In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import plotly.express as px
from pandas_profiling import ProfileReport
from plotly.offline import iplot
!pip install joypy
import joypy
from sklearn.cluster import KMeans

plt.rcParams['figure.figsize'] = 8, 5
plt.style.use("fivethirtyeight")

data = pd.read_csv('../input/palmer-archipelago-antarctica-penguin-data/penguins_si
study_data = pd.read_csv('../input/palmer-archipelago-antarctica-penguin-data/pengu
```

```
Collecting joypy
  Downloading joypy-0.2.2-py2.py3-none-any.whl (8.3 kB)
Requirement already satisfied: scipy>=0.11.0 in /opt/conda/lib/python3.7/site-pack
ages (from joypy) (1.4.1)
Requirement already satisfied: matplotlib in /opt/conda/lib/python3.7/site-package
s (from joypy) (3.2.1)
Requirement already satisfied: numpy in /opt/conda/lib/python3.7/site-packages (fr
om joypy) (1.18.1)
Requirement already satisfied: pandas>=0.20.0 in /opt/conda/lib/python3.7/site-pac
kages (from joypy) (1.0.3)
Requirement already satisfied: python-dateutil>=2.1 in /opt/conda/lib/python3.7/si
te-packages (from matplotlib->joypy) (2.8.1)
Requirement already satisfied: cycler>=0.10 in /opt/conda/lib/python3.7/site-packa
ges (from matplotlib->joypy) (0.10.0)
Requirement already satisfied: kiwisolver>=1.0.1 in /opt/conda/lib/python3.7/site-
packages (from matplotlib->joypy) (1.2.0)
Requirement already satisfied: pyparsing!=2.0.4,!=2.1.2,!=2.1.6,>=2.0.1 in /opt/co
nda/lib/python3.7/site-packages (from matplotlib->joypy) (2.4.7)
Requirement already satisfied: pytz>=2017.2 in /opt/conda/lib/python3.7/site-packa
ges (from pandas>=0.20.0->joypy) (2019.3)
Requirement already satisfied: six>=1.5 in /opt/conda/lib/python3.7/site-packages
(from python-dateutil>=2.1->matplotlib->joypy) (1.14.0)
Installing collected packages: joypy
Successfully installed joypy-0.2.2
```

Columns in the dataset

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

Various observations of the data

In [2]:

```python
# description

data.describe(include='all')
```

Out[2]:

	species	island	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
count	344	344	342.000000	342.000000	342.000000	342.000000
unique	3	3	NaN	NaN	NaN	NaN
top	Adelie	Biscoe	NaN	NaN	NaN	NaN
freq	152	168	NaN	NaN	NaN	NaN
mean	NaN	NaN	43.921930	17.151170	200.915205	4201.754386
std	NaN	NaN	5.459584	1.974793	14.061714	801.954536
min	NaN	NaN	32.100000	13.100000	172.000000	2700.000000
25%	NaN	NaN	39.225000	15.600000	190.000000	3550.000000
50%	NaN	NaN	44.450000	17.300000	197.000000	4050.000000
75%	NaN	NaN	48.500000	18.700000	213.000000	4750.000000
max	NaN	NaN	59.600000	21.500000	231.000000	6300.000000

In [3]:

```python
#Covariance

data.cov()
```

Out[3]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
culmen_length_mm	29.807054	-2.534234	50.375765	2605.591912
culmen_depth_mm	-2.534234	3.899808	-16.212950	-747.370093
flipper_length_mm	50.375765	-16.212950	197.731792	9824.416062
body_mass_g	2605.591912	-747.370093	9824.416062	643131.077327

In [4]:

```python
#correlation

data.corr()
```

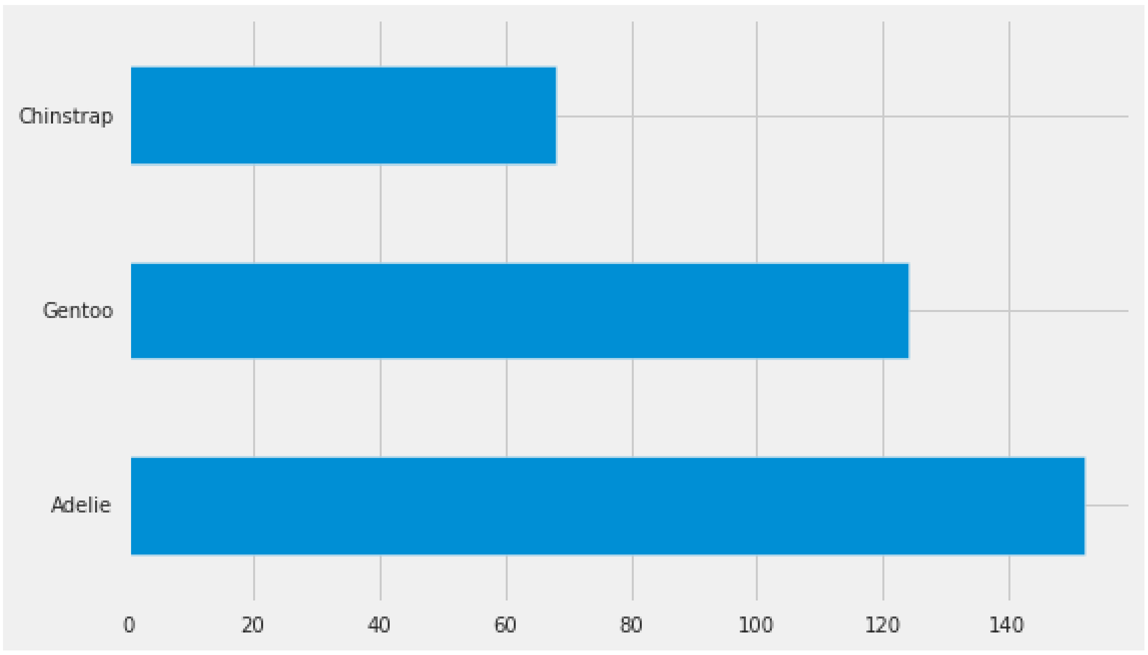
Out[4]:

	culmen_length_mm	culmen_depth_mm	flipper_length_mm	body_mass_g
culmen_length_mm	1.000000	-0.235053	0.656181	0.595110
culmen_depth_mm	-0.235053	1.000000	-0.583851	-0.471916
flipper_length_mm	0.656181	-0.583851	1.000000	0.871202
body_mass_g	0.595110	-0.471916	0.871202	1.000000

Number of entries in data for each species

In [5]:

```python
data['species'].value_counts().plot(kind='barh')
plt.show()
```



It can be observed that unlike the Iris dataset, this data contains different number of entries for each species

Filling in missing values

```
In [6]: #checking number of null values in the data
        data.isnull().sum()
```

```
Out[6]: 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 [7]: # Dropping the 2 rows with null values for all variables

        data.drop(data[data['body_mass_g'].isnull()].index,axis=0, inplace=True)
```

```
In [8]: #imputing the null values in sex with its mode

        data['sex'] = data['sex'].fillna('MALE')
```

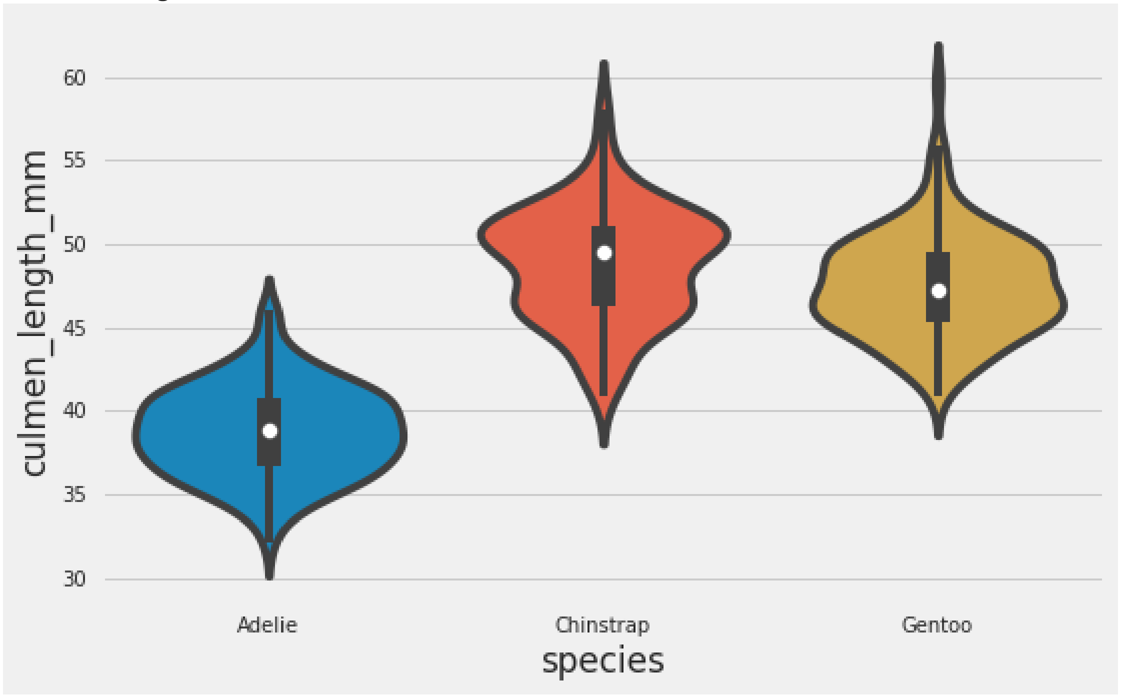
```
In [9]: #dropping the 336th row due to its faulty value in sex variable

        data.drop(data[data['sex']=='.'].index, inplace=True)
```

Distribution of the variables

