PIC 16A Group Project

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Group Contributions Statement

The group consisted of Diya Gopinath, Sumedha Goyal, and Hannah Kwon. Diya led the data acquisition and preparation. Under the exploratory analysis, Diya worked on the summary table and boxplots, Sumedha worked on the scatterplots, and Hannah worked on the histograms. Diya and Sumedha collaborated on the feature selection. Diya led the multinomial logistic regression model. Sumedha led the random forest model. Hannah led the nearest-neighbour classifiers model. We all worked on the explanations for the parts we worked on. Hannah worked on the conclusion. We all checked each other’s work and made revisions to code and writing.

Data Acquisition and Preparation

§1. Data Import

In [79]:
```
#Importing all the required
import pandas as pd
from matplotlib import pyplot as plt
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn import preprocessing
from sklearn.model_selection import cross_val_score
import seaborn as sns
```

In [80]:
```
#importing the penguin dataset as a pandas DataFrame called penguins
url = 'https://philchodrow.github.io/PIC16A/datasets/palmer_penguins.csv'
penguins = pd.read_csv(url)
```

In [81]:
```
#displaying the first five rows of the penguins dataset
penguins.head()
```

Out[81]:

	studyName	Sample Number	Species	Region	Island	Stage	Individual ID	Clutch Completion	Date Egg
0	PAL0708	1	Adelie Penguin (Pygoscelis adeliae)	Anvers	Torgersen	Adult, 1 Egg Stage	N1A1	Yes	11/11/07
1	PAL0708	2	Adelie Penguin (Pygoscelis adeliae)	Anvers	Torgersen	Adult, 1 Egg Stage	N1A2	Yes	11/11/07
2	PAL0708	3	Adelie Penguin (Pygoscelis adeliae)	Anvers	Torgersen	Adult, 1 Egg Stage	N2A1	Yes	11/16/07
3	PAL0708	4	Adelie Penguin (Pygoscelis adeliae)	Anvers	Torgersen	Adult, 1 Egg Stage	N2A2	Yes	11/16/07
4	PAL0708	5	Adelie Penguin (Pygoscelis adeliae)	Anvers	Torgersen	Adult, 1 Egg Stage	N3A1	Yes	11/16/07

§2. Data Splitting

To aid us in our data exploration and model building, we can split our penguins dataset into training and test data sets. Splitting the data allows us to holdout some data (test data) which the model will not be able to see at first, which can later be used to test the accuracy of the model.

In [82]:
```
#Setting the seed to 1234 to ensure reproducibility
np.random.seed(1234)

# Splitting and holding out 20% of data as test dataset
train, test = train_test_split(penguins, test_size = 0.2)
```

§3. Data Cleaning

We clean the given dataset to allow for easier data exploration and analysis. We shorten the species name, remove rows wherein the sex of a penguin is entered as '.' in place of an actual gender. We also drop columns from the dataset which will not have an impact of predicting the species of the penguin, such as studyName, Sample Number, Individual ID, Clutch Completion, Date Egg, and Comments. Region was also dropped as it was constant across all penguin species.

In [83]:
```
#shortens the species name
penguins["Species"] = penguins["Species"].str.split().str.get(0)

#removes rows where Sex is .
```

```
penguins = penguins[penguins['Sex'] != '.']

#drops the columns which will not have an impact on the model
penguins = penguins.drop(['studyName', 'Sample Number', 'Region', 'Stage', 'Inc
                          'Date Egg', 'Comments'],axis=1)
```

In [84]:
```
#displaying the first five columns of this cleaned penguins data set
penguins.head()
```

Out[84]:

	Species	Island	Culmen Length (mm)	Culmen Depth (mm)	Flipper Length (mm)	Body Mass (g)	Sex	Delta 15 N (o/oo)	Delta 13 C (o/oo)
0	Adelie	Torgersen	39.1	18.7	181.0	3750.0	MALE	NaN	NaN
1	Adelie	Torgersen	39.5	17.4	186.0	3800.0	FEMALE	8.94956	-24.69454
2	Adelie	Torgersen	40.3	18.0	195.0	3250.0	FEMALE	8.36821	-25.33302
3	Adelie	Torgersen	NaN	NaN	NaN	NaN	NaN	NaN	NaN
4	Adelie	Torgersen	36.7	19.3	193.0	3450.0	FEMALE	8.76651	-25.32426

In [85]:
```
def prep_data(data_df):

    """
    A function that cleans the data in a given data frame and splits it into a

    Args:
        data_df: a DataFrame

    Returns:
        X: the values of the DataFrame in which the Sex column has been changec
        from which the Species column has been dropped
        y: the values of the DataFrame consisting of only the Species column
        df_copy: a copy of the cleaned dataframe before splitting into predicto
    """

    #creates a copy of the DataFrame
    df = data_df.copy()

    le = preprocessing.LabelEncoder()

    #drops all the NaN values
    df = df[["Culmen Length (mm)","Culmen Depth (mm)","Sex","Island","Species",
             "Delta 15 N (o/oo)", "Delta 13 C (o/oo)"]].dropna()

    #encodes the column Sex, Species, and Island as integers
    df['Sex'] = le.fit_transform(df['Sex'])
    df['Species'] = le.fit_transform(df['Species'])
    df['Island'] = le.fit_transform(df['Island'])

    #creates a copy of the cleaned dataframe
    df_copy = df.copy()

    #dividing our data into predictor and target datasets
    X = df.drop(['Species'], axis = 1)
    y = df['Species']

    return(X, y, df_copy)
```

In [86]:
```
#cleaning the datasets based on the penguins dataframe
X,y,df_copy = prep_data(penguins)
#cleaning the datasets based on the training dataframe
X_train, y_train, cleaned_train = prep_data(train)
#cleaning the datasets based on the test dataframe
X_test,  y_test, clean_test  = prep_data(test)
```

Exploratory Analysis

To help us visualise the relationship between the species of the penguins and other recorded features, we can construct a summary table. This summary table will showcase the median values of the different features for the penguins, grouped by Species, then Sex, and then Island.

In [87]:
```
def summary_table (df, groups):
    """
    Functions that creates and displays a summary table grouped by the columns

    Args:
        df: a DataFrame
        groups: the columns by which to group the summary table

    Returns:
        summary_table: a summary table grouped by the columns of the DataFrame
    """
    #creating a copy of the dataframe
    values = df.copy()
    #dropping the columns in groups from the values dataframe
    values = values.drop(groups, axis=1).columns.values
    #creating a summary table grouped by the columns in groups
    summary_table = penguins.groupby(groups)[values].median()
    #returning the summary table
    return summary_table
```

In [88]:
```
#displaying the summary table
summary_table(penguins, ["Species", "Sex", "Island"])
```

Out[88]:

Species	Sex	Island	Culmen Length (mm)	Culmen Depth (mm)	Flipper Length (mm)	Body Mass (g)	Delta 15 N (o/oo)	Delta 13 C (o/oo)
Adelie	**FEMALE**	**Biscoe**	37.75	17.70	187.0	3375.0	8.755420	-26.094190
		Dream	36.80	17.80	188.0	3400.0	8.934650	-25.830600
		Torgersen	37.60	17.45	189.0	3400.0	8.791595	-25.835025
	MALE	**Biscoe**	40.80	18.90	191.0	4000.0	8.828740	-25.942600
		Dream	40.25	18.65	190.5	3987.5	8.975330	-26.015490
		Torgersen	41.10	19.20	195.0	4000.0	8.900020	-26.024500
Chinstrap	**FEMALE**	**Dream**	46.30	17.65	192.0	3550.0	9.352770	-24.587305
	MALE	**Dream**	50.95	19.30	200.5	3950.0	9.458270	-24.555925
Gentoo	**FEMALE**	**Biscoe**	45.50	14.25	212.0	4700.0	8.208700	-26.210945
	MALE	**Biscoe**	49.50	15.70	221.0	5500.0	8.289135	-26.251185

From the above table, we can see that male and female populations were observed across all species. Interestingly, Adelie penguins were found on all three islands: Biscoe, Dream, and Torgersen. Chinstrap Penguins were found only on the Dream island, while Gentoo penguins were found only on Biscoe island. This indicates that the qualitative feature of Island could be a better feature to include in our model compared to the qualitative feature of Sex.

