Multivariate Analysis of Canine skull measurement data

Dataset Information:

The accompanied dataset, from Higham et al. (1980), gives 9 skull measurement for different canine groups.

The variables

- X1 = length of mandible
- X2 = breadth of mandible below 1st molar
- X3 = breadth of articular condyle
- X4 = height of mandible below first molar
- X5 length of first molar, X6 = breadth of first molar
- X7 = length of first to third molar inclusive (first to second for Cuon)
- X8 = length from first to fourth premolar inclusive
- X9 = breadth of lower canine

All measured in millimeters

Objective:

To perform the multivariate analysis techniques to address the questions as mentioned below:

1. Using suitable graphical method, to compare the distribution of the nine variables for the prehistoric and modern Thai dog.
    a. Create a Draftsman plot for the 9 variables showing each species as a different color
2. To Create a distance matrix between the 5 canine groups
3. To Use principal components analysis to investigate the relationships between the species on the basis of these variables
4. To Carry out cluster analysis to study relation between different specifies.
    a. Who is Indian Wolf related to?
5. To Identify the important factors underlying the Skull measurement
    a. Is there a relationship between the species with respect to these factors?
6. To Carry out a discriminant function analysis to see how well it is possible to separate the groups using the measurements.
7. To investigate each canine group separately to see whether logistic regression shows a significant difference between males and females for the measurements.

Note that in view of the small sample sizes available for each group, it is unreasonable to expect to fit a logistic function involving all nine variables with good estimates of parameters. Therefore, consideration should be given to fitting functions using only a subset of the variables.

8. To Show ROC containing both your discriminant and logistic function for gender classification for the Prehistoric Thai Dog
9. To Predict the Gender for the Prehistoric Thai Dog
    a. Explain the reason for choosing the MVA technique for prediction
    b. What is the Hit Ratio (Accuracy) of your classification technique?
10. To Create a model to predict length of the Mandible length for Prehistoric Thai Dog.
    a. What is the accuracy of your model?

#Installing Libraries

```
library(readxl)
library(cluster)

## Warning: package 'cluster' was built under R version 3.6.2

library(data.table)#Data. table is an extension of data. frame package in R.
It is widely used for fast aggregation of large datasets,

## Warning: package 'data.table' was built under R version 3.6.2

library(Hmisc)#data analysis funs

## Warning: package 'Hmisc' was built under R version 3.6.2

## Loading required package: lattice

## Warning: package 'lattice' was built under R version 3.6.2

## Loading required package: survival

## Warning: package 'survival' was built under R version 3.6.2

## Loading required package: Formula

## Loading required package: ggplot2

##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##     format.pval, units

library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.6.2

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:Hmisc':
##
##     src, summarize

## The following objects are masked from 'package:data.table':
##
##     between, first, last

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

library(tidyverse)

## Warning: package 'tidyverse' was built under R version 3.6.2

## -- Attaching packages ------------------------------------- tidyverse
1.3.0 --

## v tibble  2.1.3     v purrr   0.3.3
## v tidyr   1.0.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.4.0

## Warning: package 'tidyr' was built under R version 3.6.2

## Warning: package 'purrr' was built under R version 3.6.2

## Warning: package 'stringr' was built under R version 3.6.3

## -- Conflicts ----------------------------------------
tidyverse_conflicts() --
## x dplyr::between()   masks data.table::between()
## x dplyr::filter()    masks stats::filter()
## x dplyr::first()     masks data.table::first()
## x dplyr::lag()       masks stats::lag()
## x dplyr::last()      masks data.table::last()
## x dplyr::src()       masks Hmisc::src()
## x dplyr::summarize() masks Hmisc::summarize()
## x purrr::transpose() masks data.table::transpose()

library(ggplot2)
library(plotly)

## Warning: package 'plotly' was built under R version 3.6.2
```

```
##
## Attaching package: 'plotly'

## The following object is masked from 'package:Hmisc':
##
##     subplot

## The following object is masked from 'package:ggplot2':
##
##     last_plot

## The following object is masked from 'package:stats':
##
##     filter

## The following object is masked from 'package:graphics':
##
##     layout

library(GGally)

## Warning: package 'GGally' was built under R version 3.6.2

## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2

##
## Attaching package: 'GGally'

## The following object is masked from 'package:dplyr':
##
##     nasa

library(ggthemes)

## Warning: package 'ggthemes' was built under R version 3.6.2

library(psych)

## Warning: package 'psych' was built under R version 3.6.2

##
## Attaching package: 'psych'

## The following object is masked from 'package:Hmisc':
##
##     describe

## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha

library(relaimpo)
```

```
## Warning: package 'relaimpo' was built under R version 3.6.2

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:plotly':
##
##     select

## The following object is masked from 'package:dplyr':
##
##     select

## Loading required package: boot

## Warning: package 'boot' was built under R version 3.6.2

##
## Attaching package: 'boot'

## The following object is masked from 'package:psych':
##
##     logit

## The following object is masked from 'package:survival':
##
##     aml

## The following object is masked from 'package:lattice':
##
##     melanoma

## Loading required package: survey

## Warning: package 'survey' was built under R version 3.6.2

## Loading required package: grid

## Loading required package: Matrix

##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack

##
## Attaching package: 'survey'
```

```
## The following object is masked from 'package:Hmisc':
##
##     deff

## The following object is masked from 'package:graphics':
##
##     dotchart

## Loading required package: mitools

## Warning: package 'mitools' was built under R version 3.6.2

## This is the global version of package relaimpo.

## If you are a non-US user, a version with the interesting additional metric
pmvd is available

## from Ulrike Groempings web site at prof.beuth-hochschule.de/groemping.

library(e1071)

## Warning: package 'e1071' was built under R version 3.6.2

##
## Attaching package: 'e1071'

## The following object is masked from 'package:Hmisc':
##
##     impute

library(corrplot)

## Warning: package 'corrplot' was built under R version 3.6.3

## corrplot 0.84 loaded

library(factoextra)

## Warning: package 'factoextra' was built under R version 3.6.3

## Welcome! Want to learn more? See two factoextra-related books at
https://goo.gl/ve3WBa

library(fpc)

## Warning: package 'fpc' was built under R version 3.6.3

library(cowplot)

## Warning: package 'cowplot' was built under R version 3.6.2

##
## ********************************************************

## Note: As of version 1.0.0, cowplot does not change the
```

```
##   default ggplot2 theme anymore. To recover the previous
##   behavior, execute:
##   theme_set(theme_cowplot())
## ********************************************************
##
## Attaching package: 'cowplot'
## The following object is masked from 'package:ggthemes':
##
##     theme_map
```

```
library(regclass)
```

```
## Warning: package 'regclass' was built under R version 3.6.3
## Loading required package: bestglm
## Warning: package 'bestglm' was built under R version 3.6.3
## Loading required package: leaps
## Warning: package 'leaps' was built under R version 3.6.3
## Loading required package: VGAM
## Warning: package 'VGAM' was built under R version 3.6.3
## Loading required package: stats4
## Loading required package: splines
##
## Attaching package: 'VGAM'
## The following object is masked from 'package:survey':
##
##     calibrate
## The following objects are masked from 'package:boot':
##
##     logit, simplex
## The following objects are masked from 'package:psych':
##
##     fisherz, logistic, logit
## The following object is masked from 'package:tidyr':
##
##     fill
## Loading required package: rpart
```

```
## Loading required package: randomForest

## Warning: package 'randomForest' was built under R version 3.6.3

## randomForest 4.6-14

## Type rfNews() to see new features/changes/bug fixes.

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:psych':
##
##     outlier

## The following object is masked from 'package:dplyr':
##
##     combine

## The following object is masked from 'package:ggplot2':
##
##     margin

## Important regclass change from 1.3:
## All functions that had a . in the name now have an _
## all.correlations -> all_correlations, cor.demo -> cor_demo, etc.

##
## Attaching package: 'regclass'

## The following object is masked from 'package:lattice':
##
##     qq

library(caret)

## Warning: package 'caret' was built under R version 3.6.2

##
## Attaching package: 'caret'

## The following object is masked from 'package:VGAM':
##
##     predictors

## The following object is masked from 'package:purrr':
##
##     lift

## The following object is masked from 'package:survival':
##
##     cluster
```

```
#library(pRoc) #Unable to install and knit this package
library(ROCR)

## Warning: package 'ROCR' was built under R version 3.6.3

## Loading required package: gplots

## Warning: package 'gplots' was built under R version 3.6.2

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##     lowess

library(memisc)

## Warning: package 'memisc' was built under R version 3.6.3

##
## Attaching package: 'memisc'

## The following object is masked from 'package:VGAM':
##
##     Max

## The following object is masked from 'package:Matrix':
##
##     as.array

## The following objects are masked from 'package:plotly':
##
##     rename, style

## The following object is masked from 'package:purrr':
##
##     %@%

## The following object is masked from 'package:tibble':
##
##     view

## The following objects are masked from 'package:dplyr':
##
##     collect, recode, rename, syms

## The following objects are masked from 'package:Hmisc':
##
##     %nin%, html, Mean
```

```
## The following object is masked from 'package:ggplot2':
##
##     syms

## The following objects are masked from 'package:stats':
##
##     contr.sum, contr.treatment, contrasts

## The following object is masked from 'package:base':
##
##     as.array

library(MASS)
library(scales)

## Warning: package 'scales' was built under R version 3.6.2

##
## Attaching package: 'scales'

## The following object is masked from 'package:memisc':
##
##     percent

## The following objects are masked from 'package:psych':
##
##     alpha, rescale

## The following object is masked from 'package:purrr':
##
##     discard

## The following object is masked from 'package:readr':
##
##     col_factor

library(gridExtra)

##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:randomForest':
##
##     combine

## The following object is masked from 'package:dplyr':
##
##     combine

#install.packages("klaR")
library(klaR)

## Warning: package 'klaR' was built under R version 3.6.3
```

```r
library(tidyverse)
library(caret)
```

#Reading the file from the directory

```r
Canine_Data <-
read_excel("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinalExamToUpload_Kals/Final_Data_MVA.xlsx")
```

#Exploratory data analysis:

```r
#View(Canine_Data)
head(Canine_Data)

## # A tibble: 6 x 11
##   CanineGroup    X1    X2    X3    X4    X5    X6    X7    X8    X9 Gender
##   <chr>       <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
## 1 ModernDog     123  10.1    23    23    19   7.8    32    33   5.6 Male
## 2 ModernDog     137   9.6    19    22    19   7.8    32    40   5.8 Male
## 3 ModernDog     121  10.2    18    21    21   7.9    35    38   6.2 Male
## 4 ModernDog     130  10.7    24    22    20   7.9    32    37   5.9 Male
## 5 ModernDog     149  12      25    25    21   8.4    35    43   6.6 Male
## 6 ModernDog     125   9.5    23    20    20   7.8    33    37   6.3 Male

dim(Canine_Data)

## [1] 77 11

attach(Canine_Data)
names(Canine_Data)

##  [1] "CanineGroup" "X1"          "X2"          "X3"          "X4"
##  [6] "X5"          "X6"          "X7"          "X8"          "X9"
## [11] "Gender"

Canine_Data <-  data.frame(Canine_Data)
#Numerical data only
Canine_num <- Canine_Data[2:10]
str(Canine_Data)

## 'data.frame':    77 obs. of  11 variables:
##  $ CanineGroup: chr  "ModernDog" "ModernDog" "ModernDog" "ModernDog" ...
##  $ X1         : num  123 137 121 130 149 125 126 125 121 122 ...
##  $ X2         : num  10.1 9.6 10.2 10.7 12 9.5 9.1 9.7 9.6 8.9 ...
##  $ X3         : num  23 19 18 24 25 23 20 19 22 20 ...
##  $ X4         : num  23 22 21 22 25 20 22 19 20 20 ...
##  $ X5         : num  19 19 21 20 21 20 19 19 18 19 ...
##  $ X6         : num  7.8 7.8 7.9 7.9 8.4 7.8 7.5 7.5 7.6 7.6 ...
##  $ X7         : num  32 32 35 32 35 33 32 32 31 31 ...
##  $ X8         : num  33 40 38 37 43 37 35 37 35 35 ...
```

```
## $ X9         : num  5.6 5.8 6.2 5.9 6.6 6.3 5.5 6.2 5.3 5.7 ...
## $ Gender     : chr  "Male" "Male" "Male" "Male" ...
```

```r
#Converting the 2 character variables into categorical variables
Canine_Data$CanineGroup <- as.factor(Canine_Data$CanineGroup)
Canine_Data$Gender <- as.factor(Canine_Data$Gender)
str(Canine_Data)
```

```
## 'data.frame':    77 obs. of  11 variables:
## $ CanineGroup: Factor w/ 5 levels "Cuons","GoldenJackal",..: 4 4 4 4 4 4
4 4 4 4 ...
## $ X1         : num  123 137 121 130 149 125 126 125 121 122 ...
## $ X2         : num  10.1 9.6 10.2 10.7 12 9.5 9.1 9.7 9.6 8.9 ...
## $ X3         : num  23 19 18 24 25 23 20 19 22 20 ...
## $ X4         : num  23 22 21 22 25 20 22 19 20 20 ...
## $ X5         : num  19 19 21 20 21 20 19 19 18 19 ...
## $ X6         : num  7.8 7.8 7.9 7.9 8.4 7.8 7.5 7.5 7.6 7.6 ...
## $ X7         : num  32 32 35 32 35 33 32 32 31 31 ...
## $ X8         : num  33 40 38 37 43 37 35 37 35 35 ...
## $ X9         : num  5.6 5.8 6.2 5.9 6.6 6.3 5.5 6.2 5.3 5.7 ...
## $ Gender     : Factor w/ 3 levels "Female","Male",..: 2 2 2 2 2 2 2 2 1 1
...
```

#Printing Descriptive statistics

```r
summary(Canine_Data)
```

```
##       CanineGroup       X1              X2                X3
## Cuons       :17   Min.   :105   Min.   : 7.200   Min.   : 2.00
## GoldenJackal:20   1st Qu.:114   1st Qu.: 8.700   1st Qu.:19.00
## IndianWolves:14   Median :125   Median :10.000   Median :21.00
## ModernDog   :16   Mean   :129   Mean   : 9.961   Mean   :21.64
## ThaiDogs    :10   3rd Qu.:137   3rd Qu.:10.900   3rd Qu.:25.00
##                   Max.   :177   Max.   :13.400   Max.   :32.00
##       X4              X5              X6             X7              X8
## Min.   :15.00   Min.   :17.00   Min.   : 6.0   Min.   :26.00   Min.
:31.0
## 1st Qu.:18.00   1st Qu.:19.00   1st Qu.: 7.1   1st Qu.:30.00   1st
Qu.:34.0
## Median :22.00   Median :20.00   Median : 7.9   Median :31.00   Median
:36.0
## Mean   :21.49   Mean   :20.49   Mean   : 8.0   Mean   :32.52   Mean
:37.4
## 3rd Qu.:24.00   3rd Qu.:22.00   3rd Qu.: 8.7   3rd Qu.:33.00   3rd
Qu.:39.0
## Max.   :28.00   Max.   :27.00   Max.   :10.5   Max.   :43.00   Max.
:50.0
##       X9            Gender
## Min.   :4.300   Female :32
## 1st Qu.:5.300   Male   :35
## Median :6.100   Unknown:10
```

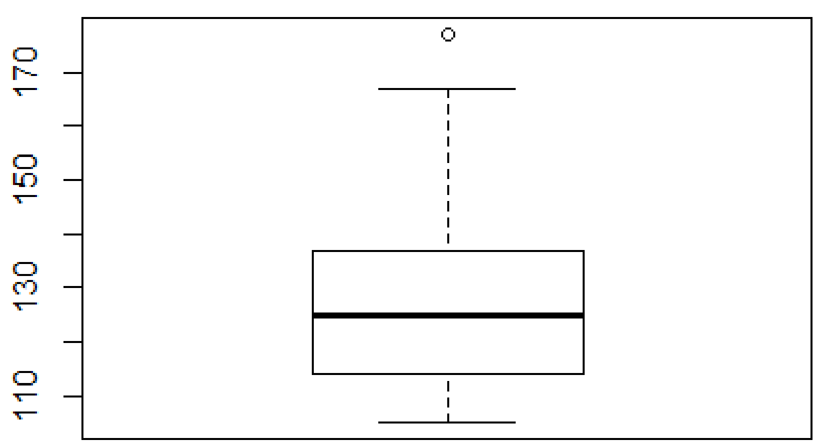
```
##   Mean   :6.075
##   3rd Qu.:6.800
##   Max.   :8.500

unique(CanineGroup)

## [1] "ModernDog"    "GoldenJackal" "Cuons"        "ThaiDogs"
"IndianWolves"

#There are 5 Canine groups
unique(Gender)

## [1] "Male"    "Female"  "Unknown"

#Gender is UNKNOWN for Thai dogs
```

#Checking for null/missing values

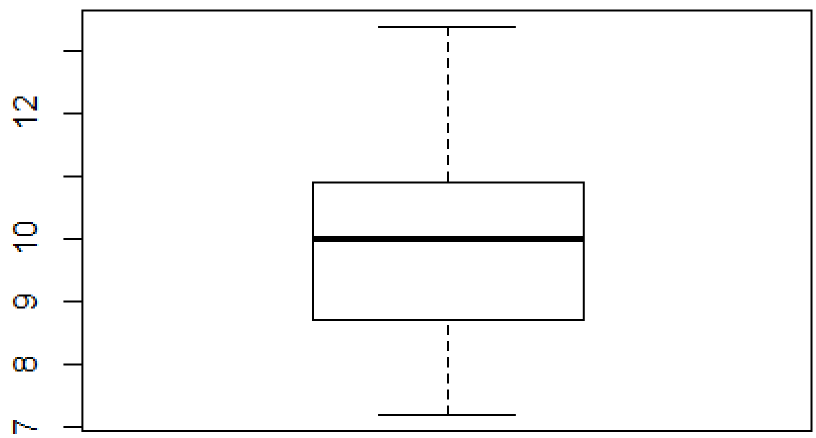
```
grep('NA',Canine_Data)

## integer(0)

#There are NO null values
```

#Looking for the outliers

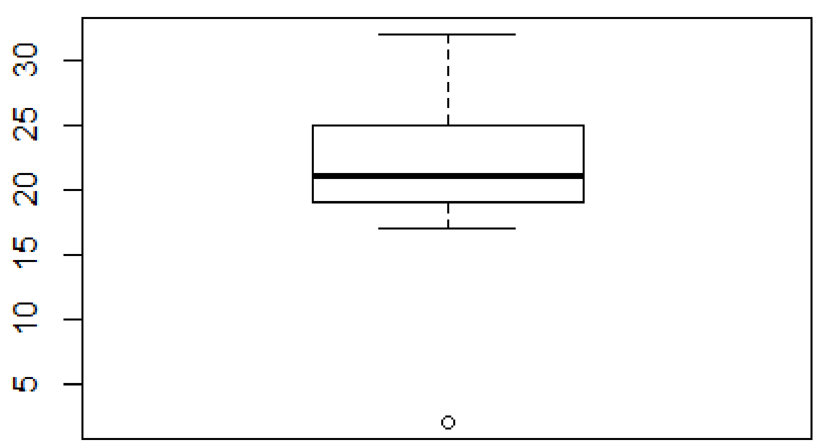
```
boxplot(Canine_Data$X1)
```



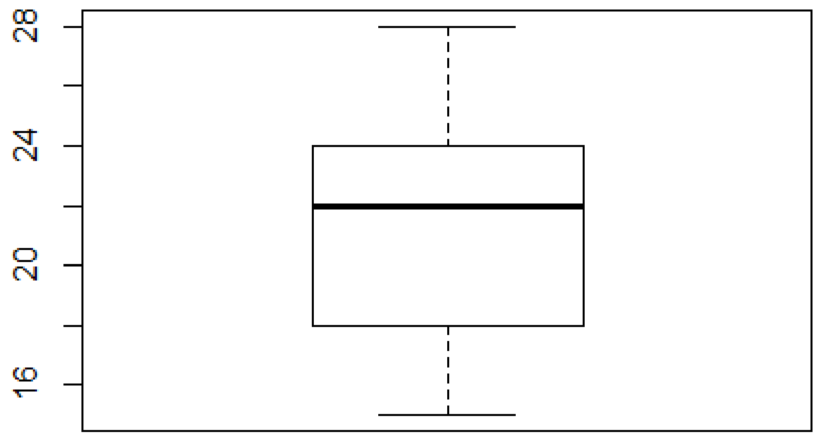

```
boxplot(Canine_Data$X2)
```



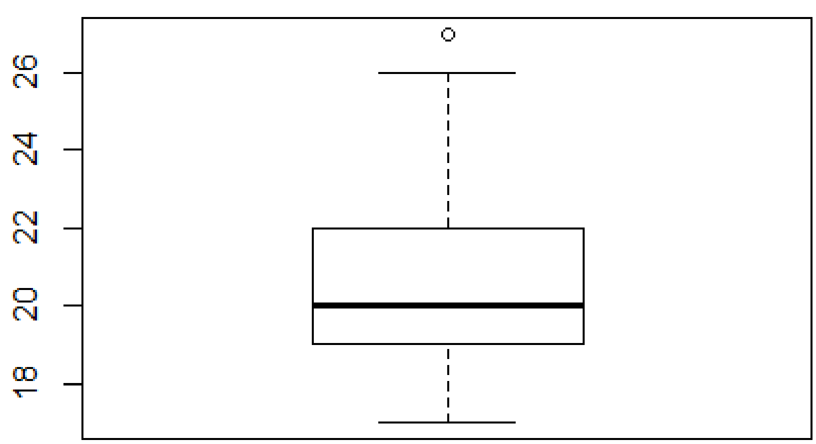

```r
boxplot(Canine_Data$X3)
```



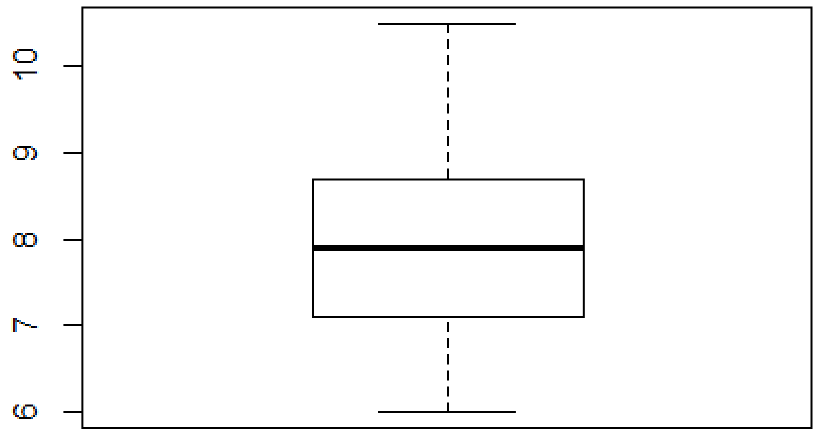

```r
boxplot(Canine_Data$X4)
```



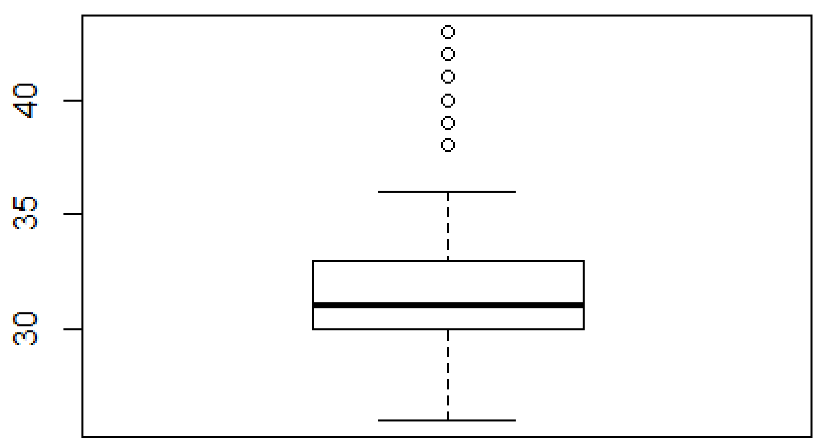

```
boxplot(Canine_Data$X5)
```



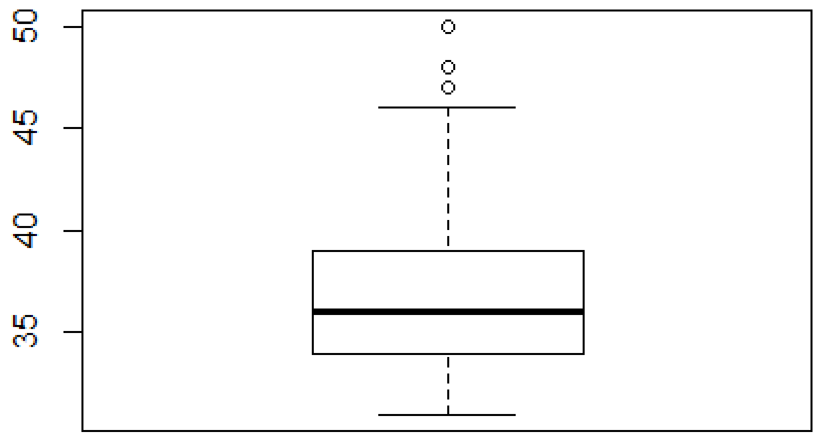

```
boxplot(Canine_Data$X6)
```



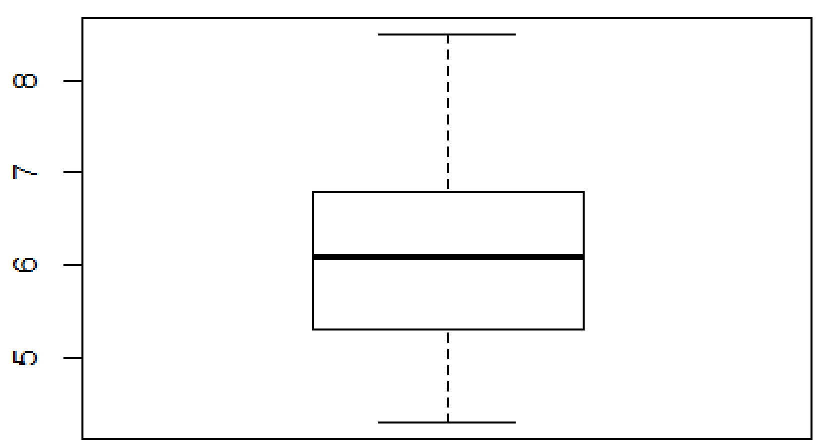

```
boxplot(Canine_Data$X7)
```




```
boxplot(Canine_Data$X8)
```




```r
boxplot(Canine_Data$X9)
```