```
In [10]: print('Culmen Length Distribution')
         sns.violinplot(data=data, x="species", y="culmen_length_mm", size=8)
```

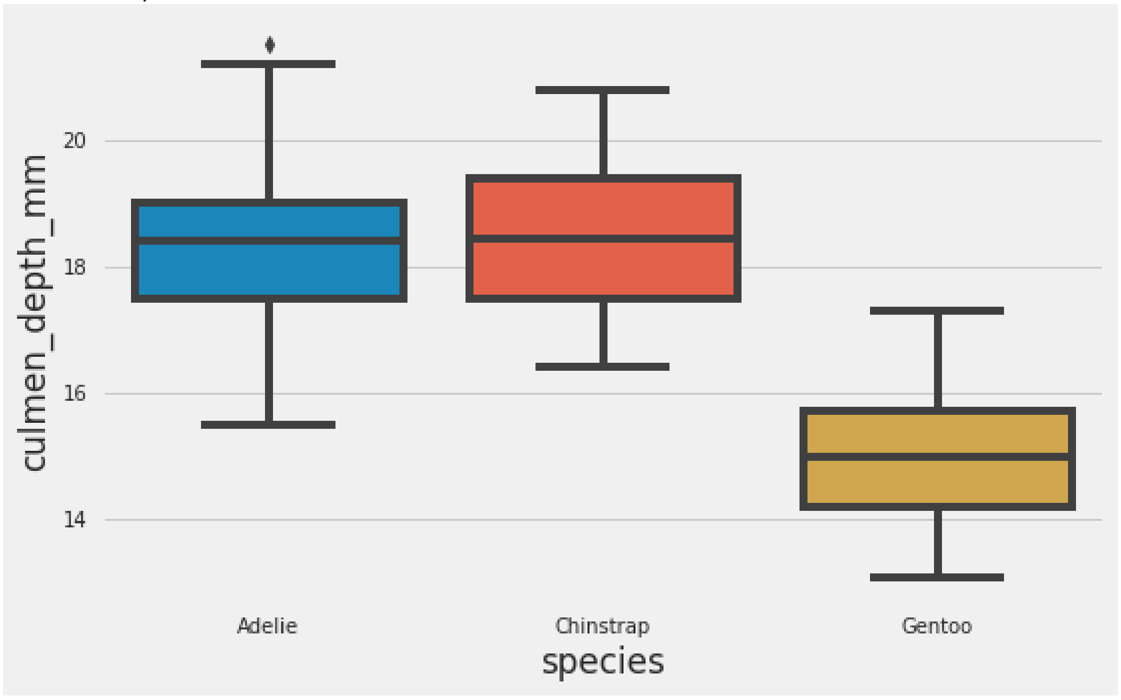
```
plt.show()
```

```
Culmen Length Distribution
```



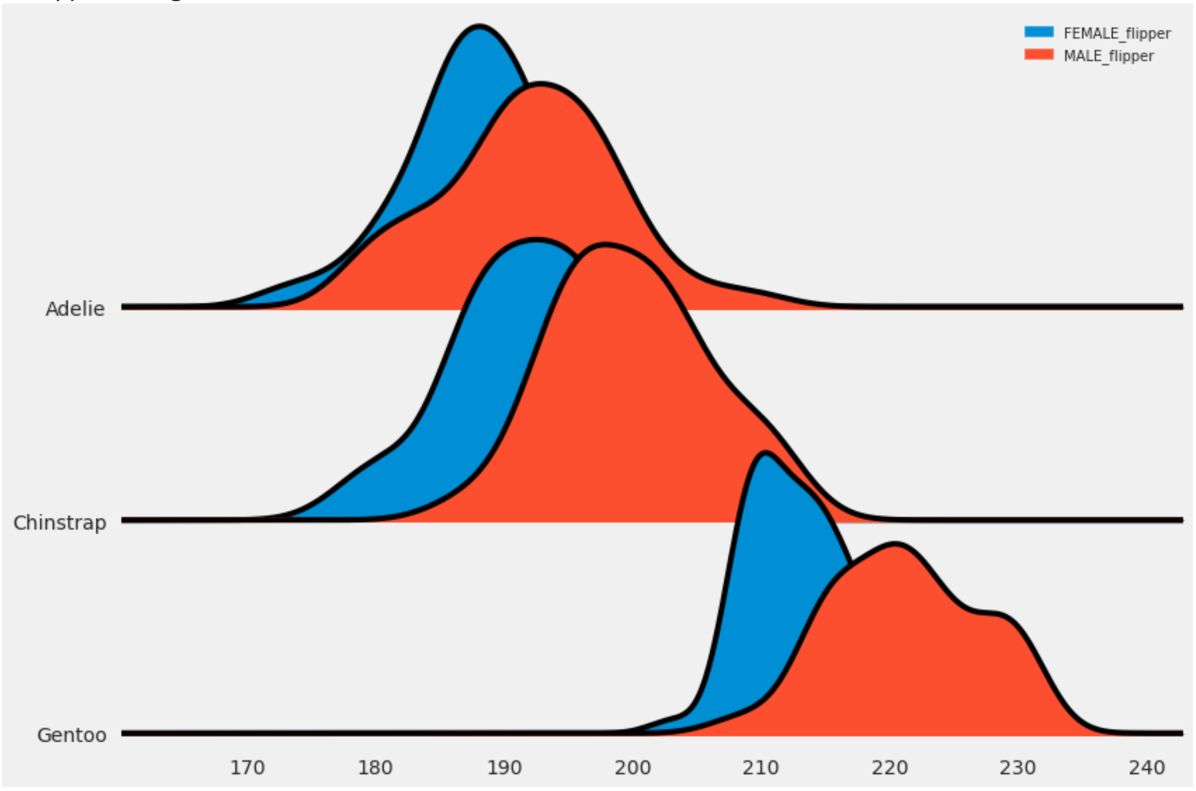
In [11]:
```
print('Culmen Depth Distribution')
sns.boxplot(data=data, x="species", y="culmen_depth_mm")
plt.show()
```