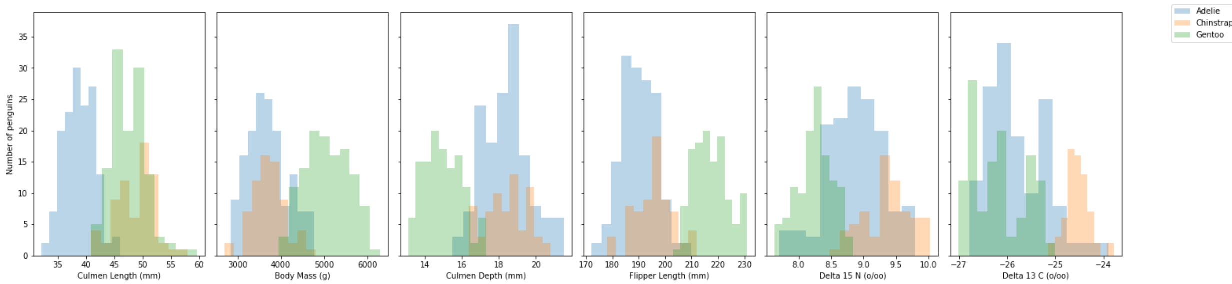
Adelie Penguins had the shortest culmen, with the culmen length of the femeales being the shortest, while Chinstrap penguins had the longest culmen. In terms of culmen depth, Gentoo penguins had the least depth while Chinstrap penguins had the greatest. When it comes to flipper length, Adelie penguins had the shortest flippers, while Gentoo penguins had the longest ones. Gentoo penguins had the greatest body mass, while that of Adelie and Chinstrap were relatively the same. No interesting trends could be observed in the two delat features. This points to the first four features of culmen length, culmen depth, flipper length, and body mass being the stronger quantitative features which could be included in our model.

In [89]:

```
#creating a plot
fig, ax = plt.subplots(1,6, figsize = (20,5), sharey = True)
#setting the y-axis label
ax[0].set(ylabel = "Number of penguins")
data = ["Culmen Length (mm)", "Body Mass (g)",
            "Culmen Depth (mm)","Flipper Length (mm)", "Delta 15 N (o/oo)","Del
unique_species = penguins["Species"].unique()

#iterating through a for loop to plot the histograms
for i in range(len(data)):
    for j in unique_species:
        df = penguins[penguins["Species"] == j]
        ax[i].hist(df[data[i]], label = j, alpha = 0.3)
        ax[i].set(xlabel = data[i])
```

```
plt.tight_layout()
#displaying the legend
plt.legend(bbox_to_anchor=(1.7, 1.05))
```

Out[89]: <matplotlib.legend.Legend at 0x7fd9dac6ad00>



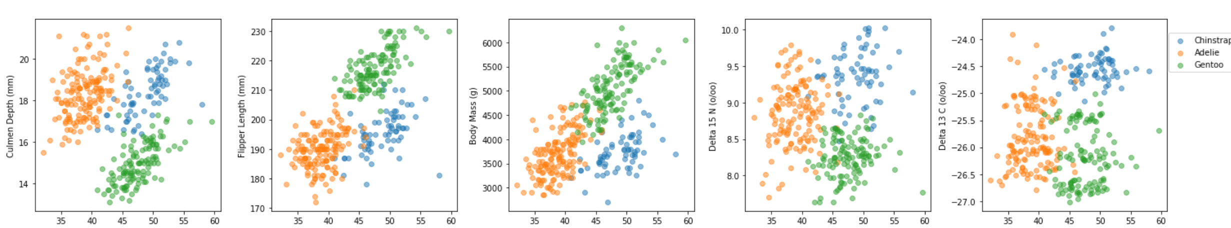
From the above histogram, we can see number of penguins for each features. There are some notable features by looking at this histogram. For `Culmen Length (mm)`, Gentoo penguin has notably higher than the other species. For `Culmen Depth (mm)` it's notable that Adelie penguins have the highest.

Other than that, we can see that Adelie penguins had the shortest culmen, Chrinstrap penguins had the longest culmen. Chinstrap had smaller in almost every features. This points to the first four features of culmen length, culmen depth, flipper length, and body mass being the stronger quantitative features which could be included in our model.

In [126…

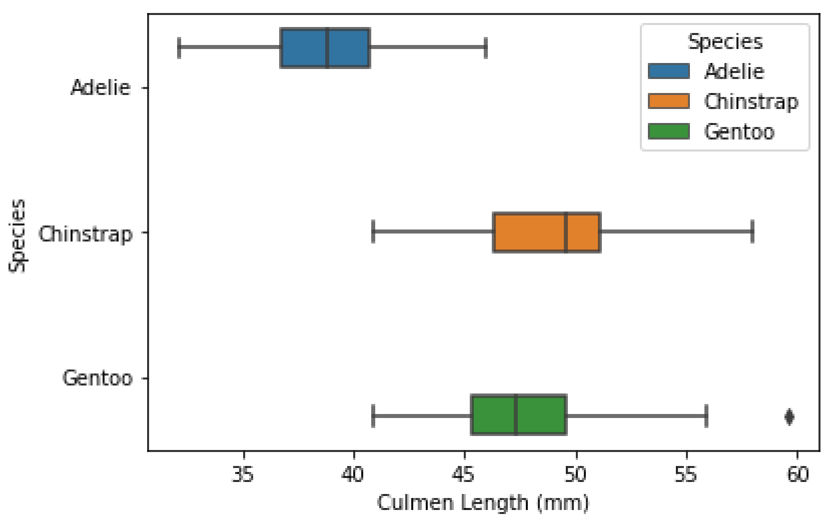
```
#creating the plot
fig, ax = plt.subplots(1, 5, figsize = (20,4))
species = set(penguins['Species'])
y_vars = ['Culmen Depth (mm)','Flipper Length (mm)', 'Body Mass (g)', 'Delta 15

#iterating through the feature names to plot relations on scatterplots
for i in range(len(y_vars)):

    #setting the axis labels
    ax[i].set(xlabel = 'Culmen Length (mm)', ylabel = y_vars[i])

    for s in species:

        sub = penguins[penguins['Species'] == s]
        ax[i].scatter(sub['Culmen Length (mm)'], sub[y_vars[i]], label = s, alp


plt.tight_layout()
plt.legend(bbox_to_anchor=(1.4, 0.95))
```

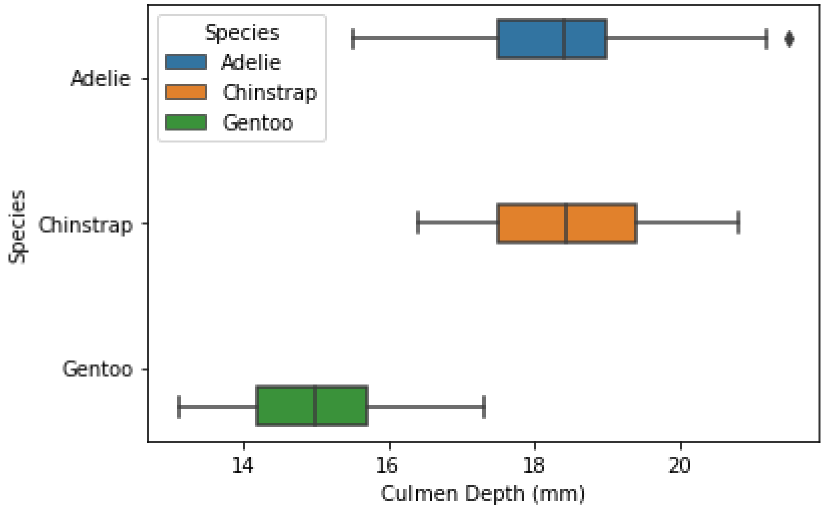
Out[126]: <matplotlib.legend.Legend at 0x7fd9c9b1f160>

