DSC424Problem2HomeWork4RSyntaxfile

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#load the necessary packages

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

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

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

```
library(corrplot) # correlation visualization
```

```
## Warning: package 'corrplot' was built under R version 4.0.3
```

```
## corrplot 0.84 loaded
```

```
library(MASS) #for CV
```

```
##
## Attaching package: 'MASS'
```

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

```
library(caTools) # for splitting the data set into training and testing
```

```
## Warning: package 'caTools' was built under R version 4.0.3
```

#set the working directory

```
setwd("C:/Users/rejalu1/OneDrive - Henry Ford Health
System/DSC424/HomeWork4")
```

#Load the data set

```
heartds <- read.csv(file="../HomeWork4/datasets/heart.csv", header=TRUE,
sep=",")
```

#the top 6 rows of this data set

```
head(heartds)
```

```
##   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
## 1  52   1  0      125  212   0       1     168     0     1.0     2  2    3
## 2  53   1  0      140  203   1       0     155     1     3.1     0  0    3
## 3  70   1  0      145  174   0       1     125     1     2.6     0  0    3
## 4  61   1  0      148  203   0       1     161     0     0.0     2  1    3
## 5  62   0  0      138  294   1       1     106     0     1.9     1  3    2
## 6  58   0  0      100  248   0       0     122     0     1.0     1  0    2
##   heartdisease
## 1            0
## 2            0
## 3            0
## 4            0
## 5            0
## 6            1
```

#structure of the ds

```
str(heartds)
```

```
## 'data.frame':    1025 obs. of  14 variables:
##  $ age         : int  52 53 70 61 62 58 58 55 46 54 ...
##  $ sex         : int  1 1 1 1 0 0 1 1 1 1 ...
##  $ cp          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ trestbps    : int  125 140 145 148 138 100 114 160 120 122 ...
##  $ chol        : int  212 203 174 203 294 248 318 289 249 286 ...
##  $ fbs         : int  0 1 0 0 1 0 0 0 0 0 ...
##  $ restecg     : int  1 0 1 1 1 0 2 0 0 0 ...
##  $ thalach     : int  168 155 125 161 106 122 140 145 144 116 ...
##  $ exang       : int  0 1 1 0 0 0 0 1 0 1 ...
##  $ oldpeak     : num  1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 ...
##  $ slope       : int  2 0 0 2 1 1 0 1 2 1 ...
##  $ ca          : int  2 0 0 1 3 0 3 1 0 2 ...
##  $ thal        : int  3 3 3 3 2 2 1 3 3 2 ...
##  $ heartdisease: int  0 0 0 0 0 1 0 0 0 0 ...
```

#check if there are any missing values

```
sum(is.na(heartds))
```

```
## [1] 0
```

#Convert all the variables to numeric

```
heartdscleansed <- heartds %>%
  transmute(age = as.numeric(age)
        , sex = as.numeric(sex)
        , cp = as.numeric(cp)
        , trestbps = as.numeric(trestbps)
        , chol = as.numeric(chol)
        , fbs = as.numeric(fbs)
```

```
        , restecg = as.numeric(restecg)
        , thalach = as.numeric(thalach)
        , exang = as.numeric(exang)
        , oldpeak = oldpeak
        ,  slope = as.numeric(slope)
        , ca = as.numeric(ca)
        , thal = as.numeric(thal)
        , heartdisease =  as.factor(heartdisease)
        )
```

#structure of the heartdscleansed data set

```
str(heartdscleansed)
```

```
## 'data.frame':    1025 obs. of  14 variables:
##  $ age         : num  52 53 70 61 62 58 58 55 46 54 ...
##  $ sex         : num  1 1 1 1 0 0 1 1 1 1 ...
##  $ cp          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ trestbps    : num  125 140 145 148 138 100 114 160 120 122 ...
##  $ chol        : num  212 203 174 203 294 248 318 289 249 286 ...
##  $ fbs         : num  0 1 0 0 1 0 0 0 0 0 ...
##  $ restecg     : num  1 0 1 1 1 0 2 0 0 0 ...
##  $ thalach     : num  168 155 125 161 106 122 140 145 144 116 ...
##  $ exang       : num  0 1 1 0 0 0 0 1 0 1 ...
##  $ oldpeak     : num  1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 ...
##  $ slope       : num  2 0 0 2 1 1 0 1 2 1 ...
##  $ ca          : num  2 0 0 1 3 0 3 1 0 2 ...
##  $ thal        : num  3 3 3 3 2 2 1 3 3 2 ...
##  $ heartdisease: Factor w/ 2 levels "0","1": 1 1 1 1 1 2 1 1 1 1 ...
```