```
Culmen Depth Distribution
```



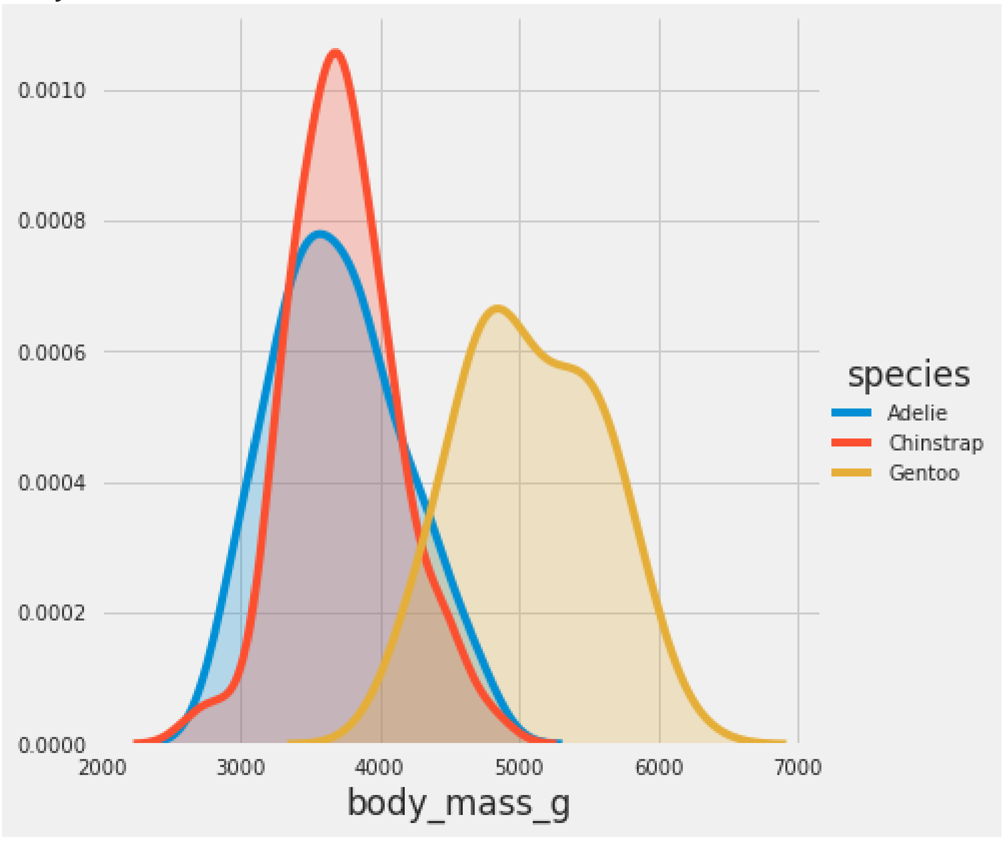
In [12]:
```
print('Flipper Length Distribution')
df = data.copy()
df["MALE_flipper"] = df.apply(lambda row: row["flipper_length_mm"] if row["sex"] ==
df["FEMALE_flipper"] = df.apply(lambda row: row["flipper_length_mm"] if row["sex"]
fig, axes = joypy.joyplot(df,
                          column=['FEMALE_flipper', 'MALE_flipper'],
                          by = "species",
                          ylim = 'own',
                          figsize = (12,8),
                         legend = True
                        )
```

```
Flipper Length Distribution
```



In [13]:
```
print('Body Mass Distribution')
sns.FacetGrid(data, hue="species", height=6,).map(sns.kdeplot, "body_mass_g",shade=
plt.show()
```

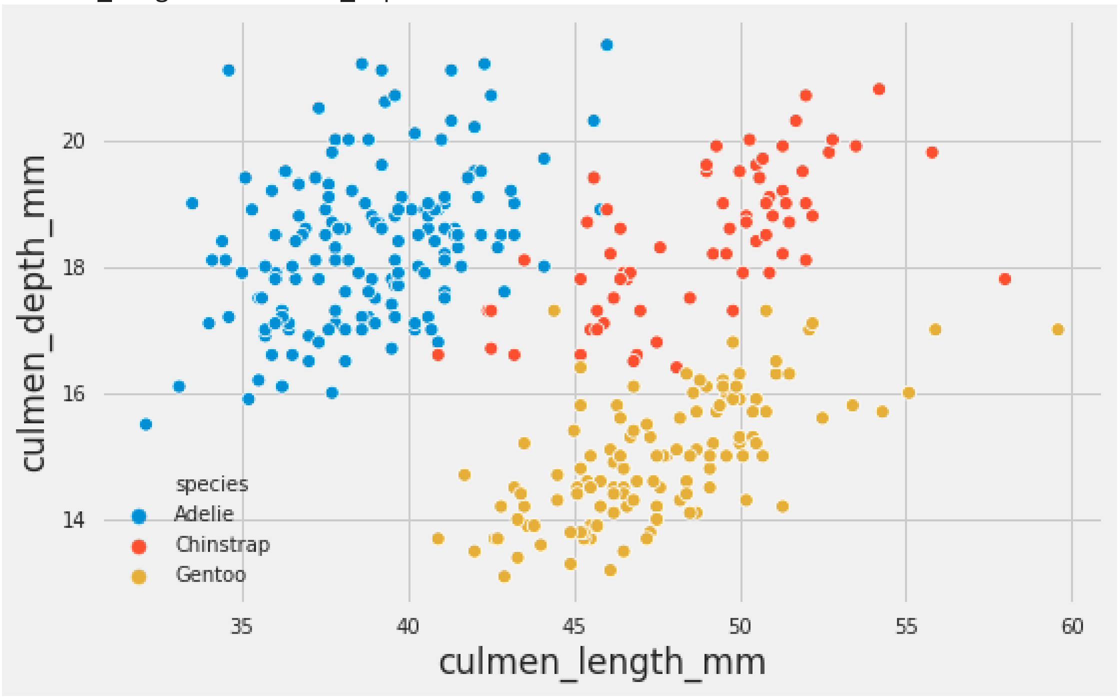
```
Body Mass Distribution
```



Correlation of the variables

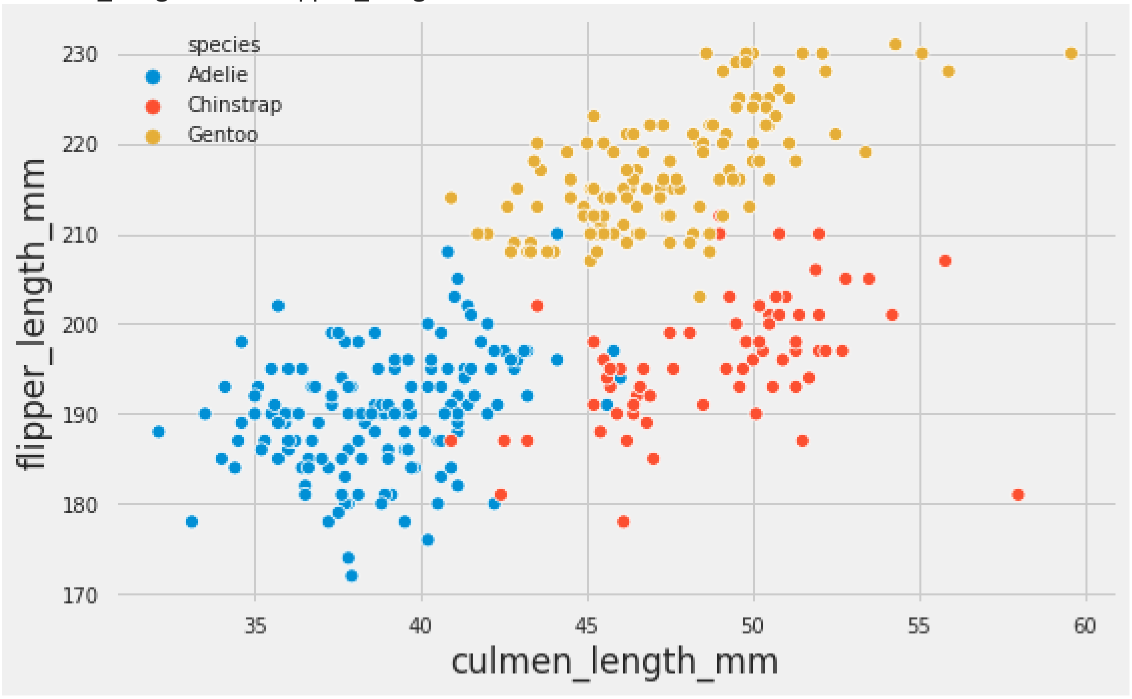
In [14]:
```
print('culmen_length vs culmen_depth')
sns.scatterplot(data=data, x='culmen_length_mm', y='culmen_depth_mm', hue='species
plt.show()
```

```
culmen_length vs culmen_depth
```



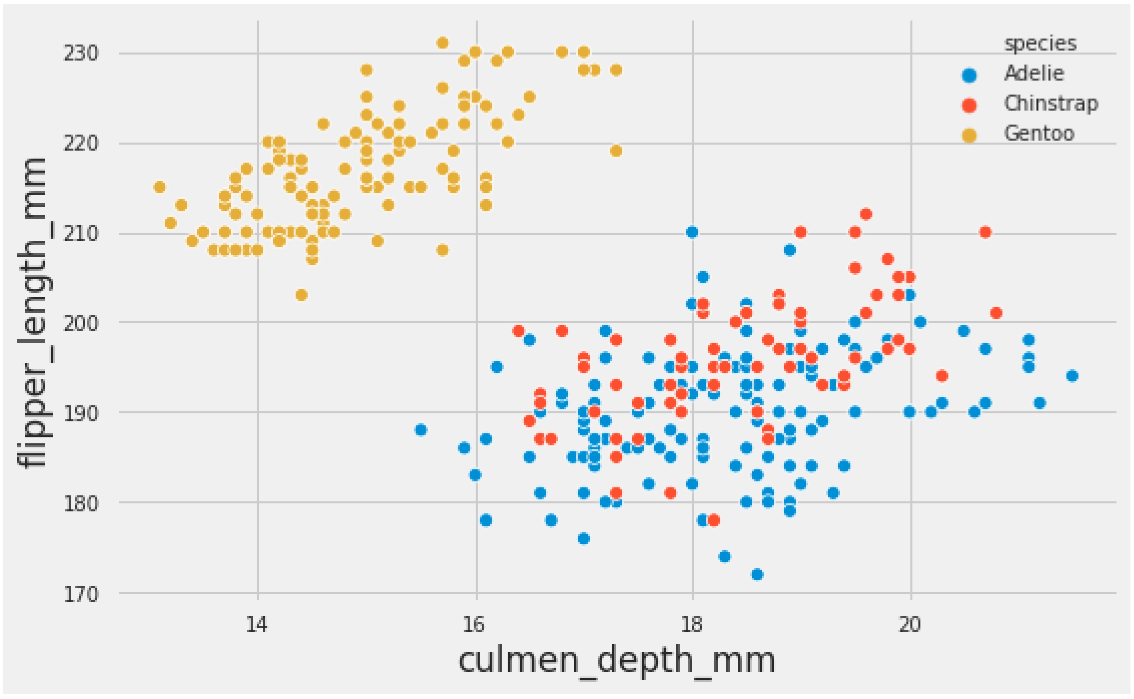
In [15]:
```
print('culmen_length vs flipper_length')
sns.scatterplot(data=data, x='culmen_length_mm', y='flipper_length_mm', hue='specie
plt.show()
```