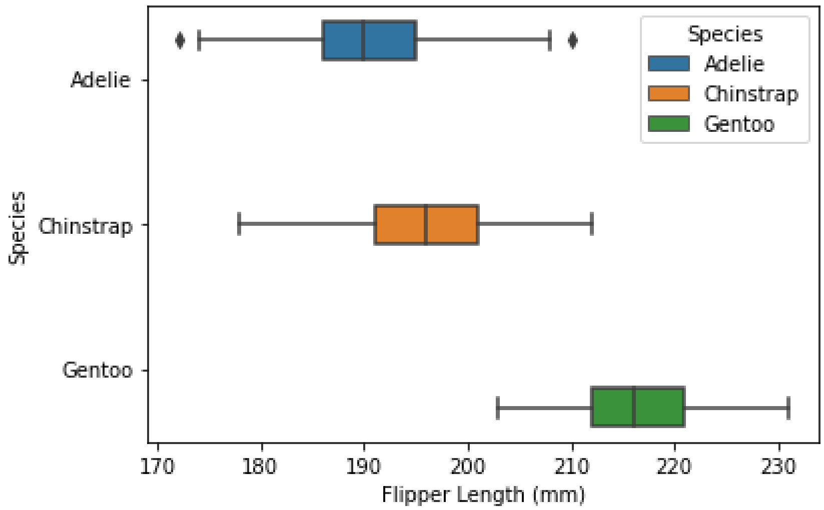


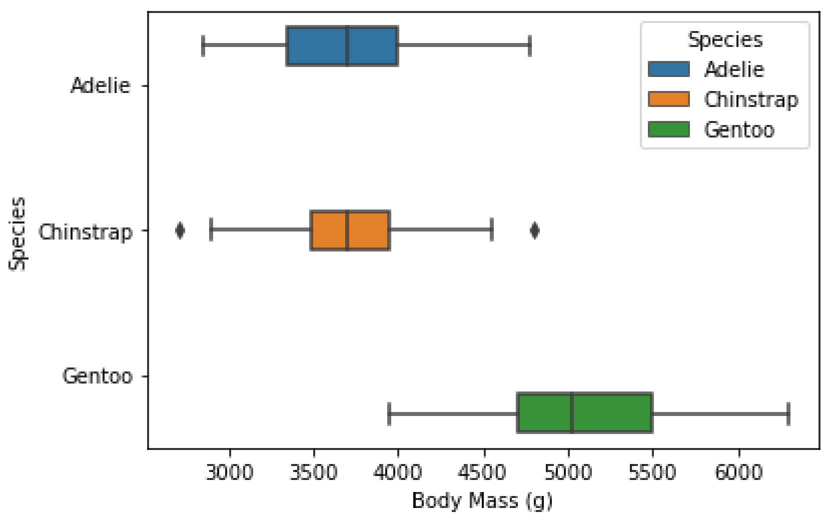
In these scatterplots, the correlation of `Delta 15 N`, `Delta 13 N`, and `Body Mass (g)`, with `Culmen Length (mm)` is weak, compared to the correlation of `Culmen Depth (mm)` and `Flipper Length (mm)` to `Culmen Length (mm)`, which have stronger correlations among the different penguin species. To distinguish Adelie penguins from Chinstrap and Gentoo penguins, `Culmen Length (mm)` is a good candidate for our model's first quantitative feature. Our second quantitative feature should be `Culmen Depth (mm)` or `Flipper Length (mm)`. The Adelie and Chinstrap penguins seem to have larger `Culmen Depth (mm)` than the Gentoo penguin. The Gentoo penguin has a larger `Flipper Length (mm)` and `Body Mass (g)` than the Adelie and Chinstrap penguins. The Chinstrap penguin has more `Delta 15 N (o/oo)` and `Delta 13 N (o/oo)` than the Gentoo and Adelie penguins.

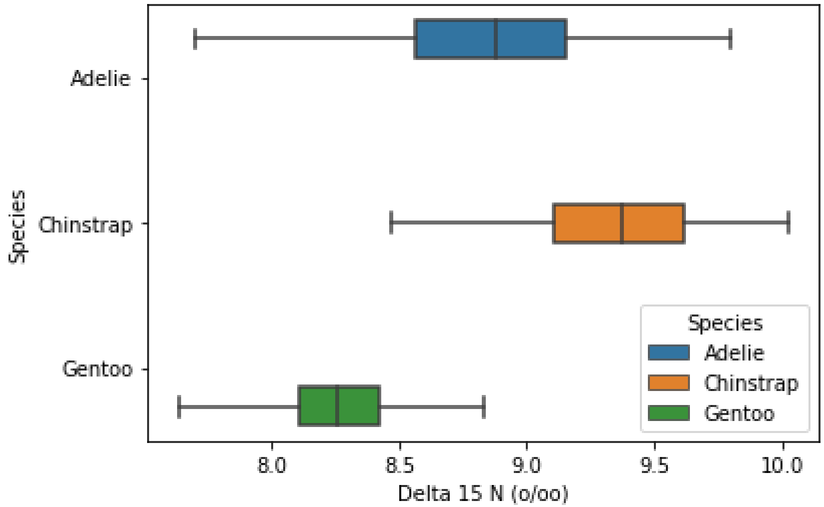
In [91]:
```
#creating a copy of penguins data set
x_ax = penguins.copy()
#dropping qualitative features
x_ax = x_ax.drop(["Species","Sex","Island"], axis=1).columns.values
species = penguins["Species"].unique

for i in range(len(x_ax)):
#Using sns.boxplot to plot a boxplot of the gdpPerCap across continents
    boxplot = sns.boxplot(x = x_ax[i],
                          y = "Species",
                          data = penguins,
                          hue = "Species")
    plt.show()
```

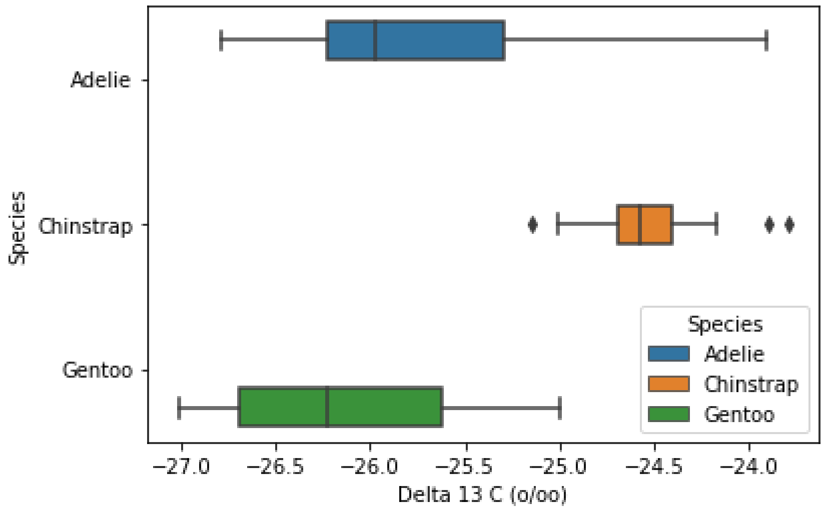



Species
Adelie
Chinstrap
Gentoo
Species
Adelie
Chinstrap
Gentoo
14
16
18
20
Culmen Depth (mm)


Species
Adelie
Chinstrap
Gentoo
Species
Adelie
Chinstrap
Gentoo
170
180
190
200
210
220
230
Flipper Length (mm)


Species
Adelie
Chinstrap
Gentoo
Species
Adelie
Chinstrap
Gentoo
3000
3500
4000
4500
5000
5500
6000
Body Mass (g)