#determine how heartdisease is split

```
tabulate(heartds$heartdisease)
```

```
## [1] 526
```

#Run the correlation matrix and check for VIF

```
#m <- cor(heartdscleansedss)
#round(m, 2)
#m <- cor(heartdscleansedss, use='pairwise.complete.obs')
#round(m,2)
# M <- cor(heartdscleansedss)
# m <- corrplot(M, method="ellipse")
# m
# m <- corrplot(M, method="number")
# m
# model <- lm(heartdisease ~., data = heartds)
# VIF(model)
```

#Running LDA with cross-validation
##

#The depedent variable must be categorical

```
heartLDA <- lda(heartdisease ~., data = heartdscleansed)
#heartLDA
```

#plotting the model #we have to create a new without cross validation

```
#heartdiseaseLDA <- lda(heartdisease ~., data=heartdscleansed)
#heartdiseaseLDA
#plot(heartdiseaseLDA, xlab = "LDA1", ylab = "LDA2")
```

Try to predict the class from the original data

Note … this is JUST a test to see how this works

In practice you will want to use cross-validation!

```
p <- predict(heartLDA, newdata=heartdscleansed[,1:13])$class
p
```

```
##   [1] 0 0 0 0 0 1 0 0 0 0 1 0 1 0 1 1 1 0 1 1 1 1 0 1 1 0 1 1 1 0 0 1 0 0
1 1 1
##  [38] 1 0 1 1 1 1 0 1 1 1 0 1 0 1 0 1 0 0 0 1 1 1 1 1 1 0 1 1 1 1 0 1 0 0
0 0 0
##  [75] 0 1 1 0 1 1 1 0 1 1 1 1 1 1 0 0 1 1 0 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0
1 0 1
## [112] 0 0 0 1 0 0 0 1 1 1 0 0 1 0 1 0 1 1 1 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1
0 1 1
## [149] 1 1 0 0 0 1 0 1 1 1 1 1 0 1 0 0 0 0 0 1 1 1 1 0 1 1 0 0 0 0 1 0 0 1
0 1 1
## [186] 0 0 0 0 0 0 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 0 1 0
0 1 0
## [223] 1 1 1 1 1 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 1 1 1 1 1 1 0 0 1 1 0 1 0 0 0 1
1 1 1
## [260] 0 1 1 1 1 1 0 0 0 0 0 1 1 1 1 0 0 0 0 1 0 1 1 1 1 1 0 1 1 1 1 1 1 1 0 1
1 0 0
## [297] 0 0 1 1 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1 1 1 1 0 1 1 1 0 0 1 1 0 0 0 1
1 0 1
## [334] 1 0 0 1 1 1 0 1 1 1 1 1 0 0 1 0 1 0 0 0 0 1 1 0 0 1 1 1 0 1 1 1 1 0
1 1 1
## [371] 0 0 1 1 1 0 1 0 0 1 0 0 0 0 0 1 1 0 0 1 1 1 1 0 0 1 0 0 0 1 0 1 1 1
0 1 1
```

```
##  [408] 0 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 0 0 1 1 0 1 1 0 1 1 1 1 1 0 1 1 1
0 0 1
##  [445] 1 1 1 0 1 1 0 1 0 1 0 1 1 1 1 1 0 1 1 1 1 1 1 0 1 0 1 1 1 1 1 1 0 1
1 0 0
##  [482] 0 0 1 1 0 1 0 1 1 1 1 0 0 1 0 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 0 1
0 0 1
##  [519] 0 0 0 0 1 0 0 1 0 1 0 1 0 1 1 1 1 1 1 1 0 1 0 1 1 1 1 1 0 1 1 1 0 0
0 1 0
##  [556] 0 0 1 1 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 0 1 1 0 1 0 1 1 1 0 0 1 0 0 0
0 1 0
##  [593] 0 0 0 0 1 1 1 1 1 0 1 1 1 1 0 0 0 0 0 0 0 0 0 1 1 1 1 1 0 0 0 1 0 0
0 1 1
##  [630] 1 1 1 1 0 0 1 1 1 1 1 1 0 0 1 1 0 1 0 1 1 0 1 1 0 1 1 1 1 0 1 0 0 1
1 1 1
##  [667] 1 1 1 0 1 0 1 1 0 0 0 0 1 0 1 0 0 0 1 0 1 0 0 1 1 1 0 1 0 0 1 1 0 0
1 0 1
##  [704] 0 1 0 1 1 1 1 1 0 1 1 1 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 1 1 1 1 1 1 0
0 0 0
##  [741] 1 1 0 0 1 1 1 0 1 0 1 1 1 1 1 1 0 0 1 1 0 1 1 1 0 0 0 0 1 1 1 1 1 0
1 1 0
##  [778] 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 1 1 1 1 0 1 1 0 1 1 1 1 0 0 1 1 1 0
1 0 0
##  [815] 1 1 1 1 1 0 0 0 0 1 0 1 1 1 1 0 1 0 1 0 0 0 1 1 1 1 0 1 0 1 0 0 1 0
1 0 1
##  [852] 1 0 0 1 1 1 1 1 1 0 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 1 0 1 0 0 0
0 0 0
##  [889] 0 0 0 1 0 1 0 1 0 1 1 0 1 1 0 1 1 0 1 1 0 0 1 1 0 0 0 0 0 1 1 1 0 0
1 1 1
##  [926] 0 0 1 0 0 0 1 1 1 1 1 1 1 0 1 0 1 1 1 0 1 1 1 0 0 0 1 1 1 1 0 1 1 1
1 1 1
##  [963] 0 0 1 1 0 1 0 1 1 1 1 1 1 0 0 1 1 0 1 0 1 0 0 0 0 1 0 1 1 0 1 0 0 1
0 0 0
## [1000] 0 0 1 0 0 1 0 1 1 1 1 0 1 1 0 1 0 1 0 1 1 1 0 0 1 0
## Levels: 0 1
```

