Linear Discriminant Analysis, Quadratic Discriminant Analysis, and Naive Bayes

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Instructions

Use Penguine dataset for this assignment. Please use "Species" as your target variable. For this assignment, you may want to drop/ignore the variable "year".

Using the target variable, Species, please conduct:

(*a.*) Linear Discriminant Analysis (30 points):

- You want to evaluate all the 'features' or dependent variables and see what should be in your model. Please comment on your choices.
- Just a suggestion: You might want to consider exploring featurePlot on the caret package. Basically, you look at each of the features/dependent variables and see how they are different based on species. Simply eye-balling this might give you an idea about which would be strong 'classifiers' (aka predictors).
- Fit your LDA model using whatever predictor variables you deem appropriate. Feel free to split the data into training and test sets before fitting the model.
- Look at the fit statistics/ accuracy rates.

Linear Discriminant Analysis (LDA)

Linear discriminant analysis is an extremely popular dimensionality reduction technique. Dimensionality reduction techniques have become critical in machine learning since many multi-dimensional datasets exist these days.

Multi-dimensional data is data that has multiple features which have a correlation with one another. Dimensionality reduction simply means plotting multi-dimensional data in just 2 or 3 dimensions.

```
library(palmerpenguins)
library(stats)
library(dplyr)
library(PerformanceAnalytics)
library(DT)
library(tidyr)
library(caret)
library(e1071)
library(kableExtra)
library(caTools)
library(MASS)
```

```
library(devtools)
library(ggord)
library(klaR)
library(naivebayes)
```

Load libraries

Load data Load the data from `palmerpenguins` library and drop year, sex and island columns from dataset.

```
penguine_data <- glimpse(penguins)
```

```
## Rows: 344
## Columns: 8
## $ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, A...
## $ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torge...
## $ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34....
## $ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18....
## $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, ...
## $ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 347...
## $ sex               <fct> male, female, female, NA, female, male, female, m...
## $ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2...
```

```
penguine_data <- penguine_data %>% dplyr::select(-c(year, island, sex))
DT::datatable(head(penguine_data,5))
```

Show 10 entries Search:

	species	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g
1	Adelie	39.1	18.7	181	3750
2	Adelie	39.5	17.4	186	3800
3	Adelie	40.3	18	195	3250
4	Adelie				
5	Adelie	36.7	19.3	193	3450

Showing 1 to 5 of 5 entries Previous 1 Next

EDA Have a look on summary statistics.

```
summary(penguine_data)
```

```
##       species    bill_length_mm  bill_depth_mm   flipper_length_mm
##  Adelie   :152   Min.   :32.10   Min.   :13.10   Min.   :172.0
##  Chinstrap: 68   1st Qu.:39.23   1st Qu.:15.60   1st Qu.:190.0
##  Gentoo   :124   Median :44.45   Median :17.30   Median :197.0
##                  Mean   :43.92   Mean   :17.15   Mean   :200.9
##                  3rd Qu.:48.50   3rd Qu.:18.70   3rd Qu.:213.0
##                  Max.   :59.60   Max.   :21.50   Max.   :231.0
##                  NA's   :2       NA's   :2       NA's   :2
```

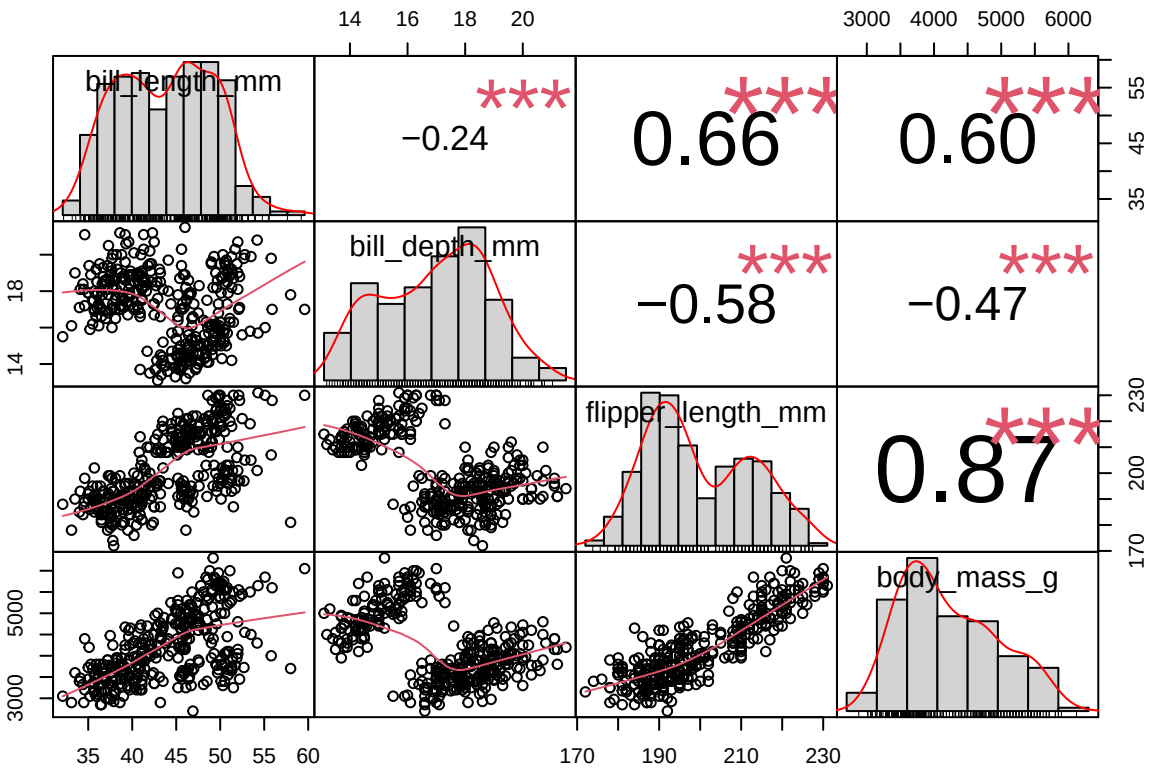
```
##   body_mass_g
##  Min.   :2700
##  1st Qu.:3550
##  Median :4050
##  Mean   :4202
##  3rd Qu.:4750
##  Max.   :6300
##  NA's   :2
```

