breast_cancer_model_analysis.R

```
setwd("C:/Users/shraddha/Desktop/Acadgild students projects/project4")
library(readr)
CancerData <- read_csv("CancerData.csv")

## Warning: Missing column names filled in: 'X33' [33]

## Parsed with column specification:
## cols(
##   .default = col_double(),
##   id = col_integer(),
##   diagnosis = col_character(),
##   X33 = col_character()
## )

## See spec(...) for full column specifications.

## Warning in rbind(names(probs), probs_f): number of columns of result is
not
## a multiple of vector length (arg 1)

## Warning: 569 parsing failures.
## row #  A tibble: 5 x 5 col      row col    expected   actual     file
expected    <int> <chr> <chr>      <chr>       <chr>            actual 1       1
<NA>   33  columns 32 columns 'CancerData.csv' file 2     2 <NA>    33 columns 32
columns 'CancerData.csv' row 3      3 <NA>   33 columns 32 columns
'CancerData.csv' col 4      4 <NA>   33 columns 32 columns 'CancerData.csv'
expected  5      5 <NA> 33 columns 32 columns 'CancerData.csv'


dim(CancerData)

 ## [1] 569   33

library(mice)

## Loading required package: lattice

##
## Attaching package: 'mice'
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```r
library(readr,dplyr)
library("ggplot2")
library("corrplot")
```

```
## corrplot 0.84 loaded
```

```r
library("gridExtra")
library("pROC")
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```r
library("MASS")
library("caTools")
library("caret")
library(randomForest)
```

```
## randomForest 4.6-14
```

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

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:gridExtra':
##
##     combine
```

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

```r
library(rpart)
library(rpart.plot)
library(rattle)
```

```
## Rattle: A free graphical interface for data science with R.
## Version 5.2.0 Copyright (c) 2006-2018 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
```

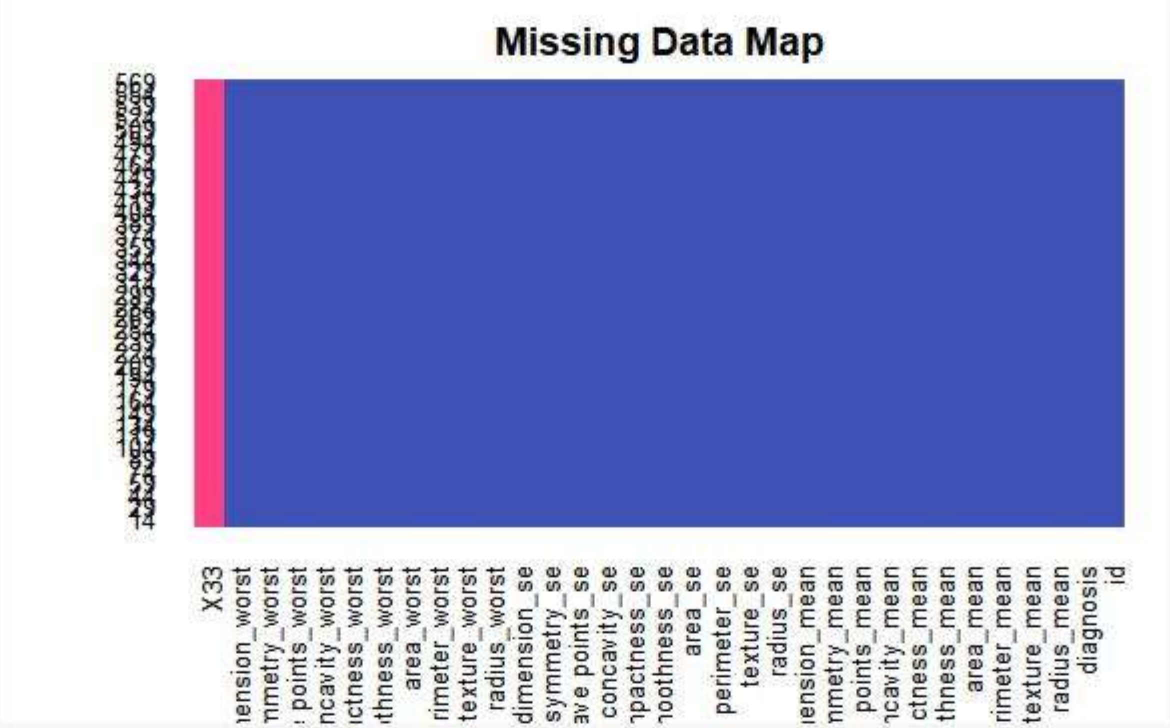
```
##
## Attaching package: 'rattle'
## The following object is masked from 'package:randomForest':
##
##     importance
```

```
data<-CancerData
library(Amelia)
```

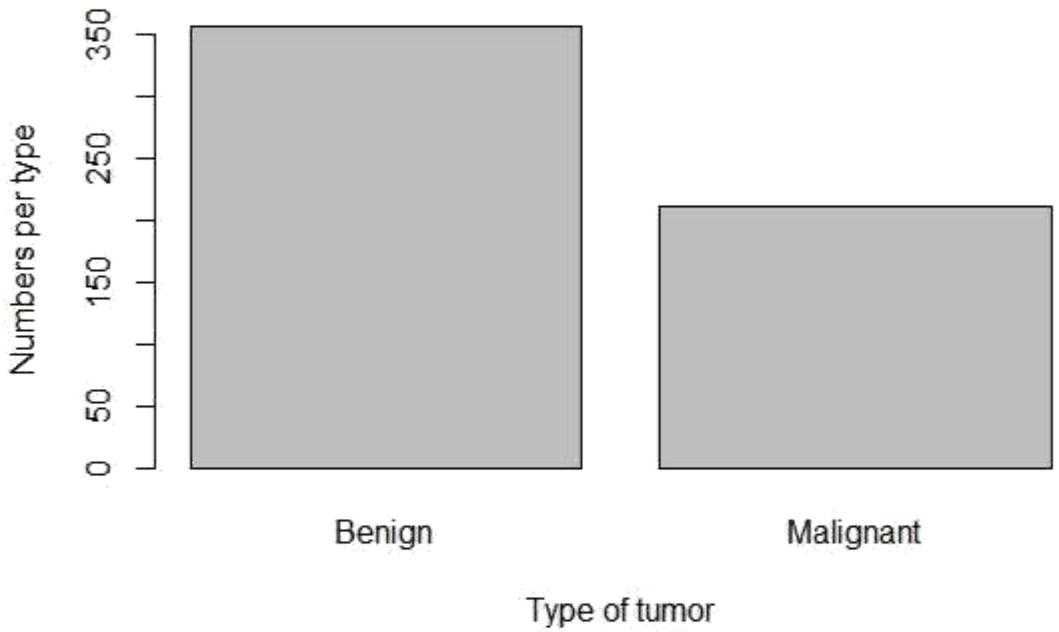
```
any(is.na(data))
```

```
## [1] TRUE
```

```
missmap(CancerData, main="Missing Data Map", col=c("#FF4081", "#3F51B5"),
    legend=FALSE)
```

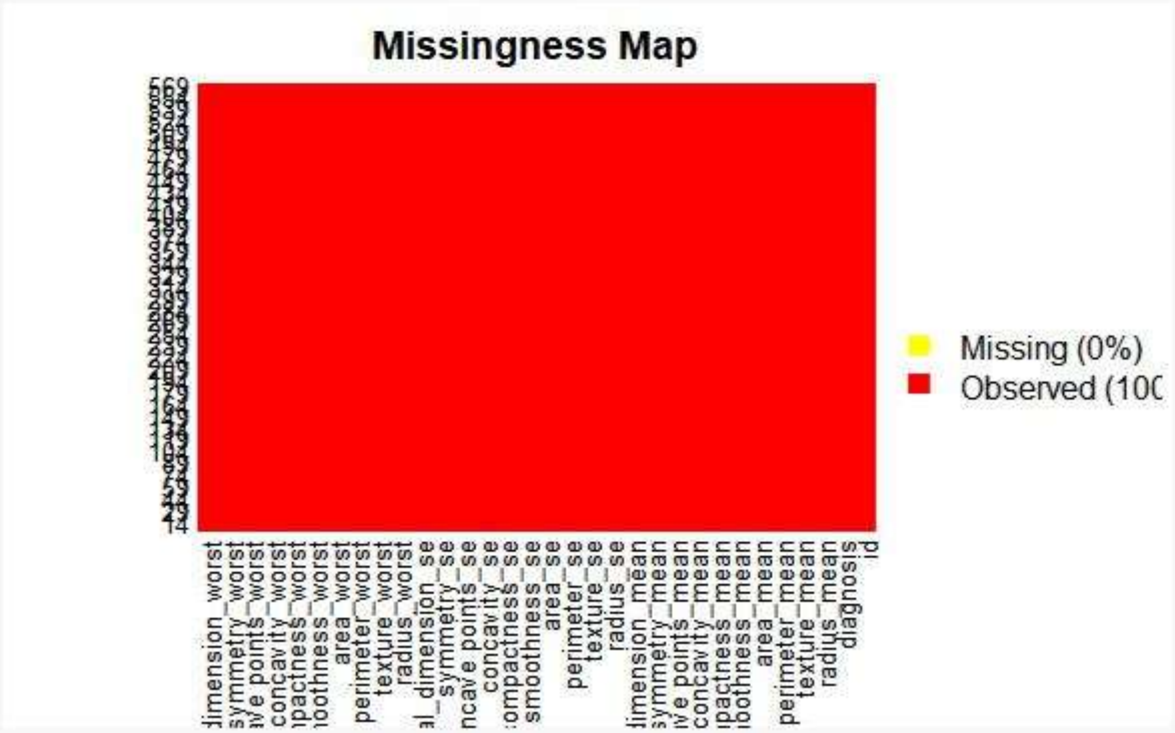


```
data<-CancerData

data[,33]<-NULL


barplot(table(data$diagnosis), xlab = "Type of tumor", ylab="Numbers per type")
```



```
# visualize the missing values using the missing map from the Amelia
package missmap(data,col=c("yellow","red"))
```

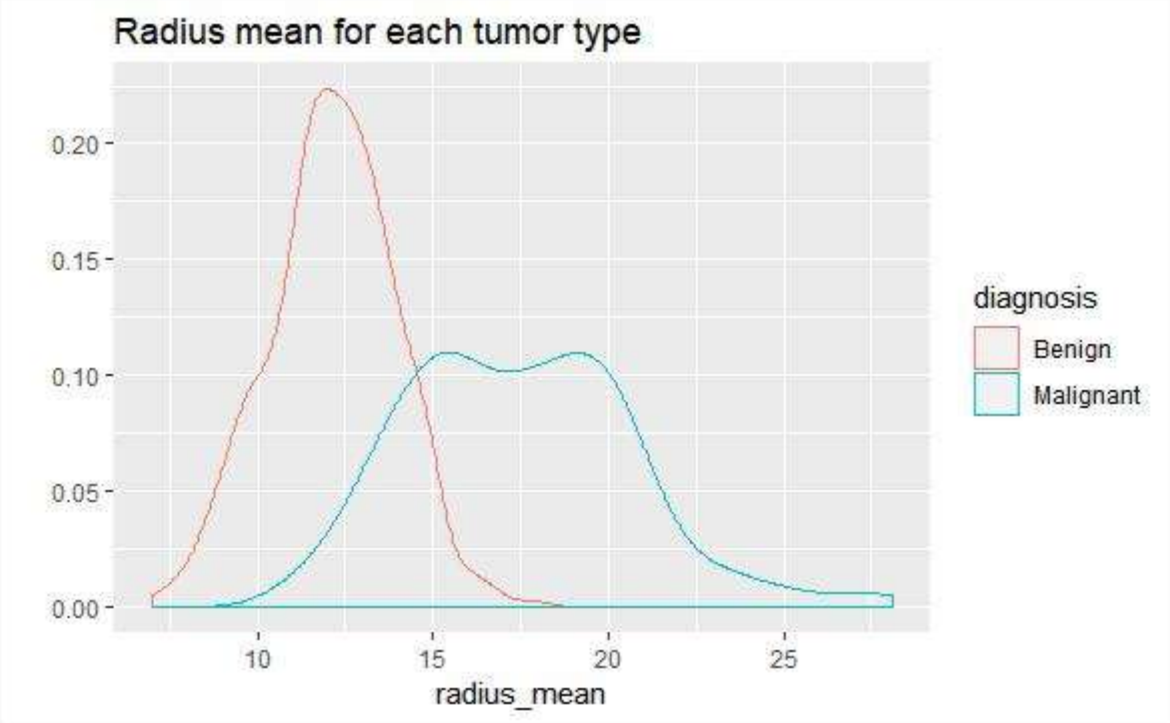
```
## Warning in if (class(obj) == "amelia") {: the condition has length > 1 and
## only the first element will be used
```



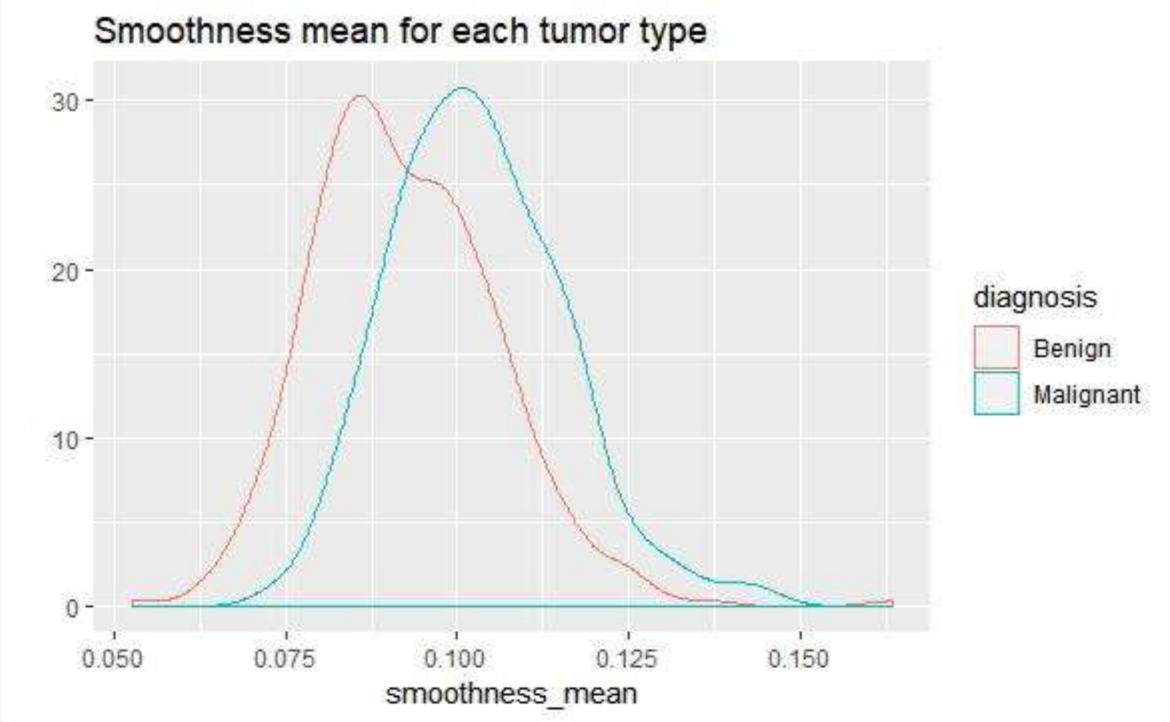
```r
data$diagnosis<-as.factor(data$diagnosis)
data[,33]<-NULL
summary(data)
```

```
##        id             diagnosis  radius_mean      texture_mean
##  Min.   :     8670   B:357     Min.   : 6.981   Min.   : 9.71
##  1st Qu.:   869218   M:212     1st Qu.:11.700   1st Qu.:16.17
##  Median :   906024             Median :13.370   Median :18.84
##  Mean   : 30371831             Mean   :14.127   Mean   :19.29
##  3rd Qu.:  8813129             3rd Qu.:15.780   3rd Qu.:21.80
##  Max.   :911320502             Max.   :28.110   Max.   :39.28
##  perimeter_mean     area_mean      smoothness_mean   compactness_mean
##  Min.   : 43.79   Min.   : 143.5   Min.   :0.05263   Min.   :0.01938
##  1st Qu.: 75.17   1st Qu.: 420.3   1st Qu.:0.08637   1st Qu.:0.06492
##  Median : 86.24   Median : 551.1   Median :0.09587   Median :0.09263
##  Mean   : 91.97   Mean   : 654.9   Mean   :0.09636   Mean   :0.10434
##  3rd Qu.:104.10   3rd Qu.: 782.7   3rd Qu.:0.10530   3rd Qu.:0.13040
##  Max.   :188.50   Max.   :2501.0   Max.   :0.16340   Max.   :0.34540
##  concavity_mean    concave points_mean symmetry_mean
##  Min.   :0.00000   Min.   :0.00000     Min.   :0.1060
##  1st Qu.:0.02956   1st Qu.:0.02031     1st Qu.:0.1619
##  Median :0.06154   Median :0.03350     Median :0.1792
##  Mean   :0.08880   Mean   :0.04892     Mean   :0.1812
##  3rd Qu.:0.13070   3rd Qu.:0.07400     3rd Qu.:0.1957
##  Max.   :0.42680   Max.   :0.20120     Max.   :0.3040
##  fractal_dimension_mean   radius_se        texture_se      perimeter_se
##  Min.   :0.04996        Min.   :0.1115   Min.   :0.3602   Min.   : 0.757
##  1st Qu.:0.05770        1st Qu.:0.2324   1st Qu.:0.8339   1st Qu.: 1.606
##  Median :0.06154        Median :0.3242   Median :1.1080   Median : 2.287
##  Mean   :0.06280        Mean   :0.4052   Mean   :1.2169   Mean   : 2.866
##  3rd Qu.:0.06612        3rd Qu.:0.4789   3rd Qu.:1.4740   3rd Qu.: 3.357
##  Max.   :0.09744        Max.   :2.8730   Max.   :4.8850   Max.   :21.980
##     area_se        smoothness_se      compactness_se      concavity_se
##  Min.   :  6.802   Min.   :0.001713   Min.   :0.002252   Min.   :0.00000
##  1st Qu.: 17.850   1st Qu.:0.005169   1st Qu.:0.013080   1st Qu.:0.01509
##  Median : 24.530   Median :0.006380   Median :0.020450   Median :0.02589
##  Mean   : 40.337   Mean   :0.007041   Mean   :0.025478   Mean   :0.03189
##  3rd Qu.: 45.190   3rd Qu.:0.008146   3rd Qu.:0.032450   3rd Qu.:0.04205
##  Max.   :542.200   Max.   :0.031130   Max.   :0.135400   Max.   :0.39600
##  concave points_se   symmetry_se       fractal_dimension_se
##  Min.   :0.000000   Min.   :0.007882   Min.   :0.0008948
##  1st Qu.:0.007638   1st Qu.:0.015160   1st Qu.:0.0022480
##  Median :0.010930   Median :0.018730   Median :0.0031870
##  Mean   :0.011796   Mean   :0.020542   Mean   :0.0037949
##  3rd Qu.:0.014710   3rd Qu.:0.023480   3rd Qu.:0.0045580
##  Max.   :0.052790   Max.   :0.078950   Max.   :0.0298400
##  radius_worst   texture_worst   perimeter_worst    area_worst
## Min.    : 7.93  Min.    :12.02  Min.    : 50.41  Min.    : 185.2
##  1st Qu.:13.01   1st Qu.:21.08  1st Qu.:  84.11  1st Qu.: 515.3
## Median :14.97   Median :25.41   Median :  97.66  Median :  686.5
## Mean    :16.27  Mean    :25.68  Mean    :107.26  Mean    :  880.6
## 3rd Qu.:18.79   3rd Qu.:29.72   3rd Qu.:125.40   3rd Qu.:1084.0
## Max.   :36.04   Max.   :49.54   Max.   :251.20   Max.   :4254.0
## smoothness_worst   compactness_worst concavity_worst   concave points_worst
## Min.   :0.07117   Min.    :0.02729  Min.    :0.0000  Min.    :0.00000
## 1st Qu.:0.11660    1st Qu.:0.14720   1st Qu.:0.1145   1st Qu.:0.06493
## Median :0.13130   Median :0.21190   Median :0.2267   Median :0.09993
## Mean   :0.13237   Mean    :0.25427  Mean    :0.2722  Mean    :0.11461
## 3rd Qu.:0.14600    3rd Qu.:0.33910   3rd Qu.:0.3829   3rd Qu.:0.16140
## Max.   :0.22260   Max.    :1.05800  Max.    :1.2520  Max.    :0.29100
## symmetry_worst   fractal_dimension_worst
## Min.   :0.1565   Min.    :0.05504
## 1st Qu.:0.2504    1st Qu.:0.07146
## Median :0.2822   Median :0.08004
## Mean   :0.2901   Mean    :0.08395
## 3rd Qu.:0.3179    3rd Qu.:0.09208
## Max.   :0.6638   Max.    :0.20750
```

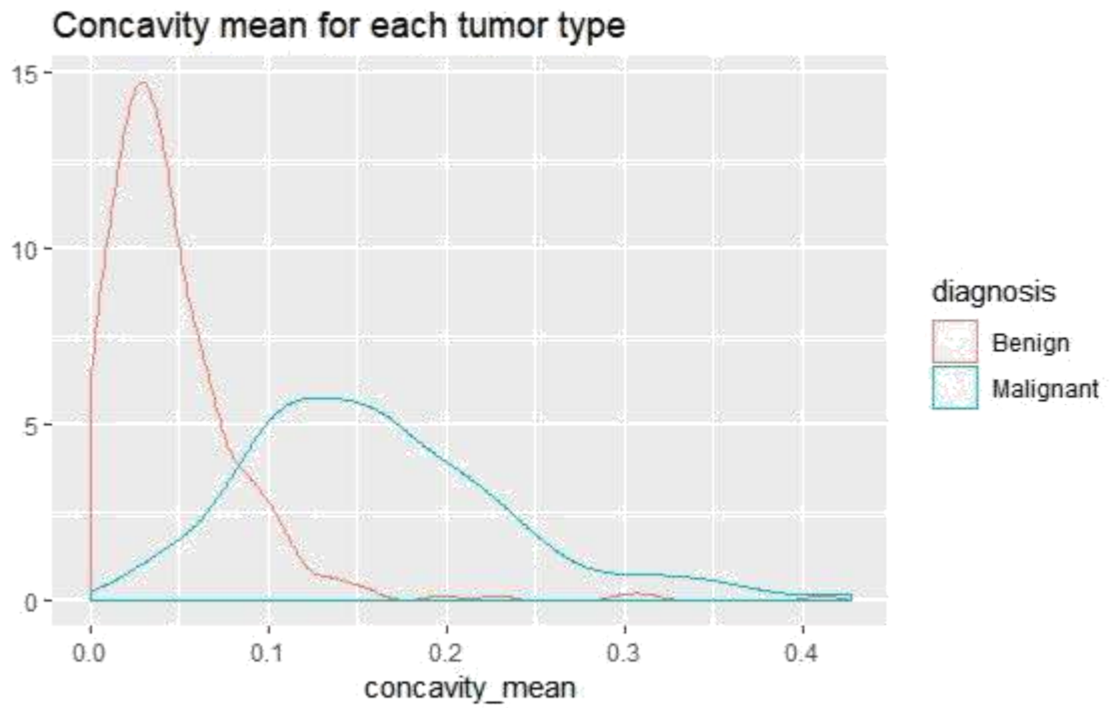
```
qplot(radius_mean, data=data, colour=diagnosis,