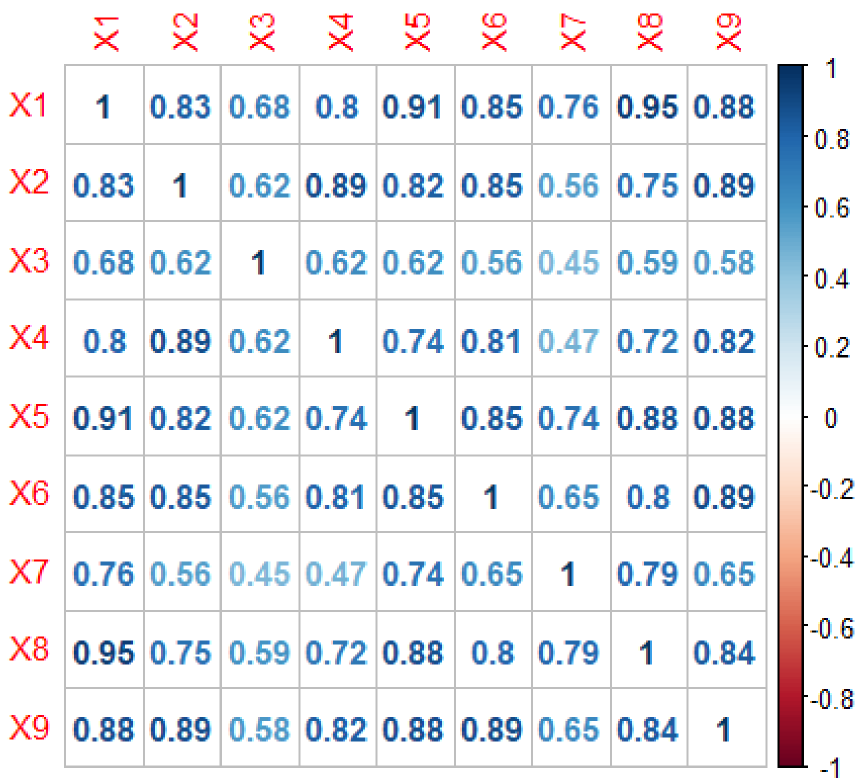


#X8 and x9 have some outliers but they are not extreme others look ok
#So no need to remove outliers

```
# Computing the means of each variable in data frame
colMeans(Canine_num)

##         X1         X2         X3         X4         X5         X6
X7
## 128.974026   9.961039  21.636364  21.493506  20.493506   8.000000
32.519481
##         X8         X9
##  37.402597   6.075325

# Covariance matrix
cov(Canine_num)

##           X1        X2        X3        X4        X5         X6        X7
## X1 306.31511 20.281869 50.464115 47.157724 39.512987 15.2565789 55.421565
## X2  20.28187  1.968462  3.656699  4.216849  2.869481  1.2147368  3.277085
## X3  50.46411  3.656699 17.760766  8.826555  6.471292  2.4197368  7.941388
## X4  47.15772  4.216849  8.826555 11.411141  6.226931  2.7960526  6.634997
## X5  39.51299  2.869481  6.471292  6.226931  6.200615  2.1763158  7.713944
## X6  15.25658  1.214737  2.419737  2.796053  2.176316  1.0478947  2.757895
## X7  55.42157  3.277085  7.941388  6.634997  7.713944  2.7578947 17.410800
## X8  73.19481  4.610629 10.964115 10.640807  9.627649  3.6000000 14.459159
## X9  15.76514  1.269684  2.471172  2.834706  2.241285  0.9334211  2.756408
##           X8         X9
## X1 73.194805 15.7651401
## X2  4.610629  1.2696839
## X3 10.964115  2.4711722
## X4 10.640807  2.8347061
## X5  9.627649  2.2412850
## X6  3.600000  0.9334211
## X7 14.459159  2.7564081
## X8 19.401572  3.7640123
## X9  3.764012  1.0397779

# Finding correlation -Correlation matrix takes units out and gives
normalized values
cor.PT<-cor(Canine_num)
cor.PT

##           X1        X2        X3        X4        X5        X6        X7
## X1 1.0000000 0.8259623 0.6841756 0.7976348 0.9066471 0.8515578 0.7589012
## X2 0.8259623 1.0000000 0.6184360 0.8897336 0.8213389 0.8457847 0.5597767
## X3 0.6841756 0.6184360 1.0000000 0.6200059 0.6166557 0.5608910 0.4516023
## X4 0.7976348 0.8897336 0.6200059 1.0000000 0.7402734 0.8085781 0.4707245
## X5 0.9066471 0.8213389 0.6166557 0.7402734 1.0000000 0.8537794 0.7424201
## X6 0.8515578 0.8457847 0.5608910 0.8085781 0.8537794 1.0000000 0.6456683
## X7 0.7589012 0.5597767 0.4516023 0.4707245 0.7424201 0.6456683 1.0000000
```

```
## X8 0.9494620 0.7460676 0.5906419 0.7151408 0.8777774 0.7984086 0.7867110
## X9 0.8833714 0.8874866 0.5750451 0.8229495 0.8826925 0.8942284 0.6478342
##           X8        X9
## X1 0.9494620 0.8833714
## X2 0.7460676 0.8874866
## X3 0.5906419 0.5750451
## X4 0.7151408 0.8229495
## X5 0.8777774 0.8826925
## X6 0.7984086 0.8942284
## X7 0.7867110 0.6478342
## X8 1.0000000 0.8380353
## X9 0.8380353 1.0000000
```

```
#Plotting correlation
corrplot(cor.PT,method="number")
```



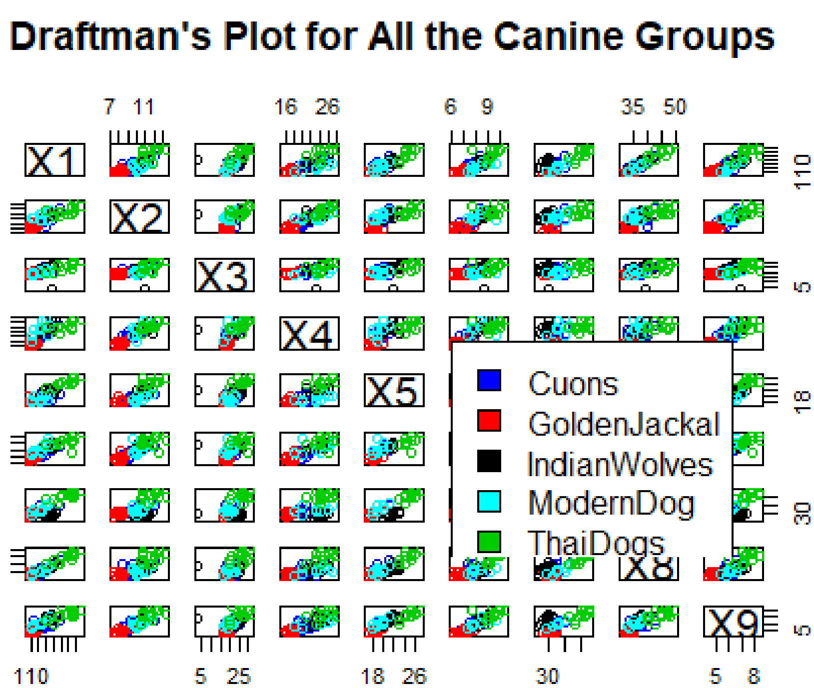

```
#As per above Correlation plot, there is High Positive correlation between variables
#X1 and X2 are very much correlated with almost all other variables.
```

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

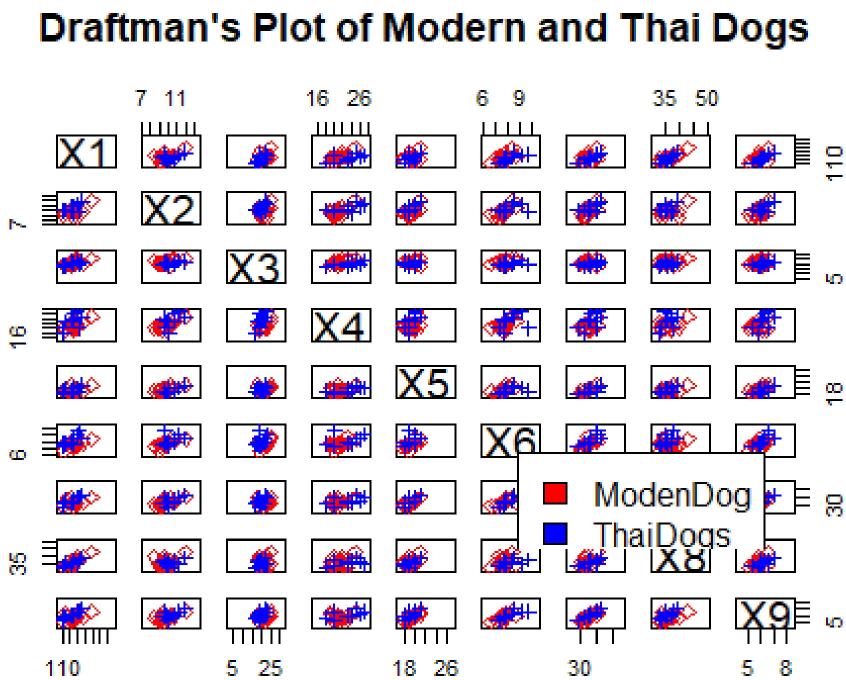
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
#@@@@@@@ Question 1 @@@@@@@@@@@@@@@@@@@@@@@@@@
#1. Using suitable graphical method, compare the distribution of the nine variables for the prehistoric and modern Thai dog.
#a. Create a Draftsman plot for the 9 variables showing each species as a different color
#First Trying to plot for all the Canine groups
pairs(Canine_Data[2:10], main = "Draftman's Plot for All the Canine Groups",
col = as.numeric(Canine_Data$CanineGroup),
      bg = c("red", "green2","black", "green3",
"blue")[unclass(Canine_Data$CanineGroup)])
legend("bottomright", fill = unique(Canine_Data$CanineGroup),legend =
c(levels(Canine_Data$CanineGroup)))
```

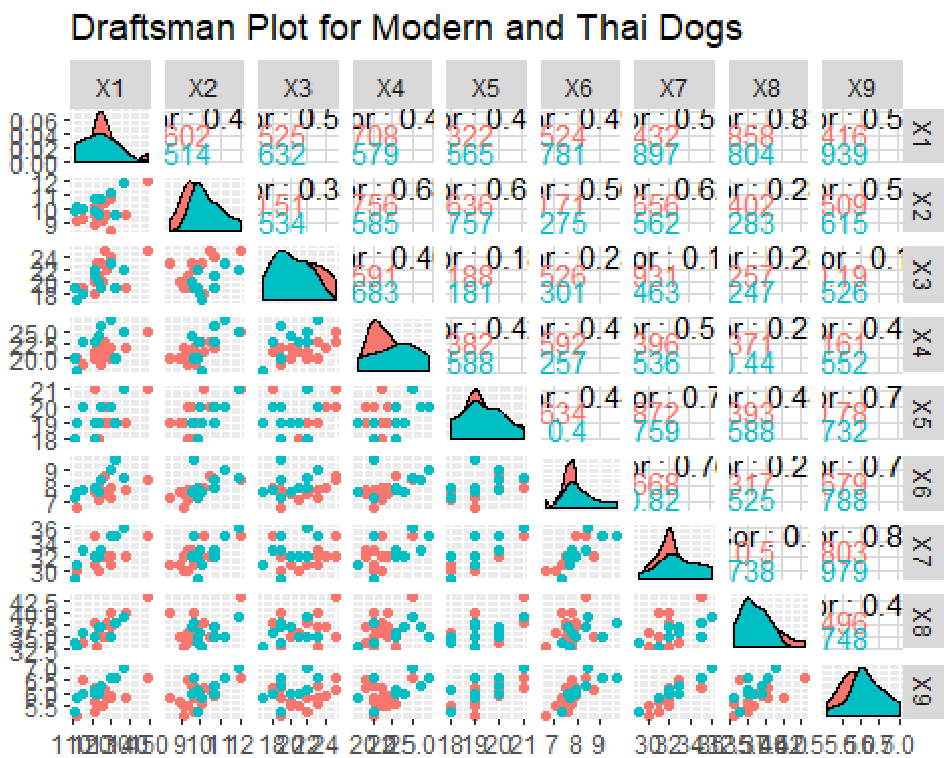



```
#unclassturns the list of canine grps from a list of categories (a "factor"
data type in R terminology) into a list of ones, twos and threes, 4, 5:

#Plotting Draftsman plot only for 2 groups Moderndog and Thaigdog below
group <- NA
group[Canine_Data$CanineGroup == 'ModernDog'] <- 1
group[Canine_Data$CanineGroup == 'ThaiDogs'] <- 2

pairs(Canine_Data[,2:10],
      col = c("red", "blue")[group],    # Change color by group
```

```
      pch = c(5, 3)[group],                                   # Change points by
group
      main = "Draftman's Plot of Modern and Thai Dogs")
legend("bottomright", fill = c("red","blue"), legend =
c("ModenDog","ThaiDogs"),col=c("red","blue"))
```




```
#Doing ggpairs for only 2 grps
datapr<-(Canine_Data$CanineGroup %in% c("ModernDog","ThaiDogs"))
datapr1<- Canine_Data %>% filter(Canine_Data$CanineGroup %in%
c("ModernDog","ThaiDogs"))
head(datapr1)

##   CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 1   ModernDog 123 10.1 23 23 19 7.8 32 33 5.6   Male
## 2   ModernDog 137  9.6 19 22 19 7.8 32 40 5.8   Male
## 3   ModernDog 121 10.2 18 21 21 7.9 35 38 6.2   Male
## 4   ModernDog 130 10.7 24 22 20 7.9 32 37 5.9   Male
## 5   ModernDog 149 12.0 25 25 21 8.4 35 43 6.6   Male
## 6   ModernDog 125  9.5 23 20 20 7.8 33 37 6.3   Male

ggpairs(datapr1,column=2:10,ggplot2::aes(colour=CanineGroup),title="Draftsman
Plot for Modern and Thai Dogs")
```




```
##Conclusion: Red= Modern dog and Green is Thai dogs
#For Modern dog = x1 is correlated with X2 and X8
#For Thai dogs= X7 and x8 , X8 and x9 are highly corelated
#There is Left skewed distributions for almost all fields from X1 to X8
for both canine groups

#X9 looks a bit normal for Thai dogs and left skewed for Modern dogs.
#=============Question 1 end ======================

#@@@@@@@@@@ Question 2 - Distance Matrix @@@@@@@@@@@@@
#2. Create a distance matrix between the 5 canine groups

#Creating Distance matrix after scaling
#By default is euclidean dist
x<- dist(scale(Canine_Data[2:10],center = FALSE))
x

##             1           2           3           4           5           6
7
## 2  0.28915229
## 3  0.32238260 0.21720720
## 4  0.16257847 0.27287512 0.30988348
## 5  0.45793170 0.44992594 0.48539766 0.33243206
```

```
## 6  0.22279192 0.25564100 0.25632848 0.17639236 0.44007723
## 7  0.18726311 0.18063959 0.24989879 0.26479680 0.53694457 0.22866779
## 8  0.29924963 0.19761930 0.18547771 0.29644276 0.54080485 0.19963379
0.19976694
## 9  0.18011973 0.26324676 0.31993936 0.23811327 0.55325283 0.21309728
0.15746496
## 10 0.23609125 0.21783901 0.25466845 0.29090480 0.58179465 0.20266994
0.10851861
## 11 0.31759542 0.29815271 0.19998805 0.34425907 0.59567636 0.21937470
0.24404876
## 12 0.31643105 0.34581251 0.35693150 0.40303214 0.70475336 0.35350430
0.21144980
## 13 0.20670079 0.21873760 0.30946955 0.26288427 0.55540763 0.23017100
0.11770997
## 14 0.18460200 0.17101688 0.25101200 0.16719493 0.44433640 0.12861267
0.14660424
## 15 0.29946713 0.24995402 0.35439399 0.27786563 0.52248649 0.18924848
0.23154663
## 16 0.18579768 0.35118429 0.37110786 0.13627414 0.34856519 0.23222024
0.32497939
## 17 0.42498666 0.35907532 0.38228670 0.47875029 0.75984167 0.37641304
0.28057801
## 18 0.47482051 0.42954248 0.39182003 0.53569349 0.81916577 0.42273608
0.33670041
## 19 0.48166994 0.47532497 0.46849676 0.55256277 0.85633404 0.46243502
0.36626654
## 20 0.35929414 0.38502945 0.41390833 0.43830557 0.74449524 0.36942241
0.25863299
## 21 0.36229303 0.36100818 0.35930187 0.43609526 0.73287101 0.34115683
0.24712936
## 22 0.43689415 0.43642567 0.44337880 0.49901306 0.80711468 0.40882837
0.33383843
## 23 0.44037853 0.40063104 0.41522301 0.51279085 0.80351216 0.44623822
0.30478703
## 24 0.36763807 0.36812175 0.39703812 0.42163793 0.72879354 0.33470249
0.26691798
## 25 0.24168389 0.29035844 0.29909867 0.29373907 0.60803948 0.23134788
0.17897616
## 26 0.41943347 0.40539256 0.41515876 0.47966499 0.78313837 0.38355429
0.29911262
## 27 0.42906597 0.41746122 0.40772812 0.49851666 0.79982561 0.41265225
0.30913660
## 28 0.43766806 0.47211003 0.50952534 0.52718380 0.83915368 0.45525821
0.33703255
## 29 0.60771960 0.56024517 0.59587003 0.67497565 0.96672008 0.58257821
0.47370149
## 30 0.51104819 0.49855035 0.51892483 0.58215843 0.88666848 0.49837331
0.39779238
## 31 0.58362774 0.57547237 0.60663574 0.65186360 0.95422064 0.55982187
0.47143174
```

```
## 32 0.48316817 0.50990257 0.53447362 0.56817653 0.88142213 0.50153460
0.38872665
## 33 0.51497184 0.53387679 0.54973099 0.60066569 0.90969006 0.54056119
0.41342782
## 34 0.48307521 0.50853997 0.52808153 0.57426740 0.87997738 0.50320014
0.37660542
## 35 0.49942246 0.45705492 0.46625104 0.56238689 0.85642167 0.47945347
0.37202117
## 36 0.48724910 0.46590527 0.50359554 0.55424446 0.85258134 0.46806712
0.36260153
## 37 0.22356464 0.26580165 0.31540363 0.21834735 0.49983525 0.19884848
0.22573574
## 38 0.43051684 0.47518575 0.44293671 0.30411278 0.31119486 0.35761229
0.51897499
## 39 0.43016304 0.48093985 0.48884268 0.33512387 0.26730698 0.41405362
0.52802759
## 40 0.34679547 0.41180116 0.47831984 0.24651835 0.25568732 0.35403723
0.44593168
## 41 0.34376575 0.40482334 0.44705612 0.24531742 0.24955383 0.35452699
0.44568482
## 42 0.32790742 0.30928940 0.31356781 0.23258867 0.26558479 0.29664823
0.37397356
## 43 0.31838097 0.36486631 0.34562627 0.24710115 0.35925871 0.27816984
0.38154708
## 44 0.30050823 0.36680932 0.42965762 0.20695356 0.30399717 0.30414582
0.39256713
## 45 0.34416022 0.39400805 0.44221677 0.25657123 0.28269182 0.33238577
0.43055476
## 46 0.23938880 0.38291362 0.41683649 0.17887112 0.33866580 0.30035376
0.37104559
## 47 0.33300575 0.35352847 0.34279525 0.25593773 0.34073417 0.30971616
0.39884670
## 48 0.45725935 0.43671788 0.48198508 0.35759284 0.23642213 0.42963915
0.51763247
## 49 1.01155790 0.82166575 0.77505426 1.02092370 1.06826221 0.99374867
0.90028793
## 50 0.20100918 0.32737031 0.39051810 0.23466146 0.52343533 0.27355917
0.25572393
## 51 0.41942706 0.50804319 0.53708385 0.32313161 0.26148668 0.43912973
0.53569635
## 52 0.28661309 0.30162826 0.30668621 0.23499306 0.39135731 0.24972347
0.32184476
## 53 0.22112909 0.28545527 0.35057187 0.23295566 0.50503952 0.26448673
0.24465924
## 54 0.36669773 0.33990701 0.26786476 0.41302041 0.68184771 0.34445480
0.28194219
## 55 0.26133614 0.22202842 0.14421321 0.30849293 0.51888715 0.28439952
0.19227659
## 56 0.39910250 0.39785699 0.36183651 0.31589214 0.21120194 0.38855421
0.46693882
```

```
## 57 0.27835933 0.30749463 0.32001254 0.35363492 0.65199956 0.32486358
0.20653631
## 58 0.33625069 0.42752006 0.41829028 0.31979126 0.31313184 0.40779816
0.44193598
## 59 0.29600125 0.27392516 0.26131622 0.30742611 0.39836208 0.35653074
0.30887124
## 60 0.40610294 0.30379121 0.27799820 0.37998472 0.50065805 0.31509662
0.36657784
## 61 0.13774366 0.23565178 0.23218199 0.17452051 0.42222427 0.22448656
0.19870628
## 62 0.12134793 0.23683099 0.27949256 0.18691589 0.44754291 0.19069968
0.17331791
## 63 0.19963239 0.16802746 0.22986785 0.24687905 0.46039236 0.24063105
0.13991834
## 64 0.79102702 0.79750933 0.81056061 0.68672025 0.41623034 0.75804989
0.87013881
## 65 0.84806298 0.82132562 0.80504680 0.73099818 0.44746862 0.78402394
0.91497817
## 66 0.77471659 0.68424897 0.62017063 0.67118778 0.46872864 0.67088560
0.79086742
## 67 0.55556212 0.59910477 0.58912705 0.43588511 0.26404329 0.49637162
0.65067818
## 68 1.04583947 1.03386687 1.03377971 0.92605406 0.64492435 0.98595682
1.12174315
## 69 0.91637303 0.94566424 0.94811009 0.79402552 0.51672857 0.88376727
1.01781328
## 70 0.83883693 0.81488879 0.78611505 0.71971462 0.46648931 0.75387435
0.90339097
## 71 0.79478733 0.82225227 0.81672260 0.67791299 0.42749673 0.74591872
0.88427311
## 72 0.43907011 0.39717038 0.30439201 0.36681990 0.31408418 0.41431899
0.46916483
## 73 0.68766338 0.63759123 0.66116808 0.56000523 0.32016323 0.60279742
0.73405764
## 74 0.78261592 0.70290478 0.67424794 0.66904073 0.46063102 0.67539159
0.80251582
## 75 0.44755191 0.32724271 0.30219494 0.37004778 0.34430844 0.38659120
0.42732479
## 76 0.52141176 0.52651435 0.49423310 0.40519200 0.32302790 0.41293034
0.57793151
## 77 0.68476576 0.63753660 0.62884200 0.57949848 0.35256324 0.60856989
0.72824568
##             8          9         10         11         12         13
14
## 2
## 3
## 4
## 5
## 6
## 7
```

```
## 8
## 9  0.22057089
## 10 0.14575767 0.13945389
## 11 0.14350991 0.27397167 0.18021970
## 12 0.27208728 0.21837261 0.19103915 0.29517496
## 13 0.19988577 0.10940698 0.12115206 0.27379207 0.18850604
## 14 0.17920484 0.14524583 0.15712399 0.25660460 0.28956906 0.13185882
## 15 0.25396904 0.21997500 0.20853266 0.32125822 0.33374761 0.19373999
0.15069800
## 16 0.37446784 0.30374630 0.34896086 0.38346498 0.47527953 0.34247268
0.25955944
## 17 0.26210017 0.27768885 0.21706448 0.29698589 0.20951930 0.26695003
0.33238705
## 18 0.31688119 0.35431708 0.27108644 0.29567159 0.22926300 0.34462724
0.40227580
## 19 0.37172503 0.34151471 0.30366474 0.36988976 0.23444442 0.35626761
0.43055454
## 20 0.31194371 0.21586397 0.21870681 0.33620689 0.16960788 0.23951292
0.31737056
## 21 0.27592632 0.23882437 0.18253823 0.26272989 0.21401163 0.26582588
0.31651860
## 22 0.31821834 0.28130554 0.25802611 0.33189128 0.20811580 0.29855087
0.37623125
## 23 0.33410775 0.30847866 0.26420679 0.35865805 0.17617383 0.30126153
0.38626437
## 24 0.25676333 0.20754206 0.19109473 0.29212167 0.17182024 0.21690654
0.29451837
## 25 0.20207862 0.09915612 0.12083645 0.23195435 0.16841156 0.14719968
0.18940565
## 26 0.29832795 0.27493552 0.22826690 0.31213223 0.16726297 0.26893568
0.34741656
## 27 0.31201870 0.29132742 0.24850025 0.31793266 0.17010656 0.29722892
0.37384762
## 28 0.40356076 0.30601891 0.29782782 0.41566553 0.20515003 0.30856291
0.40458979
## 29 0.47559649 0.45891059 0.41877404 0.50162782 0.32175675 0.43154159
0.52981159
## 30 0.39298432 0.35847114 0.33595323 0.41538269 0.23856981 0.35336685
0.45079736
## 31 0.48134596 0.43117733 0.41487852 0.50159278 0.32620863 0.42829529
0.51761435
## 32 0.41961424 0.34020374 0.34086755 0.43814758 0.21970185 0.34372510
0.44801003
## 33 0.44828234 0.38384079 0.37459254 0.46584443 0.22834090 0.38011049
0.48426512
## 34 0.43465659 0.35838775 0.34553800 0.44505398 0.21456221 0.35151599
0.44923688
## 35 0.35972160 0.34713097 0.31074838 0.38376805 0.23652172 0.34928152
0.43155863
## 36 0.39159634 0.33755953 0.31212774 0.41865502 0.22921178 0.32677082
```

```
0.41524221
## 37 0.23337777 0.21054904 0.19746929 0.26820465 0.30928771 0.19489956
0.18254475
## 38 0.46888869 0.50313030 0.51455195 0.47872916 0.64570826 0.52719691
0.42434027
## 39 0.52643964 0.54492960 0.55066184 0.53784294 0.68403539 0.54705414
0.45421282
## 40 0.48097098 0.45325534 0.48011199 0.52158561 0.59737770 0.44459053
0.36073263
## 41 0.46692981 0.45362639 0.47623136 0.49966713 0.59648440 0.45100127
0.36602203
## 42 0.36517450 0.41968842 0.40398962 0.39796446 0.52593870 0.40097743
0.30913876
## 43 0.38133828 0.41146461 0.39020021 0.37301968 0.52370014 0.41456596
0.32944760
## 44 0.42226790 0.39574791 0.41637743 0.45848238 0.53861326 0.39089979
0.31298662
## 45 0.45351547 0.44914789 0.45719694 0.47921281 0.58648711 0.43779247
0.35273493
## 46 0.42064720 0.36313404 0.39957656 0.43895939 0.50835074 0.37957486
0.31178455
## 47 0.36624066 0.41538951 0.40605982 0.38193232 0.53417158 0.41394869
0.33811174
## 48 0.52781743 0.55688689 0.55094657 0.56015593 0.68945246 0.54184168
0.44566047
## 49 0.84147863 1.00057417 0.90655208 0.85477352 0.93666047 0.95564984
0.96091469
## 50 0.32877321 0.22373163 0.25420732 0.35341075 0.33324301 0.23429315
0.24286762
## 51 0.57736445 0.54295531 0.57280756 0.59858479 0.68471826 0.55065711
0.46032703
## 52 0.32892944 0.35922348 0.32794363 0.33025514 0.46717811 0.35369301
0.27967626
## 53 0.29663567 0.22765596 0.24013448 0.33210760 0.33196279 0.22633613
0.22565812
## 54 0.19608466 0.27940378 0.22294929 0.19123304 0.24137007 0.28849272
0.32536494
## 55 0.22010524 0.28624799 0.22626503 0.22242375 0.29833852 0.26001302
0.24636316
## 56 0.45411466 0.50920972 0.50904496 0.47639495 0.62975248 0.50814325
0.40744424
## 57 0.22896705 0.17530555 0.17622438 0.26786276 0.13678648 0.17007711
0.25870101
## 58 0.49577283 0.48580404 0.49805972 0.49458254 0.61488104 0.49562380
0.41794322
## 59 0.35741126 0.39694721 0.37027790 0.37405476 0.46719007 0.37413834
0.32479369
## 60 0.30268648 0.39939610 0.34871694 0.30328263 0.52009592 0.42066639
0.34595049
## 61 0.24174774 0.22351328 0.23895293 0.27075393 0.33132801 0.22559585
```

```
0.18646438
## 62 0.24509690 0.19533418 0.20872611 0.26860894 0.32880230 0.19104054
0.15550333
## 63 0.23625253 0.24675841 0.20775063 0.27549107 0.31051112 0.19539281
0.17268120
## 64 0.89198165 0.90291602 0.91663704 0.91350200 1.05181556 0.91151348
0.79323884
## 65 0.89539707 0.94494685 0.94780751 0.91344009 1.09275820 0.95594235
0.83114475
## 66 0.72750928 0.84822124 0.80890942 0.73076232 0.95152368 0.84097256
0.72484386
## 67 0.64704286 0.65763247 0.67363379 0.65586637 0.81334053 0.67753487
0.55740117
## 68 1.11517862 1.14282894 1.15523790 1.13537022 1.29874627 1.15772848
1.03297848
## 69 1.02104922 1.02276387 1.05581923 1.04835849 1.17953955 1.04106727
0.92263420
## 70 0.86543488 0.92821711 0.92517242 0.87542423 1.07535627 0.94168129
0.81575006
## 71 0.87545644 0.90236042 0.92088960 0.90026738 1.03507707 0.90318528
0.79038725
## 72 0.45130606 0.52362270 0.50804834 0.46272184 0.61802983 0.53135586
0.43122171
## 73 0.72512550 0.75819869 0.76372342 0.76238073 0.91029363 0.76550676
0.63941838
## 74 0.76714171 0.84829595 0.82485760 0.78193462 0.97340398 0.85371650
0.72788412
## 75 0.42552411 0.49224835 0.46514496 0.46006107 0.59422492 0.49547080
0.38842867
## 76 0.54975443 0.58928000 0.58868193 0.55491139 0.73468494 0.61440457
0.48835597
## 77 0.71837528 0.77139135 0.76031936 0.73277726 0.91427690 0.77963787
0.65514261
##            15         16         17         18         19         20
21
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16 0.35096139
```

