# Roll no. 33140

# Batch: L9

# PS. Using Naive-Bayes algorithm to predict Breast Cancer

```
R version 3.6.2 (2019-12-12) -- "Dark and Stormy Night"
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Platform: x86_64-w64-mingw32/x64 (64-bit)

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[Workspace loaded from G:/College/SL6/Assignment6/.RData]

> # set the working directory

> setwd("G:/College/SL6/Assignment6")

> # Load libraries
> library('caTools')

> # Read the dataset
> breast_cancer = read.csv2("../../Sl-VI DataSets/BreastCancer/BreastCancerWc.csv",
                header = T,sep =',')

> names(breast_cancer)

 [1] "X1000025" "X5"       "X1"       "X1.1"     "X1.2"     "X2"       "X1.3"
     "X3"       "X1.4"     "X1.5"
[11] "X2.1"

> # Set the labels
> names(breast_cancer)[1] = "ID"
> names(breast_cancer)[2] = "CT" # Clump thickness
> names(breast_cancer)[3] = "CellSize"
> names(breast_cancer)[4] = "CellShape"
> names(breast_cancer)[5] = "MA" # Marginal adhesion
> names(breast_cancer)[6] = "ECellSize" # Epithelial cell size
> names(breast_cancer)[7] = "BN" # Bare nuclei
> names(breast_cancer)[8] = "BC" # Bland chromatin
> names(breast_cancer)[9] = "NN" # Normal nuclei
> names(breast_cancer)[10] = "Mit" # Mitoses
> names(breast_cancer)[11] = "Class" # class
> names(breast_cancer)
 [1] "ID"        "CT"        "CellSize"  "CellShape" "MA" "ECellSize" "BN"  "BC"
     "NN"
[10] "Mit"       "Class"

> breast_cancer$Class