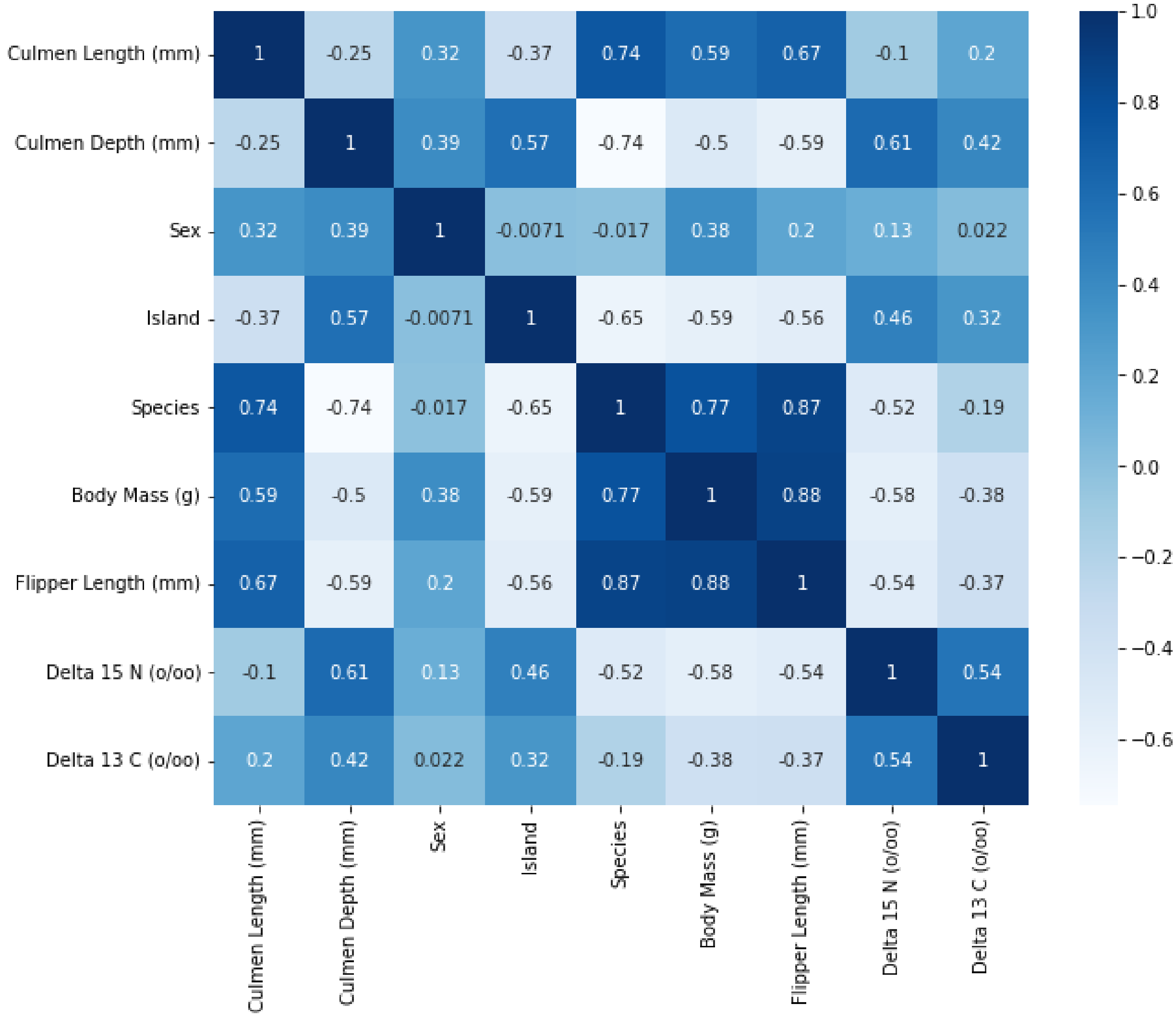


Based on the above plots, we can better visualise the relationship between the different qualitative features and the penguin species. From the above boxplots, we can see that Chinstrap penguins tend to have the higher values in Delta 15N(o/oo) and Culmen Length (mm). Adelie penguins have higher Delta 13 C(o/oo) and Culmen Depth (mm). Gentoo penguins have higher Body Mass (g) and Flipper Length (mm). Additionally, Delta 13 C(o/oo) and Delta 15 N(o/oo) seem to have the different species overlapping, which would not be beneficial when trying to gauging levels at which a penguin can be classified under each Species based on either of those factors.

Feature Selection

To visualise the correlations between the different quantiative and qualitative features of the penguins dataset, we plot a correlation heatmap.

In [92]:
```
#plotting the heatmap
import seaborn as sns
plt.figure(figsize=(10,8))
cor = cleaned_train.corr()
sns.heatmap(cor, annot=True, cmap=plt.cm.Blues)
plt.show()
```



In [93]:
```
#Correlation of quantitative and qualitative features with the target variable
corr_target = abs(cor["Species"])

#Visualising the features with the highest correlation
imp_features = corr_target[corr_target>0.5].sort_values(ascending=False)
imp_features
```

Out[93]:
```
Species                1.000000
Flipper Length (mm)    0.867907
Body Mass (g)          0.773947
Culmen Depth (mm)      0.744324
Culmen Length (mm)     0.736564
Island                 0.647180
Delta 15 N (o/oo)      0.516752
Name: Species, dtype: float64
```

Based on the heatmap and the analysis done on it, the qualitative feature with the highest correlation coefficient to our target variable, Species is Island. The quantitative features with the highest correlation coefficients are Flipper Length (mm), Body Mass (g), Culmen Depth (mm), Delta 15 N (o/oo), and Culmen Length (mm). When inspecting the heat map of correlation coefficients, we observe that Culmen Length (mm) is least correlated to Island, so we pick Culmen Length (mm) to be our second feature. Among Culmen Depth (mm), Flipper Length (mm), Delta 15 N (o/oo), and Body Mass (g), Delta 15 N (o/oo) is least correlated to Culmen Length (mm), but it is very borderline, so we picked the next least correlated feature Culmen Depth (mm), to be our third feature.

The features we selected using the heatmap based on correlation coefficients supports the graphs in our exploratory analysis of the features. Our summary table showed us that Island is a better qualitative feature to use in our model than Sex. The scatter plot also supported that Culmen Depth (mm) should be one of our model's quantitative features because the species have more distinct points, but with Delta 15 N (o/oo), there are more overlapping points between species. The heatmap shows us that Culmen Depth (mm) is our third feature which corroborates the theory that our second quantitative feature should be Culmen Depth (mm), Flipper Length (mm), Delta 15 N (o/oo), or Body Mass (g), Delta 15 N (o/oo). The histograms and boxplots of the different features of penguins support our analysis for this heatmap plot.

We also confirmed our choice of qualitative features using an exhaustive search. We first generated a list of the different combinations of 1 qualitative and 2 quantative features which could predict the species of penguin.

In [94]:
```
from itertools import combinations

#two lists combs1 and combs2 with different combinations of 2 quantitative feat
combs1 = list(combinations(list(x_ax),2))
combs2 = list(combinations(list(x_ax),2))

#for loop to append the qualitative feature of Sex to the list of combinations
for i in range(len(combs1)):
    combs1[i]=list(combs1[i])
    combs1[i].append('Sex')

#for loop to append the qualitative feature of Island to the list of combinatic
for i in range(len(combs2)):
    combs2[i]=list(combs2[i])
    combs2[i].append('Island')

#combining the 2 lists with different combinations of 1 qualitiative and 2 quan
combs = combs1 + combs2

#displaying the different combinations of quantitative and qualitative features
combs
```

Out[94]:
```
[['Culmen Length (mm)', 'Culmen Depth (mm)', 'Sex'],
 ['Culmen Length (mm)', 'Flipper Length (mm)', 'Sex'],
 ['Culmen Length (mm)', 'Body Mass (g)', 'Sex'],
 ['Culmen Length (mm)', 'Delta 15 N (o/oo)', 'Sex'],
 ['Culmen Length (mm)', 'Delta 13 C (o/oo)', 'Sex'],
 ['Culmen Depth (mm)', 'Flipper Length (mm)', 'Sex'],
 ['Culmen Depth (mm)', 'Body Mass (g)', 'Sex'],
 ['Culmen Depth (mm)', 'Delta 15 N (o/oo)', 'Sex'],
 ['Culmen Depth (mm)', 'Delta 13 C (o/oo)', 'Sex'],
 ['Flipper Length (mm)', 'Body Mass (g)', 'Sex'],
 ['Flipper Length (mm)', 'Delta 15 N (o/oo)', 'Sex'],
 ['Flipper Length (mm)', 'Delta 13 C (o/oo)', 'Sex'],
 ['Body Mass (g)', 'Delta 15 N (o/oo)', 'Sex'],
 ['Body Mass (g)', 'Delta 13 C (o/oo)', 'Sex'],
 ['Delta 15 N (o/oo)', 'Delta 13 C (o/oo)', 'Sex'],
 ['Culmen Length (mm)', 'Culmen Depth (mm)', 'Island'],
 ['Culmen Length (mm)', 'Flipper Length (mm)', 'Island'],
 ['Culmen Length (mm)', 'Body Mass (g)', 'Island'],
 ['Culmen Length (mm)', 'Delta 15 N (o/oo)', 'Island'],
 ['Culmen Length (mm)', 'Delta 13 C (o/oo)', 'Island'],
 ['Culmen Depth (mm)', 'Flipper Length (mm)', 'Island'],
 ['Culmen Depth (mm)', 'Body Mass (g)', 'Island'],
 ['Culmen Depth (mm)', 'Delta 15 N (o/oo)', 'Island'],
 ['Culmen Depth (mm)', 'Delta 13 C (o/oo)', 'Island'],
 ['Flipper Length (mm)', 'Body Mass (g)', 'Island'],
 ['Flipper Length (mm)', 'Delta 15 N (o/oo)', 'Island'],
 ['Flipper Length (mm)', 'Delta 13 C (o/oo)', 'Island'],
 ['Body Mass (g)', 'Delta 15 N (o/oo)', 'Island'],
 ['Body Mass (g)', 'Delta 13 C (o/oo)', 'Island'],
 ['Delta 15 N (o/oo)', 'Delta 13 C (o/oo)', 'Island']]
```

In [95]:
```python
def exhaustive_search(model, X, y, min_cols, max_cols):
    """
    A function that iterates through the list of quantitative and qualitative f
    feature set with the best CV score.

    Args:
        model: the chosen machine learning model
        X: the cleaned penguins data set without the target column
        y: the target column from the cleaned penguins data set
        min_cols: the minimum number of features for the model
        max_cols: the maximum number of features for the model

    Returns:
        best_cv: the higher cv score
        best_cols: the combination of features with the highest cv score
    """
    #setting the best cv score to 0
    best_cv = 0

    #setting the best combination of features as None
    best_cols = None

    #for loop to iterate through the different feature combinations
    for n_cols in range(min_cols, max_cols + 1):
        for cols in combs:
            #assigns the cv score based on the combinations of features
            cv = cross_val_score(model, X[list(cols)], y, cv = 10).mean()
            #if statement to check if the cv score for the current feature comb
            #combinations and reassign it to best_cv if so
```

```
            if cv > best_cv:
                best_cv = cv
                #assigns the features combination with the highest cv score to
                best_cols = cols

    #returns the best features combination and best cv score
    return best_cv, best_cols
```

We then run the multinomial logistic regression model through the exhaustive search function to visualise the best combination of features along with its cv score.

