National Institute Of Technology – Calicut
Data Mining

R programming

T.G. Deshan K. Sumanathilaka
B150413CS
Computer Science and Engineering

DATA-MINING ASSIGNMENT #02

01. Decision Tree with Gini index as the impurity measure...

case A:

A Random sample of 80: 20 for Train-Set and Data-Set

```
kidney <- read.csv("/home/deshan/Desktop/clean_kidney.csv")
```

```
str(kidney)
```

```
'data.frame':   400 obs. of  25 variables:
 $ age  : num  48 7 62 48 51 60 68 24 52 53 ...
 $ bp   : num  80 50 80 70 80 ...
 $ sg   : num  1.02 1.02 1.01 1 1.01 ...
 $ al   : int  1 4 2 4 2 3 0 2 3 2 ...
 $ su   : int  0 0 3 0 0 0 0 4 0 0 ...
 $ rbc  : Factor w/ 2 levels "abnormal","normal": 2 2 2 2 2 2 2 2 2 1 ...
 $ pc   : Factor w/ 2 levels "abnormal","normal": 2 2 2 1 2 2 2 1 1 1 ...
 $ pcc  : Factor w/ 2 levels "notpresent","present": 1 1 1 2 1 1 1 1 2 2 ...
 $ ba   : Factor w/ 2 levels "notpresent","present": 1 1 1 1 1 1 1 1 1 1 ...
 $ bgr  : num  121 148 423 117 106 ...
 $ bu   : num  36 18 53 56 26 25 54 31 60 107 ...
 $ sc   : num  1.2 0.8 1.8 3.8 1.4 1.1 24 1.1 1.9 7.2 ...
 $ sod  : num  138 138 138 111 138 ...
 $ pot  : num  4.63 4.63 4.63 2.5 4.63 ...
 $ hemo : num  15.4 11.3 9.6 11.2 11.6 12.2 12.4 12.4 10.8 9.5 ...
 $ pcv  : num  44 38 31 32 35 39 36 44 33 29 ...
 $ wbcc : num  7800 6000 7500 6700 7300 ...
 $ rbcc : num  5.2 4.71 4.71 3.9 4.6 ...
 $ htn  : Factor w/ 2 levels "no","yes": 2 1 1 2 1 2 1 1 2 2 ...
 $ dm   : Factor w/ 2 levels "no","yes": 2 1 2 1 1 2 1 2 2 2 ...
 $ cad  : Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1 ...
 $ appet: Factor w/ 2 levels "good","poor": 1 1 2 2 1 1 1 1 1 2 ...
 $ pe   : Factor w/ 2 levels "no","yes": 1 1 1 2 1 2 1 2 1 1 ...
 $ ane  : Factor w/ 2 levels "no","yes": 1 1 2 2 1 1 1 1 2 2 ...
 $ class: Factor w/ 2 levels "ckd","notckd": 1 1 1 1 1 1 1 1 1 1 ...
```

```
summary(kidney)
```

```
      age              bp               sg              al              su              rbc
 Min.   : 2.00   Min.   : 50.00   Min.   :1.005   Min.   :0.0   Min.   :0.000   abnormal: 47
 1st Qu.:42.00   1st Qu.: 70.00   1st Qu.:1.015   1st Qu.:0.0   1st Qu.:0.000   normal  :353
 Median :54.00   Median : 78.23   Median :1.020   Median :0.0   Median :0.000
 Mean   :51.48   Mean   : 76.47   Mean   :1.018   Mean   :0.9   Mean   :0.395
 3rd Qu.:64.00   3rd Qu.: 80.00   3rd Qu.:1.020   3rd Qu.:2.0   3rd Qu.:0.000
 Max.   :90.00   Max.   :180.00   Max.   :1.025   Max.   :5.0   Max.   :5.000
         pc              pcc              ba           bgr             bu               sc
 abnormal: 76   notpresent:358   notpresent:378   Min.   : 22   Min.   :  1.50   Min.   :
0.400
 normal  :324   present   : 42   present   : 22   1st Qu.:101   1st Qu.: 27.00   1st Qu.:
0.900
                                                   Median :126   Median : 44.00
Median : 1.400
                                                   Mean   :148   Mean   : 57.43
Mean   : 3.072
                                                   3rd Qu.:150   3rd Qu.: 61.75   3rd
Qu.: 3.072
```

```
                                                  Max.   :490   Max.   :391.00
Max.   :76.000
      sod              pot              hemo            pcv              wbcc            rbcc
 Min.   :  4.5   Min.   : 2.500   Min.   : 3.10   Min.   : 9.00   Min.   : 2200   Min.   :
2.100
 1st Qu.:135.0   1st Qu.: 4.000   1st Qu.:10.88   1st Qu.:34.00   1st Qu.: 6975   1st
Qu.:4.500
 Median :137.5   Median : 4.627   Median :12.53   Median :38.88   Median : 8406   Median :
4.707
 Mean   :137.5   Mean   : 4.627   Mean   :12.53   Mean   :38.88   Mean   : 8406   Mean   :
4.707
 3rd Qu.:141.0   3rd Qu.: 4.800   3rd Qu.:14.62   3rd Qu.:44.00   3rd Qu.: 9400   3rd
Qu.:5.100
 Max.   :163.0   Max.   :47.000   Max.   :17.80   Max.   :54.00   Max.   :26400   Max.   :
8.000
  htn        dm       cad       appet       pe       ane         class
 no :253   no :263   no :366   good:318   no :324   no :340   ckd   :250
 yes:147   yes:137   yes: 34   poor: 82   yes: 76   yes: 60   notckd:150
```

