

EXPLORATORY DATA ANALYSIS ON PENGUIN DATASET

Introduction

The dataset in use is penguin dataset: the new iris. The dataset is originally published by [Dr.Kristen Gorman](https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0090081) (<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0090081>). This dataset contains penguin species and culmen and flipper measurements, body mass, sex and islands they are found at. The data used is in the file `penguins_size.csv` found on [Kaggle](https://www.kaggle.com/parulpandey/penguin-dataset-the-new-iris/data?select=penguins_size.csv) (https://www.kaggle.com/parulpandey/penguin-dataset-the-new-iris/data?select=penguins_size.csv).

Summary

`penguins_size.csv` : Simplified data from original penguin data sets. Contains variables:

- `species` : penguin species (Chinstrap, Adélie, or Gentoo)
- `culmen_length_mm` : culmen length (mm)
- `culmen_depth_mm` : culmen depth (mm)
- `flipper_length_mm` : flipper length (mm)
- `body_mass_g` : body mass (g)
- `island` : island name (Dream, Torgersen, or Biscoe) in the Palmer Archipelago (Antarctica)
- `sex` : penguin sex (Male, Female)

Initial Plans:

- **retrieve data**
- **analyse**: shape, columns, groupby, visualise
- **data cleaning**: remove null, check for skew, transform, scale
- **visualise**
- **hypothesis testing**: Significance test

Data Retrieving and Analysis

```
In [ ]: import os
import numpy as np
import pandas as pd
```

```
In [ ]: filepath = "data/penguins_size.csv"
data = pd.read_csv(filepath)
data.head()
```

```
Out[ ]:
```

	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
2	Adelie	Torgersen	40.3	18.0	195.0	3250.0
3	Adelie	Torgersen	NaN	NaN	NaN	NaN
4	Adelie	Torgersen	36.7	19.3	193.0	3450.0

```
In [ ]: data.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      342 non-null   float64
3   culmen_depth_mm       342 non-null   float64
4   flipper_length_mm     342 non-null   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 [ ]: data.shape
```

```
Out[ ]: (344, 7)
```

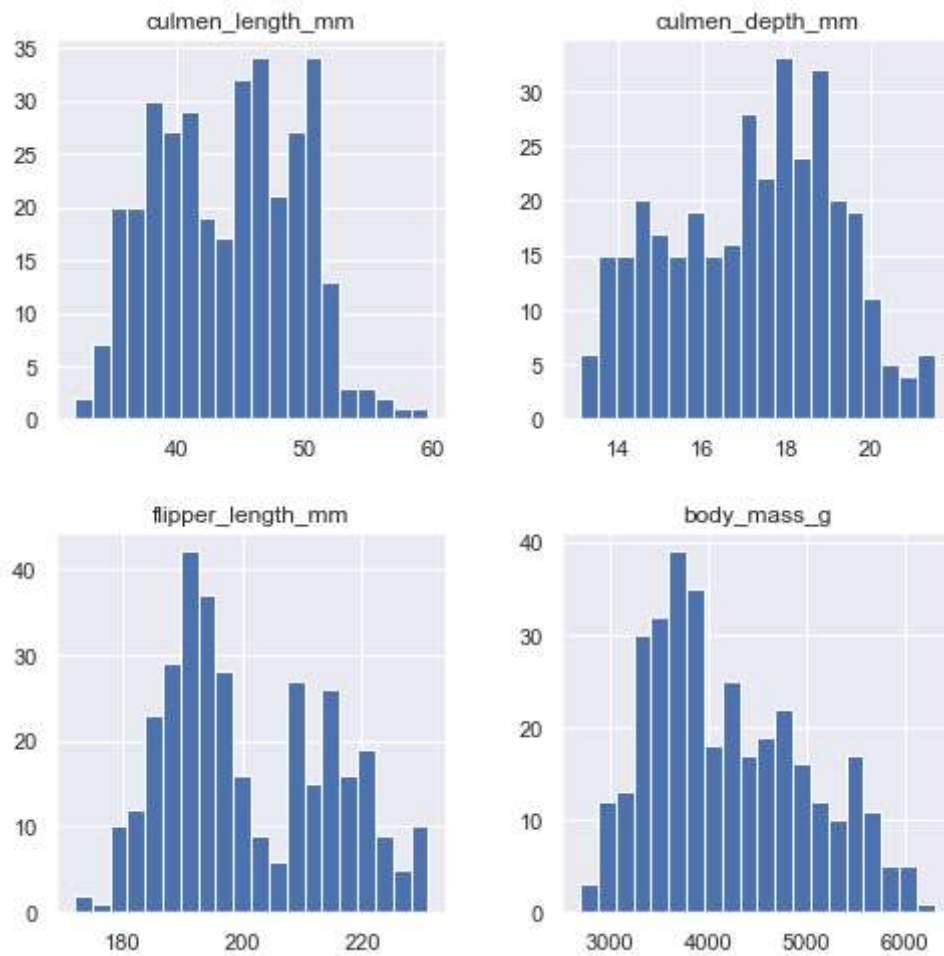
```
In [ ]: data.drop(["island"], axis=1, inplace=True)
```

```
In [ ]: data.columns.tolist()
```

```
Out[ ]: ['species',
'culmen_length_mm',
'culmen_depth_mm',
'flipper_length_mm',
'body_mass_g',
'sex']
```