```
## 17 0.32735910 0.55075893
## 18 0.40170018 0.59634266 0.15159426
## 19 0.43011694 0.61169179 0.15545428 0.14342165
## 20 0.32799582 0.50092327 0.14651174 0.21929171 0.15511834
## 21 0.33076271 0.47707101 0.15449836 0.17405414 0.16399833 0.13905354
## 22 0.37632559 0.56157211 0.13178251 0.17546546 0.09961932 0.13359332
0.16033906
## 23 0.40310399 0.58028993 0.15509951 0.16305374 0.12815287 0.16050358
0.17220003
## 24 0.29463902 0.49183448 0.12434810 0.20871466 0.17104923 0.11644786
0.16223743
## 25 0.24372522 0.35955895 0.22376291 0.27090979 0.26933526 0.17339946
0.17730094
## 26 0.33627015 0.54814544 0.11539182 0.13454366 0.11696102 0.13469699
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## 65 1.22207038 0.87942488 0.56877579 0.53993575 0.62647764 0.61600475
0.61977157
## 66 1.08209405 0.76578529 0.51415222 0.50837271 0.61773023 0.58823558
0.50963965
## 67 0.94645495 0.57896269 0.28017017 0.26979432 0.33158725 0.32996370
0.36918544
## 68 1.41614428 1.07737160 0.76131580 0.73263946 0.79915976 0.80258476
0.83291690
## 69 1.31266782 0.96113378 0.64324730 0.61782994 0.66329369 0.67027980
0.72311554
## 70 1.20021512 0.85879169 0.53284986 0.52905969 0.62699960 0.61709793
0.61077491
## 71 1.17633848 0.83590408 0.54882192 0.52395592 0.55272481 0.57529928
0.59387019
## 72 0.77970669 0.48590772 0.35751266 0.37208446 0.42764700 0.37960119
0.27133525
## 73 1.01274879 0.70355219 0.46332187 0.45426447 0.47319707 0.48611510
0.48734639
## 74 1.07600527 0.79329155 0.54095642 0.55617979 0.62098623 0.61687742
0.56306042
## 75 0.71112710 0.47417017 0.41743834 0.43823276 0.44377791 0.42126242
0.31623286
## 76 0.84439616 0.54472897 0.30011495 0.36933560 0.40481685 0.40855617
0.37514560
## 77 1.03078257 0.71479438 0.46786845 0.43881870 0.50758106 0.49981932
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## 45 0.18861591 0.09135319
## 46 0.18305032 0.11448677 0.16916219
## 47 0.14803346 0.19636655 0.19683651 0.20503246
## 48 0.25006917 0.21348790 0.15508145 0.28489191 0.24952740
## 49 0.95459680 1.04477858 1.04428210 1.05291520 0.90856018 1.00591852
## 50 0.30097021 0.27008527 0.33673629 0.23469071 0.31973505 0.45565092
1.00789366
## 51 0.26437535 0.19317343 0.18001329 0.21071218 0.30316107 0.20527880
1.13896172
## 52 0.09533796 0.18769230 0.20183172 0.19665697 0.15231790 0.27109682
0.91319190
## 53 0.28652269 0.26477096 0.32456426 0.24547656 0.28979408 0.43018237
0.95555712
## 54 0.48234839 0.54512172 0.58443889 0.51189158 0.46108392 0.66444690
0.80722895
## 55 0.35404115 0.41442258 0.42835562 0.38816793 0.34370856 0.48951203
0.78670368
## 56 0.28986881 0.32172765 0.28789846 0.32307791 0.24969189 0.26472905
0.93155305
## 57 0.47637835 0.48605970 0.53441746 0.45174481 0.45746279 0.63477064
0.90182321
## 58 0.29605022 0.31116541 0.28107456 0.26989294 0.28329299 0.30090348
0.99163835
## 59 0.30322164 0.34228653 0.33260772 0.32280133 0.27047486 0.35681943
0.80558469
## 60 0.36961325 0.44946773 0.45248934 0.44462354 0.35756799 0.46850226
0.82913962
## 61 0.28745631 0.29795265 0.32589582 0.25466834 0.25750985 0.41625919
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0.90519504
## 62 0.30823013 0.29686675 0.31930812 0.26784123 0.29726490 0.42532038
0.95906452
## 63 0.32799638 0.33325481 0.34756878 0.32624358 0.32532563 0.42392259
0.87151029
## 64 0.63504513 0.62227003 0.57947749 0.65194697 0.67565293 0.48859166
1.32362295
## 65 0.65790259 0.67487357 0.62651764 0.70773979 0.67475919 0.51871668
1.26246397
## 66 0.56009574 0.63744346 0.58291279 0.67671615 0.56348219 0.47963132
0.99219928
## 67 0.36462931 0.37112334 0.33635733 0.39450495 0.41253020 0.29666001
1.19617282
## 68 0.85739296 0.85527466 0.81245823 0.89056038 0.88870467 0.70942024
1.49035872
## 69 0.75518687 0.72725364 0.69432634 0.75275563 0.77836101 0.61572703
1.46738823
## 70 0.63604235 0.66849821 0.62183128 0.70142795 0.65509350 0.52767147
1.25449244
## 71 0.64405920 0.62212266 0.58407888 0.65753563 0.66799156 0.53137929
1.35819981
## 72 0.33452445 0.41789856 0.40156901 0.40431976 0.33058892 0.36587082
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## 73 0.52688379 0.51796497 0.48561304 0.56771810 0.56523895 0.39750496
1.20417089
## 74 0.59414948 0.64881668 0.61102396 0.68723058 0.63687278 0.51363447
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## 75 0.36641430 0.42975627 0.42544931 0.43912418 0.39802160 0.38294334
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## 76 0.36518070 0.41782962 0.40346978 0.43323373 0.42904666 0.38509021
1.12683955
## 77 0.50733077 0.54154239 0.49560461 0.57512882 0.54406253 0.39614316
1.12923717
##              50          51          52          53          54          55
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## 54 0.37934796 0.69148257 0.43064058 0.35495260
## 55 0.33215656 0.53127841 0.29779404 0.29551225 0.26123333
## 56 0.48852724 0.32542821 0.31963336 0.46365561 0.56801854 0.38997577
## 57 0.28095353 0.63805151 0.41357493 0.26543583 0.18038635 0.25518700
0.57111943
## 58 0.43635062 0.30852510 0.31181080 0.42760621 0.58222222 0.38823303
0.20310361
## 59 0.37336877 0.41985140 0.26464028 0.33778937 0.43132462 0.19978242
0.26027641
## 60 0.44574015 0.55763776 0.33066305 0.40994257 0.38945502 0.33486595
0.39984255
## 61 0.24330163 0.42243872 0.24626235 0.22406011 0.31343541 0.17103187
0.32266748
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## 62 0.23304922 0.43730760 0.25849069 0.22524686 0.34441656 0.21692049
0.36879133
## 63 0.27779482 0.46666175 0.26538613 0.24929169 0.34427653 0.14802796
0.37397737
## 64 0.85696418 0.48705469 0.69212562 0.85015933 1.03549628 0.85555469
0.52651198
## 65 0.90988948 0.56119948 0.71553834 0.89191591 1.03318634 0.87110253
0.51964868
## 66 0.83222198 0.59647066 0.60261018 0.79845903 0.85571869 0.70481602
0.42365233
## 67 0.59773334 0.26231808 0.43260049 0.59285467 0.78042468 0.63576225
0.33998532
## 68 1.09555981 0.71854607 0.91803744 1.08423942 1.25716838 1.09698102
0.75349298
## 69 0.96794459 0.57317291 0.82084671 0.96311027 1.15516875 0.99825060
0.64856828
## 70 0.89806270 0.57427847 0.69935330 0.88222001 1.00286122 0.86191200
0.51756183
## 71 0.86406099 0.50880490 0.71466846 0.86258853 1.02163600 0.86842411
0.52879555
## 72 0.52540872 0.41483544 0.35458937 0.49270913 0.53841448 0.36519797
0.18241403
## 73 0.73614427 0.43995417 0.56904021 0.71879160 0.88293612 0.73029473
0.44733507
## 74 0.84275539 0.58724393 0.64096663 0.81966991 0.91019718 0.76666816
0.49820595
## 75 0.51586921 0.45190135 0.36232057 0.48028377 0.54302998 0.38126265
0.30397752
## 76 0.58402125 0.38797072 0.42405515 0.57757601 0.68663352 0.57535068
0.35072098
## 77 0.74984781 0.46622492 0.55221306 0.73003926 0.86174384 0.69597347
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##            57         58         59         60         61         62
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## 62 0.27438603 0.32271616 0.25157875 0.34029872 0.11211534
## 63 0.27887949 0.35247166 0.19942949 0.35282898 0.15113473 0.13435986
## 64 1.02068429 0.57295294 0.72200254 0.77708001 0.78451686 0.79104969
0.79959105
## 65 1.04781057 0.61088113 0.74232238 0.75236683 0.81300309 0.83075423
0.83894756
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## 66 0.91006840 0.56640082 0.60862393 0.59409767 0.70121080 0.72782078
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## 67 0.77180740 0.39413620 0.53575523 0.56061093 0.54728689 0.55524732
0.58943758
## 68 1.25967655 0.82185707 0.96799678 0.97482573 1.02958733 1.04042138
1.05308737
## 69 1.13841512 0.71352381 0.87006127 0.92741750 0.90760278 0.92705873
0.95039892
## 70 1.03152585 0.61965772 0.74915691 0.72276276 0.80330444 0.81785257
0.83455022
## 71 1.01062766 0.62554859 0.75919848 0.83707329 0.78273622 0.79675132
0.81522752
## 72 0.56824710 0.29794580 0.27896029 0.37861272 0.35787345 0.42283476
0.39901737
## 73 0.87780933 0.53852478 0.63203079 0.61939742 0.67108107 0.67331494
0.67580251
## 74 0.94683356 0.61322835 0.68218967 0.62955634 0.74589384 0.75883149
0.74667197
## 75 0.56211201 0.38547147 0.33406579 0.33700938 0.39505316 0.42852402
0.38426559
## 76 0.70750325 0.43554066 0.52495940 0.46433563 0.51306698 0.51820992
0.54602994
## 77 0.87734459 0.47792634 0.58337361 0.56425595 0.65446542 0.66045634
0.66000467
##            64          65          66          67          68          69
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## 65 0.20853293
## 66 0.47492488 0.34291327
## 67 0.31902659 0.35223100 0.43385353
## 68 0.28672324 0.25454081 0.57243708 0.51881224
## 69 0.24886632 0.28996951 0.59734671 0.41310573 0.24541725
## 70 0.28348771 0.12582386 0.31018747 0.33874455 0.31500068 0.35145476
## 71 0.29671118 0.33811563 0.50326773 0.35066019 0.42839451 0.29750484
0.33646266
## 72 0.57402872 0.55203470 0.41761438 0.40717544 0.78484705 0.70035834
0.55492942
## 73 0.24874454 0.26910729 0.39402860 0.25838714 0.41561509 0.38812906
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0.29120398
## 74 0.35022140 0.26722448 0.25770215 0.37948027 0.44395661 0.49538179
0.24636343
## 75 0.57550288 0.57601043 0.45768920 0.43427412 0.78786797 0.73167244
0.58330856
## 76 0.42346683 0.42592744 0.41198240 0.20874329 0.60957651 0.54379510
0.38053077
## 77 0.25879623 0.22454338 0.28786224 0.27265030 0.43197448 0.44426769
0.23642457
##            71         72         73         74         75         76
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## 72 0.61134885
## 73 0.36651712 0.47510721
## 74 0.44771163 0.47613184 0.23647538
## 75 0.65689310 0.19989080 0.42362057 0.43730605
## 76 0.43926595 0.36430250 0.28322504 0.32308339 0.34679712
## 77 0.41282275 0.41402409 0.17701301 0.17493639 0.39182244 0.28081725
```
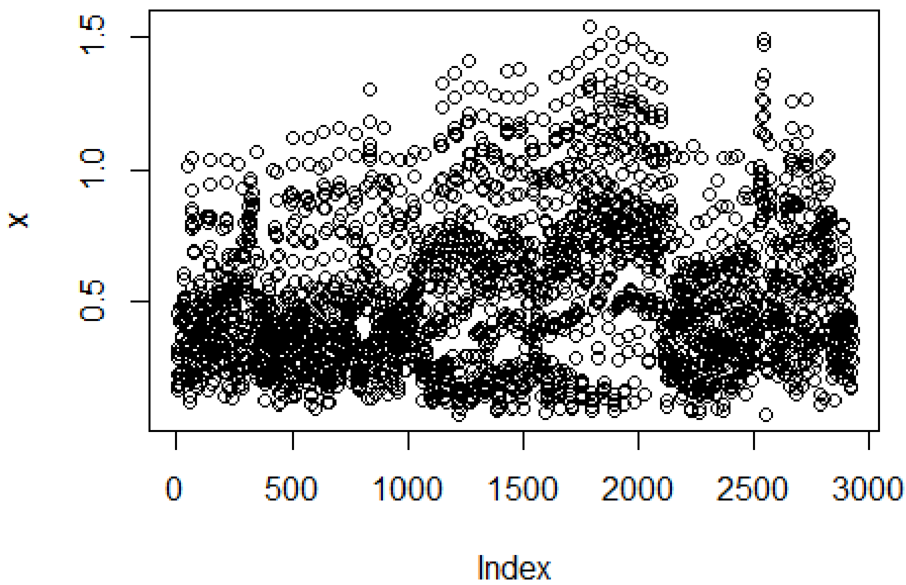

```r
plot(x)
```




```
#Distance matrix with original data (Without scaling)

dist.mat <- dist(Canine_Data[2:10])
dist.mat

##             1           2           3           4           5           6
7
## 2  16.1953697
## 3   8.4486685 16.5990964
## 4   8.2740558  9.2320095 11.3727745
## 5  28.3190748 14.7566934 29.6251582 20.4799902
## 6   5.6435804 13.2385800  6.9649121  5.7105166 25.5479941
## 7   4.9091751 12.1420756  7.3389373  6.3150614 25.5035292  4.5705580
## 8   7.2532751 12.7381317  5.9506302  7.8262379 26.5190498  4.3749286
3.9812058
## 9   4.5144213 17.2130764  7.2291078  9.9829855 30.2504545  5.4817880
5.9413803
## 10  5.0487622 16.0168661  6.0852280  9.6628153 29.5645057  5.2687759
4.5923850
## 11 10.0224747 23.0560187  7.9315824 16.4720976 36.3546421 11.2285351
11.6245430
## 12 12.3567795 26.1568347 11.8789730 19.4650970 39.6598033 14.6301059
14.4903416
## 13  4.9132474 13.9882093  7.6118329  7.6000000 27.3895966  4.6010868
3.4928498
## 14  7.4417740  9.7514102  8.8701747  3.5185224 22.6099536  3.7881394
4.2825226
```

```
## 15 10.5441927  8.4669947 11.6086175  4.6540305 20.8281060  6.3804389
7.4578817
## 16  5.1205468 12.8339394 10.4278473  3.9648455 23.7611027  4.8836462
5.6356011
## 17  8.9112289 18.5461586  7.0576200 13.2872119 32.4709101  8.4581322
8.1945104
## 18 18.3185698 31.1412909 15.6815178 24.9200722 44.7600268 19.5754949
19.9682248
## 19 15.8208723 28.8955014 14.4672043 22.5353056 42.5735834 17.3496398
17.5442298
## 20  9.3733665 22.6033183  9.3155784 15.9662143 36.0353993 10.9110036
11.0526015
## 21 11.2191800 24.4225306 10.1098961 17.9134028 37.9465413 12.7334206
12.8891427
## 22 14.7448296 27.7189466 13.7829605 21.2671108 41.3702792 16.1300961
16.4854481
## 23 13.0403221 25.2812183 11.1843641 19.3693056 39.2038263 14.4006944
14.1537981
## 24  9.4741754 21.6520207  9.4899947 15.2413910 35.2535105 10.3193992
10.6066017
## 25 10.3281170 23.8407215  9.6234090 16.7991071 37.0170231 11.6661905
12.4551194
## 26 13.5225737 26.3334388 12.2237474 19.9022612 39.9781190 14.7353317
15.1148933
## 27 15.3195953 28.4193596 13.6890467 22.0374681 42.0844389 16.8404275
17.0578428
## 28 13.8629001 27.7220129 13.9133030 20.9380037 41.2163802 15.9590100
16.0810447
## 29 19.4283298 31.5469491 17.6312223 25.6963032 45.5017582 20.6177108
20.7966343
## 30 17.8308721 30.7351590 16.7008982 24.4830554 44.5453701 19.4069575
19.5780489
## 31 16.3993902 29.0666476 15.4447402 22.7982455 42.7760447 17.6343415
18.0055547
## 32 19.9032661 33.6313842 19.2213423 26.9755445 47.2303928 21.9401459
22.1729565
## 33 18.3885834 31.9882791 17.7690743 25.4899980 45.7065641 20.5370397
20.4846284
## 34 18.5010810 32.4154284 17.5467946 25.7011673 45.9055552 20.5684224
20.7987980
## 35 15.4706173 27.5733567 13.5018517 21.6919340 41.5033734 16.5653252
16.6547291
## 36 14.6266879 27.1685480 13.0873985 20.8868380 40.8530293 15.6904430
16.1263759
## 37  6.3568860 15.7511904  9.4482803  9.0027773 28.6513525  6.5635356
6.4660653
## 38 14.1545046  8.3510478 16.4124952  6.4536811 16.0480528 11.2312065
12.0337027
## 39 16.6439178  8.3624159 19.5923454  9.3091353 13.1609270 14.7665162
14.5182644
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## 40 19.6870516  9.4957885 22.7499451 12.1876987 10.8871484 17.6881316
17.4201033
## 41 14.2797059  8.1767964 17.3092461  7.0887234 15.7689568 12.3911259
12.2821008
## 42 14.8101317  5.2962251 16.4024388  7.3443856 14.5989726 12.3527325
11.8177832
## 43  9.7642204  9.5629493 12.7687118  4.3058100 20.3147729  8.1160335
7.7987178
## 44 15.7260930  8.1080207 19.0633156  8.5164547 14.8653961 13.8744369
13.5236829
## 45 14.2551745  8.0857900 17.2867001  7.0915443 15.8221364 12.3174673
12.1954910
## 46  9.3536089 10.7861022 14.2776048  4.5265881 20.6489709  8.9140339
8.4693565
## 47  9.1219515  9.2811637 11.8528478  4.1484937 21.1362248  7.5193085
6.8212902
## 48 23.4296820 10.5517771 25.1827322 15.7305435  7.4793048 20.9652093
20.6254697
## 49 27.3704220 17.6553108 24.7511616 24.0765446 26.0074989 25.8094944
23.0139088
## 50  6.2593929 16.8869772 11.3384302  9.7948966 29.2904421  8.1651699
7.5405570
## 51 16.7349933 10.2562176 19.8479218  9.6104110 13.9495520 14.9026843
15.1419946
## 52  7.8625696 10.9366357 10.3846040  4.8600412 23.0453900  6.3364028
5.8702640
## 53  7.0149840 16.9487463 10.2190998 10.2844543 29.7196904  8.0423877
7.6922038
## 54 13.5295972 26.3677834 11.6709040 20.1843999 40.0841615 15.1861779
15.0708328
## 55 10.0084964 22.4543982  7.0064256 16.2637634 35.6050558 11.6335721
11.4083303
## 56 15.3521985  6.8716810 16.2138829  8.5445889 13.9706836 12.9514478
12.6526677
## 57 13.4305622 26.9553334 12.8163957 20.3312567 40.4760423 15.5695215
15.5473470
## 58  9.1049437 11.3969294 12.4338248  6.4171645 20.8597699  9.3096724
8.2571181
## 59  6.9433421 13.1461021  6.9649121  8.2103593 25.6082018  7.3348483
5.2924474
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##            64         65         66         67         68         69
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## 2
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## 62
## 63
## 64
## 65  4.8352870
## 66 19.2803008 15.4754645
## 67 23.3051496 21.0030950 11.2578861
## 68 11.8448301 14.1513250 29.4042514 34.4149677
## 69  4.5409250  6.0679486 19.8517002 22.9458057 11.9733036
## 70  5.6329388  2.8653098 15.3218798 20.4289011 14.9869944  7.0604532
## 71  4.3520110  5.9481089 18.0036107 20.8189817 14.6928554  5.2191953
5.2201533
## 72 37.8427007 34.8518292 20.3798921 16.3370744 48.9102239 37.9959208
34.4607023
## 73  7.1147734  4.4384682 14.7224319 19.5777935 15.9705980  7.4793048
4.8856934
## 74  8.2945765  4.7853944 14.6112970 21.6242919 15.7473807 10.0189820
4.3139309
## 75 28.3197811 25.1282709 10.6122571  9.6093704 39.1557148 28.7236836
24.7422715
## 76 21.2181526 18.5986559  9.0675245  5.7113921 32.1498056 21.4077089
17.4911406
## 77 10.3812331  7.0604532  9.2249661 14.8579945 21.0387737 11.5494589
6.7660919
##            71         72         73         74         75         76
## 2
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## 58
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## 69
## 70
## 71
## 72 35.7884059
## 73  7.0922493 33.7699571
## 74  8.8848185 34.5240496  5.6973678
## 75 26.5120727 10.5933942 23.7118114 24.4542430
## 76 18.6346452 18.3766156 17.2953751 18.2682785 10.0518655
## 77  9.4482803 28.1606108  6.5977269  7.2890329 18.2991803 12.1235308

plot(dist.mat)
```
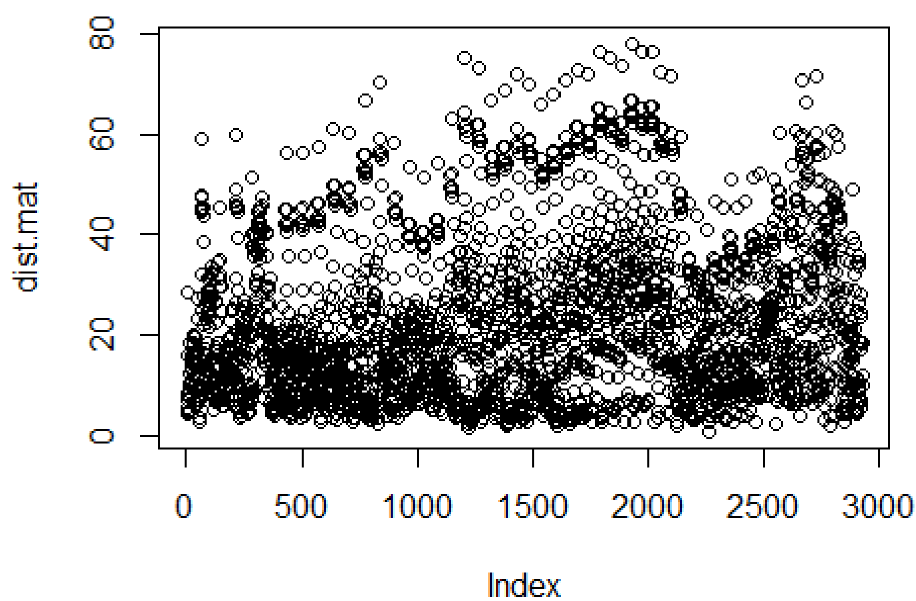




```
#Both show similar distributions of distances
#=============Question 1 end ======================
```

#@@@@@@@@@@@ Question 2 - PCA @@@@@@@@@@@@@@@

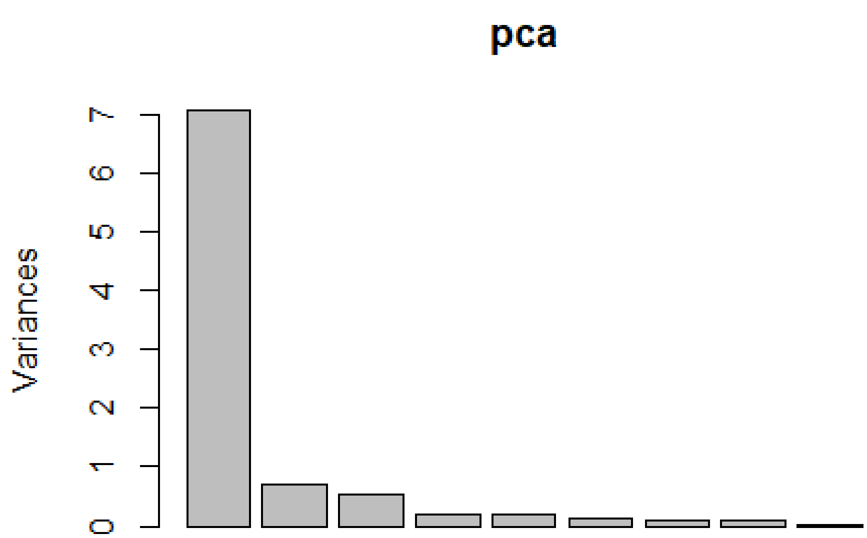
#3. Use principal components analysis to investigate the relationships between the species on the basis of these variables

```
#PC generation
pca <- prcomp(Canine_Data[2:10],scale=TRUE)
pca

## Standard deviations (1, .., p=9):
## [1] 2.6555963 0.8391652 0.7365758 0.4390554 0.4241988 0.3627806 0.3031519
## [8] 0.2652189 0.1857418
##
## Rotation (n x k) = (9 x 9):
##          PC1         PC2         PC3         PC4         PC5         PC6
## X1 0.3636408 -0.11451510  0.08210471 -0.30326354  0.24950692 -0.07899550
## X2 0.3424554  0.31490128 -0.19979188  0.33605928  0.01517931  0.49451257
## X3 0.2665621  0.32018675  0.87894338  0.04161625 -0.18169514 -0.04568559
## X4 0.3265349  0.44638084 -0.16540131  0.26534253  0.54545187 -0.21526217
## X5 0.3539586 -0.14160855 -0.03861441 -0.26352534 -0.33012092  0.43239890
## X6 0.3459444  0.06792334 -0.26250857  0.05378069 -0.51974026 -0.68294862
## X7 0.2859405 -0.68736531  0.13651981  0.64014932  0.05443187 -0.01170970
## X8 0.3470802 -0.28877388  0.03666665 -0.47256682  0.40753260 -0.10978603
## X9 0.3544268  0.07362113 -0.25111557 -0.13231892 -0.24254817  0.18765482
##            PC7         PC8          PC9
## X1  0.05543869  0.16005914  0.811637429
## X2  0.13657790  0.60411640 -0.048224206
## X3  0.08257828 -0.03476461 -0.094992855
## X4 -0.30849700 -0.39244126 -0.057608736
## X5 -0.67024916 -0.19081879 -0.046144083
## X6 -0.08734948  0.23986950 -0.046794522
## X7  0.03463451 -0.11415807  0.002559605
## X8  0.12889717  0.23397418 -0.567438948
## X9  0.63372357 -0.54081471 -0.016253801
```

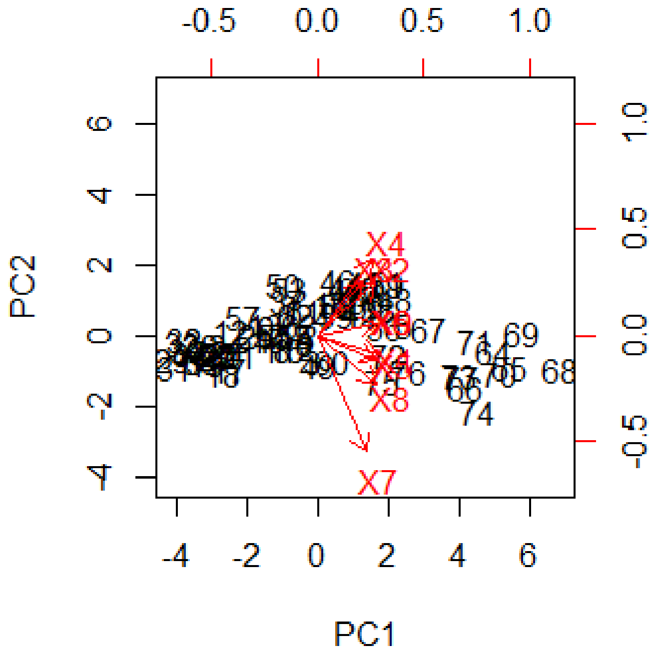
#Total 9 principal components are generated
#PC1 has all the variables positively contributing to it
#PC2 -ve contribution of of x7 which is length of first to third molar inclusive
#PC3 has positive contribution of X3 i.e.breadth of articular condyle

```
summary(pca)

## Importance of components:
##                            PC1     PC2     PC3     PC4     PC5     PC6
PC7
## Standard deviation     2.6556 0.83917 0.73658 0.43906 0.42420 0.36278
0.30315
```