** install.packages("rpart")

** install.packages("rpart.plot")

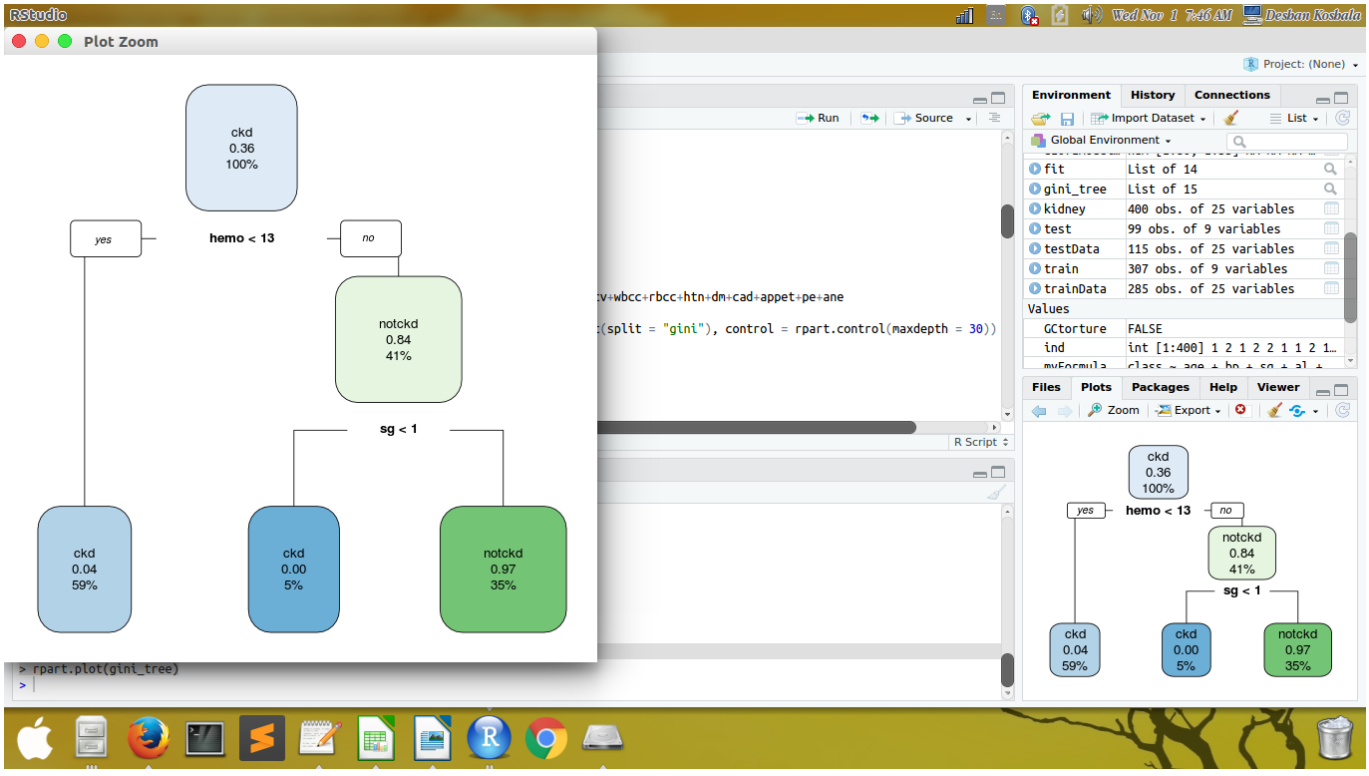
```
library(rpart)

library(rpart.plot)

set.seed(123)

> ind <- sample(2, nrow(kidney), replace=TRUE, prob=c(0.7, 0.3))

> trainData <- kidney[ind==1,]

> testData <- kidney[ind==2,]

> summary(trainData)
```

```
 age              bp               sg              al               su               rbc
 Min.   : 3.00   Min.   : 50.00   Min.   :1.005   Min.   :0.0000   Min.   :0.0000
abnormal: 35
 1st Qu.:43.00   1st Qu.: 70.00   1st Qu.:1.015   1st Qu.:0.0000   1st Qu.:0.0000
normal  :250
 Median :54.00   Median : 80.00   Median :1.020   Median :0.0000   Median :0.0000
 Mean   :51.99   Mean   : 76.91   Mean   :1.018   Mean   :0.9368   Mean   :0.4456
 3rd Qu.:64.00   3rd Qu.: 80.00   3rd Qu.:1.020   3rd Qu.:2.0000   3rd Qu.:0.0000
 Max.   :90.00   Max.   :180.00   Max.   :1.025   Max.   :5.0000   Max.   :5.0000
         pc              pcc              ba           bgr              bu              sc
 abnormal: 51   notpresent:257   notpresent:264   Min.   : 70.0   Min.   : 10.00   Min.   :
0.400
 normal  :234   present   : 28   present   : 21   1st Qu.:102.0   1st Qu.: 27.00   1st Qu.:
0.900
                                                  Median :129.0   Median : 44.00
Median : 1.400
                                                  Mean   :148.4   Mean   : 58.91
Mean   : 3.346
                                                  3rd Qu.:158.0   3rd Qu.: 68.00
3rd Qu.: 3.072
                                                  Max.   :490.0   Max.   :391.00
Max.   :76.000
      sod              pot              hemo            pcv              wbcc            rbcc
 Min.   :  4.5   Min.   : 2.700   Min.   : 4.80   Min.   :14.00   Min.   : 2200   Min.   :
2.100
 1st Qu.:135.0   1st Qu.: 3.900   1st Qu.:10.80   1st Qu.:33.00   1st Qu.: 7000   1st
Qu.:4.300
```

```
 Median :137.5   Median : 4.627   Median :12.53   Median :38.88   Median : 8406   Median :
4.707
 Mean   :137.1   Mean   : 4.696   Mean   :12.44   Mean   :38.67   Mean   : 8474   Mean   :
4.658
 3rd Qu.:140.0   3rd Qu.: 4.800   3rd Qu.:14.50   3rd Qu.:44.00   3rd Qu.: 9400   3rd
Qu.:5.000
 Max.   :163.0   Max.   :47.000   Max.   :17.80   Max.   :54.00   Max.   :26400   Max.   :
6.500
   htn         dm         cad         appet        pe         ane          class
 no :174   no :181   no :259   good:226   no :227   no :241   ckd    :181
 yes:111   yes:104   yes: 26   poor: 59   yes: 58   yes: 44   notckd:104
```

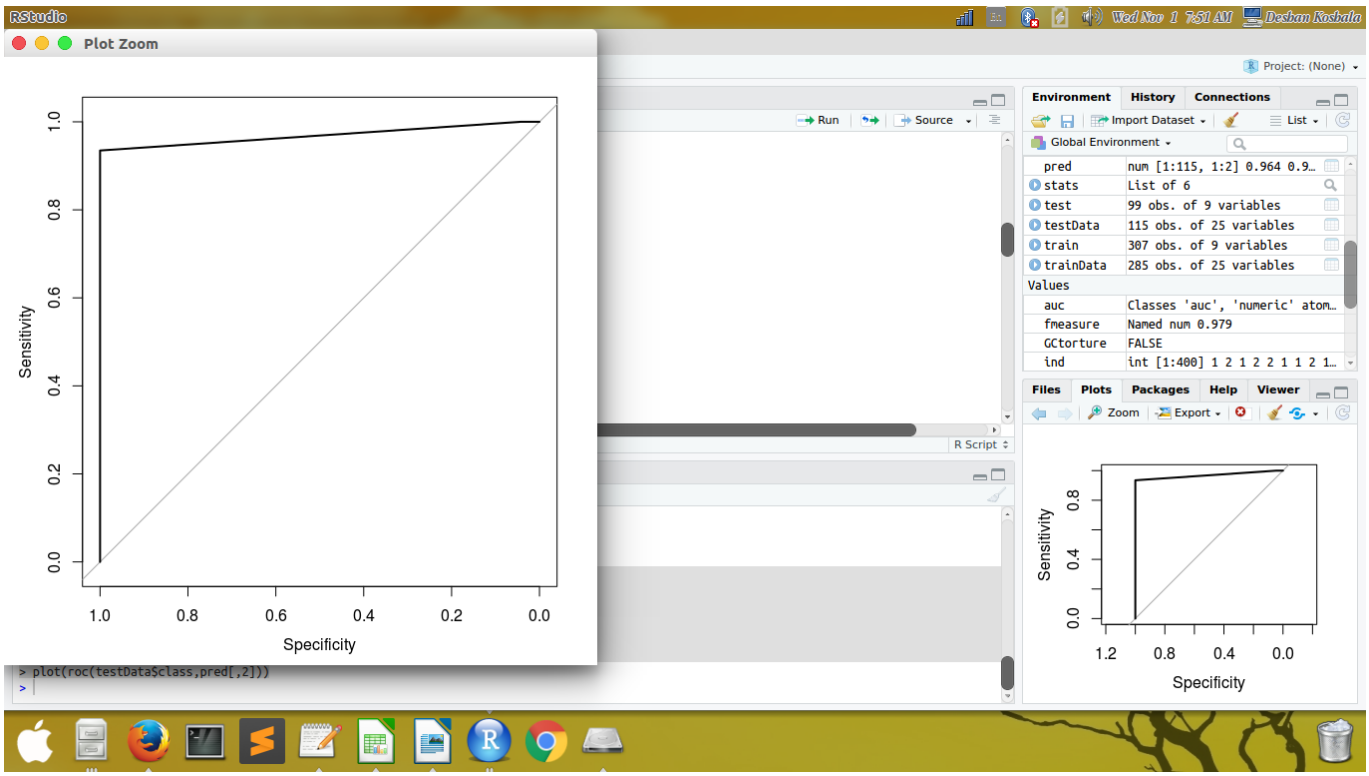
** install.packages("party")

```
library(party)

myFormula <- class ~
age+bp+sg+al+su+rbc+pc+pcc+ba+bgr+bu+sc+sod+pot+hemo+pcv+wbcc+rbcc+htn+dm+cad+appet+pe+ane

gini_tree <- rpart(myFormula, data = trainData, method="class", parms = list(split = "gini"),
control = rpart.control(maxdepth = 30))


 plot(gini_tree)

 rpart.plot(gini_tree)
```




```
 # confusion matrix
testPred <- predict(gini_tree, newdata = testData, type = "class")

 table(testPred, testData$class)

testPred ckd notckd
  ckd     69       3
  notckd   0      43
```