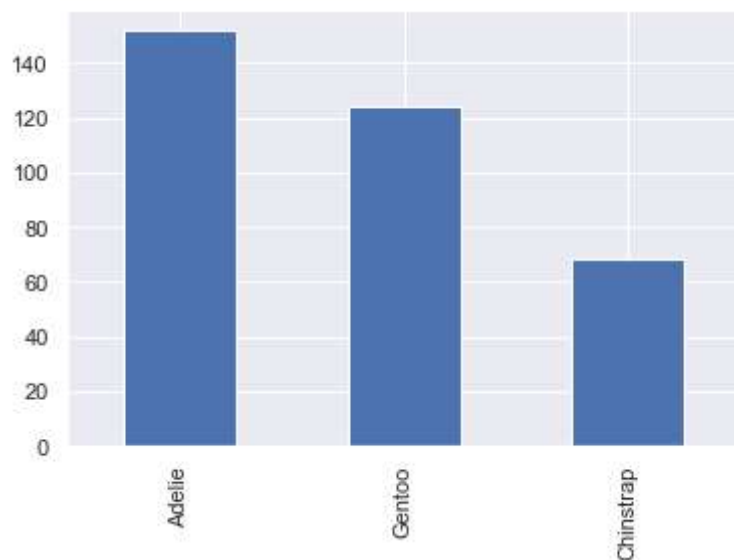
```
In [ ]: data.hist(bins=20, figsize=(8, 8))
```

```
Out[ ]: array([[<AxesSubplot:title={'center':'culmen_length_mm'}>,  
               <AxesSubplot:title={'center':'culmen_depth_mm'}>],  
             [<AxesSubplot:title={'center':'flipper_length_mm'}>,  
               <AxesSubplot:title={'center':'body_mass_g'}>]], dtype=object)
```



```
In [ ]: data["species"].value_counts().plot(kind="bar")
data["species"].value_counts()
```

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



```
In [ ]: stats_df = data.describe()
stats_df.loc['range'] = stats_df.loc['max'] - stats_df.loc['min']
stats_df
```

```
Out[ ]:
```

	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
range	27.500000	8.400000	59.000000	3600.000000

```
In [ ]: stats_df.loc['range'] = stats_df.loc['max'] - stats_df.loc['min']

out_fields = ['mean', '25%', '50%', '75%', 'range']
stats_df = stats_df.loc[out_fields]
stats_df.rename({'50%': 'median'}, inplace=True) #renaming 50% to median
stats_df
```

Out[]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
mean	43.92193	17.15117	200.915205	4201.754386
25%	39.22500	15.60000	190.000000	3550.000000
median	44.45000	17.30000	197.000000	4050.000000
75%	48.50000	18.70000	213.000000	4750.000000
range	27.50000	8.40000	59.000000	3600.000000

calculating for each species in a separate dataframe.

```
In [ ]: data.groupby('species').mean()
```

Out[]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
species				
Adelie	38.791391	18.346358	189.953642	3700.662252
Chinstrap	48.833824	18.420588	195.823529	3733.088235
Gentoo	47.504878	14.982114	217.186992	5076.016260

```
In [ ]: data.groupby('species').agg([np.mean, np.median])
```

Out[]:

	culmen_length_mm		culmen_depth_mm		flipper_length_mm		body_mass_g	
	mean	median	mean	median	mean	median	mean	median
species								
Adelie	38.791391	38.80	18.346358	18.40	189.953642	190.0	3700.662252	3700.0
Chinstrap	48.833824	49.55	18.420588	18.45	195.823529	196.0	3733.088235	3700.0
Gentoo	47.504878	47.30	14.982114	15.00	217.186992	216.0	5076.016260	5000.0

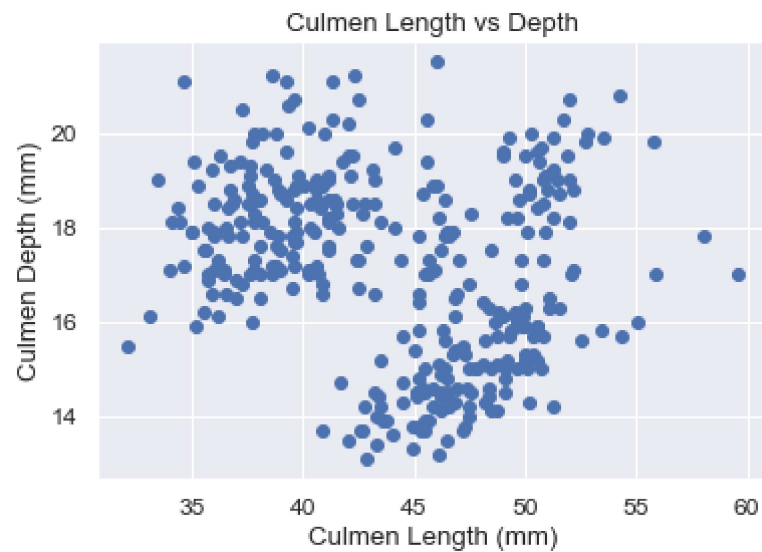
Making a scatter plot for culmen_length vs culmen_depth

```
In [ ]: import matplotlib.pyplot as plt
%matplotlib inline
```