   geom="density", main="Radius mean for each tumor type")
```



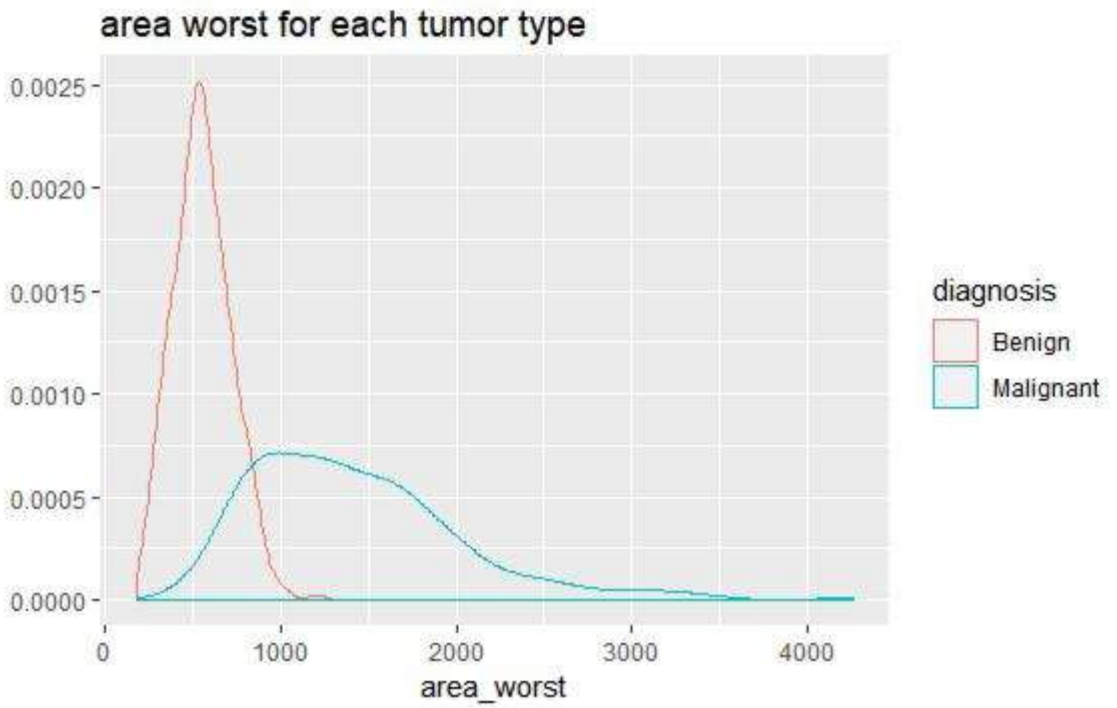
```
qplot(smoothness_mean, data=data, colour=diagnosis,
    geom="density", main="Smoothness mean for each tumor type")
```



```
qplot(concavity_mean, data=data, colour=diagnosis, geom="density",
    main="Concavity mean for each tumor type")
```

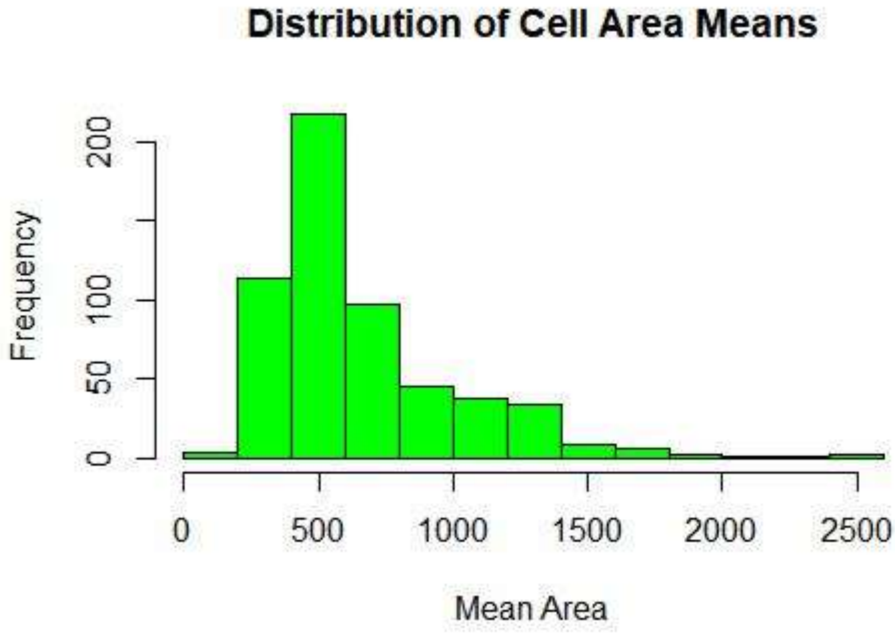


```
qplot(area_worst , data=data, colour=diagnosis, geom="density",
     main="area worst for each tumor type")
```

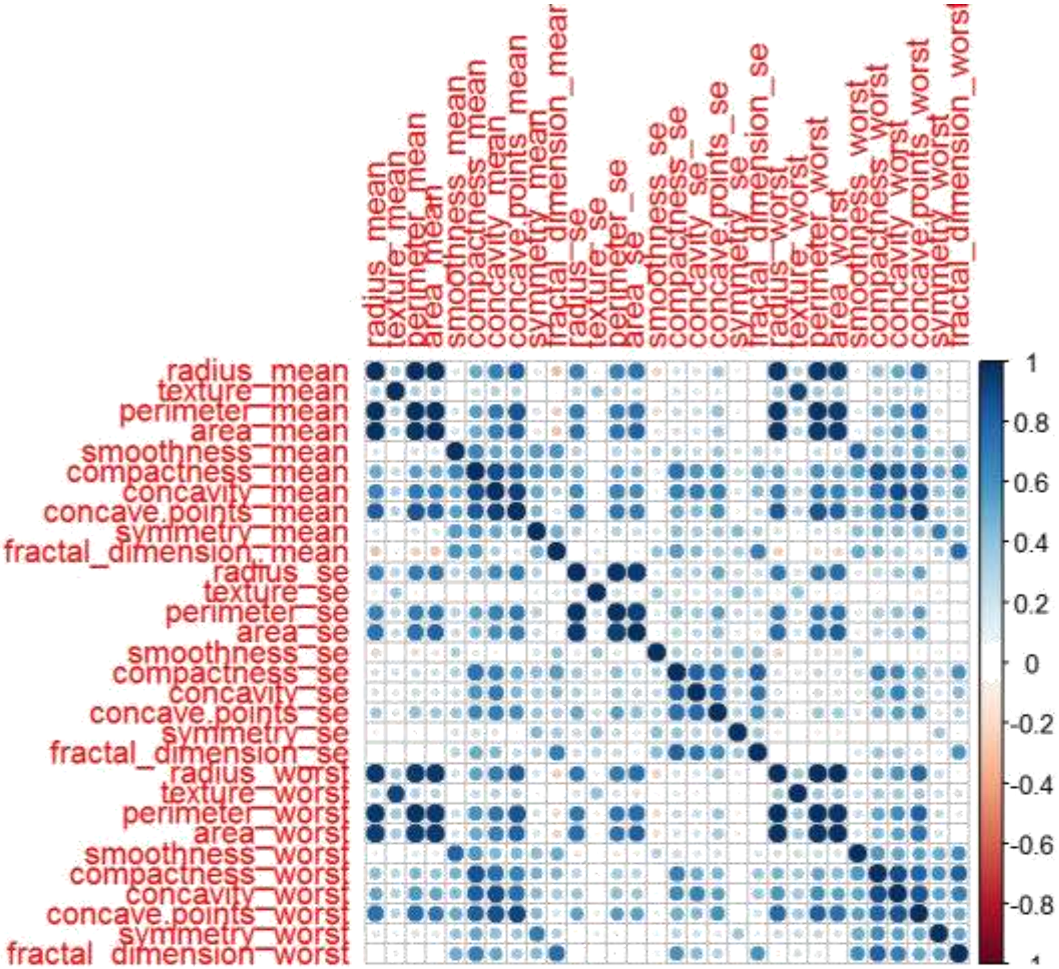


```
# Looking at distribution for area.mean
variable plot.new()
```

```r
hist(CancerData$area_mean,
     main = 'Distribution of Cell Area Means',
     xlab = 'Mean Area',
     col = 'green')
```

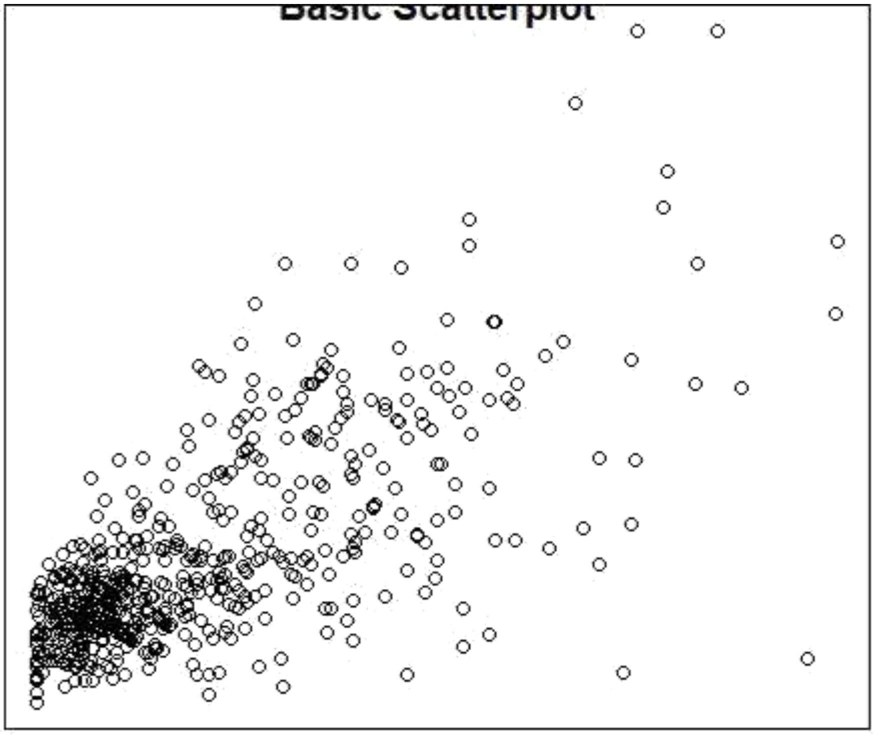


```r
#we find that the data is imbalanced and also there is a lot of
corelation between the attributes
## we find that there are no missing values
## we find that data is little unbalanced
prop.table(table(data$diagnosis))

##
##         B         M
## 0.6274165 0.3725835

## we then show some correlation
corr_mat<-cor(data[,3:ncol(data)])
corrplot(corr_mat)
```

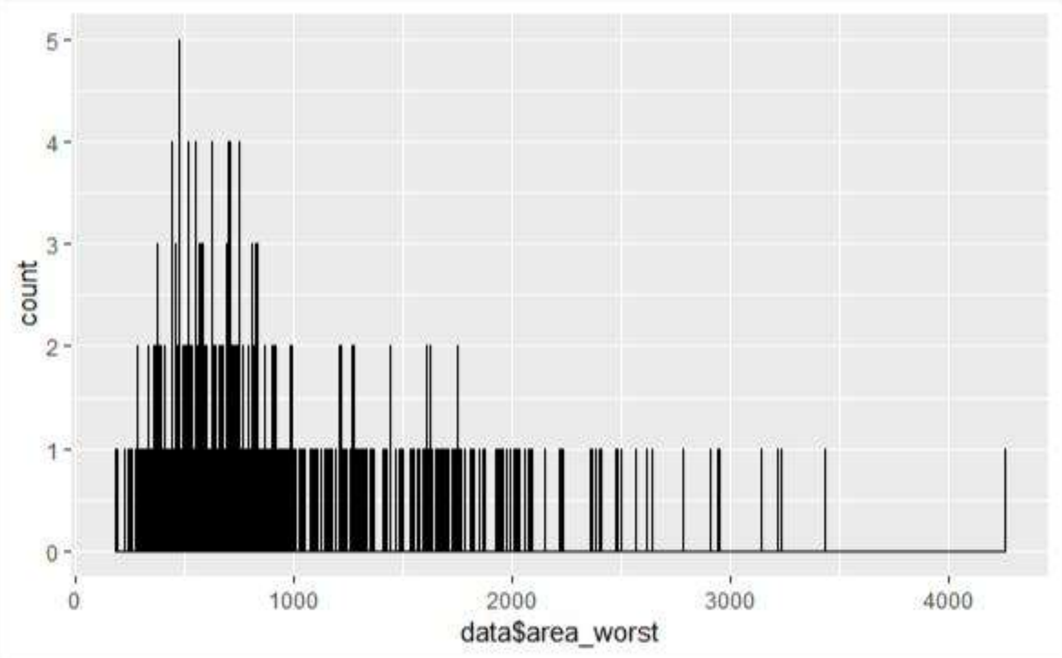


```
plot.new()
```

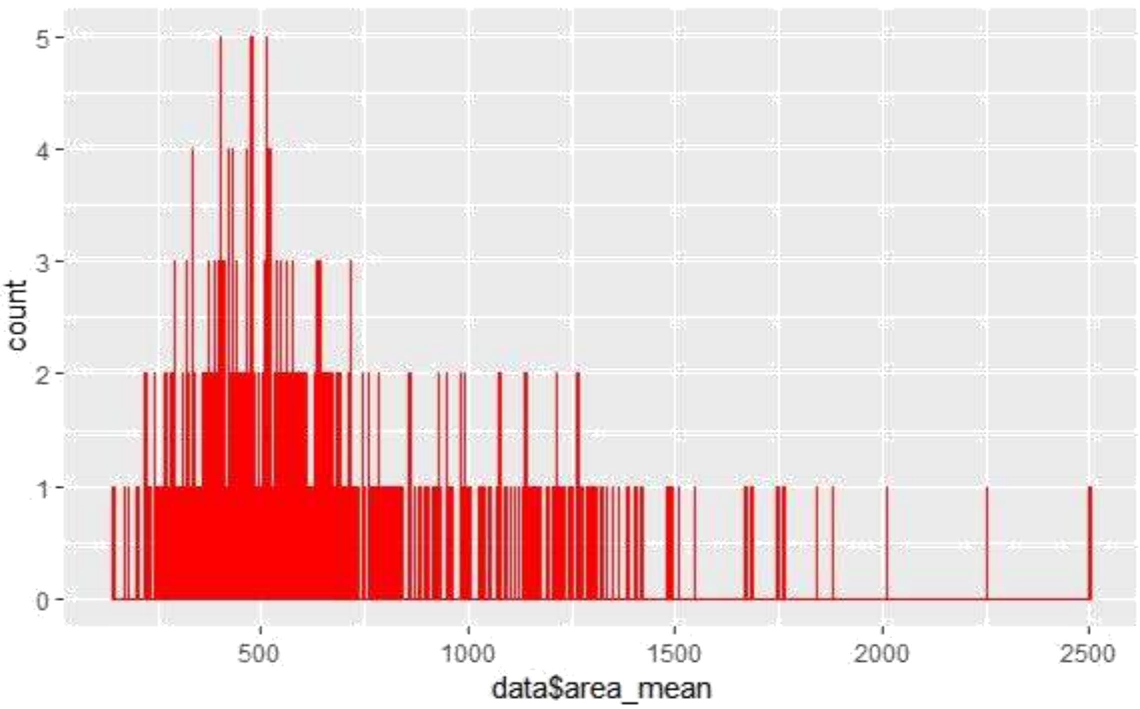
```
plot(data$area_mean ~data$concavity_mean)
title('Basic Scatterplot')
```



```
ggplot(data, aes(x=data$area_worst)) + geom_histogram(binwidth = 1, fill = "yellow", color = "black")
```



```
ggplot(data, aes(x=data$area_mean)) + geom_histogram(binwidth = 1, fill = "green", color = "red")
```



```
#Modelling
#We are going to get a training and a testing set to use when building
some models:
set.seed(1234)
data_index<-createDataPartition (data$diagnosis,p=0.75,list = FALSE)
train_data<-data[data_index,-1]
test_data<-data[data_index,-1]

## Applying learning models
fitControl <- trainControl(method="cv" , number = 5,

                           preProcOptions = list(thresh = 0.99), # threshold
for pca preprocess
                           classProbs = TRUE,
                           summaryFunction = twoClassSummary)
#Model1: Random Forest
#Building the model on the training data
## random forest
model_rf <- train(diagnosis~.,
                  train_data,
                  method="ranger",
                  metric="ROC",
                  #tuneLength=10,
                  #tuneGrid = expand.grid(mtry = c(2, 3,
                  6)), preProcess = c('center', 'scale'),
                  trControl=fitControl)
```

```
#Testing on the testing data
## testing for random forets
pred_rf <- predict(model_rf, test_data)
cm_rf <- confusionMatrix(pred_rf, test_data$diagnosis, positive = "M")
cm_rf
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   B   M
##          B 268   0
##          M   0 159
 ##
 ##                Accuracy : 1
 ##                  95% CI : (0.9914, 1)
##     No Information Rate : 0.6276
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 1
##  Mcnemar's Test P-Value : NA
##
 ##             Sensitivity :  1.0000
 ##             Specificity :  1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 1.0000
##              Prevalence : 0.3724
##          Detection Rate : 0.3724
##    Detection Prevalence : 0.3724
##       Balanced Accuracy : 1.0000
##
##        'Positive' Class : M
##
```

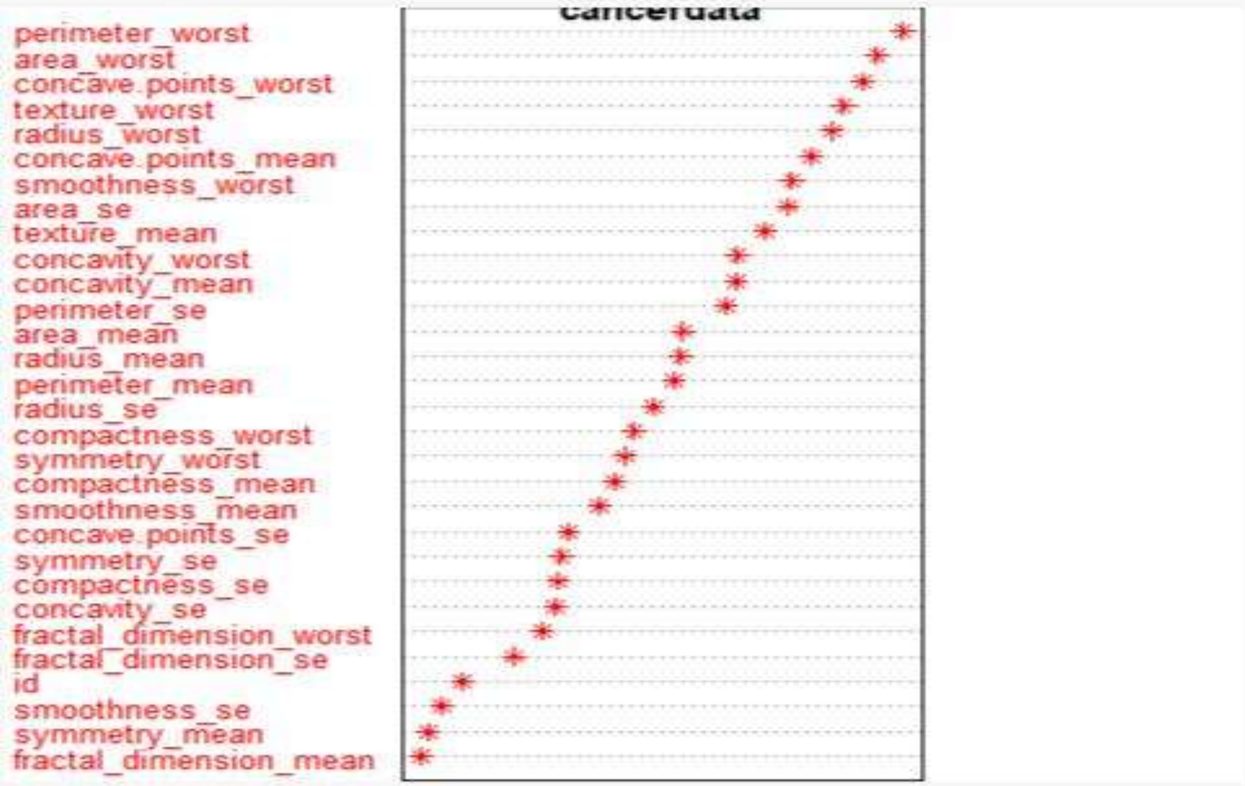
```
# We find the accuracy of the model is 100%
#Random forest model- takes decision trees and averages them
normalize<-function(x){return((x-min(x))/(max(x)-min(x)))}
data$diagnosis<-as.numeric(data$diagnosis)
data_n<-as.data.frame(lapply (data,normalize))
traindata_n<--data_n[1:426,]
testdata_n<-data_n[427:569,]
rf <- randomForest (diagnosis ~., data= traindata_n, ntree =300, mtry =
5, importance = TRUE)
```