In [96]:
```
from sklearn.linear_model import LogisticRegression
LR = LogisticRegression(solver = "liblinear", random_state=16)

best_cv, best_cols = exhaustive_search(LR, X, y, 3, 3)
```

In [97]:
```
best_cv, best_cols
```

Out[97]:
```
(0.9628787878787879, ['Culmen Length (mm)', 'Culmen Depth (mm)', 'Island'])
```

The exhaustive search function returns 'Culmen Length (mm)', 'Culmen Depth (mm)', and 'Island' as the combination of 1 qualitative and 2 quantative features to predict the penguin species with the highest cv score of 0.963. This aligns with the inference we made based on our correlation heatmap as well. So, we choose these three features to be used across our three models.

We then assign these finalised predictor variables to our X training and X test data set to be used in the 3 models.

Multinomial Logistic Regression Model

§1. MLR modelling and cross validation

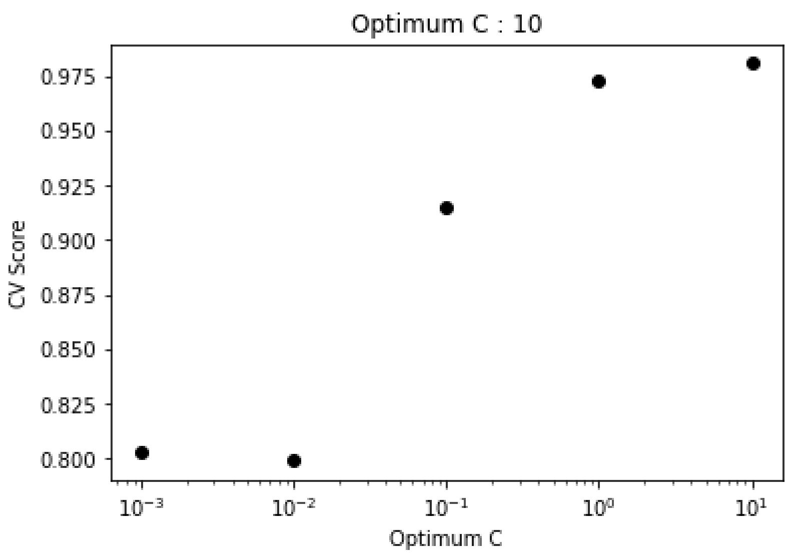
In [98]:
```
#getting the training and test data sets for the 1st model
X_train1 = X_train[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
X_test1 = X_test[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
y_train1 = y_train
y_test1 = y_test
```

We use cross-validation to check the optimum hyperparameter value. In the case of the MLR model, this is C or the inverse regularisation.

In [99]:
```
#creating the plot
fig, ax = plt.subplots(1)

best_score = 0

#setting the hyperparameter values for the model
params = [0.001, 0.01, 0.1, 1, 10]

#iterating through a for loop to check the combination of features with the hig
```

```
for c in params:
    LR = LogisticRegression(solver = "liblinear", random_state=16, C = c)
    cv_score = cross_val_score(LR, X_train1, y_train1, cv=10).mean()
    print ("For C = " + str(c) + " , the cv score is " + str(cv_score))

    ax.scatter(c, cv_score, color = "black")
    if cv_score > best_score:
        best_C = c
        best_score = cv_score

#setting the title and axis labels
l = ax.set(title = "Optimum C : " + str(best_C),
       xlabel = "Optimum C",
       ylabel = "CV Score")

#scaling the x-axis to log
plt.xscale("log")
```

```
For C = 0.001 , the cv score is 0.803076923076923
For C = 0.01 , the cv score is 0.7992307692307692
For C = 0.1 , the cv score is 0.9152307692307691
For C = 1 , the cv score is 0.9726153846153848
For C = 10 , the cv score is 0.9806153846153848
```



From the above plot, we see the highest cv score is achieved with C = 10. However, the different between C=10 and C=1, the next highest cv score, is quite minute, a difference of around 0.008. So, we choose C=1 to prevent overfitting of the model.

We create the Multinomial Logistic Regression model and assign it to LR with C=1.

In [100…
```
LR = LogisticRegression(solver = "liblinear", random_state=16, C=1)
```

We calculate the cv scores for the model to understand the accuracy of the MLR model.

In [101…
```
#calculating the cv scores for the MLR model
cv_scores = cross_val_score(LR, X_train1, y_train1, cv=10)

print("The mean cross-validation score is "+ str(cv_scores.mean())+ ".")
print("The standard deviation of the cross-validation score is "+ str(cv_scores
```

```
The mean cross-validation score is 0.9726153846153848.
The standard deviation of the cross-validation score is 0.03971972815533519.
```

For the MLR model, we get a mean cross-validation score of 0.973, with a standard deviation of 0.040. This implies that the MLR model has a high accuracy when it comes to predicting the species of penguins given our chosen features.

We train the MLR model on our training data set, based on the chosen features of Island, Culmen Length (mm), and Culmen Length (mm).

In [102…

```
LR.fit(X_train1, y_train1)
```

Out[102]:

```
LogisticRegression(C=1, random_state=16, solver='liblinear')
```

§2. Evaluating model on test set

We also scored and evaluated our model against our test data set.

In [104…

```
print("Accuracy: "+ str(LR.score(X_test1, y_test1)))
```

```
Accuracy: 0.9393939393939394
```

On the test data set, the MLR model scores 0.939. This is a relatively high accuracy score and suggests that the MLR model fits the test data well.

§3. Confusion matrix

To gain a better understanding of the accuracy of the MLR model and where it went wrong, we can use the confusion matrix. First, we look at the predictions made by the model of the penguin species based on the chosen features in the test set.

In [105…

```
#assigns predictions of penguin species based on the MLR model on the test set
y_pred1 = LR.predict(X_test1)
y_pred1
```

Out[105]:

```
array([0, 2, 0, 0, 0, 2, 2, 1, 0, 0, 0, 0, 0, 2, 2, 2, 1, 0, 0, 1, 2, 0,
       0, 0, 0, 0, 2, 0, 1, 0, 1, 2, 2, 0, 0, 2, 0, 0, 0, 0, 0, 2, 0, 1,
       1, 2, 0, 2, 2, 2, 1, 0, 1, 0, 0, 1, 0, 2, 2, 0, 1, 2, 1, 2, 0, 2])
```

Then, we create and display a confusion matrix to see what our model predicts as the penguin species and what the penguin species actually is.

In [106…

```
# import the metrics class
from sklearn import metrics

def conf_matrix (y_test, y_pred):
    """
    Function that calculates and displays the confusion matrix for a given mode

    Args:
        y_test: the test data set with the penguin species
        y_pred: the predictor set with the penguin species
```

```
    Returns:
        None (displays the dataFrame with the confusion matrix)
    """
    #creates and assigns the confusion matrix to a pandas dataframe based on th
    cm = pd.DataFrame(metrics.confusion_matrix(y_test, y_pred),
                      index = ['Actual ' + i for i in np.unique(penguins['Species
                      columns = ['Predicted ' + i for i in np.unique(penguins['Sp
    #prints confusion matrix
    print('Confusion Matrix:')

    #displays the confusion matrix dataFrame
    display(cm)

conf_matrix (y_test1, y_pred1)
```

```
Confusion Matrix:
```

	Predicted Adelie	Predicted Chinstrap	Predicted Gentoo
Actual Adelie	30	0	0
Actual Chinstrap	3	12	1
Actual Gentoo	0	0	20

Based on the above confusion matrix, we can see that most of the time, the MLR model predicts the penguin species correctly. However, we do have instances where the model incorrectly classified the penguins. In the above dataframe, the second row represented the number of penguins that are actually of the Chinstrap species. This row highlights that 3 penguins that are actually Chinstrap were predicted to be of the Adelie species and 1 was predicted to be Gentoo, while the remaining 12 penguins were correctly predicted to be Chinstrap.