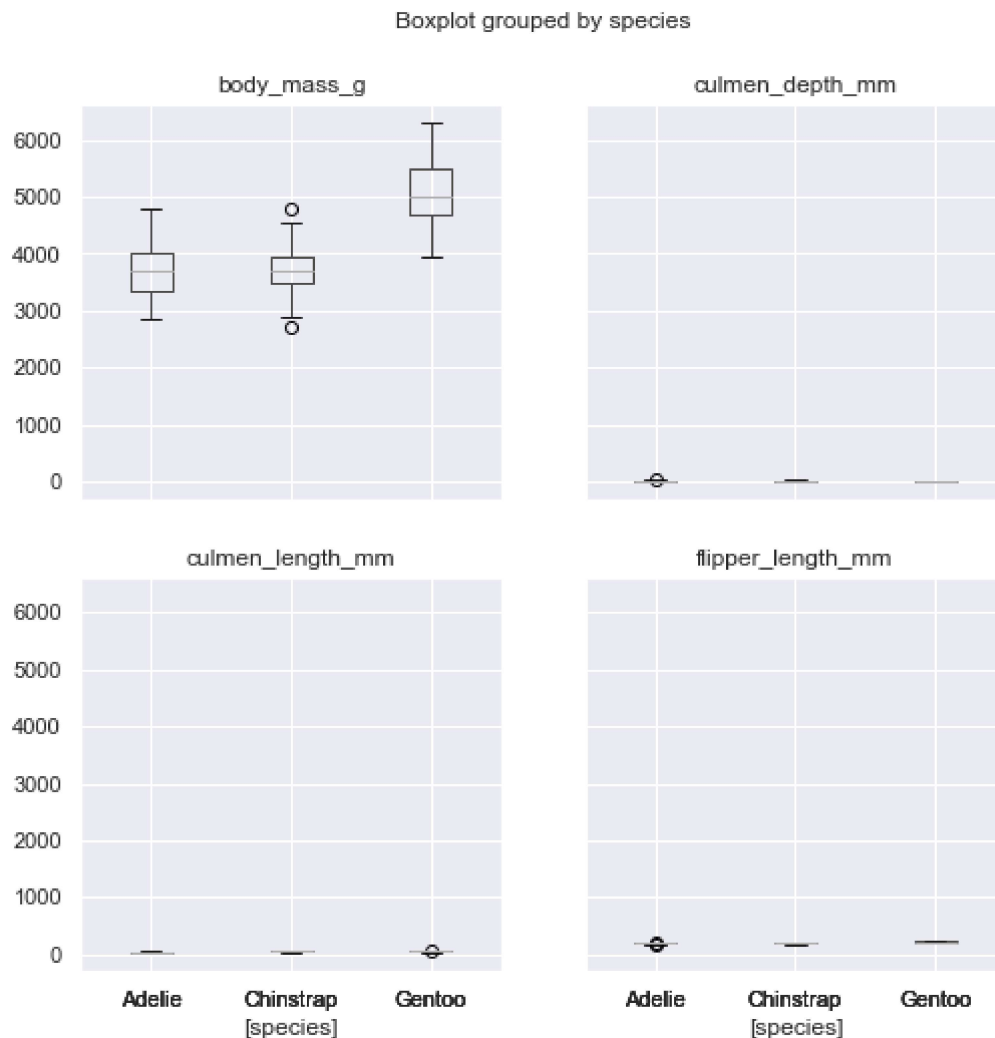
```
In [ ]: ax = plt.axes()

ax.scatter(data.culmen_length_mm, data.culmen_depth_mm)

# Label the axes
ax.set(xlabel='Culmen Length (mm)',
       ylabel='Culmen Depth (mm)',
       title='Culmen Length vs Depth');
```



```
In [ ]: data.boxplot(by='species', figsize=(8,8));
```



Data Cleaning

```
In [ ]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 344 entries, 0 to 343
Data columns (total 6 columns):
#   Column                Non-Null Count  Dtype
---  -
0   species               344 non-null   object
1   culmen_length_mm      342 non-null   float64
2   culmen_depth_mm       342 non-null   float64
3   flipper_length_mm     342 non-null   float64
4   body_mass_g           342 non-null   float64
5   sex                   334 non-null   object
dtypes: float64(4), object(2)
memory usage: 16.2+ KB
```

```
In [ ]: df = data.copy()
```

```
In [ ]: one_hot_encode_cols = data.dtypes[df.dtypes == np.object] # filtering by string categoricals
one_hot_encode_cols = one_hot_encode_cols.index.tolist() # list of categorical fields

df[one_hot_encode_cols].head().T
```

Out[]:

	0	1	2	3	4
species	Adelie	Adelie	Adelie	Adelie	Adelie
sex	MALE	FEMALE	FEMALE	NaN	FEMALE

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

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

- There are a *lot* of null values.
- For numerical columns replacing by mean
- For categorical columns replacing by mode.

```
In [ ]: for i in df.columns:
        if(df[i].isnull()).any():
            if(df[i].dtype) == 'float64':
                df[i] = df[i].replace(np.nan, df[i].mean())
            if(df[i].dtype) == 'object':
                df[i] = df[i].replace(np.nan, df[i].mode()[0])
```

```
In [ ]: df['sex'] = df['sex'].replace('.', 'MALE')
```