```
## Warning in randomForest.default(m, y, ...): The response has five or fewer
## unique values. Are you sure you want to do regression?
```

```
print(rf)
```

```
##
## Call:
##  randomForest(formula = diagnosis ~ ., data = traindata_n, ntree = 300,
mtry = 5, importance = TRUE)
##                Type of random forest: regression
##                      Number of trees: 300
## No. of variables tried at each split: 5
##
##           Mean of squared residuals: 0.03693862
##                     % Var explained: 84.79
```

```
plot.new()

varImpPlot(rf, type = 1, pch =8, col = 2, cex =0.8, main = "cancerdata")
abline(v= 45, col= "red")
```



```
library(party)
```

		MeanDecreaseAccuracy	MeanDecreaseGini
area_worst	15.13 10.84	17.79	13.78
concave.points_worst	13.84 11.08	17.58	12.86
radius_worst	13.19 11.08	15.99	12.32

perimeter_worst	13.16 10.67	15.65	14.85
concave.points_mean	9.53 10.94	13.77	13.81
concavity_worst	7.32 9.27	11.99	3.33
texture_mean	8.28 9.79	11.95	2.1
texture_worst	8.63 10.24	11.74	2.3
area_se	8.40 7.98	11.33	5.83
smoothness_worst	6.42 8.05	10.23	1.57
perimeter_mean	8.58 5.62	9.6	7.04
radius_mean	8.55 5.14	9.37	4.99
area_mean	8.50 5.28	9.3	4.07
concavity_mean	5.31 6.54	9.03	3.9
perimeter_se	5.63 6.26	8.33	1.88
radius_se	5.66 4.59	7.6	1.23
smoothness_	4.07 6.30	7.34	0.92
compactness_mean	5.84 3.89	6.92	1.51
compactness_worst	4.29 4.11	6.37	1.44
compactness_se	4.34 2.83	5.35	0.59
concavity_se	3.20 3.77	5.33	0.76
smoothness_se	3.65 3.47	5.3	0.58
symmetry_worst		5.15	1.17

fractal_dimension_worst	4.31 2.39	5.05	1.06
texture_se	3.97 1.92	4.44	0.55
concave.points_se	3.70 2.72	4.39	0.51
symmetry_mean	0.22 3.69	3.03	0.45
fractal_dimension_mean	2.10 1.25	2.57	0.43
fractal_dimension_se	1.96 1.34	2.56	0.64
symmetry_se	0.96 0.48	1.03	0.55

```r
library(Boruta)
```

```
## Loading required package: ranger

##
## Attaching package: 'ranger'
```

```
## The following object is masked from 'package:rattle':
##
##     importance

## The following object is masked from 'package:randomForest':
##
##     importance
```

```
# Decide if a variable is important or not using Boruta

boruta_output <- Boruta ( diagnosis~ ., data=na.omit(train_data), doTrace=2)
# perform Boruta search
```

```
##  1. run of importance source...

...

## After 77 iterations, +19 secs:

##  rejected 1 attribute: texture_se;

##  no more attributes left.
```

```
boruta_signif <-
names(boruta_output$finalDecision[boruta_output$finalDecision %in%
c("Confirmed" , "Tentative")])
boruta_signif
```

```
 ##  [1] "radius_mean"             "texture_mean"
 ##  [3] "perimeter_mean"          "area_mean"
 ##  [5] "smoothness_mean"         "compactness_mean"
 ##  [7] "concavity_mean"          "`concave points_mean`"
 ##  [9] "symmetry_mean"           "fractal_dimension_mean"
## [11] "radius_se"               "perimeter_se"
## [13] "area_se"                 "compactness_se"
## [15] "concavity_se"            "`concave points_se`"
## [17] "fractal_dimension_se"    "radius_worst"
## [19] "texture_worst"           "perimeter_worst"
## [21] "area_worst"              "smoothness_worst"
## [23] "compactness_worst"       "concavity_worst"
## [25] "`concave points_worst`"  "symmetry_worst"
## [27] "fractal_dimension_worst"
```

```
#Model2: Naive Bayes
#Building and testing the model
model_nb <- train(diagnosis~.,
                  train_data,
                  method="nb",
                  metric="ROC",
                  preProcess=c('center', 'scale'),
                  trace=FALSE,
                  trControl=fitControl)

cm_nb <- confusionMatrix(pred_nb, test_data$diagnosis, positive = "M")
cm_nb
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   B   M
##          B 259  17
##          M   9 142
##
##                Accuracy : 0.9391
##                  95% CI : (0.9121, 0.9598)
##     No Information Rate : 0.6276
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.8684
##  Mcnemar's Test P-Value : 0.1698
##
##             Sensitivity : 0.8931
##             Specificity : 0.9664
##          Pos Pred Value : 0.9404
##          Neg Pred Value : 0.9384
##              Prevalence : 0.3724
##          Detection Rate : 0.3326
##    Detection Prevalence : 0.3536
##       Balanced Accuracy : 0.9297
##
##        'Positive' Class : M
##
```

```
#Accuracy of the model is 93.9%
#Model3: glm
#Building and testing the model
model_glm <- train(diagnosis~.,
                  train_data,
                  method="glm",
                  metric="ROC",
                  preProcess=c('center', 'scale'),
                  trace=FALSE,
                  trControl=fitControl)


## predicting for test data
pred_glm <- predict(model_glm, test_data)
```

```r
cm_glm <- confusionMatrix(pred_glm, test_data$diagnosis, positive = "M")
cm_glm
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   B   M
##          B 265   4
##          M   3 155
 ##
 ##               Accuracy : 0.9836
 ##                 95% CI : (0.9665, 0.9934)
##     No Information Rate : 0.6276
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9649
##  Mcnemar's Test P-Value : 1
##
 ##            Sensitivity  :  0.9748
 ##            Specificity  :  0.9888
##          Pos Pred Value : 0.9810
##          Neg Pred Value : 0.9851
##              Prevalence : 0.3724
##          Detection Rate : 0.3630
##    Detection Prevalence : 0.3700
##       Balanced Accuracy : 0.9818
##
##        'Positive' Class : M
##
```

```r
#Accuracy of the model is 98.3%
#algorithm for decision tree
library(C50)
data$diagnosis<-as.factor(data$diagnosis)
tree <- C5.0( diagnosis~., data = data)
summary(tree)
```

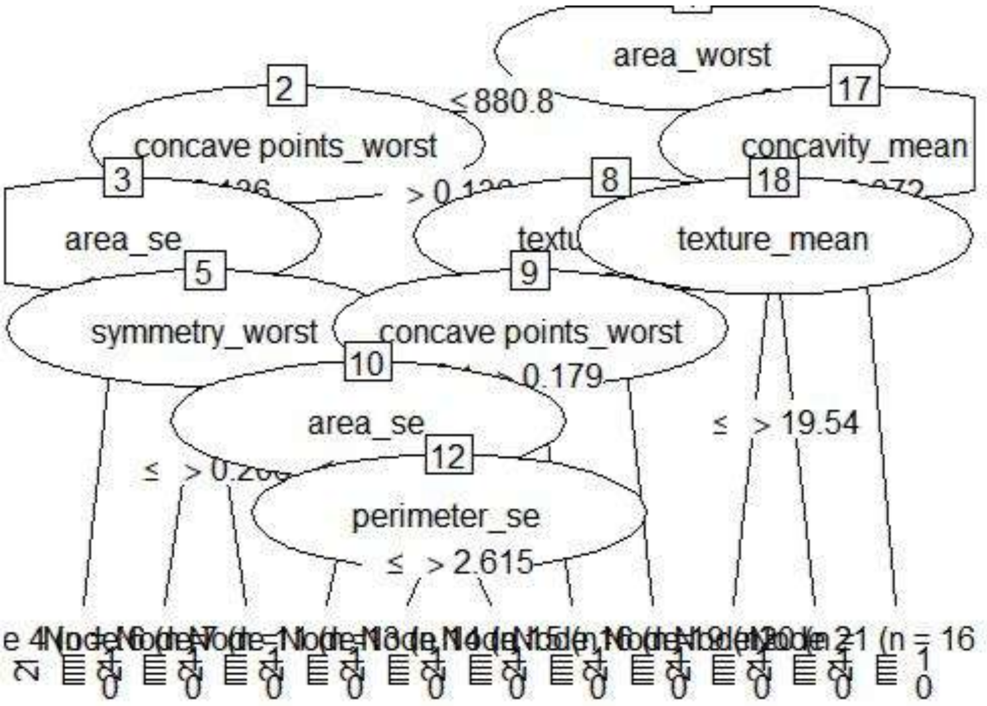
```
##
## Call:
## C5.0.formula(formula = diagnosis ~ ., data = data)
##
##
## C5.0 [Release 2.07 GPL Edition]      Sat Nov 03 17:35:50 2018
## -------------------------------
##
## Class specified by attribute `outcome'
##
## Read 569 cases (32 attributes) from undefined.data
##
## Decision tree:
```

```
##
## area_worst > 880.8:
## :...concavity_mean > 0.0716: 2 (164)
## :   concavity_mean <= 0.0716:
## :   :...texture_mean <= 19.54: 1 (9/1)
## :texture_mean > 19.54: 2 (10)
## area_worst <= 880.8:
## :...concave points_worst <= 0.1357:
##     :...area_se <= 36.46: 1 (319/3)
##     :   area_se > 36.46:
##     :   :...symmetry_worst <= 0.206: 2 (2)
##     :symmetry_worst > 0.206: 1 (16/2)
##     concave points_worst > 0.1357:
##     :...texture_worst > 27.37: 2 (21)
##         texture_worst <= 27.37:
##         :...concave points_worst > 0.1789: 2 (4)
##             concave points_worst  <= 0.1789:
##             :...area_se <= 21.91: 1 (12)
##                 area_se > 21.91:
##                 :...perimeter_se <= 2.615: 2 (6/1)
##                     perimeter_se > 2.615: 1  (6)
##
##
## Evaluation on training data (569 cases):
##
##      Decision Tree
##    ----------------
##    Size      Errors
##
##      11    7( 1.2%)   <<
##
##
##     (a)  (b)     <-classified as
##    ----  ----
##     356     1   (a): class  1
##       6   206   (b): class  2
##
##
##  Attribute usage:
##
##  100.00% area_worst
##   67.84% concave points_worst
##   63.44% area_se
##   32.16% concavity_mean
##    8.61% texture_worst
##    3.34% texture_mean
##    3.16% symmetry_worst
##    2.11% perimeter_se
##
```

```
##
## Time: 0.0 secs
```

```r
plot.new()
```

```r
plot(tree)
```

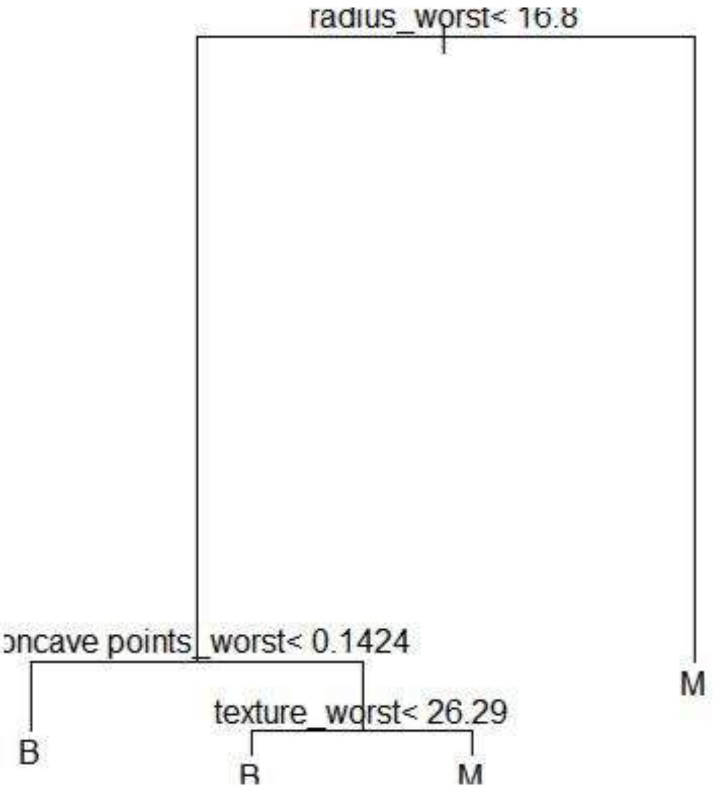


```r
results <- C5.0(diagnosis ~., data = data, rules = TRUE)
summary(results)
```

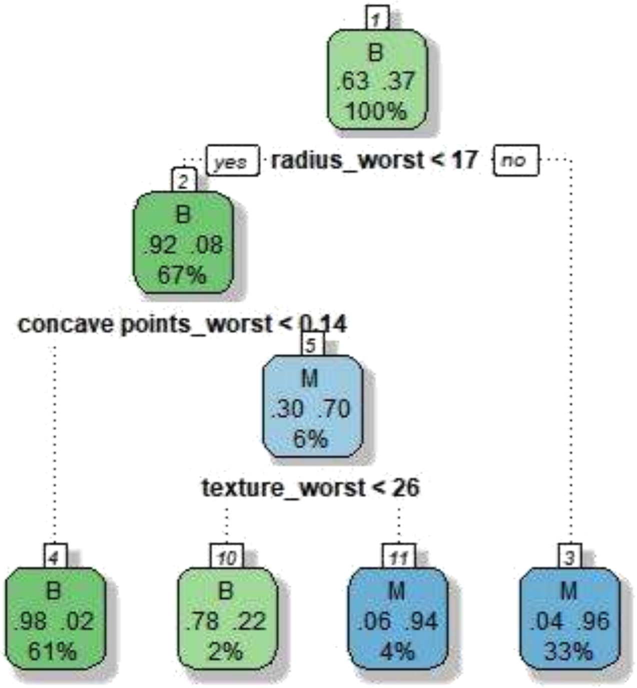
```
##
## Call:
## C5.0.formula(formula = diagnosis ~ ., data = data, rules = TRUE)
##
##
## C5.0 [Release 2.07 GPL Edition]      Sat Nov 03 17:35:51 2018
## -------------------------------
##
## Class specified by attribute `outcome'
##
## Read 569 cases (32 attributes) from undefined.data
##
## Rules:
##
## Rule 1: (223/2, lift 1.6)
##  texture_mean <= 19.54
##  concavity_mean <= 0.0716
##  ->  class 1  [0.987]
##
## Rule 2: (386/37, lift 1.4)
##  area_worst <= 880.8
##  ->  class 1  [0.902]
##
## Rule 3: (164, lift 2.7)
##  concavity_mean > 0.0716
##  area_worst > 880.8
##  ->  class 2  [0.994]
##
## Rule 4: (126, lift 2.7)
##  texture_mean > 19.54
##  area_worst > 880.8
##  ->  class 2  [0.992]
##
## Rule 5: (109, lift 2.7)
##  concave points_worst > 0.1789
##  ->  class 2  [0.991]
##
## Rule 6: (114, lift 2.7)
##  texture_worst > 27.37
##  concave points_worst > 0.1357
##  ->  class 2  [0.991]
##
## Default class: 1
##
##
## Evaluation on training data (569 cases):
##
##          Rules
##    ----------------
 ##     No      Errors
 ##
##       6   13( 2.3%)   <<
##
##
##     (a)   (b)    <-classified as
##    ----  ----
 ##     357         (a): class  1
 ##      13   199   (b): class  2
 ##
 ##
##  Attribute usage:
##
##   98.42% area_worst
##   68.01% concavity_mean
##   61.34% texture_mean
##   26.89% concave points_worst
##   20.04% texture_worst
```

```
##
##
## Time: 0.0 secs
```

```
data<-as.data.frame(data)
library(rpart)
tree<-rpart(diagnosis~.,data =train_data,method="class")
plot(tree)
text(tree, pretty=0)
library(rattle)
library(rpart.plot)
library(RColorBrewer)
plot.new()
```



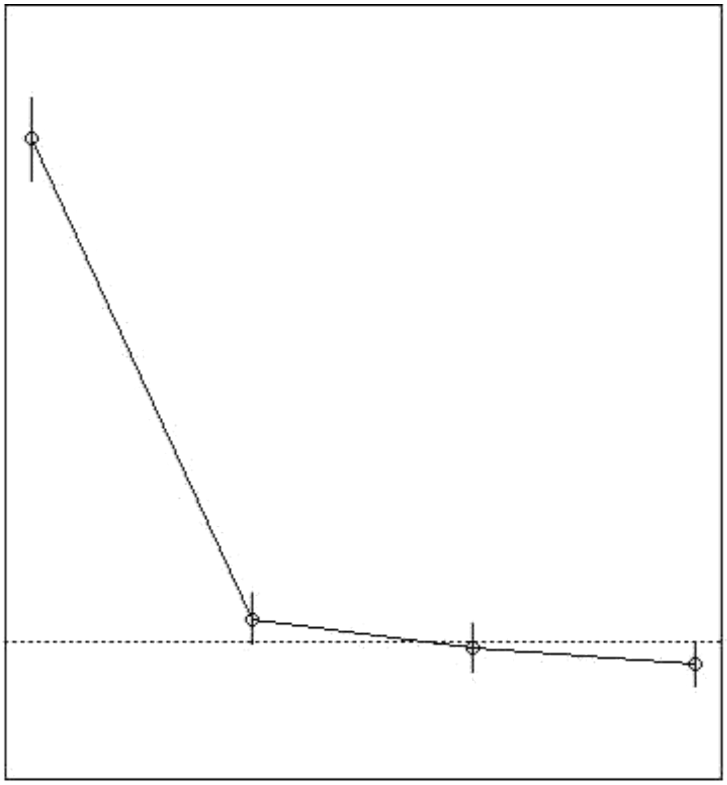
```
fancyRpartPlot(tree)
plot.new()
```



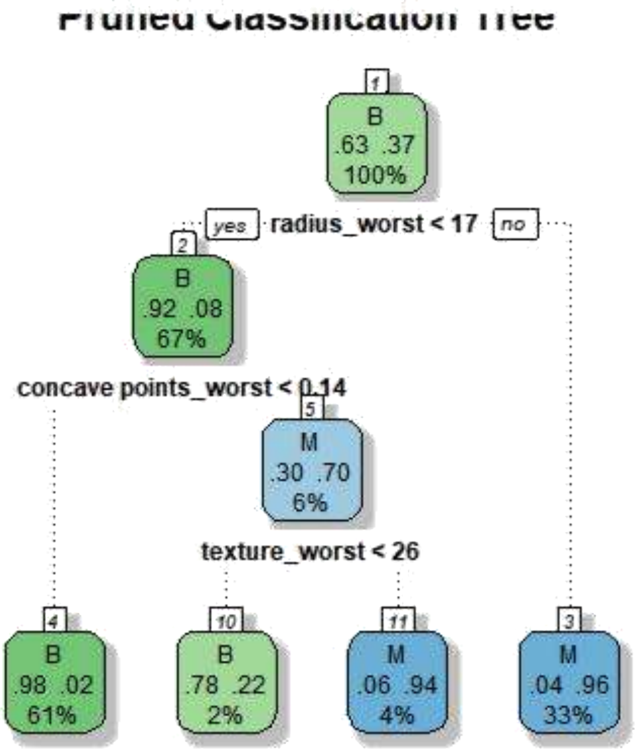
```
printcp(tree)
```

```
##
## Classification tree:
## rpart(formula = diagnosis ~ ., data = train_data, method = "class")
##
## Variables actually used in tree construction:
## [1] concave points_worst radius_worst         texture_worst
##
## Root node error: 159/427 = 0.37237
##
## n= 427
##
##           CP nsplit rel error  xerror     xstd
## 1 0.811321      0   1.00000 1.00000 0.062828
## 2 0.069182      1   0.18868 0.26415 0.038703
## 3  0.031447      2   0.11950 0.22013 0.035651
## 4  0.010000      3   0.08805 0.19497 0.033722
```

```
plotcp(tree)
ptree<- prune(tree, cp=
tree$cptable[which.min(tree$cptable[,"xerror"]),"CP"])
plot.new()
```