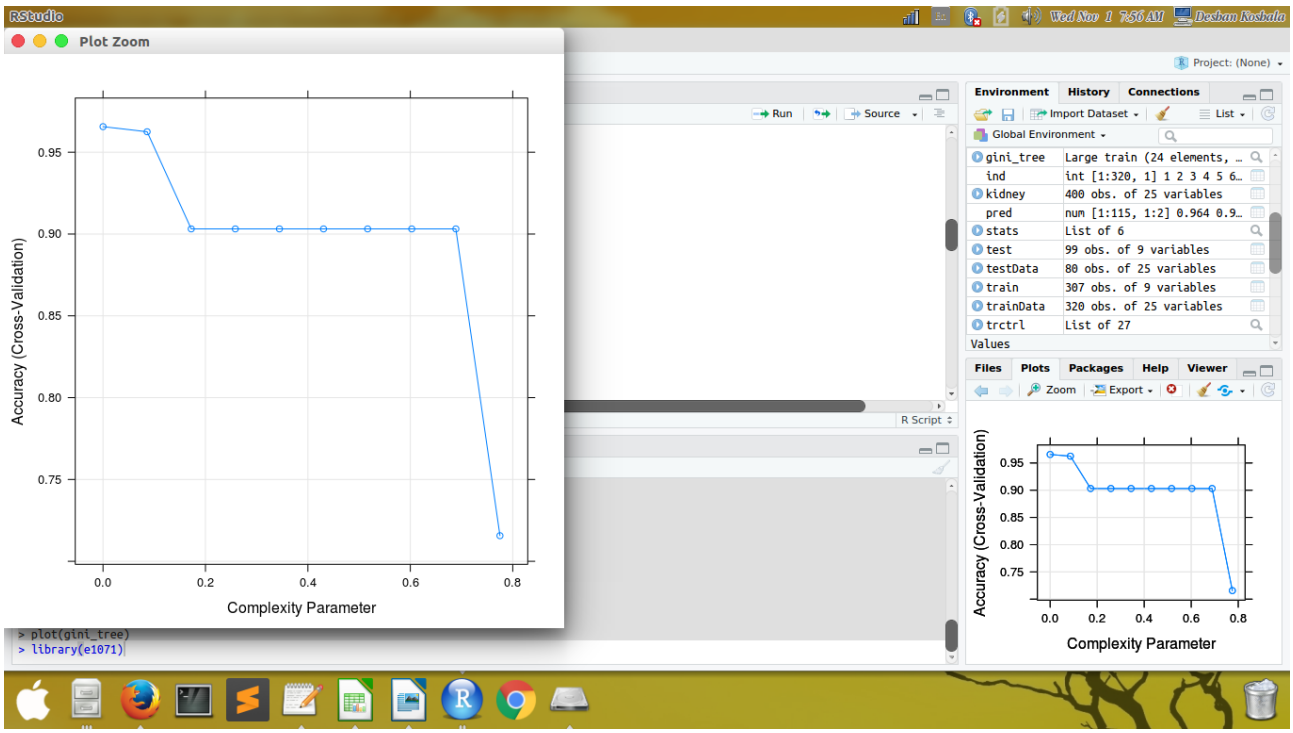
```
ibrary(caret)

 stats <- confusionMatrix(data = testPred, testData$class)

 precision <- stats$byClass['Pos Pred Value']

 recall <- stats$byClass['Sensitivity']

 fmeasure <- 2 * ((precision * recall) / (precision + recall))

> precision
Pos Pred Value
      0.9583333
> recall
Sensitivity
          1
> fmeasure
Pos Pred Value
      0.9787234


 # ROC curve

pred<-predict(gini_tree,testData,type='prob')

library(ROCR)

library(pROC)

auc<-auc(testData$class,pred[,2])

>auc
Area under the curve: 0.9688

>auc<-auc(testData$class,pred[,1])

>auc
Area under the curve: 0.9688

> plot(roc(testData$class,pred[,2]))
```



case B:

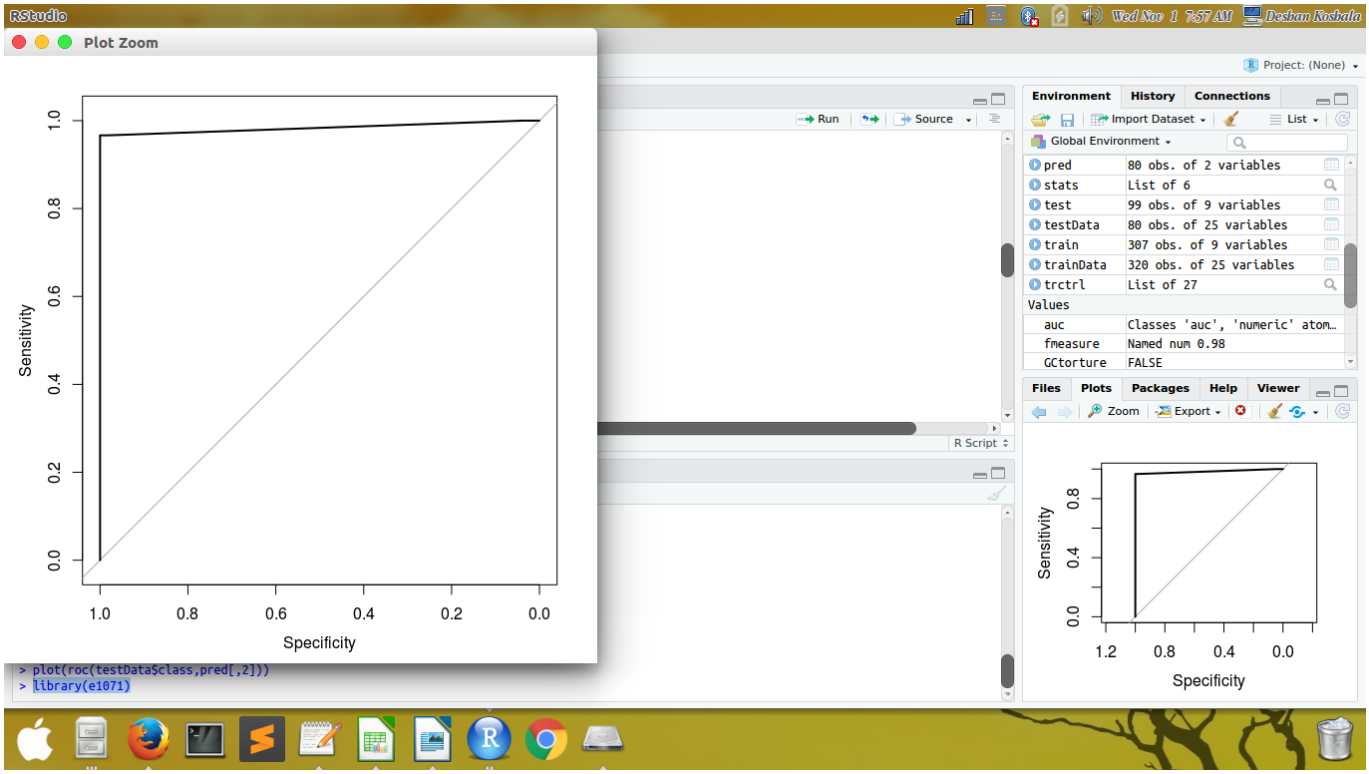
A 10-fold cross validation

```
library(caret)

library(e1071)

ind=createDataPartition(kidney$class, p=0.8,list=FALSE)

 trainData<-kidney[ind,]

 testData<-kidney[-ind,]

 trctrl <- trainControl(method = "cv", number = 10)

 set.seed(3333)

 gini_tree <- train(myFormula, data = trainData, method = "rpart",
+                    parms = list(split = "gini"),
+                    trControl=trctrl,
+                    tuneLength = 10)

plot(gini_tree)
```




```
 # confusion matrix
testPred <- predict(gini_tree, newdata = testData)

 table(testPred, testData$class)

testPred ckd notckd
  ckd     49      1
  notckd   1     29


 stats <- confusionMatrix(data = testPred, testData$class)

 precision <- stats$byClass['Pos Pred Value']
 recall <- stats$byClass['Sensitivity']
 fmeasure <- 2 * ((precision * recall) / (precision + recall))

 precision
Pos Pred Value
          0.98
 recall
Sensitivity
       0.98
 fmeasure
Pos Pred Value
          0.98

 # ROC curve
 pred<-predict(gini_tree,testData,type='prob')

 library(ROCR)

 library(pROC)

 auc<-auc(testData$class,pred[,2])

 auc
Area under the curve: 0.9837

 auc<-auc(testData$class,pred[,1])
```

```
auc
Area under the curve: 0.9837

plot(roc(testData$class,pred[,2]))
```