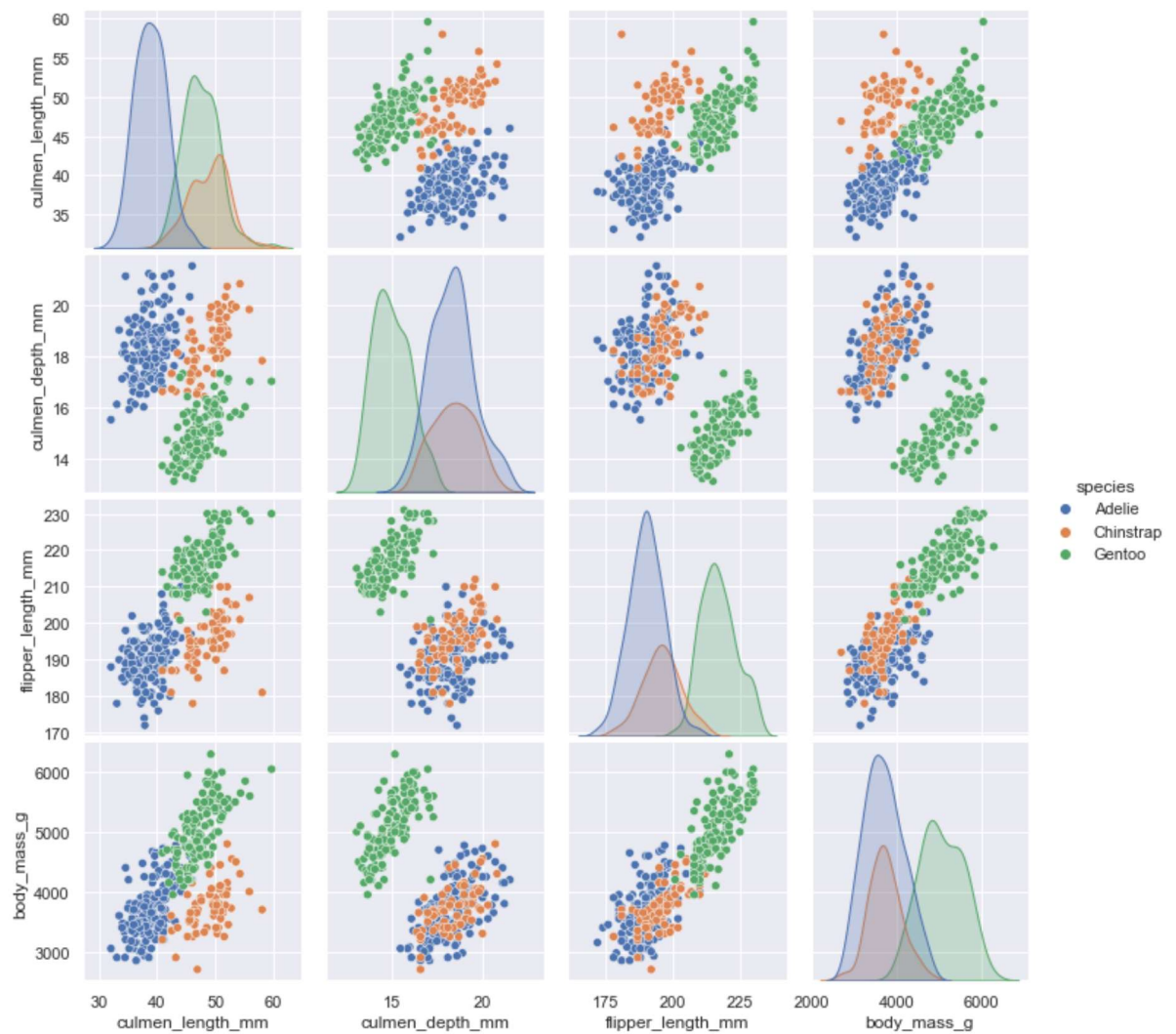
```
In [ ]: df.isnull().sum()
```

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

PairPlot for numerical columns


```
In [ ]: sns.pairplot(df, hue= 'species')
```

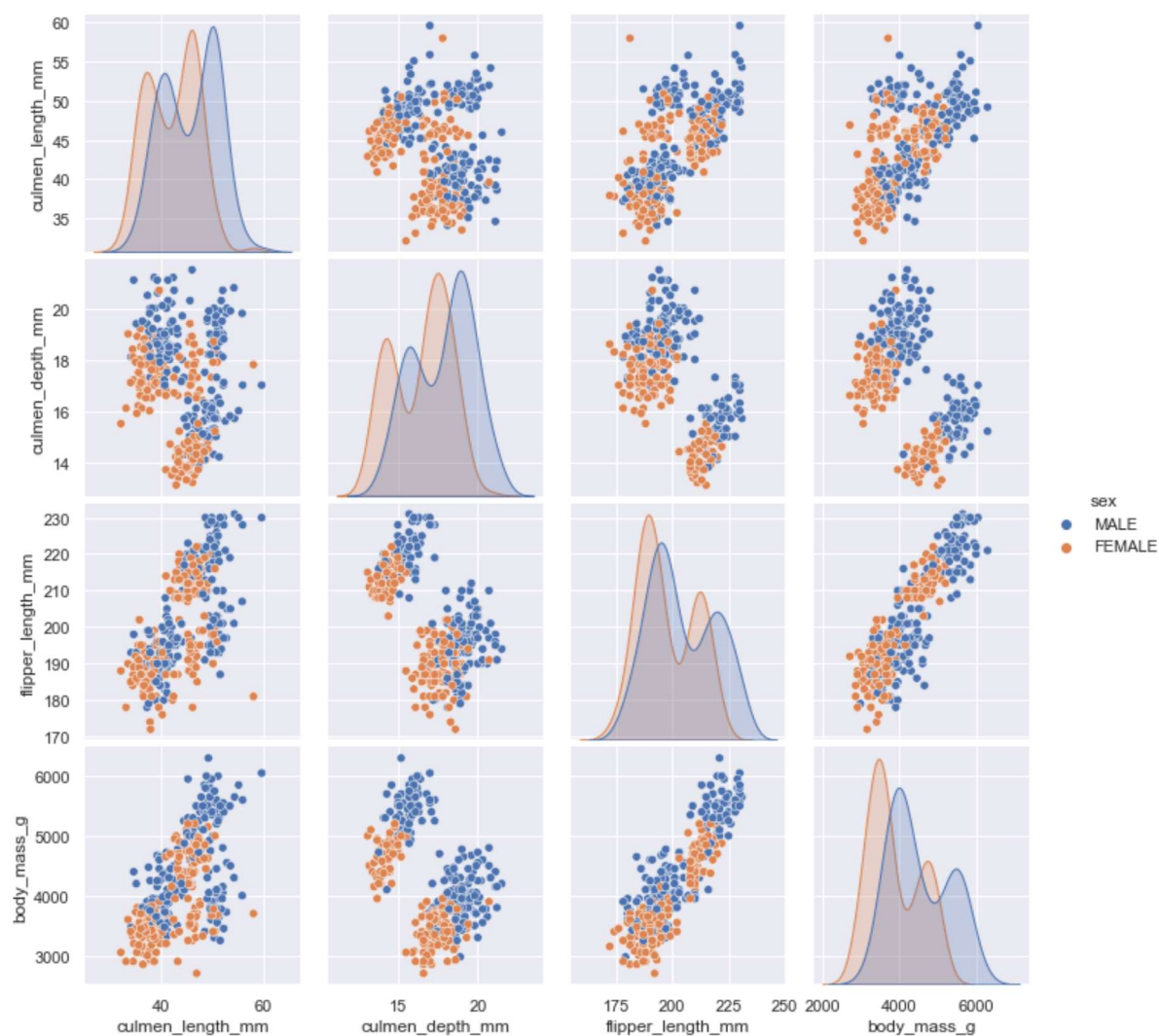
```
Out[ ]: <seaborn.axisgrid.PairGrid at 0x2846e0b7e80>
```



