

Assignment - III

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First Problem

The data on features given in the table below are collected to estimate the published relative performance (PRP) of a centralised processing unit. The data is given in the CPU_Data file.

Feature Name	Description	Unit
MYCT	Machine Cycle Time	Nanoseconds
MMIN	Minimum Main Memory	Kilobytes
MMAx	Maximum Main Memory	Kilobytes
CACH	Cache Memory	Kilobytes
CHMIN	Minimum Channels	Channels
CHMAX	Maximum Channels	Channels

Load the Data

```
df<- readxl::read_excel("CPU_data.xlsx")

# Head of Data
attach(df)

# Head of Data
head(df)

## # A tibble: 6 × 7
##   MYCT  MMIN  MMAx  CACH  CHMIN  CHMAX  PRP
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1   125   256  6000   256    16   128   198
## 2    29  8000 32000    32     8    32   269
## 3    29  8000 32000    32     8    32   220
## 4    29  8000 32000    32     8    32   172
```

```
## 5      29  8000 16000      32      8      16      132
## 6      26  8000 32000      64      8      32      318
```

- a. Split the data randomly into training (80%) and test (20%). Develop a CART model for PRP using training data

```
library(rpart)
library(caret)

## Loading required package: ggplot2
## Loading required package: lattice

set.seed(1)
indexes = createDataPartition(PRP, p = 0.80, list = F)
train = df[indexes, ]
test = df[-indexes, ]

train_x = train[, -7]
train_y = train[, 7] # PRP

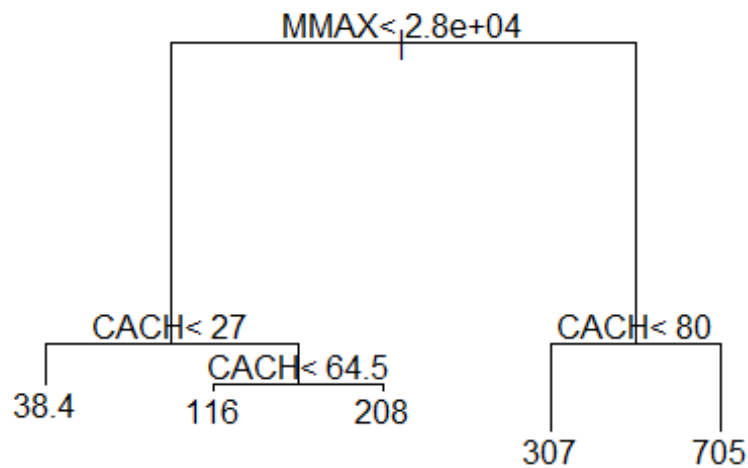
test_x = test[, -7]
test_y = test[, 7] # PRP

dim(train_x)

## [1] 169 6

fit = rpart(PRP ~ ., data = train)

par(xpd = NA) # otherwise on some devices the text is clipped
plot(fit)
text(fit, digits = 3)
```



```

print(fit, digits = 2)

## n= 169
##
## node), split, n, deviance, yval
##      * denotes terminal node
##
## 1) root 169 5000000 110
##    2) MMAX< 2.8e+04 147 500000 61
##      4) CACH< 27 113 58000 38 *
##      5) CACH>=27 34 190000 140
##        10) CACH< 64 26 76000 120 *
##        11) CACH>=64 8 59000 210 *
##    3) MMAX>=2.8e+04 22 1800000 430
##      6) CACH< 80 15 290000 310 *
##      7) CACH>=80 7 760000 700 *