```
## Proportion of Variance 0.7836 0.07824 0.06028 0.02142 0.01999 0.01462
0.01021
## Cumulative Proportion  0.7836 0.86182 0.92210 0.94352 0.96352 0.97814
0.98835
##                            PC8     PC9
## Standard deviation     0.26522 0.18574
## Proportion of Variance 0.00782 0.00383
## Cumulative Proportion  0.99617 1.00000

#Reading from the summary of pca table we can see that upto pc3 about 92% of
variance is captured.
plot(pca)
```

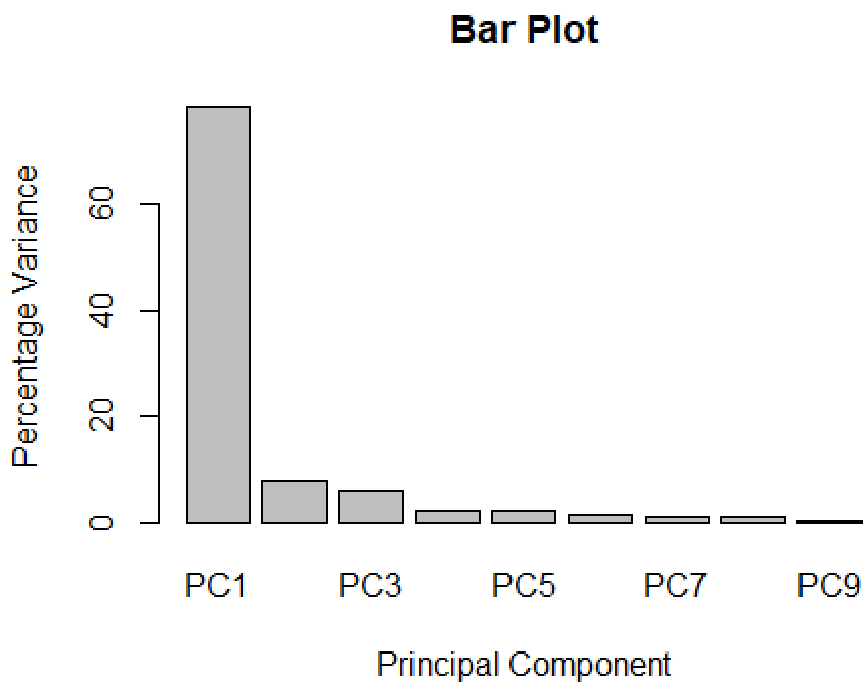



```
#Above plot shows that PC1 explains majority of variance which is 78%
biplot(pca,scale=0)
```

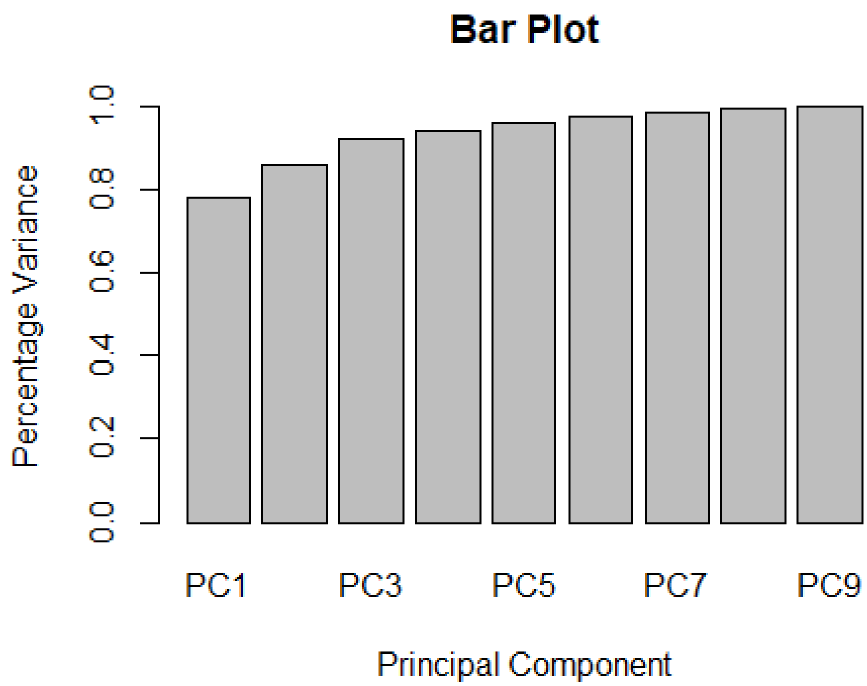



```
#$x gives the new dataset #u need to rename these columns
head(pca$x)

##                PC1        PC2        PC3         PC4          PC5
PC6
## [1,] -0.68594144  0.7845059  0.3006808  0.87047017  0.099293422 -
0.13703394
## [2,] -0.24567287 -0.2998432 -0.3386984 -0.38688425  0.904531523 -
0.40703561
## [3,] -0.08646546 -0.7099032 -0.7324535  0.36215960  0.007597324
0.34684409
## [4,]  0.16794155  0.5263915  0.4238685  0.25556873  0.116376021
0.15817439
## [5,]  2.46605602  0.3055451  0.2215356  0.12938866  0.883927889
0.13952874
## [6,] -0.31165997 -0.1929752  0.4205179 -0.01594082 -0.279041559
0.03359648
##                PC7         PC8         PC9
## [1,] -0.12574305 -0.08103187  0.27299561
## [2,]  0.21201705  0.24663975  0.14167354
## [3,] -0.04042272 -0.04720248 -0.36986352
## [4,]  0.09155686  0.34942670  0.02832178
## [5,]  0.34760207  0.63208273 -0.03260669
## [6,]  0.38738491 -0.23534059 -0.10684702

#From Summary of Pincipal components,
#Proportion of Variance, PC1, PC2 and PC3 explain 78%,7% and 6% of variance
```

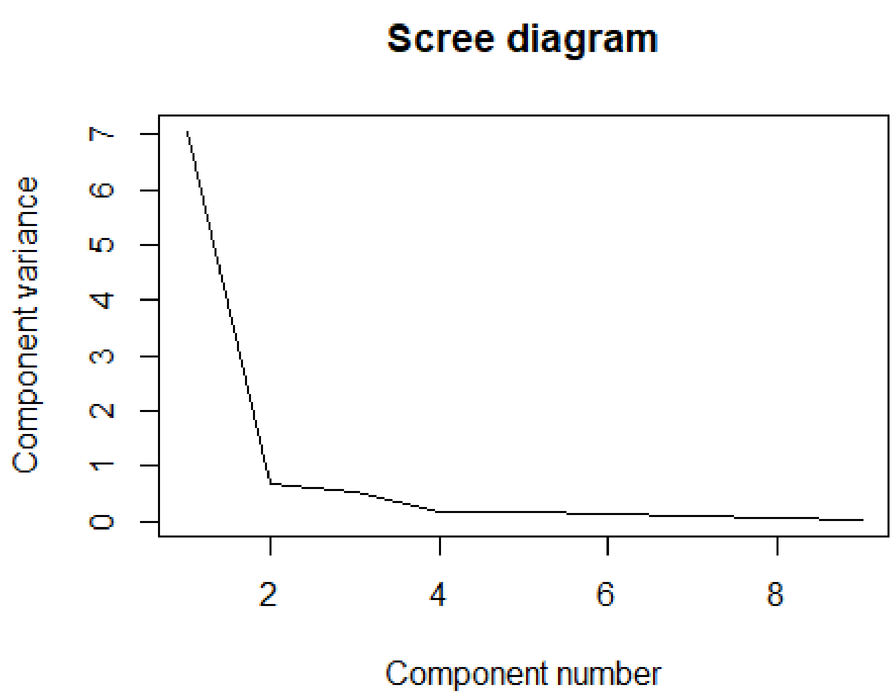
```
respectively.
#'Cumulative Proportion' field, 92% of Cummulative variance is explained by
PC1, PC2, PC3
#So I will include PC1,PC2 and PC3 in my data input
#So My input variables will be reduced from 11 to 3

(eigen_dog <- pca$sdev^2) #singular values (square roots of eigenvalues)
stored in sparrow_pca$sdev

## [1] 7.05219159 0.70419829 0.54254392 0.19276967 0.17994462 0.13160975
0.09190108
## [8] 0.07034106 0.03450002

names(eigen_dog) <- paste("PC",1:9,sep="") #Naming PC components
eigen_dog

##        PC1        PC2        PC3        PC4        PC5        PC6
PC7
## 7.05219159 0.70419829 0.54254392 0.19276967 0.17994462 0.13160975
0.09190108
##        PC8        PC9
## 0.07034106 0.03450002

sumlambdas <- sum(eigen_dog)
sumlambdas #sum of genvalues is total var of ur dataset

## [1] 9

propvar <- eigen_dog/sumlambdas
#Printing Proper variance per PC
propvar

##         PC1         PC2         PC3         PC4         PC5         PC6
## 0.783576843 0.078244255 0.060282658 0.021418853 0.019993847 0.014623306
##         PC7         PC8         PC9
## 0.010211231 0.007815673 0.003833335

#Percentage of total variance
percentvar <- (eigen_dog/sumlambdas) *100
percentvar

##        PC1        PC2        PC3        PC4        PC5        PC6
PC7
## 78.3576843  7.8244255  6.0282658  2.1418853  1.9993847  1.4623306
1.0211231
##        PC8        PC9
##  0.7815673  0.3833335

#Bar plot of Percentage variance
barplot(percentvar, main = "Bar Plot", xlab = "Principal Component", ylab =
"Percentage Variance")
```



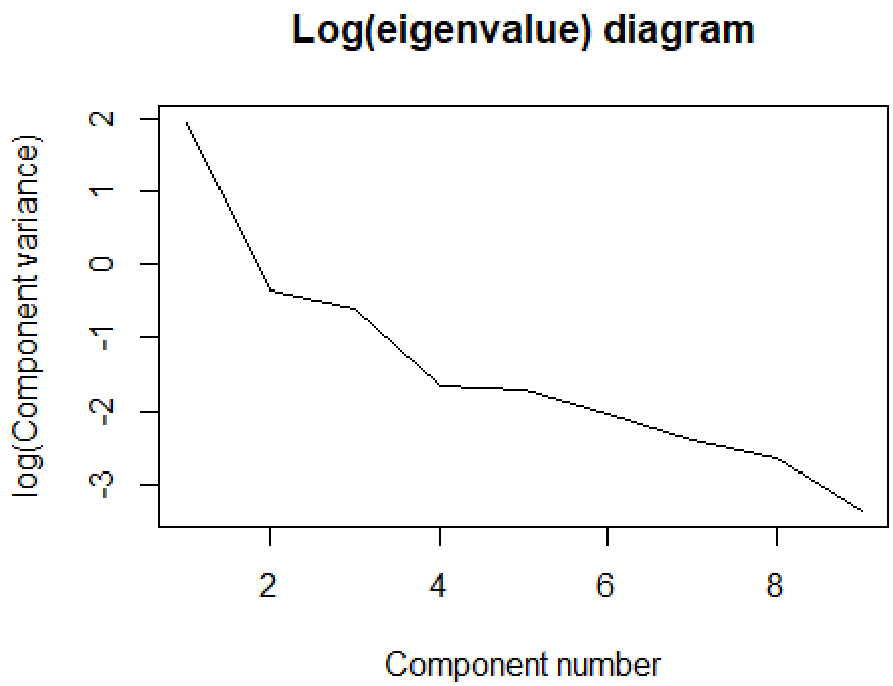

```
#As per above graph, PC1 holds 78% of ur total var, PC2 14% and so on
#Cummulative variance
cumvar_dog <- cumsum(propvar)
cumvar_dog

##       PC1       PC2       PC3       PC4       PC5       PC6       PC7
PC8
## 0.7835768 0.8618211 0.9221038 0.9435226 0.9635165 0.9781398 0.9883510
0.9961667
##       PC9
## 1.0000000

#Bar plot of Cummulative Percentage variance
barplot(cumvar_dog, main = "Bar Plot", xlab = "Principal Component", ylab =
"Percentage Variance")
```




```
#Plotting Scree diagram
plot(eigen_dog, xlab = "Component number", ylab = "Component variance", type
= "l", main = "Scree diagram")
```



```
#Plotting log scree diagram
plot(log(eigen_dog), xlab = "Component number",ylab = "log(Component
variance)", type="l",main = "Log(eigenvalue) diagram")
```




```
# Scree diagram suggests to use 4 PCs but I beleive 92% variance by PC1,2,3
is enough for question at hand.

#Printing our new Dataset after PCA
#Binding with categorical columns from the original dataset
pca.cty <- cbind(data.frame(CanineGroup,Gender),pca$x)
head(pca.cty)

##   CanineGroup Gender         PC1        PC2        PC3         PC4
PC5
## 1   ModernDog   Male -0.68594144  0.7845059  0.3006808  0.87047017
0.099293422
## 2   ModernDog   Male -0.24567287 -0.2998432 -0.3386984 -0.38688425
0.904531523
## 3   ModernDog   Male -0.08646546 -0.7099032 -0.7324535  0.36215960
0.007597324
## 4   ModernDog   Male  0.16794155  0.5263915  0.4238685  0.25556873
0.116376021
## 5   ModernDog   Male  2.46605602  0.3055451  0.2215356  0.12938866
0.883927889
## 6   ModernDog   Male -0.31165997 -0.1929752  0.4205179 -0.01594082 -
0.279041559
##            PC6          PC7          PC8          PC9
```

```
## 1 -0.13703394 -0.12574305 -0.08103187  0.27299561
## 2 -0.40703561  0.21201705  0.24663975  0.14167354
## 3  0.34684409 -0.04042272 -0.04720248 -0.36986352
## 4  0.15817439  0.09155686  0.34942670  0.02832178
## 5  0.13952874  0.34760207  0.63208273 -0.03260669
## 6  0.03359648  0.38738491 -0.23534059 -0.10684702
```

```
#Renaming 1st 3 Principal components as we have decided to select 1st 3
components
names(pca.cty)[names(pca.cty) == 'PC1'] <- 'Mix_all'
names(pca.cty)[names(pca.cty) == 'PC2'] <- 'Neg_len_1_3molar'
names(pca.cty)[names(pca.cty) == 'PC3'] <- 'Postv_articular_condyle'
#This is our new dataset that can be passed to models
head(pca.cty)
```

```
##   CanineGroup Gender     Mix_all Neg_len_1_3molar Postv_articular_condyle
## 1   ModernDog   Male -0.68594144        0.7845059               0.3006808
## 2   ModernDog   Male -0.24567287       -0.2998432              -0.3386984
## 3   ModernDog   Male -0.08646546       -0.7099032              -0.7324535
## 4   ModernDog   Male  0.16794155        0.5263915               0.4238685
## 5   ModernDog   Male  2.46605602        0.3055451               0.2215356
## 6   ModernDog   Male -0.31165997       -0.1929752               0.4205179
##           PC4          PC5         PC6         PC7         PC8         PC9
## 1  0.87047017  0.099293422 -0.13703394 -0.12574305 -0.08103187  0.27299561
## 2 -0.38688425  0.904531523 -0.40703561  0.21201705  0.24663975  0.14167354
## 3  0.36215960  0.007597324  0.34684409 -0.04042272 -0.04720248 -0.36986352
## 4  0.25556873  0.116376021  0.15817439  0.09155686  0.34942670  0.02832178
## 5  0.12938866  0.883927889  0.13952874  0.34760207  0.63208273 -0.03260669
## 6 -0.01594082 -0.279041559  0.03359648  0.38738491 -0.23534059 -0.10684702
```

```
#PCA Conclusion:
#Principal Component analysis is a statistical technique
that uses Orthogonal Transformation.
#It helps in reducing the number of input variables to be
passed to a model.
#The principal components are Non-correlated with each
other.
#After performing PCA on this dataset, it can be concluded
that:
#Contents of Principal Components:
#PC1 has all factors contributing to it
#PC2 is dominated by Negative effect of x7 which is length
of first to third molar inclusive
#PC3 is dominated by positive effect of breadth of articular
condyle
#PC components renamed accordingly.
```

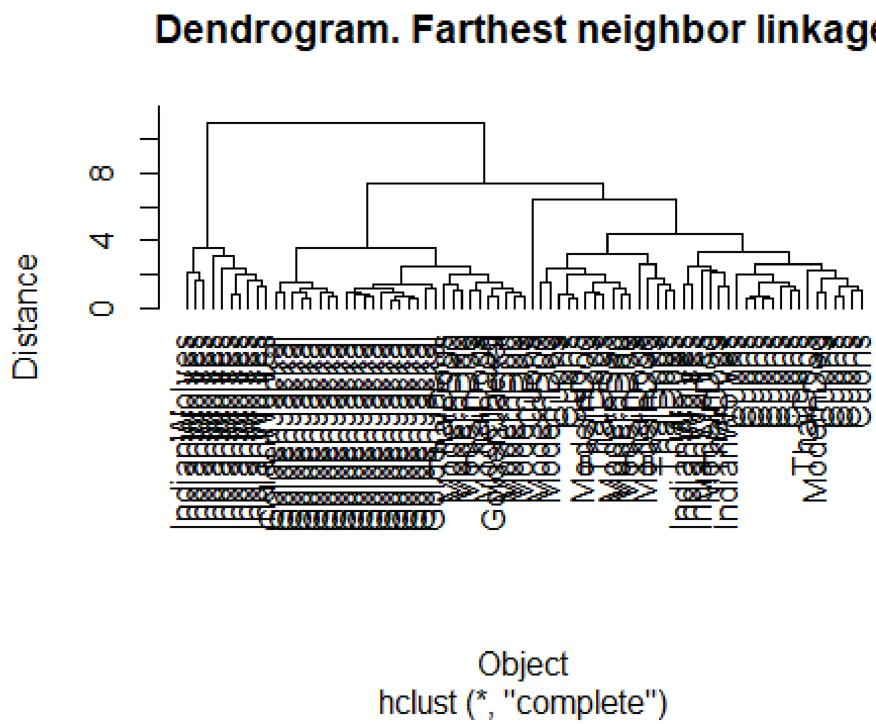
```
#From Summary of Principal components,
#Proportion of Variance, PC1 and PC2 explain 78% , 7% and 6%
of variance respectively.
#'Cumulative Proportion' field, 92% of Cumulative variance
is explained by PC1, PC2, PC3
#So I will include PC1 and PC2 , PC3 in my data input to
models.
#So My input variables will be reduced from 11 to 3
#As there is high correlation between measurements of
different canine groups, they must be
#related to each other which can further be conformed with
the help of cluster analysis.

#==============Question 3 end ======================
```

Including Plots

You can also embed plots, for example:

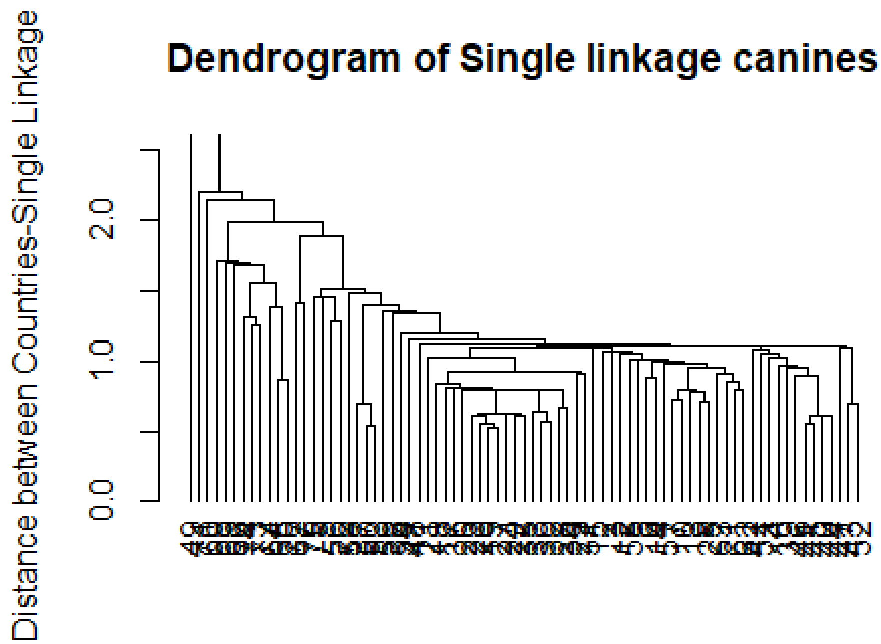
```
#@@@@@@@@@@  Question 4 - Cluster Analysis  @@@@@@@@@@@

#4. Carry out cluster analysis to study relation between
different specifies.
#a. Who is Indian Wolf related to?

#DG_Clust_1 <-
read.csv("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/lastyearmidterm/Butterf
ly_colonies_Updated.csv",row.names=1, fill = TRUE)
#DG_Clust_1 <-
read_excel("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinal_old/Final_Da
ta.xlsx",row.names=1, fill = TRUE)

head(Canine_Data)

##   CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 1   ModernDog 123 10.1 23 23 19 7.8 32 33 5.6   Male
## 2   ModernDog 137  9.6 19 22 19 7.8 32 40 5.8   Male
## 3   ModernDog 121 10.2 18 21 21 7.9 35 38 6.2   Male
## 4   ModernDog 130 10.7 24 22 20 7.9 32 37 5.9   Male
## 5   ModernDog 149 12.0 25 25 21 8.4 35 43 6.6   Male
## 6   ModernDog 125  9.5 23 20 20 7.8 33 37 6.3   Male

######## Hierarchical Clustering ##########
#Scaling
```

```
matstd.dog <- scale(Canine_Data[,2:10])
head(matstd.dog)

##                X1          X2         X3         X4         X5          X6
## [1,] -0.34133663  0.09904431  0.3235696  0.4459670 -0.5997769 -0.19537598
## [2,]  0.45857835 -0.25733007 -0.6255679  0.1499372 -0.5997769 -0.19537598
## [3,] -0.45561020  0.17031919 -0.8628523 -0.1460926  0.2034026 -0.09768799
## [4,]  0.05862086  0.52669357  0.5608540  0.1499372 -0.1981871 -0.09768799
## [5,]  1.14421975  1.45326697  0.7981384  1.0380266  0.2034026  0.39075196
## [6,] -0.22706306 -0.32860495  0.3235696 -0.4421225 -0.1981871 -0.19537598
##               X7          X8         X9
## [1,] -0.1244973 -0.99951775 -0.4661440
## [2,] -0.1244973  0.58968599 -0.2700069
## [3,]  0.5944746  0.13562778  0.1222673
## [4,] -0.1244973 -0.09140133 -0.1719384
## [5,]  0.5944746  1.27077331  0.5145414
## [6,]  0.1151600 -0.09140133  0.2203358

#Complete linkage method
# Creating a (Euclidean) distance matrix of the standardized data
dist.PT_Clust_1 <- dist(matstd.dog, method="euclidean")

#Default - Complete Linkage
clusPT.fn <- hclust(dist.PT_Clust_1)
plot(clusPT.fn,hang=-1,xlab="Object",ylab="Distance",
     main="Dendrogram. Farthest neighbor 
linkage",labels=Canine_Data$CanineGroup)#can add for labels instead of row
numbers
```

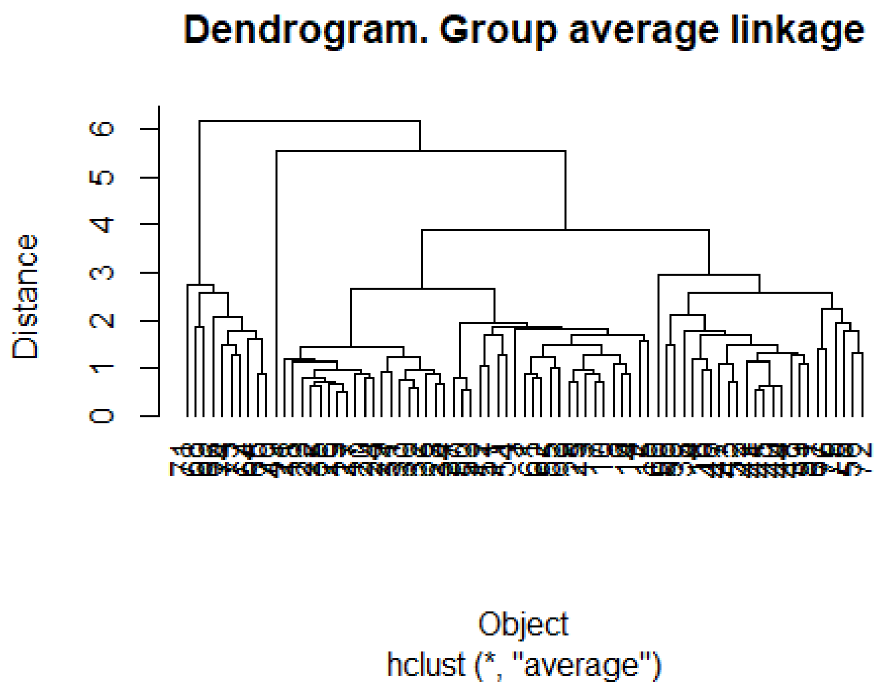


##As per this dendogram , if you cut around level 4, Indian Wolves are related to Modern Dog and Thai dog as they are clustered in same group.
#Dendogram shows that canines have roughly 4 main group which are subdivided into smaller groups.

```
#Single linkage
# Invoking hclust command (cluster analysis by single linkage method)
clusPT.nn <- hclust(dist.PT_Clust_1, method = "single")
# Plotting vertical dendrogram
# create extra margin room in the dendrogram, on the bottom
par(mar=c(6, 4, 4, 2) + 0.1)
plot(as.dendrogram(clusPT.nn),ylab="Distance between Countries-Single
Linkage",ylim=c(0,2.5),main="Dendrogram of Single linkage canines")
```




```
#Average
clusPT.avl <- hclust(dist.PT_Clust_1,method="average")
plot(clusPT.avl,hang=-1,xlab="Object",ylab="Distance",
     main="Dendrogram. Group average linkage")
```

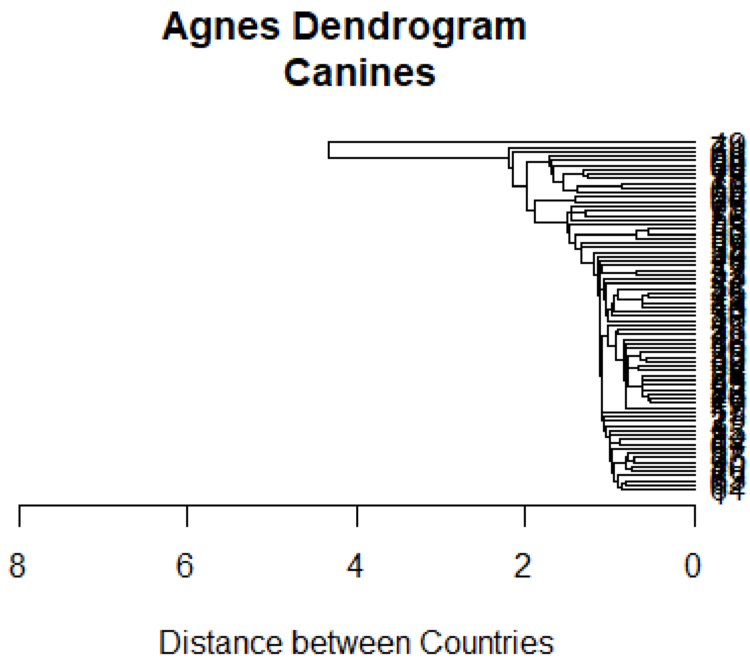



```
#Dendogrm shows that canines have roughly 4 main group which are subdivided
into smalled grps.

