CS5900/STAT 46700 Topics in Data Science Spring 2025

Lab 10

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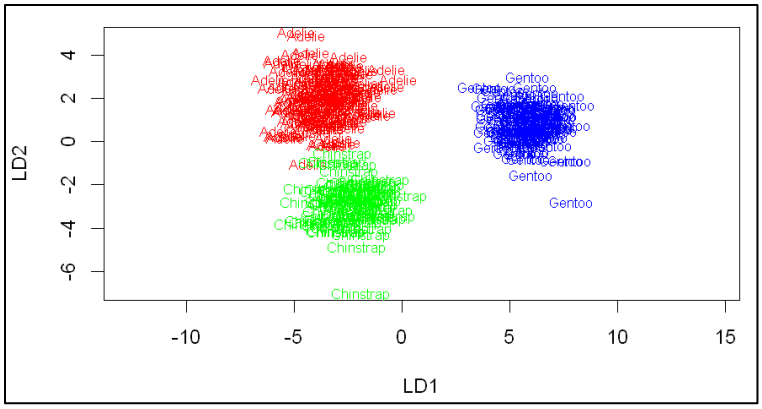
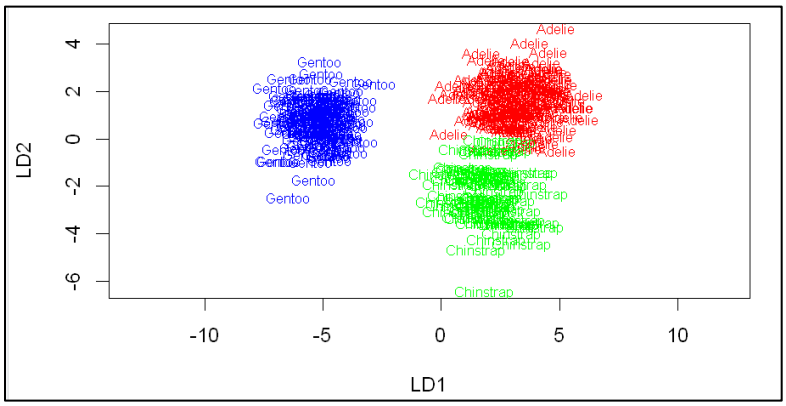
1. The penguins dataset included in the palmerpenguins package provides the size measurements for adult foraging penguins near Palmer Station, Antarctica.
   a) Access the data and determine its dimension.
   b) How many species of penguins are provided in the dataset?
   c) Perform the LDA and QDA to classify the species of penguins.

```
> ########################################################################################### Q1
>
> # a
>
> install.packages("palmerpenguins")
> library(palmerpenguins)
> data(penguins, package = "palmerpenguins")
> head(penguins)
# A tibble: 6 × 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
  <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
4 Adelie  Torgersen           NA            NA                  NA          NA NA      2007
5 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
6 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
> names(penguins)
[1] "species"           "island"            "bill_length_mm"    "bill_depth_mm"
[5] "flipper_length_mm" "body_mass_g"       "sex"               "year"
> dim(penguins)
[1] 344   8
> cat("There are 344 rows and 8 columns in the penguins dataset!")
There are 344 rows and 8 columns in the penguins dataset!

###########################################################################################################

> # b
>
> # attach(penguins)
> table(penguins$species)

   Adelie Chinstrap    Gentoo
      152        68       124
> cat("There are 3 different species in the penguins dataset namely:\n1. Adelie -- 152\n2. Chinstra
p -- 68\n3. Gentoo -- 124")
There are 3 different species in the penguins dataset namely:
1. Adelie -- 152
2. Chinstrap -- 68
3. Gentoo -- 124

###########################################################################################################

> # c
>
> # Before, performing the LDA and QDA. Let's remove the NA values in the dataset, if any!!