- PairPlots for categorical columns

```
In [ ]: sns.pairplot(df, hue= 'sex')
```

```
Out[ ]: <seaborn.axisgrid.PairGrid at 0x2846da16820>
```



Converting sex column to integer value by Label Encoder, Nominal to Numeric value conversion

```
In [ ]: from sklearn.preprocessing import LabelEncoder
lb = LabelEncoder()
df["sex"] = lb.fit_transform(df["sex"])
```

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

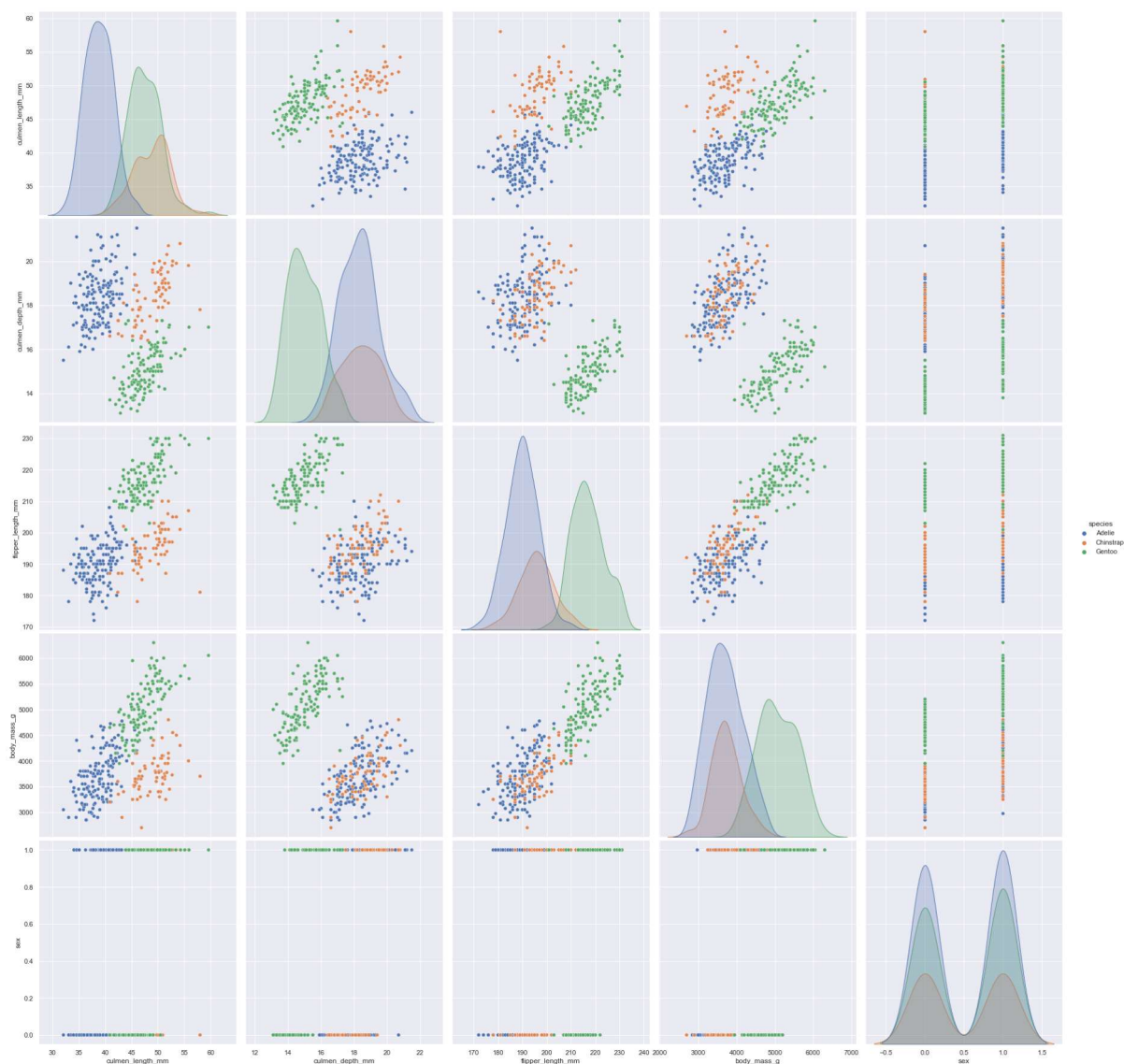
```
Out[ ]:
```

	species	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
0	Adelie	39.10000	18.70000	181.000000	3750.000000	1
1	Adelie	39.50000	17.40000	186.000000	3800.000000	0
2	Adelie	40.30000	18.00000	195.000000	3250.000000	0
3	Adelie	43.92193	17.15117	200.915205	4201.754386	1
4	Adelie	36.70000	19.30000	193.000000	3450.000000	0