#Lazy option --> agnes is 1 liner command for clustering
# We will use agnes function as it allows us to select option for data
standardization, the distance measure and clustering algorithm in one single
function
(agn.PT <- agnes(dist.PT_Clust_1, metric="euclidean", stand=TRUE, method =
"single"))

## Call:     agnes(x = dist.PT_Clust_1, metric = "euclidean", stand = TRUE,
method = "single")
## Agglomerative coefficient:  0.7649879
## Order of objects:
##  [1]  1 61 62 63  7 10  9 25 13 57  6 14  8 55 12  3  2 15 17 19 27 26 23
22 35
## [26] 24 28 34 30 32 33 20 36 18 29 31 21  4 16 39 40 44 41 45 46 51 42 43
52 47
## [51] 11 48 54 38 59 37 50 53 58  5 56 72 75 67 76 64 65 70 73 77 74 66 69
68 60
## [76] 71 49
## Height (summary):
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.5181  0.7897  1.0007  1.0926  1.2928  4.3361
##
## Available components:
## [1] "order"  "height" "ac"     "merge"  "diss"   "call"   "method"
```

```
#  Description of cluster merging
agn.PT$merge
```

```
##       [,1] [,2]
##  [1,]  -19  -27
##  [2,]  -50  -53
##  [3,]  -41  -45
##  [4,]    1  -26
##  [5,]  -30  -32
##  [6,]  -40  -44
##  [7,]  -22  -35
##  [8,]    6    3
##  [9,]    4  -23
## [10,]    7  -24
## [11,]    9   10
## [12,]    5  -33
## [13,]  -28  -34
## [14,]  -37    2
## [15,]  -43  -52
## [16,]   -9  -25
## [17,]   -7  -10
## [18,]   16  -13
## [19,]   13   12
## [20,]   11   19
## [21,]  -61  -62
## [22,]   20  -20
## [23,]   17   18
## [24,]   22  -36
## [25,]  -17   24
## [26,]   25  -18
## [27,]   -1   21
## [28,]  -65  -70
## [29,]   -6  -14
## [30,]    8  -46
## [31,]  -29  -31
## [32,]   27  -63
## [33,]   26   31
## [34,]   32   23
## [35,]  -39   30
## [36,]  -16   35
## [37,]   34  -57
## [38,]   37   29
## [39,]   38   -8
## [40,]   39  -55
## [41,]   33  -21
## [42,]   -4   36
## [43,]   40  -12
## [44,]   42  -51
## [45,]   43   -3
## [46,]   45   -2
```

```
## [47,]   44  -42
## [48,]   15  -47
## [49,]   46  -15
## [50,]   49   41
## [51,]   47   48
## [52,]   50   51
## [53,]   52  -11
## [54,]   53  -48
## [55,]   54  -54
## [56,]  -73  -77
## [57,]  -56  -72
## [58,]   56  -74
## [59,]   55  -38
## [60,]   59  -59
## [61,]  -64   28
## [62,]   60   14
## [63,]  -67  -76
## [64,]   -5   57
## [65,]   64  -75
## [66,]   62  -58
## [67,]   66   65
## [68,]   61   58
## [69,]   68  -66
## [70,]   69  -69
## [71,]   70  -68
## [72,]   67   63
## [73,]   72   71
## [74,]   73  -60
## [75,]   74  -71
## [76,]   75  -49

#Dendogram
plot(as.dendrogram(agn.PT), xlab= "Distance between Countries",xlim=c(8,0),
     horiz = TRUE,main="Agnes Dendrogram  \n Canines")
```




```
######## Non Hierarchical clustering -- K-Means Clustering##########
##DG_Clust_1 <-
read_excel("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinal_old/finaloldCluster.xlsx",row.names=1)#, fill = TRUE)
##DG_Clust_1 <-
read_xlsx("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinal_old/finaloldCluster.xlsx",rowNames=TRUE)#, fill = TRUE)

#Converted xlsx into csv and importing it with row names for cluster analysis
(csv has row id column)
DG_Clust_1 <-
read.csv("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinal_old/finaloldClustercsvform.csv",row.names=1, fill = TRUE)
head(DG_Clust_1)

##   CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 1   ModernDog 123 10.1 23 23 19 7.8 32 33 5.6   Male
## 2   ModernDog 137  9.6 19 22 19 7.8 32 40 5.8   Male
## 3   ModernDog 121 10.2 18 21 21 7.9 35 38 6.2   Male
## 4   ModernDog 130 10.7 24 22 20 7.9 32 37 5.9   Male
## 5   ModernDog 149 12.0 25 25 21 8.4 35 43 6.6   Male
## 6   ModernDog 125  9.5 23 20 20 7.8 33 37 6.3   Male

#names(Final_Data)
#Imporing without row names the csv (csv has ro ID column)
Dg_Norowname <-
read.csv("C:/Alok/OneDrive/Rutgers_MITA/Semester2/MVA/MVAFinal_old/finaloldCl
```

```
ustercsvform.csv") #,row.names=1, fill = TRUE)
#View(Dg_Norowname)
names(Dg_Norowname)

##  [1] "ï..ID_C"     "CanineGroup" "X1"          "X2"          "X3"
##  [6] "X4"          "X5"          "X6"          "X7"          "X8"
## [11] "X9"          "Gender"

# Standardizing the data with scale()
matstd.dog <- scale(DG_Clust_1[,2:10])#quantitative
head(matstd.dog)

##            X1          X2         X3         X4         X5          X6
## 1 -0.34133663  0.09904431  0.3235696  0.4459670 -0.5997769 -0.19537598
## 2  0.45857835 -0.25733007 -0.6255679  0.1499372 -0.5997769 -0.19537598
## 3 -0.45561020  0.17031919 -0.8628523 -0.1460926  0.2034026 -0.09768799
## 4  0.05862086  0.52669357  0.5608540  0.1499372 -0.1981871 -0.09768799
## 5  1.14421975  1.45326697  0.7981384  1.0380266  0.2034026  0.39075196
## 6 -0.22706306 -0.32860495  0.3235696 -0.4421225 -0.1981871 -0.19537598
##           X7          X8         X9
## 1 -0.1244973 -0.99951775 -0.4661440
## 2 -0.1244973  0.58968599 -0.2700069
## 3  0.5944746  0.13562778  0.1222673
## 4 -0.1244973 -0.09140133 -0.1719384
## 5  0.5944746  1.27077331  0.5145414
## 6  0.1151600 -0.09140133  0.2203358

# Creating a (Euclidean) distance matrix of the standardized data
#dist.PT_Clust_1 <- dist(matstd.dog, method="euclidean")

#Implementing K-Means Clustering with different values of k.
# K-means, k=2, 3, 4, 5, 6
# Centers (k's) are numbers thus, 10 random sets are chosen
#k=2
(kmeans2.dog <- kmeans(matstd.dog,2,nstart = 10))

## K-means clustering with 2 clusters of sizes 33, 44
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  0.8723872  0.8917073  0.7334245  0.8675852  0.8970576  0.9176751
0.5799499
## 2 -0.6542904 -0.6687805 -0.5500683 -0.6506889 -0.6727932 -0.6882563 -
0.4349624
##           X8         X9
## 1  0.7960761  0.9068156
## 2 -0.5970571 -0.6801117
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
```

```
26
##  2  2  2  2  1  2  2  2  2  2  2  2  2  2  2  1  2  2  2  2  2  2  2  2  2
2
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  2  2  2  2  2  2  2  2  2  2  2  1  1  1  1  1  1  1  1  1  1  1  2  2  1
1
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  2  2  2  1  2  1  1  1  2  2  2  1  1  1  1  1  1  1  1  1  1  1  1  1  1
##
## Within cluster sum of squares by cluster:
## [1] 183.3078 137.6728
##  (between_SS / total_SS =  53.1 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
# Computing the percentage of variation accounted for. Two clusters
perc.var.2 <- round(100*(1 - kmeans2.dog$betweenss/kmeans2.dog$totss),1)
names(perc.var.2) <- "Perc. 2 clus"
perc.var.2
```

```
## Perc. 2 clus
##         46.9
```

```
#46% variance with k=2

# Computing the percentage of variation accounted for. Three clusters
(kmeans3.dog <- kmeans(matstd.dog,3,nstart = 10))
```

```
## K-means clustering with 3 clusters of sizes 35, 12, 30
##
## Cluster means:
##           X1         X2          X3         X4         X5         X6
X7
## 1  0.1108602  0.4370909  0.07272612  0.5474629  0.1001367  0.3544678 -
0.2614443
## 2  1.8250998  1.2097445  1.33202825  1.0133575  1.8097616  1.3839132
1.9325611
## 3 -0.8593768 -0.9938371 -0.61765844 -1.0440497 -0.8407307 -0.9671111 -
0.4680061
##            X8         X9
## 1  0.05130268  0.3128004
## 2  1.80050789  1.4952269
## 3 -0.78005628 -0.9630246
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
```

```
26
##  1  1  1  1  1  1  3  3  3  3  3  3  3  1  3  1  3  3  3  3  3  3  3  3  3
3
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  3  3  3  3  3  3  3  3  3  3  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
1
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  1  3  1  1  3  1  1  1  1  1  1  2  2  2  2  2  2  2  2  1  2  2  1  2  2
##
## Within cluster sum of squares by cluster:
## [1] 111.50575  33.56015  48.65771
##  (between_SS / total_SS =  71.7 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
perc.var.3 <- round(100*(1 - kmeans3.dog$betweenss/kmeans3.dog$totss),1)
names(perc.var.3) <- "Perc. 3 clus"
perc.var.3
```

```
## Perc. 3 clus
##         28.3
```

```
#28% variance with k=3

# Computing the percentage of variation accounted for. Four clusters
(kmeans4.dog <- kmeans(matstd.dog,4,nstart = 10))
```

```
## K-means clustering with 4 clusters of sizes 20, 20, 25, 12
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  0.3357343  0.7583369  0.4422118  0.8456072  0.4242770  0.6007811 -
0.2323431
## 2 -1.0326917 -1.2801246 -0.7442101 -1.3154104 -0.9210487 -1.2015623 -
0.5319147
## 3 -0.3184819 -0.1632472 -0.3977749 -0.1105691 -0.4712682 -0.1836534 -
0.3162231
## 4  1.8250998  1.2097445  1.3320283  1.0133575  1.8097616  1.3839132
1.9325611
##           X8         X9
## 1  0.2264394  0.5733826
## 2 -0.9427605 -1.2555957
## 3 -0.2911869 -0.1719384
## 4  1.8005079  1.4952269
##
```

```
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
26
##  3  3  3  3  1  3  3  3  3  3  3  2  3  3  3  1  2  2  2  2  2  2  2  2  3
2
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  2  2  2  2  2  2  2  2  2  2  3  1  1  1  1  1  1  1  1  1  1  1  3  3  1
1
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  3  3  3  1  3  1  1  3  3  3  3  4  4  4  4  4  4  4  4  1  4  4  1  4  4
##
## Within cluster sum of squares by cluster:
## [1] 37.30154 16.21449 61.66440 33.56015
##  (between_SS / total_SS =  78.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
perc.var.4 <- round(100*(1 - kmeans4.dog$betweenss/kmeans4.dog$totss),1)
names(perc.var.4) <- "Perc. 4 clus"
perc.var.4
```

```
## Perc. 4 clus
##         21.7
```

```
#21%

# Computing the percentage of variation accounted for. Five clusters
(kmeans5.dog <- kmeans(matstd.dog,5,nstart = 10))
```

```
## K-means clustering with 5 clusters of sizes 12, 20, 22, 17, 6
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  1.8250998  1.2097445  1.3320283  1.0133575  1.8097616  1.3839132
1.9325611
## 2 -1.0326917 -1.2801246 -0.7442101 -1.3154104 -0.9210487 -1.2015623 -
0.5319147
## 3 -0.3750993 -0.2119733 -0.1725705 -0.1191808 -0.5450146 -0.3108254 -
0.3859416
## 4  0.3611097  0.7656740  0.6027277  0.8464779  0.3923860  0.5861279 -
0.4346420
## 5  0.1443260  0.4554187 -1.2583263  0.3966287  0.3372658  0.7163786
0.5545317
##           X8         X9
## 1  1.8005079  1.4952269
```

```
## 2 -0.9427605 -1.2555957
## 3 -0.3597085 -0.2610916
## 4  0.1623371  0.6414537
## 5  0.4004951  0.3347491
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
26
##  3  3  5  3  4  3  3  3  3  3  3  2  3  3  3  4  2  2  2  2  2  2  2  2  3
2
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  2  2  2  2  2  2  2  2  2  2  3  4  4  4  4  4  4  4  4  4  4  4  5  3  4
4
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  3  3  3  4  3  4  5  5  3  3  3  1  1  1  1  1  1  1  1  5  1  1  5  1  1
##
## Within cluster sum of squares by cluster:
## [1] 33.56015 16.21449 29.00083 24.00051 26.60738
##  (between_SS / total_SS =  81.1 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
perc.var.5 <- round(100*(1 - kmeans5.dog$betweenss/kmeans5.dog$totss),1)
names(perc.var.5) <- "Perc. 5 clus"
perc.var.5
```

```
## Perc. 5 clus
##         18.9
```

```
(kmeans6.dog <- kmeans(matstd.dog,6,nstart = 10))
```

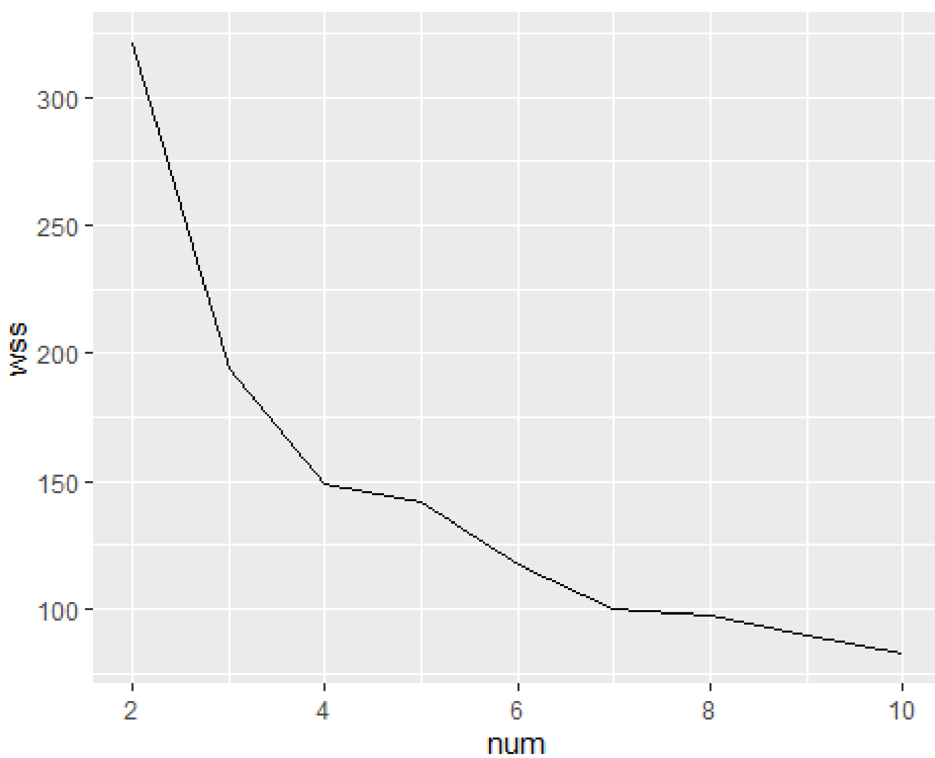
```
## K-means clustering with 6 clusters of sizes 6, 16, 24, 20, 1, 10
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  0.7252167  0.9781011  0.4422118  0.6433202  0.8727188  0.7652226
1.0737891
## 2  0.2728838  0.6692433  0.5460237  0.8530080  0.3790981  0.5922334 -
0.5438975
## 3 -0.3556208 -0.1979343 -0.2202071 -0.1337581 -0.5161124 -0.2197980 -
0.3042403
## 4 -1.0326917 -1.2801246 -0.7442101 -1.3154104 -0.9210487 -1.2015623 -
0.5319147
## 5  0.5728519  0.6692433 -4.6594025  0.4459670  0.6049923  0.6838159 -
0.6038119
```

```
## 6  1.9898442  1.3107172  1.3438925  1.1564386  1.8900795  1.4555510
2.0803498
##            X8         X9
## 1  0.81671510  0.6289547
## 2  0.06468118  0.6064807
## 3 -0.31843043 -0.2128002
## 4 -0.94276048 -1.2555957
## 5  0.36265688  0.8087471
## 6  2.01996936  1.5932954
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
26
##  3  3  3  3  1  3  3  3  3  3  3  4  3  3  3  2  4  4  4  4  4  4  4  4  3
4
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  4  4  4  4  4  4  4  4  4  4  3  2  2  2  2  2  2  2  2  2  2  2  5  3  2
2
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  3  3  3  1  3  2  2  3  3  3  3  6  6  6  1  6  6  6  6  1  6  6  1  1  6
##
## Within cluster sum of squares by cluster:
## [1] 10.41048 20.39985 37.35032 16.21449  0.00000 23.61837
##  (between_SS / total_SS =  84.2 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"

# Computing the percentage of variation accounted for. Six clusters
perc.var.6 <- round(100*(1 - kmeans6.dog$betweenss/kmeans6.dog$totss),1)
names(perc.var.6) <- "Perc. 6 clus"
perc.var.6

## Perc. 6 clus
##         15.8

#
#It can be seen that Variance goes down as K increases...
```

#To Identify the Best number of K Clusters, plotting Elbow Plot

```
wss=c()########## empty vector to hold wss
for(i in 2:10)#### from 2 to 10 cluster
{
  km = kmeans(matstd.dog[,1:9],i)
  wss[i-1]=km$tot.withinss
```

```
}
wss

## [1] 320.98060 193.72361 148.74059 141.75197 117.59048 100.48292  97.53825
## [8]  89.83151  82.85621

#Creating a 'elbowdt' data table with column names num and wss with the
contents of wss
elbowdt = data.table(num=2:10,wss)
elbowdt

##    num       wss
## 1:   2 320.98060
## 2:   3 193.72361
## 3:   4 148.74059
## 4:   5 141.75197
## 5:   6 117.59048
## 6:   7 100.48292
## 7:   8  97.53825
## 8:   9  89.83151
## 9:  10  82.85621

#Plotting
ggplot(elbowdt,aes(x=num,y=wss)) + geom_line()
```



#For k = 6 the between sum of square/total sum of square ratio tends to change slowly

#and remain less changing as compared to others.
#Also this dataset has only 77 rows so more than 6/7 clusters would not make much sense to me.
#Therefore, k = 6 should be a good choice for the number of clusters.
#For 6 clusters, k-means = 6

```
# Centers (k's) are numbers thus, 10 random sets are chosen
(kmeans6.dog <- kmeans(matstd.dog,6,nstart = 10))

## K-means clustering with 6 clusters of sizes 10, 1, 6, 24, 16, 20
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  1.9898442  1.3107172  1.3438925  1.1564386  1.8900795  1.4555510
2.0803498
## 2  0.5728519  0.6692433 -4.6594025  0.4459670  0.6049923  0.6838159 -
0.6038119
## 3  0.7252167  0.9781011  0.4422118  0.6433202  0.8727188  0.7652226
1.0737891
## 4 -0.3556208 -0.1979343 -0.2202071 -0.1337581 -0.5161124 -0.2197980 -
0.3042403
## 5  0.2728838  0.6692433  0.5460237  0.8530080  0.3790981  0.5922334 -
0.5438975
## 6 -1.0326917 -1.2801246 -0.7442101 -1.3154104 -0.9210487 -1.2015623 -
0.5319147
##            X8         X9
## 1  2.01996936  1.5932954
## 2  0.36265688  0.8087471
## 3  0.81671510  0.6289547
## 4 -0.31843043 -0.2128002
## 5  0.06468118  0.6064807
## 6 -0.94276048 -1.2555957
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
26
##  4  4  4  4  3  4  4  4  4  4  4  6  4  4  4  5  6  6  6  6  6  6  6  6  4
6
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  6  6  6  6  6  6  6  6  6  6  4  5  5  5  5  5  5  5  5  5  5  5  2  4  5
5
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
##  4  4  4  3  4  5  5  4  4  4  4  1  1  1  3  1  1  1  1  3  1  1  3  3  1
##
## Within cluster sum of squares by cluster:
## [1] 23.61837  0.00000 10.41048 37.35032 20.39985 16.21449
##  (between_SS / total_SS =  84.2 %)
```

```
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
perc.var.6 <- round(100*(1 - kmeans6.dog$betweenss/kmeans6.dog$totss),1)
names(perc.var.6) <- "Perc. 3 clus"
perc.var.6
```

```
## Perc. 3 clus
##         15.8
```

```
kmeans6.dog
```

```
## K-means clustering with 6 clusters of sizes 10, 1, 6, 24, 16, 20
##
## Cluster means:
##           X1         X2         X3         X4         X5         X6
X7
## 1  1.9898442  1.3107172  1.3438925  1.1564386  1.8900795  1.4555510
2.0803498
## 2  0.5728519  0.6692433 -4.6594025  0.4459670  0.6049923  0.6838159 -
0.6038119
## 3  0.7252167  0.9781011  0.4422118  0.6433202  0.8727188  0.7652226
1.0737891
## 4 -0.3556208 -0.1979343 -0.2202071 -0.1337581 -0.5161124 -0.2197980 -
0.3042403
## 5  0.2728838  0.6692433  0.5460237  0.8530080  0.3790981  0.5922334 -
0.5438975
## 6 -1.0326917 -1.2801246 -0.7442101 -1.3154104 -0.9210487 -1.2015623 -
0.5319147
##            X8         X9
## 1  2.01996936  1.5932954
## 2  0.36265688  0.8087471
## 3  0.81671510  0.6289547
## 4 -0.31843043 -0.2128002
## 5  0.06468118  0.6064807
## 6 -0.94276048 -1.2555957
##
## Clustering vector:
##  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
26
##  4  4  4  4  3  4  4  4  4  4  4  6  4  4  4  5  6  6  6  6  6  6  6  6  4
6
## 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
52
##  6  6  6  6  6  6  6  6  6  6  4  5  5  5  5  5  5  5  5  5  5  5  2  4  5
5
## 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77
```

```
##   4   4   4   3   4   5   5   4   4   4   4   1   1   1   3   1   1   1   1   3   1   1   3   3   1
##
## Within cluster sum of squares by cluster:
## [1] 23.61837  0.00000 10.41048 37.35032 20.39985 16.21449
##  (between_SS / total_SS =  84.2 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
"tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

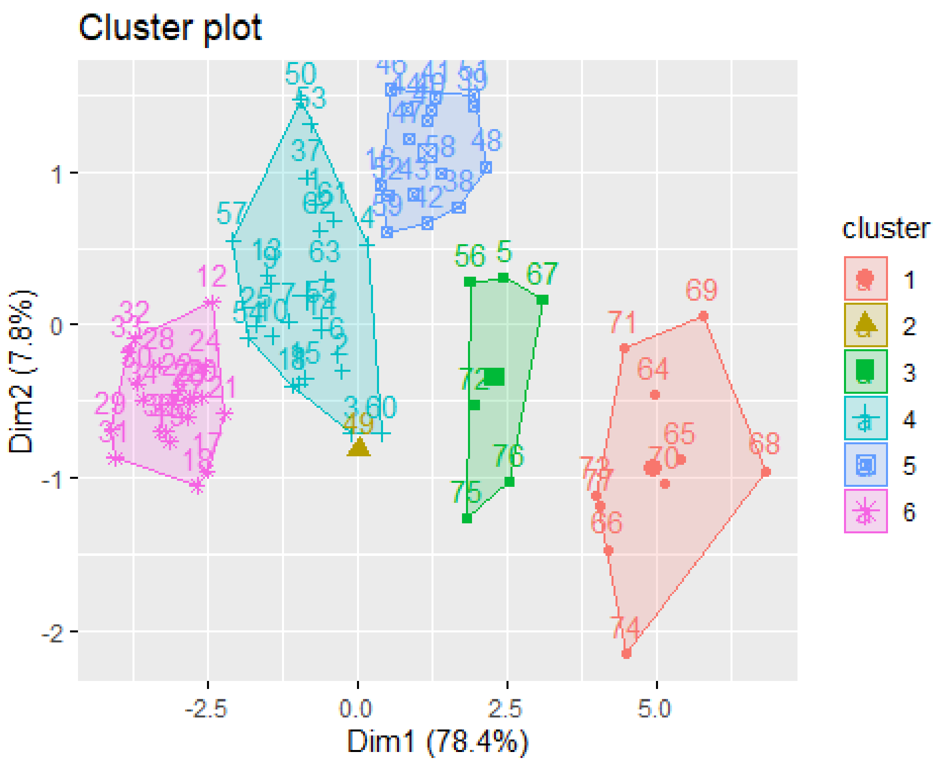
```
kmeans6.dog$cluster
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21  22  23  24  25
26
##   4   4   4   4   3   4   4   4   4   4   4   6   4   4   4   5   6   6   6   6   6   6   6   6   4
6
##  27  28  29  30  31  32  33  34  35  36  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51
52
##   6   6   6   6   6   6   6   6   6   6   4   5   5   5   5   5   5   5   5   5   5   5   2   4   5
5
##  53  54  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77
##   4   4   4   3   4   5   5   4   4   4   4   1   1   1   3   1   1   1   1   3   1   1   3   3   1
```

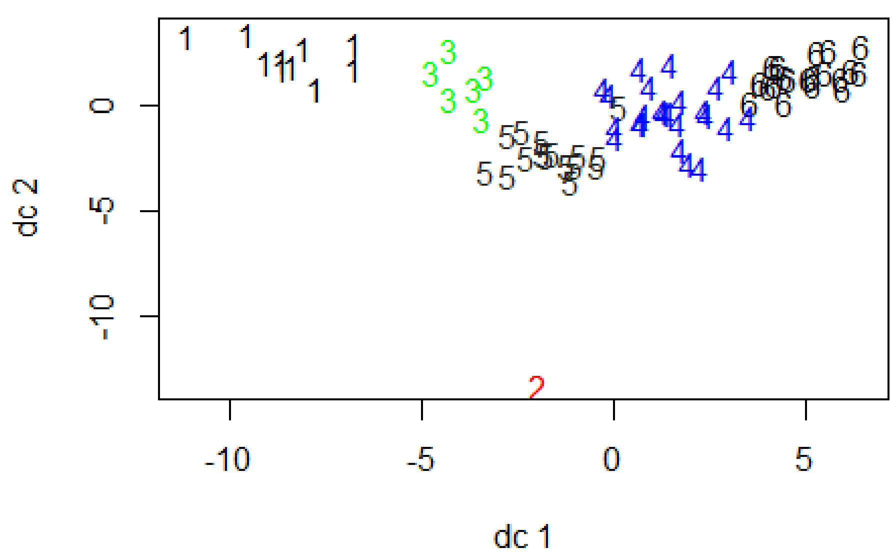
```
#typeof(kmeans6.dog$cluster)
```

#plotting output of kmeans for 6 clusters

```
fviz_cluster(kmeans6.dog,data=matstd.dog)
```




```
#Clusters plotting in another way to see them more clearly
plotcluster(matstd.dog,kmeans6.dog$cluster)
```



```
#Clear 6 groups can be seen after Plotting the clusters.
#Creating separate matrices for clusters
##b<-names(kmeans6.dog$cluster[kmeans6.dog$cluster == 1])
##b
##(kmeans6.dog$cluster[kmeans6.dog$cluster == 1])

clus1 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 1]),
                ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 1]))
colnames(clus1) <- "Cluster 1"
clus1

##       Cluster 1
##  [1,] "64"
##  [2,] "65"
##  [3,] "66"
##  [4,] "68"
##  [5,] "69"
##  [6,] "70"
##  [7,] "71"
##  [8,] "73"
##  [9,] "74"
## [10,] "77"

clus2 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 2]),
                ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 2]))
colnames(clus2) <- "Cluster 2"
clus2

##      Cluster 2
## [1,] "49"

clus3 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 3]),
                ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 3]))
colnames(clus3) <- "Cluster 3"
clus3

##      Cluster 3
## [1,] "5"
## [2,] "56"
## [3,] "67"
## [4,] "72"
## [5,] "75"
## [6,] "76"

clus4 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 4]),
                ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 4]))
```

```
colnames(clus4) <- "Cluster 4"
clus4

##       Cluster 4
##  [1,] "1"
##  [2,] "2"
##  [3,] "3"
##  [4,] "4"
##  [5,] "6"
##  [6,] "7"
##  [7,] "8"
##  [8,] "9"
##  [9,] "10"
## [10,] "11"
## [11,] "13"
## [12,] "14"
## [13,] "15"
## [14,] "25"
## [15,] "37"
## [16,] "50"
## [17,] "53"
## [18,] "54"
## [19,] "55"
## [20,] "57"
## [21,] "60"
## [22,] "61"
## [23,] "62"
## [24,] "63"

clus5 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 5]),
              ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 5]))
colnames(clus5) <- "Cluster 5"
clus5

##       Cluster 5
##  [1,] "16"
##  [2,] "38"
##  [3,] "39"
##  [4,] "40"
##  [5,] "41"
##  [6,] "42"
##  [7,] "43"
##  [8,] "44"
##  [9,] "45"
## [10,] "46"
## [11,] "47"
## [12,] "48"
## [13,] "51"
## [14,] "52"
```

```
## [15,] "58"
## [16,] "59"
```

```r
clus6 <- matrix(names(kmeans6.dog$cluster[kmeans6.dog$cluster == 6]),
               ncol=1, nrow=length(kmeans6.dog$cluster[kmeans6.dog$cluster
== 6]))
colnames(clus6) <- "Cluster 6"
clus6
```

```
##       Cluster 6
##  [1,] "12"
##  [2,] "17"
##  [3,] "18"
##  [4,] "19"
##  [5,] "20"
##  [6,] "21"
##  [7,] "22"
##  [8,] "23"
##  [9,] "24"
## [10,] "26"
## [11,] "27"
## [12,] "28"
## [13,] "29"
## [14,] "30"
## [15,] "31"
## [16,] "32"
## [17,] "33"
## [18,] "34"
## [19,] "35"
## [20,] "36"
```

```r
#Displaying all the Canine group row numbers in their respective clusters
list(clus1,clus2,clus3,clus4,clus5,clus6)
```

```
## [[1]]
##       Cluster 1
##  [1,] "64"
##  [2,] "65"
##  [3,] "66"
##  [4,] "68"
##  [5,] "69"
##  [6,] "70"
##  [7,] "71"
##  [8,] "73"
##  [9,] "74"
## [10,] "77"
##
## [[2]]
##      Cluster 2
## [1,] "49"
##
```

```
## [[3]]
##      Cluster 3
## [1,] "5"
## [2,] "56"
## [3,] "67"
## [4,] "72"
## [5,] "75"
## [6,] "76"
##
## [[4]]
##       Cluster 4
##  [1,] "1"
##  [2,] "2"
##  [3,] "3"
##  [4,] "4"
##  [5,] "6"
##  [6,] "7"
##  [7,] "8"
##  [8,] "9"
##  [9,] "10"
## [10,] "11"
## [11,] "13"
## [12,] "14"
## [13,] "15"
## [14,] "25"
## [15,] "37"
## [16,] "50"
## [17,] "53"
## [18,] "54"
## [19,] "55"
## [20,] "57"
## [21,] "60"
## [22,] "61"
## [23,] "62"
## [24,] "63"
##
## [[5]]
##       Cluster 5
##  [1,] "16"
##  [2,] "38"
##  [3,] "39"
##  [4,] "40"
##  [5,] "41"
##  [6,] "42"
##  [7,] "43"
##  [8,] "44"
##  [9,] "45"
## [10,] "46"
## [11,] "47"
## [12,] "48"
```

```
## [13,] "51"
## [14,] "52"
## [15,] "58"
## [16,] "59"
##
## [[6]]
##       Cluster 6
##  [1,] "12"
##  [2,] "17"
##  [3,] "18"
##  [4,] "19"
##  [5,] "20"
##  [6,] "21"
##  [7,] "22"
##  [8,] "23"
##  [9,] "24"
## [10,] "26"
## [11,] "27"
## [12,] "28"
## [13,] "29"
## [14,] "30"
## [15,] "31"
## [16,] "32"
## [17,] "33"
## [18,] "34"
## [19,] "35"
## [20,] "36"

#Making Subsets for 6 clusters using Row filtering from the Original dataset
#(Not the scaled one)
```