  [1] 2 2 2 2 4 2 2 2 2 2 2 4 2 4 4 2 2 4 2 4 4 2 4 2 4 2 2 2 2 2 2 4 2 2 2 4 2 4 4 2 4 4
 [59] 4 4 2 4 4 2 4 2 4 4 2 2 4 2 4 4 2 2 2 2 2 2 2 2 2 4 4 4 4 2 2 2 2 2 2 2 2 2 2 4 4 4
[117] 4 2 2 2 2 4 4 4 2 4 2 4 2 2 2 4 2 2 2 2 2 2 2 2 2 4 2 2 2 4 2 2 4 2 4 4 2 2 4 2 2 2
[175] 4 2 4 2 4 2 2 2 4 4 2 4 4 4 2 4 4 2 2 2 2 2 2 2 2 4 4 2 2 2 4 4 2 2 2 4 4 2 4 4 4 2
[233] 4 2 2 4 4 4 4 2 2 2 2 2 2 4 4 2 2 2 4 2 4 4 4 2 2 2 2 4 4 4 4 4 2 4 4 4 2 4 2 4 4 2
[291] 2 4 4 2 4 2 2 2 4 4 2 4 2 4 4 2 2 4 2 2 2 4 2 2 2 4 4 2 2 4 2 2 4 2 2 4 2 4 4 4 2 2
[349] 4 2 2 2 4 2 2 4 4 4 4 4 4 2 2 2 2 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 4 2 2 2 2 4 2 2 2 2
[407] 2 2 2 2 2 4 2 4 2 4 2 2 2 2 4 2 2 2 4 2 4 2 2 2 2 2 2 2 4 4 2 2 2 4 2 2 2 2 2 2 2 2
[465] 4 4 4 2 2 2 2 2 2 2 2 2 2 2 4 2 2 4 4 2 2 2 4 4 4 2 4 2 4 2 2 2 2 2 2 2 2 2 2 2 2 4
[523] 4 2 2 2 2 2 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 4 2 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[581] 4 4 2 2 2 4 2 4 2 4 4 4 2 4 2 2 2 2 2 2 2 2 4 4 4 2 2 4 2 4 4 4 2 2 2 2 2 2 2 2 2 2
[639] 2 2 2 2 2 2 2 2 2 4 2 2 2 2 2 2 2 2 2 4 2 2 2 2 2 2 2 2 2 4 4 4 2 2 2 2 2 2 2 2 2 4
[697] 4 4

> # Set 1 for malignant, 0 for benign (Clean the data)
> breast_cancer$Class <- replace(breast_cancer$Class, breast_cancer$Class == 4,1)
> breast_cancer$Class <- replace(breast_cancer$Class, breast_cancer$Class == 2,0)

> breast_cancer$Class
  [1] 0 0 0 0 1 0 0 0 0 0 0 1 0 1 1 0 0 1 0 1 1 0 1 0 1 0 0 0 0 0 0 1 0 0 0 1 0 1 1 0 1 1