```

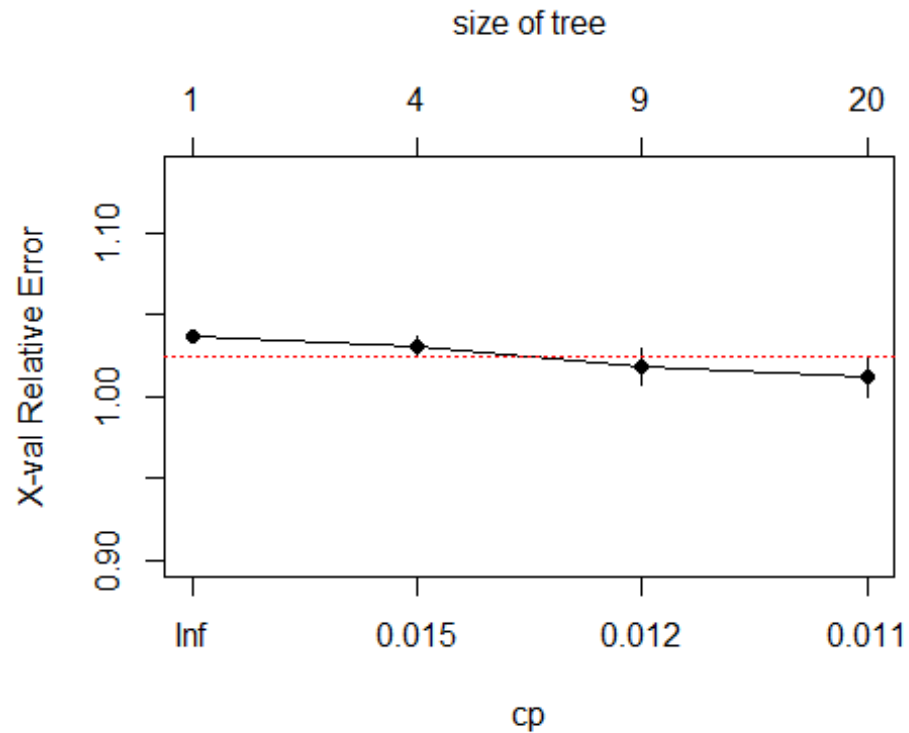
b. Show the cp plot and give the optimum cp value

```

library(rpart.plot)
mymodel = rpart(PRP ~. ,data = train, method = 'class', control = rpart.contr
ol(minsplit = 2))

# Cross validation and identification of cp
plotcp(mymodel, pch = 19, col = "red")

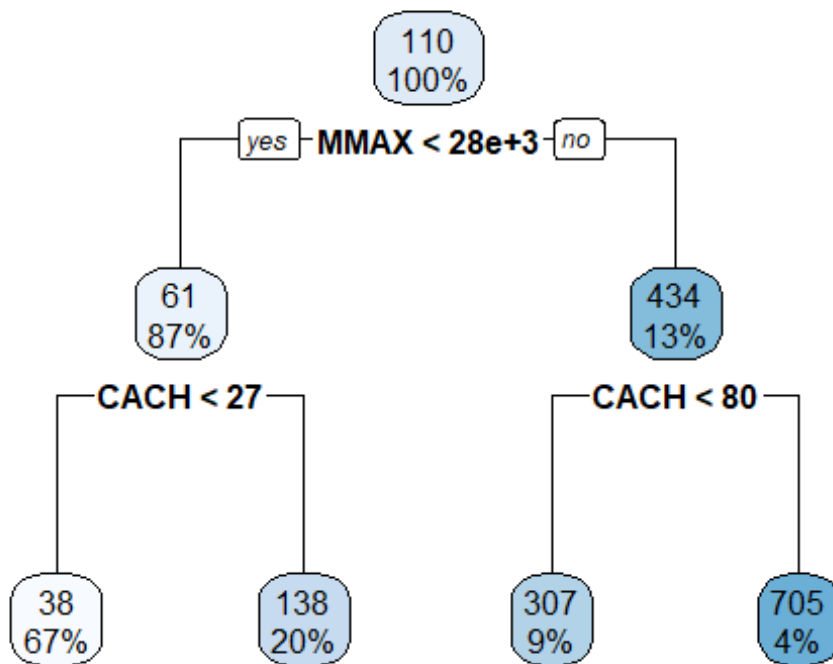
```



Optimum $cp = 0.019$ Corresponding to minimum cross validation relative error

c. Display the best CART model obtained (rpart.plot) and give your interpretation

```
library(rpart.plot)
fit.pruned = prune(fit, cp = 0.019)
rpart.plot(fit.pruned)
```



- d. Compute the mean square error (MSE) and root mean square error (RMSE) for training data. Is the model reasonably accurate?

```
pred_y_tr = predict(fit.pruned, train_x)
```

#Accuracy checking

#Next, we'll check the prediction accuracy with MSE, MAE, and RMSE metrics.

```
print(head(data.frame(train_y, pred_y_tr)))
```

```
## PRP pred_y_tr
## 1 198 137.9118
## 2 269 307.4000
## 3 220 307.4000
## 4 132 137.9118
## 5 318 307.4000
## 6 367 307.4000
```

```
msetr = sapply((train_y - pred_y_tr)^2, mean, 2)
```

```
maetr = sapply(as.data.frame(train_y, pred_y_tr), caret::MAE, 2)
```

```
rmsetr = sapply(as.data.frame(train_y, pred_y_tr), caret::RMSE, 2)
```

```
tr_acc <- cat("MSE: ", msetr, "MAE: ", maetr, " RMSE: ", rmsetr)
```

```
## MSE: 458.2631 MAE: 107.8994 RMSE: 202.5156
```