So below are the 6 cluster sets of Original entire dataset

```
#Using original dataframe to capture Row ID as clusters are identified based
on these IDs
head(DG_Clust_1)

##   CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 1   ModernDog 123 10.1 23 23 19 7.8 32 33 5.6   Male
## 2   ModernDog 137  9.6 19 22 19 7.8 32 40 5.8   Male
## 3   ModernDog 121 10.2 18 21 21 7.9 35 38 6.2   Male
## 4   ModernDog 130 10.7 24 22 20 7.9 32 37 5.9   Male
## 5   ModernDog 149 12.0 25 25 21 8.4 35 43 6.6   Male
## 6   ModernDog 125  9.5 23 20 20 7.8 33 37 6.3   Male

#head(Final_Data)
#Dg_Norowname$ï..ID_C
#Dg_Norowname
#Dg_Norowname$ï..ID_C %in% clus4
DG_Cl1_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus1)
#DG_Cl1_Dt
DG_Cl2_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus2)
```

```r
#DG_Cl2_Dt
DG_Cl3_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus3)
#DG_Cl3_Dt
DG_Cl4_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus4)
#DG_Cl4_Dt
DG_Cl5_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus5)
#DG_Cl5_Dt
DG_Cl6_Dt<-subset(Dg_Norowname,Dg_Norowname$ï..ID_C %in% clus6)
#DG_Cl6_Dt
```

#Printing all the columns of the Clusters formed

```r
#Original observations after clustering with all the variables
list(DG_Cl1_Dt,DG_Cl2_Dt,DG_Cl3_Dt,DG_Cl4_Dt,DG_Cl5_Dt,DG_Cl6_Dt)
```

```
## [[1]]
##    ï..ID_C  CanineGroup  X1   X2 X3 X4 X5   X6 X7 X8  X9 Gender
## 64      64 IndianWolves 167 11.5 29 28 25  9.5 41 45 7.2   Male
## 65      65 IndianWolves 164 12.3 27 26 25 10.0 42 47 7.9   Male
## 66      66 IndianWolves 150 11.5 21 24 25  9.3 41 46 8.5   Male
## 68      68 IndianWolves 177 12.4 31 27 27 10.5 43 50 7.9   Male
## 69      69 IndianWolves 166 13.4 32 27 26  9.5 40 47 7.3   Male
## 70      70 IndianWolves 164 12.1 27 24 25  9.9 42 45 8.3   Male
## 71      71 IndianWolves 165 12.6 30 26 25  7.7 40 43 7.9   Male
## 73      73 IndianWolves 163 10.8 27 24 24  9.2 39 48 7.0 Female
## 74      74 IndianWolves 164 10.7 24 23 26  9.5 43 47 7.6 Female
## 77      77 IndianWolves 158 10.7 25 25 24  9.8 41 45 7.4 Female
##
## [[2]]
##    ï..ID_C CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 49      49       Cuons 139 10.9  2 23 22 8.7 30 39 6.9 Female
##
## [[3]]
##    ï..ID_C  CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9  Gender
## 5        5    ModernDog 149 12.0 25 25 21 8.4 35 43 6.6    Male
## 56      56     ThaiDogs 136 11.9 22 25 21 8.5 36 39 7.0 Unknown
## 67      67 IndianWolves 145 11.3 28 24 24 9.2 36 41 7.2    Male
## 72      72 IndianWolves 131 11.8 20 24 23 8.8 38 40 6.5  Female
## 75      75 IndianWolves 141 10.4 20 23 23 8.9 38 43 6.0  Female
## 76      76 IndianWolves 148 10.6 26 21 24 8.9 39 40 7.0  Female
##
## [[4]]
##    ï..ID_C  CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9  Gender
## 1        1    ModernDog 123 10.1 23 23 19 7.8 32 33 5.6    Male
## 2        2    ModernDog 137  9.6 19 22 19 7.8 32 40 5.8    Male
## 3        3    ModernDog 121 10.2 18 21 21 7.9 35 38 6.2    Male
## 4        4    ModernDog 130 10.7 24 22 20 7.9 32 37 5.9    Male
## 6        6    ModernDog 125  9.5 23 20 20 7.8 33 37 6.3    Male
## 7        7    ModernDog 126  9.1 20 22 19 7.5 32 35 5.5    Male
## 8        8    ModernDog 125  9.7 19 19 19 7.5 32 37 6.2    Male
```

```
## 9        9    ModernDog 121  9.6 22 20 18 7.6 31 35 5.3  Female
## 10      10    ModernDog 122  8.9 20 20 19 7.6 31 35 5.7  Female
## 11      11    ModernDog 115  9.3 19 19 20 7.8 33 34 6.5  Female
## 13      13    ModernDog 124  9.3 21 21 18 7.1 30 36 5.5  Female
## 14      14    ModernDog 128  9.6 22 21 19 7.5 32 38 5.8  Female
## 15      15    ModernDog 130  8.4 23 20 19 7.3 31 40 5.8  Female
## 25      25 GoldenJackal 114  9.4 21 19 19 7.5 31 35 5.3    Male
## 37      37        Cuons 123  9.7 22 21 20 7.8 27 36 6.1    Male
## 50      50        Cuons 123  9.8 23 22 20 8.1 26 34 5.6  Female
## 53      53        Cuons 122  9.9 22 22 20 8.2 26 36 5.7  Female
## 54      54     ThaiDogs 112 10.1 17 18 19 7.7 31 33 5.8 Unknown
## 55      55     ThaiDogs 115 10.0 18 23 20 7.8 33 36 6.0 Unknown
## 57      57     ThaiDogs 111  9.9 19 20 18 7.3 29 34 5.3 Unknown
## 60      60     ThaiDogs 132  9.6 19 20 19 9.7 35 38 6.6 Unknown
## 61      61     ThaiDogs 121 10.7 21 23 19 7.9 32 35 6.0 Unknown
## 62      62     ThaiDogs 122  9.8 22 23 18 7.9 32 35 6.1 Unknown
## 63      63     ThaiDogs 124  9.5 20 24 19 7.6 32 37 6.0 Unknown
##
## [[5]]
##    ï..ID_C CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9  Gender
## 16      16   ModernDog 127 10.5 25 23 20 8.7 32 35 6.1  Female
## 38      38       Cuons 135 11.8 25 21 23 8.9 31 38 7.1    Male
## 39      39       Cuons 138 11.4 25 25 22 9.0 30 38 7.3    Male
## 40      40       Cuons 141 10.8 26 25 21 8.1 29 39 6.6    Male
## 41      41       Cuons 135 11.2 25 25 21 8.5 29 39 6.7    Male
## 42      42       Cuons 136 11.0 22 24 22 8.1 31 39 6.8    Male
## 43      43       Cuons 131 10.4 23 23 23 8.7 30 36 6.8    Male
## 44      44       Cuons 137 10.6 25 24 21 8.3 28 38 6.5    Male
## 45      45       Cuons 135 10.5 25 25 21 8.4 29 39 6.9    Male
## 46      46       Cuons 131 10.9 25 24 21 8.5 29 35 6.2  Female
## 47      47       Cuons 130 11.3 22 23 21 8.7 29 37 7.0  Female
## 48      48       Cuons 144 10.8 24 26 22 8.9 30 42 7.1  Female
## 51      51       Cuons 137 11.3 27 26 23 8.7 30 39 6.5  Female
## 52      52       Cuons 128 10.0 22 23 22 8.7 29 37 6.6  Female
## 58      58    ThaiDogs 130 11.2 23 27 20 9.1 35 35 6.6 Unknown
## 59      59    ThaiDogs 125 10.7 19 26 20 8.4 33 37 6.3 Unknown
##
## [[6]]
##    ï..ID_C  CanineGroup  X1  X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 12      12    ModernDog 112 9.1 19 20 19 6.6 30 33 5.1 Female
## 17      17 GoldenJackal 120 8.2 18 17 18 7.0 32 35 5.2   Male
## 18      18 GoldenJackal 107 7.9 17 17 20 7.0 32 34 5.3   Male
## 19      19 GoldenJackal 110 8.1 18 16 19 7.1 31 32 4.7   Male
## 20      20 GoldenJackal 116 8.5 20 18 18 7.1 32 33 4.7   Male
## 21      21 GoldenJackal 114 8.2 19 18 19 7.9 32 33 5.1   Male
## 22      22 GoldenJackal 111 8.5 19 16 18 7.1 30 33 5.0   Male
## 23      23 GoldenJackal 113 8.5 17 18 19 7.1 30 34 4.6   Male
## 24      24 GoldenJackal 117 8.7 20 17 18 7.0 30 34 5.2   Male
## 26      26 GoldenJackal 112 8.2 19 17 19 6.8 30 34 5.1   Male
## 27      27 GoldenJackal 110 8.5 18 17 19 7.0 31 33 4.9 Female
```

```
## 28      28 GoldenJackal 111 7.7 20 18 18 6.7 30 32 4.5 Female
## 29      29 GoldenJackal 107 7.2 17 16 17 6.0 28 35 4.7 Female
## 30      30 GoldenJackal 108 8.2 18 16 17 6.5 29 33 4.8 Female
## 31      31 GoldenJackal 110 7.3 19 15 17 6.1 30 33 4.5 Female
## 32      32 GoldenJackal 105 8.3 19 17 17 6.5 29 32 4.5 Female
## 33      33 GoldenJackal 107 8.4 18 17 18 6.2 29 31 4.3 Female
## 34      34 GoldenJackal 106 7.8 19 18 18 6.2 31 32 4.4 Female
## 35      35 GoldenJackal 111 8.4 17 16 18 7.0 30 34 4.7 Female
## 36      36 GoldenJackal 111 7.6 19 17 18 6.5 30 35 4.6 Female
```

#Conclusion:

#Cluster analysis is a technique that groups the observations into clusters based on similarities
#Clustering types: Hierarchical and nonhierarchical
#Hierarchical and non hierarchical clustering has been performed on Canines dataset above.
#Clear 6 groups can be seen after Plotting the clusters.
#In one of the cluster (cluster 1), Indian wolves, Modern dog and Thai dogs are clubbed together.

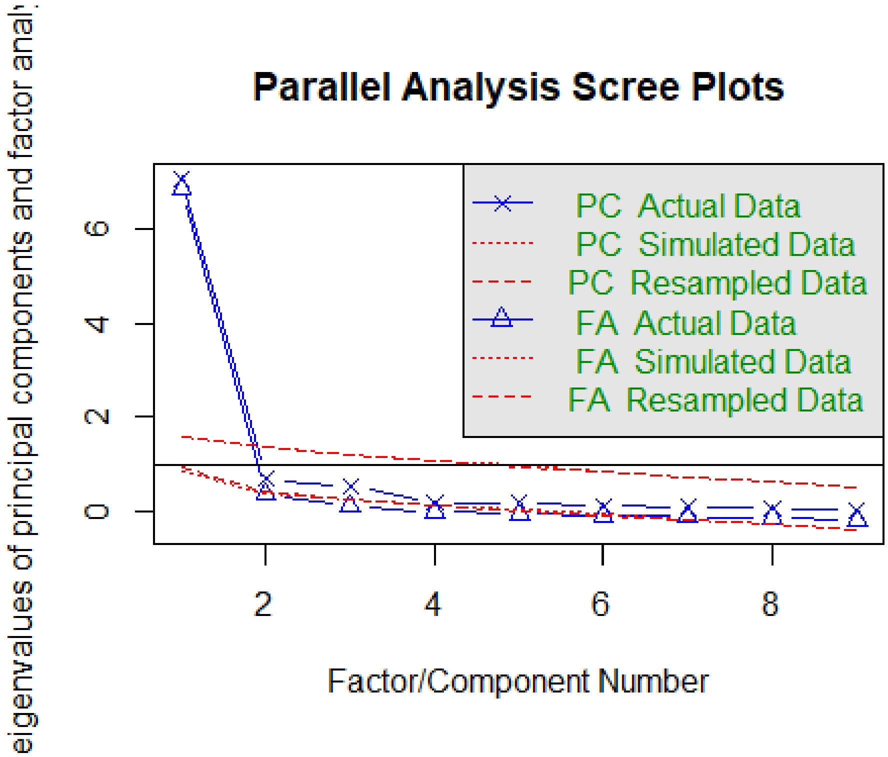
#Also, in hierarchical complete linkage dendogram, Indian wolves are clustered together with Modern dog and Thai dogs
#So Indian Wolves are related to Thai dogs and Modern Dogs

```
#==============Question 4 end =======================
```

#@@@@@@@@@@@ Question 5 - Factor Analysis @@@@@@@@@@
#5. Identify the important factors underlying the Skull measurement
#a. Is there a relationships between the species with respect to these factors?

```
#library(psych)
fa.parallel(Canine_Data[2:10]) # See factor recommendation

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
## different factor score estimation method.

## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,
: An
## ultra-Heywood case was detected. Examine the results carefully

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
```

```
## different factor score estimation method.

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
## different factor score estimation method.

## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,
: An
## ultra-Heywood case was detected. Examine the results carefully

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
## different factor score estimation method.

## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,
: An
## ultra-Heywood case was detected. Examine the results carefully

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
## different factor score estimation method.

## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate,
: An
## ultra-Heywood case was detected. Examine the results carefully

## Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs =
np.obs, :
## The estimated weights for the factor scores are probably incorrect. Try a
## different factor score estimation method.
```




```
## Parallel analysis suggests that the number of factors =  1  and the number
of components =  1
```

#we can see that after 2 factors the eigen value crosses at 1 and hence 1 is the number of recommended factors

```
#Do an eigen value decomposition removing the non numeric columns
fcdg <- principal(Canine_Data[2:10], nfactors=2, rotate="varimax")
fcdg

## Principal Components Analysis
## Call: principal(r = Canine_Data[2:10], nfactors = 2, rotate = "varimax")
## Standardized loadings (pattern matrix) based upon correlation matrix
##     RC1  RC2   h2    u2 com
## X1 0.67 0.70 0.94 0.058 2.0
## X2 0.86 0.39 0.90 0.103 1.4
## X3 0.71 0.26 0.57 0.427 1.3
## X4 0.90 0.28 0.89 0.108 1.2
## X5 0.64 0.70 0.90 0.102 2.0
## X6 0.74 0.55 0.85 0.153 1.9
## X7 0.20 0.93 0.91 0.091 1.1
## X8 0.54 0.78 0.91 0.092 1.8
## X9 0.76 0.56 0.89 0.110 1.9
##
##                        RC1  RC2
## SS loadings           4.38 3.38
```

```
## Proportion Var        0.49 0.38
## Cumulative Var        0.49 0.86
## Proportion Explained  0.56 0.44
## Cumulative Proportion 0.56 1.00
##
## Mean item complexity =  1.6
## Test of the hypothesis that 2 components are sufficient.
##
## The root mean square of the residuals (RMSR) is  0.04
##  with the empirical chi square  9.66  with prob <  0.96
##
## Fit based upon off diagonal values = 1
```

```
summary(fcdg)
```

```
##
## Factor analysis with Call: principal(r = Canine_Data[2:10], nfactors = 2,
rotate = "varimax")
##
## Test of the hypothesis that 2 factors are sufficient.
## The degrees of freedom for the model is 19  and the objective function was
1.18
## The number of observations was  77  with Chi Square =  83.28  with prob <
5e-10
##
## The root mean square of the residuals (RMSA) is  0.04
```

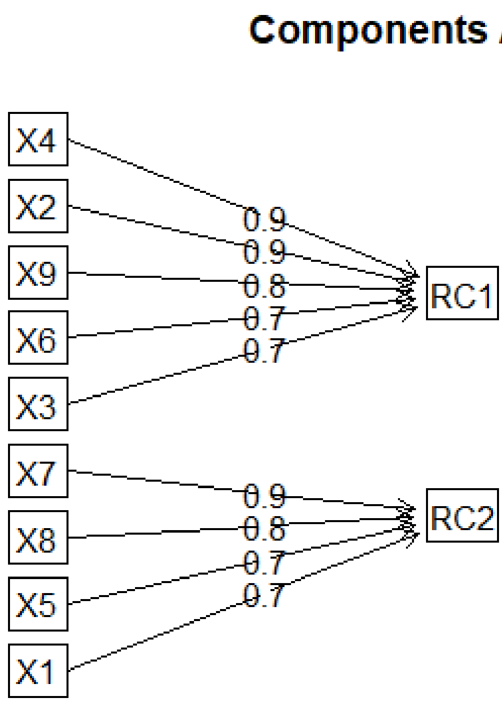
```
#From the summary we can see that 2 factors the variables explain about 80%
of the variance
round(fcdg$values, 3)
```

```
## [1] 7.052 0.704 0.543 0.193 0.180 0.132 0.092 0.070 0.035
```

```
fcdg$loadings
```

```
##
## Loadings:
##    RC1   RC2
## X1 0.672 0.700
## X2 0.863 0.390
## X3 0.713 0.255
## X4 0.903 0.278
## X5 0.638 0.701
## X6 0.736 0.553
## X7 0.203 0.932
## X8 0.544 0.783
## X9 0.756 0.564
##
##                  RC1   RC2
## SS loadings    4.375 3.381
```

```
## Proportion Var 0.486 0.376
## Cumulative Var 0.486 0.862

# Communalities
fcdg$communality

##        X1        X2        X3        X4        X5        X6        X7
X8
## 0.9417787 0.8968812 0.5732902 0.8922558 0.8976670 0.8472377 0.9093146
0.9082632
##        X9
## 0.8897015

# Plotting the relationship and mapping between variables and factors with
weights
fa.diagram(fcdg)
```




```
#Above, output gives weights going in RCs

#fa.graph(fcdg)
#cluster.plot(fcdg)
#plot(fcdg)
#Now lets rename these factors as per their contributing variables as per
above graph
colnames(fcdg$loadings) <- c("x_42963","x_7851")
#fcdg
```

```
#Factor Analysis Conclusion:
#Factor analysis is a technique used to reduce number of columns.
#Factor analysis tries to find if there is any underlying latent variable in your input columns.
#After performing Factor analysis on Canine dataset, it can be concluded that:
#Based on per Measurements for the canine groups,
#Total 2 factors have been formed with common variance of different Measurements contributing to them.
#RC1 is made up with Positive contributions of Breadth and Height measurements.
#RC2 is made up with Positive contributions of Length measurements
#This shows that there is an underlying latent variable within Breadth and Height related skull measurements for canine dogs.
#Also there is an underlying latent variable within length related measurements.
#As per above diagram, almost all the factors have significant contribution and so
#So, its better not to loose any of 2 factors
#Hence I will take All 2 Factors, RC1 and RC2 as inputs for our models
#Above factor analysis, we can conclude to reduce number of 9 Measurements to 2 in our input dataset.
#==============Question 5 end =======================
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
#@@@@@@@ Question 6 - Discriminant Function Analysis @@@@@@@@@

#6. Carry out a discriminant function analysis to see how well it is possible to separate the groups using the measurements.

#library(MASS)
#library(scales)
#library(gridExtra)
#install.packages("klaR")
#library(klaR)
#library(tidyverse)
#library(caret)

#splitting the data into training and testing sets with 80% and 20% respectively.
set.seed(123)
training.samples <- Canine_Data$CanineGroup %>% createDataPartition(p = 0.8,
```

```r
list = FALSE)
#So sample has a random mix of canine groups
train.data <- Canine_Data[training.samples, ]
test.data <- Canine_Data[-training.samples, ]
dim(Canine_Data) #Total data  77 11

## [1] 77 11

dim(train.data) #Training data  63 11

## [1] 63 11

dim(test.data) #Test data 14 11

## [1] 14 11

#Estimating preprocessing parameters
#Pre-processing transformation (centering, scaling etc.) can be estimated
from the training data and applied to any data set with the same variables.
#So the properties of training and test data remain the same
preproc.param <- train.data %>% preProcess(method = c("center", "scale"))
#preproc.param

# Transform the data using the estimated parameters
train.transformed <- preproc.param %>% predict(train.data)
test.transformed <- preproc.param %>% predict(test.data)
head(train.transformed)

##   CanineGroup         X1          X2         X3         X4         X5
## 1   ModernDog -0.3497343  0.06197983  0.2928336  0.4622625 -0.5938638
## 2   ModernDog  0.4514751 -0.28665672 -0.8085703  0.1589027 -0.5938638
## 3   ModernDog -0.4641927  0.13170714 -1.0839213 -0.1444570  0.1937871
## 5   ModernDog  1.1382260  1.38679871  0.8435355  1.0689820  0.1937871
## 6   ModernDog -0.2352758 -0.35638403  0.2928336 -0.4478168 -0.2000383
## 8   ModernDog -0.2352758 -0.21692941 -0.8085703 -0.7511765 -0.5938638
##           X6         X7         X8         X9 Gender
## 1 -0.1609105 -0.1085148 -1.0196587 -0.4512798   Male
## 2 -0.1609105 -0.1085148  0.5471340 -0.2578742   Male
## 3 -0.0615246  0.5987026  0.0994789  0.1289371   Male
## 5  0.4354048  0.5987026  1.2186165  0.5157483   Male
## 6 -0.1609105  0.1272243 -0.1243486  0.2256399   Male
## 8 -0.4590681 -0.1085148 -0.1243486  0.1289371   Male

head(test.transformed)

##     CanineGroup          X1         X2         X3         X4         X5
## 4     ModernDog  0.05087044  0.4803437  0.5681846  0.1589027 -0.2000383
## 7     ModernDog -0.17804653 -0.6352933 -0.5332194  0.1589027 -0.5938638
## 11    ModernDog -0.80756818 -0.4958386 -0.8085703 -0.7511765 -0.2000383
## 18 GoldenJackal -1.26540211 -1.4720210 -1.3592723 -1.3578961 -0.2000383
## 22 GoldenJackal -1.03648515 -1.0536571 -0.8085703 -1.6612558 -0.9876892
## 28 GoldenJackal -1.03648515 -1.6114756 -0.5332194 -1.0545363 -0.9876892
```