We can see 8 NAs are present in the dataset. Remove NAs from data.

```
penguine_data <- drop_na(penguine_data)
```

To see the variables co-related to each other plot a co-relation graph.

```
my_data <- penguine_data[, c(2,3,4,5)]
chart.Correlation(my_data, histogram=TRUE, pch=19)
```



Above plot shows:

- Positive co-relation between body_mass_g and flipper_length_mm
- Negative Co-relation between bill_depth_mm and flipper_length_mm
- Positive co-relation between bill_length_mm and flipper_length_mm
- Positive co-relation between body_mass_g and bill_length_mm

Split data Split data in to 2 sets train and test. Train data and Test data ration is 70:30.

```r
set.seed(123)


# Data split
sample = sample.split(penguine_data$species, SplitRatio = 0.70)

penguine_train = subset(penguine_data, sample == TRUE)
penguine_test = subset(penguine_data, sample == FALSE)

dim(penguine_train)
```

```
## [1] 240   5
```

```r
dim(penguine_test)
```

```
## [1] 102   5
```

Train test has 240 and Test test has 102 rows.

LDA for all variables The linear Discriminant analysis estimates the probability that a new set of inputs belongs to every class. In our dataset dependant variable is `species` and all other 4 variables/fields are independent.

Load library `MASS` to perform LDA. Apply LDA on train dataset and look at the model structure.

```r
lda_all <- lda(species ~ ., data = penguine_train)
lda_all
```

```
## Call:
## lda(species ~ ., data = penguine_train)
##
## Prior probabilities of groups:
##    Adelie Chinstrap    Gentoo
## 0.4416667 0.2000000 0.3583333
##
## Group means:
##           bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
## Adelie          38.70283      18.33585          190.0566    3704.481
## Chinstrap       49.02708      18.48958          197.1250    3766.667
## Gentoo          47.78023      15.02558          217.6860    5116.279
##
## Coefficients of linear discriminants:
##                             LD1          LD2
## bill_length_mm     0.089443430 -0.383958867
## bill_depth_mm     -0.985577100 -0.053402145
## flipper_length_mm  0.082416295  0.006036714
## body_mass_g        0.001263067  0.001683273
##
## Proportion of trace:
##    LD1    LD2
## 0.8709 0.1291
```

Above model shows, *Prior probabilities of groups:*

- 44.2% belongs to Adelie in training data
- 20% belongs to Chinstrap in training data
- 35.9% belongs to Gentoo in training data

Group means: This table shows for ecah species and each variables we have averages. For examaple, Adelie's average bill_length_mm is 38.7.

Coefficients of linear discriminants:

The first discreminant function is a linear combination of the four variables. Example: $0.089443430 * bill_length_mm - 0.985577100 * bill_depth_mm + 0.082416295 * flipper_length_mm + 0.001263067 * body_mass_g$

Proportion of trace: Percentage separations achieved by the first discreminant function is 87%. Percentage separations achieved by the second discreminant function is 13%.

LDA for body mass and bill depth From EDA, we relation between body mass and flipper length, and body mass and bill length. So to avoid co-linearty exclude body mass and flipper length variables from the model.