> sum(is.na(penguins))
[1] 19
> cat("There are NA values in the penguin dataset")
There are NA values in the penguin dataset
> clean_data = na.omit(penguins)
```

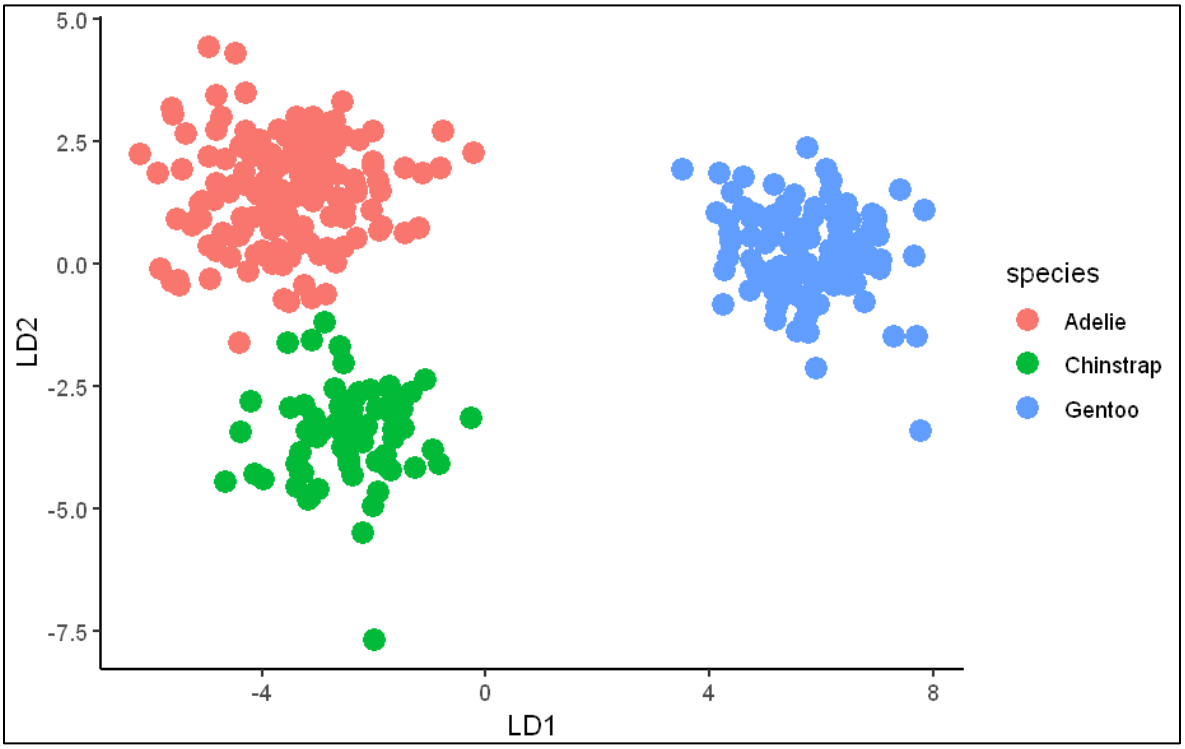
```
> head(clean_data)
# A tibble: 6 × 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g sex     year
  <fct>   <fct>              <dbl>         <dbl>             <int>       <int> <fct>  <int>
1 Adelie  Torgersen           39.1          18.7               181        3750 male    2007
2 Adelie  Torgersen           39.5          17.4               186        3800 female  2007
3 Adelie  Torgersen           40.3          18                 195        3250 female  2007
4 Adelie  Torgersen           36.7          19.3               193        3450 female  2007
5 Adelie  Torgersen           39.3          20.6               190        3650 male    2007
6 Adelie  Torgersen           38.9          17.8               181        3625 female  2007
> dim(clean_data)
[1] 333   8
> cat("There are there are 11 such rows in the main dataset 'penguins', which has been removed!!")
There are there are 11 such rows in the main dataset 'penguins', which has been removed!!
>
>
> attach(clean_data)
> names(clean_data)
[1] "species"           "island"            "bill_length_mm"    "bill_depth_mm"
[5] "flipper_length_mm" "body_mass_g"       "sex"               "year"
> install.packages("MASS")
> library(MASS)

> ###############################################################################
>
> # 1. Performing LDA
>
> lda_penguins = lda(species~., data = clean_data)
> lda_penguins
Call:
lda(species ~ ., data = clean_data)

Prior probabilities of groups:
   Adelie Chinstrap    Gentoo
0.4384384 0.2042042 0.3573574

Group means:
          islandDream islandTorgersen bill_length_mm bill_depth_mm flipper_length_mm
Adelie      0.3767123       0.3219178       38.82397      18.34726          190.1027
Chinstrap   1.0000000       0.0000000       48.83382      18.42059          195.8235
Gentoo      0.0000000       0.0000000       47.56807      14.99664          217.2353
          body_mass_g  sexmale     year
Adelie       3706.164 0.500000 2008.055
Chinstrap    3733.088 0.500000 2007.971
Gentoo       5092.437 0.512605 2008.067

Coefficients of linear discriminants:
                           LD1          LD2
islandDream       -1.20784332 -1.615747171
islandTorgersen   -1.08912081 -0.128942981
bill_length_mm     0.09371102 -0.396269193
bill_depth_mm     -0.92018212 -0.071302456
flipper_length_mm  0.10433497 -0.001273443
body_mass_g        0.00131498  0.001015129
sexmale           -0.54812118  0.912511570
year              -0.35906682  0.134141729

Proportion of trace:
   LD1    LD2
0.8458 0.1542
> cat("Inference: LD1 accounts for 84.58% of the variance between the species groups. i.e., (LD1) i
s sufficient to capture most of the class separability in the data.")