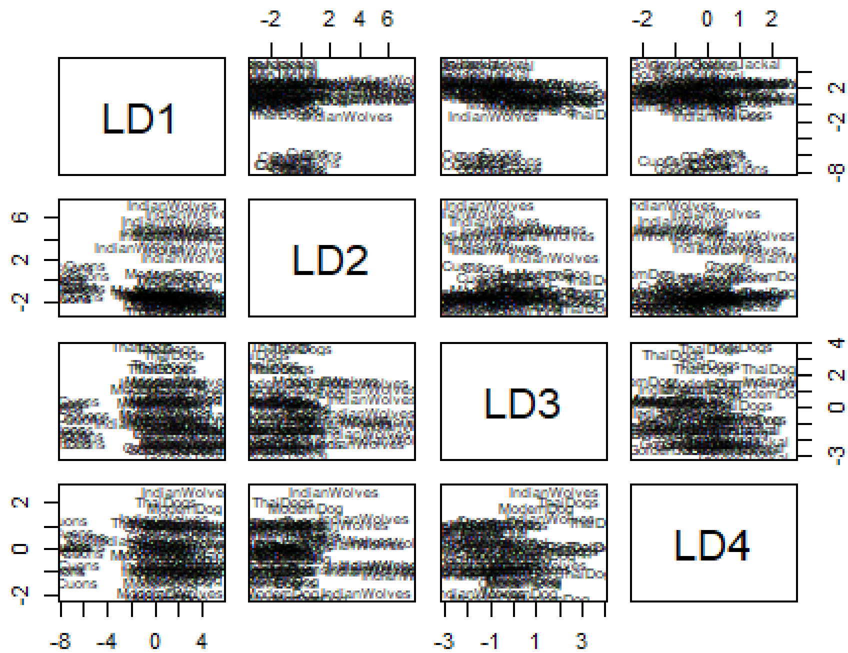
```
##            X6         X7         X8         X9 Gender
## 4  -0.0615246 -0.1085148 -0.1243486 -0.1611713   Male
## 7  -0.4590681 -0.1085148 -0.5720037 -0.5479826   Male
## 11 -0.1609105  0.1272243 -0.7958312  0.4190455 Female
## 18 -0.9559976 -0.1085148 -0.7958312 -0.7413882   Male
## 22 -0.8566117 -0.5799931 -1.0196587 -1.0314966   Male
## 28 -1.2541553 -0.5799931 -1.2434863 -1.5150106 Female
```

```
#Fitting the LDA model with Canine group as dependent variable and all the
measurements as predictors
#Fitting with Training data
fit_lda <- lda(CanineGroup ~ X1+X2+X3+X4+X5+X6+X7+X8+X9, data =
train.transformed)
fit_lda
```

```
## Call:
## lda(CanineGroup ~ X1 + X2 + X3 + X4 + X5 + X6 + X7 + X8 + X9,
##     data = train.transformed)
##
## Prior probabilities of groups:
##        Cuons GoldenJackal IndianWolves    ModernDog     ThaiDogs
##    0.2222222    0.2539683    0.1904762    0.2063492    0.1269841
##
## Group means:
##                      X1         X2         X3         X4         X5
X6
## Cuons         0.2143826  0.5152073  0.5485166  0.6572795  0.3344391
0.49929577
## GoldenJackal -1.0007169 -1.2628391 -0.9290364 -1.3578961 -0.9138469 -
1.14234613
## IndianWolves  1.5674453  1.1485637  1.1418324  0.8920221  1.6706325
1.31331352
## ModernDog    -0.1516330 -0.1954749 -0.1307833 -0.0977863 -0.4726867 -
0.29852171
## ThaiDogs     -0.4785000  0.2188663 -0.6020571  0.3864225 -0.4954074 -
0.07394783
##                       X7         X8           X9
## Cuons        -0.84940930  0.0195405  0.474304244
## GoldenJackal -0.49159096 -0.9077450 -1.224902222
## IndianWolves  1.79704325  1.6103147  1.313546462
## ModernDog    -0.10851484 -0.1415661 -0.213242087
## ThaiDogs     -0.04958006 -0.4041330 -0.004029284
##
## Coefficients of linear discriminants:
##            LD1         LD2        LD3          LD4
## X1 -1.97072716  0.31966418 -1.6475816 -1.791634507
## X2  0.06807624 -0.19192502  0.6369900  0.004391232
## X3  0.99095629  0.13693446 -0.1322325 -0.573740739
## X4 -0.76054550 -0.28871452  1.6031046  0.501051689
## X5 -2.43079790  2.21886698 -2.7044257  2.188532378
```

```
## X6 -0.55809049 -0.07197145  0.2410220 -0.015939568
## X7  5.26574802  0.60720401  1.5297908  0.264218219
## X8  0.99632709  0.23806894  0.2776807 -0.510735191
## X9 -1.46257979 -0.38760990  1.2142292 -0.165711380
##
## Proportion of trace:
##    LD1    LD2    LD3    LD4
## 0.6347 0.2757 0.0831 0.0064
```

```r
#We get 4 functions LD1 to LD4 as there are canine 5 groups
plot(fit_lda)
```




```r
summary(fit_lda)
```

```
##         Length Class  Mode
## prior    5     -none- numeric
## counts   5     -none- numeric
## means   45     -none- numeric
## scaling 36     -none- numeric
## lev      5     -none- character
## svd      4     -none- numeric
## N        1     -none- numeric
## call     3     -none- call
## terms    3     terms  call
## xlevels  0     -none- list
```

```r
#chk coeffs they r gd
print(fit_lda)

## Call:
## lda(CanineGroup ~ X1 + X2 + X3 + X4 + X5 + X6 + X7 + X8 + X9,
##     data = train.transformed)
##
## Prior probabilities of groups:
##        Cuons GoldenJackal IndianWolves    ModernDog     ThaiDogs
##    0.2222222    0.2539683    0.1904762    0.2063492    0.1269841
##
## Group means:
##                      X1         X2         X3         X4         X5
X6
## Cuons         0.2143826  0.5152073  0.5485166  0.6572795  0.3344391
0.49929577
## GoldenJackal -1.0007169 -1.2628391 -0.9290364 -1.3578961 -0.9138469 -
1.14234613
## IndianWolves  1.5674453  1.1485637  1.1418324  0.8920221  1.6706325
1.31331352
## ModernDog    -0.1516330 -0.1954749 -0.1307833 -0.0977863 -0.4726867 -
0.29852171
## ThaiDogs     -0.4785000  0.2188663 -0.6020571  0.3864225 -0.4954074 -
0.07394783
##                       X7         X8           X9
## Cuons        -0.84940930  0.0195405  0.474304244
## GoldenJackal -0.49159096 -0.9077450 -1.224902222
## IndianWolves  1.79704325  1.6103147  1.313546462
## ModernDog    -0.10851484 -0.1415661 -0.213242087
## ThaiDogs     -0.04958006 -0.4041330 -0.004029284
##
## Coefficients of linear discriminants:
##            LD1         LD2        LD3          LD4
## X1 -1.97072716  0.31966418 -1.6475816 -1.791634507
## X2  0.06807624 -0.19192502  0.6369900  0.004391232
## X3  0.99095629  0.13693446 -0.1322325 -0.573740739
## X4 -0.76054550 -0.28871452  1.6031046  0.501051689
## X5 -2.43079790  2.21886698 -2.7044257  2.188532378
## X6 -0.55809049 -0.07197145  0.2410220 -0.015939568
## X7  5.26574802  0.60720401  1.5297908  0.264218219
## X8  0.99632709  0.23806894  0.2776807 -0.510735191
## X9 -1.46257979 -0.38760990  1.2142292 -0.165711380
##
## Proportion of trace:
##    LD1    LD2    LD3    LD4
## 0.6347 0.2757 0.0831 0.0064

fit_lda$counts #IT gives no of observations put in respective groups
```

```
##        Cuons GoldenJackal IndianWolves    ModernDog     ThaiDogs
##           14           16           12           13            8
```

```
fit_lda$means
```

```
##                     X1         X2         X3         X4         X5
X6
## Cuons         0.2143826  0.5152073  0.5485166  0.6572795  0.3344391
0.49929577
## GoldenJackal -1.0007169 -1.2628391 -0.9290364 -1.3578961 -0.9138469 -
1.14234613
## IndianWolves  1.5674453  1.1485637  1.1418324  0.8920221  1.6706325
1.31331352
## ModernDog    -0.1516330 -0.1954749 -0.1307833 -0.0977863 -0.4726867 -
0.29852171
## ThaiDogs     -0.4785000  0.2188663 -0.6020571  0.3864225 -0.4954074 -
0.07394783
##                      X7         X8           X9
## Cuons        -0.84940930  0.0195405  0.474304244
## GoldenJackal -0.49159096 -0.9077450 -1.224902222
## IndianWolves  1.79704325  1.6103147  1.313546462
## ModernDog    -0.10851484 -0.1415661 -0.213242087
## ThaiDogs     -0.04958006 -0.4041330 -0.004029284
```

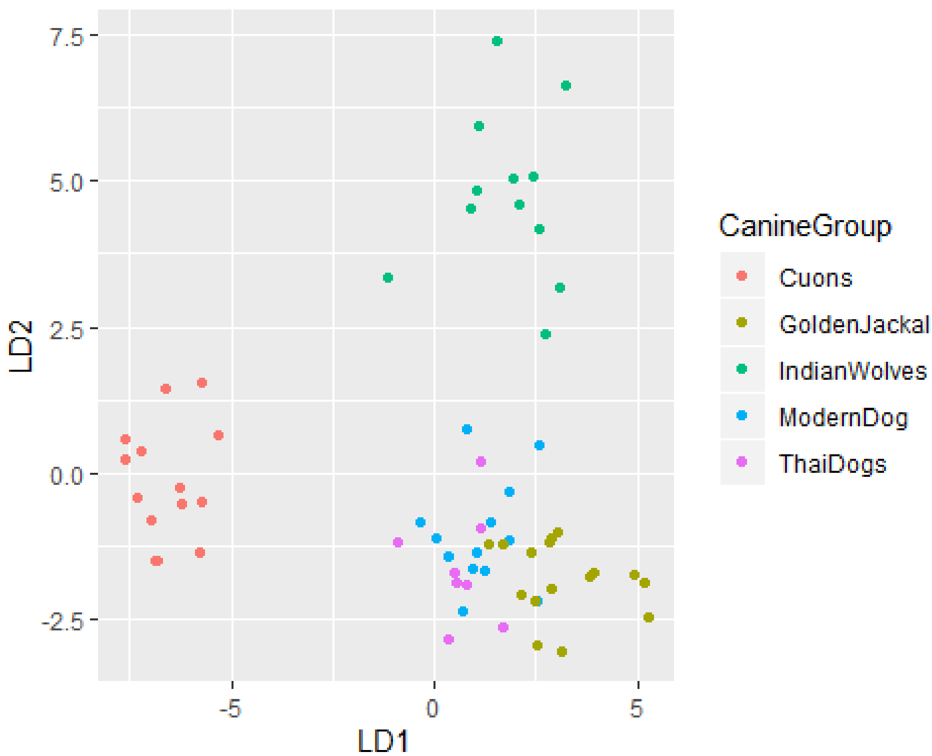
#Here we can see how means r different for the measurements in different canine grps
#For example Indian wolves have higher (Positive) values of means for all the measurements.
#On the contrary, Golden Jackal has the smallest values (negative) for all the measurements.
#This shows that there is a large difference between the measurements of Indian wolves and Golden Jackal.
#This is how the Canine groups are being separated using the measurements.

```
fit_lda$scaling
```

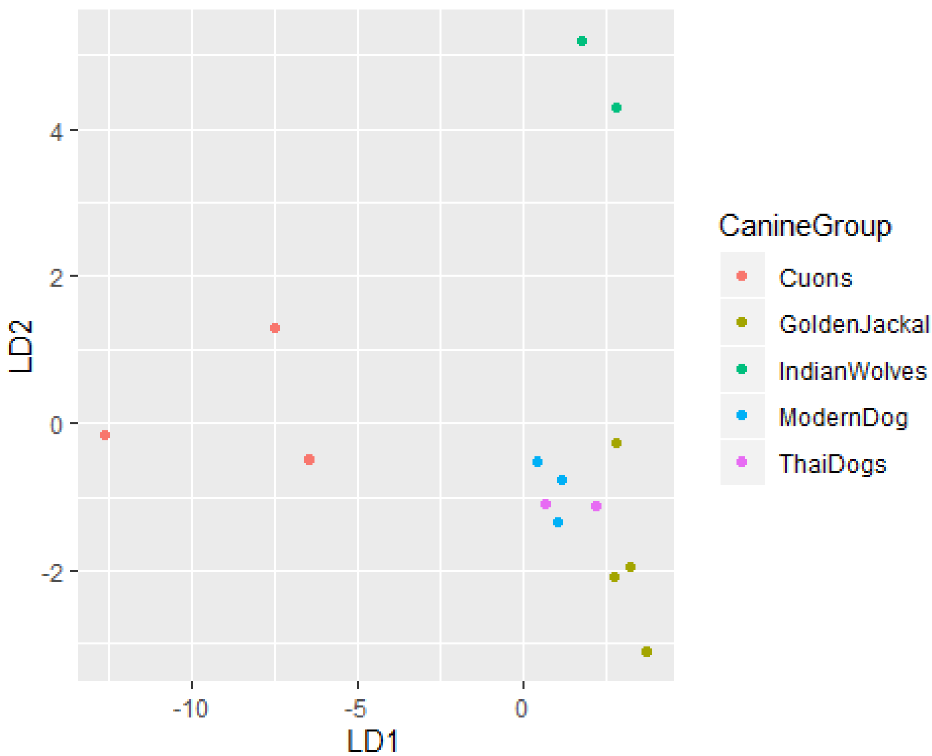
```
##            LD1         LD2        LD3          LD4
## X1 -1.97072716  0.31966418 -1.6475816 -1.791634507
## X2  0.06807624 -0.19192502  0.6369900  0.004391232
## X3  0.99095629  0.13693446 -0.1322325 -0.573740739
## X4 -0.76054550 -0.28871452  1.6031046  0.501051689
## X5 -2.43079790  2.21886698 -2.7044257  2.188532378
## X6 -0.55809049 -0.07197145  0.2410220 -0.015939568
## X7  5.26574802  0.60720401  1.5297908  0.264218219
## X8  0.99632709  0.23806894  0.2776807 -0.510735191
## X9 -1.46257979 -0.38760990  1.2142292 -0.165711380
```

```
fit_lda$prior
```

```
##        Cuons GoldenJackal IndianWolves    ModernDog     ThaiDogs
##    0.2222222    0.2539683    0.1904762    0.2063492    0.1269841

#above gives prior probabilities
fit_lda$lev

## [1] "Cuons"        "GoldenJackal" "IndianWolves" "ModernDog"    "ThaiDogs"

fit_lda$svd

## [1] 14.361791  9.465986  5.197737  1.440606

#singular values (svd) that gives the ratio of the between- and within-group
standard deviations on the linear discriminant variables.
#fit_lda$N
#fit_lda$call

#Predictions for test data==>
predictions <- fit_lda %>% predict(test.transformed)
names(predictions)

## [1] "class"     "posterior" "x"

#Linear discriminants -- Functions
head(predictions$x, 9)

##           LD1        LD2        LD3         LD4
## 4   0.4356528 -0.5164550  0.5316930 -0.71066819
## 7   1.0183009 -1.3282084  0.7191164 -0.23634222
## 11  1.1679786 -0.7637476  0.9020575  1.46762903
## 18  2.8191202 -0.2591108 -1.8265538  2.43825960
## 22  2.7506776 -2.0852008 -1.4779341 -0.12556377
## 28  3.2301641 -1.9528649 -1.6421005  0.21878152
## 32  3.7201019 -3.0957270 -0.6032432 -0.07921485
## 43 -7.4892226  1.3040956 -1.9033387  1.91440481
## 45 -6.4840681 -0.4828682  0.6652580 -0.64769490

#Plotting Training data predictions
lda.dataTrn <- cbind(train.transformed, predict(fit_lda)$x)
ggplot(lda.dataTrn, aes(LD1, LD2,LD3,LD4)) +
  geom_point(aes(color = CanineGroup))

## Warning: Duplicated aesthetics after name standardisation:
```




```
#Plotting for Testing data predictions
lda.dataTst <- cbind(test.transformed, predictions$x)
ggplot(lda.dataTst, aes(LD1, LD2,LD3,LD4)) +
  geom_point(aes(color = CanineGroup))

## Warning: Duplicated aesthetics after name standardisation:
```



#Both the Training and Testing prediction plots clearly shows 5 canine groups without any overlap
#So Model predictions look good.

```
# Lets try to compare Actual and predicted groups
#For training data
lda.train <- predict(fit_lda,train.transformed)
lda.train

## $class
##  [1] ModernDog    ModernDog    ModernDog    ModernDog    ModernDog
##  [6] ModernDog    ModernDog    ModernDog    ModernDog    ModernDog
## [11] ModernDog    ModernDog    ModernDog    GoldenJackal GoldenJackal
## [16] GoldenJackal GoldenJackal GoldenJackal GoldenJackal GoldenJackal
## [21] GoldenJackal GoldenJackal GoldenJackal GoldenJackal GoldenJackal
## [26] GoldenJackal GoldenJackal GoldenJackal GoldenJackal Cuons
## [31] Cuons        Cuons        Cuons        Cuons        Cuons
## [36] Cuons        Cuons        Cuons        Cuons        Cuons
## [41] Cuons        Cuons        Cuons        ModernDog    ThaiDogs
## [46] ThaiDogs     ModernDog    ThaiDogs     ThaiDogs     ThaiDogs
## [51] ThaiDogs     IndianWolves IndianWolves IndianWolves IndianWolves
## [56] IndianWolves IndianWolves IndianWolves IndianWolves IndianWolves
## [61] IndianWolves IndianWolves IndianWolves
## Levels: Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##
## $posterior
```

```
##            Cuons GoldenJackal IndianWolves    ModernDog     ThaiDogs
## 1  1.388956e-15 9.090607e-04 2.431872e-10 5.319940e-01 4.670969e-01
## 2  5.481175e-11 3.361494e-04 3.520329e-09 9.875639e-01 1.209998e-02
## 3  2.926527e-18 6.203807e-02 1.121008e-03 6.665732e-01 2.702677e-01
## 5  1.544167e-13 1.197820e-05 7.890816e-05 9.643060e-01 3.560314e-02
## 6  3.910723e-16 4.991412e-02 3.864008e-06 9.414455e-01 8.636515e-03
## 8  4.922102e-14 8.294856e-03 3.253250e-09 9.666672e-01 2.503792e-02
## 9  8.495759e-20 1.126659e-01 3.864376e-11 8.706160e-01 1.671810e-02
## 10 3.371585e-11 1.536991e-02 3.334777e-09 9.669817e-01 1.764837e-02
## 12 9.587465e-13 3.065208e-01 3.829167e-09 6.665146e-01 2.696462e-02
## 13 1.589935e-13 3.213183e-03 4.583587e-12 9.622972e-01 3.448961e-02
## 14 7.113746e-17 1.715308e-02 1.163483e-08 9.722371e-01 1.060985e-02
## 15 1.270871e-14 7.822919e-02 7.767764e-08 9.215826e-01 1.881692e-04
## 16 1.390227e-09 5.474358e-05 1.579850e-08 7.016953e-01 2.982499e-01
## 17 5.316199e-25 9.891208e-01 9.733194e-11 1.087563e-02 3.593184e-06
## 19 9.733673e-22 9.996605e-01 1.310722e-09 3.394680e-04 3.749826e-08
## 20 3.837107e-29 9.984586e-01 2.428819e-11 1.540358e-03 9.939077e-07
## 21 2.528531e-20 9.730982e-01 1.258661e-08 2.683574e-02 6.606309e-05
## 23 1.906400e-14 9.671754e-01 7.655723e-09 3.279955e-02 2.502515e-05
## 24 7.118567e-18 8.760949e-01 4.660528e-11 1.238461e-01 5.902458e-05
## 25 2.864106e-18 6.217499e-01 1.131495e-08 3.739170e-01 4.333135e-03
## 26 7.591279e-16 9.791913e-01 5.210808e-09 2.080194e-02 6.744070e-06
## 27 1.506685e-20 9.962582e-01 2.629577e-09 3.738426e-03 3.384120e-06
## 29 1.729664e-20 9.926945e-01 4.666467e-14 7.303140e-03 2.350636e-06
## 30 1.023272e-22 9.881341e-01 3.277515e-14 1.185065e-02 1.523788e-05
## 31 9.421078e-32 9.999751e-01 1.287257e-14 2.491210e-05 4.541537e-10
## 33 5.472563e-20 9.982589e-01 2.718295e-12 1.740229e-03 9.189538e-07
## 34 1.178817e-30 9.998725e-01 3.257114e-12 1.273348e-04 1.822945e-07
## 35 2.400741e-21 9.959632e-01 1.296541e-11 4.035412e-03 1.379568e-06
## 36 4.209467e-25 9.992773e-01 1.378137e-11 7.225713e-04 8.137076e-08
## 37 1.000000e+00 1.500233e-17 3.598527e-21 1.214922e-11 4.083535e-13
## 38 1.000000e+00 4.724516e-19 7.701868e-15 5.107151e-13 2.746634e-15
## 39 1.000000e+00 3.423873e-27 5.149038e-24 2.556475e-17 4.949800e-17
## 40 1.000000e+00 6.010167e-21 2.297556e-20 1.030553e-12 4.770873e-14
## 41 1.000000e+00 7.236201e-21 1.813379e-20 4.366551e-12 4.096487e-12
## 42 1.000000e+00 1.767055e-17 6.243559e-15 2.149333e-10 4.508467e-11
## 44 1.000000e+00 6.776174e-25 1.204115e-24 1.263339e-16 4.958700e-18
## 46 1.000000e+00 2.407349e-18 6.563207e-19 2.580120e-11 5.316656e-12
## 47 1.000000e+00 7.763885e-24 7.239035e-24 7.341319e-15 2.757431e-14
## 48 1.000000e+00 2.823590e-27 2.965386e-23 2.410889e-17 8.437128e-18
## 50 1.000000e+00 7.207557e-22 1.320856e-25 1.260816e-15 3.722618e-17
## 51 1.000000e+00 3.286344e-23 3.484540e-18 1.334834e-15 8.889384e-17
## 52 1.000000e+00 9.180986e-25 1.081374e-22 1.722856e-17 2.821341e-18
## 53 1.000000e+00 1.194451e-21 3.582945e-25 4.547906e-15 3.202027e-16
## 54 4.767648e-12 1.826275e-02 3.888271e-10 7.050458e-01 2.766915e-01
## 55 3.350196e-16 1.920233e-05 1.577227e-09 2.425356e-02 9.757272e-01
## 56 8.297904e-17 1.394484e-07 1.804986e-07 3.525646e-02 9.647432e-01
## 57 1.427678e-12 2.186544e-03 2.831961e-13 5.217713e-01 4.760422e-01
## 59 1.166786e-11 5.191057e-10 1.283781e-12 1.464206e-03 9.985358e-01
## 61 1.177734e-15 4.224614e-06 2.410703e-12 5.600662e-02 9.439892e-01
```

```
## 62 9.147629e-20 4.441405e-06 1.814597e-14 5.859564e-02 9.413999e-01
## 63 2.994048e-14 5.586607e-06 1.406942e-11 1.098247e-01 8.901697e-01
## 65 1.378969e-24 1.651718e-12 1.000000e+00 1.277048e-08 4.184558e-11
## 66 8.585340e-18 6.745086e-12 9.999997e-01 2.839354e-07 5.725258e-08
## 67 2.048285e-07 3.373233e-08 9.996900e-01 3.090435e-04 6.786096e-07
## 68 1.058976e-25 4.388552e-18 1.000000e+00 9.095769e-15 7.583324e-20
## 69 5.953963e-21 2.276260e-14 1.000000e+00 5.693822e-11 3.873198e-15
## 70 1.807904e-22 3.435237e-12 1.000000e+00 1.522104e-08 1.245093e-11
## 71 1.160407e-18 1.368711e-11 1.000000e+00 4.807964e-08 1.109413e-11
## 72 5.111515e-20 8.941127e-05 9.751777e-01 9.652944e-03 1.507999e-02
## 73 1.138890e-21 1.544656e-09 9.999999e-01 9.539803e-08 4.507628e-13
## 74 6.736745e-30 3.370249e-14 1.000000e+00 5.333068e-14 2.252133e-19
## 75 2.132274e-22 2.639185e-05 9.999353e-01 3.825453e-05 4.339422e-08
## 76 2.255239e-22 1.820291e-07 9.999997e-01 1.113720e-07 1.680672e-12
##
## $x
##            LD1        LD2         LD3         LD4
## 1   1.23813637 -1.6568988  1.88820506 -0.03976406
## 2   0.05288003 -1.0990658  0.67530012 -1.82911366
## 3   2.58593958  0.4912730  1.32160202  1.89285593
## 5   0.77255447  0.7569585  2.07157582 -2.11404908
## 6   1.86225159 -0.3095102  0.34028535 -0.34791908
## 8   1.03482253 -1.3575570  0.60359869 -0.77079436
## 9   2.55648217 -2.1851874  0.86074357 -1.23582080
## 10  0.34169764 -1.4247120 -0.06702892 -0.22673716
## 12  0.92208542 -1.6254106 -0.42788377  1.23553095
## 13  0.67643544 -2.3445037  0.78394387 -1.43509386
## 14  1.83761836 -1.1481275  0.73219247 -1.29886216
## 15  1.37427088 -0.8479240 -0.79633696 -2.10533461
## 16 -0.36596176 -0.8332142  1.47780543 -0.22574974
## 17  3.91910055 -1.6806524 -0.88060878 -0.87383368
## 19  3.05694715 -1.0115197 -2.64374704  1.22030259
## 20  4.90517710 -1.7324614 -0.64415374 -0.31956801
## 21  2.87685956 -1.0999166 -0.95617117  0.82768862
## 23  1.34938948 -1.2221268 -2.09365470  1.10100859
## 24  2.12121434 -2.0666067 -1.23189769 -0.89091779
## 25  2.39248555 -1.3556030 -0.10699164  0.35076905
## 26  1.68359395 -1.2032352 -2.17651551  0.65929357
## 27  2.84081595 -1.1671604 -1.70673006  1.22874432
## 29  2.54945212 -2.9222417 -1.75299723 -0.55305449
## 30  3.13356234 -3.0367454 -0.96602475 -0.54353239
## 31  5.25636955 -2.4702235 -2.16451591 -0.94463734
## 33  2.49537612 -2.1932415 -2.14492252  0.88702198
## 34  5.18607632 -1.8790336 -0.96638410  0.97596938
## 35  2.90298774 -1.9743402 -1.76358865  0.12543203
## 36  3.82178882 -1.7529211 -1.88045444 -0.13134971
## 37 -5.79446003 -1.3353237 -1.32035671 -0.05961330
## 38 -5.71462683  1.5634569 -1.81903204  0.67100872
## 39 -7.61720953  0.2224246  0.62893878  0.01235801
## 40 -6.28296065 -0.2416378 -0.22776530 -1.36713294
```

```
## 41 -6.22343586 -0.5087321  0.76528262 -0.61508623
## 42 -5.32777054  0.6620547 -0.11713067  0.58049360
## 44 -7.31730863 -0.4114213 -0.88163937 -0.88674219
## 46 -5.74066825 -0.4799077 -0.31282946  0.17952197
## 47 -6.99316774 -0.7848591  0.69360494  0.24522234
## 48 -7.59561000  0.5824589  0.30925135 -0.71833613
## 50 -6.89414626 -1.4823439 -1.82620508  0.17642962
## 51 -6.63059151  1.4537938 -0.92182684  0.83115815
## 52 -7.22087711  0.3763021 -1.22996730  1.37230840
## 53 -6.80036809 -1.4897887 -1.38541054  0.19100765
## 54  0.52643382 -1.8573975  0.56252128  1.18324259
## 55  1.15865833 -0.9514794  2.73185516  2.08723868
## 56  1.14351984  0.1923134  3.96781213  0.14639520
## 57  0.34067999 -2.8395022  1.19084158  0.25887277
## 59 -0.88934157 -1.1893432  4.08054369  1.19016398
## 61  0.77126413 -1.8997037  3.03403590  0.18878461
## 62  1.70449522 -2.6345920  3.68608633 -0.95240952
## 63  0.48478332 -1.6814901  2.79334960 -0.03639300
## 65  2.43610774  5.0878462  1.62643524 -0.62242996
## 66  0.87667417  4.5164708  1.95104829  1.42144816
## 67 -1.12918083  3.3541447 -0.52046134  0.43580104
## 68  1.55380442  7.3904521 -0.67752413 -0.99977023
## 69  1.08228991  5.9263940 -0.37992914 -0.62063516
## 70  1.93176517  5.0404281  0.88638730 -0.76092184
## 71  1.05716493  4.8441969  0.03534136 -0.82885641
## 72  2.71953662  2.3796178  2.11938715  2.63214693
## 73  2.11206450  4.5900422 -1.12122207 -1.83466665
## 74  3.21940491  6.6168045 -1.61040471  0.37079589
## 75  3.07669631  3.1776184 -0.30833201  1.18611236
## 76  2.59597071  4.1626108 -1.78733085  0.32399780
```

```r
train.transformed$lda <- lda.train$class
train.transformed$lda
```

```
##  [1] ModernDog    ModernDog    ModernDog    ModernDog    ModernDog
##  [6] ModernDog    ModernDog    ModernDog    ModernDog    ModernDog
## [11] ModernDog    ModernDog    ModernDog    GoldenJackal GoldenJackal
## [16] GoldenJackal GoldenJackal GoldenJackal GoldenJackal GoldenJackal
## [21] GoldenJackal GoldenJackal GoldenJackal GoldenJackal GoldenJackal
## [26] GoldenJackal GoldenJackal GoldenJackal GoldenJackal Cuons
## [31] Cuons        Cuons        Cuons        Cuons        Cuons
## [36] Cuons        Cuons        Cuons        Cuons        Cuons
## [41] Cuons        Cuons        Cuons        ModernDog    ThaiDogs
## [46] ThaiDogs     ModernDog    ThaiDogs     ThaiDogs     ThaiDogs
## [51] ThaiDogs     IndianWolves IndianWolves IndianWolves IndianWolves
## [56] IndianWolves IndianWolves IndianWolves IndianWolves IndianWolves
## [61] IndianWolves IndianWolves IndianWolves
## Levels: Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
```

```r
table(train.transformed$lda,train.transformed$CanineGroup)
```

```
##
##                Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##   Cuons           14            0            0         0        0
##   GoldenJackal     0           16            0         0        0
##   IndianWolves     0            0           12         0        0
##   ModernDog        0            0            0        13        2
##   ThaiDogs         0            0            0         0        6
```

```
# running accuracy on the training set shows how good the model is.
#It predicted 2 values wrong out of 63 observations (2 Modern dogs are
incorrectly predicted as Thai dogs)
#It is not an indication of "true" accuracy. We will use the test set to
approximate accuracy
#For test data
lda.test <- predict(fit_lda,test.transformed)
test.transformed$lda <- lda.test$class
table(test.transformed$lda,test.transformed$CanineGroup)
```

```
##
##                Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##   Cuons            3            0            0         0        0
##   GoldenJackal     0            4            0         0        0
##   IndianWolves     0            0            2         0        0
##   ModernDog        0            0            0         3        1
##   ThaiDogs         0            0            0         0        1
```

```
#This shows that out of 4 Moderndogs, 3 are predicted correctly but 1 is
incorrectly predicted as a Thai dog

#Fig margin too large to produce graph
#par(mar = c(5, 5, 5, 5))
#partimat(CanineGroup ~ X1+X2+X3+X4+X5+X6+X7+X8+X9, data=train.transformed,
method="lda")
```

#Now lets check accuracy %

```
mean(predictions$class==test.transformed$CanineGroup)
```

```
## [1] 0.9285714
```

```
#Model Accuracy for train and test is 92.85%
```

#Discriminant Analysis Conclusion:

#Discriminant analysis is used when dependent variable is categorical with more than 2 values.

#Multiple discriminant analysis helps to classify the observations using functions.