#Compare the results of the prediction

```
t <- table(p, heartdscleansed$heartdisease)
t

##
## p     0   1
##   0 376  41
##   1 123 485
```

#determine the accuracy

```
acc <- mean(p==heartdscleansed$heartdisease)
acc

## [1] 0.84
```

#splitting the data set into training and testing
##
##
####################

#you're going to do a set seed, because every set seed will give you a different randomization #So if you want to have the same exact. #If you want to know exactly where you got that randomization from, you want to set the seed to the same number

```
set.seed(123)
```

#put in sample split the original data set in this case we're going to do a 7030 split #so 70% is going into training #and 30% is going into testing.

```
sample <- sample.split(heartdscleansed, SplitRatio = 0.70)#Splits the data in the ratio mentioned in the SplitRatio
train <- subset(heartdscleansed, sample==TRUE)
test <- subset(heartdscleansed, sample==FALSE)
```

#The depedent variable must be categorial (Assuming No Cross-Validation)

```
heartLDA <- lda(heartdisease ~., data = train)
heartLDA

## Call:
## lda(heartdisease ~ ., data = train)
##
## Prior probabilities of groups:
##        0        1
## 0.508346 0.491654
##
## Group means:
##        age       sex        cp trestbps     chol       fbs   restecg
thalach
## 0 56.45373 0.8179104 0.5104478 133.3373 252.4657 0.1701493 0.4537313
138.7045
## 1 52.27778 0.5370370 1.4444444 129.6265 241.7068 0.1450617 0.5956790
158.5679
##       exang   oldpeak    slope        ca     thal
## 0 0.5611940 1.6435821 1.146269 1.1671642 2.543284
## 1 0.1450617 0.5496914 1.629630 0.3364198 2.104938
##
## Coefficients of linear discriminants:
##                    LD1
## age      -0.006501605
## sex      -0.855971953
## cp        0.373364594
## trestbps -0.001604870
## chol     -0.002299697
```

```
## fbs       0.076949989
## restecg   0.154638530
## thalach   0.010245005
## exang    -0.606056064
## oldpeak  -0.196089733
## slope     0.510724746
## ca       -0.428958496
## thal     -0.456359144

#plot(heartLDA)
#ls(heartLDA)
```