```r
fancyRpartPlot(ptree, uniform=TRUE,main="Pruned Classification Tree")
```



```r
library(rpart)
```

```
fit1 <- rpart(diagnosis~.,data=train_data)
fit1
```

```
## n= 427
##
## node), split, n, loss, yval, (yprob)
##       * denotes terminal node
##
##  1) root 427 159 B (0.62763466 0.37236534)
##    2) radius_worst< 16.795 286  24 B (0.91608392 0.08391608)
##      4) concave points_worst< 0.14235 259   5 B (0.98069498 0.01930502) *
##      5) concave points_worst>=0.14235 27   8 M (0.29629630 0.70370370)
##       10) texture_worst< 26.285 9   2 B (0.77777778 0.22222222) *
##       11) texture_worst>=26.285 18   1 M  (0.05555556 0.94444444) *
##    3) radius_worst>=16.795 141   6  M (0.04255319 0.95744681) *
```

```
summary(fit1)
```

```
## Call:
## rpart(formula = diagnosis ~ ., data = train_data)
##   n= 427
##
##            CP nsplit  rel error    xerror       xstd
## 1 0.811320750 1.00000000 1.0000000 0.06282824
## 2 0.069182391 0.18867925 0.2201258 0.03565053
## 3 0.031446542 0.11949686 0.1635220 0.03107762
## 4 0.010000003 0.08805031 0.1823899 0.03269862
##
## Variable importance
##          radius_worst            area_worst       perimeter_worst
##                    16                    16                    15
##             area_mean           radius_mean        perimeter_mean
##                    14                    14                    14
## concave points_worst       concavity_worst        concavity_mean
##                    3                     2                     1
##     compactness_worst   concave points_mean      compactness_mean
##                     1                     1                     1
##        texture_worst
##                    1
##
## Node number 1: 427 observations,    complexity param=0.8113208
##   predicted class=B  expected loss=0.3723653  P(node) =1
##     class counts:   268   159
##    probabilities: 0.628 0.372
##   left son=2 (286 obs) right son=3 (141 obs)
##   Primary splits:
##       radius_worst         < 16.795   to the left,  improve=144.1264, (0
missing)
##       perimeter_worst      < 112.6    to the left,  improve=143.9985, (0
missing)
```

```
##       area_worst           < 884.55   to the left,  improve=140.9804, (0
missing)
##       concave points_worst < 0.14235  to the left,  improve=138.8752, (0
missing)
##       concave points_mean  < 0.05593  to the left,  improve=132.0683, (0
missing)
##   Surrogate splits:
##       area_worst      < 868.2     to the left, agree=0.993, adj=0.979, (0
split)
##       perimeter_worst < 111.7     to the left, agree=0.974, adj=0.922, (0
split)
##       area_mean       < 697.8     to the left, agree=0.960, adj=0.879, (0
split)
##       radius_mean     < 15.045    to the left, agree=0.958, adj=0.872, (0
split)
##       perimeter_mean  < 96.405    to the left, agree=0.946, adj=0.837, (0
split)
##
## Node number 2: 286 observations,    complexity param=0.06918239
##   predicted class=B   expected loss=0.08391608 P(node) =0.6697892
##     class counts:   262    24
##    probabilities: 0.916 0.084
##   left son=4 (259 obs) right son=5 (27 obs)
##   Primary splits:
##       concave points_worst < 0.14235  to the left,  improve=22.90582, (0
missing)
##       concavity_mean       < 0.11865  to the left,  improve=19.46751, (0
missing)
##       concavity_worst      < 0.3782   to the left,  improve=19.39395, (0
missing)
##       compactness_worst    < 0.3849   to the left,  improve=17.79391, (0
missing)
##       concave points_mean  < 0.05593  to the left,  improve=17.40573, (0
missing)
##   Surrogate splits:
##       concavity_worst     < 0.4383   to the left,  agree=0.969, adj=0.667,
(0 split)
##       compactness_worst   < 0.3849   to the left,  agree=0.955, adj=0.519,
(0 split)
##       concavity_mean      < 0.1563   to the left,  agree=0.951, adj=0.481,
(0 split)
##       concave points_mean < 0.06687  to the left,  agree=0.948, adj=0.444,
(0 split)
##       compactness_mean    < 0.15     to the left,  agree=0.937, adj=0.333,
(0 split)
##
## Node number 3: 141 observations
##   predicted class=M   expected loss=0.04255319 P(node) =0.3302108
##     class counts:     6   135
##    probabilities: 0.043 0.957
```

```
## 
## Node number 4: 259 observations
##   predicted class=B  expected loss=0.01930502  P(node) =0.6065574
##     class counts:   254     5
##    probabilities: 0.981 0.019 
## 
## Node number 5: 27 observations,    complexity param=0.03144654
##   predicted class=M  expected loss=0.2962963  P(node) =0.06323185
##     class counts:     8    19
##    probabilities: 0.296 0.704 
##   left son=10 (9 obs) right son=11 (18 obs)
##   Primary splits:
##       texture_worst        < 26.285   to the left,  improve=6.259259, (0
missing)
##       smoothness_worst     < 0.1405   to the left,  improve=4.680312, (0
missing)
##       smoothness_mean      < 0.1083   to the left,  improve=4.402116, (0
missing)
##       texture_mean         < 20.3     to the left,  improve=3.792593, (0
missing)
##       concave points_worst < 0.17175  to the left,  improve=3.792593, (0
missing)
##   Surrogate splits:
##       texture_mean      < 16.22    to the left,  agree=0.852, adj=0.556, (0
split)
##       smoothness_worst < 0.13145  to the left,  agree=0.815, adj=0.444, (0
split)
##       concavity_mean   < 0.089375 to the left,  agree=0.778, adj=0.333, (0
split)
##       smoothness_se    < 0.005373 to the left,  agree=0.778, adj=0.333, (0
split)
##       concavity_se     < 0.11138  to the right, agree=0.778, adj=0.333, (0
split)
## 
## Node number 10: 9 observations
##   predicted class=B  expected loss=0.2222222  P(node) =0.02107728
##     class counts:     7     2
##    probabilities: 0.778 0.222 
## 
## Node number 11: 18 observations
##   predicted class=M  expected loss=0.05555556  P(node) =0.04215457
##     class counts:     1    17
##    probabilities: 0.056 0.944
```

```
#Kernlab Classification
require(kernlab)
```

```
## Loading required package: kernlab
```

```
##
## Attaching package: 'kernlab'
```

```
## The following object is masked from 'package:modeltools':
##
##     prior
```

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

```
installed.packages("kernlab")
```

```
##      Package LibPath Version Priority Depends Imports LinkingTo Suggests
##      Enhances License License_is_FOSS License_restricts_use OS_type Archs
##      MD5sum NeedsCompilation Built
```

```
library(kernlab)
data_classifier<-ksvm(diagnosis ~., data =train_data , kernel='vanilladot')
```

```
##  Setting default kernel parameters
```

```
data_classifier
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 1
##
## Linear (vanilla) kernel function.
##
## Number of Support Vectors : 28
##
## Objective Function Value : -13.7674
## Training error : 0.007026
```

```
data_predictions<-predict(data_classifier,test_data)
head(data_predictions)
```

```
## [1] M M M M M M
## Levels: B M
```

```
table(data_predictions, test_data$diagnosis)
```

```
##
## data_predictions   B   M
##                B 267   2
##                M   1 157
```

```
agreement<-data_ predictions ==
test_data$diagnosis table(agreement)
```

```
## agreement
## FALSE   TRUE
##     3    424
```

```
prop.table(table(agreement))
```

```
## agreement
##       FALSE       TRUE
## 0.007025761 0.992974239
```

```
Agreement
```

```
##    [1]   TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
##   [12]   TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
##   [23]   TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
##   [34]   TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [342]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [353]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [364]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [375]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [386]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [397]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [408]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
## [419]    TRUE  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE
```

```
set.seed(12345)
data_classifier_rbf<-ksvm(diagnosis ~., data = train_data, kernel='rbfdot')
data_predictions_rbf<-predict(data_classifier_rbf,test_data)
agreement_rbf<-data_predictions_rbf == test_data$diagnosis
table(agreement_rbf)
```

```
## agreement_rbf
## FALSE  TRUE
##     2   425
```

```
prop.table(table(agreement_rbf))
```

```
## agreement_rbf
##       FALSE        TRUE
## 0.004683841 0.995316159
```

```
# logistic regression model:
fit <- glm(diagnosis~.,data = train_data,family = binomial(link='logit'))
```

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

```
summary(fit)
```

```
##
## Call:
## glm(formula = diagnosis ~ ., family = binomial(link = "logit"),
##      data = train_data)
## 
## Deviance Residuals: 
##     Min       1Q   Median       3Q      Max  
##   -8.49     0.00     0.00     0.00     8.49  
## 
## Coefficients:
##                           Estimate Std. Error    z value Pr(>|z|)    
## (Intercept)             -5.487e+15  1.418e+08  -38703923   <2e-16 ***
## radius_mean             -1.401e+13  5.949e+07    -235423   <2e-16 ***
## texture_mean            -5.783e+13  2.594e+06  -22293459   <2e-16 ***
## perimeter_mean          -1.954e+14  8.518e+06  -22935779   <2e-16 ***
## area_mean                7.231e+12  1.723e+05   41962794   <2e-16 ***
## smoothness_mean          1.141e+16  6.970e+08   16374586   <2e-16 ***
## compactness_mean        -1.560e+16  4.601e+08  -33898361   <2e-16 ***
## concavity_mean           3.612e+15  3.663e+08    9859481   <2e-16 ***
## `concave points_mean`    3.368e+16  6.496e+08   51839897   <2e-16 ***
## symmetry_mean            7.166e+14  2.485e+08    2883416   <2e-16 ***
## fractal_dimension_mean  -1.875e+16  1.853e+09  -10119625   <2e-16 ***
## radius_se               -1.780e+14  1.147e+08   -1552350   <2e-16 ***
## texture_se              -5.141e+14  1.143e+07  -44982769   <2e-16 ***
## perimeter_se            -1.506e+14  1.516e+07   -9929607   <2e-16 ***
## area_se                  3.909e+12  4.713e+05    8294154   <2e-16 ***
## smoothness_se            6.741e+16  2.230e+09   30224242   <2e-16 ***
## compactness_se          -1.263e+16  7.957e+08  -15868906   <2e-16 ***
## concavity_se            -6.112e+15  4.465e+08  -13688233   <2e-16 ***
## `concave points_se`      2.479e+16  1.882e+09   13170418   <2e-16 ***
## symmetry_se              3.309e+16  8.953e+08   36963236   <2e-16 ***
## fractal_dimension_se     2.482e+16  4.032e+09    6155984   <2e-16 ***
## radius_worst             7.751e+14  2.067e+07   37495454   <2e-16 ***
## texture_worst            1.151e+14  2.192e+06   52500738   <2e-16 ***
## perimeter_worst          7.806e+13  2.049e+06   38088467   <2e-16 ***
## area_worst              -5.352e+12  1.108e+05  -48313624   <2e-16 ***
## smoothness_worst        -4.364e+15  4.930e+08   -8850467   <2e-16 ***
## compactness_worst        1.527e+15  1.306e+08   11684310   <2e-16 ***
## concavity_worst          2.629e+15  9.403e+07   27964084   <2e-16 ***
## `concave points_worst`  -5.585e+15  3.231e+08  -17282850   <2e-16 ***
## symmetry_worst          -1.380e+15  1.615e+08   -8543749   <2e-16 ***
## fractal_dimension_worst  8.968e+15  7.758e+08   11560246   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
##     Null deviance: 563.81   on 426  degrees of freedom
## Residual deviance: 504.61   on 396  degrees of freedom
## AIC: 566.61
## 
## Number of Fisher Scoring iterations: 19
```

```r
library(MASS)
step_fit <- stepAIC(fit,method='backward')
```

```
## Start:  AIC=566.61
## diagnosis ~ radius_mean + texture_mean + perimeter_mean + area_mean + 
##     smoothness_mean + compactness_mean + concavity_mean + 
`concave points_mean` + 
##     symmetry_mean + fractal_dimension_mean + radius_se + texture_se + 
##     perimeter_se + area_se + smoothness_se + compactness_se + 
##     concavity_se + `concave points_se` + symmetry_se + 
fractal_dimension_se + 
##     radius_worst + texture_worst + perimeter_worst + area_worst + 
##     smoothness_worst + compactness_worst + concavity_worst + 
##     `concave points_worst` + symmetry_worst + fractal_dimension_worst
```

```
##                             Df Deviance    AIC
## - perimeter_se               1     0.00  60.00
## - area_mean                  1     0.00  60.00
## - radius_mean                1     0.00  60.00
## - area_se                    1     0.00  60.00
## - symmetry_se                1     0.00  60.00
## - radius_worst               1     0.00  60.00
## - radius_se                  1     0.00  60.00
## - texture_mean               1     0.00  60.00
## - smoothness_worst           1     0.00  60.00
## - compactness_mean           1     0.00  60.00
## - area_worst                 1     0.00  60.00
## - smoothness_mean            1     0.00  60.00
## - compactness_se             1     0.00  60.00
## - `concave points_se`        1     0.00  60.00
## - perimeter_worst            1     0.00  60.00
## - compactness_worst          1     0.00  60.00
## - concavity_se               1     0.00  60.00
## - `concave points_mean`      1     0.00  60.00
## - smoothness_se              1     0.00  60.00
## - symmetry_mean              1     0.00  60.00
## - `concave points_worst`     1     0.00  60.00
## - symmetry_worst             1     0.00  60.00
## - fractal_dimension_mean     1     0.00  60.00
## - fractal_dimension_se       1     0.00  60.00
## - texture_se                 1     0.00  60.00
## - perimeter_mean             1     0.00  60.00
## - fractal_dimension_worst    1     0.00  60.00
## - texture_worst              1     0.00  60.00
## - concavity_mean             1     0.00  60.00
## - concavity_worst            1     0.00  60.00
## <none>                          504.61 566.61
```

```
## 
## Step:  AIC=22
## diagnosis ~ concavity_mean + `concave points_mean` + symmetry_mean +
##     texture_se + smoothness_se + fractal_dimension_se + texture_worst +
##     perimeter_worst + compactness_worst + fractal_dimension_worst
```

```
##                            Df Deviance    AIC
## - texture_se                1    0.000 20.000
## - `concave points_mean`     1    0.000 20.000
## <none>                           0.000 22.000
## - symmetry_mean             1   11.359 31.359
## - concavity_mean            1   12.771 32.771
## - compactness_worst         1   21.067 41.067
## - fractal_dimension_worst   1   31.257 51.257
## - smoothness_se             1   42.914 62.914
## - fractal_dimension_se      1   46.981 66.981
## - texture_worst             1   47.144 67.144
## - perimeter_worst           1   69.590 89.590
```

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

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

```
## 
## Step:  AIC=20
## diagnosis ~ concavity_mean + `concave points_mean` + symmetry_mean +
##     smoothness_se + fractal_dimension_se + texture_worst + perimeter_worst
+
##     compactness_worst + fractal_dimension_worst
```

```
##                            Df Deviance     AIC
## <none>                           0.000  20.000
## - concavity_mean            1   18.073  36.073
## - `concave points_mean`     1   19.949  37.949
## - symmetry_mean             1   25.134  43.134
## - compactness_worst         1   27.324  45.324
## - fractal_dimension_worst   1   43.464  61.464
## - smoothness_se             1   45.694  63.694
## - fractal_dimension_se      1   54.866  72.866
## - texture_worst             1   56.170  74.170
## - perimeter_worst           1  101.702 119.702
```

```
summary(step_fit)
```

```
## 
## Call:
## glm(formula = diagnosis ~ concavity_mean + `concave points_mean` +
##     symmetry_mean + smoothness_se + fractal_dimension_se + texture_worst +
##     perimeter_worst + compactness_worst + fractal_dimension_worst,
##     family = binomial(link = "logit"), data = train_data)
## 
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -9.155e-04  -2.000e-08  -2.000e-08   2.000e-08   1.028e-03
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -1.434e+04  3.496e+05  -0.041    0.967
## concavity_mean           4.805e+03  1.196e+05   0.040    0.968
## `concave points_mean`    8.822e+03  2.173e+05   0.041    0.968
## symmetry_mean            7.239e+03  1.808e+05   0.040    0.968
## smoothness_se            1.715e+05  4.174e+06   0.041    0.967
## fractal_dimension_se    -5.041e+05  1.225e+07  -0.041    0.967
## texture_worst            7.016e+01  1.710e+03   0.041    0.967
## perimeter_worst          5.920e+01  1.446e+03   0.041    0.967
## compactness_worst       -6.023e+03  1.469e+05  -0.041    0.967
## fractal_dimension_worst  7.318e+04  1.785e+06   0.041    0.967
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 5.6381e+02  on 426  degrees of freedom
## Residual deviance: 5.6950e-06  on 417  degrees of freedom
## AIC: 20
##
## Number of Fisher Scoring iterations: 25
```

```
confint(step_fit)
```

```
##                                 2.5 %       97.5 %
## (Intercept)             -2.004980e+05   -22898.638
## concavity_mean          -6.092841e+03    78980.638
## `concave points_mean`   -1.650539e+04   144613.722
## symmetry_mean           -1.076787e+04   121654.932
## smoothness_se           -2.475484e+05 2738198.040
## fractal_dimension_se    -7.894729e+06   765781.958
## texture_worst           -8.660910e+01     1047.087
## perimeter_worst         -5.280658e+01      917.796
## compactness_worst       -9.344200e+04    12900.424
## fractal_dimension_worst -1.312846e+05 1169411.619
```

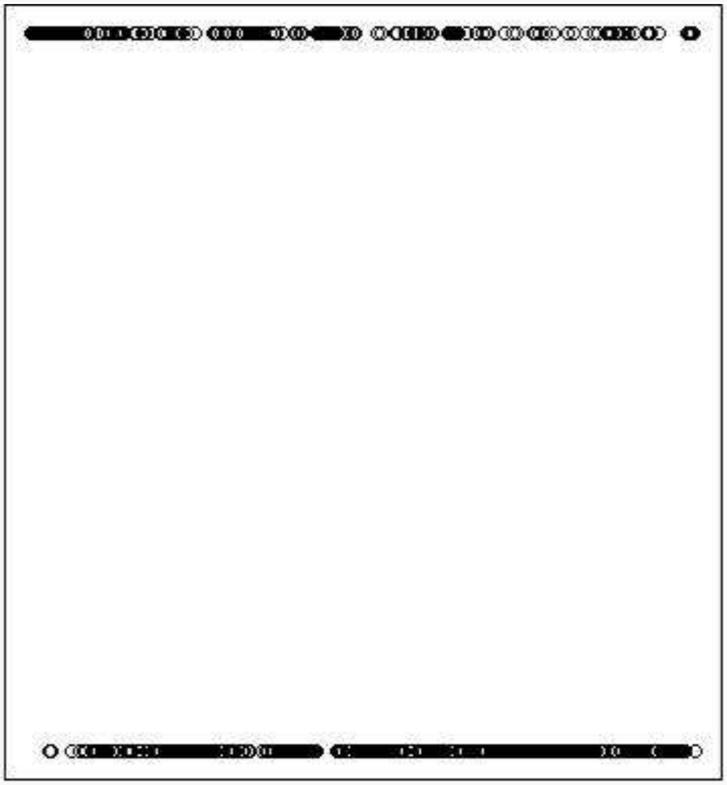
```
#ANOVA on base model
anova(fit,test = 'Chisq')
```