Analysing the data visually.

```
In [ ]: sns.pairplot(df, hue = 'species', height=5)
```

```
Out[ ]: <seaborn.axisgrid.PairGrid at 0x2846ea20550>
```



observation

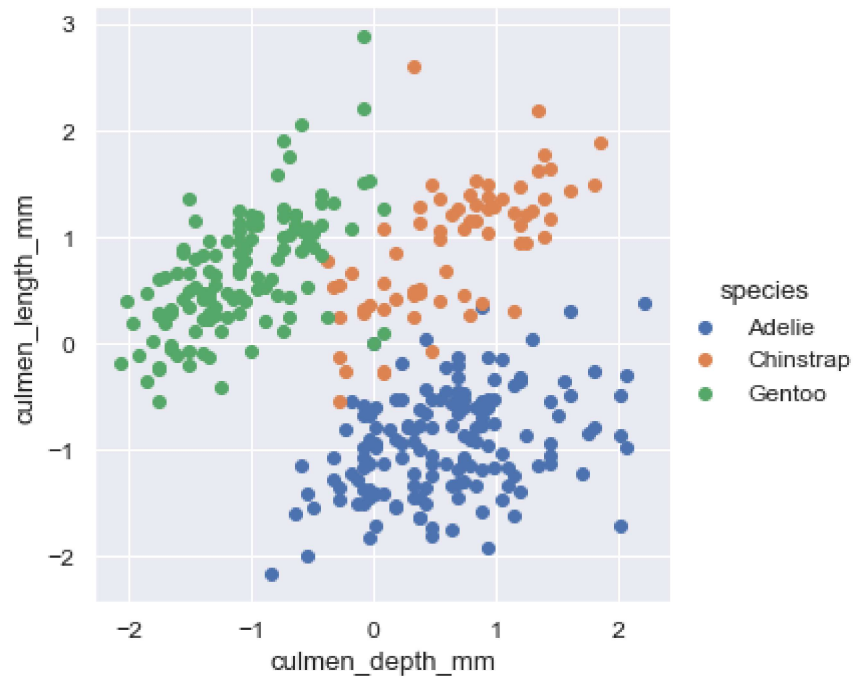
From above plot we can see that,

- In case of culmen length, Adelia is easily identifiable.
- In case of culmen depth, flipper length and body mass, Gentoo is easily identifiable.
- In all cases, Chinstrap remains hard to identify.

1. Scatter Plot for culmen_depth vs culmen_length

```
In [ ]: sns.FacetGrid(df, hue="species", height=5) \
        .map(plt.scatter, "culmen_depth_mm", "culmen_length_mm") \
        .add_legend()
```

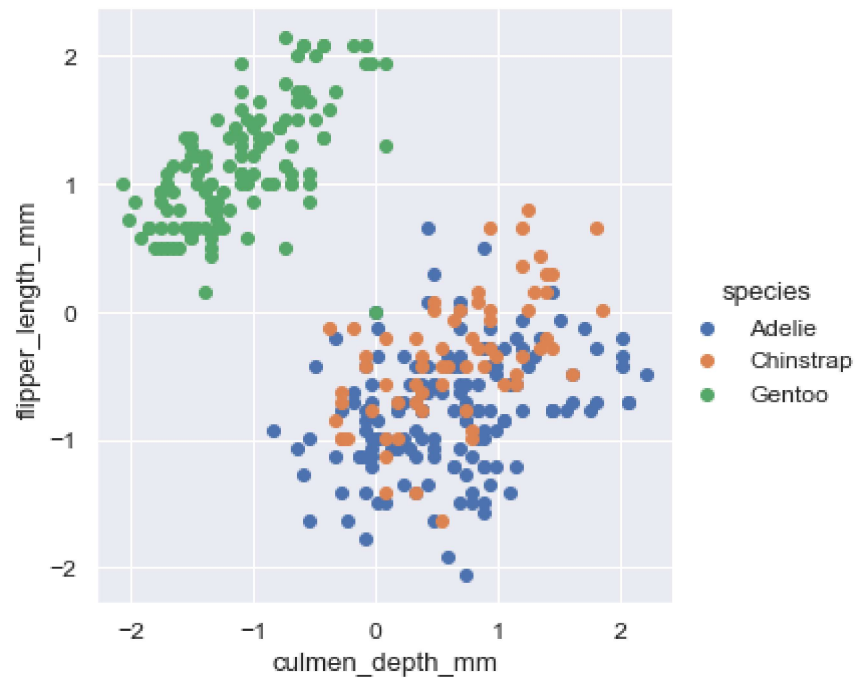
```
Out[ ]: <seaborn.axisgrid.FacetGrid at 0x28471fac220>
```



2. Scatter Plot for culmen_depth vs Flipper_length

```
In [ ]: sns.FacetGrid(df, hue="species", height=5) \
        .map(plt.scatter, "culmen_depth_mm", "flipper_length_mm") \
        .add_legend()
```