 [59] 1 1 0 1 1 0 1 0 1 1 0 0 1 0 1 1 0 0 0 0 0 0 0 0 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0 1 1 1
[117] 1 0 0 0 0 1 1 1 0 1 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 1 0 1 1 0 0 1 0 0 0
[175] 1 0 1 0 1 0 0 0 1 1 0 1 1 1 0 1 1 0 0 0 0 0 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 1 1 1 0
[233] 1 0 0 1 1 1 1 0 0 0 0 0 0 1 1 0 0 0 1 0 1 1 1 0 0 0 0 1 1 1 1 1 0 1 1 1 0 1 0 1 1 0
[291] 0 1 1 0 1 0 0 0 1 1 0 1 0 1 1 0 0 1 0 0 0 1 0 0 0 1 1 0 0 1 0 0 1 0 0 1 0 1 1 1 0 0
[349] 1 0 0 0 1 0 0 1 1 1 1 1 1 0 0 0 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 1 0 0 0 0
[407] 0 0 0 0 0 1 0 1 0 1 0 0 0 0 1 0 0 0 1 0 1 0 0 0 0 0 0 0 1 1 0 0 0 1 0 0 0 0 0 0 0 0
[465] 1 1 1 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 1 0 0 0 1 1 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 1
[523] 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[581] 1 1 0 0 0 1 0 1 0 1 1 1 0 1 0 0 0 0 0 0 0 0 1 1 1 0 0 1 0 1 1 1 0 0 0 0 0 0 0 0 0 0
[639] 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 1
[697] 1 1

> # Check for missing value
> '?' %in% breast_cancer$CT
[1] FALSE

> '?' %in% breast_cancer$CellSize
[1] FALSE

> '?' %in% breast_cancer$CellShape
[1] FALSE

> '?' %in% breast_cancer$MA
[1] FALSE

> '?' %in% breast_cancer$ECellSize
[1] FALSE
```
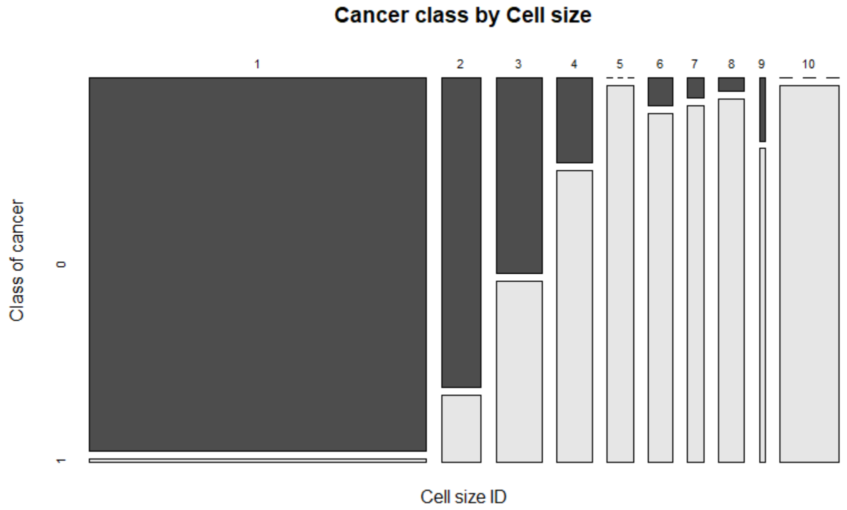
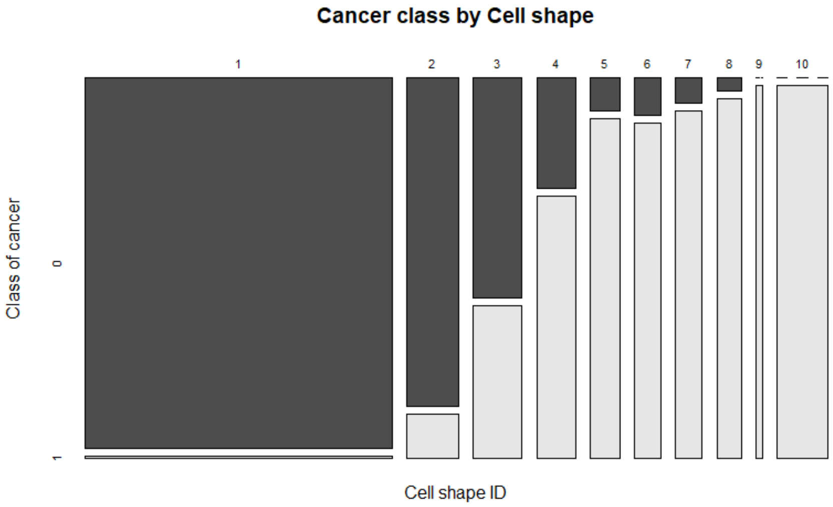
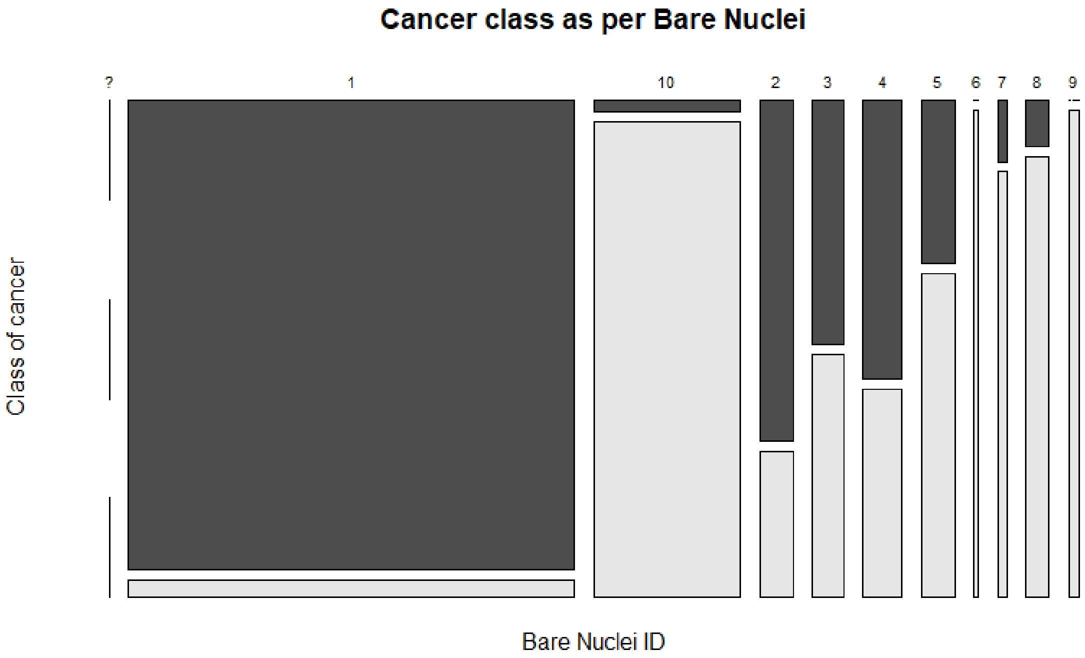

```
> '?' %in% breast_cancer$BN # Returned true (16 values are '?')
[1] TRUE  #i.e. There is a missing value here.