```
## Model: binomial, link: logit
##
## Response: diagnosis
##
## Terms added sequentially (first to last)
##
##
##                          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                                       426     563.81
## radius_mean               1   312.35       425     251.46 < 2.2e-16 ***
## texture_mean              1     22.22       424     229.24 2.431e-06 ***
## perimeter_mean           1    60.59       423     168.65 7.016e-15 ***
## area_mean                1     7.82       422     160.83 0.0051568 **
## smoothness_mean          1    34.03       421     126.79 5.416e-09 ***
## compactness_mean         1     0.02       420     126.77 0.8900612
## concavity_mean           1    11.89       419     114.88 0.0005637 ***
## `concave points_mean`    1     2.64       418     112.24 0.1041743
## symmetry_mean            1     3.55       417     108.69 0.0595695 .
## fractal_dimension_mean   1     0.48       416     108.21 0.4872629
## radius_se                1     4.78       415     103.42 0.0287116 *
## texture_se               1     9.47       414      93.95 0.0020869 **
## perimeter_se             1     0.05       413      93.90 0.8153014
## area_se                  1    12.15       412      81.75 0.0004913 ***
## smoothness_se            1     1.73       411      80.02 0.1883121
## compactness_se           1    20.73       410      59.29 5.295e-06 ***
## concavity_se             1     6.22       409      53.07 0.0126083 *
## `concave points_se`      1     1.12       408      51.94 0.2891473
## symmetry_se              1     1.00       407      50.94 0.3161479
## fractal_dimension_se     1     1.34       406      49.59 0.2461846
## radius_worst             1     0.00       405     648.79 1.0000000
## texture_worst            1   648.79       404       0.00 < 2.2e-16 ***
## perimeter_worst          1     0.00       403       0.00 0.9999778
## area_worst               1     0.00       402       0.00 0.9998569
## smoothness_worst         1     0.00       401       0.00 0.9998323
## compactness_worst        1     0.00       400       0.00 0.9998844
## concavity_worst          1     0.00       399       0.00 1.0000000
## `concave points_worst`   1     0.00       398       0.00 0.9999370
## symmetry_worst           1     0.00       397       0.00 1.0000000
## fractal_dimension_worst  1     0.00       396     504.61 1.0000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#ANOVA from reduced model after applying the Step AIC
anova(step_fit,test = 'Chisq')
```

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

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

## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: diagnosis
##
## Terms added sequentially (first to last)
##
##
##                          Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                                       426     563.81
## concavity_mean           1  290.218       425     273.60 < 2.2e-16 ***
## `concave points_mean`      1    76.300        424      197.30 <  2.2e-16 ***
## symmetry_mean              1     4.970        423      192.32    0.02578 *
## smoothness_se              1     6.224        422      186.10    0.01260 *
## fractal_dimension_se       1    33.111        421      152.99 8.706e-09 ***
## texture_worst              1    46.144        420      106.85 1.099e-11 ***
## perimeter_worst            1    59.618        419       47.23 1.152e-14 ***
## compactness_worst          1     3.765        418       43.46   0.05234 .
## fractal_dimension_worst    1    43.464        417        0.00 4.319e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#plot the fitted model
```



```
plot.new()

plot(fit$fitted.values)
pred_link <- predict(fit,newdata = test_data,type = 'link')
#check for multicollinearity
library(car)
```

```
## Loading required package: carData

##
## Attaching package: 'car'
## The following object is masked from 'package:modeltools':
##
##     Predict
```

```r
vif(fit)
```

```
##              radius_mean            texture_mean          perimeter_mean
##              4231.240532               12.057374             4114.484019
##                area_mean         smoothness_mean        compactness_mean
##               357.762613                9.570587               55.757803
##           concavity_mean   `concave points_mean`           symmetry_mean
##                79.562151               59.693761                4.277740
##  fractal_dimension_mean                radius_se              texture_se
##                16.406891              100.057360                3.980190
##             perimeter_se                 area_se           smoothness_se
##                92.303083               47.935390                4.114137
##           compactness_se            concavity_se     `concave points_se`
##                17.218922               16.063111               13.374578
##              symmetry_se    fractal_dimension_se            radius_worst
##                 5.415910               11.916743              960.040406
##            texture_worst         perimeter_worst              area_worst
##                18.054760              454.037215              386.858470
##         smoothness_worst       compactness_worst         concavity_worst
##                12.427398               37.442475               34.364483
##   `concave points_worst`          symmetry_worst fractal_dimension_worst
##                43.557508                9.363305               17.264083
```

```r
vif(step_fit)
```

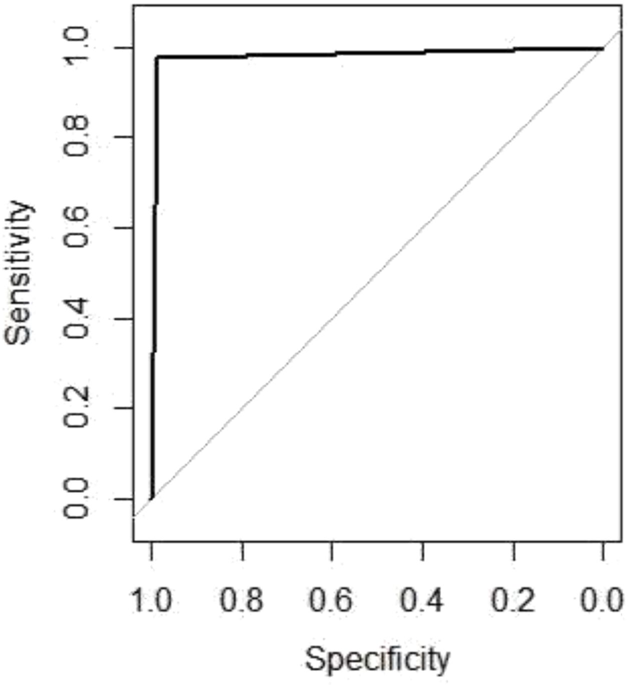
```
##           concavity_mean   `concave points_mean`           symmetry_mean
##                244.05337                99.94645               317.05513
##            smoothness_se    fractal_dimension_se           texture_worst
##               4608.37740              6335.09066              1093.86196
##          perimeter_worst       compactness_worst fractal_dimension_worst
##               1517.71228              5118.72975              6430.41696
```

```r
pred <- predict(fit,newdata =test_data ,type ='response')
#check the AUC curve
library(pROC)
g <- roc(diagnosis ~ pred, data = test_data)
g
```

```
##
## Call:
## roc.formula(formula = diagnosis ~ pred, data = test_data)
##
## Data: pred in 268 controls (diagnosis B) < 159 cases (diagnosis M).
## Area under the curve: 0.9818
```

```r
plot.new()
```

```r
plot(g)
```



```
library(caret)
#with default prob cut 0.50
test_data$pred_diagnosis <- ifelse(pred<0.5,'yes','no')

table(test_data$pred_diagnosis,test_data$diagnosis)
```

```
##
##         B   M
##   no    3 155
##   yes 265   4
```

```
#training split of diagnosis classes
round(table(train_data$diagnosis)/nrow(train_data),2)*100
```

```
##
##  B  M
## 63 37
```

```
# test split of diagnosis
round(table(test_data$diagnosis)/nrow(test_data),2)*100
```

```
##
##  B  M
## 63 37
```

```
#predicted split of diagnosis
round(table(test_data$pred_diagnosis)/nrow(test_data),2)*100
```

```
## 
##  no yes
##  37  63
```

```
#create confusion matrix
#confusionMatrix(test_data$diagnosis,test_data$pred_diagnosis)
#how do we create a cross validation scheme
control <- trainControl(method = 'repeatedcv',
                        number = 10,
                        repeats = 3)
seed <-7
metric <- 'Accuracy'
set.seed(seed)
fit_default <- train(diagnosis~.,
                     data = train_data,
                     method = 'glm',
                     metric =metric ,
                     trControl = control)
```

```
print(fit_default)
```

```
## Generalized Linear Model
## 
## 427 samples
##  30 predictor
##   2 classes: 'B', 'M'
## 
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 384, 384, 385, 384, 385, 384, ...
## Resampling results:
## 
##   Accuracy   Kappa
##   0.9516242  0.8968547
```

```
library(caret)
varImp(step_fit)
```

```
##                                Overall
## concavity_mean           0.04016248
## `concave points_mean`    0.04060020
## symmetry_mean            0.04004251
## smoothness_se            0.04107363
## fractal_dimension_se     0.04113828
## texture_worst            0.04104256
## perimeter_worst          0.04095488
## compactness_worst        0.04099049
## fractal_dimension_worst 0.04099415
```

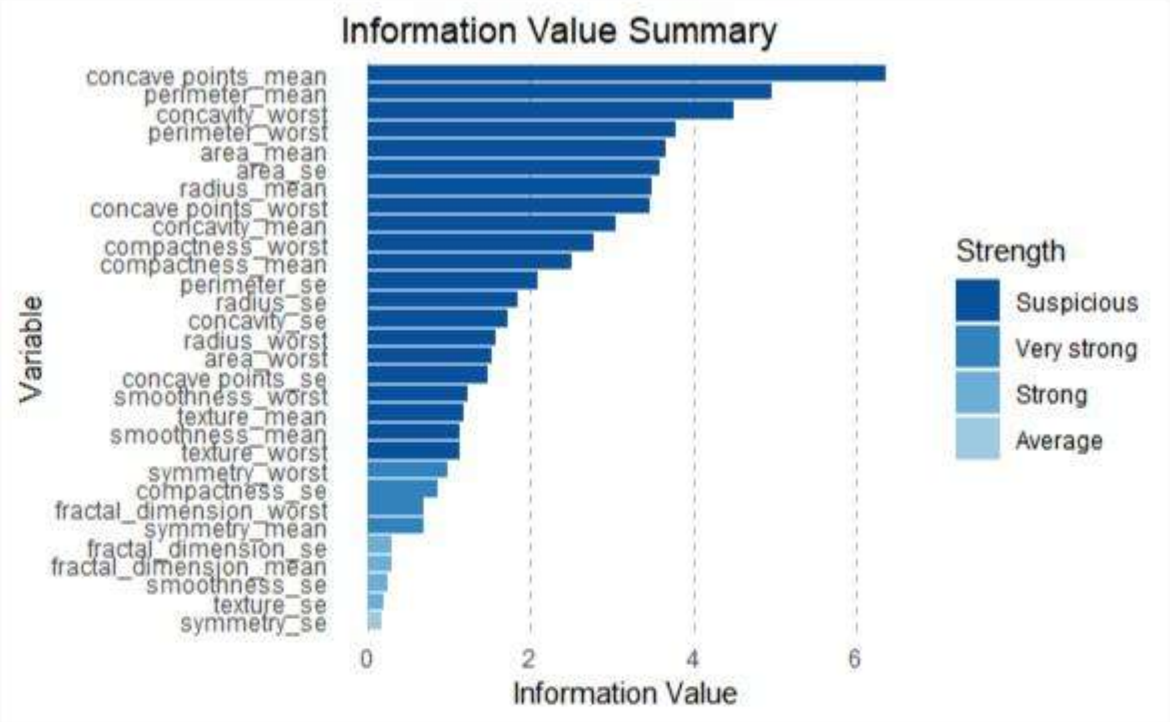
```
varImp(fit_default)
```

```
## glm variable importance
##
##   only 20 most important variables shown (out of 30)
##
##                                Overall
## texture_worst                  100.00
## `\\`concave points_mean\\``     98.74
## area_worst                      91.99
## texture_se                      85.62
## area_mean                       79.84
## perimeter_worst                 72.42
## radius_worst                    71.29
## symmetry_se                     70.27
## compactness_mean                64.41
## smoothness_se                   57.38
## concavity_worst                 53.05
## perimeter_mean                  43.43
## texture_mean                    42.20
## `\\`concave points_worst\\``    32.62
## smoothness_mean                 30.88
## compactness_se                  29.91
## concavity_se                    25.74
## `\\`concave points_se\\``       24.75
## compactness_worst               21.91
## fractal_dimension_worst         21.67
```

```
library(woe)

library(riv)

train_data<-as.data.frame(train_data)

iv_df <- iv.mult(train_data, y="diagnosis", summary=TRUE, verbose=TRUE)

iv_df

iv <- iv.mult(train_data, y="diagnosis", summary=FALSE, verbose=TRUE)
```

```
Calling iv.num for variable: radius_mean
  Building rpart model
  Model finished
  Sending model to tree parser
  Rules parsed: 5
  Mapping nodes to data
    SQL Merge
    DF Merge
  Calling iv.str for nodes
Information Value 3.48
  Formatting output
Calling iv.num for variable: texture_mean
  Building rpart model
  Model finished
  Sending model to tree parser
  Rules parsed: 6
  Mapping nodes to data
    SQL Merge
    DF Merge
  Calling iv.str for nodes
Information Value 1.17
  Formatting output
  Calling iv.str for nodes
Information Value 0.7
  Formatting output
Preparing summary
> iv_df
                   Variable InformationValue Bins ZeroBins   Strength
1       concave points_mean        6.3541081    5        0 Suspicious
2            perimeter_mean        4.9638289    4        0 Suspicious
3           concavity_worst        4.4909270    4        0 Suspicious
4           perimeter_worst        3.7922674    5        1 Suspicious
5                 area_mean        3.6702849    4        1 Suspicious
6                   area_se        3.5749979    4        0 Suspicious
7               radius_mean        3.4772020    5        1 Suspicious
8      concave points_worst        3.4756344    5        1 Suspicious
9            concavity_mean        3.0356262    6        1 Suspicious
10        compactness_worst        2.7665883    5        0 Suspicious
11         compactness_mean        2.5078805    5        0 Suspicious
12             perimeter_se        2.0849968    6        1 Suspicious
13                radius_se        1.8363325    5        1 Suspicious
14             concavity_se        1.7134338    5        0 Suspicious
15             radius_worst        1.5670693    5        2 Suspicious
16               area_worst        1.5115545    5        2 Suspicious
17        concave points_se        1.4623521    5        0 Suspicious
18         smoothness_worst        1.2334093    5        0 Suspicious
19             texture_mean        1.1714620    6        0 Suspicious
20          smoothness_mean        1.1352591    6        0 Suspicious
21            texture_worst        1.1186736    5        0 Suspicious
22           symmetry_worst        0.9764180    5        0Very strong
23           compactness_se        0.8494686    6        0Very strong
24  fractal_dimension_worst        0.6992234    5        0Very strong
25            symmetry_mean        0.6878786    6        0Very strong
26     fractal_dimension_se        0.3035412    5        0     Strong
27   fractal_dimension_mean        0.2839318    6        0     Strong
28            smoothness_se        0.2490128    6        0     Strong
29               texture_se        0.2015776    6        0     Strong
30              symmetry_se        0.1679877    6        0    Average
> iv <- iv.mult(train_data, y="diagnosis", summary=FALSE, verbose=TRUE)
Started processing of data frame: train_data
Calling iv.num for variable:
  radius_mean Building rpart model
  Model finished
  Sending model to tree parser
  Rules parsed: 5
  Mapping nodes to data
    SQL Merge
    DF Merge
  Calling iv.str for nodes
Information Value 3.48
  Building rpart model
  Model finished
  Sending model to tree parser
  Rules parsed: 5
  Mapping nodes to data
    SQL Merge
    DF Merge
  Calling iv.str for nodes
Information Value 0.7
  Formatting output
```

```
# Plot information value

summary iv.plot.summary(iv_df)
```



```
#4. MARS (earth package)
#The earth package implements variable importance based on Generalized cross validation (GCV),
#number of subset models the variable occurs (nsubsets) and residual sum of squares (RSS).
library(earth)
```

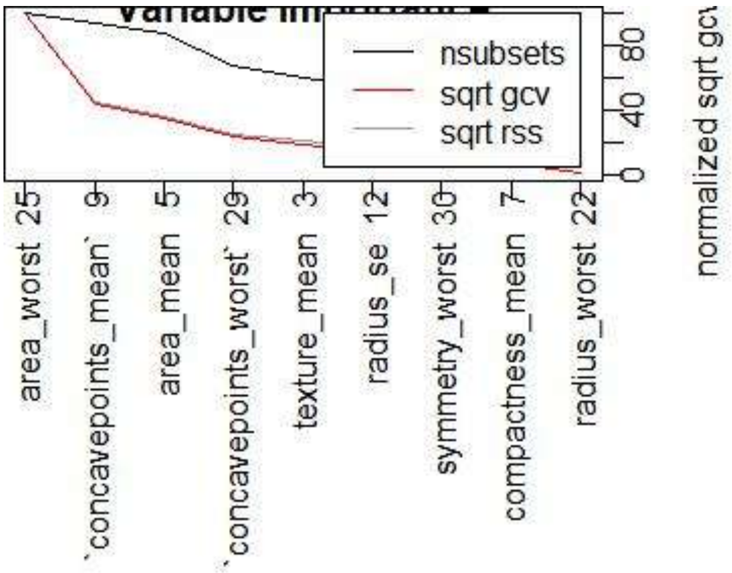
```
## Loading required package: plotmo

## Loading required package: plotrix

## Loading required package: TeachingDemos
```

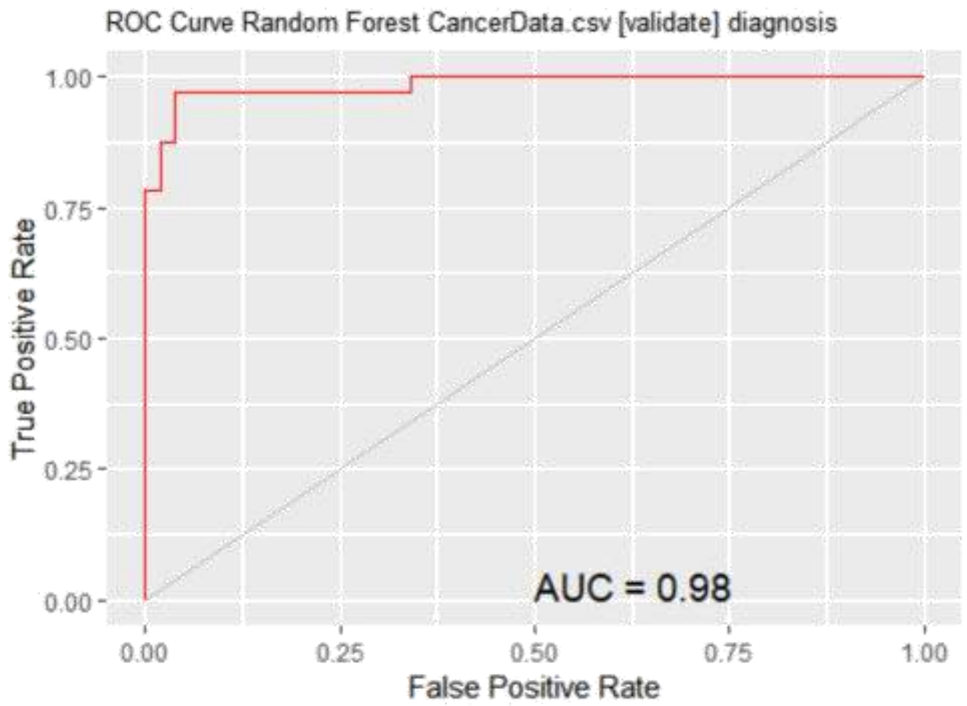
```
marsModel<-earth(diagnosis~ ., data=data) # build model
ev <- evimp (marsModel) # estimate variable importance
ev
```

```
##                         nsubsets   gcv    rss
## area_worst                    15 100.0  100.0
## `concavepoints_mean`          14  43.1   44.5
## area_mean                     13  34.5   36.2
## `concavepoints_worst`         10  22.9   24.9
## texture_mean                   9  18.2   20.5
## radius_se                      8  13.3   16.2
## symmetry_worst                 7   9.6   13.0
## compactness_mean               6   7.6   11.1
## radius_worst                   2   1.5    5.1
```