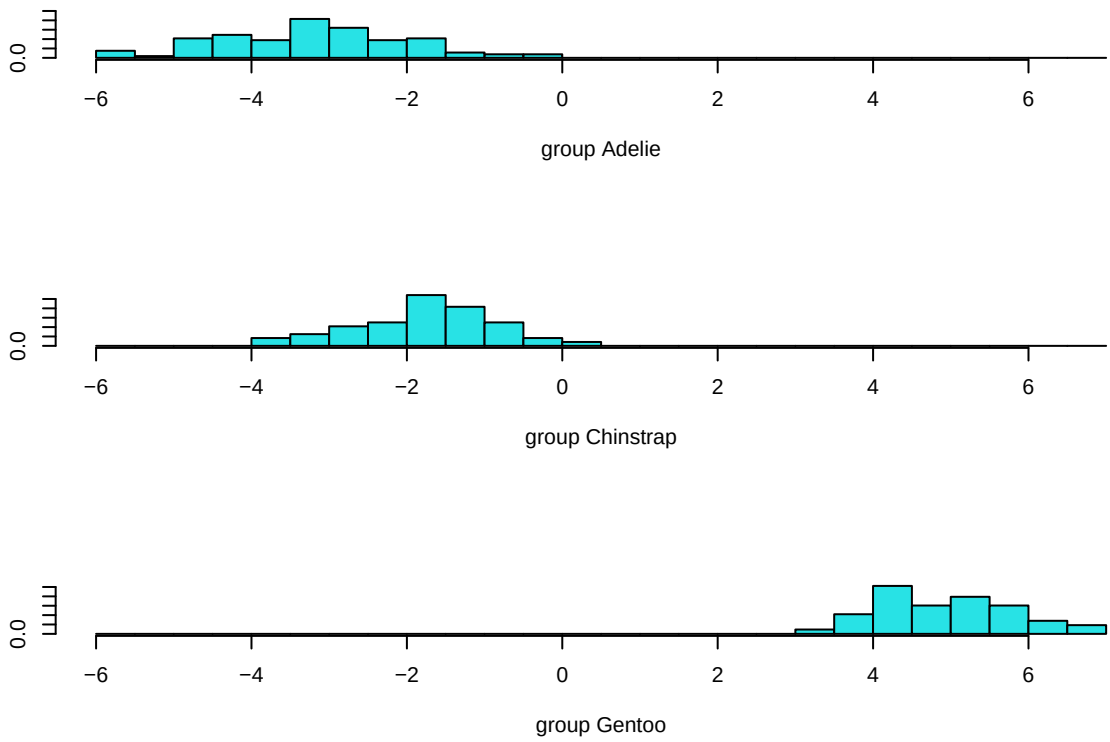
```
lda_2 <- lda(species ~ bill_length_mm + bill_depth_mm, data = penguine_train)
lda_2
```

```
## Call:
## lda(species ~ bill_length_mm + bill_depth_mm, data = penguine_train)
##
## Prior probabilities of groups:
##    Adelie Chinstrap    Gentoo
## 0.4416667 0.2000000 0.3583333
##
## Group means:
##           bill_length_mm bill_depth_mm
## Adelie          38.70283      18.33585
## Chinstrap       49.02708      18.48958
## Gentoo          47.78023      15.02558
##
## Coefficients of linear discriminants:
##                        LD1        LD2
## bill_length_mm  0.3367164 -0.1673935
## bill_depth_mm  -0.8441757 -0.5163900
##
## Proportion of trace:
##   LD1   LD2
## 0.922 0.078
```

Proportion of trace: Percentage separations achieved by the first discreminant function is 99.9%. Percentage separations achieved by the second discreminant function is 0.1%. Which is quite higher than our first model.

LDA Advantage Histogram and Bi-plot provides useful insights and are helpful for interpretaion of the analysis.

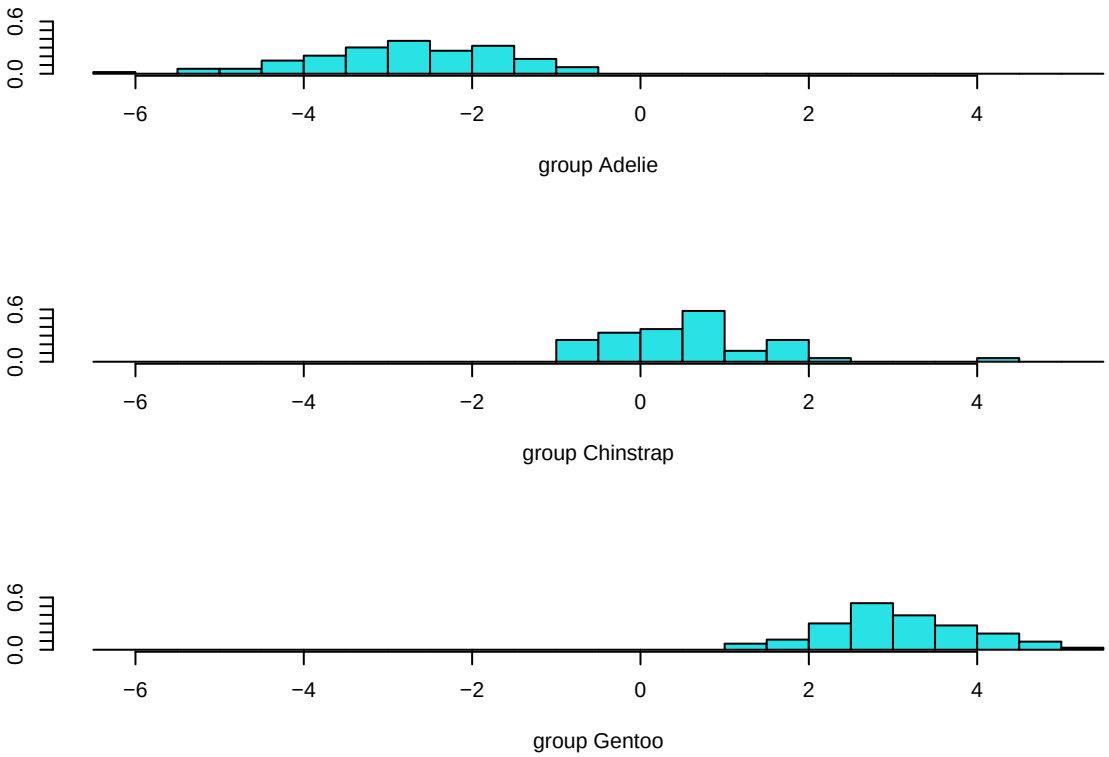
```r
# predict for train data
P_lda_all <- predict(lda_all, penguine_train)
P_lda_2 <- predict(lda_2, penguine_train)

# histigram of all variables lda models
ldahist(data = P_lda_all$x[,1], g = penguine_train$species)
```