02 .Decision Tree with Entropy as the impurity measure

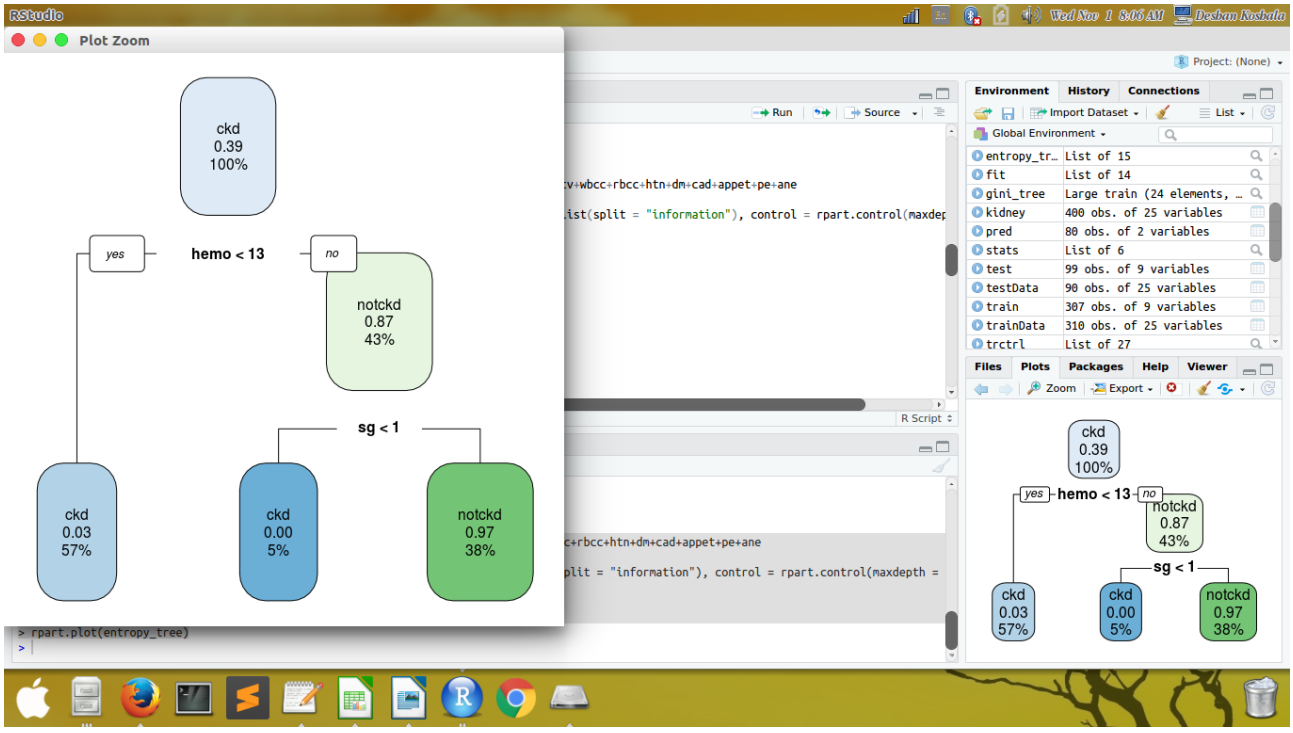
case A:

A Random sample of 80: 20 for Train-Set and Data-Set

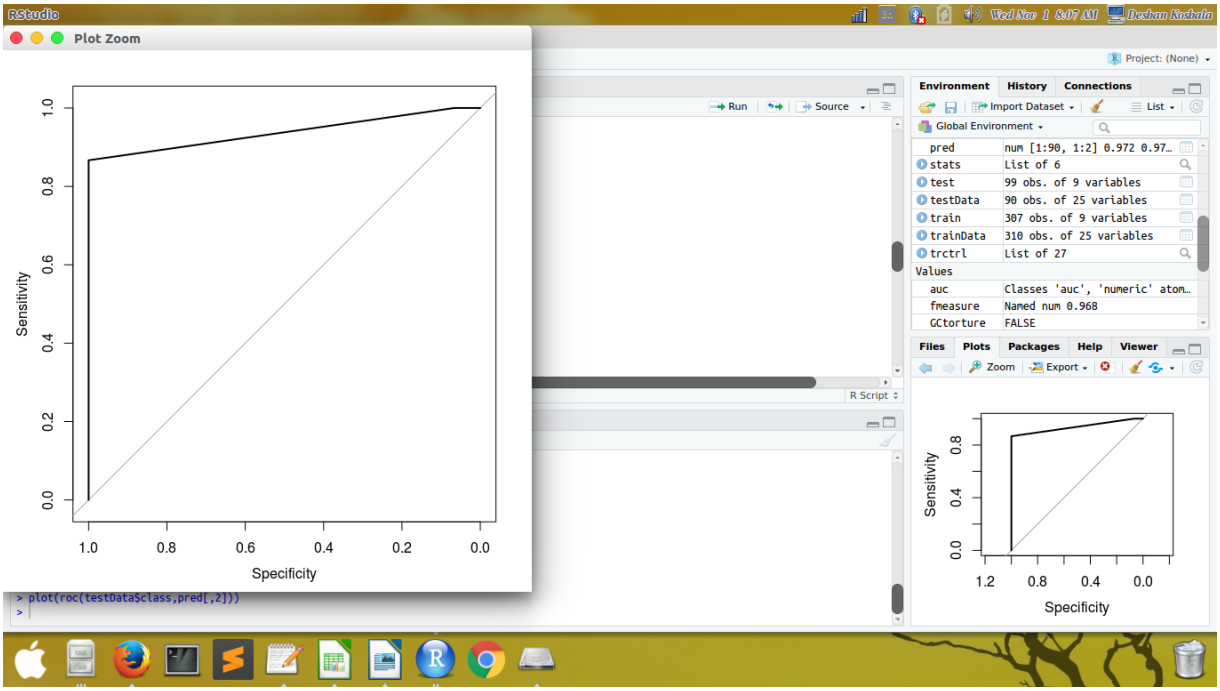
```
library(rpart)
library(rpart.plot)

set.seed(456)

ind <- sample(2, nrow(kidney), replace=TRUE, prob=c(0.8, 0.2))

trainData <- kidney[ind==1,]

testData <- kidney[ind==2,]

summary(trainData)
       age              bp               sg               al               su              rbc
pc              pcc
 Min.   : 2.00   Min.   : 50.00   Min.   :1.005   Min.   :0.0000   Min.   :0.0   abnormal:
35   abnormal: 54   notpresent:281
 1st Qu.:41.00   1st Qu.: 70.00   1st Qu.:1.015   1st Qu.:0.0000   1st Qu.:0.0   normal   :
275   normal  :256   present    : 29
 Median :55.00   Median : 80.00   Median :1.020   Median :0.0000   Median :0.0
 Mean   :50.98   Mean   : 76.76   Mean   :1.018   Mean   :0.8677   Mean   :0.4
```

```
 3rd Qu.:64.00   3rd Qu.: 80.00   3rd Qu.:1.020   3rd Qu.:2.0000   3rd Qu.:0.0
 Max.   :90.00   Max.   :180.00   Max.   :1.025   Max.   :5.0000   Max.   :5.0
           ba           bgr              bu              sc              sod
pot              hemo            pcv
 notpresent:293   Min.   : 22.0   Min.   :  1.50   Min.   : 0.400   Min.   :  4.5   Min.   :
2.500   Min.   : 3.10   Min.   : 9.00
 present   : 17   1st Qu.:100.2   1st Qu.: 27.00   1st Qu.: 0.900   1st Qu.:136.0   1st Qu.:
4.000   1st Qu.:10.90   1st Qu.:34.00
                  Median :124.0   Median : 43.00   Median : 1.300   Median :137.5
Median : 4.627   Median :12.53   Median :38.88
                  Mean   :146.6   Mean   : 57.07   Mean   : 3.160   Mean   :137.4   Mean
: 4.704   Mean   :12.59   Mean   :39.22
                  3rd Qu.:152.2   3rd Qu.: 59.50   3rd Qu.: 3.072   3rd Qu.:141.0   3rd
Qu.: 4.800   3rd Qu.:14.57   3rd Qu.:44.75
                  Max.   :490.0   Max.   :391.00   Max.   :76.000   Max.   :163.0   Max.
:47.000   Max.   :17.80   Max.   :54.00
      wbcc            rbcc        htn        dm       cad       appet        pe       ane
class
 Min.   : 2200   Min.   :2.100   no :202   no :205   no :284   good:252   no :253   no :271
ckd   :190
 1st Qu.: 6900   1st Qu.:4.500   yes:108   yes:105   yes: 26   poor: 58   yes: 57   yes: 39
notckd:120
 Median : 8406   Median :4.707
 Mean   : 8282   Mean   :4.713
 3rd Qu.: 9100   3rd Qu.:5.075
 Max.   :26400   Max.   :8.000
```

```
myFormula <- class ~
age+bp+sg+al+su+rbc+pc+pcc+ba+bgr+bu+sc+sod+pot+hemo+pcv+wbcc+rbcc+htn+dm+cad+appet+pe+ane

 entropy_tree <- rpart(myFormula, data = trainData, method="class", parms = list(split =
"information"), control = rpart.control(maxdepth = 30))

 plot(entropy_tree)

rpart.plot(entropy_tree)
```