§4. Decision regions

In [107…

```
from matplotlib import patches as mpatches

def decision_regions(model,X_test, y_test):
# plot the decision regions of the classifier

    fig, ax = plt.subplots(3, figsize = (12,20), sharey = True)

    uniqueQualValues = [int(i) for i in np.unique(X_test["Island"])] # as list

# create a meshgrid of the dataset
    f1_min, f1_max = X["Culmen Length (mm)"].min() - 1, X["Culmen Length (mm)"]
    f2_min, f2_max = X["Culmen Depth (mm)"].min() - 1, X["Culmen Depth (mm)"].m
    f1, f2 = np.meshgrid(np.arange(f1_min, f1_max, 0.1), np.arange(f2_min, f2_m

    for i in uniqueQualValues:
    # predict the class of each point in the meshgrid
        Z = model.predict(np.c_[f1.ravel(), f2.ravel(), np.ones(f1.ravel().shap
        Z = Z.reshape(f1.shape)

        # plot the test set samples as a scatter plot
        ax[i].scatter(X_test[X_test["Island"]==i]["Culmen Length (mm)"], X_test
                      c=y_test[X_test["Island"]==i], cmap='jet', vmin = 0, vmax
```

```
        # plot the decision regions
        ax[i].contourf(f1, f2, Z, alpha=0.2, cmap="jet")

        #setting axis labels
        ax[i].set_xlabel('Culmen Length (mm)')
        ax[i].set_ylabel('Culmen Depth (mm)')

    #setting plot titles
    ax[0].set_title('Torgensen')
    ax[1].set_title('Dream')
    ax[2].set_title('Biscoe')

    #setting the legend
    legend0 = mpatches.Patch(color = 'red', label = 'Adelie', alpha = 0.2)
    legend1 = mpatches.Patch(color = 'green', label = 'Chinstrap', alpha = 0.2)
    legend2 = mpatches.Patch(color = 'blue', label = 'Gentoo', alpha = 0.2)
    fig.legend(handles = [legend0, legend1, legend2],loc = (0.9,0.92), fontsize
```

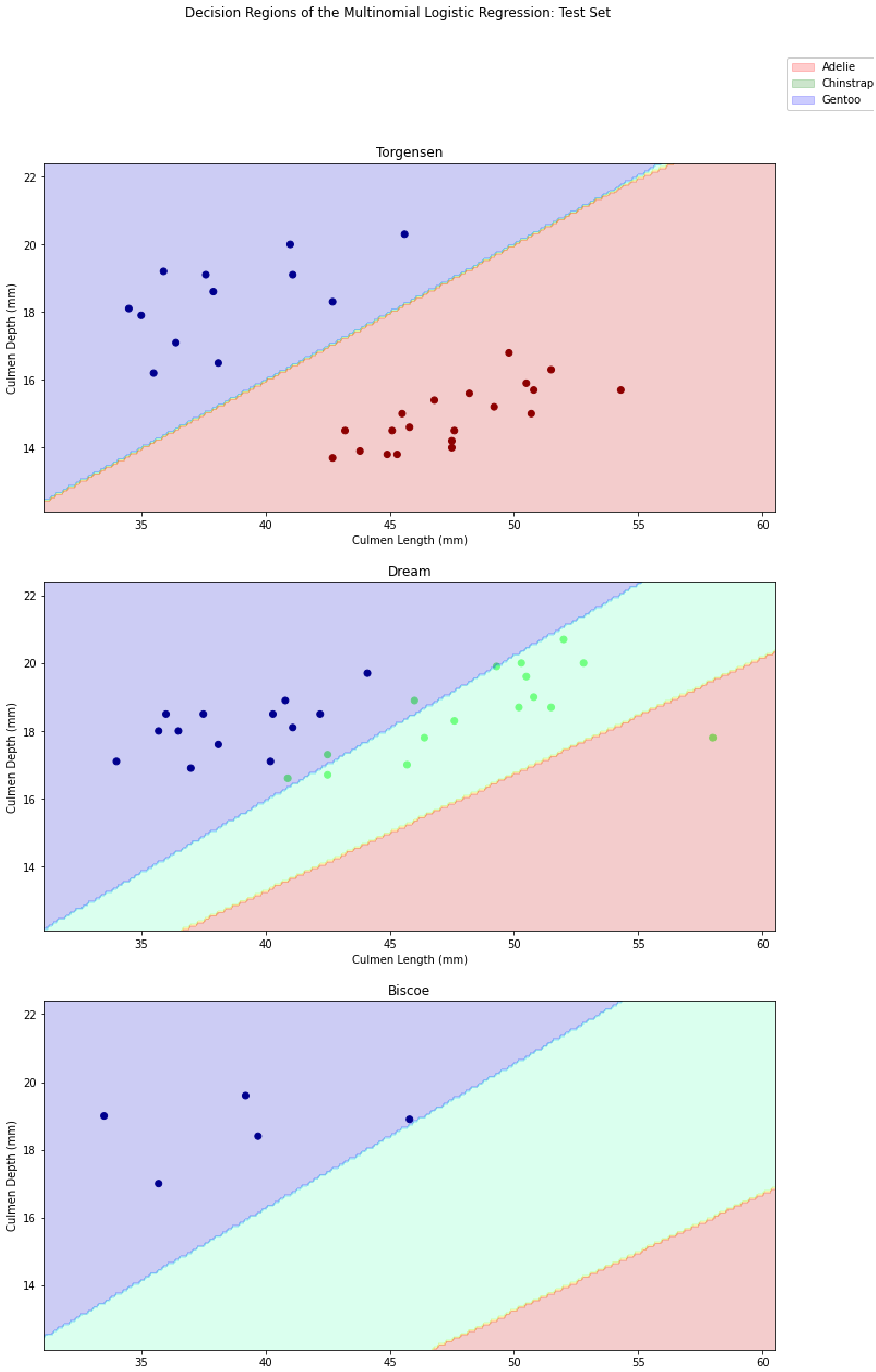
In [109…

```
#plotting the decision regions
decision_regions(LR,X_test1, y_test1)
plt.suptitle('Decision Regions of the Multinomial Logistic Regression: Test Set
```

```
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but LogisticRegression
was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but LogisticRegression
was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but LogisticRegression
was fitted with feature names
  warnings.warn(
```

Out[109]:

```
Text(0.5, 0.98, 'Decision Regions of the Multinomial Logistic Regression: Test
Set')
```


Decision Regions of the Multinomial Logistic Regression: Test Set
Adelie
Chinstrap
Gentoo
Torgensen
Dream
Biscoe
Culmen Depth (mm)
Culmen Length (mm)
22
20
18
16
14
35
40
45
50
55
60

Through the decision regions and boundary, we can see that the majority of the time, the MLR model predicts the species of the penguins accurately. On both Torgen and Biscoe islands, all penguins were accurately classified as their respective species. However, there are some errors. On Dream Island, some Chinstrap penguins were incorrectly classified as Gentoo and Adelie. Overall, the decision regions seem to show that our model well fits the data.

Nearest-Neighbour Classifiers Model

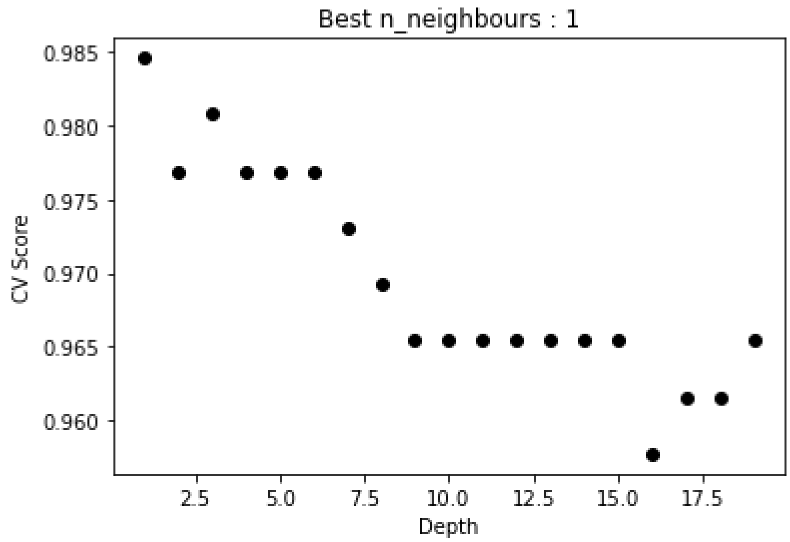
§1. Nearest-Neighbour Classifiers modelling and cross validation

In [110…

```
#getting the training and test data sets for the 2nd model
X_train2 = X_train[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
X_test2 = X_test[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
y_train2 = y_train
y_test2 = y_test
```

In [123…

```
from sklearn.neighbors import KNeighborsClassifier
from sklearn.model_selection import GridSearchCV

#creating the plot
fig, ax = plt.subplots(1)

best_score = 0

#iterating through the range of hyperparameters
for d in range(1,20):
    rf = KNeighborsClassifier(n_neighbors = d)
    cv_score = cross_val_score(rf, X_train2, y_train2, cv=5).mean()
    ax.scatter(d, cv_score, color = "black")
    if cv_score > best_score:
        best_depth = d
        best_score = cv_score

#setting the title and axis labels for the plot
l = ax.set(title = "Best n_neighbours : " + str(best_depth),
       xlabel = "Depth",
       ylabel = "CV Score")
```



From the above plot, we see that the optimum value of the hyperparameter n_neighbours is 1 as it had the highest cv score.