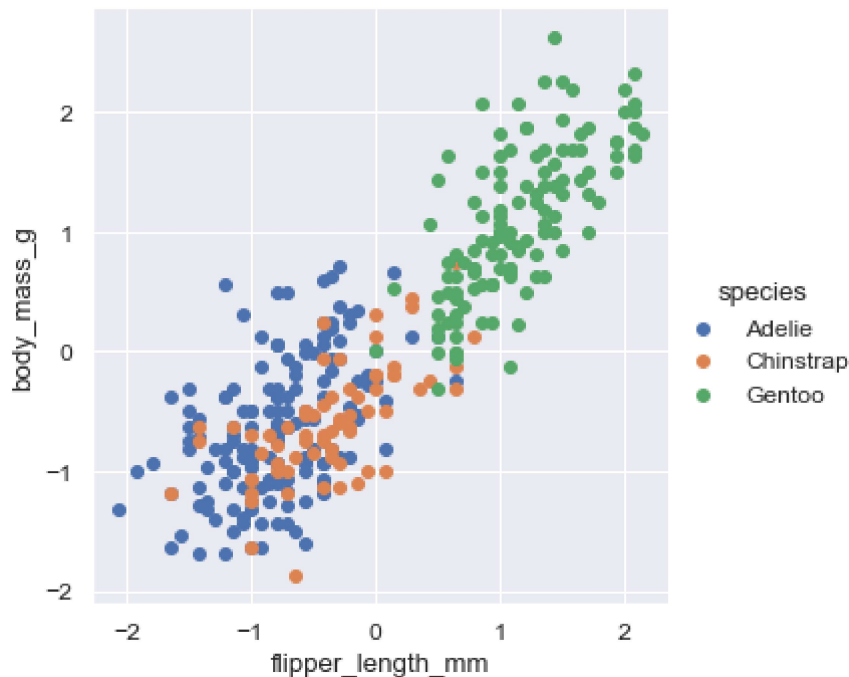
```
Out[ ]: <seaborn.axisgrid.FacetGrid at 0x2847200bf40>
```



3. Scatter Plot for Flipper_Length vs body_mass

```
In [ ]: sns.set_context("notebook", font_scale=1.1)
sns.FacetGrid(df, hue="species", height=5) \
    .map(plt.scatter, "flipper_length_mm", "body_mass_g") \
    .add_legend()
```

Out[]: <seaborn.axisgrid.FacetGrid at 0x28471e0b370>



Covariance and Correlation

- Covariance

```
In [ ]: df.cov()
```

Out[]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
culmen_length_mm	29.633252	-2.519457	50.082029	2590.398957
culmen_depth_mm	-2.519457	3.877069	-16.118414	-743.012250
flipper_length_mm	50.082029	-16.118414	196.578837	9767.130837
body_mass_g	2590.398957	-743.012250	9767.130837	639381.041890
sex	0.877896	0.349105	1.708480	163.307503