#we can predict on the training

```
p <- predict(heartLDA, newdata = heartdscleansed[,1:13])$class
p

##   [1] 0 0 0 0 0 1 0 0 0 0 1 0 1 0 1 1 1 0 1 1 1 1 0 1 1 0 1 1 0 0 0 1 0 0
1 1 1
##  [38] 1 0 0 1 1 1 0 1 1 1 0 1 0 1 0 1 0 0 0 1 1 1 1 1 1 0 1 1 1 1 0 1 0 0
0 0 0
##  [75] 0 1 1 0 1 1 1 0 1 1 1 1 1 1 0 0 1 1 0 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0
1 0 1
## [112] 0 0 0 1 0 0 0 1 1 1 0 0 1 0 1 0 1 0 1 1 1 1 1 1 0 1 1 1 1 0 1 0 1 1
0 1 1
## [149] 1 1 0 1 0 1 0 1 1 1 1 1 0 1 0 0 0 0 0 1 1 1 1 0 1 1 0 0 0 0 1 0 0 1
0 1 1
## [186] 0 0 0 0 0 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 0 1 0
0 1 0
## [223] 1 1 1 1 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 1 1 1 1 1 1 0 1 1 0 1 0 0 0 1
1 1 0
## [260] 0 1 1 1 1 0 0 0 0 0 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1 1 1 1 0 0 0
1 0 0
## [297] 0 0 1 1 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1 1 1 1 0 1 1 1 0 0 1 1 1 0 0 1
1 0 1
## [334] 1 0 0 1 0 0 0 1 1 1 1 1 0 0 1 0 0 0 0 0 0 1 1 0 0 1 1 1 0 1 1 1 1 0
0 0 1
## [371] 0 0 1 0 1 1 1 0 0 1 0 0 0 0 0 1 1 0 0 1 1 1 1 0 0 1 0 0 1 1 0 1 1 1
0 0 1
## [408] 0 1 1 1 0 0 0 1 1 0 0 1 1 1 1 1 1 0 0 1 1 0 1 1 0 1 1 1 1 1 0 1 0 1
0 0 1
## [445] 1 1 1 0 1 1 0 1 0 1 0 1 1 1 1 1 0 1 1 1 1 1 1 0 0 0 1 1 1 1 0 1 0 0
1 0 0
## [482] 0 0 1 1 0 1 0 1 0 1 1 0 0 1 0 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 0 1
0 0 1
## [519] 0 0 0 0 1 0 0 1 0 1 0 1 0 1 1 1 1 1 1 1 0 1 0 1 1 1 0 0 0 1 1 1 0 0
0 1 0
## [556] 0 0 1 1 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 0 1 1 0 1 0 1 1 1 0 0 1 0 0 0
0 1 0
## [593] 0 0 0 0 1 1 0 1 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 1 1 1 1 1 0 0 0 0 0 0
0 0 1
```

```
##  [630] 1 1 1 1 0 0 1 1 1 1 1 1 0 0 1 1 0 1 0 1 1 0 1 1 0 1 1 1 1 0 1 0 0 1
1 1 1
##  [667] 1 1 1 0 1 0 1 1 0 0 0 0 1 0 1 0 0 0 1 0 1 0 0 1 0 1 0 1 0 0 1 1 0 0
1 0 1
##  [704] 0 1 0 0 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 1 1 1 0 0 1 0 1 1 1 1 1 1 1 0
0 0 0
##  [741] 1 1 0 0 1 1 1 0 1 0 1 1 1 1 1 1 0 1 1 1 0 1 1 1 0 0 0 0 1 1 1 1 1 0
1 1 0
##  [778] 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 1 0 1 1 0 1 1 0 1 1 1 1 0 0 1 1 1 0
1 0 0
##  [815] 1 0 1 1 1 0 0 0 0 1 0 1 1 0 1 0 1 0 1 0 0 0 1 1 1 1 0 1 0 1 0 0 1 0
1 0 0
##  [852] 1 0 0 1 1 1 1 1 0 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 1 0 1 0 0 0
0 0 0
##  [889] 0 0 0 1 0 1 0 0 0 1 1 0 0 1 0 1 1 0 1 1 0 0 1 1 0 0 0 0 0 1 1 0 0 0
1 1 1
##  [926] 0 0 1 0 0 0 1 1 0 1 1 1 1 0 1 0 1 1 1 0 1 1 1 0 0 0 0 1 1 1 0 1 1 1
1 1 1
##  [963] 0 0 1 1 0 1 0 1 1 1 1 1 1 0 0 1 1 0 1 0 1 0 0 0 0 1 0 1 1 0 1 0 0 1
0 0 0
## [1000] 0 0 1 0 0 1 0 1 1 1 1 0 1 0 0 1 0 1 0 1 1 1 0 0 1 0
## Levels: 0 1
```