#As per LDA model means -

#Here we can see how means r different for the measurements in different

canine groups.
#For example Indian wolves have higher (Positive) values of means for all the measurements.
#On the contrary, Golden Jackal has the smallest values (negative) for all the measurements.
#This shows that there is a large difference between the measurements of Indian wolves and Golden Jackal.
#This is how the Canine groups are being separated using the measurements.
#As per LDA model Plots -
#Both the Training and Testing prediction plots clearly shows 5 canine groups without any overlap
#So Model predictions look good.
 # running accuracy on the training set shows how good the model is.
#For training set, It predicted 2 values wron out of 63 observations (2 Modern dogs are incorrectly predicted as Thai dogs)
#For test set, This shows that out of 4 Moderndogs, 3 are predicted correctly but 1 is incorrectly predicted as a Thai dog
#With above outputs you can see that the canine groups are very well separated with LDA
#with 92% accuracy

```
#==============Question 6 end =======================
```

#@@@@@@@@@ Question 7 - Logistic Regression @@@@@@@@

#7. investigate each canine group separately to see whether logistic regression shows a significant difference between males and females for the measurements. Note that in view of the small sample sizes available for each group, it is unreasonable to expect to fit a logistic function involving all nine variables with good estimates of parameters. Therefore, consideration should be given to fitting functions using only a subset of the variables.

```
#
#library(regclass)
#Sample size is very small for the individual canine groups
#So to avoid curse of dimensionality, I am trying to fit logistic regression model using few measure variables
```

#For Modern Dogs

```
moderncanine <- Canine_Data[1:16,]
xtabs(~Gender + CanineGroup, data=moderncanine)

##          CanineGroup
## Gender    Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
```

```
##   Female      0            0            0         8        0
##   Male        0            0            0         8        0
##   Unknown     0            0            0         0        0

#using the variables X1, X2, X3 for the logistic model
logistic_modern <- glm(Gender~ X2+X3+X4, data=moderncanine,
family="binomial")
#Viewing the summary statistics
summary(logistic_modern)

##
## Call:
## glm(formula = Gender ~ X2 + X3 + X4, family = "binomial", data =
moderncanine)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.44704  -0.86076  -0.01154   0.71505   2.18570
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -22.2726    13.6466  -1.632    0.103
## X2            2.6844     1.8691   1.436    0.151
## X3           -0.7248     0.5481  -1.322    0.186
## X4            0.5574     0.6326   0.881    0.378
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 22.181  on 15  degrees of freedom
## Residual deviance: 14.893  on 12  degrees of freedom
## AIC: 22.893
##
## Number of Fisher Scoring iterations: 6

#AIC = 22
#plotting the confusion matrix
confusion_matrix(logistic_modern)

##               Predicted Female Predicted Male Total
## Actual Female                7              1     8
## Actual Male                  2              6     8
## Total                        9              7    16
```

#X2, X3 and X4 give Good predictions for Modern Dogs.

```
#@@@@@@
#predicted.data <-
data.frame(probability.of.gender=logistic_modern$fitted.values,X2=moderncanin
e$X2)
#predicted.data #finding hrt desease prob based on sex for each data pt
## we can use a table to summarize the predicted probabilities.
#xtabs(~ probability.of.gender + X2, data=predicted.data)
```

```r
#@@@@@@@@@@
#Computing the logistic model for the 2nd group of canines using the X7 variable
```

#For Golden Jackals

```r
can2<- Canine_Data[17:36,]
xtabs(~Gender + CanineGroup, data=can2)

##          CanineGroup
## Gender    Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##   Female      0           10            0         0        0
##   Male        0           10            0         0        0
##   Unknown     0            0            0         0        0

lo2 <- glm(Gender~ X1+X5, data=can2, family="binomial")
summary(lo2)

##
## Call:
## glm(formula = Gender ~ X1 + X5, family = "binomial", data = can2)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.63576  -0.08276   0.01137   0.19238   1.77995
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -175.1802   105.5058  -1.660   0.0968 .
## X1             1.0143     0.7254   1.398   0.1620
## X5             3.4023     1.7502   1.944   0.0519 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 27.7259  on 19  degrees of freedom
## Residual deviance:  8.5094  on 17  degrees of freedom
## AIC: 14.509
##
## Number of Fisher Scoring iterations: 8

confusion_matrix(lo2)

##                Predicted Female Predicted Male Total
## Actual Female                 9              1    10
## Actual Male                   1              9    10
## Total                        10             10    20
```

#X5 is more significant role to predict gender of Golden jackals
#However, X1 and X5 do not have significant difference between them and so do not predict Golden jackal gender very well.

```r
#For Cuons
#Now for the 3rd group, using the X4 and X7 predictors
can3<- Canine_Data[37:53,]
xtabs(~Gender + CanineGroup, data=can3)

##          CanineGroup
## Gender    Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##   Female      8            0            0         0        0
##   Male        9            0            0         0        0
##   Unknown     0            0            0         0        0

lo3 <- glm(Gender~ X4+X7, data=can3, family="binomial")
summary(lo3)

##
## Call:
## glm(formula = Gender ~ X4 + X7, family = "binomial", data = can3)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.458  -1.264   0.679   1.207   1.326
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -8.5235    11.1110  -0.767    0.443
## X4           -0.1463     0.3741  -0.391    0.696
## X7            0.4176     0.4065   1.027    0.304
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 23.508  on 16  degrees of freedom
## Residual deviance: 22.326  on 14  degrees of freedom
## AIC: 28.326
##
## Number of Fisher Scoring iterations: 4

confusion_matrix(lo3)

##               Predicted Female Predicted Male Total
## Actual Female                2              6     8
## Actual Male                  5              4     9
## Total                        7             10    17

#Similarly for the 4th group, I have used the X1, X6, X7, X8 and X9
predictors
#For Indian wolves
can4<- Canine_Data[64:77,]
xtabs(~Gender + CanineGroup, data=can4)
```

```
##          CanineGroup
## Gender    Cuons GoldenJackal IndianWolves ModernDog ThaiDogs
##   Female      0            0            6         0        0
##   Male        0            0            8         0        0
##   Unknown     0            0            0         0        0
```

```r
lo4 <- glm(Gender~ X1+X6+X7+X8+X9, data=can4, family="binomial")
```

```
## Warning: glm.fit: algorithm did not converge

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```r
summary(lo4)
```

```
## 
## Call:
## glm(formula = Gender ~ X1 + X6 + X7 + X8 + X9, family = "binomial", 
##     data = can4)
## 
## Deviance Residuals: 
##        Min          1Q      Median          3Q         Max  
## -1.131e-05  -5.000e-07   2.110e-08   2.280e-06   1.450e-05  
## 
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.454e+02  2.774e+06   0.000        1
## X1           7.706e+00  1.330e+04   0.001        1
## X6          -2.628e+00  3.149e+05   0.000        1
## X7          -2.336e+01  1.373e+05   0.000        1
## X8          -1.411e+01  4.181e+04   0.000        1
## X9           1.112e+02  2.325e+05   0.000        1
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 1.9121e+01  on 13  degrees of freedom
## Residual deviance: 5.9190e-10  on  8  degrees of freedom
## AIC: 12
## 
## Number of Fisher Scoring iterations: 25
```

```r
confusion_matrix(lo4)
```

```
##               Predicted Female Predicted Male Total
## Actual Female                6              0     6
## Actual Male                  0              8     8
## Total                        6              8    14
```

#Logistic regression Conclusion:

#Sample size is very small for the individual canine groups

#So to avoid curse of dimensionality, I am trying to fit logistic regression model

using few measure variables
#As per confusion matrices above, most of the logistic regression models are working well
#Because measurements are different for different Canine Groups so they predict gender correctly for given measurements.
#X2, X3 and X4 very well classify Modern Dogs into Male and Female groups.
#X5 is more significant role to predict gender of Golden jackals
#However, X1 and X5 do not have significant difference between them and so do not predict Golden jackal gender very well.
#Hence, the above logistic regression models shows that there is significant difference between males and females for the measurements.
#And so they classify observations into correct Male / Female groups given the values of Measurements.

```
#==============Question 7 end =======================
```

#@@@@@@@@@@@ Question 8 - ROC @@@@@@@@

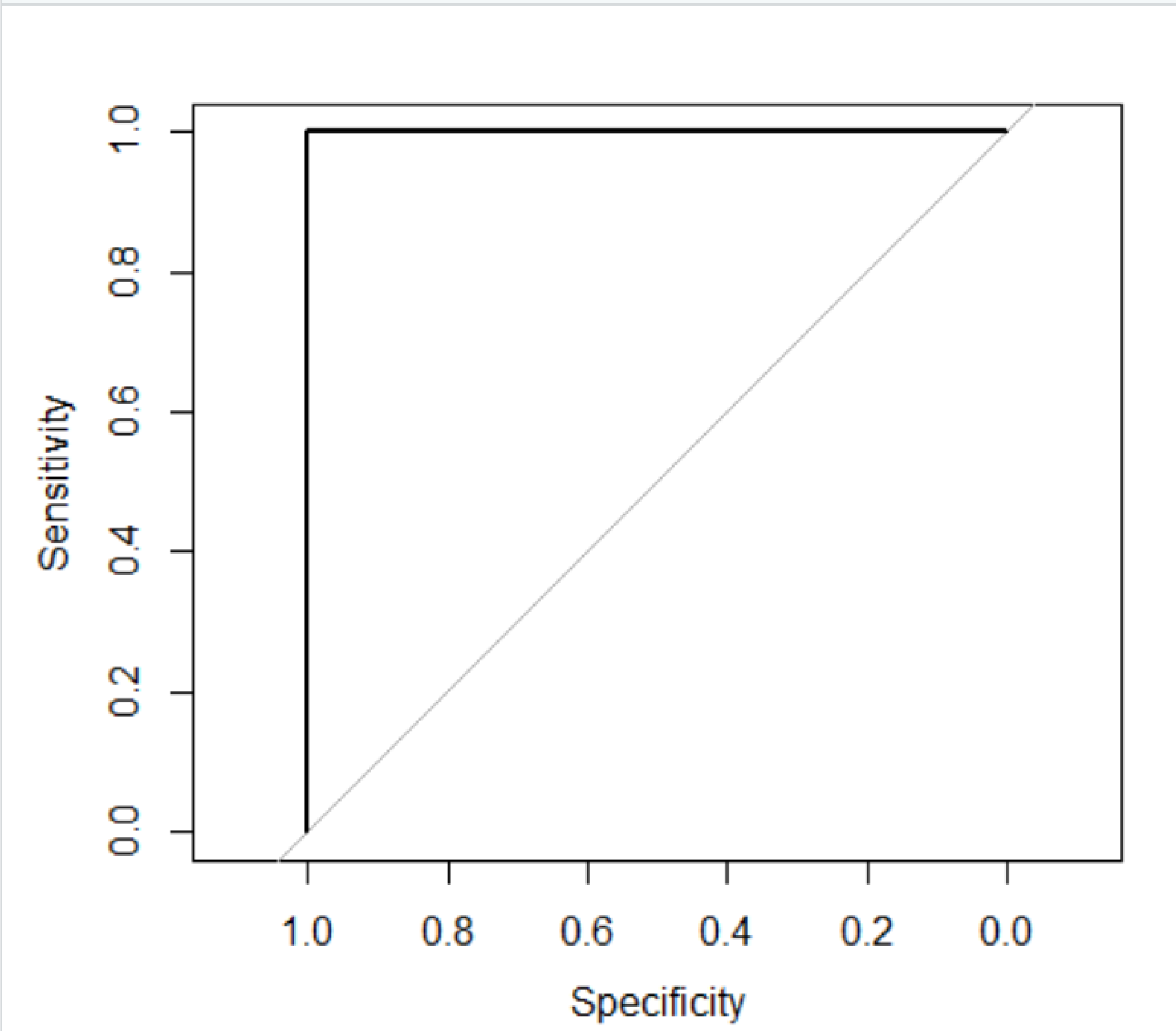
#8. Show ROC containing both your discriminant and logistic function for gender classification for the Prehistoric Thai Dog

#For Thai dogs:

```
Canine_Data$Gender[53:63] <- c("Female", "Male", "Female", "Male", "Male",
"Male", "Female","Female","Male","Male","Female")
Canine_Data$Gender <- as.factor(Canine_Data$Gender)
dataThai <- Canine_Data[c(54:63),]
dataThai

##    CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 54    ThaiDogs 112 10.1 17 18 19 7.7 31 33 5.8   Male
## 55    ThaiDogs 115 10.0 18 23 20 7.8 33 36 6.0 Female
## 56    ThaiDogs 136 11.9 22 25 21 8.5 36 39 7.0   Male
## 57    ThaiDogs 111  9.9 19 20 18 7.3 29 34 5.3   Male
## 58    ThaiDogs 130 11.2 23 27 20 9.1 35 35 6.6   Male
## 59    ThaiDogs 125 10.7 19 26 20 8.4 33 37 6.3 Female
## 60    ThaiDogs 132  9.6 19 20 19 9.7 35 38 6.6 Female
## 61    ThaiDogs 121 10.7 21 23 19 7.9 32 35 6.0   Male
## 62    ThaiDogs 122  9.8 22 23 18 7.9 32 35 6.1   Male
## 63    ThaiDogs 124  9.5 20 24 19 7.6 32 37 6.0 Female

#Fitting Logistic regression model

lo_Thai <- glm(Gender ~ .,data=dataThai[c(-1)], family="binomial")
summary(lo_Thai)
```

```
##
## Call:
## glm(formula = Gender ~ ., family = "binomial", data = dataThai[c(-1)])
##
## Deviance Residuals:
##  [1]  0  0  0  0  0  0  0  0  0  0
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.942e+02  6.328e+06       0        1
## X1          -4.115e+00  9.167e+04       0        1
## X2          -7.501e+00  7.185e+05       0        1
## X3           2.629e+01  3.948e+05       0        1
## X4          -1.099e+01  1.131e+05       0        1
## X5           4.108e+01  1.054e+06       0        1
## X6           2.782e+01  7.972e+05       0        1
## X7          -3.841e+01  8.190e+05       0        1
## X8          -8.144e-02  1.456e+05       0        1
## X9           1.215e+02  2.369e+06       0        1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1.3460e+01  on 9  degrees of freedom
## Residual deviance: 4.2867e-10  on 0  degrees of freedom
## AIC: 20
##
## Number of Fisher Scoring iterations: 23
```

```
#library(pROC)
roc(dataThai$Gender,lo_Thai$fitted.values,plot=TRUE)
#par(pty = "s")
```




```
#The Area under curve is 1 which is overfitting which might be due to the
small sample size

#Fitting lda model on thai dog data
lin_thai <- lda(Gender ~ ., data = dataThai[c(-1)])#, family="binomial")

## Warning in lda.default(x, grouping, ...): group Unknown is empty

## Warning in lda.default(x, grouping, ...): variables are collinear

lin_thai

## Call:
## lda(Gender ~ ., data = dataThai[c(-1)])
##
## Prior probabilities of groups:
## Female   Male
```

```
##    0.4    0.6
##
## Group means:
##          X1    X2       X3       X4       X5       X6    X7       X8
X9
## Female 124  9.95 19.00000 23.25000 19.50000 8.375000 33.25 37.00000
6.225000
## Male   122 10.60 20.66667 22.66667 19.16667 8.066667 32.50 35.16667
6.133333
##
## Coefficients of linear discriminants:
##           LD1
## X1  0.1056632
## X2 11.9779780
## X3  2.8973871
## X4 -2.4125649
## X5 -4.6606775
## X6 -5.0227080
## X7  1.1399154
## X8 -2.8151482
## X9  2.0090869
```

```r
lin_thai$prior
```

```
## Female   Male
##    0.4    0.6
```

```r
summary(lin_thai)
```

```
##         Length Class  Mode
## prior    2     -none- numeric
## counts   2     -none- numeric
## means   18     -none- numeric
## scaling  9     -none- numeric
## lev      3     -none- character
## svd      1     -none- numeric
## N        1     -none- numeric
## call     3     -none- call
## terms    3     terms  call
## xlevels  0     -none- list
```

```r
# Lets add the other graph
#plot.roc(dataThai$Gender, lin_thai$fitted.values, percent=TRUE,
col="#4daf4a", lwd=4, print.auc=TRUE, add=TRUE, print.auc.y=40)
#legend("bottomright", legend=c("Simple", "Non Simple"), col=c("#377eb8",
"#4daf4a"), lwd=4) # Make it user friendly
```

#Conclusion for Thai dogs ROC:

#The Area under curve is 1 which is overfitting which might be due to the small sample size

```
#==============Question 8 end =======================
```

#@@@@ Question 9 - Gender prediction for prehistoric thai dogs @@@

#9. Predict the Gender for the Prehistoric Thai Dog

```
data9 = Canine_Data[-c(54:63),-1] #removing the unknown gender rows and the canine group column
data9$Gender <- as.factor(data9$Gender)
#Fitting model on Thai dog data
logistic_T <- glm(Gender ~ ., data=data9, family="binomial")
summary(logistic_T)

##
## Call:
## glm(formula = Gender ~ ., family = "binomial", data = data9)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.9718  -1.1021   0.3837   1.0086   1.7916
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.94892    2.92170  -0.325    0.745
## X1           0.05571    0.07781   0.716    0.474
## X2           0.76742    0.59927   1.281    0.200
## X3           0.09570    0.09692   0.987    0.323
## X4          -0.26780    0.25630  -1.045    0.296
## X5          -0.16317    0.36040  -0.453    0.651
## X6          -0.84409    0.97851  -0.863    0.388
## X7           0.07344    0.13052   0.563    0.574
## X8          -0.24511    0.23483  -1.044    0.297
## X9           1.12319    0.85645   1.311    0.190
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 92.747  on 66  degrees of freedom
## Residual deviance: 81.939  on 57  degrees of freedom
## AIC: 101.94
##
## Number of Fisher Scoring iterations: 4
```

#a. Explain the reason for choosing the MVA technique for prediction

#The Logistic regression technique is chosen because

#We want to predict the Gender of Thai dogs, which is a categorical variable having 2 values as 'Male' & 'Female'
#This falls under the Binomial classification problem which works on the maximum likelihood principle
#The Linear discriminant analysis or random forest will also work for this problem.

#b. What is the Hit Ratio (Accuracy) of your classification technique?

```
#To check accuracy
pdata <- predict(logistic_T,newdata=data9,type="response")
pdata

##         1         2         3         4         5         6         7
8
## 0.6373411 0.3438914 0.4611295 0.7082149 0.7660123 0.6757455 0.4001009
0.7317289
##         9        10        11        12        13        14        15
16
## 0.5517566 0.4553697 0.7044623 0.4771642 0.5273017 0.5376575 0.3340535
0.6067306
##        17        18        19        20        21        22        23
24
## 0.4914652 0.2585982 0.3664417 0.4356189 0.2524704 0.5230936 0.2008980
0.6158678
##        25        26        27        28        29        30        31
32
## 0.4397013 0.4030895 0.3906903 0.2808497 0.2311434 0.4927282 0.4574246
0.4052972
##        33        34        35        36        37        38        39
40
## 0.4550128 0.2984661 0.3377446 0.2143183 0.4981630 0.8878184 0.7479240
0.6699633
##        41        42        43        44        45        46        47
48
## 0.5889636 0.6629109 0.5727399 0.5973199 0.5328368 0.6441110 0.7435923
0.3722040
##        49        50        51        52        53        64        65
66
## 0.2063523 0.3773638 0.4563857 0.3414591 0.2615866 0.6053135 0.7624328
0.7631413
##        67        68        69        70        71        72        73
74
## 0.7414619 0.6619095 0.8545097 0.9290440 0.9891649 0.4995653 0.4642971
0.6106067
##        75        76        77
## 0.1634855 0.8568749 0.4669179
```

```r
#Above are the probabilities
pdataF <- as.factor(ifelse(test=as.numeric(pdata>0.5) == 0, yes="Female",
no="Male"))
pdataF
```

```
##  [1] Male   Female Female Male   Male   Male   Female Male   Male   Female
## [11] Male   Female Male   Male   Female Male   Female Female Female Female
## [21] Female Male   Female Male   Female Female Female Female Female Female
## [31] Female Female Female Female Female Female Female Male   Male   Male
## [41] Male   Male   Male   Male   Male   Male   Male   Female Female Female
## [51] Female Female Female Male   Male   Male   Male   Male   Male   Male
## [61] Male   Female Female Male   Female Male   Female
## Levels: Female Male
```

```r
#if Probability >0.5 then classified as male, else female
#install.packages("e1071",
lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/library")
#library(e1071)
confusionMatrix(pdataF, data9$Gender)
```

```
## Warning in levels(reference) != levels(data): longer object length is not
a
## multiple of shorter object length
```

```
## Warning in confusionMatrix.default(pdataF, data9$Gender): Levels are not
in the
## same order for reference and data. Refactoring data to match.
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Female Male Unknown
##    Female      23   12       0
##    Male         9   23       0
##    Unknown      0    0       0
##
## Overall Statistics
##
##                Accuracy : 0.6866
##                  95% CI : (0.5616, 0.7944)
##     No Information Rate : 0.5224
##     P-Value [Acc > NIR] : 0.004694
##
##                   Kappa : 0.3744
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: Female Class: Male Class: Unknown
## Sensitivity                 0.7188      0.6571             NA
```

```
## Specificity                   0.6571      0.7188              1
## Pos Pred Value                0.6571      0.7188             NA
## Neg Pred Value                0.7188      0.6571             NA
## Prevalence                    0.4776      0.5224              0
## Detection Rate                0.3433      0.3433              0
## Detection Prevalence          0.5224      0.4776              0
## Balanced Accuracy             0.6879      0.6879             NA
```

```
#If error comment below 4 lines
data9$Gender <- "Female"
data9$Gender[2] <- "Male"
#finalthai$Gender = as.factor(finalthai$Gender)
head(data9)
```

```
##    X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 1 123 10.1 23 23 19 7.8 32 33 5.6 Female
## 2 137  9.6 19 22 19 7.8 32 40 5.8   Male
## 3 121 10.2 18 21 21 7.9 35 38 6.2 Female
## 4 130 10.7 24 22 20 7.9 32 37 5.9 Female
## 5 149 12.0 25 25 21 8.4 35 43 6.6 Female
## 6 125  9.5 23 20 20 7.8 33 37 6.3 Female
```

#Conclusion for gender prediction for prehistoric dog gender predictions:

#As per balanced class output, the Accuracy is 68.79%

#It can also be seen that for Female class sensitivity is more and for male class specificity is more.

```
#//////Q 9
#Predicting the gender of thai dogs
#install.packages("caret",
lib="/Library/Frameworks/R.framework/Versions/3.5/Resources/library")
#library(caret)
#finalthai <- Canine_Data[c(54:63),-1]
#finalthai$Gender <- "Female"
#finalthai$Gender[2] <- "Male"
#finalthai$Gender = as.factor(finalthai$Gender)
#head(finalthai)
#Using a threshold of 0.5 for determining the gender
#pdata <- predict(logistic,newdata=finalthai,type="response")
#Printing probabilities
#pdata
#If Prob > 0 then male else female
#pdataF <- as.factor(ifelse(test=as.numeric(pdata>0.5) == 0, yes="Female",
no="Male"))
#pdataF

#==============Question 9 end =======================
```

#@@@@@@@@@ Question 10 - Multiple Regression @@@@@@@@@@

#10. Create a model to predict length of the Mandible length for Prehistoric Thai Dog.
#a. What is the accuracy of your model

```
#From the above prediction, we are filling the unknown values with the predicted values.
Canine_Data$Gender[53:63] <- c("Female", "Male", "Female", "Male", "Male",
"Male", "Female","Female","Male","Male","Female")
Canine_Data$Gender <- as.factor(Canine_Data$Gender)

#Dataset with only thai dog data as asked in question
datamult <- Canine_Data[c(54:63),]

#X1 is the madible length
head(datamult)

##    CanineGroup  X1   X2 X3 X4 X5  X6 X7 X8  X9 Gender
## 54    ThaiDogs 112 10.1 17 18 19 7.7 31 33 5.8   Male
## 55    ThaiDogs 115 10.0 18 23 20 7.8 33 36 6.0 Female
## 56    ThaiDogs 136 11.9 22 25 21 8.5 36 39 7.0   Male
## 57    ThaiDogs 111  9.9 19 20 18 7.3 29 34 5.3   Male
## 58    ThaiDogs 130 11.2 23 27 20 9.1 35 35 6.6   Male
## 59    ThaiDogs 125 10.7 19 26 20 8.4 33 37 6.3 Female

#View(data10)
#View(data10[c(-1)])
```

#multiple regression with all the predictors

```
Regrn_all <-lm(X1~.,data = datamult[c(-1)])
summary(Regrn_all)

##
## Call:
## lm(formula = X1 ~ ., data = datamult[c(-1)])
##
## Residuals:
## ALL 10 residuals are 0: no residual degrees of freedom!
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -41.21667         NA      NA       NA
## X2           -1.82292         NA      NA       NA
## X3            6.38958         NA      NA       NA
## X4           -2.66979         NA      NA       NA
## X5            9.98333         NA      NA       NA
## X6            6.76042         NA      NA       NA
```

```
## X7          -9.33438         NA       NA       NA
## X8          -0.01979         NA       NA       NA
## X9          29.53125         NA       NA       NA
## GenderMale  -11.93958        NA       NA       NA
##
## Residual standard error: NaN on 0 degrees of freedom
## Multiple R-squared:      1,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 9 and 0 DF,  p-value: NA
```

```
#Output not good so trying with different variables
#The significance of X8,X2 is very less and, we can compute the model by removing these factors.

Regrn_2 <- lm(X1~X3+X4+X5+X6+X7+X9+Gender,data = datamult[c(-1)])
summary(Regrn_2)
```

```
##
## Call:
## lm(formula = X1 ~ X3 + X4 + X5 + X6 + X7 + X9 + Gender, data =
datamult[c(-1)])
##
## Residuals:
##       54       55       56       57       58       59       60       61
##  0.24198 -0.14447 -0.06360 -0.05624  0.26174 -0.13215 -0.06032 -0.29805
##       62       63
## -0.08583  0.33693
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -31.3926     7.4642  -4.206  0.05215 .
## X3            6.0040     0.4359  13.773  0.00523 **
## X4           -2.5810     0.2347 -10.997  0.00817 **
## X5            7.9530     0.8099   9.820  0.01021 *
## X6            5.8603     0.5694  10.292  0.00931 **
## X7           -8.2167     0.6461 -12.718  0.00613 **
## X9           27.3681     1.6798  16.293  0.00375 **
## GenderMale  -12.7080     0.8867 -14.332  0.00483 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4393 on 2 degrees of freedom
## Multiple R-squared:  0.9994, Adjusted R-squared:  0.9973
## F-statistic: 471.7 on 7 and 2 DF,  p-value: 0.002117
```

#The adjusted R-squared is nearly 1 (99.73) which indicates over-fitting.
#This is due the small sample size.

```
#dropping x5 as it is not significant
Regrn_3 <- lm(X1~X3+X4+X6+X7+X9+Gender,data = datamult[c(-1)])
summary(Regrn_3)
```

```
##
## Call:
## lm(formula = X1 ~ X3 + X4 + X6 + X7 + X9 + Gender, data = datamult[c(-1)])
##
## Residuals:
##       54       55       56       57       58       59       60       61
## -0.72426 -1.25310  1.39135  1.88972  0.00323 -0.35111  0.32467  0.48804
##       62       63
## -3.04808  1.27955
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  34.2404    19.0378   1.799   0.1699
## X3            2.0440     0.9486   2.155   0.1202
## X4           -0.4988     0.5765  -0.865   0.4506
## X6            1.7902     2.2366   0.800   0.4820
## X7           -3.2363     2.2928  -1.412   0.2529
## X9           24.9215     9.5158   2.619   0.0791 .
## GenderMale   -5.2884     2.6586  -1.989   0.1408
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.516 on 3 degrees of freedom
## Multiple R-squared:  0.9702, Adjusted R-squared:  0.9106
## F-statistic: 16.28 on 6 and 3 DF,  p-value: 0.0217
```

```
#Predictions
predk <- predict(Regrn_3,datamult[c(-1)])
predk #Predictions
```

```
##       54       55       56       57       58       59       60       61
## 112.7243 116.2531 134.6086 109.1103 129.9968 125.3511 131.6753 120.5120
##       62       63
## 125.0481 122.7205
```

```
datamult$X1 #Actual Data
```

```
##  [1] 112 115 136 111 130 125 132 121 122 124
```

#If you compare visually, the actual and predicted data,, the predictions are quiet impressive.

```
#Here accuracy is 91.06

##step<-stepAIC(Regrn_2,direction = "both") we can also use stepaic if needed
but here we already got 91 % accuracy
```

#Conclusion for Multiple Regression:

#Multiple Regression model is used to predict length of the Mandible length for

Prehistoric Thai Dogs.
#Multiple regression is used because the dependent variable is quantitative here.
#Different combinations of predictors were tried in order to achieve better accuracy
#The predictions were made
#The model with predictors - 'X3+X4+X6+X7+X9+Gender'is selected.
#Accuracy of this model is 91.06%
#==============Question 10 end ======================