Inference: LD1 accounts for 84.58% of the variance between the species groups. i.e., (LD1) is suffi
cient to capture most of the class separability in the data.

> plot(lda_penguins, col = c("red","green","blue")[as.integer(clean_data$species)])
```




```
> # let's consider only numerical variables in the model
>
> lda_numerical = lda(species~bill_length_mm+bill_depth_mm+flipper_length_mm+body_mass_g, data = cl
ean_data)
> lda_numerical
Call:
lda(species ~ bill_length_mm + bill_depth_mm + flipper_length_mm +
    body_mass_g, data = clean_data)

Prior probabilities of groups:
   Adelie Chinstrap    Gentoo
0.4384384 0.2042042 0.3573574

Group means:
          bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
Adelie           38.82397      18.34726          190.1027    3706.164
Chinstrap        48.83382      18.42059          195.8235    3733.088
Gentoo           47.56807      14.99664          217.2353    5092.437

Coefficients of linear discriminants:
                        LD1         LD2
bill_length_mm    -0.085926709 -0.41660160
bill_depth_mm      1.041646762 -0.01042272
flipper_length_mm -0.084552842  0.01424552
body_mass_g       -0.001347375  0.00168559

Proportion of trace:
   LD1    LD2
0.8655 0.1345
> cat("Inference: LD1 accounts for 86.55% of the variance between the species groups. i.e., (LD1) i
s sufficient to capture most of the class separability in the data.")
Inference: LD1 accounts for 86.55% of the variance between the species groups. i.e., (LD1) is suffi
cient to capture most of the class separability in the data.
> plot(lda_numerical, col = c("red","green","blue")[as.integer(clean_data$species)])
```



```
> # or
>
> # install.packages("ggplot2")
> library(ggplot2)
> lda_pred <- predict(lda_penguins)
> lda_df <- data.frame(species = clean_data[, "species"], LD1 = lda_pred$x[, 1], LD2 = lda_pred$x[,
2])
> ggplot(lda_df) + geom_point(aes(x = LD1, y = LD2, color = species), size = 4) + theme_classic()
>
```




```
> ################################################################################
>
> # 2. Performing QDA
>
> library(MASS)
> library(ggplot2)
> set.seed(037831852)
> index <- sample(1:nrow(clean_data), 0.7 * nrow(clean_data))
> train <- clean_data[index, ]
> test <- clean_data[-index, ]
>
> qda_numerical <- qda(species~bill_length_mm+bill_depth_mm+flipper_length_mm+body_mass_g, data = t
rain)
> qda_numerical
Call:
qda(species ~ bill_length_mm + bill_depth_mm + flipper_length_mm +
    body_mass_g, data = train)

Prior probabilities of groups:
   Adelie Chinstrap    Gentoo
0.4506438 0.2103004 0.3390558

Group means:
          bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
Adelie          38.71714      18.26190          190.2571    3695.714
Chinstrap       48.89592      18.52245          195.6531    3777.551
Gentoo          47.20380      14.95696          216.7089    5070.253
>
```

```
> predicted <- predict(qda_numerical, test)
>
> head(predicted$class)
[1] Adelie Adelie Adelie Adelie Adelie Adelie
Levels: Adelie Chinstrap Gentoo
>
> head(predicted$posterior)
     Adelie    Chinstrap       Gentoo
1 0.8285099 1.714901e-01 6.453494e-29
2 0.9995185 4.814871e-04 2.792383e-30
3 0.9999980 2.010203e-06 4.009137e-34
4 0.9999929 7.108147e-06 6.439711e-40
5 0.9999980 2.046592e-06 1.779171e-37
6 0.9999999 9.497511e-08 1.197489e-34
>
> mean(predicted$class == test$species)
[1] 0.99
> cat("Accuracy: 99%")
Accuracy: 99%
>
> install.packages("klaR")
> library(klaR)
> partimat(species ~ bill_length_mm + bill_depth_mm + flipper_length_mm + body_mass_g,
+          data = train, method = "qda")
```