- Correlation

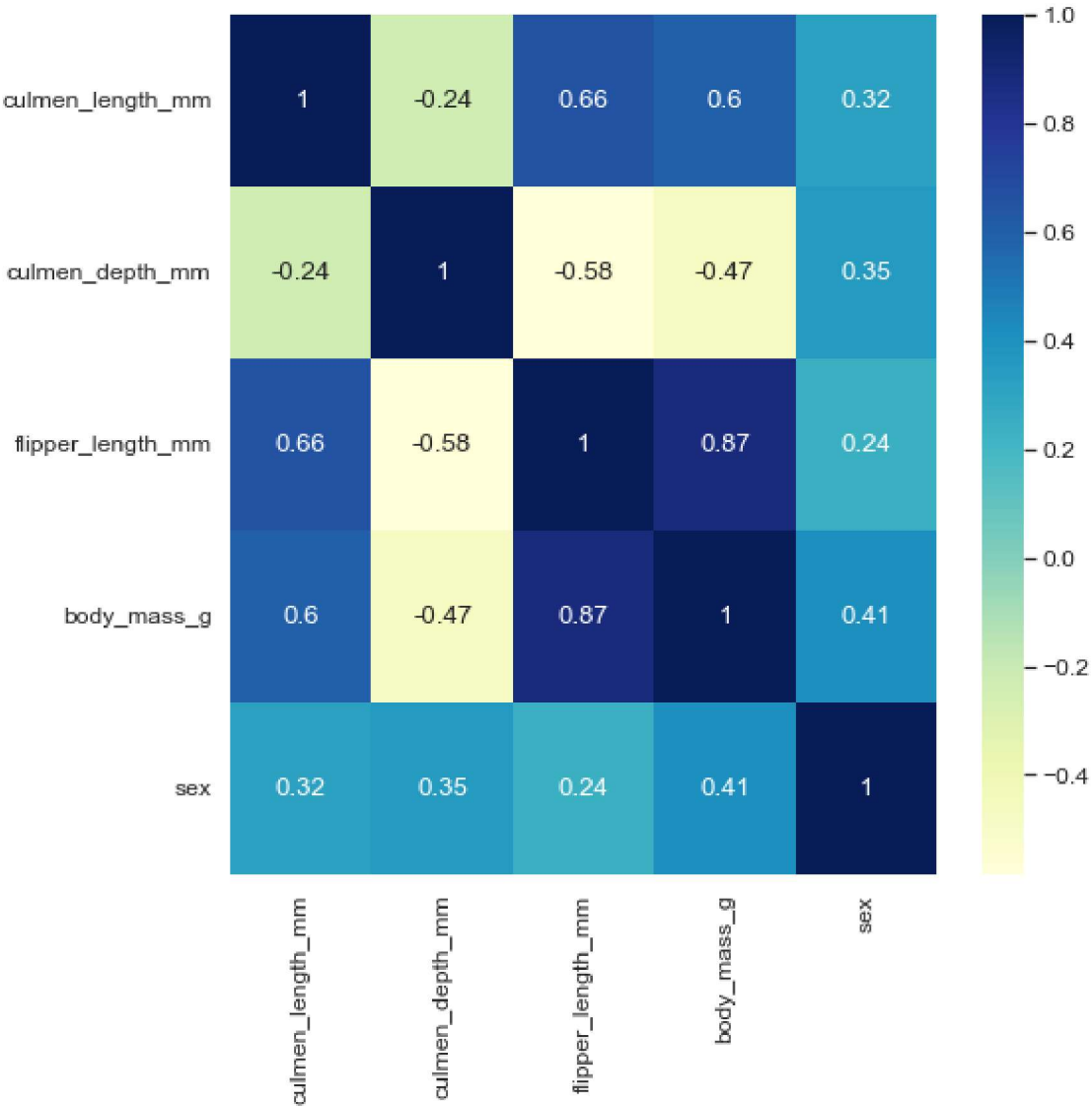
```
In [ ]: df.corr()
```

Out[]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g	sex
culmen_length_mm	1.000000	-0.235053	0.656181	0.595110	0.322338
culmen_depth_mm	-0.235053	1.000000	-0.583851	-0.471916	0.354374
flipper_length_mm	0.656181	-0.583851	1.000000	0.871202	0.243556
body_mass_g	0.595110	-0.471916	0.871202	1.000000	0.408210
sex	0.322338	0.354374	0.243556	0.408210	1.000000

```
In [ ]: plt.figure(figsize=(8,8))
sns.heatmap(df.corr(), cmap="YlGnBu", annot=True)
```

Out[]: <AxesSubplot:>



Observations

from the above heatmap we can determine the following:

- The flipper length is highly correlated to body mass with a value of 0.87
conclusion: The heavier penguins have longer flippers.

Outliers Detection

- plotting the Box Plot.

```
In [ ]: plt.figure(figsize = (10,5))  
sns.boxplot(data = df.drop(['sex'], axis = 1), palette = "Set2")
```

```
Out[ ]: <AxesSubplot:>
```



- Scaling data for handling outliers

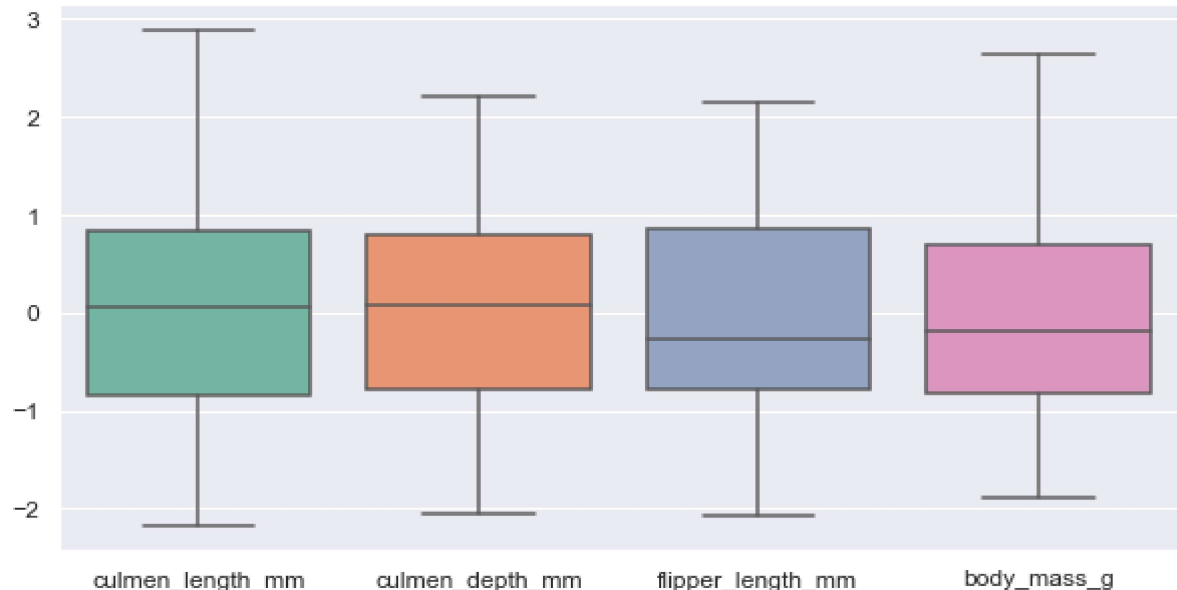
```
In [ ]: from sklearn.preprocessing import StandardScaler  
sc = StandardScaler()
```

```
In [ ]: for i in df.columns:  
    if df[i].dtype == 'float64':  
        a = np.asarray(df[i])  
        a = a.reshape(-1, 1)  
        df[i] = sc.fit_transform(a)
```



```
In [ ]: plt.figure(figsize=(10,5))  
sns.boxplot(data = df.drop(['sex'], axis = 1), palette = "Set2")
```

Out[]: <AxesSubplot:>



Hypothesis testing

- to be completed

key Findings

- In case of culmen length, Adelie is easily identifiable.
- In case of culmen depth, flipper length and body mass, Gentoo is easily identifiable.
- In all cases, Chinstrap remains hard to identify.
- The heavier penguins have longer flippers.

Steps Summarised:

- Data was cleaned for missing values by one_hot_encoding method and filling with mean and mode values for numeric and categorical columns respectively.
- There was no significant deviation but there were a few outliers which were handled *after* standard Scaling.
- One column was dropped as it was outside the scope of this study that was performed.
- One of the categorical column was Encoded to yield numeric value by label encoding method.
- One significant Correlation was found as observed in heat map.
- Each of the above step is accompanied by visual plots and their observations respectively.

Data Summary

The given dataset is clean with minimal skewness and insignificant outliers. Can be used further for training the machine.