#we can use the table to get the same confusion matrix

```
t1 <- table(p, heartdscleansed$heartdisease)
t1
```

```
##
## p     0   1
##   0 401  49
##   1  98 477
```

#calculate the accuracy by using the mean

```
acc1 <- mean(p==heartdscleansed$heartdisease)
acc1
```

```
## [1] 0.8565854
```

#We can also do as we said before the Cross validation come up with the table, #and if we use coefficients remember if we do Ls. # Setting “CV = T” will have the lda function perform # “Leave-one-out” cross-validation

```
heartLDA2 <- lda(heartdisease ~., data=heartdscleansed, CV=T)
heartLDA2
```

```
## $class
##    [1] 0 0 0 0 0 1 0 0 0 0 1 0 1 0 1 1 1 0 1 1 1 1 0 1 1 0 1 1 1 0 0 1 0 0
1 1 1
##   [38] 1 0 1 1 1 1 0 1 1 1 0 1 0 1 0 1 0 0 0 1 1 1 1 1 1 0 1 1 1 1 0 1 0 0
0 0 0
```

```
##   [75] 0 1 1 0 1 1 1 0 1 1 1 1 1 1 0 0 1 1 0 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0
1 0 1
##  [112] 0 0 0 1 0 0 0 1 1 1 0 0 1 0 1 0 1 1 1 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1
0 1 1
##  [149] 1 1 0 1 0 1 0 1 1 1 1 1 0 1 0 0 0 0 0 1 1 1 1 0 1 1 0 0 0 0 1 0 0 1
0 1 1
##  [186] 0 0 0 0 0 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 0 1 0
0 1 0
##  [223] 1 1 1 1 0 1 1 0 0 1 0 1 1 1 0 1 0 1 1 1 1 1 1 1 1 0 1 1 0 1 0 0 0 1
1 1 1
##  [260] 0 1 1 1 1 0 0 0 0 0 1 1 1 1 0 0 0 0 1 0 1 1 1 1 1 0 1 1 1 1 1 1 0 0
1 0 0
##  [297] 0 0 1 1 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1 1 1 1 0 1 1 1 0 0 1 1 1 0 0 1
1 0 1
##  [334] 1 0 0 1 1 1 0 1 1 1 1 1 0 0 1 0 1 0 0 0 0 1 1 0 0 1 1 1 0 1 1 1 1 0
1 0 1
##  [371] 0 0 1 1 1 0 1 0 0 1 0 0 0 0 0 1 1 0 0 1 1 1 1 0 0 1 0 0 0 1 0 1 1 1
0 1 1
##  [408] 0 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 0 0 1 1 0 1 1 0 1 1 1 1 1 0 1 1 1
0 0 1
##  [445] 1 1 1 0 1 1 0 1 0 1 0 1 1 1 1 1 0 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 0 1
1 0 0
##  [482] 0 0 1 1 0 1 0 1 0 1 1 0 0 1 0 0 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 0 1
0 0 1
##  [519] 0 0 0 0 1 0 0 1 0 1 0 1 0 1 1 1 1 1 1 1 0 1 0 1 1 1 1 1 0 1 1 1 0 0
0 1 0
##  [556] 0 0 1 1 0 1 1 1 1 0 1 1 1 1 1 1 0 1 1 0 1 1 0 1 0 1 1 1 0 0 1 0 0 0
0 1 0
##  [593] 0 0 0 0 1 1 1 1 1 0 1 1 1 1 0 0 0 0 0 0 0 0 0 1 1 1 1 1 0 0 0 1 0 0
0 1 1
##  [630] 1 1 1 1 0 0 1 1 1 1 1 1 0 0 0 1 0 1 0 1 1 0 1 1 0 1 1 1 1 0 1 0 0 1
1 1 1
##  [667] 1 1 1 0 1 0 1 1 0 0 0 0 1 0 1 0 0 0 1 0 1 0 0 1 0 1 0 1 0 0 1 1 0 0
1 0 1
##  [704] 0 1 0 1 1 1 1 1 0 1 1 1 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 1 1 1 1 1 1 0
0 0 0
##  [741] 1 1 0 0 1 1 1 0 1 0 1 1 1 0 1 1 0 0 1 1 0 1 1 1 0 0 0 0 1 1 1 1 1 0
1 1 0
##  [778] 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 1 1 1 1 0 1 1 0 1 1 1 1 0 0 1 1 1 0
1 0 0
##  [815] 1 0 1 1 1 0 0 0 0 1 0 1 1 1 1 0 1 0 1 0 0 0 1 1 1 1 0 1 0 1 0 0 1 0
1 0 1
##  [852] 1 0 0 1 1 1 1 1 1 0 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 1 0 1 0 0 0
0 0 0
##  [889] 0 0 0 1 0 1 0 1 0 1 1 0 1 1 0 1 1 0 1 1 0 0 1 1 0 0 0 0 0 1 1 1 0 0
1 1 1
##  [926] 0 0 1 0 0 0 1 1 1 1 1 1 1 0 1 0 1 1 0 0 1 1 1 0 0 0 1 1 1 1 0 1 1 1
1 1 1
##  [963] 0 0 1 1 0 1 0 1 1 1 1 1 1 0 0 1 1 0 1 0 1 0 0 0 0 1 0 1 1 0 1 0 0 1
0 0 0
```

```