```
culmen_length vs flipper_length
```



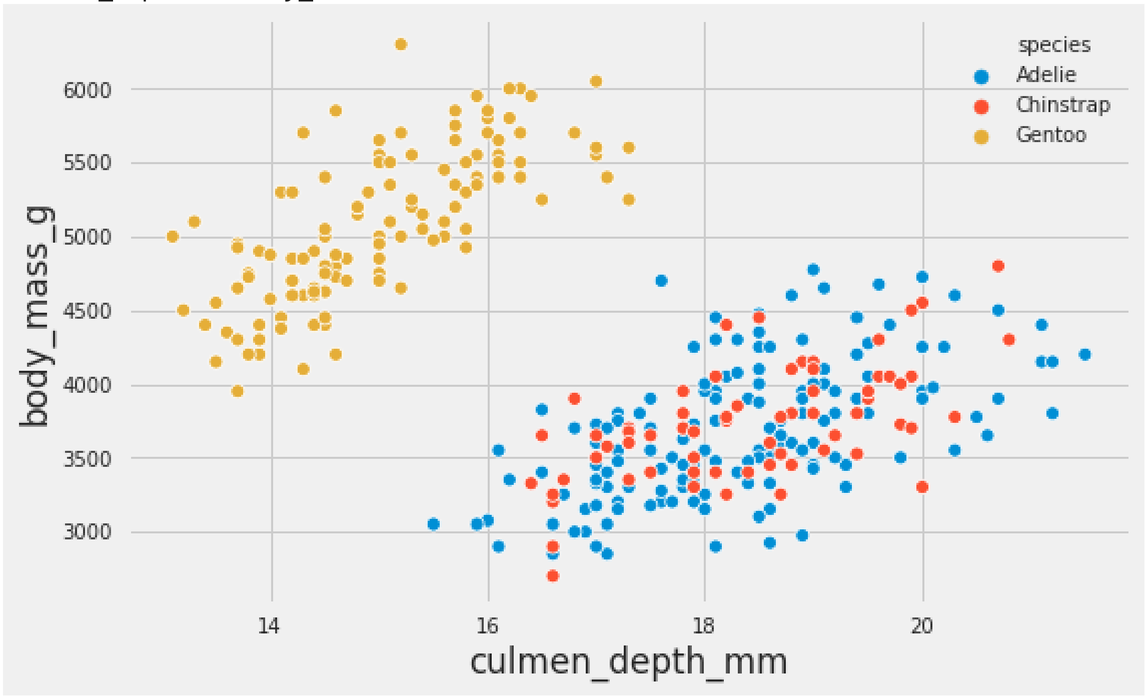
In [16]:
```
print('culmen_depth vs flipper_length')
sns.scatterplot(data=data, x='culmen_depth_mm', y='flipper_length_mm', hue='species
plt.show()
```

```
culmen_depth vs flipper_length
```



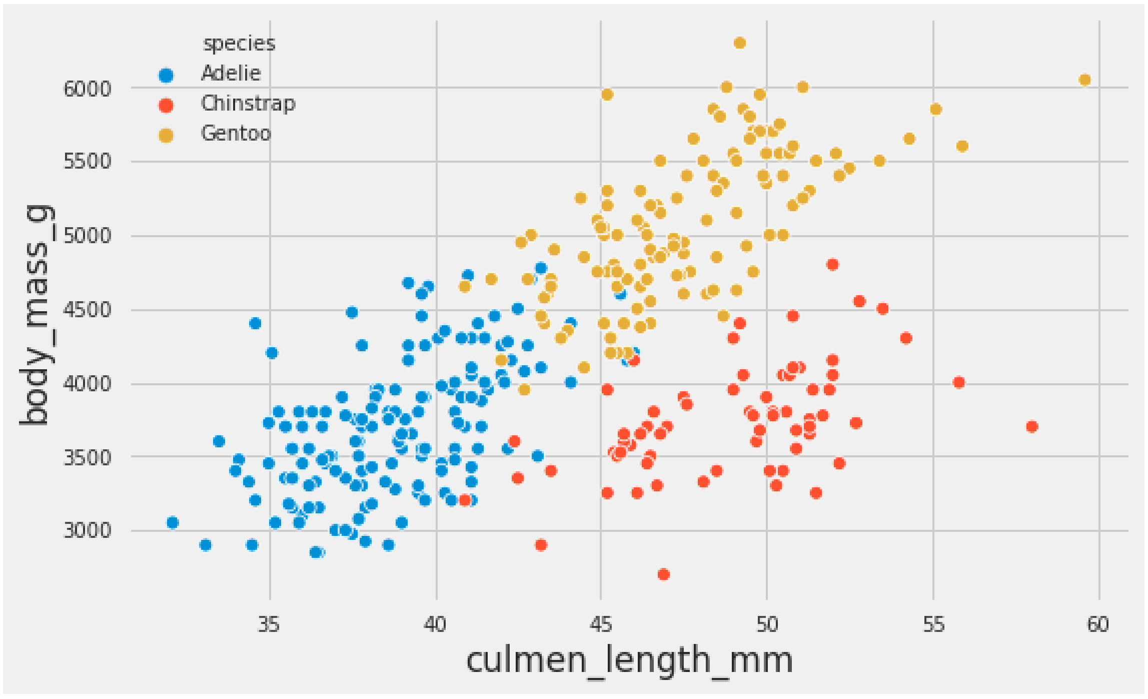
In [17]:
```
print('culmen_depth vs body_mass')
sns.scatterplot(data=data, x='culmen_depth_mm', y='body_mass_g', hue='species')
plt.show()
```

```
culmen_depth vs body_mass
```



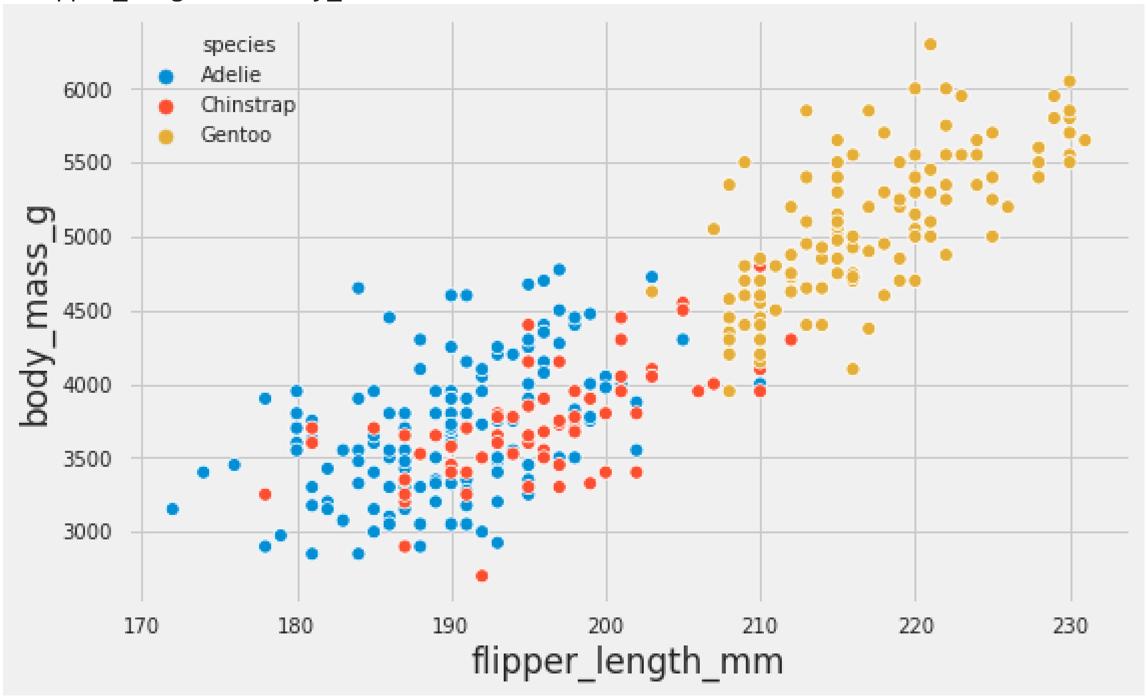
In [18]:
```
print('culmen_length vs body_mass')
sns.scatterplot(data=data, x='culmen_length_mm', y='body_mass_g', hue='species')
plt.show()
```