bi-Plot

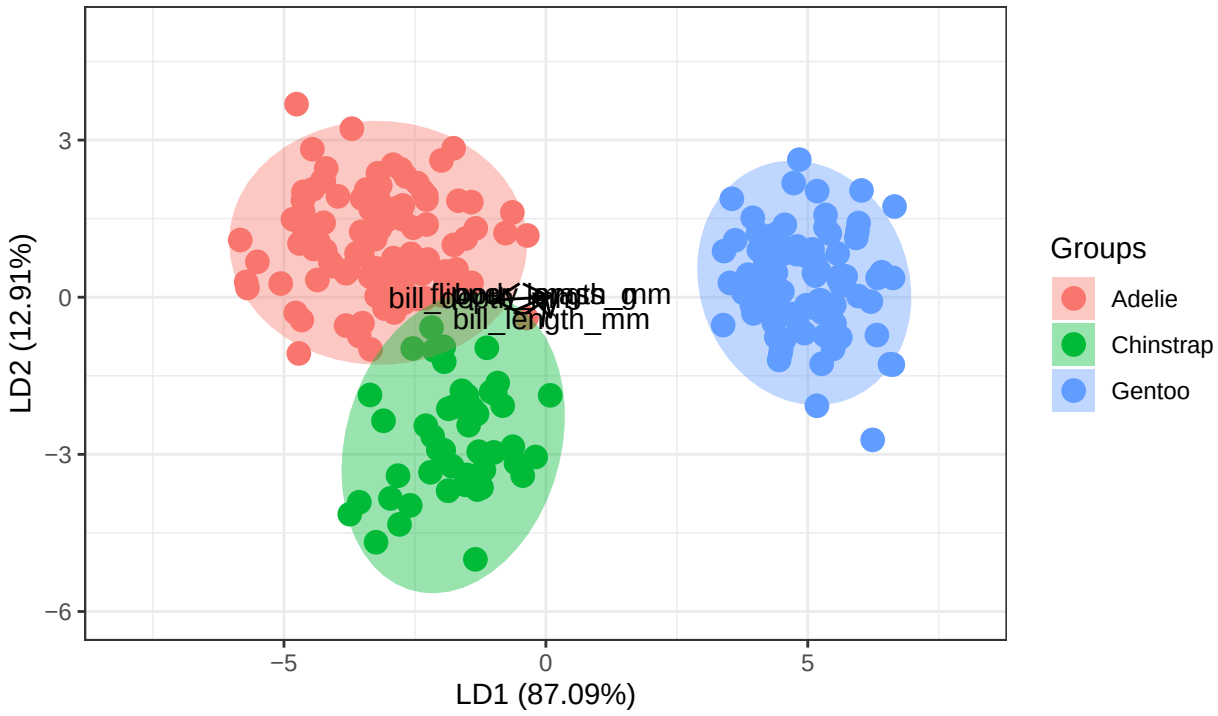
We see using our first model there is little over-lap between Adile and Chinstrap

```r
# histigram of 2nd lda models
ldahist(data = P_lda_2$x[,1], g = penguine_train$species)
```



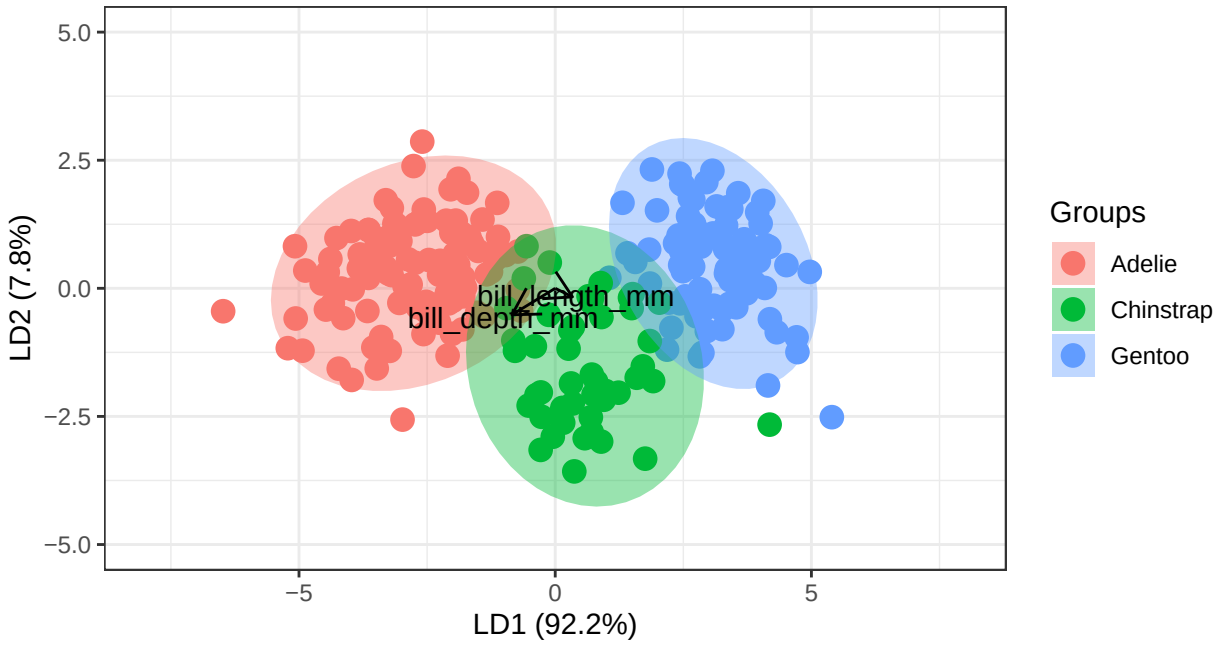
This model separates 3 species better than first model. Very few over-lap we see between species.

```
ggord(lda_all, penguine_train$species, ylim = c(-6,5), xlim = c(-8,8))
```