## [1000] 0 0 1 0 0 1 0 1 1 1 1 0 1 1 0 1 0 1 0 1 1 1 0 0 1 0
## Levels: 0 1
##
## $posterior
##                0           1
## 1    0.767608548 0.2323914521
## 2    0.981677756 0.0183222441
## 3    0.986367250 0.0136327504
## 4    0.616250115 0.3837498846
## 5    0.918466648 0.0815333518
## 6    0.251656048 0.7483439524
## 7    0.974792687 0.0252073126
## 8    0.980252913 0.0197470874
## 9    0.607370801 0.3926291988
## 10   0.993671030 0.0063289698
## 11   0.222754578 0.7772454220
## 12   0.905451979 0.0945480210
## 13   0.006597333 0.9934026675
## 14   0.999185014 0.0008149864
## 15   0.217150645 0.7828493546
## 16   0.006597333 0.9934026675
## 17   0.093848688 0.9061513118
## 18   0.992083114 0.0079168859
## 19   0.023115111 0.9768848890
## 20   0.050017267 0.9499827326
## 21   0.336276742 0.6637232580
## 22   0.225861676 0.7741383241
## 23   0.884010942 0.1159890579
## 24   0.009117245 0.9908827549
## 25   0.006133200 0.9938667997
## 26   0.793932563 0.2060674366
## 27   0.080120249 0.9198797509
## 28   0.164587517 0.8354124827
## 29   0.368723635 0.6312763652
## 30   0.886773991 0.1132260088
## 31   0.782648686 0.2173513137
## 32   0.023115111 0.9768848890
## 33   0.968479141 0.0315208589
## 34   0.974220731 0.0257792685
## 35   0.027867276 0.9721327245
## 36   0.400501761 0.5994982389
## 37   0.390364797 0.6096352031
## 38   0.223109894 0.7768901056
## 39   0.978840223 0.0211597767
## 40   0.460641091 0.5393589085
## 41   0.049034060 0.9509659399
## 42   0.296769131 0.7032308691
## 43   0.065517555 0.9344824452
## 44   0.607370801 0.3926291988
## 45   0.040134255 0.9598657454
```

```
## 46   0.133843716 0.8661562836
## 47   0.101218565 0.8987814355
## 48   0.909796444 0.0902035563
## 49   0.077114795 0.9228852049
## 50   0.941783465 0.0582165351
## 51   0.009708566 0.9902914341
## 52   0.677749448 0.3222505521
## 53   0.344096257 0.6559037435
## 54   0.851796776 0.1482032238
## 55   0.997693244 0.0023067557
## 56   0.997693244 0.0023067557
## 57   0.167630558 0.8323694423
## 58   0.147893241 0.8521067586
## 59   0.413600088 0.5863999120
## 60   0.278650711 0.7213492885
## 61   0.032737956 0.9672620442
## 62   0.077114795 0.9228852049
## 63   0.971867702 0.0281322984
## 64   0.105723767 0.8942762334
## 65   0.032737956 0.9672620442
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## 71   0.996055392 0.0039446075
## 72   0.969334291 0.0306657090
## 73   0.921913239 0.0780867612
## 74   0.802740885 0.1972591149
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## 76   0.063803953 0.9361960465
## 77   0.104182533 0.8958174668
## 78   0.994118557 0.0058814432
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## 82   0.505213604 0.4947863962
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## 85   0.003381987 0.9966180130
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## 87   0.050017267 0.9499827326
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## 91   0.006516781 0.9934832195
## 92   0.034714706 0.9652852936
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## 95   0.174443466 0.8255565337
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## 987  0.886773991 0.1132260088
## 988  0.278650711 0.7213492885
## 989  0.946564124 0.0534358758
## 990  0.193692580 0.8063074196
## 991  0.076488428 0.9235115724
## 992  0.941783465 0.0582165351
## 993  0.045420369 0.9545796310
## 994  0.994732495 0.0052675054
## 995  0.963836109 0.0361638911
```

```