```
culmen_length vs body_mass
```



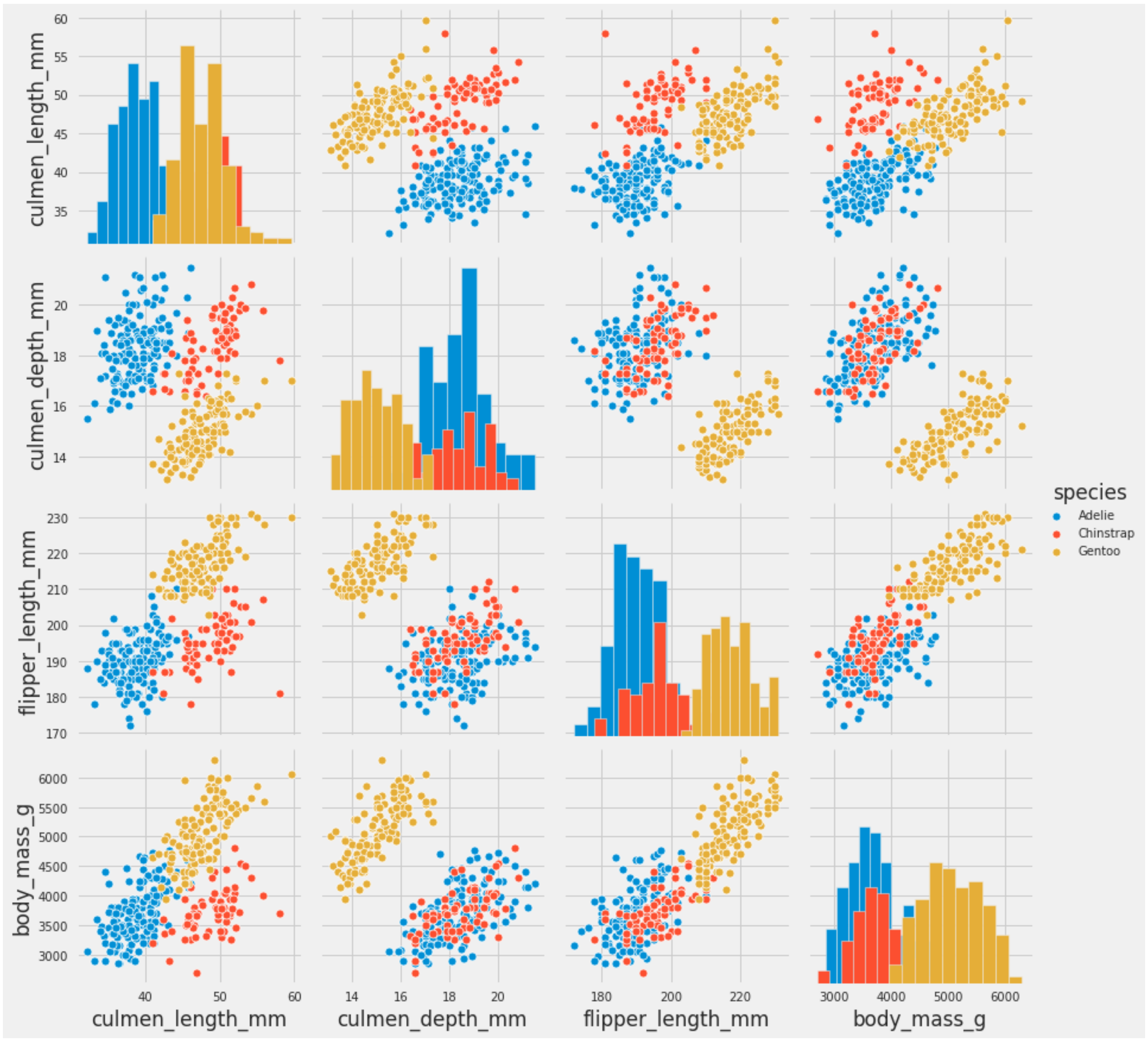
In [19]:
```
print('flipper_length vs body_mass')
sns.scatterplot(data=data, x='flipper_length_mm', y='body_mass_g', hue='species')
plt.show()
```

```
flipper_length vs body_mass
```



In [20]:
```
print('Pairplot')
sns.pairplot(data=data[['species','culmen_length_mm','culmen_depth_mm','flipper_ler
plt.show()
```

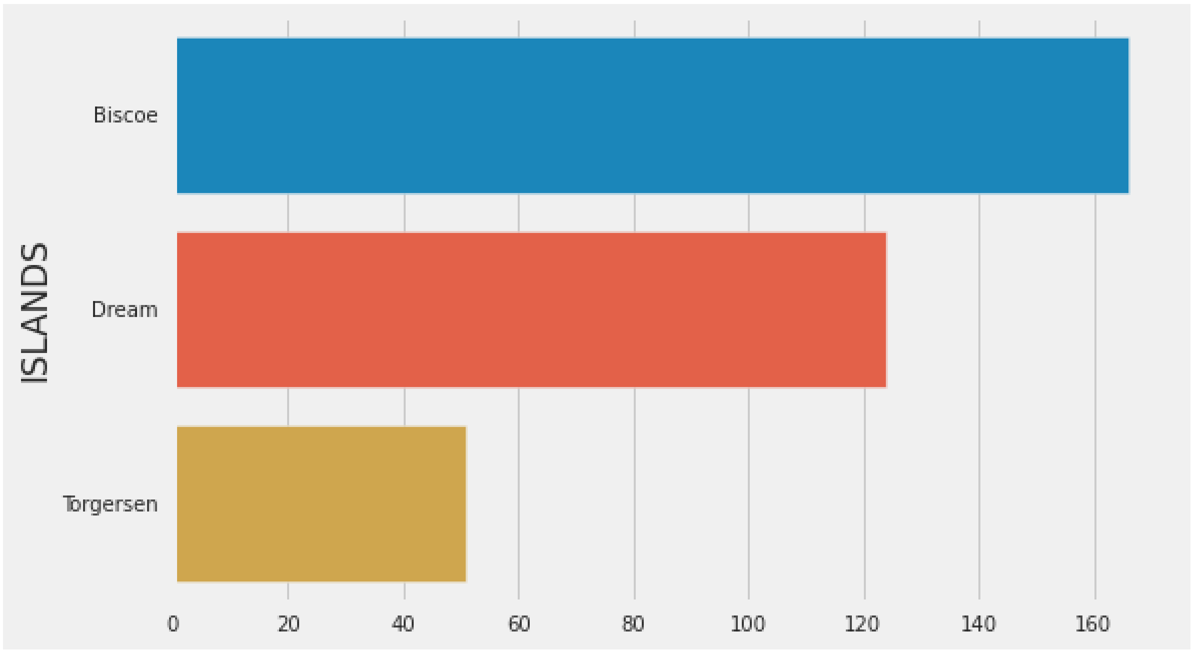
```
Pairplot
```



Extreme values of the variables

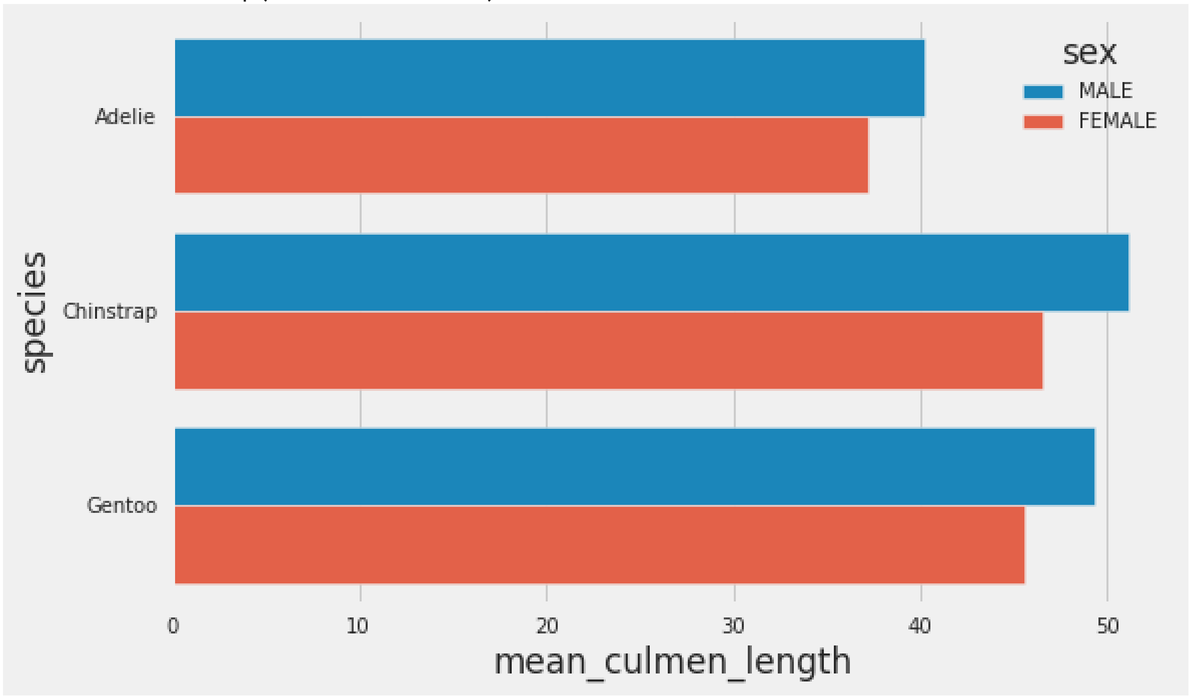
In [21]:
```
print('Which island consists of most Penguins?')
print('Answer: Biscoe')
df = data['island'].value_counts().reset_index()