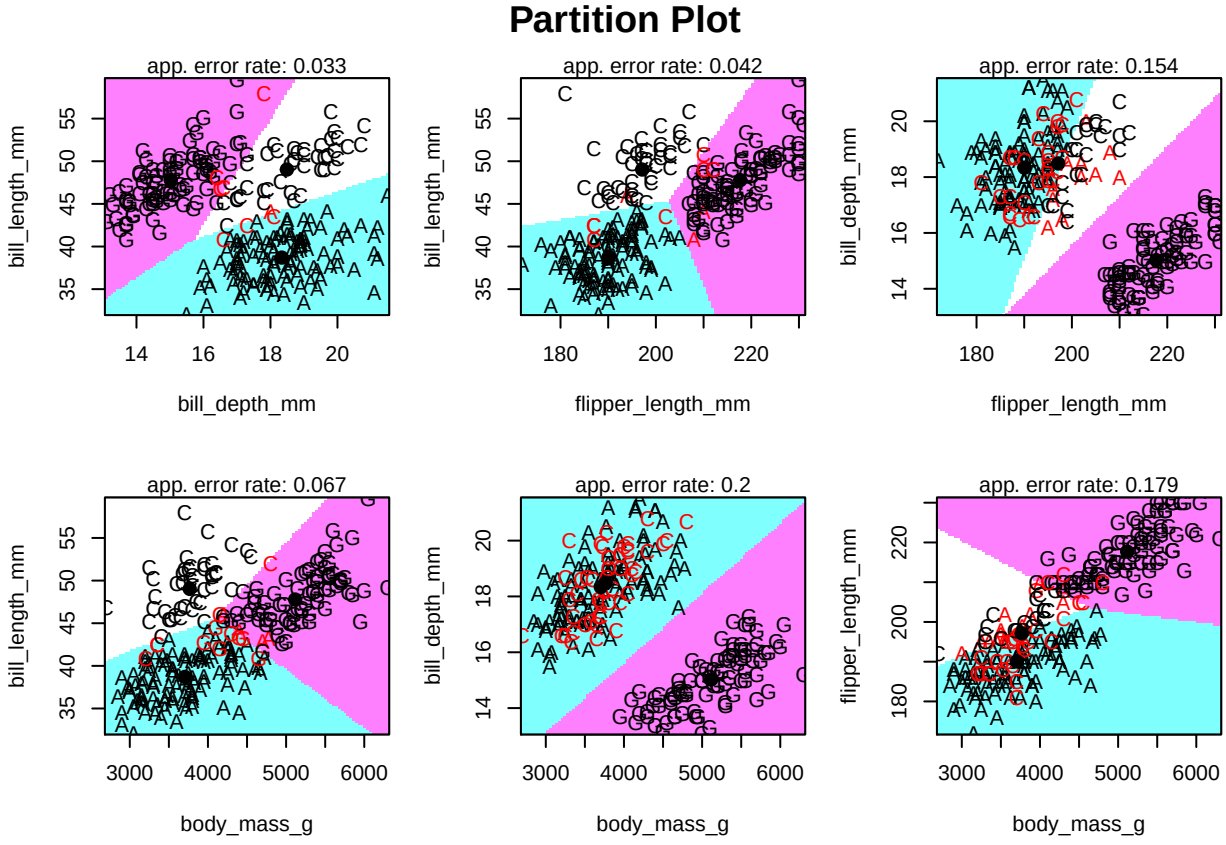


Bi-plots

```
ggord(lda_2, penguine_train$species, ylim = c(-5,5), xlim = c(-8,8))
```




```
partimat(species ~ ., data = penguine_train, method = 'lda')
```



Partition Plot

This plot gives classification of each and every observation in the training dataset based on LDA method.