> # replace the NA values
> breast_cancer$BN <- replace(breast_cancer$BN, breast_cancer$BN == '?',NA)
                    # replace ? with NA
> levels(breast_cancer)[levels(breast_cancer)]
NULL

> summary(breast_cancer$CT)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  1.000   2.000   4.000   4.417   6.000  10.000 

> breast_cancer$BN[is.na(breast_cancer$BN)] <- 4.0 # Median value (replace NA)

> # Mosiac plots of some of the factors vs the class of cancer

> mosaicplot(breast_cancer$CellSize ~ breast_cancer$Class, main = "Cancer class by Cell
+             size",color = TRUE, shade = FALSE, xlab = "Cell size ID", ylab = "Class
+             of cancer")
```



```
> mosaicplot(breast_cancer$CellShape ~ breast_cancer$Class, main = "Cancer class by
+            Cell shape", color = TRUE, shade = FALSE, xlab = "Cell shape ID",
+            ylab = "Class of cancer")
```



```
> mosaicplot(breast_cancer$BN ~ breast_cancer$Class, main = "Cancer class as per
+            Bare Nuclei", color = TRUE, shade = FALSE, xlab = "Bare Nuclei ID",
+            ylab = "Class of cancer")
```



```
> # Create the dataframes for training and testing

> brcdata<-breast_cancer
> brcdata$ID=factor(brcdata$ID)
> brcdata$CT=factor(brcdata$CT)
> brcdata$TCellSize=factor(brcdata$CellSize)
> brcdata$CellShape=factor(brcdata$CellShape)
> brcdata$MA=factor(brcdata$MA)
> brcdata$ECellSize=factor(brcdata$ECellSize)
> brcdata$BN=factor(brcdata$BN)
> brcdata$BC=factor(brcdata$BC)
> brcdata$NN=factor(brcdata$NN)
> brcdata$Mit=factor(brcdata$Mit)
> brcdata$Class=factor(brcdata$Class)

> # Dividing dataset into training and testing
> split = sample.split(brcdata$Class, SplitRatio = 2/3)
> train_brcdata = subset(brcdata,split == TRUE)
> test_brcdata = subset(brcdata,split == FALSE)

> train_brcdata
        ID CT CellSize CellShape MA ECellSize BN BC NN Mit Class TCellSize
1  1002945  5        4         4  5         7 10  3  2   1     0         4
2  1015425  3        1         1  1         2  2  3  1   1     0         1
8  1033078  2        1         1  1         2  1  1  1   5     0         1
9  1033078  4        2         1  1         2  1  2  1   1     0         2
10 1035283  1        1         1  1         1  1  3  1   1     0         1
11 1036172  2        1         1  1         2  1  2  1   1     0         1
12 1041801  5        3         3  3         2  3  4  4   1     1         3
14 1044572  8        7         5 10         7  9  5  5   4     1         7
15 1047630  7        4         6  4         6  1  4  3   1     1         4
16 1048672  4        1         1  1         2  1  2  1   1     0         1
18 1050670 10        7         7  6         4 10  4  1   2     1         7
19 1050718  6        1         1  1         2  1  3  1   1     0         1
21 1054593 10        5         5  3         6  7  7 10   1     1         5
22 1056784  3        1         1  1         2  1  2  1   1     0         1
23 1057013  8        4         5  1         2  4  7  3   1     1         4
24 1059552  1        1         1  1         2  1  3  1   1     0         1
25 1065726  5        2         3  4         2  7  3  6   1     1         2
27 1066979  5        1         1  1         2  1  2  1   1     0         1
28 1067444  2        1         1  1         2  1  2  1   1     0         1
29 1070935  1        1         3  1         2  1  1  1   1     0         1
30 1070935  3        1         1  1         1  1  2  1   1     0         1
31 1071760  2        1         1  1         2  1  3  1   1     0         1
33 1074610  2        1         1  2         2  1  3  1   1     0         1
35 1079304  2        1         1  1         2  1  2  1   1     0         1
36 1080185 10       10        10  8         6  1  8  9   1     1        10
37 1081791  6        2         1  1         1  1  7  1   1     0         2
38 1084584  5        4         4  9         2 10  5  6   1     1         4
39 1091262  2        5         3  3         6  7  7  5   1     1         5
40 1096800  6        6         6  9         6  4  7  8   1     0         6
41 1099510 10        4         3  1         3  3  6  5   2     1         4
42 1100524  6       10        10  2         8 10  7  3   3     1        10
45 1103722  1        1         1  1         2  1  2  1   2     0         1