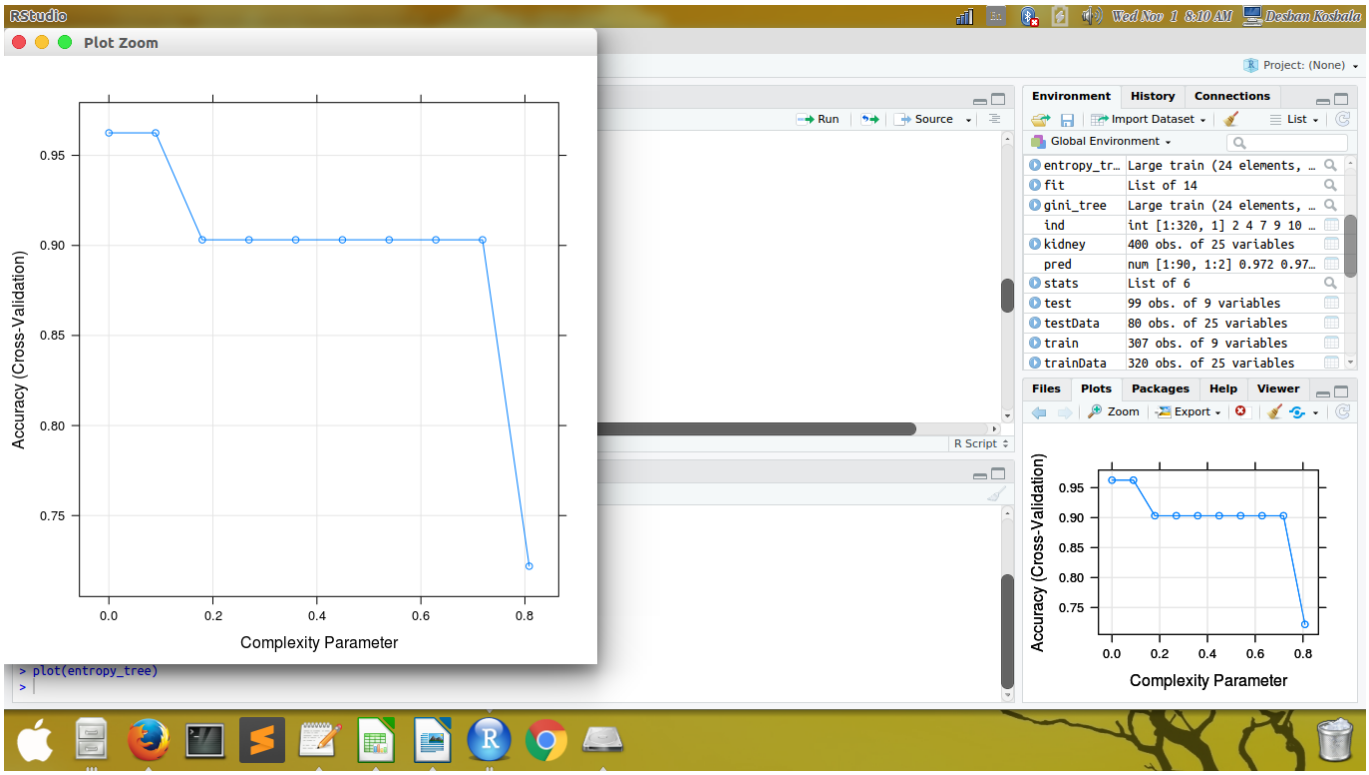
```
 # confusion matrix
testPred <- predict(entropy_tree, newdata = testData, type = "class")

table(testPred, testData$class)

testPred ckd notckd
  ckd     60      4
  notckd   0     26

stats <- confusionMatrix(data = testPred, testData$class)

precision <- stats$byClass['Pos Pred Value']

recall <- stats$byClass['Sensitivity']

fmeasure <- 2 * ((precision * recall) / (precision + recall))

> precision
Pos Pred Value
         0.9375
> recall
Sensitivity
          1
> fmeasure
Pos Pred Value
     0.9677419

 # ROC curve
pred<-predict(entropy_tree,testData,type='prob')

library(ROCR)

library(pROC)

auc<-auc(testData$class,pred[,2])

auc
Area under the curve: 0.9378

plot(roc(testData$class,pred[,2]))
```



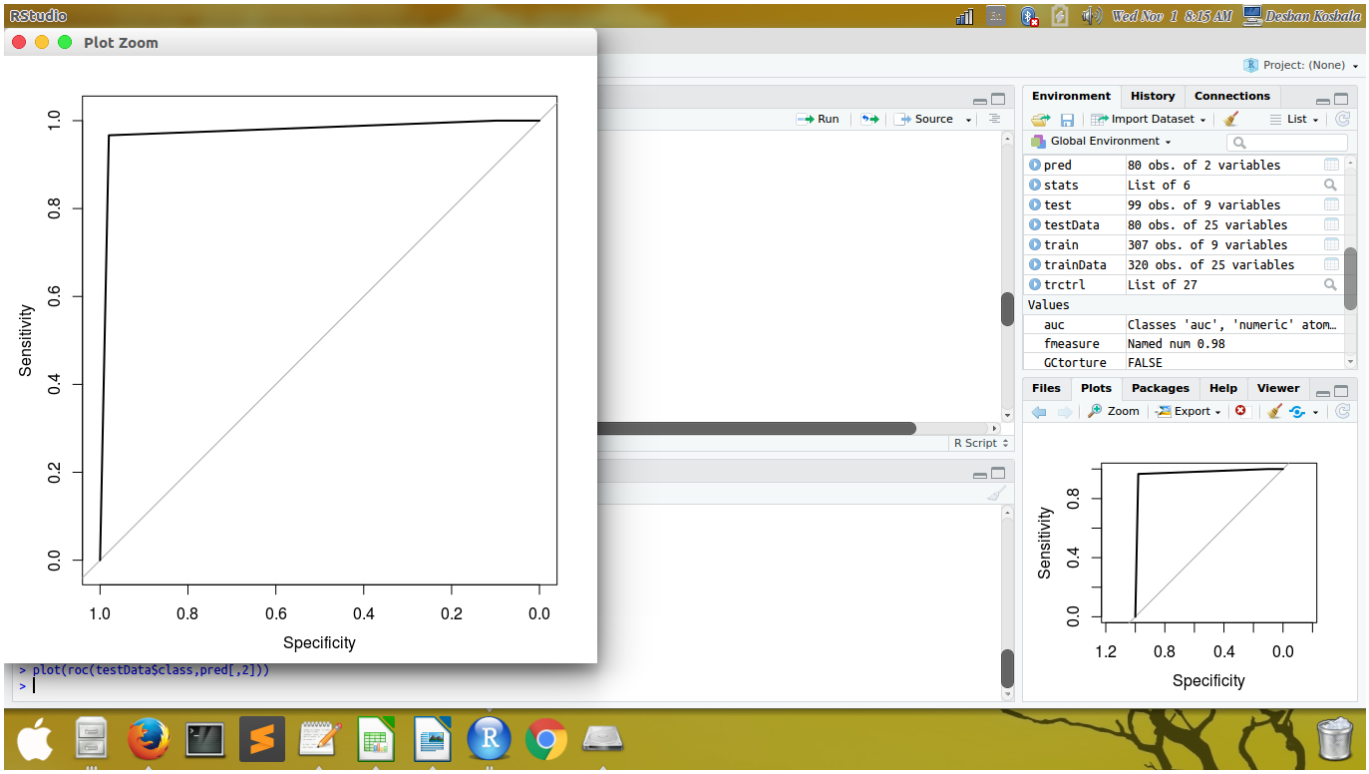
case B:

A 10-fold cross validation

```
 library(caret)

 library(e1071)

 ind=createDataPartition(kidney$class, p=0.8,list=FALSE)

trainData<-kidney[ind,]

testData<-kidney[-ind,]

trctrl <- trainControl(method = "cv", number = 10)

set.seed(4444)

entropy_tree <- train(myFormula, data = trainData, method = "rpart",
+                      parms = list(split = "information"),
+                      trControl=trctrl,
+                      tuneLength = 10)

plot(entropy_tree)
```



```
 # confusion matrix
 testPred <- predict(entropy_tree, newdata = testData)
 table(testPred, testData$class)

testPred ckd notckd
  ckd     49      1
  notckd   1     29

stats <- confusionMatrix(data = testPred, testData$class)



 precision <- stats$byClass['Pos Pred Value']

 recall <- stats$byClass['Sensitivity']

 fmeasure <- 2 * ((precision * recall) / (precision + recall))

 precision

Pos Pred Value
          0.98
recall
Sensitivity
        0.98
 fmeasure
Pos Pred Value
          0.98

 # ROC curve
pred<-predict(entropy_tree,testData,type='prob')

 library(ROCR)

library(pROC)

 auc<-auc(testData$class,pred[,2])

 auc
Area under the curve: 0.975

 plot(roc(testData$class,pred[,2]))
```



03.Naive Bayesian Classifier

case A:

A Random sample of 80: 20 for Train-Set and Data-Set

```
library(rpart)

library(rpart.plot)

set.seed(456)

ind <- sample(2, nrow(kidney), replace=TRUE, prob=c(0.8, 0.2))

trainData <- kidney[ind==1,]

testData <- kidney[ind==2,]


myFormula <- class ~
age+bp+sg+al+su+rbc+pc+pcc+ba+bgr+bu+sc+sod+pot+hemo+pcv+wbcc+rbcc+htn+dm+cad+appet+pe+ane


nb <-naiveBayes(class ~., data = trainData)

nb

Naive Bayes Classifier for Discrete Predictors

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

A-priori probabilities:
Y
       ckd    notckd
0.6129032 0.3870968

Conditional probabilities:
          age
Y            [,1]     [,2]
  ckd    54.27588 17.78416
  notckd 45.75403 15.00247

          bp
Y            [,1]      [,2]
  ckd    79.95659 15.309744
  notckd 71.69115  8.321532

          sg
Y            [,1]        [,2]
  ckd    1.014842 0.004794873
  notckd 1.022417 0.002509087

          al
Y            [,1]     [,2]
  ckd    1.415789 1.418235
  notckd 0.000000 0.000000

          su
Y             [,1]     [,2]
  ckd    0.6526316 1.282923
  notckd 0.0000000 0.000000
```

```
         rbc
Y         abnormal    normal
  ckd    0.1842105 0.8157895
  notckd 0.0000000 1.0000000

         pc
Y         abnormal    normal
  ckd    0.2842105 0.7157895
  notckd 0.0000000 1.0000000

         pcc
Y        notpresent   present
  ckd     0.8473684 0.1526316
  notckd  1.0000000 0.0000000

         ba
Y        notpresent    present
  ckd    0.91052632 0.08947368
  notckd 1.00000000 0.00000000

         bgr
Y            [,1]     [,2]
  ckd    170.1313 84.53242
  notckd 109.2426 19.29568

         bu
Y            [,1]     [,2]
  ckd    71.88886 60.12010
  notckd 33.61419 12.16525

         sc
Y             [,1]      [,2]
  ckd    4.5606555 7.5658380
  notckd 0.9432485 0.4730002

         sod
Y            [,1]      [,2]
  ckd    134.9786 11.442888
  notckd 141.3387  4.698008

         pot
Y            [,1]      [,2]
  ckd    4.920803 4.0251108
  notckd 4.360302 0.5689374

         hemo
Y            [,1]     [,2]
  ckd    11.03343 2.111330
  notckd 15.04171 1.338804

         pcv
Y            [,1]     [,2]
  ckd    34.78479 6.734479
  notckd 46.24807 4.109710

         wbcc
Y            [,1]     [,2]
  ckd    8683.598 2685.747
  notckd 7646.139 1753.444

         rbcc
Y            [,1]      [,2]
  ckd    4.336954 0.7245245
  notckd 5.309538 0.5992003
```

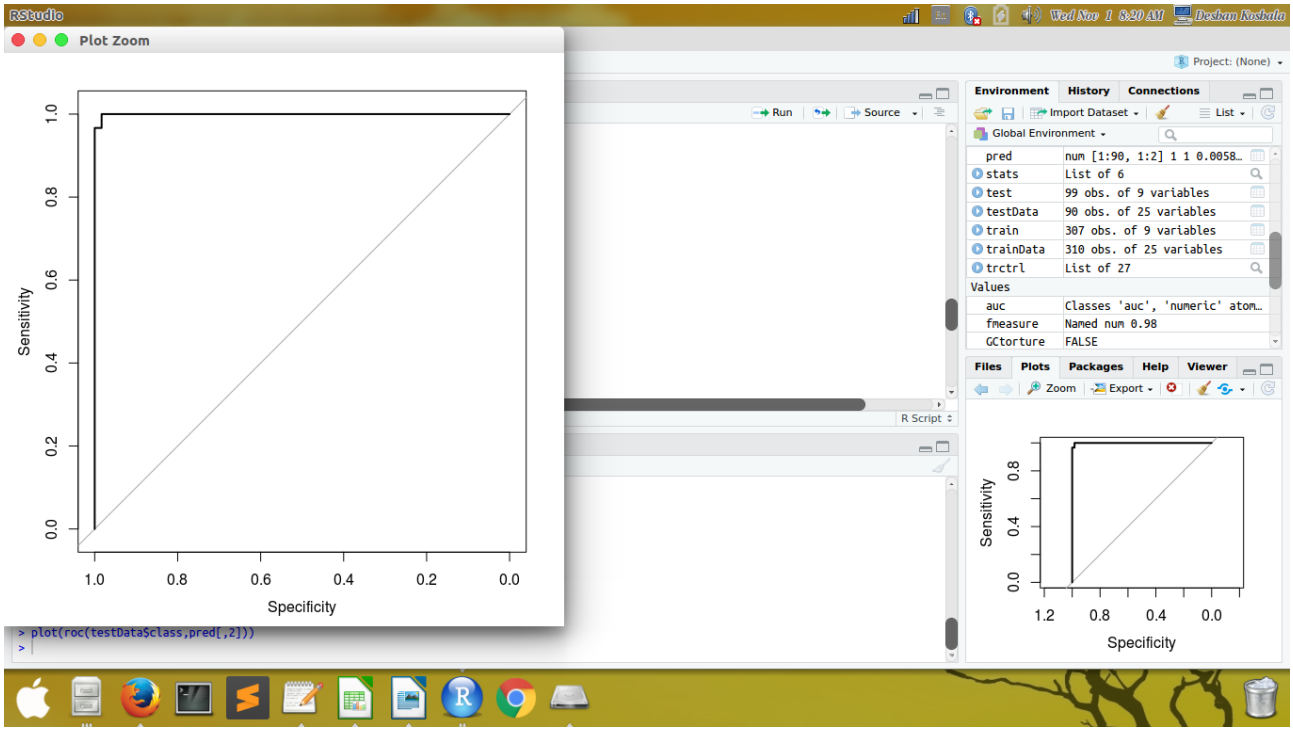
```
         htn
Y               no       yes
  ckd    0.4315789 0.5684211
  notckd 1.0000000 0.0000000

         dm
Y               no       yes
  ckd    0.4473684 0.5526316
  notckd 1.0000000 0.0000000

         cad
Y               no       yes
  ckd    0.8631579 0.1368421
  notckd 1.0000000 0.0000000

         appet
Y            good      poor
  ckd    0.6947368 0.3052632
  notckd 1.0000000 0.0000000

         pe
Y         no yes
  ckd    0.7 0.3
  notckd 1.0 0.0

         ane
Y               no       yes
  ckd    0.7947368 0.2052632
  notckd 1.0000000 0.0000000
```

```
# confusion matrix
pred <- predict(nb,testData)


testPred <- predict(nb, newdata = testData)
table(testPred, testData$class)
```

```
testPred ckd notckd
  ckd     54      0
  notckd   6     30
```

```
precision <- stats$byClass['Pos Pred Value']

recall <- stats$byClass['Sensitivity']

fmeasure <- 2 * ((precision * recall) / (precision + recall))

precision
Pos Pred Value
          0.98
recall
Sensitivity
        0.98
fmeasure
Pos Pred Value

          0.98
```

```
 # ROC curve
pred<-predict(nb,testData,type="raw")

library(ROCR)

library(pROC)

auc<-auc(testData$class,pred[,2])

auc
Area under the curve: 0.9994

plot(roc(testData$class,pred[,2]))
```



case B:

A 10-fold cross validation

```
library(caret)

library(e1071)

ind=createDataPartition(kidney$class, p=0.8,list=FALSE)

trainData<-kidney[ind,]

testData<-kidney[-ind,]

trctrl <- trainControl(method = "cv", number = 10)

nb_c <- train(class~ age+hemo, data = trainData,trControl=trctrl,  method = "nb")

nb_c
Naive Bayes

320 samples
  2 predictors
  2 classes: 'ckd', 'notckd'
```

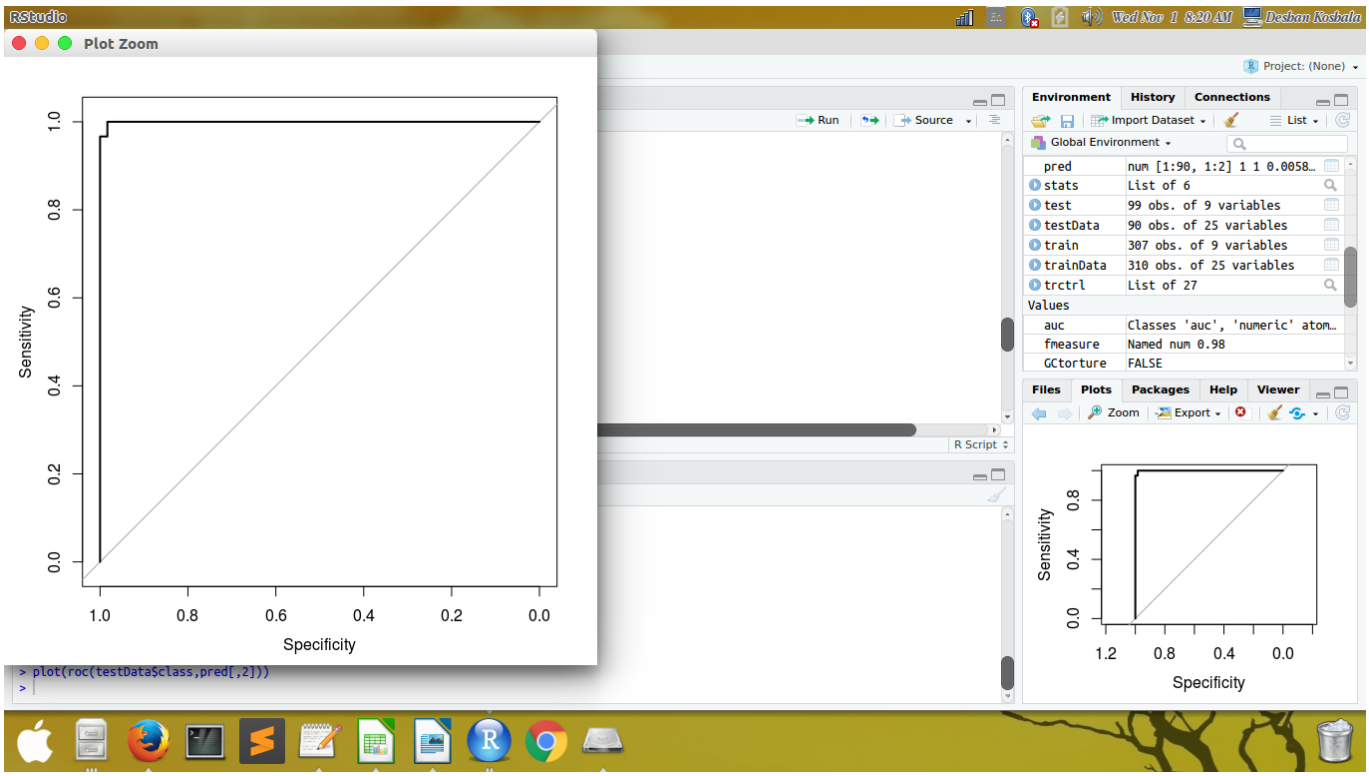
```
No pre-processing
Resampling: Cross-Validated (10 fold)
Summary of sample sizes: 288, 288, 288, 288, 288, 288, ...
Resampling results across tuning parameters:

  usekernel  Accuracy  Kappa
  FALSE      0.896875  0.7759446
   TRUE      0.906250  0.8007512

Tuning parameter 'fL' was held constant at a value of 0
Tuning parameter 'adjust' was held constant at a value of 1
Accuracy was used to select the optimal model using  the largest value.
The final values used for the model were fL = 0, usekernel = TRUE and adjust = 1.
```

```
 # confusion matrix

 testPred <- predict(nb_c, newdata = testData)
table(testPred, testData$class)
```

```
testPred ckd notckd
  ckd     47      1
  notckd   3     29
```

```
> stats <- confusionMatrix(data = testPred, testData$class)

> precision <- stats$byClass['Pos Pred Value']
> recall <- stats$byClass['Sensitivity']
> fmeasure <- 2 * ((precision * recall) / (precision + recall))

> precision
Pos Pred Value
     0.9791667
> recall
Sensitivity
       0.94
> fmeasure
Pos Pred Value
     0.9591837
```

```
 # ROC curve

library(ROCR)
library(pROC)

trctrl <- trainControl(method = "cv", number = 10)

model<-train(class~ age+hemo , data=trainData, trControl=trctrl,method="nb")

pred <- predict(model, testData)

auc<-auc(testData$class,pred[,2])

> auc
Area under the curve: 0.9994

plot(roc(testData$class,model[,2]))
```



04.Artificial Neural Network – with and without hidden layers

case A: A Random sample of 80: 20 for Train-Set and Data-Set

**** with HIDDEN layers

install.packages("neuralnet")

```
ind <- sample(2, nrow(kidney), replace = TRUE, prob=c(0.8, 0.2))

trainset <- kidney[ind == 1,]

testset <- kidney[ind == 2,]

trainset$yes= trainset$class == "yes"

trainset$no= trainset$class == "no"

library(neuralnet)

network = neuralnet(yes + no ~ age+hemo+pcv+wbcc+rbcc, trainset, hidden=c(3,2))

network

network$result.matrix
```