Confusion matrix and accuracy training data LDA Model 1 with all variables

```
p1_train_all <- predict(lda_all, penguine_train)$class
tab_train_all <- table(Predicted = p1_train_all, Actual = penguine_train$species)
tab_train_all
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie       105         2      0
##   Chinstrap      1        46      0
##   Gentoo         0         0     86
```

There are 3 mis-classification occures in Chinstrap.

```
lda_train_accuracy_all <- sum(diag(tab_train_all))/sum(tab_train_all) * 100
lda_train_accuracy_all
```

```
## [1] 98.75
```

Accuracy in training data : 98.75

Confusion matrix and accuracy for test data LDA Model 1 with all variables

```
p1_test_all <- predict(lda_all, penguine_test)$class
tab_test_all <- table(Predicted = p1_test_all, Actual = penguine_test$species)
tab_test_all
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie        44         1      0
##   Chinstrap      1        19      0
##   Gentoo         0         0     37
```

There are total 2 mis-classification occures in test data.

```
lda_test_accuracy_all <- sum(diag(tab_test_all))/sum(tab_test_all) * 100
lda_test_accuracy_all
```

```
## [1] 98.03922
```

Accuracy in test data : 98.0392157

Confusion matrix and accuracy training data (LDA Model 2) LDA Model 2 with two variables

```
p1_train_2 <- predict(lda_2, penguine_train)$class
tab_train_2 <- table(Predicted = p1_train_2, Actual = penguine_train$species)
tab_train_2
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie       105         3      0
##   Chinstrap      1        41      0
##   Gentoo         0         4     86
```

There are 8 mis-classification occures in Chinstrap and Adile.

```
lda_train_accuracy_2 <- sum(diag(tab_train_2))/sum(tab_train_2) * 100
lda_train_accuracy_2
```

```
## [1] 96.66667
```

Accuracy in training data : 96.6666667

Confusion matrix and accuracy for test data (LDA model 2) LDA Model 2 with two variables

```
p1_test_2 <- predict(lda_2, penguine_test)$class
tab_test_2 <- table(Predicted = p1_test_2, Actual = penguine_test$species)
tab_test_2
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie        44         2      0
##   Chinstrap      1        18      1
##   Gentoo         0         0     36
```

There are total 4 mis-classification occures in test data.

```
lda_test_accuracy_2 <- sum(diag(tab_test_2))/sum(tab_test_2) * 100
lda_test_accuracy_2
```

```
## [1] 96.07843
```

Accuracy in test data : 96.0784314

Quadratic Discriminant Analysis

(*a*) Same steps as above to consider

For QDA use same `MASS` package to perform analysis.

First we will build the model, then calculate the prediction of train and test data and accuracy. QDA will create 2 models i.e one with 4 variable and another one with bill length and bill depth.

QDA model building With all 4 variables

```r
qda_all <- qda(species ~ ., data = penguine_train)
qda_all
```

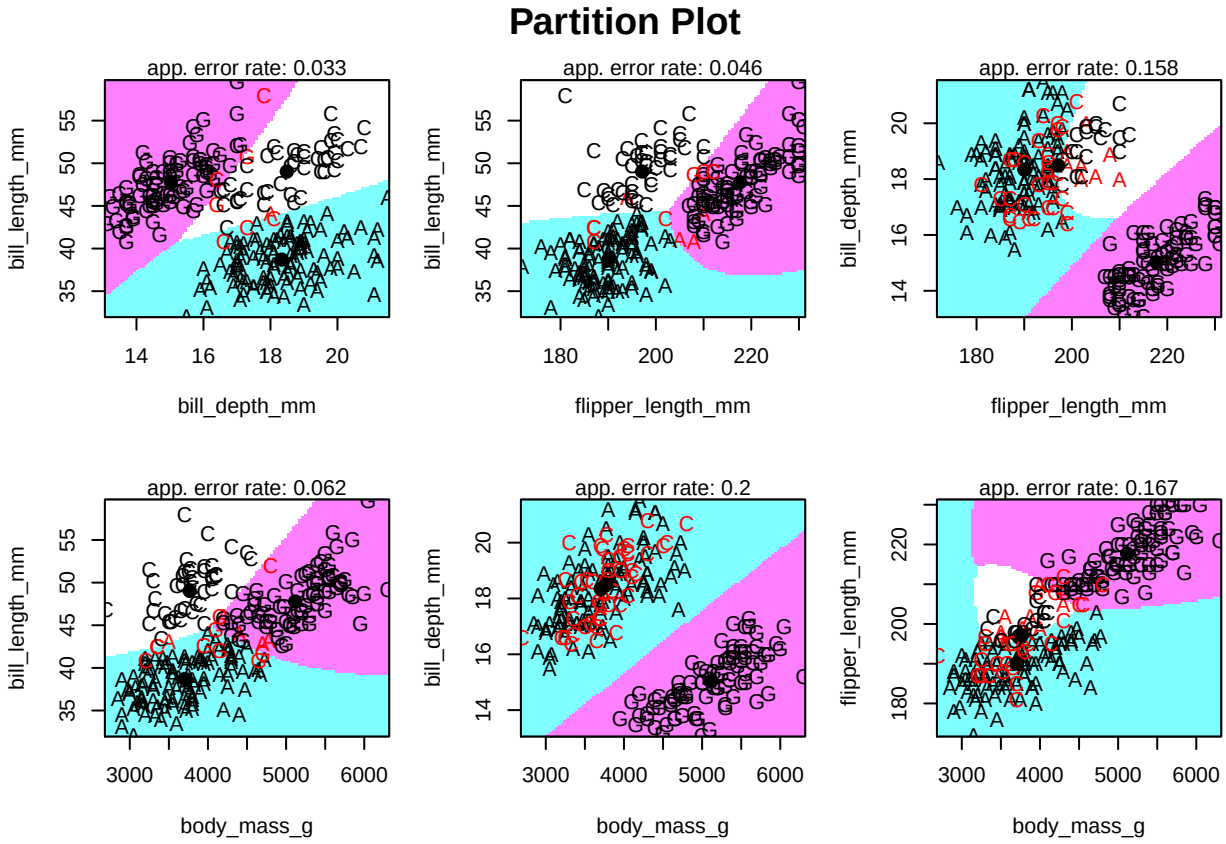
```
## Call:
## qda(species ~ ., data = penguine_train)
##
## Prior probabilities of groups:
##    Adelie Chinstrap    Gentoo
## 0.4416667 0.2000000 0.3583333
##
## Group means:
##           bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
## Adelie          38.70283      18.33585          190.0566    3704.481
## Chinstrap       49.02708      18.48958          197.1250    3766.667
## Gentoo          47.78023      15.02558          217.6860    5116.279
```