- e. Validate the model on test data. Compute MSE and RMSE on test data

```
pred_y = predict(fit.pruned, test_x)
#Accuracy checking

#Next, we'll check the prediction accuracy with MSE, MAE, and RMSE metrics.

print(head(data.frame(test_y, pred_y)))

##   PRP   pred_y
## 1 172 307.40000
## 2  40  38.40708
## 3  28  38.40708
## 4  31  38.40708
## 5  69  38.40708
## 6  33  38.40708

mse = sapply((test_y - pred_y)^2, mean, 2)

mae = sapply(as.data.frame(test_y, pred_y), caret::MAE, 2)

rmse = sapply(as.data.frame(test_y, pred_y), caret::RMSE, 2)

test_acc<- cat("MSE: ", mse, "MAE: ", mae, " RMSE: ", rmse)

## MSE:  529.3516 MAE:  85.55  RMSE:  131.649
```

- f. Provide the comparison table of MSE & RMSE for training and test data. Give your comments on the model accuracy and generalizability?

```
data.frame(Errors = c("MSE", "MAE", "RMSE"),
           Training_accuracy = c(458.26, 107.89, 202.52),
           Test_accuracy = c(529.35, 85.55, 131.6)
)

##   Errors Training_accuracy Test_accuracy
## 1    MSE             458.26           529.35
## 2    MAE             107.89            85.55
## 3    RMSE             202.52           131.60
```

- g. Validate the model on test data? Compute mean square error and root mean square on test data. Give your comments on model generalizability.

- h. Develop a model to predict PRP using the Bagging method.

```
library(randomForest)

## randomForest 4.7-1.1

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

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

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

mymodel = randomForest(PRP ~., data = train, mtry = 13, importance = TRUE)

## Warning in randomForest.default(m, y, ...): invalid mtry: reset to within
## valid
## range

mymodel

##
## Call:
## randomForest(formula = PRP ~ ., data = train, mtry = 13, importance = TRUE)
##
##           Type of random forest: regression
##           Number of trees: 500
## No. of variables tried at each split: 6
##
##           Mean of squared residuals: 3468.082
##           % Var explained: 88.19
```

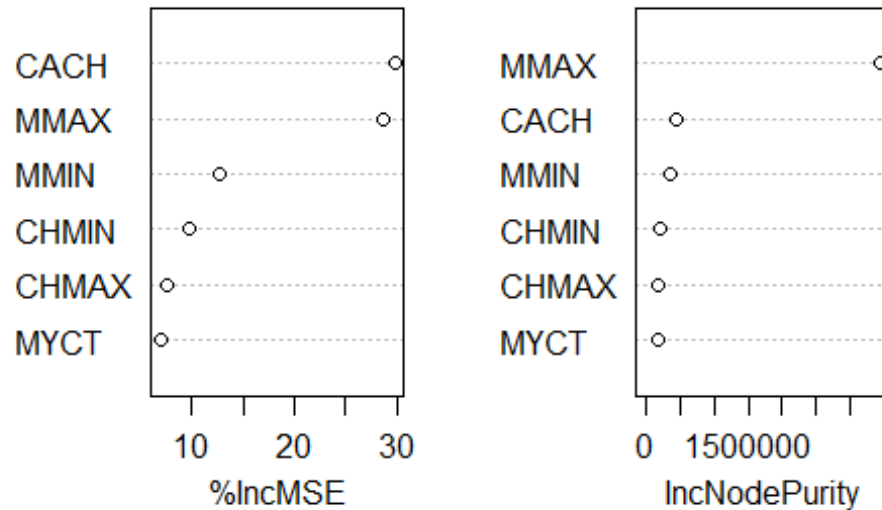
i. Provide variable importance plot and give your comments?

```
importance(mymodel)

##           %IncMSE IncNodePurity
## MYCT      7.000670      162707.3
## MMIN     12.671986      358981.4
## MMAX     28.691670     3433065.4
## CACH     29.818329      446125.0
## CHMIN     9.734622      214210.2
## CHMAX     7.480474      184521.4

varImpPlot(mymodel)
```

mymodel



- j. Compute the R2, mean square error and root mean square on training data. Give your comments on model accuracy.

```
predtrain = predict(mymodel, newdata = train)
restrain = train$PRP - predtrain
mset = mean(restrain^2)

R2t<- R2(predtrain, train$PRP, form = "traditional")

rmset = sqrt(mse)
cat("MSE: ", mset, " RMSE: ", rmset, " R2: ", R2t)

## MSE:  988.0823  RMSE:  23.00764 R2:  0.9663577
```