## 996  0.134440101 0.8655598987
## 997  0.969453585 0.0305464149
## 998  0.917133740 0.0828662604
## 999  0.797080181 0.2029198190
## 1000 0.860231859 0.1397681408
## 1001 0.888916630 0.1110833704
## 1002 0.133843716 0.8661562836
## 1003 0.798418405 0.2015815953
## 1004 0.877021434 0.1229785661
## 1005 0.093848688 0.9061513118
## 1006 0.827248769 0.1727512309
## 1007 0.050017267 0.9499827326
## 1008 0.167630558 0.8323694423
## 1009 0.079090984 0.9209090163
## 1010 0.283356555 0.7166434454
## 1011 0.821896702 0.1781032984
## 1012 0.111769660 0.8882303397
## 1013 0.425161802 0.5748381983
## 1014 0.974792687 0.0252073126
## 1015 0.005208393 0.9947916067
## 1016 0.997024705 0.0029752955
## 1017 0.148792530 0.8512074701
## 1018 0.996048452 0.0039515481
## 1019 0.305358038 0.6946419620
## 1020 0.192878819 0.8071211808
## 1021 0.255066274 0.7449337256
## 1022 0.988182586 0.0118174135
## 1023 0.942196452 0.0578035482
## 1024 0.045420369 0.9545796310
## 1025 0.917133740 0.0828662604
##
## $terms
## heartdisease ~ age + sex + cp + trestbps + chol + fbs + restecg +
##     thalach + exang + oldpeak + slope + ca + thal
## attr(,"variables")
## list(heartdisease, age, sex, cp, trestbps, chol, fbs, restecg,
##     thalach, exang, oldpeak, slope, ca, thal)
## attr(,"factors")
##              age sex cp trestbps chol fbs restecg thalach exang oldpeak
slope
## heartdisease   0   0  0        0    0   0       0       0     0       0
0
## age            1   0  0        0    0   0       0       0     0       0
0
## sex            0   1  0        0    0   0       0       0     0       0
0
## cp             0   0  1        0    0   0       0       0     0       0
0
## trestbps       0   0  0        1    0   0       0       0     0       0
0
```

```
## chol           0   0  0        0    1   0       0       0     0       0
0
## fbs            0   0  0        0    0   1       0       0     0       0
0
## restecg        0   0  0        0    0   0       1       0     0       0
0
## thalach        0   0  0        0    0   0       0       1     0       0
0
## exang          0   0  0        0    0   0       0       0     1       0
0
## oldpeak        0   0  0        0    0   0       0       0     0       1
0
## slope          0   0  0        0    0   0       0       0     0       0
1
## ca             0   0  0        0    0   0       0       0     0       0
0
## thal           0   0  0        0    0   0       0       0     0       0
0
##              ca thal
## heartdisease  0    0
## age           0    0
## sex           0    0
## cp            0    0
## trestbps      0    0
## chol          0    0
## fbs           0    0
## restecg       0    0
## thalach       0    0
## exang         0    0
## oldpeak       0    0
## slope         0    0
## ca            1    0
## thal          0    1
## attr(,"term.labels")
##  [1] "age"      "sex"      "cp"       "trestbps" "chol"     "fbs"
##  [7] "restecg"  "thalach"  "exang"    "oldpeak"  "slope"    "ca"
## [13] "thal"
## attr(,"order")
##  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1
## attr(,"intercept")
## [1] 1
## attr(,"response")
## [1] 1
## attr(,".Environment")
## <environment: R_GlobalEnv>
## attr(,"predvars")
## list(heartdisease, age, sex, cp, trestbps, chol, fbs, restecg,
##     thalach, exang, oldpeak, slope, ca, thal)
## attr(,"dataClasses")
## heartdisease          age          sex           cp     trestbps
```

```
chol
##     "factor"    "numeric"    "numeric"    "numeric"    "numeric"
"numeric"
##          fbs      restecg      thalach        exang      oldpeak
slope
##    "numeric"    "numeric"    "numeric"    "numeric"    "numeric"
"numeric"
##           ca         thal
##    "numeric"    "numeric"
##
## $call
## lda(formula = heartdisease ~ ., data = heartdscleansed, CV = T)
##
## $xlevels
## named list()
```