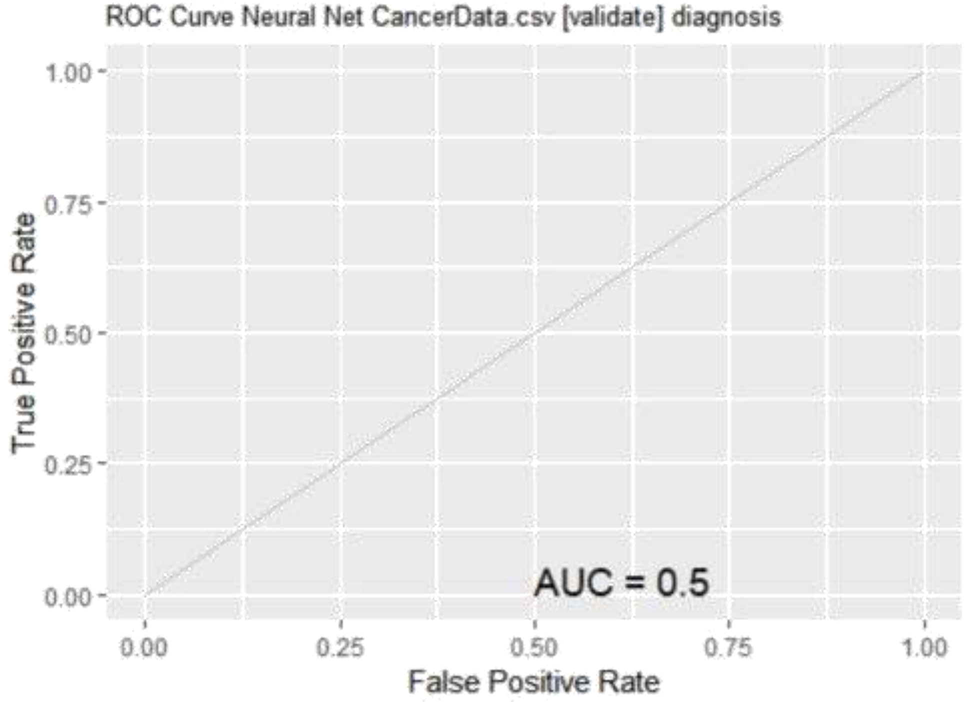
```
plot.new()
```

```
plot (ev)
```

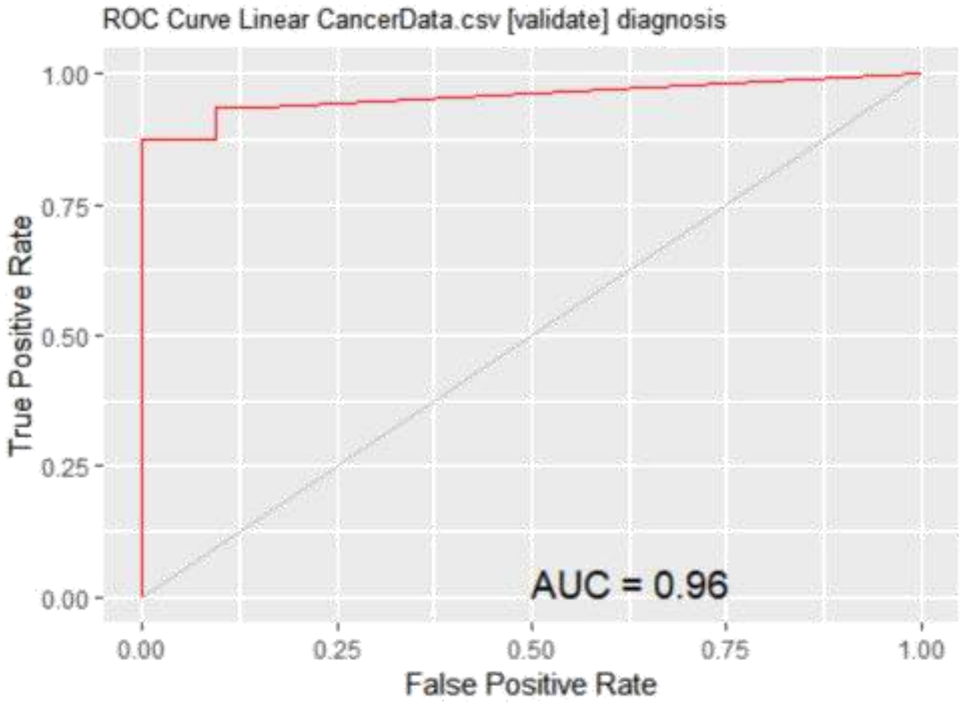


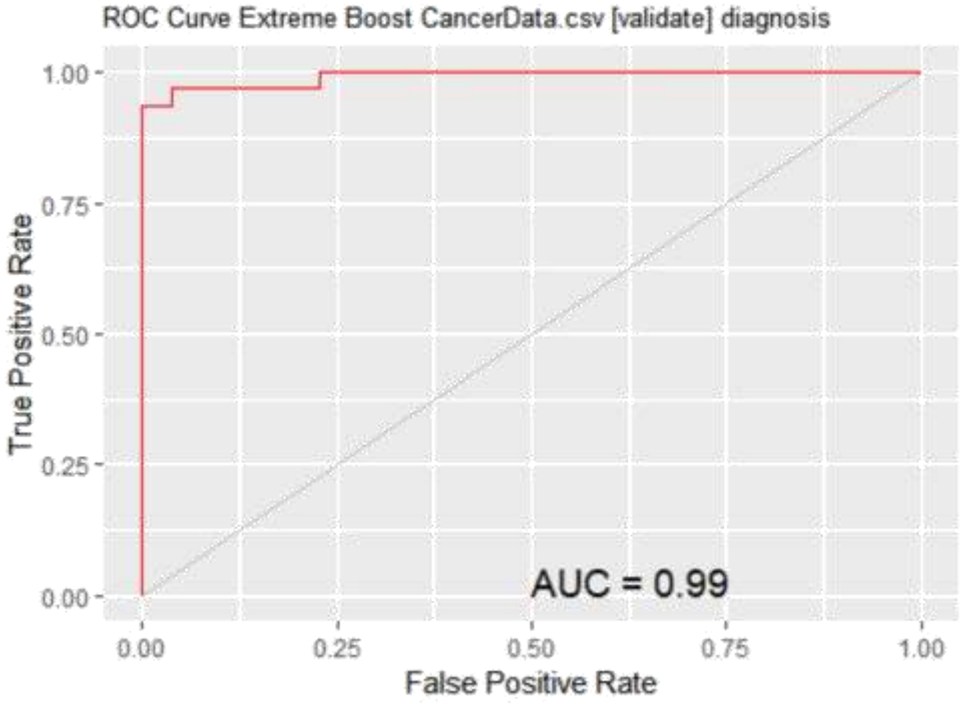


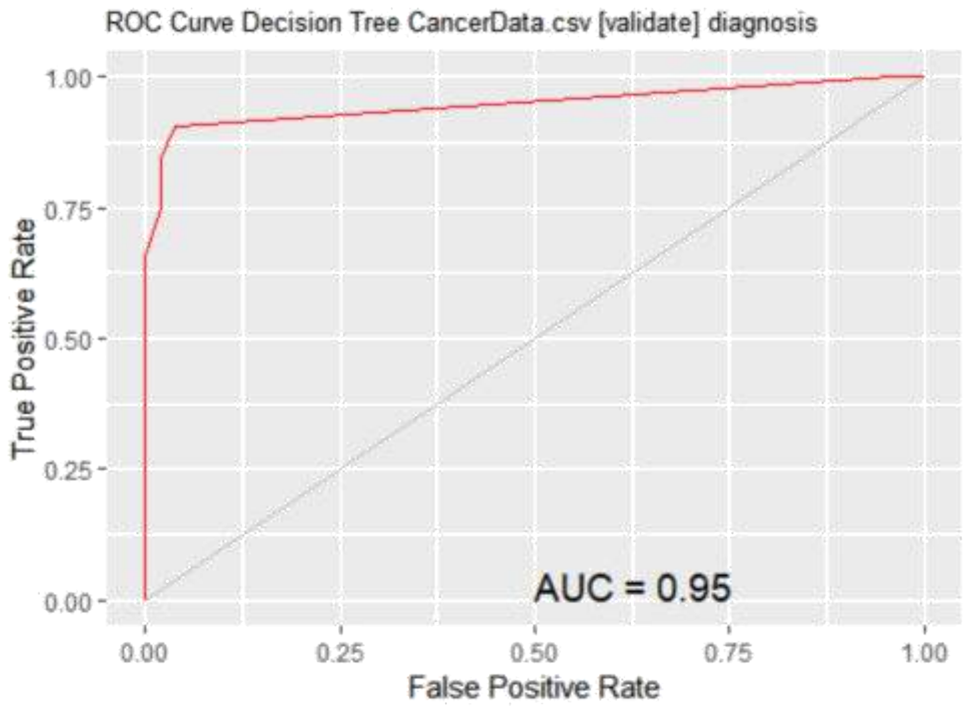
ROC Curve Random Forest CancerData.csv [validate] diagnosis

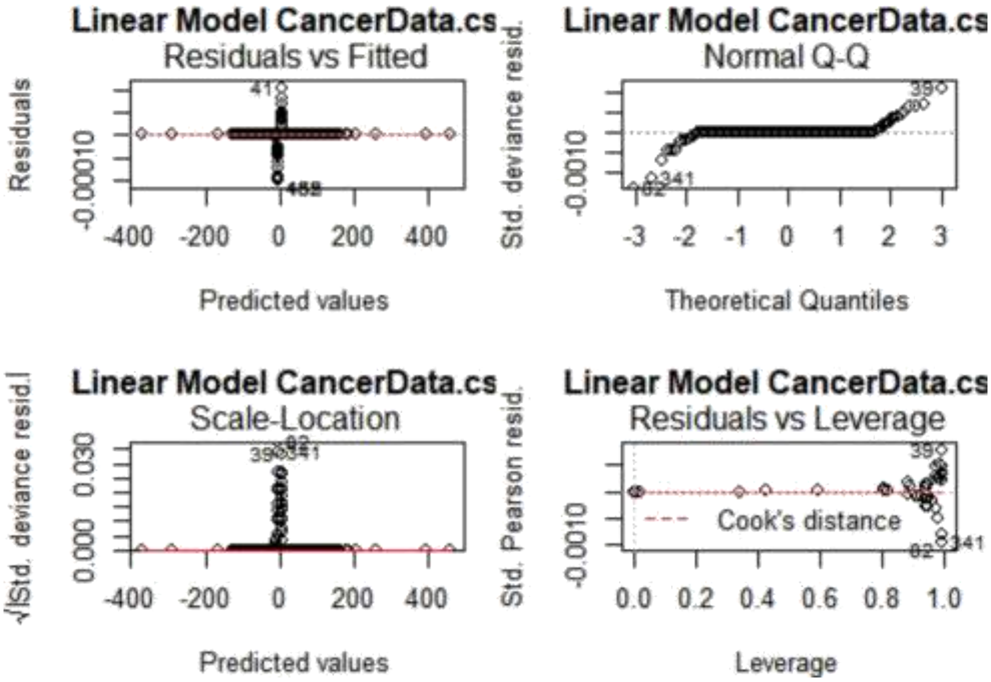


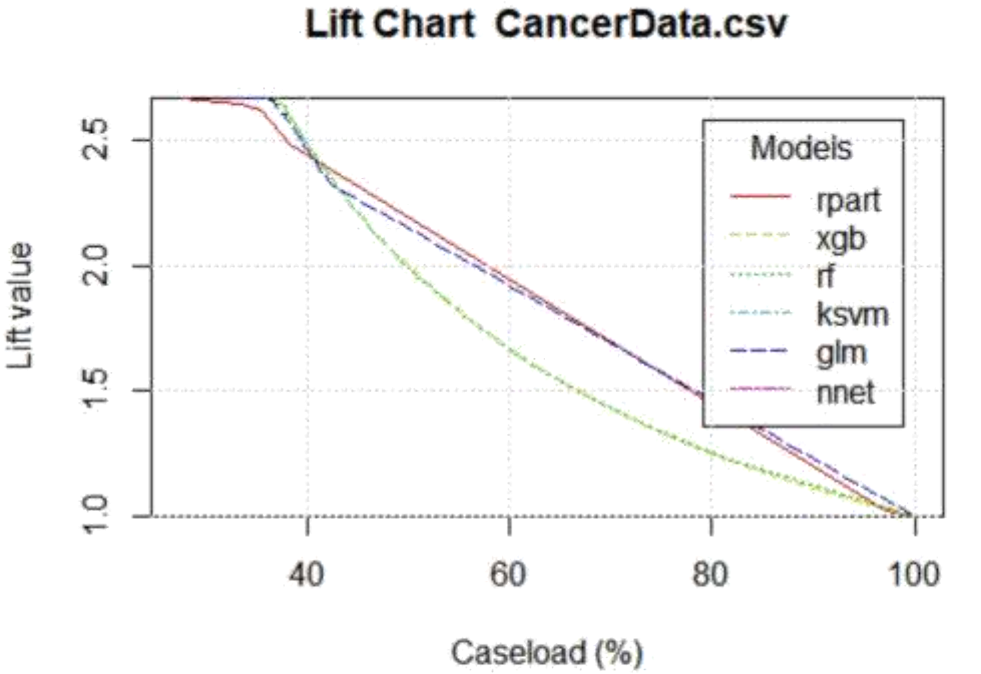
ROC Curve Neural Net CancerData.csv [validate] diagnosis


ROC Curve Linear CancerData.csv [validate] diagnosis
True Positive Rate
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
False Positive Rate
AUC = 0.96

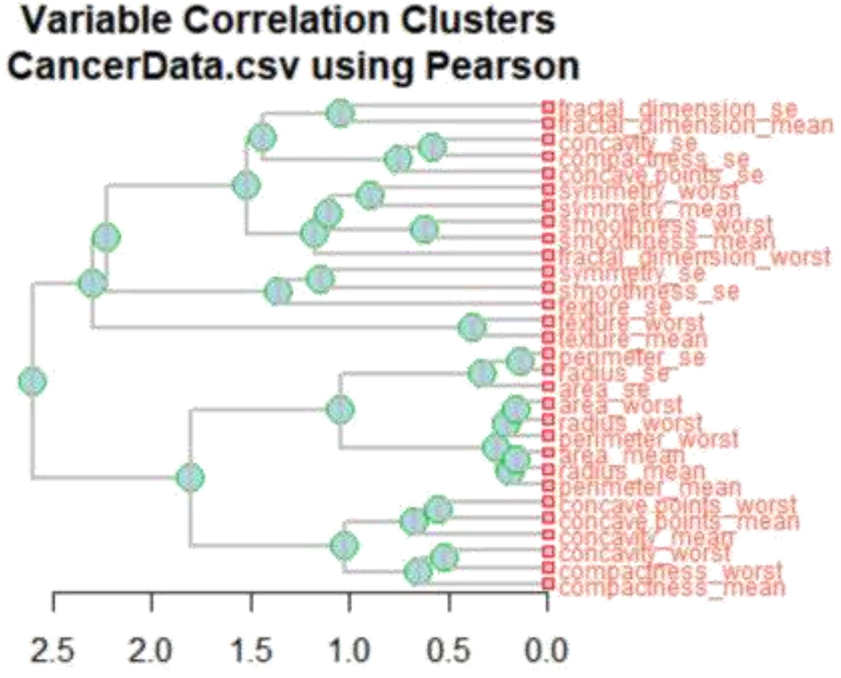

ROC Curve Extreme Boost CancerData.csv [validate] diagnosis
True Positive Rate
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
False Positive Rate
AUC = 0.99


ROC Curve Decision Tree CancerData.csv [validate] diagnosis
True Positive Rate
1.00
0.75
0.50
0.25
0.00
False Positive Rate
0.00
0.25
0.50
0.75
1.00
AUC = 0.95

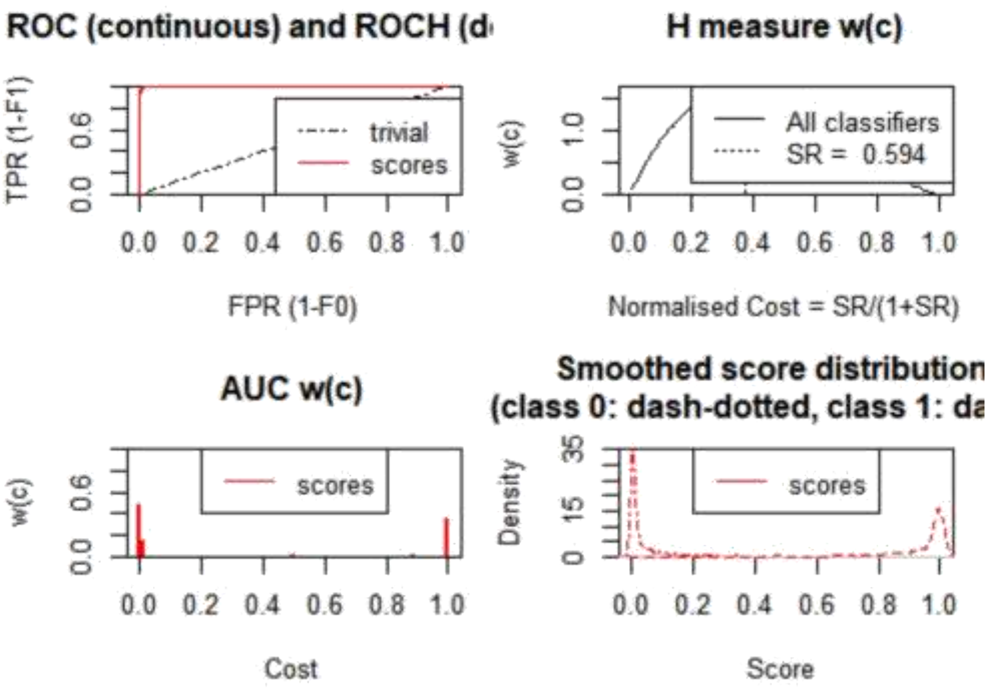

Linear Model CancerData.cs
Residuals vs Fitted
Residuals
-0.00010
41
462
-400
-200
0
200
400
Predicted values
Linear Model CancerData.cs
Normal Q-Q
Std. deviance resid.
-0.0010
39
341
62
-3
-2
-1
0
1
2
3
Theoretical Quantiles
Linear Model CancerData.cs
Scale-Location
√|Std. deviance resid.|
0.000
0.030
39
62
341
-400
-200
0
200
400
Predicted values
Linear Model CancerData.cs
Residuals vs Leverage
Std. Pearson resid.
-0.0010
39
Cook's distance
62
341
0.0
0.2
0.4
0.6
0.8
1.0
Leverage

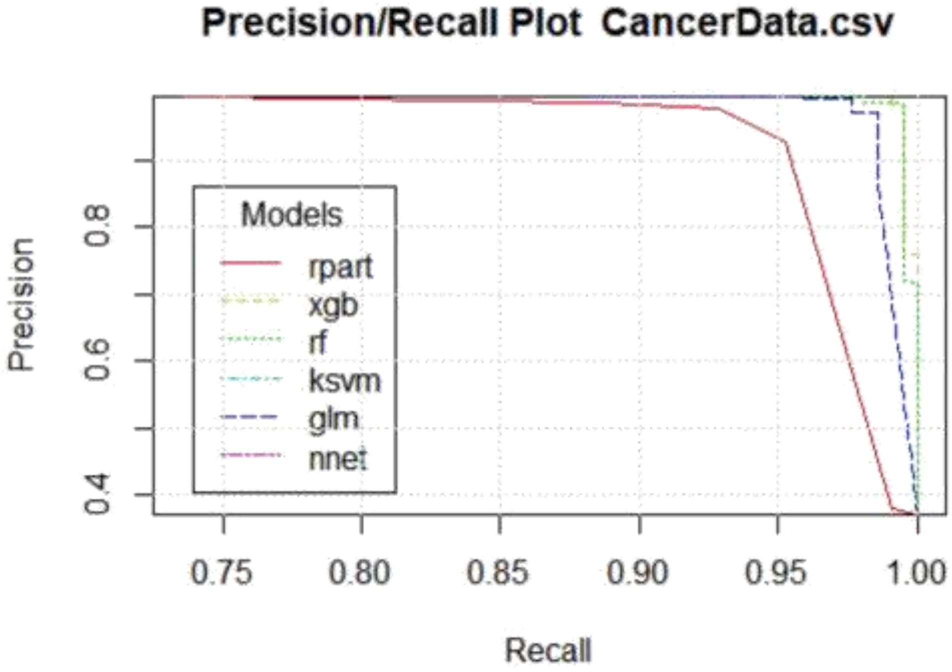


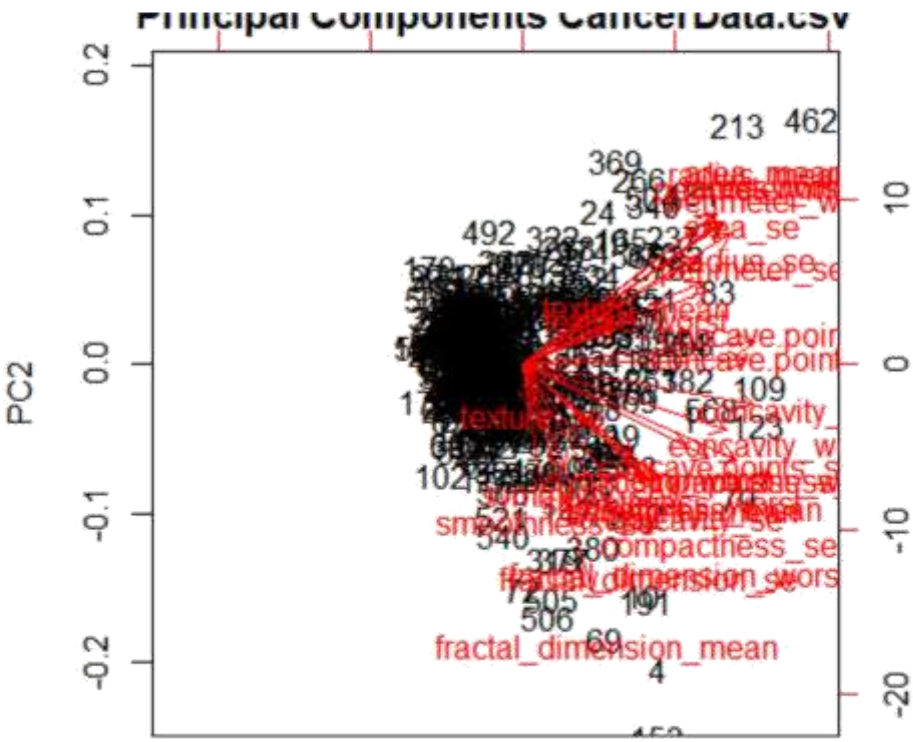
Lift Chart CancerData.csv

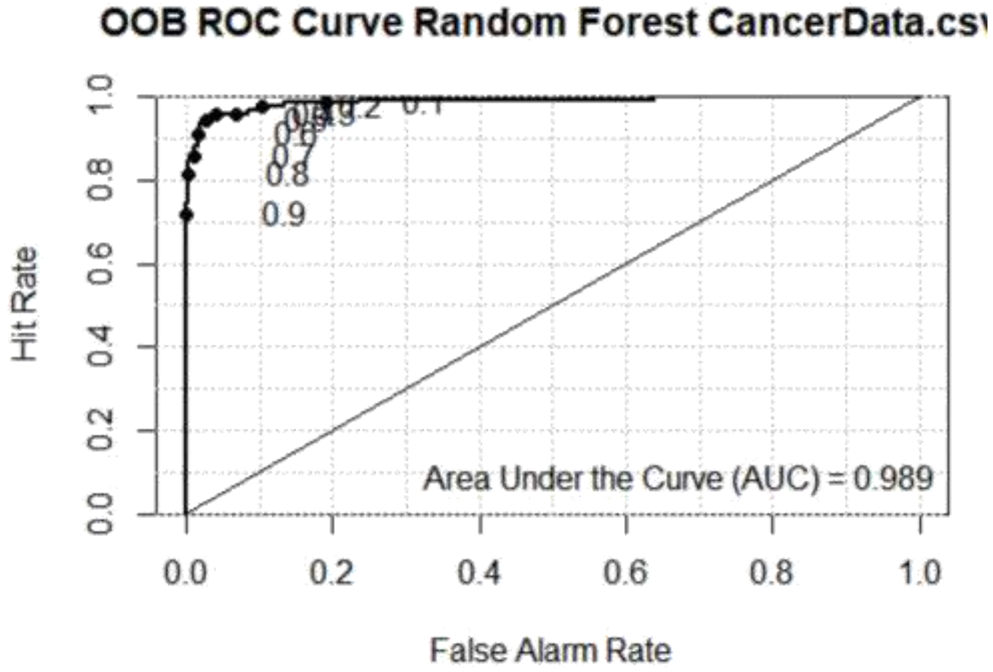


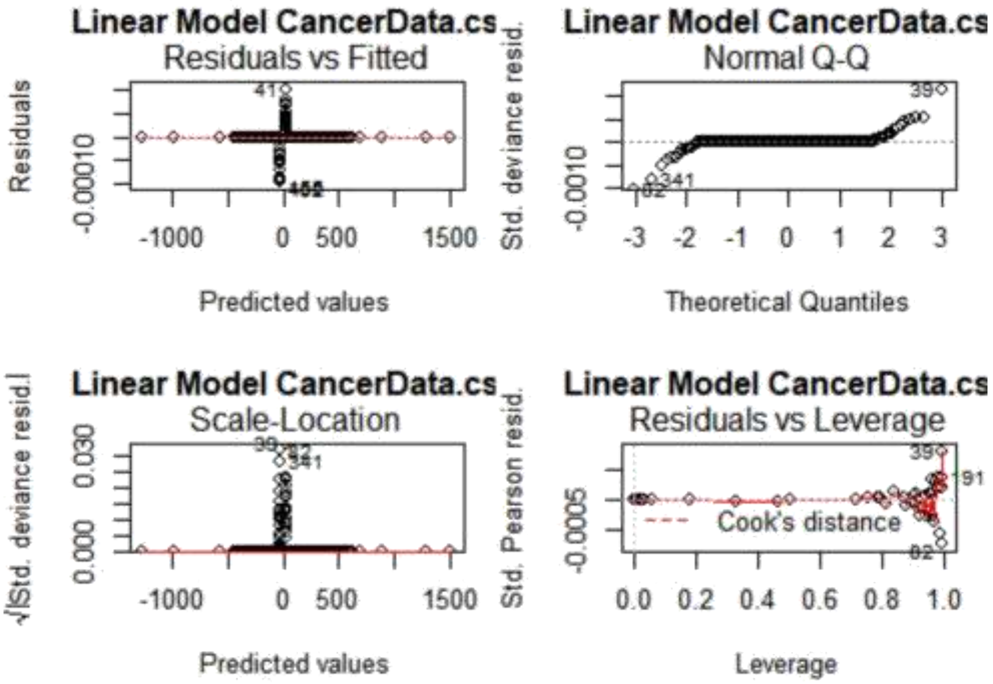
Variable Correlation Clusters
CancerData.csv using Pearson