- k. Validate the model on test data? Compute mean square error and root mean square on test data. Give your comments on model generalizability.

```
predtest = predict(mymodel, newdata = test)
retest = test$PRP - predtest
mse = mean(retest^2)

R2<- R2(predtest, test$PRP, form = "traditional")

rmse = sqrt(mse)
cat("MSE: ", mse, " RMSE: ", rmse, " R2: ", R2)

## MSE:  1352.706  RMSE:  36.77915 R2:  0.8649003
```


l. Develop a model to predict PRP using the Random Forest method.

```
mymodel = randomForest(PRP ~., data = train, importance = TRUE)
mymodel

##
## Call:
## randomForest(formula = PRP ~ ., data = train, importance = TRUE)
##              Type of random forest: regression
##              Number of trees: 500
## No. of variables tried at each split: 2
##
##              Mean of squared residuals: 3375.5
##              % Var explained: 88.51
```

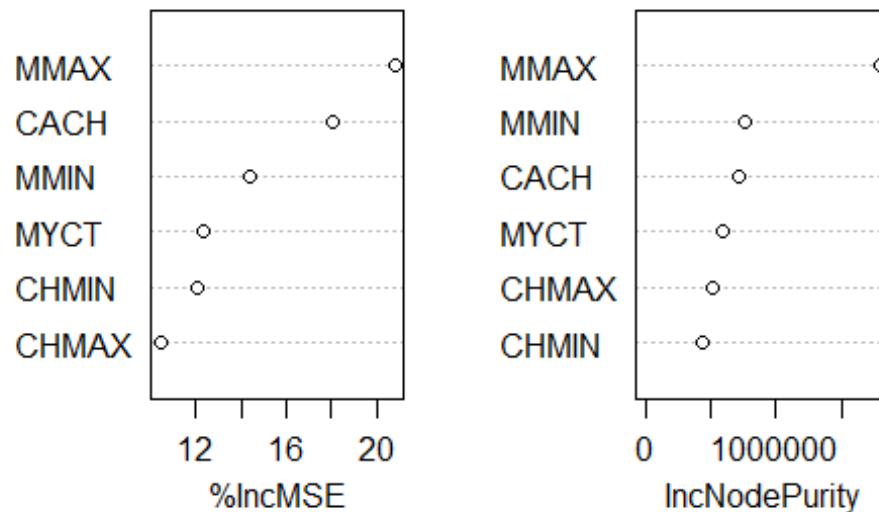
m. Provide variable importance plot and give your comments?

```
importance(mymodel)

##          %IncMSE IncNodePurity
## MYCT  12.29317      593191.2
## MMIN  14.38355      765801.3
## MMAX  20.80375     1795686.3
## CACH  18.07221      707943.6
## CHMIN 12.02622      430274.9
## CHMAX 10.46882      518347.5

varImpPlot(mymodel)
```

mymodel



- n. Compute the R2, mean square error and root mean square on training data. Give your comments on model accuracy.

```
predtrain = predict(mymodel, newdata = train)
restrain = train$PRP - predtrain
mset = mean(restrain^2)

R2t<- caret::R2(predtrain, train$PRP, form = "traditional")

rmset = sqrt(mse)
cat("MSE: ", mset, " RMSE: ", rmset, "R2: ", R2t)

## MSE:  989.406  RMSE:  36.77915 R2:  0.9663127
```

- o. Validate the model on test data? Compute mean square error and root mean square on test data. Give your comments on model generalizability.

```
predtest = predict(mymodel, newdata = test)
retest = test$PRP - predtest
mse = mean(retest^2)

R2<- R2(predtest, test$PRP, form = "traditional")

rmse = sqrt(mse)
cat("MSE: ", mse, " RMSE: ", rmse, "R2: ", R2)

## MSE:  923.7535  RMSE:  30.39331 R2:  0.9077413
```

- p. Compare the Regression tree, bgging & random forest models and give your comments.