With 2 variables

```r
qda_2 <- qda(species ~ bill_length_mm + bill_depth_mm, data = penguine_train)
qda_2
```

```
## Call:
## qda(species ~ bill_length_mm + bill_depth_mm, data = penguine_train)
##
## Prior probabilities of groups:
##    Adelie Chinstrap    Gentoo
## 0.4416667 0.2000000 0.3583333
##
## Group means:
##           bill_length_mm bill_depth_mm
## Adelie          38.70283      18.33585
## Chinstrap       49.02708      18.48958
## Gentoo          47.78023      15.02558
```

```r
partimat(species ~ ., data = penguine_train, method = 'qda')
```



Partition Plot

This plot gives classification of each and every observation in the training dataset based on QDA method.

Confusion matrix and accuracy training data QDA Model with all variables

```
p2_train_all <- predict(qda_all, penguine_train)$class
tab2_train_all <- table(Predicted = p2_train_all, Actual = penguine_train$species)
tab2_train_all
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie       105         2      0
##   Chinstrap      1        46      0
##   Gentoo         0         0     86
```

There are 3 mis-classification occures in Chinstrap.

```
qda_train_accuracy_all <- sum(diag(tab2_train_all))/sum(tab2_train_all) * 100
qda_train_accuracy_all
```

```
## [1] 98.75
```

Accuracy in training data : 98.75

Confusion matrix and accuracy for test data QDA Model with all variables

```
p2_test_all <- predict(qda_all, penguine_test)$class
tab2_test_all <- table(Predicted = p2_test_all, Actual = penguine_test$species)
tab2_test_all
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie        44         1      0
##   Chinstrap      1        19      0
##   Gentoo         0         0     37
```

There are total 2 mis-classification occures in test data.

```
qda_test_accuracy_all <- sum(diag(tab2_test_all))/sum(tab2_test_all) * 100
qda_test_accuracy_all
```

```
## [1] 98.03922
```

Accuracy in test data : 98.0392157

Confusion matrix and accuracy training data (QDA Model 2) QDA Model 2 with two variables

```
p2_train_2 <- predict(qda_2, penguine_train)$class
tab2_train_2 <- table(Predicted = p2_train_2, Actual = penguine_train$species)
tab2_train_2
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie       105         3      0
##   Chinstrap      1        43      2
##   Gentoo         0         2     84
```

There are 8 mis-classification occures in all species.

```
qda_train_accuracy_2 <- sum(diag(tab2_train_2))/sum(tab2_train_2) * 100
qda_train_accuracy_2
```

```
## [1] 96.66667
```

Accuracy in training data : 96.6666667

Confusion matrix and accuracy for test data (QDA model 2) QDA Model 2 with two variables

```
p2_test_2 <- predict(qda_2, penguine_test)$class
tab2_test_2 <- table(Predicted = p2_test_2, Actual = penguine_test$species)
tab2_test_2
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie        44         1      0
##   Chinstrap      1        19      1
##   Gentoo         0         0     36
```

There are total 3 mis-classification occures in test data.

```
qda_test_accuracy_2 <- sum(diag(tab2_test_2))/sum(tab2_test_2) * 100
qda_test_accuracy_2
```

```
## [1] 97.05882
```