#use the table() to get a confusion matrix by using the class

```
t2 <- table(heartLDA2$class, heartdscleansed$heartdisease)
t2

##
##       0   1
##   0 373  50
##   1 126 476
```

#calculate the accuracy by hand

```
accuracy <- (373 + 476)/(373 + 476 + 126 + 50)
accuracy

## [1] 0.8282927
```

#Coming up with the different performance metrics #build a model with a train()

```
library(caret)

## Warning: package 'caret' was built under R version 4.0.3

## Loading required package: lattice

## Loading required package: ggplot2

## Warning: package 'ggplot2' was built under R version 4.0.3

heartModelFit <- train(heartdisease ~., method = "lda",
preProcess=c("scale","center"), data=train)
```

#And then predict this data on the training data and come up with a confusion matrix.

```
p <- predict(heartModelFit, train)
cm <- confusionMatrix(train$heartdisease, p, dnn=c("Actual Group", "Predicted
```

```
Group"))
cm

## Confusion Matrix and Statistics
##
##             Predicted Group
## Actual Group   0   1
##            0 272  63
##            1  26 298
##
##                Accuracy : 0.8649
##                  95% CI : (0.8365, 0.8901)
##     No Information Rate : 0.5478
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.7303
##
##  Mcnemar's Test P-Value : 0.0001356
##
##             Sensitivity : 0.9128
##             Specificity : 0.8255
##          Pos Pred Value : 0.8119
##          Neg Pred Value : 0.9198
##              Prevalence : 0.4522
##          Detection Rate : 0.4127
##    Detection Prevalence : 0.5083
##       Balanced Accuracy : 0.8691
##
##        'Positive' Class : 0
##
```