From Regression tree, bgging & random forest models we can easily compute that the model using **Random Forest** is best most model as comparision because the value of **RMSE** of Random Forest Model is **36** and **30** for training and testing data respectively.

- q. Compare the Regression tree, bgging & random forest models with the linear regression model of assignment 2 and give your comments.

From Regression tree, bgging & random forest models we can easily compute that the model using **Random Forest** is best most model as comparision because the value of **RMSE** of Random Forest Model is **36** and **30** for training and testing data respectively.

Second Problem

SL No	Feature Name	Description
1	Age	Age
2	Sex	Sex
3	CP	Chest pain type
4	RestBP	Resting blood pressure
5	Cholesterol	Serum cholesterol in mg/dl
6	FBP	Fasting blood sugar > 120 mg/dl
7	RestECG	Resting electrocardiographic results
8	Max_HR	Maximum heart rate achieved
9	ExAngina	Exercise-induced angina
10	Oldpeak	ST depression induced by exercise relative to rest
11	Slope	The slope of the peak exercise ST segment
12	CA	Number of major vessels (0-3) colored by flourosopy
13	Thal	3 = normal; 6 = fixed defect; 7 = reversible defect

Load the Data

```
df<- readxl::read_excel("Heart_Disease_Data.xlsx")
```

```
# Head of Data
```

```
attach(df)
```

```
# Head of Data
```

```
head(df)
```

```
## # A tibble: 6 × 14
```

```
##   Age    Sex    CP RestBP Cholesterol    FBP RestECG Max_HR ExAngina Oldpe
```

```
ak
```

```
##   <dbl> <dbl> <dbl> <dbl>         <dbl> <dbl>   <dbl>   <dbl>   <dbl>   <db
```

```
l>
```

```
## 1    63     1     3    145           233     1       0    150       0     2
```

```
.3
```

```
## 2    37     1     2    130           250     0       1    187       0     3
```

```
.5
```

```
## 3    41     0     1    130           204     0       0    172       0     1
```

```
.4
```

```
## 4    56     1     1    120           236     0       1    178       0     0
```

```
.8
```

```
## 5    57     0     0    120           354     0       1    163       1     0
```

```
.6
```

```
## 6    57     1     0    140           192     0       1    148       0     0
```

```
.4
## # ... with 4 more variables: Slope <dbl>, CA <dbl>, Thal <dbl>, Result <dbl>

dim(df)

## [1] 303 14

names(df)

## [1] "Age"      "Sex"      "CP"      "RestBP"   "Cholesterol"
## [6] "FBP"      "RestECG"  "Max_HR"   "ExAngina" "Oldpeak"
## [11] "Slope"    "CA"       "Thal"     "Result"
```

- a. Split the data randomly into training (80%) and test (20%). Develop a classification tree model for Result

```
set.seed(1)
indexes = createDataPartition(CP, p = 0.80, list = F)
train = df[indexes, ]
test = df[-indexes, ]

train_x = train[, -14]
train_y = train[, 14] # PRP

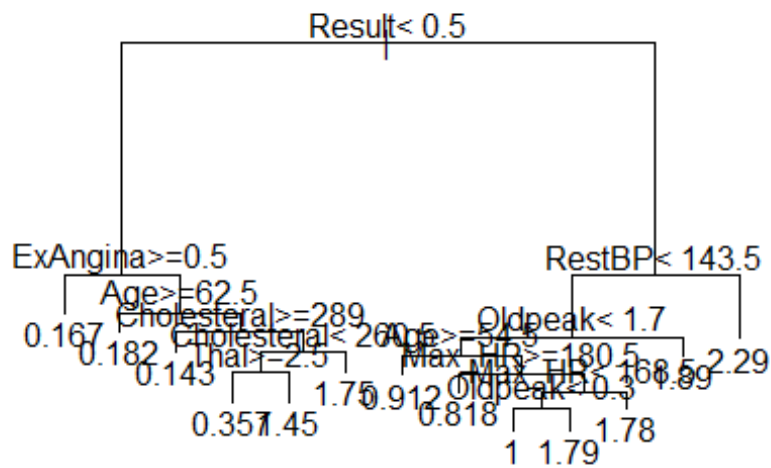
test_x = test[, -14]
test_y = test[, 14] # PRP

dim(train_x)

## [1] 244 13

fit = rpart(CP ~ ., data = train)

par(xpd = NA) # otherwise on some devices the text is clipped
plot(fit)
text(fit, digits = 3)
```