Accuracy in test data : 97.0588235

Naive Bayes

(a) Same steps as above to consider

Naive Bayes algorithem is based on Bayes theorm. Mathematical expression :

$$P(A|B) = \frac{P(A) * P(B|A)}{P(B)}$$

To develop a naive bayes classigication model we need to make sure that the independant variables are not highly co-related. From EDA, we see there are co-relation exist between flipp_length and body mass. So exclude flipper length variable for NB model.

```
NB <- naive_bayes(species ~ bill_length_mm + bill_depth_mm + body_mass_g, data = penguine_train)
NB
```

```
##
## ================================== Naive Bayes ==================================
##
##  Call:
## naive_bayes.formula(formula = species ~ bill_length_mm + bill_depth_mm +
##     body_mass_g, data = penguine_train)
##
## ---------------------------------------------------------------------------------
##
## Laplace smoothing: 0
##
## ---------------------------------------------------------------------------------
##
##  A priori probabilities:
##
##    Adelie Chinstrap    Gentoo
## 0.4416667 0.2000000 0.3583333
##
## ---------------------------------------------------------------------------------
##
##  Tables:
##
## ---------------------------------------------------------------------------------
##  ::: bill_length_mm (Gaussian)
## ---------------------------------------------------------------------------------
##
## bill_length_mm    Adelie Chinstrap    Gentoo
```

```
##           mean 38.702830 49.027083 47.780233
##           sd    2.767308  3.519232  3.343292
##
## ------------------------------------------------------------------------------
##  ::: bill_depth_mm (Gaussian)
## ------------------------------------------------------------------------------
##
## bill_depth_mm    Adelie Chinstrap    Gentoo
##          mean 18.335849 18.489583 15.025581
##          sd    1.284352  1.252443  1.031297
##
## ------------------------------------------------------------------------------
##  ::: body_mass_g (Gaussian)
## ------------------------------------------------------------------------------
##
## body_mass_g    Adelie Chinstrap    Gentoo
##        mean 3704.4811 3766.6667 5116.2791
##        sd    490.3691  390.1491  516.9021
##
## ------------------------------------------------------------------------------
```

Confusion matrix and accuracy for train data Calculate Confusion Matrix and accuracy for training data using NB model

```
p3_train <- predict(NB, penguine_train)
tab3_train <- table(Predicted = p3_train, Actual = penguine_train$species)
tab3_train
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie       104         4      0
##   Chinstrap      2        44      0
##   Gentoo         0         0     86
```

There are 6 mis-classification occures in train data.

```
NB_train_accuracy <- sum(diag(tab3_train))/sum(tab3_train) * 100
NB_train_accuracy
```

```
## [1] 97.5
```

Accuracy in training data : 97.5

Confusion matrix and accuracy for test data Calculate Confusion Matrix and accuracy for training data using NB model

```
p3_test <- predict(NB, penguine_test)
tab3_test <- table(Predicted = p3_test, Actual = penguine_test$species)
tab3_test
```

```
##            Actual
## Predicted   Adelie Chinstrap Gentoo
##   Adelie        43         2      0
##   Chinstrap      2        18      0
##   Gentoo         0         0     37
```

There are 4 mis-classification occured test data.

```
NB_test_accuracy <- sum(diag(tab3_test))/sum(tab3_test) * 100
NB_test_accuracy
```

```
## [1] 96.07843
```

Accuracy in test data : 96.0784314

(*d.*) **Comment on the models fits/strength/weakness/accuracy for all these three**

models that you worked with

We find out confusion matrix and accuracy of all 5 models. Compair all model based on F1, Sensitivity and Specificity.

Matrix result of all 5 models

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Pr
Class: Adelie	0.9777778	0.9824561	0.9777778	0.9824561	0.9777778	0.9777778	0.9777778	0
Class: Chinstrap	0.9500000	0.9878049	0.9500000	0.9878049	0.9500000	0.9500000	0.9500000	0
Class: Gentoo	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	0

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Pr
Class: Adelie	0.9565217	0.9821429	0.9777778	0.9649123	0.9777778	0.9565217	0.9670330	0
Class: Chinstrap	0.9000000	0.9756098	0.9000000	0.9756098	0.9000000	0.9000000	0.9000000	0
Class: Gentoo	1.0000000	0.9848485	0.9729730	1.0000000	0.9729730	1.0000000	0.9863014	0

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Pr
Class: Adelie	0.9777778	0.9824561	0.9777778	0.9824561	0.9777778	0.9777778	0.9777778	0
Class: Chinstrap	0.9500000	0.9878049	0.9500000	0.9878049	0.9500000	0.9500000	0.9500000	0
Class: Gentoo	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	0

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Pr
Class: Adelie	0.9777778	0.9824561	0.9777778	0.9824561	0.9777778	0.9777778	0.9777778	0
Class: Chinstrap	0.9047619	0.9876543	0.9500000	0.9756098	0.9500000	0.9047619	0.9268293	0
Class: Gentoo	1.0000000	0.9848485	0.9729730	1.0000000	0.9729730	1.0000000	0.9863014	0

	Sensitivity	Specificity	Pos Pred Value	Neg Pred Value	Precision	Recall	F1	Pr
Class: Adelie	0.9555556	0.9649123	0.9555556	0.9649123	0.9555556	0.9555556	0.9555556	0
Class: Chinstrap	0.9000000	0.9756098	0.9000000	0.9756098	0.9000000	0.9000000	0.9000000	0
Class: Gentoo	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	0

From matrix result we see, LDA and QDA performed well than Naive Bayes. Naive Bayes performed well in normalized data, however this dataset is not normalized. I will go the QDA model 2 due to high accuract, specificity, Sensitivity, and F1.

References:

LDA: https://www.youtube.com/watch?v=WUCnHx0QDSI

Naive bayes: https://www.youtube.com/watch?v=RLjSQdcg8AM&list=RDCMUCuWECsa_za4gm7B3TLgeV_A&index=4