47 1105524  1        1         1  1         2  1  2  1   1     0         1
49 1106829  7        8         7  2         4  8  3  8   2     1         8
51 1108449  5        3         3  4         2  4  3  4   1     1         3
52 1110102 10        3         6  2         3  5  4 10   2     1         3
53 1110503  5        5         5  8        10  8  7  3   7     1         5
54 1110524 10        5         5  6         8  8  7  1   1     1         5
```

```
56  1112209  8       10        10  1         3  6  3  9   1     1        10
57  1113038  8        2         4  1         5  1  5  4   4     1         2
58  1113483  5        2         3  1         6 10  5  1   1     1         2
59  1113906  9        5         5  2         2  2  5  1   1     1         5
60  1115282  5        3         5  5         3  3  4 10   1     1         3
61  1115293  1        1         1  1         2  2  2  1   1     0         1
63  1116132  6        3         4  1         5  2  3  9   1     1         3
64  1116192  1        1         1  1         2  1  2  1   1     0         1
65  1116998 10        4         2  1         3  2  4  3  10     1         4
66  1117152  4        1         1  1         2  1  3  1   1     0         1
67  1118039  5        3         4  1         8 10  4  9   1     1         3
68  1120559  8        3         8  3         4  9  8  9   8     1         3
70  1121919  5        1         3  1         2  1  2  1   1     0         1
71  1123061  6       10         2  8        10  2  7  8  10     1        10
75  1131294  1        1         2  1         2  2  4  2   1     0         1
76  1132347  1        1         4  1         2  1  2  1   1     0         1
77  1133041  5        3         1  2         2  1  2  1   1     0         3
78  1133136  3        1         1  1         2  3  3  1   1     0         1
79  1136142  2        1         1  1         3  1  2  1   1     0         1
80  1137156  2        2         2  1         1  1  7  1   1     0         2
81  1143978  4        1         1  2         2  1  2  1   1     0         1
84  1147699  3        5         7  8         8  9  7 10   7     1         5
85  1147748  5       10         6  1        10  4  4 10  10     1        10
88  1152331  4        1         1  1         2  1  3  1   1     0         1
90  1156272  1        1         1  1         2  1  3  1   1     0         1
91  1156948  3        1         1  2         2  1  1  1   1     0         1
92  1157734  4        1         1  1         2  1  3  1   1     0         1
96  1165297  2        1         1  2         2  1  1  1   1     0         1
97  1165790  5        1         1  1         2  1  3  1   1     0         1
98  1165926  9        6         9  2        10  6  2  9  10     1         6
99  1166630  7        5         6 10         5 10  7  9   4     1         5
101 1167439  2        3         4  4         2  5  2  5   1     1         3
103 1168359  8        2         3  1         6  3  7  1   1     1         2
104 1168736 10       10        10 10        10  1  8  8   8     1        10
105 1169049  7        3         4  4         3  3  3  2   7     1         3
106 1170419 10       10        10  8         2 10  4  1   1     1        10
107 1170420  1        6         8 10         8 10  5  7   1     1         6
110 1171795  1        3         1  2         2  2  5  3   2     0         3
111 1171845  8        6         4  3         5  9  3  1   1     1         6
112 1172152 10        3         3 10         2 10  7  3   3     1         3
114 1173235  3        3         2  1         2  3  3  1   1     0         3
115 1173347  1        1         1  1         2  5  1  1   1     0         1
117 1173509  4        5         5 10         4 10  7  5   8     1         5
119 1173681  3        2         1  1         2  2  3  1   1     0         2
120 1174057  1        1         2  2         2  1  3  1   1     0         1
 [ reached 'max' / getOption("max.print") -- omitted 383 rows ]
```

```
> # Applying Naive Bayes claasifier on dataset
> library(e1071)
> classifier <- naiveBayes(Class ~ CT+CellSize+CellShape+MA+ECellSize+BN+BC+NN+Mit,
                           train_brcdata)
> classifier

Naive Bayes Classifier for Discrete Predictors

Call:
naiveBayes.default(x = X, y = Y, laplace = laplace)

A-priori probabilities:
Y
        0         1
0.6545064 0.3454936