fig = sns.barplot(data=df, x='island', y='index')
fig.set(xlabel='', ylabel='ISLANDS')
plt.show()
```

```
Which island consists of most Penguins?
Answer: Biscoe
```



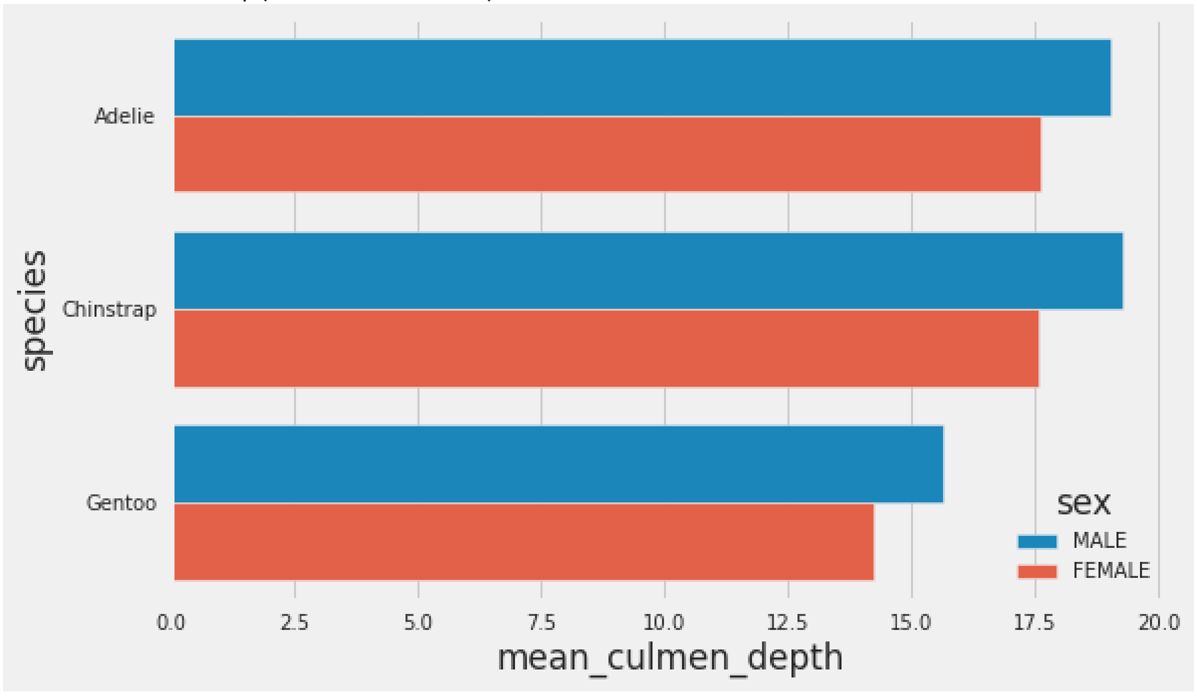
In [22]:
```
print('Which species have highest culmen_length?')
print('Answer: Chinstrap(male and female)')
df = data.loc[:,['species','culmen_length_mm','sex']]
df['mean_culmen_length'] = df.groupby(['species','sex'])['culmen_length_mm'].transf
df = df.drop('culmen_length_mm', axis=1).drop_duplicates()

sns.barplot(data=df, x='mean_culmen_length', y='species', hue='sex')
plt.show()
```

```
Which species have highest culmen_length?
Answer: Chinstrap(male and female)
```



In [23]:
```
print('Which species have highest culmen_depth?')
print('Answer: Chinstrap(male and female)')
df = data.loc[:,['species','culmen_depth_mm','sex']]
df['mean_culmen_depth'] = df.groupby(['species','sex'])['culmen_depth_mm'].transfor
df = df.drop('culmen_depth_mm', axis=1).drop_duplicates()

sns.barplot(data=df, x='mean_culmen_depth', y='species', hue='sex')
plt.show()
```

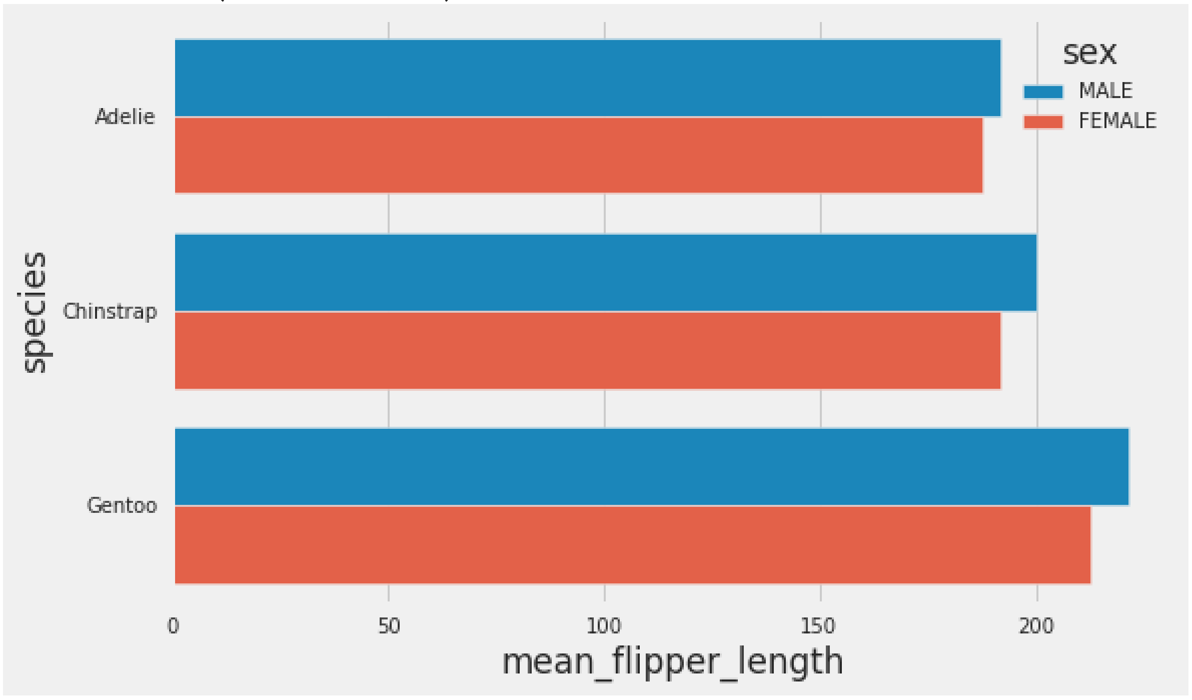
```
Which species have highest culmen_depth?
Answer: Chinstrap(male and female)
```



In [24]:

```
print('Which species have highest flipper_length?')
print('Answer: Gentoo(male and female)')
df = data.loc[:,['species','flipper_length_mm','sex']]
df['mean_flipper_length'] = df.groupby(['species','sex'])['flipper_length_mm'].tran
df = df.drop('flipper_length_mm', axis=1).drop_duplicates()

sns.barplot(data=df, x='mean_flipper_length', y='species', hue='sex')
plt.show()
```