We create an instance of the KneighborsClassifier class and assign it to knn variable.

In [112…

```
knn2 = KNeighborsClassifier(n_neighbors = 1)
cv_scores = cross_val_score(knn2, X_train2, y_train2, cv=10)

print("The mean cross-validation score is "+ str(cv_scores.mean())+ ".")

#Creating a dictionary of neighbours
neighbours= {'n_neighbors': np.arange(1, 10)}
knn_cv = GridSearchCV(knn2, neighbours, cv=5)

#fit model to data
knn2.fit(X_train2, y_train2)
```

```
The mean cross-validation score is 0.9923076923076923.
```

Out[112]:

```
KNeighborsClassifier(n_neighbors=1)
```

We create an instance of the KneighborsClassifier class and assign it to knn variable. This class requires a parameter named n_neighbors, which will be set to the K nearest neighbors algorithm. We use GridSearch CV to reconfirm the best hyper parameter as n_neighbours=1.

Here, we found out that from 1 to 10, 1 is the best k which has 0.98 accuracy. So we will be setting n_neighbors as 1.

§2. Evaluating model on test set

In [113…

```
from matplotlib.colors import ListedColormap
from sklearn import neighbors, datasets
```

In [114…

```
print("Accuracy: "+ str(knn2.score(X_test2, y_test2)))
```

```
Accuracy: 0.9393939393939394
```

We also evaluated our model against our test data set. With our test data set we have a 0.94.

§3. Confusion Matrix

In [115…

```
#assigns predictions of penguin species based on the MLR model on the test set
y_pred2 = knn2.predict(X_test2)
y_pred2
```

Out[115]:

```
array([0, 2, 0, 0, 0, 2, 2, 1, 0, 0, 0, 0, 0, 2, 2, 2, 1, 1, 0, 1, 2, 0,
       0, 0, 1, 1, 2, 0, 1, 0, 1, 2, 2, 1, 0, 2, 0, 0, 0, 0, 0, 2, 0, 1,
       1, 2, 0, 2, 2, 2, 1, 0, 1, 0, 0, 1, 0, 2, 2, 0, 1, 2, 1, 2, 0, 2])
```

In [116…

```
conf_matrix (y_test2, y_pred2)
```

```
Confusion Matrix:
```

	Predicted Adelie	Predicted Chinstrap	Predicted Gentoo
Actual Adelie	28	2	0
Actual Chinstrap	1	14	1
Actual Gentoo	0	0	20

For the Torgersen Island, our model incorrectly predicts an Adelie penguin to be a Chinstrap penguin. On Biscoe Island, the model interprets a few Gentoo penguins as Chinstrap. On Dream Island, the model incorrectly interprets a few Chinstrap penguins to be Adelie or Gentoo penguins. Also, for Chinstrap penguins one is predicted to be Adelie and one is predicted to be Gentoo. For, Gentoo penguins all penguins are classified correctly.

§4. Decision regions

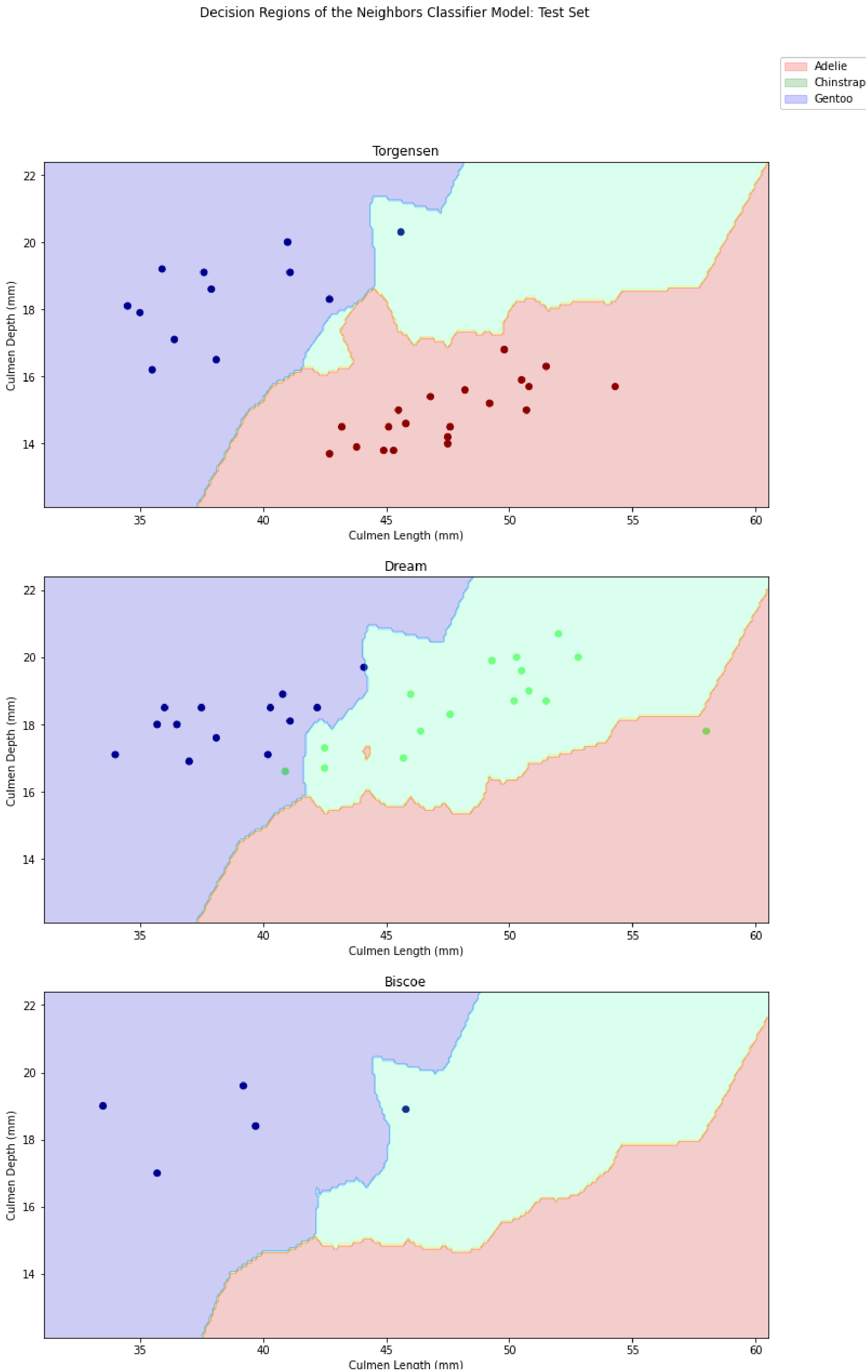
In [117…

```
decision_regions(knn2,X_test2,y_test2)
plt.suptitle('Decision Regions of the Neighbors Classifier Model: Test Set')
```

```
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but KNeighborsClassifie
r was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but KNeighborsClassifie
r was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but KNeighborsClassifie
r was fitted with feature names
  warnings.warn(
```

Out[117]:

```
Text(0.5, 0.98, 'Decision Regions of the Neighbors Classifier Model: Test Se
t')
```


Decision Regions of the Neighbors Classifier Model: Test Set
Adelie
Chinstrap
Gentoo
Torgensen
Dream
Biscoe
Culmen Depth (mm)
Culmen Length (mm)
22
20
18
16
14
35
40
45
50
55
60

As observed from the decision regions, the Neighbors Classifier Model classifies the species accurately majority of the times. For the Torgersen Island, our model incorrectly predicts two Adelie penguin to be a Chinstrap penguin. On Biscoe Island, the model interprets a two Chinstrap penguins as Adelie. On Dream Island, the model correctly classifies all the Gentoo penguins. However, we do see that there are some jagged lines present in the decision regions, which could be indiciative of overfitting.

Random Forest Classifier Model

§1. Random Forest modelling and cross validation

A random forest model is a classification model which uses several decision trees to increase the accuracy of the model's prediction and to prevent overfitting.

In [62]:
```
X_train3 = X_train[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
X_test3 = X_test[["Culmen Length (mm)","Culmen Depth (mm)", "Island"]]
y_train3 = y_train
y_test3 = y_test
```

In [63]:
```
from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier()
rf.fit(X_train3, y_train3)
```

Out[63]:
```
RandomForestClassifier()
```

For the random forest model, I used Grid Search, because there are 2 important hyperparameters in a random forest classifier model, n_estimators: which is the number of trees, and max_depth: the number of splits a tree can have.