1

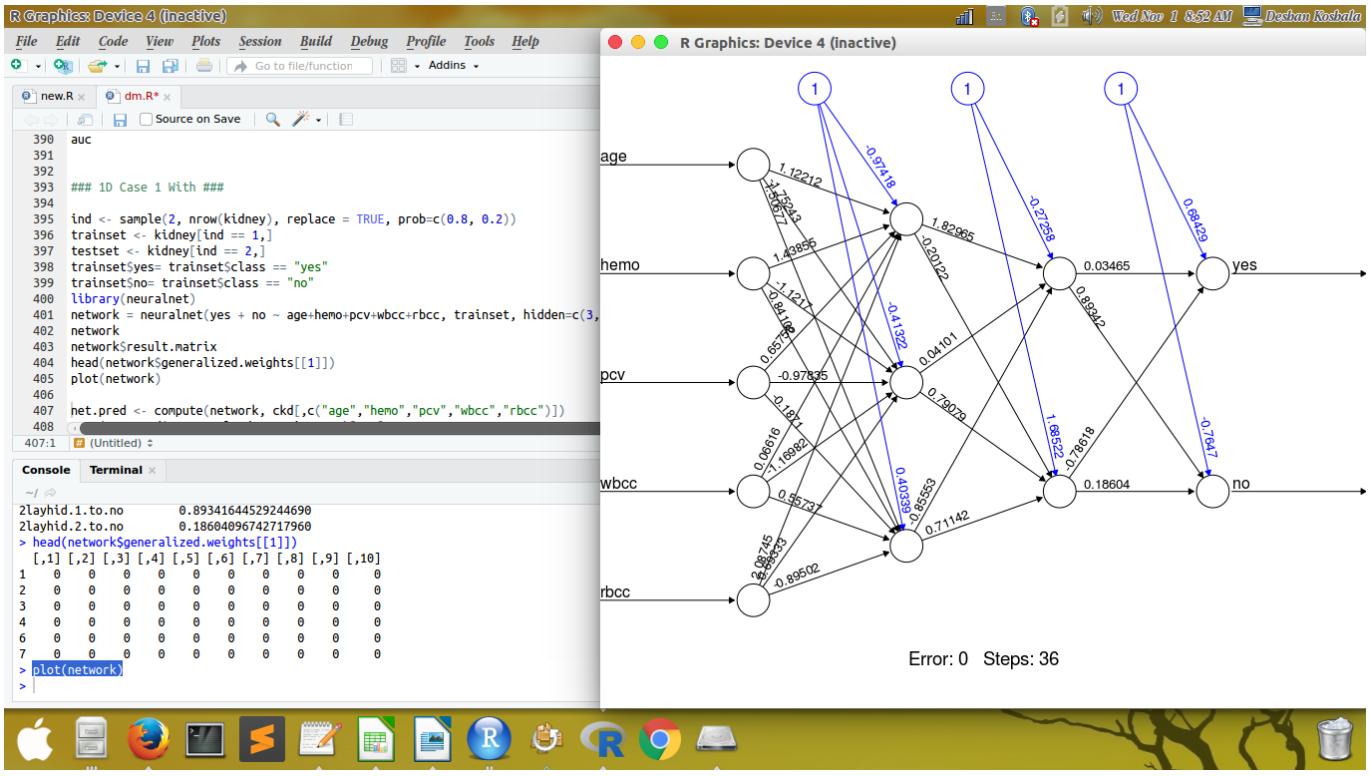
```
error                  0.00000008689132863
reached.threshold      0.00565038166051579
steps                 36.00000000000000000
Intercept.to.1layhid1 -0.97418027049069444
age.to.1layhid1        1.12211534983724848
hemo.to.1layhid1       1.43854570611994048
pcv.to.1layhid1        0.65758044271826110
wbcc.to.1layhid1       0.06616398181914837
rbcc.to.1layhid1       2.08744967510959567
Intercept.to.1layhid2 -0.41321849258162524
age.to.1layhid2       -1.75243343194728207
```

```
hemo.to.1layhid2       -1.12170275307391676
pcv.to.1layhid2        -0.97835183410832760
wbcc.to.1layhid2       -1.16981876305466281
rbcc.to.1layhid2        0.69332603036113827
Intercept.to.1layhid3   0.40339170706485139
age.to.1layhid3         1.50676946618665353
hemo.to.1layhid3       -0.84101556703836533
pcv.to.1layhid3        -0.18709525132190252
wbcc.to.1layhid3        0.55736919716509048
rbcc.to.1layhid3       -0.89502143121799416
Intercept.to.2layhid1 -0.27257607952123147
1layhid.1.to.2layhid1  1.82965123588992995
1layhid.2.to.2layhid1  0.04101025630568338
1layhid.3.to.2layhid1 -0.85553152808364741
Intercept.to.2layhid2  1.68521632429071566
1layhid.1.to.2layhid2 -0.20122452859229625
1layhid.2.to.2layhid2  0.79079430763856695
1layhid.3.to.2layhid2  0.71141793436974798
Intercept.to.yes       0.68428702149209664
2layhid.1.to.yes       0.03465144886376779
2layhid.2.to.yes      -0.78618155531096900
Intercept.to.no       -0.76469729909827666
2layhid.1.to.no        0.89341644529244690
2layhid.2.to.no        0.18604096742717960
```

```
head(network$generalized.weights[[1]])
```

```
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
1       0    0    0    0    0    0    0    0    0     0
2       0    0    0    0    0    0    0    0    0     0
3       0    0    0    0    0    0    0    0    0     0
4       0    0    0    0    0    0    0    0    0     0
6       0    0    0    0    0    0    0    0    0     0
7       0    0    0    0    0    0    0    0    0     0
```

```
plot(network)
```



case B:

*** without HIDDEN layers

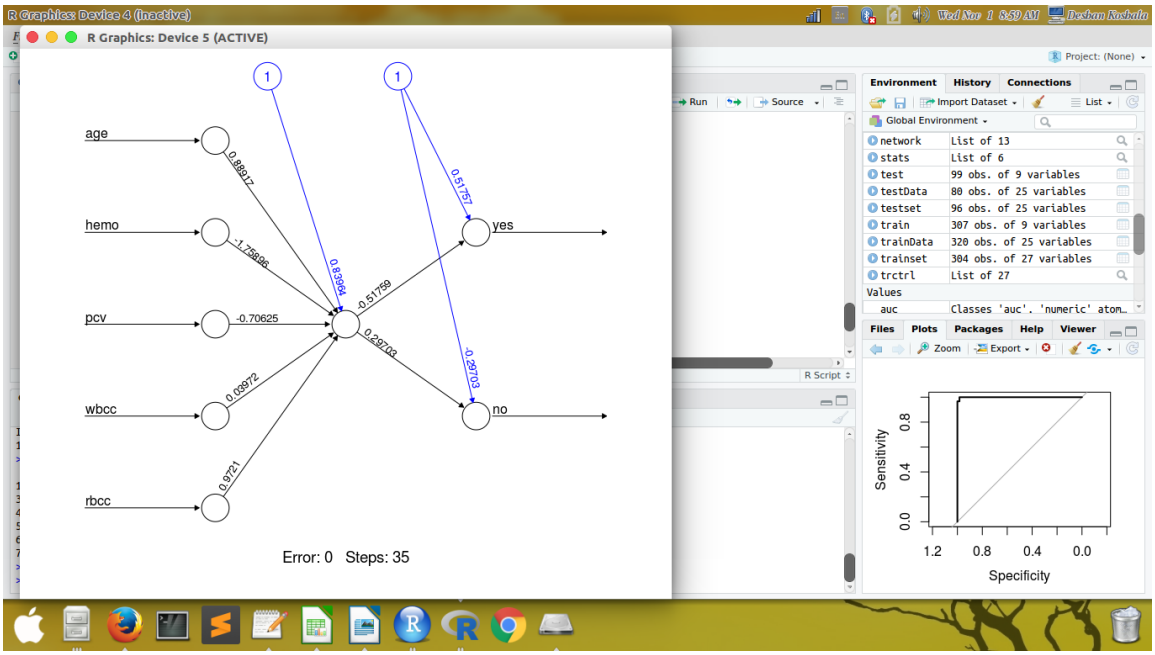
```
ind <- sample(2, nrow(kidney), replace = TRUE, prob=c(0.8, 0.2))

trainset <- kidney[ind == 1,]

testset <- kidney[ind == 2,]

trainset$yes= trainset$class == "yes"

trainset$no= trainset$class == "no"

library(neuralnet)

network = neuralnet(yes + no ~ age+hemo+pcv+wbcc+rbcc, trainset)

network$result.matrix
```

```
                                    1
error                   0.00000004075709233
reached.threshold       0.00477606654239082
steps                  35.00000000000000000
Intercept.to.1layhid1   0.83964376411589003
age.to.1layhid1         0.88916935097661853
hemo.to.1layhid1       -1.75896399687258564
pcv.to.1layhid1        -0.70624843257405345
wbcc.to.1layhid1        0.03971502344014190
rbcc.to.1layhid1        0.97209656011054346
Intercept.to.yes        0.51757322601414668
1layhid.1.to.yes       -0.51758893675935191
Intercept.to.no        -0.29702970471810164
1layhid.1.to.no         0.29702508830711549
```

```
head(network$generalized.weights[[1]])
```

```
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
1    0    0    0    0    0    0    0    0    0     0
3    0    0    0    0    0    0    0    0    0     0
4    0    0    0    0    0    0    0    0    0     0
5    0    0    0    0    0    0    0    0    0     0
6    0    0    0    0    0    0    0    0    0     0
7    0    0    0    0    0    0    0    0    0     0
```

```
plot(network)
```



We can compare the performances of different classifiers using the ROC curve and conclude that the classifier with the highest AUC (area under the curve) is the best.
Naive-Bayes has the highest area and therefore is the best.

Naive-Bayes classifier performs the best with Case 1 and Case 2