Conditional probabilities:
   CT
Y             1           2           3           4           5           6           7
           8           9
  0 0.318032787 0.101639344 0.196721311 0.157377049 0.173770492 0.042622951 0.003278689
0.006557377 0.000000000
  1 0.018633540 0.012422360 0.031055901 0.049689441 0.198757764 0.074534161 0.105590062
0.167701863 0.043478261
   CT
Y            10
  0 0.000000000
  1 0.298136646

   CellSize
Y       [,1]      [,2]
  0 1.334426 0.9352183
  1 6.515528 2.7502400

   CellShape
Y             1           2           3           4           5           6           7
          8           9
  0 0.777049180 0.118032787 0.055737705 0.032786885 0.003278689 0.006557377 0.006557377
0.000000000 0.000000000
  1 0.006211180 0.031055901 0.118012422 0.118012422 0.136645963 0.093167702 0.099378882
 0.136645963 0.031055901
   CellShape
Y            10
  0 0.000000000
  1 0.229813665

   MA
Y             1           2           3           4           5           6           7
           8           9
  0 0.819672131 0.081967213 0.062295082 0.013114754 0.013114754 0.006557377 0.000000000
0.000000000 0.003278689
  1 0.136645963 0.099378882 0.080745342 0.111801242 0.093167702 0.055900621 0.062111801
0.118012422 0.012422360
   MA
Y            10
```

```
  0 0.000000000
  1 0.229813665

   ECellSize
Y             1           2           3           4           5           6           7
           8           9
  0 0.104918033 0.780327869 0.072131148 0.009836066 0.013114754 0.006557377 0.006557377
0.003278689 0.000000000
  1 0.006211180 0.111801242 0.167701863 0.167701863 0.149068323 0.173913043 0.018633540
 0.080745342 0.012422360
   ECellSize
Y            10
  0 0.003278689
  1 0.111801242

   BN
Y             1          10           2           3           4           5           6
           7           8
  0 0.852459016 0.006557377 0.039344262 0.026229508 0.039344262 0.026229508 0.000000000
0.003278689 0.006557377
  1 0.068322981 0.540372671 0.055900621 0.037267081 0.062111801 0.074534161 0.018633540
0.037267081 0.062111801
   BN
Y             9
  0 0.000000000
  1 0.043478261

   BC
Y             1           2           3           4           5           6           7
          8           9
  0 0.337704918 0.344262295 0.262295082 0.022950820 0.013114754 0.003278689 0.016393443
 0.000000000 0.000000000
  1 0.012422360 0.037267081 0.130434783 0.136645963 0.130434783 0.018633540 0.310559006
0.111801242 0.043478261
   BC
Y            10
  0 0.000000000
  1 0.068322981

   NN
Y             1           2           3           4           5           6           7
          8           9
  0 0.865573770 0.075409836 0.029508197 0.003278689 0.003278689 0.003278689 0.003278689
0.013114754 0.003278689
  1 0.173913043 0.018633540 0.167701863 0.062111801 0.080745342 0.055900621 0.062111801
0.062111801 0.074534161
   NN
Y            10
  0 0.000000000
  1 0.242236025

   Mit
Y             1           2           3           4           5           6           7
          8          10
  0 0.957377049 0.026229508 0.006557377 0.000000000 0.003278689 0.000000000 0.003278689
```

```
0.003278689 0.000000000
  1 0.552795031 0.111801242 0.130434783 0.037267081 0.012422360 0.012422360 0.024844720
0.037267081 0.080745342

> #predict using trained model
> prediction <- predict(classifier, test_brcdata ,type="class")

> table(prediction,  test_brcdata[,11])   # put it in table

prediction   0   1
         0 147   0
         1   5  80

> # Displaying the accuracy using confusion Matrix
> library(e1071)
> library(caret)

> df1=confusionMatrix(test_brcdata[,11],prediction) #create the confusion matrix

> df1
Confusion Matrix and Statistics

          Reference
Prediction   0   1
         0 147   5
         1   0  80

               Accuracy : 0.9784
                 95% CI : (0.9504, 0.993)
    No Information Rate : 0.6336
    P-Value [Acc > NIR] : < 2e-16

                  Kappa : 0.953

 Mcnemar's Test P-Value : 0.07364

            Sensitivity : 1.0000
            Specificity : 0.9412
         Pos Pred Value : 0.9671
         Neg Pred Value : 1.0000
             Prevalence : 0.6336
         Detection Rate : 0.6336
   Detection Prevalence : 0.6552
      Balanced Accuracy : 0.9706

       'Positive' Class : 0


>
```