```
Which species have highest flipper_length?
Answer: Gentoo(male and female)
```

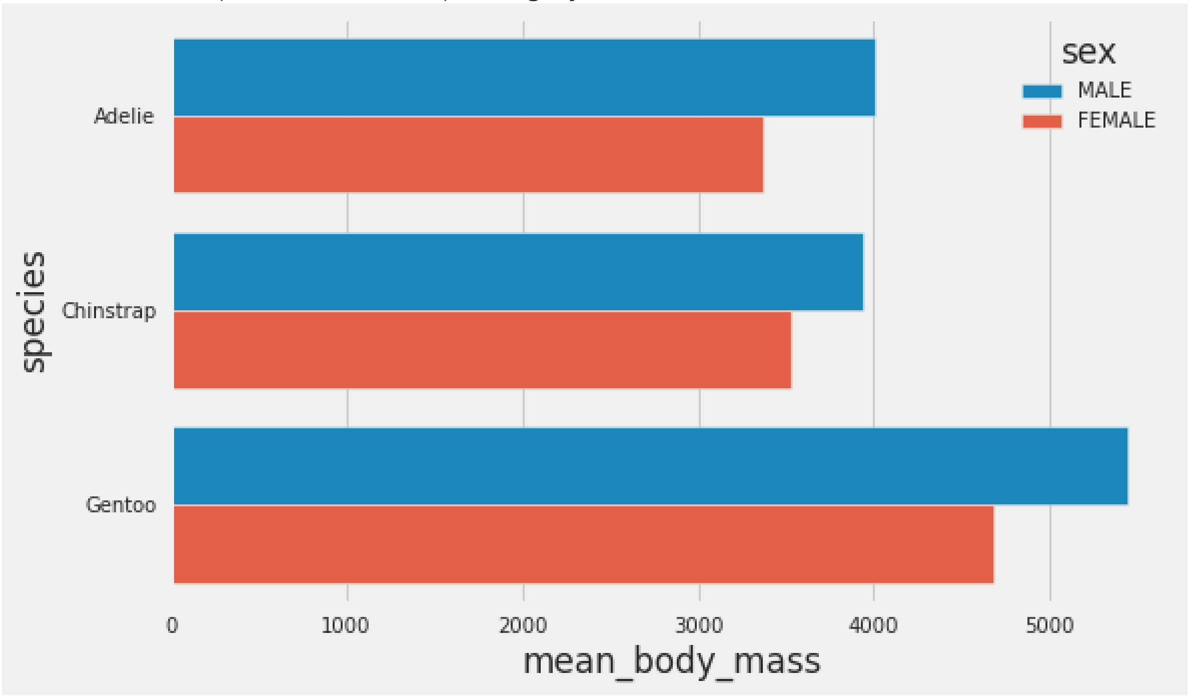


In [25]:

```
print('Which species have highest body_mass?')
print('Answer: Gentoo(male and female) - Highly diverse values noticed')
df = data.loc[:,['species','body_mass_g','sex']]
df['mean_body_mass'] = df.groupby(['species','sex'])['body_mass_g'].transform('mear
df = df.drop('body_mass_g', axis=1).drop_duplicates()
```

```
sns.barplot(data=df, x='mean_body_mass', y='species', hue='sex')
plt.show()
```

```
Which species have highest body_mass?
Answer: Gentoo(male and female) - Highly diverse values noticed
```



Creating classifier for gender prediction

Since the missing values are already we don't need to worry about that. Next step is to encode the categorical variables.

I am setting 'sex' as the target variable. So the categorical variables to be encoded are 'species' and 'island'

In [26]:
```
df = data.copy()
target = 'sex'
encode = ['species','island']

for col in encode:
    dummy = pd.get_dummies(df[col], prefix=col)
    df = pd.concat([df,dummy], axis=1)
    del df[col]
```

Lets label encode the target variable as well.

I won't be using any fit transform from the scikit learn api rather i will be using a primitive mapping.

In [27]:
```
target_mapper = {'MALE':0, 'FEMALE':1}
def target_encode(val):
    return target_mapper[val]

df['sex'] = df['sex'].apply(target_encode)
```

In [28]:
```
#separating X and y

X = df.drop('sex', axis=1)
y = df['sex']
```

In [29]:
```
# scaling the data

from sklearn import preprocessing
X = preprocessing.scale(X)
```

In [30]:
```
#splitting the data

from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.2, random_state
```

In [31]:
```
# model fitting and prediction

from sklearn.linear_model import LogisticRegression

model = LogisticRegression().fit(X_train, y_train)
pred = model.predict(X_test)
```

In [32]:
```
# checking performance of model

from sklearn.metrics import classification_report, confusion_matrix, roc_curve, ro

print('CONFUSION MATRIX')
print(confusion_matrix(y_test, pred))
```

```
CONFUSION MATRIX
[[29  7]
 [ 1 32]]
```

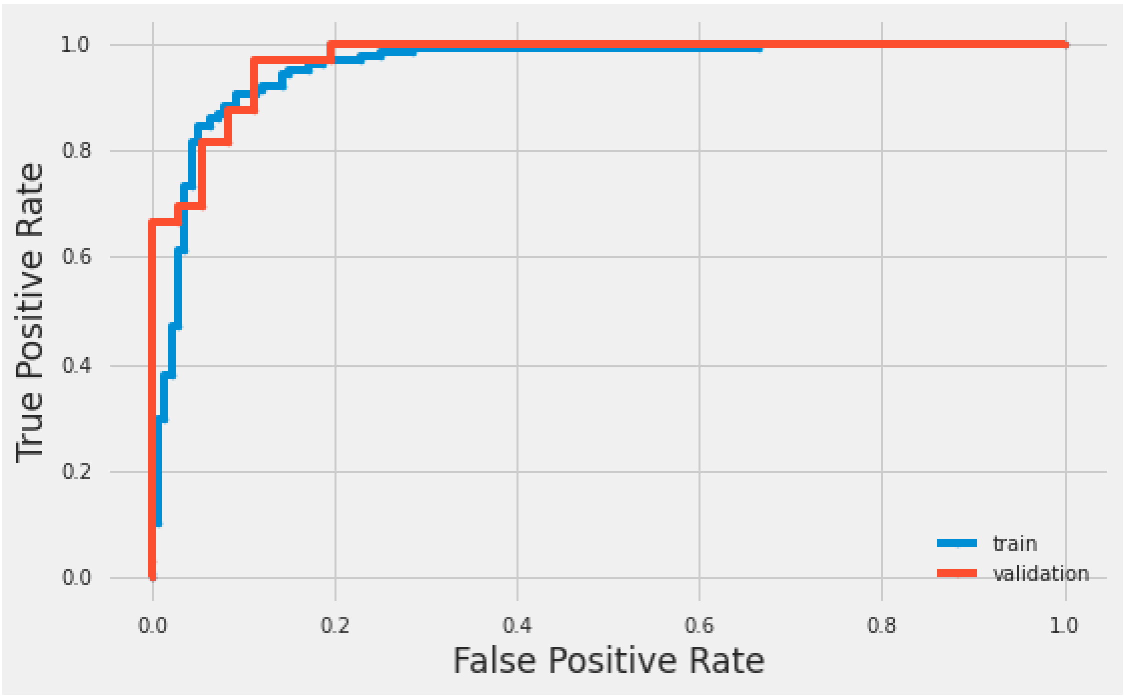
In [33]:
```
print('CLASSIFICATION REPORT\n')
print(classification_report(y_test, pred))
```

```
CLASSIFICATION REPORT

              precision    recall  f1-score   support

           0       0.97      0.81      0.88        36
           1       0.82      0.97      0.89        33

    accuracy                           0.88        69
   macro avg       0.89      0.89      0.88        69
weighted avg       0.90      0.88      0.88        69
```

In [34]:
```
# ROC CURVE

print('ROC CURVE')
train_probs = model.predict_proba(X_train)
train_probs1 = train_probs[:, 1]
fpr0, tpr0, thresholds0 = roc_curve(y_train, train_probs1)
```

```
test_probs = model.predict_proba(X_test)
test_probs1 = test_probs[:, 1]
fpr1, tpr1, thresholds1 = roc_curve(y_test, test_probs1)

plt.plot(fpr0, tpr0, marker='.', label='train')
plt.plot(fpr1, tpr1, marker='.', label='validation')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend()
plt.show()
```