In [64]:
```
from sklearn.model_selection import GridSearchCV


param_grid = {
                 'n_estimators': [5, 10, 15, 20],
                 'max_depth': [2, 5, 7, 9]
             }

grid_rf = GridSearchCV(rf, param_grid, cv=10)
grid_rf.fit(X_train3, y_train3)

grid_rf.best_params_
```

Out[64]:
```
{'max_depth': 5, 'n_estimators': 15}
```

In [65]:
```
grid_rf.best_score_
```

Out[65]:
```
0.9923076923076923
```

The best cross validation score is 99.23%, showing us that these parameters are a good fit for the model.

In [66]:
```
# new model with hyperparameters from cross-validation
clf=RandomForestClassifier( max_depth=5, n_estimators = 15)

#Train the model using the training sets y_pred=clf.predict(X_test)
clf.fit(X_train3,y_train3)
```

§2. Evaluating model on test set

In [118…
```
# score of the model on the test set
print("Accuracy: "+ str(clf.score(X_test3, y_test3)))
```

```
Accuracy: 0.9545454545454546
```

We scored our model on the test, to get an accuracy of 95%.

§3. Confusion Matrix

In [119…
```
# prediction on test set
y_pred3=clf.predict(X_test3)
y_pred3
```

Out[119]:
```
array([0, 2, 0, 0, 0, 2, 2, 1, 0, 0, 0, 0, 0, 2, 2, 1, 1, 2, 0, 1, 2, 0,
       0, 0, 1, 1, 2, 1, 1, 0, 1, 2, 2, 0, 0, 2, 0, 0, 0, 0, 0, 2, 0, 1,
       1, 2, 0, 2, 2, 2, 1, 0, 1, 0, 0, 1, 0, 2, 2, 0, 1, 2, 1, 2, 0, 2])
```

In [120…
```
conf_matrix (y_test3, y_pred3)
```

```
Confusion Matrix:
```

	Predicted Adelie	Predicted Chinstrap	Predicted Gentoo
Actual Adelie	28	1	1
Actual Chinstrap	1	15	0
Actual Gentoo	0	0	20

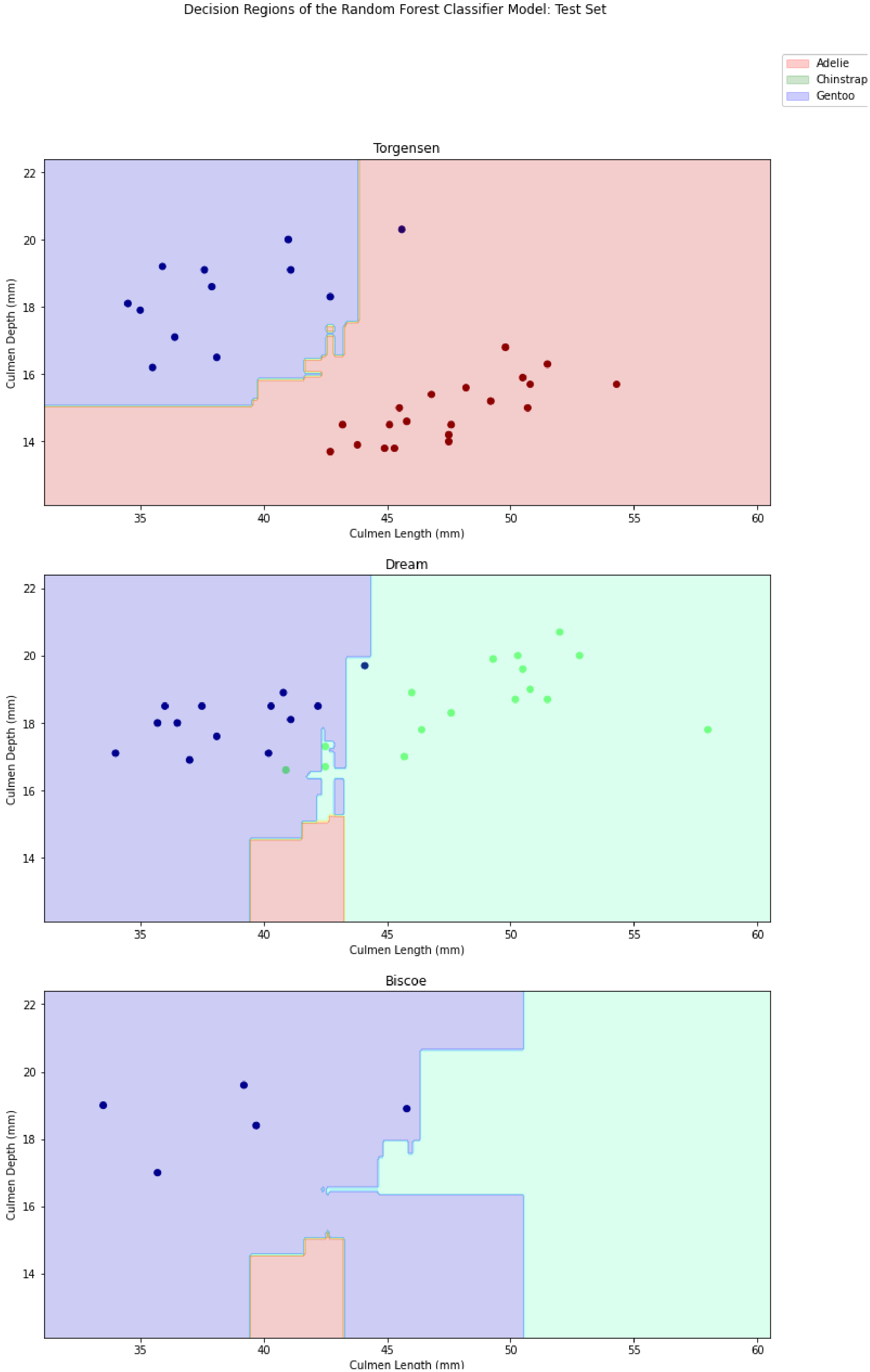
From the confusion matrix above, the model correctly predicts the species, most of the time. There are a few instances such as in row 1 and 2, where the model classified an Adelie penguin as a Chinstrap or a Gentoo, and once where it predicted a Chinstrap penguin as an Adelie.

§4. Decision regions

In [121…
```
decision_regions(clf,X_test3,y_test3)
plt.suptitle('Decision Regions of the Random Forest Classifier Model: Test Set'
```

```
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but RandomForestClassif
ier was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but RandomForestClassif
ier was fitted with feature names
  warnings.warn(
/Users/diyagopinath/opt/anaconda3/lib/python3.9/site-packages/sklearn/base.py:
450: UserWarning: X does not have valid feature names, but RandomForestClassif
ier was fitted with feature names
  warnings.warn(
```

Out[121]:
```
Text(0.5, 0.98, 'Decision Regions of the Random Forest Classifier Model: Test
Set')
```


Decision Regions of the Random Forest Classifier Model: Test Set
Adelie
Chinstrap
Gentoo
Torgensen
Dream
Biscoe
Culmen Depth (mm)
Culmen Length (mm)
22
20
18
16
14
35
40
45
50
55
60

In the decision regions, there is some overfitting going on, represented by the jagged lines. The model is sometimes predicting Chinstrap penguins as Gentoo on Dream Island. On Torgensen Island, the model correctly predicts the penguin species. On Biscoe and Dream Islands, the model interpreted a Gentoo penguin as a Chinstrap penguin. The model probably failed due to overlaps between their `Culmen Length (mm)` and `Culmen Depth (mm)`, because there are values that are close to each other between the 2 species.

Conclusion

Based on the above models, we saw that when scoring each model against the test data set, the Random Forest Classifier model had the higher accuracy score of 95.5%. The Multinomial Logistical Regression and Neighbours Classifer model both had accuracy scores of almost 94%. While the higher accuracy could indicate that the Random Forest is a better model choice, we noticed when plotting decision regions that the decision boundaries of the Random Forest Classifer and Neighbours Classifier had jagged lines. This could be indiciative of overfitting which is not a good indicator when it comes to the model's accuracy. Since the test accuracy score was not too far off, we decided that the best choice model would be the Multinomial Logistic Regression model.

These three models show how we can perform classification in machine learning. It trains data so that the model can identify which class or category a new data should fall into. We can improve our models' accuracy by accumulating and training more dataset. Also, we could experiment by using alternative values for the training parameters used with each algorithms. However, we still had a pretty high accuracy with 95.5% and 94% in average.