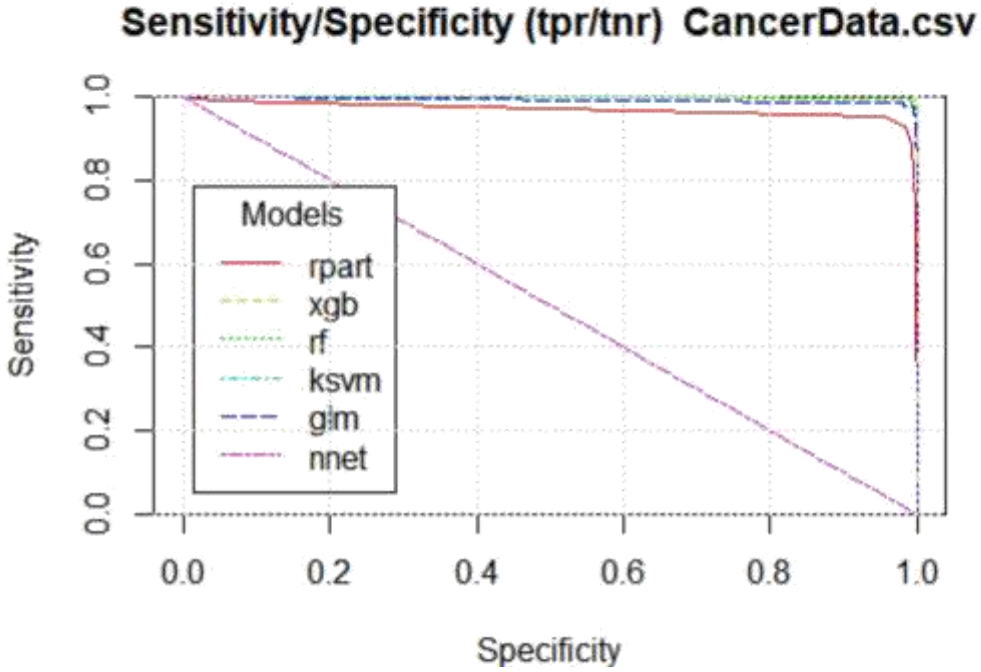

ROC (continuous) and ROCH (d
TPR (1-F1)
0.0
0.6
trivial
scores
0.0 0.2 0.4 0.6 0.8 1.0
FPR (1-F0)
H measure w(c)
w(c)
0.0
1.0
All classifiers
SR = 0.594
0.0 0.2 0.4 0.6 0.8 1.0
Normalised Cost = SR/(1+SR)
AUC w(c)
w(c)
0.0
0.6
scores
0.0 0.2 0.4 0.6 0.8 1.0
Cost
Smoothed score distribution
(class 0: dash-dotted, class 1: da
Density
0
15
35
scores
0.0 0.2 0.4 0.6 0.8 1.0
Score

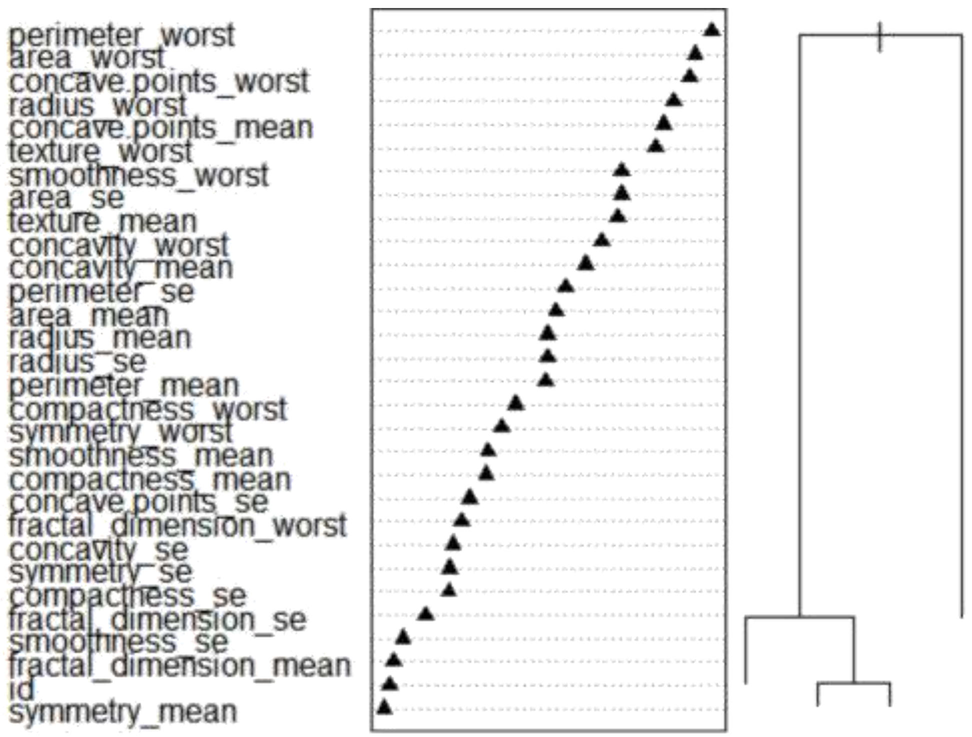

Precision/Recall Plot CancerData.csv
Precision
0.4
0.6
0.8
Models
rpart
xgb
rf
ksvm
glm
nnet
0.75
0.80
0.85
0.90
0.95
1.00
Recall

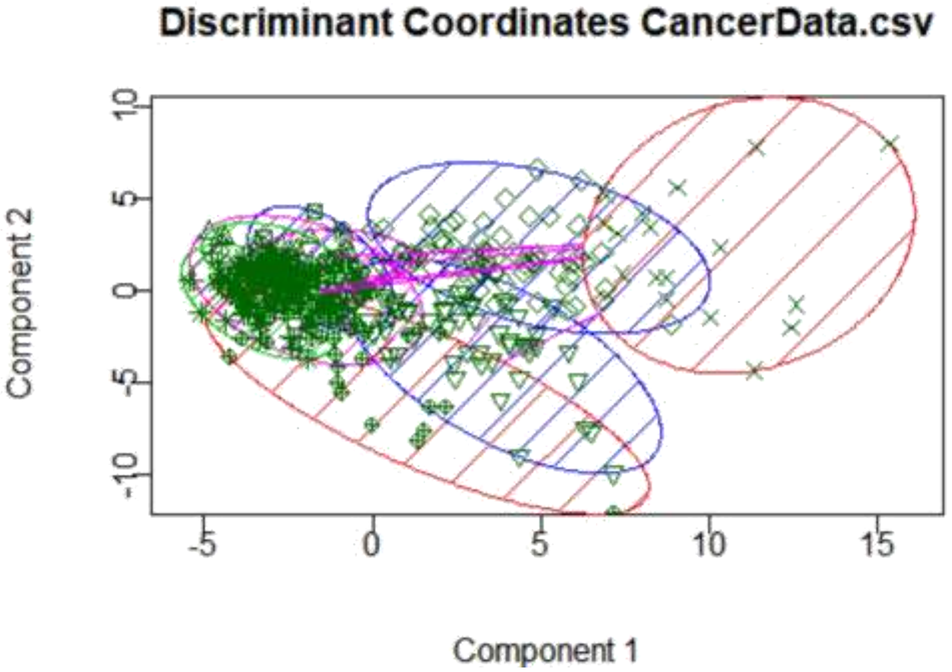

Principal Components CancerData.csv
PC2
0.2
0.1
0.0
-0.1
-0.2
10
0
-10
-20
213
462
369
24
492
83
109
123
102
540
380
505
506
69
4
191
radius_mean
perimeter_w
area_se
radius_se
perimeter_se
concave.poin
concavity_
concavity_w
texture
smoothness
compactness_se
fractal_dimension_se
fractal_dimension_mean

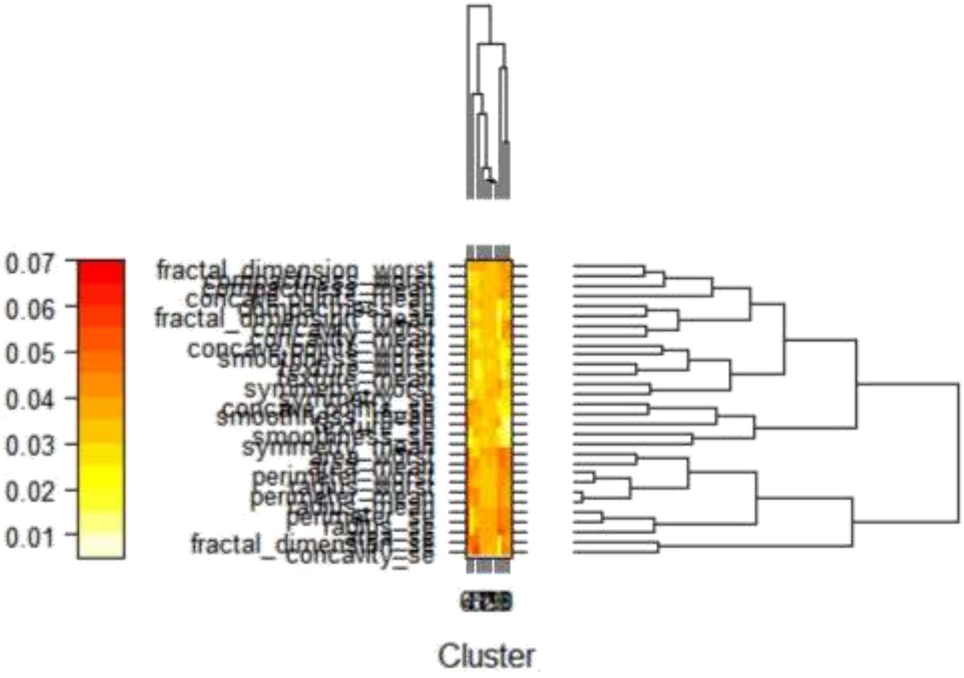

OOB ROC Curve Random Forest CancerData.csv
Hit Rate
False Alarm Rate
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
Area Under the Curve (AUC) = 0.989

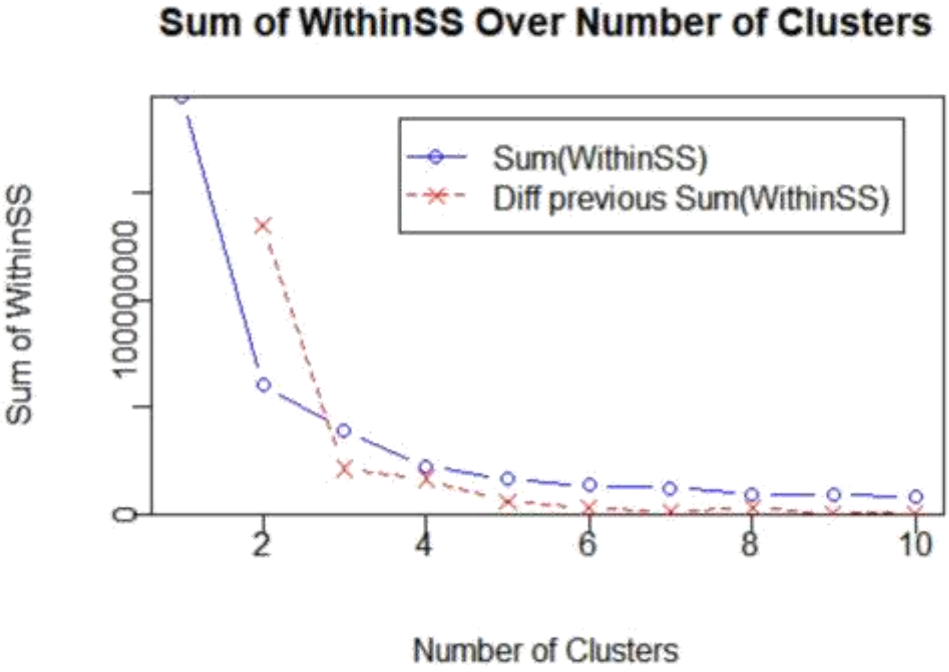

Linear Model CancerData.cs
Residuals vs Fitted
Residuals
-0.00010
41
465
-1000
0
500
1500
Predicted values
Linear Model CancerData.cs
Normal Q-Q
Std. deviance resid.
-0.0010
39
341
82
-3
-2
-1
0
1
2
3
Theoretical Quantiles
Linear Model CancerData.cs
Scale-Location
√|Std. deviance resid.|
0.000
0.030
39
82
341
-1000
0
500
1500
Predicted values
Linear Model CancerData.cs
Residuals vs Leverage
Std. Pearson resid.
-0.0005
39
191
82
Cook's distance
0.0
0.2
0.4
0.6
0.8
1.0
Leverage

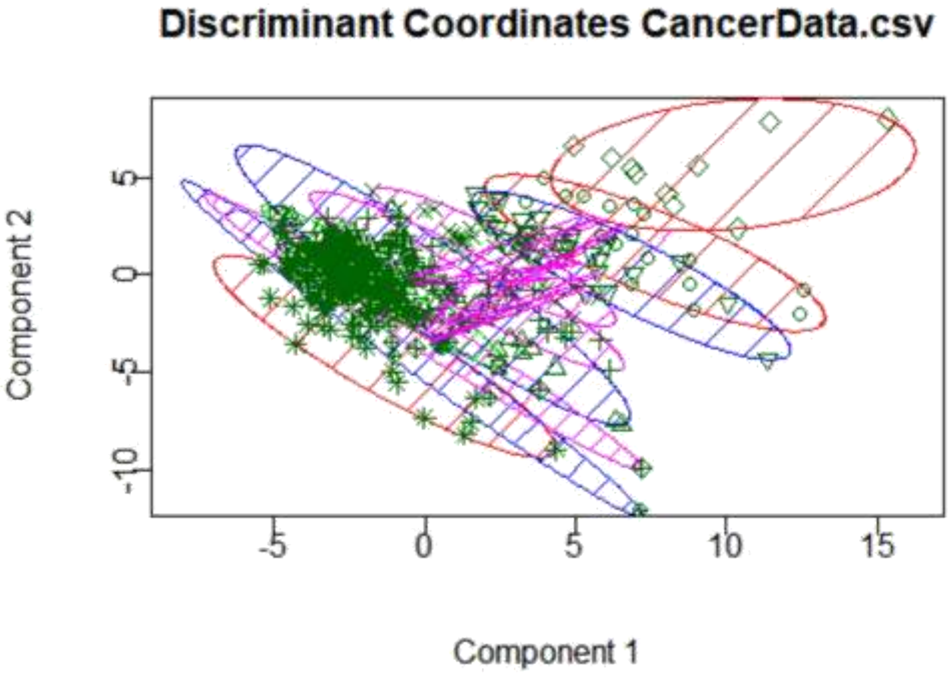

Sensitivity/Specificity (tpr/tnr) CancerData.csv
Sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
Models
rpart
xgb
rf
ksvm
glm
nnet
0.0
0.2
0.4
0.6
0.8
1.0
Specificity

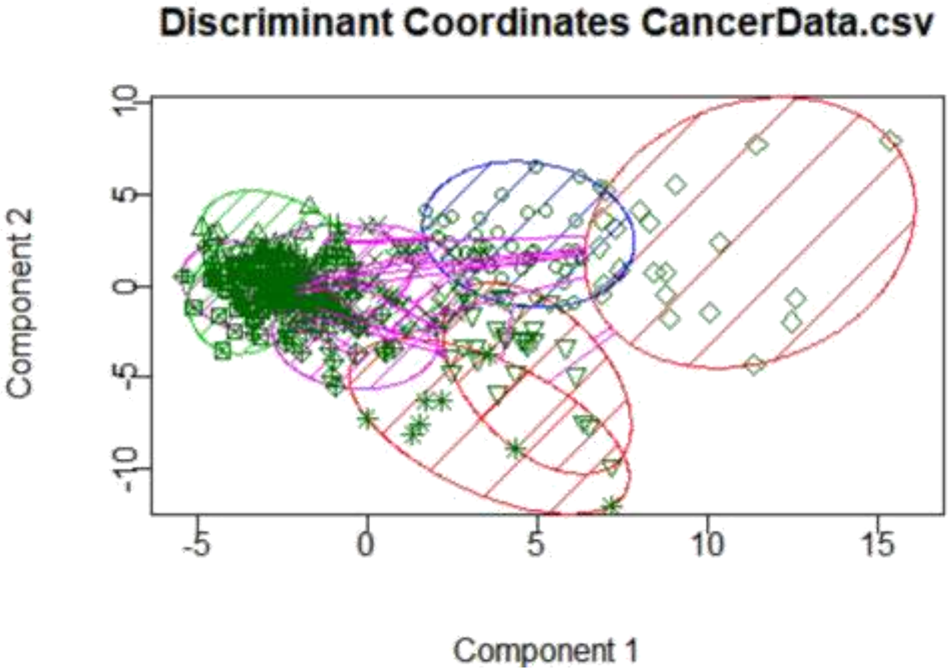

perimeter_worst
area_worst
concave.points_worst
radius_worst
concave.points_mean
texture_worst
smoothness_worst
area_se
texture_mean
concavity_worst
concavity_mean
perimeter_se
area_mean
radius_mean
radius_se
perimeter_mean
compactness_worst
symmetry_worst
smoothness_mean
compactness_mean
concave.points_se
fractal_dimension_worst
concavity_se
symmetry_se
compactness_se
fractal_dimension_se
smoothness_se
fractal_dimension_mean
id
symmetry_mean

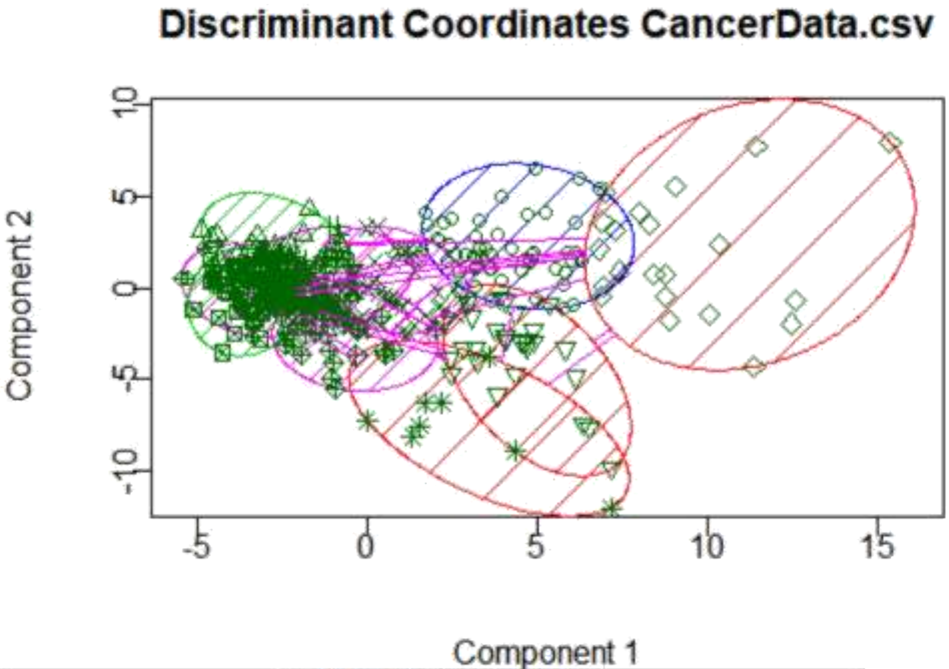

Discriminant Coordinates CancerData.csv
Component 2
10
5
0
-5
-10
-5
0
5
10
15
Component 1

