 | 1.000000 | |
| body_mass_g | -0.558500 | 0.594925 | -0.471942 | 0.871221 | |
| sex | 0.002893 | 0.322871 | 0.354791 | 0.241941 | |
| 4 | | | | | • |

To check correlation creating a label encoded copy.

```
In [47]:
```

```
df_copy = df.copy()
df_copy['species'] = le.fit_transform(df_copy['species'])
df_copy.corr().species.sort_values(ascending =False)
```

Out[47]:

```
      species
      1.000000

      flipper_length_mm
      0.850819

      body_mass_g
      0.747547

      culmen_length_mm
      0.728706

      sex
      0.010240

      island
      -0.635659

      culmen_depth_mm
      -0.741282

      Name: species, dtype: float64
```

Task 9: Spliting data to dependent and independent variables

In [48]:

```
1 Y=df['species']
2 Y
```

Out[48]:

```
0
       Adelie
       Adelie
1
2
       Adelie
3
       Adelie
4
       Adelie
        . . .
339
       Gentoo
340
       Gentoo
       Gentoo
341
342
       Gentoo
343
       Gentoo
Name: species, Length: 344, dtype: object
```

In [49]:

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

Out[49]:

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

Task 10: Scaling the data

In [50]:

- 1 from sklearn.preprocessing import MinMaxScaler
- 2 scale =MinMaxScaler()
- 3 X_scaled= pd.DataFrame(scale.fit_transform(X),columns =X.columns)
- 4 X_scaled.head()

Out[50]:

| | 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 | 1.0 |
| 1 | 1.0 | 0.269091 | 0.511905 | 0.237288 | 0.305556 | 0.0 |
| 2 | 1.0 | 0.298182 | 0.583333 | 0.389831 | 0.152778 | 0.0 |
| 3 | 1.0 | 0.449091 | 0.500000 | 0.423729 | 0.375000 | 1.0 |
| 4 | 1.0 | 0.167273 | 0.738095 | 0.355932 | 0.208333 | 0.0 |

Task 11:Split the data into training and testing

In [51]:

```
from sklearn.model_selection import train_test_split
X_train,X_test,Y_train,Y_test = train_test_split(X_scaled,Y,test_size=0.3,random_state)
```

Task 12: Check the training and testing data shape

In [52]:

```
print(X_train.shape)
print(Y_train.shape)
print(X_test.shape)
print(Y_test.shape)
```

(240, 6) (240,) (104, 6) (104,)