```
ROC CURVE
```



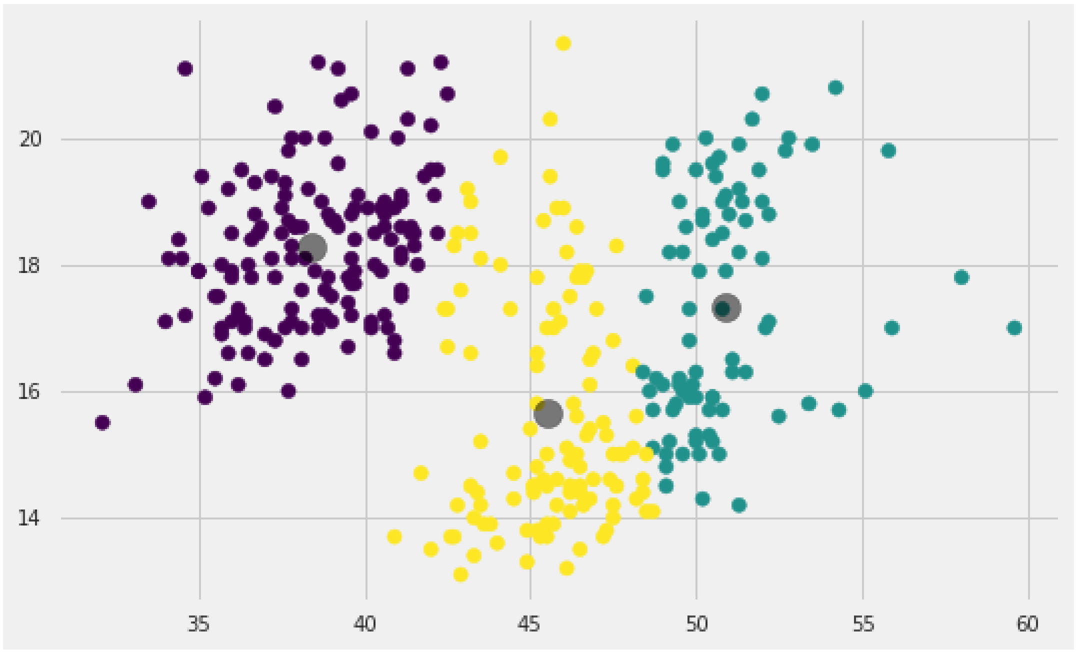
So the model achieved an accuracy of 88%.

Clustering the species

In [35]:
```
df = data.copy()
```

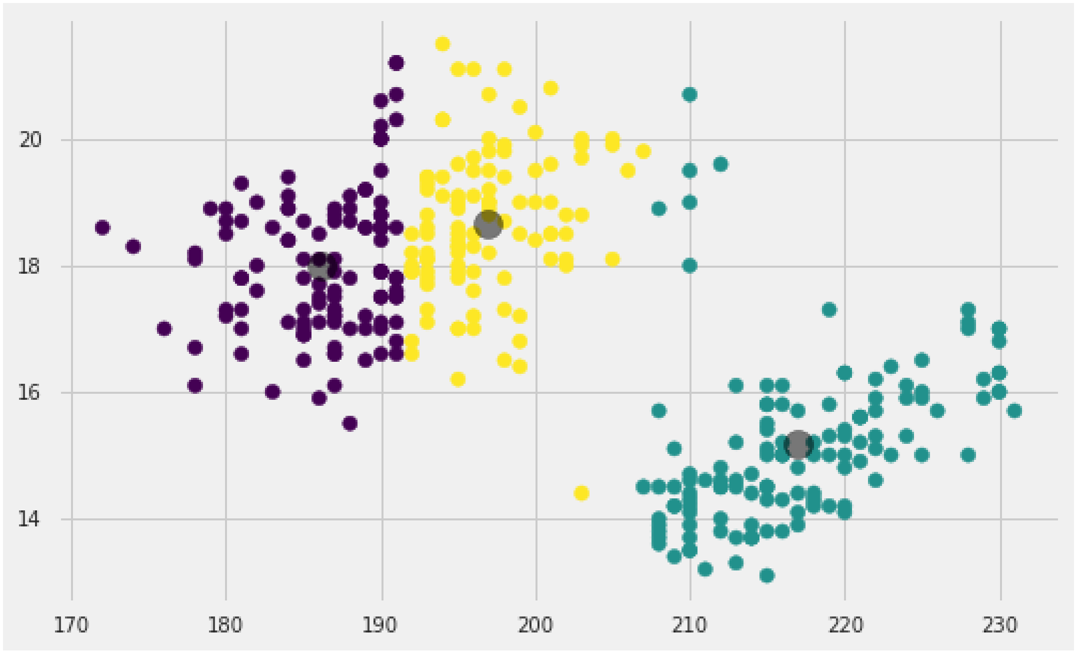
In [36]:
```
print('CLUSTERING ON CULMEN LENGTH AND CULMEN DEPTH')
X = df[['culmen_length_mm','culmen_depth_mm']]

kmeans = KMeans(n_clusters=3)
kmeans.fit(X)
y_kmeans = kmeans.predict(X)

plt.scatter(X.loc[:, 'culmen_length_mm'], X.loc[:, 'culmen_depth_mm'], c=y_kmeans,

centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.5)
plt.show()
```

```
CLUSTERING ON CULMEN LENGTH AND CULMEN DEPTH
```



In [37]:
```python
print('CLUSTERING ON FLIPPER LENGTH AND CULMEN DEPTH')
X = df[['flipper_length_mm','culmen_depth_mm']]

kmeans = KMeans(n_clusters=3)
kmeans.fit(X)
y_kmeans = kmeans.predict(X)

plt.scatter(X.loc[:, 'flipper_length_mm'], X.loc[:, 'culmen_depth_mm'], c=y_kmeans,

centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.5)
plt.show()
```

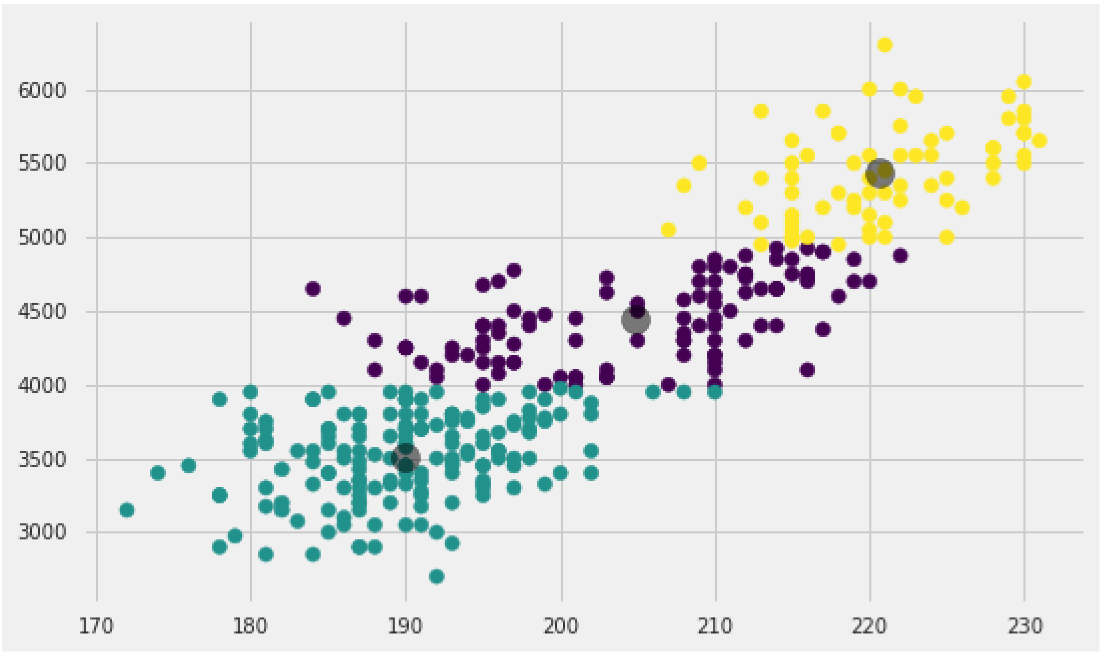
```
CLUSTERING ON FLIPPER LENGTH AND CULMEN DEPTH
```



In [38]:
```python
print('CLUSTERING ON FLIPPER LENGTH AND BODY MASS')
X = df[['flipper_length_mm','body_mass_g']]

kmeans = KMeans(n_clusters=3)
kmeans.fit(X)
y_kmeans = kmeans.predict(X)
```

```
plt.scatter(X.loc[:, 'flipper_length_mm'], X.loc[:, 'body_mass_g'], c=y_kmeans, s=

centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.5)
plt.show()
```

```
CLUSTERING ON FLIPPER LENGTH AND BODY MASS
```



```
In [ ]:
```