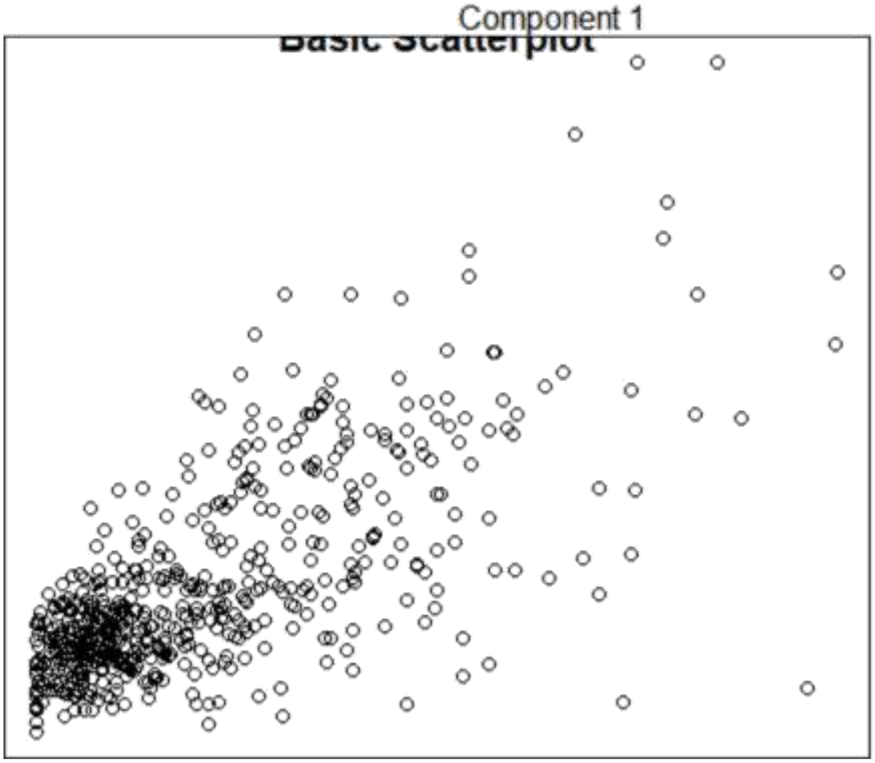



Sum of WithinSS Over Number of Clusters

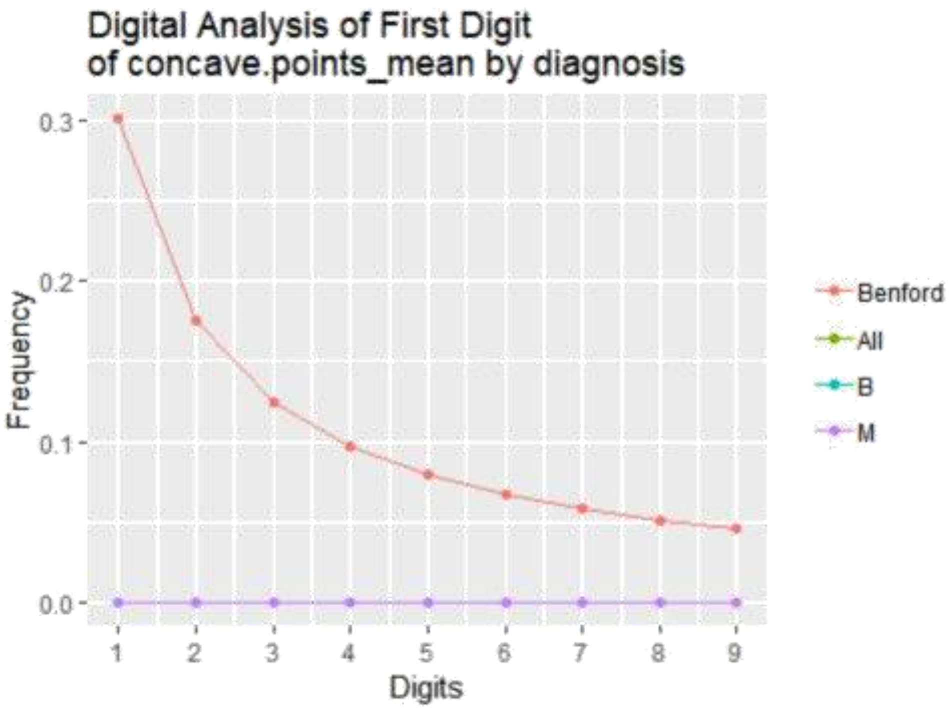

Discriminant Coordinates CancerData.csv
Component 2
5
0
-5
-10
-5
0
5
10
15
Component 1


Discriminant Coordinates CancerData.csv
Component 2
10
5
0
-5
-10
-5
0
5
10
15
Component 1

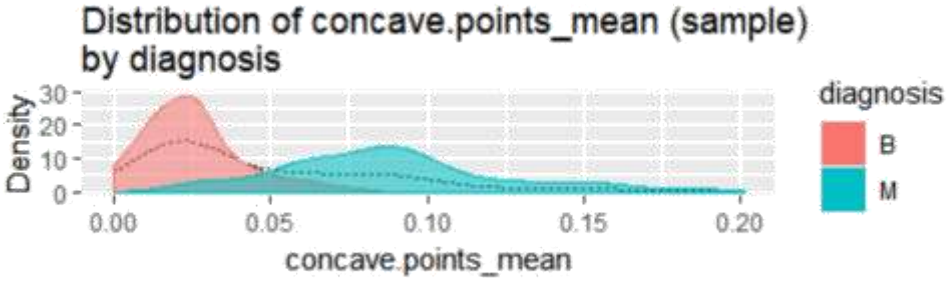




Other plots through Rattle

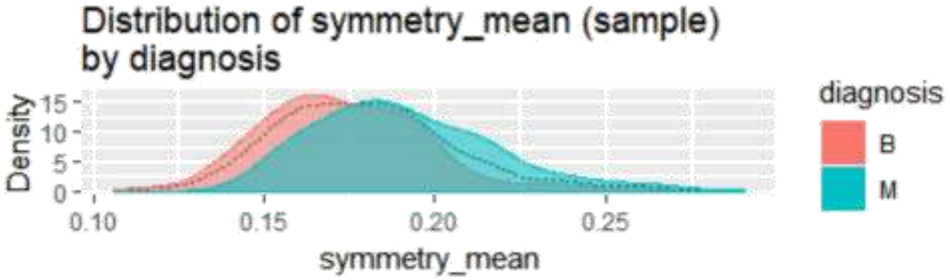


Digital Analysis of First Digit
of concave.points_mean by diagnosis



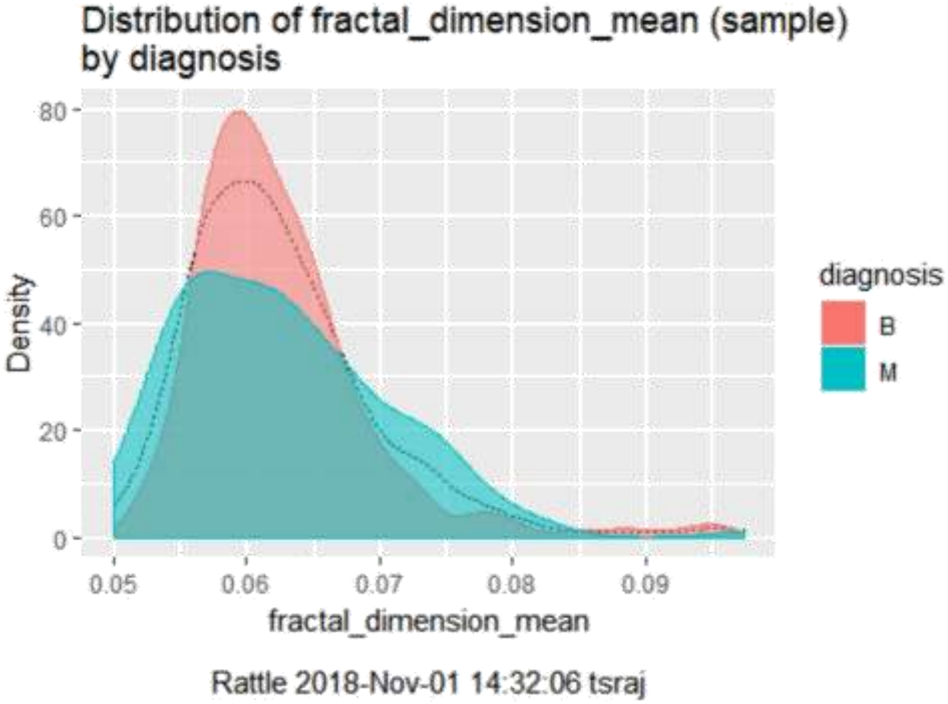
Distribution of concave.points_mean (sample)
by diagnosis

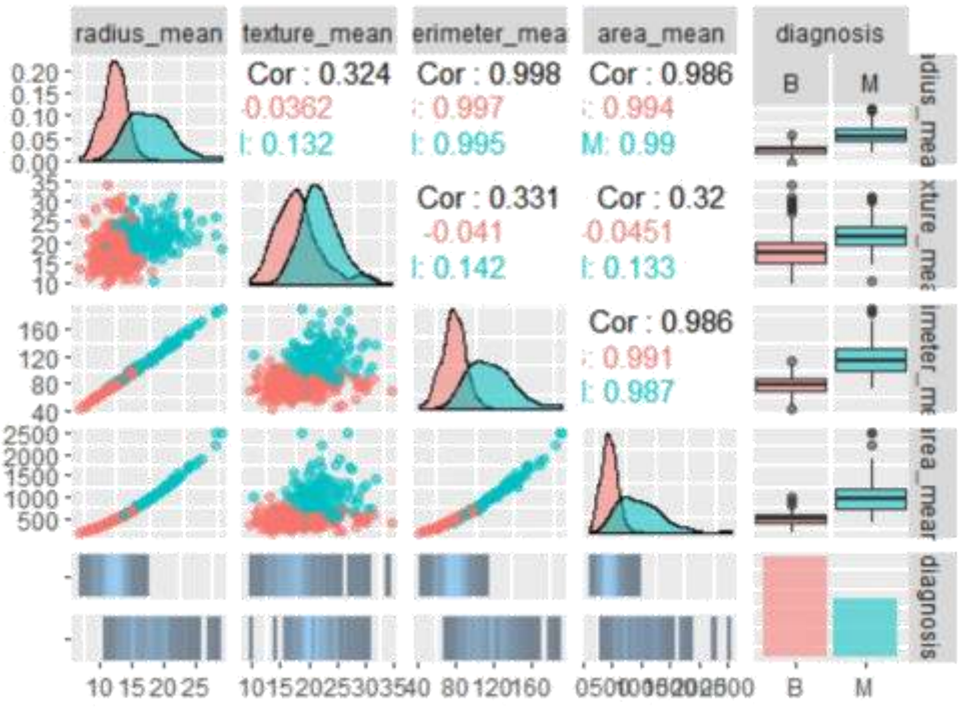
Rattle 2018-Nov-01 14:23:33 tsraj

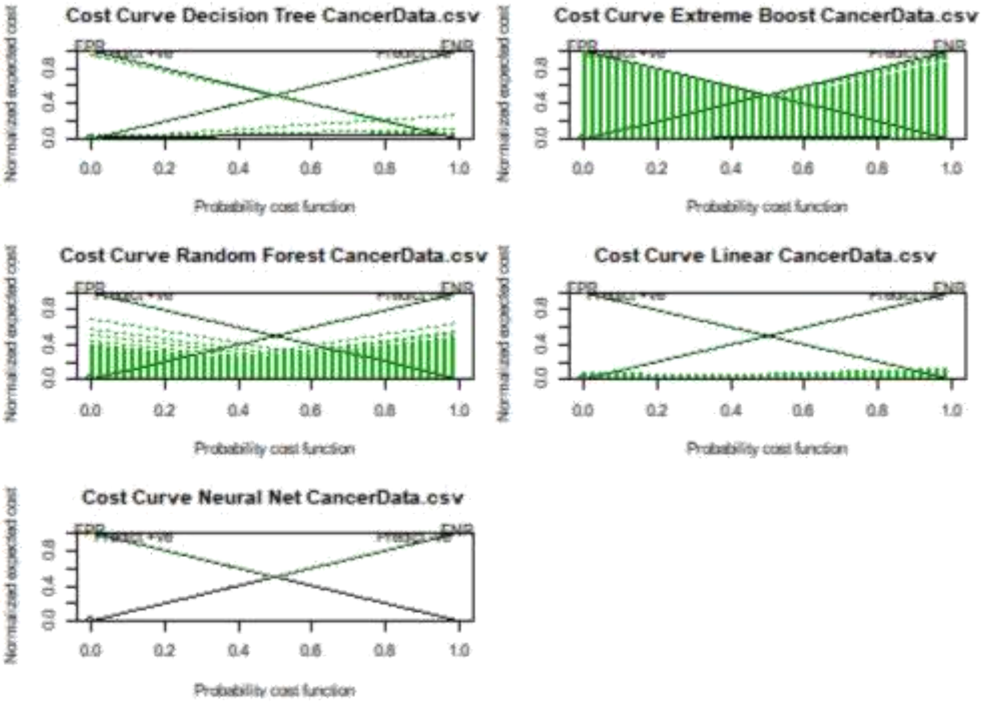


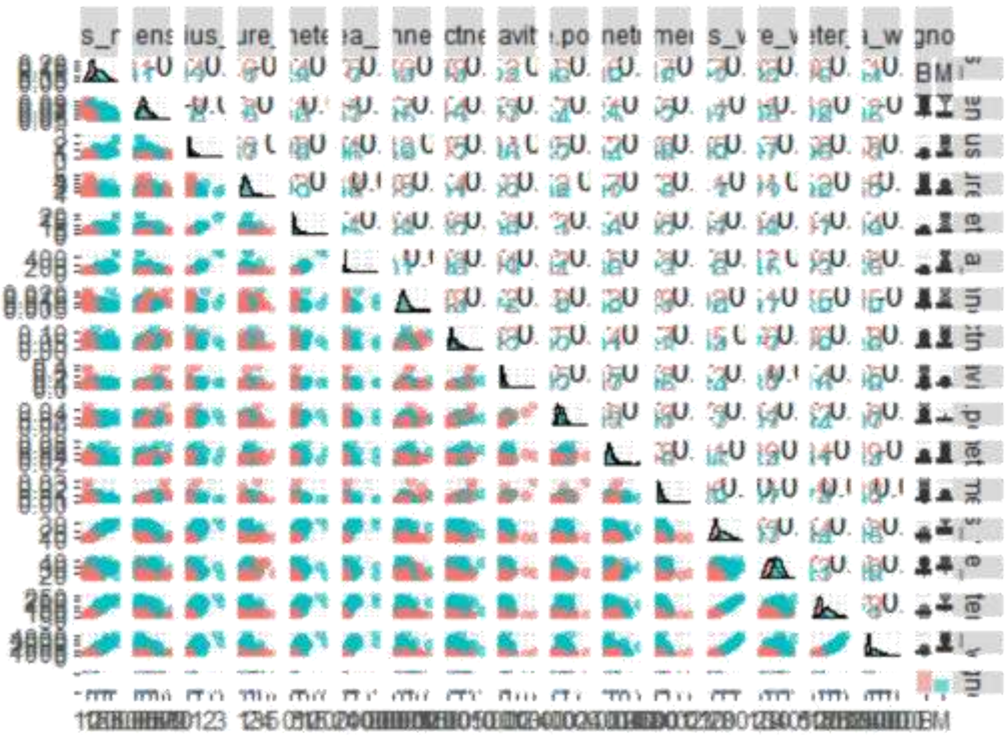
Distribution of symmetry_mean (sample)
by diagnosis

Rattle 2018-Nov-01 14:23:35 tsraj


Distribution of fractal_dimension_mean (sample)
by diagnosis
80
60
40
20
0
Density
0.05
0.06
0.07
0.08
0.09
fractal_dimension_mean
diagnosis
B
M
Rattle 2018-Nov-01 14:32:06 tsraj


radius_mean
texture_mean
erimeter_mea
area_mean
diagnosis
B
M
Cor : 0.324
-0.0362
l: 0.132
Cor : 0.998
:: 0.997
l: 0.995
Cor : 0.986
:: 0.994
M: 0.99
Cor : 0.331
-0.041
l: 0.142
Cor : 0.32
-0.0451
l: 0.133
Cor : 0.986
:: 0.991
l: 0.987
0.20
0.15
0.10
0.05
0.00
35
30
25
20
15
10
160
120
80
40
2500
2000
1500
1000
500
10 15 20 25
1015202530354
40 80 120160
0500100015002000250
B
M
idius_mea
xture_mea
imeter_mı
irea_mear
diagnosis


Cost Curve Decision Tree CancerData.csv
Cost Curve Extreme Boost CancerData.csv
Cost Curve Random Forest CancerData.csv
Cost Curve Linear CancerData.csv
Cost Curve Neural Net CancerData.csv
FPR
FNR
Normalized expected cost
Probability cost function
0.0
0.2
0.4
0.6
0.8
1.0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ure
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ctne
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mei
s_v
e_v
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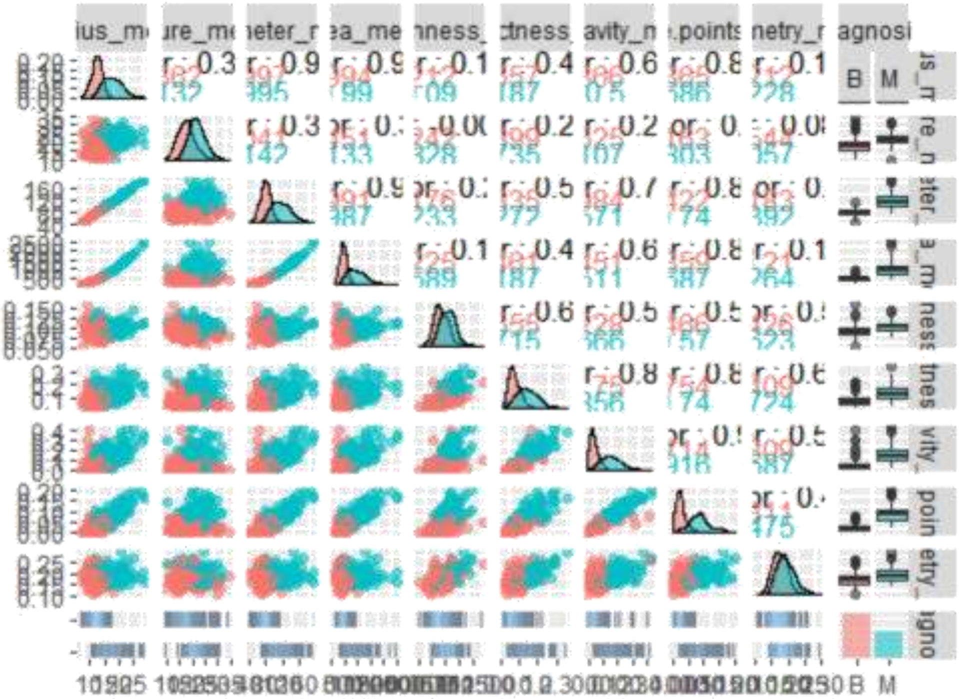
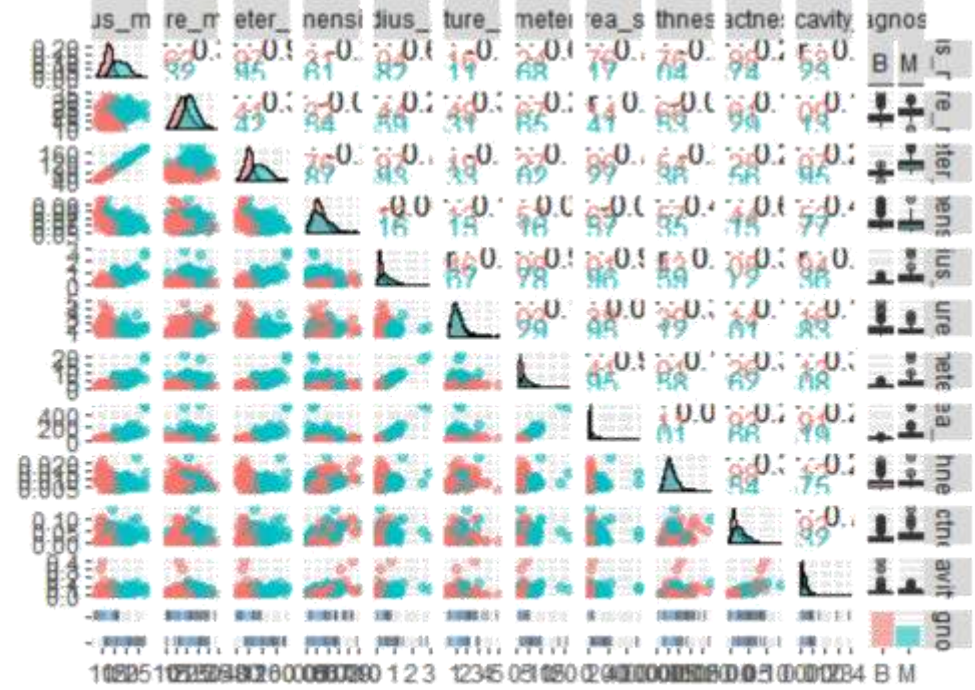
a_w
gno
BM


ius_m
ure_m
neter_r
ea_me
nness_
ctness
avity_n
.points
netry_r
agnosi
B
M


us_m
re_m
eter_
nensi
dius_
ture_
meter
rea_s
thnes
actne
cavity
agnos
B
M