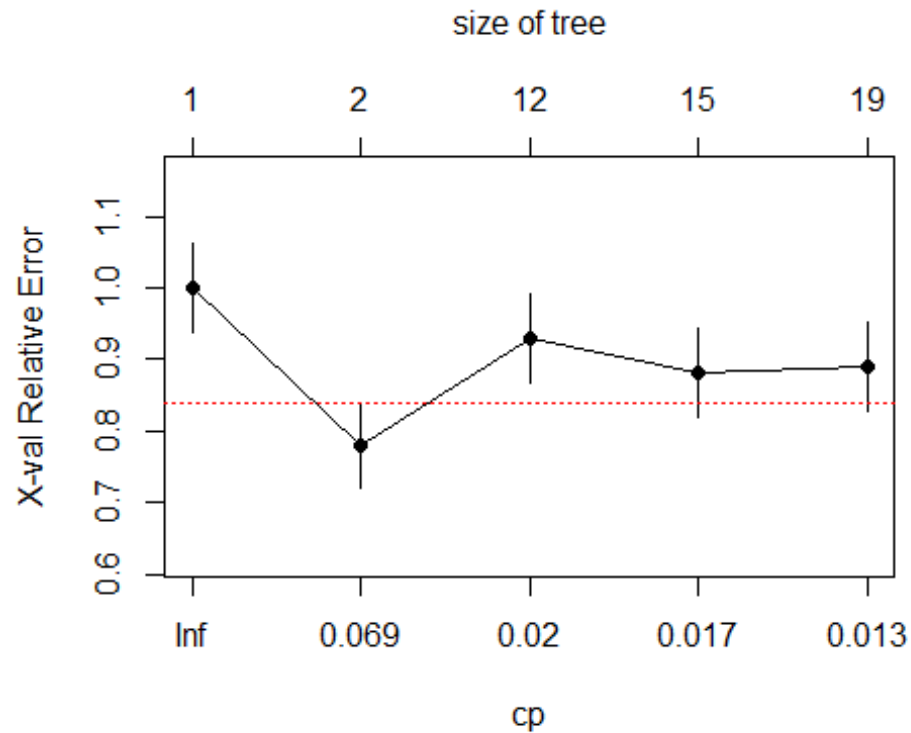


b. Show the cp plot and give the optimum cp value

```

library(rpart.plot)
mymodel = rpart(CP ~. ,data = train, method = 'class', control = rpart.control(minsplit = 2))

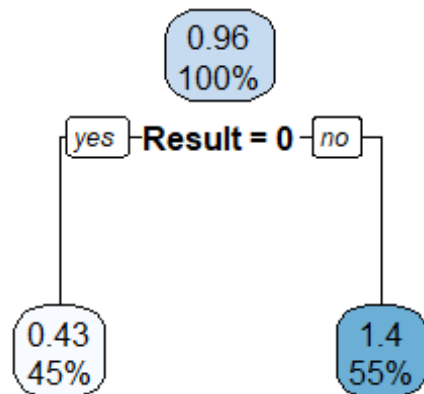
# Cross validation and identification of cp
plotcp(mymodel, pch = 19, col = "red")
  
```



Optimum $cp = 0.069$ Corresponding to minimum cross validation relative error

c. Display the best CART model obtained (rpart.plot) and give your interpretation

```
library(rpart.plot)
fit.pruned = prune(fit, cp = 0.069)
rpart.plot(fit.pruned)
```



- d. Compute the actual versus predicted table, accuracy% and misclassification % on training data. Give your comments on model accuracy.

```

library("e1071")
model<- naiveBayes(CP ~. , train)

pred_y_tr = predict(model, train_x)

# Confusion Matrix
cmt <- table(train$CP, pred_y_tr)
# Model Evaluation
confusionMatrix(cmt)

## Confusion Matrix and Statistics
##
##      pred_y_tr
##      0  1  2  3
## 0  84 20 13  0
## 1   5 22  9  2
## 2  15 25 23  7
## 3   8  3  3  5
##
## Overall Statistics
##
##              Accuracy : 0.5492
##              95% CI : (0.4844, 0.6127)

```

```
##      No Information Rate : 0.459
##      P-Value [Acc > NIR] : 0.0029191
##
##      Kappa : 0.3314
##
##      McNemar's Test P-Value : 0.0001818
##
## Statistics by Class:
##
##      Class: 0 Class: 1 Class: 2 Class: 3
## Sensitivity      0.7500  0.31429  0.47917  0.35714
## Specificity      0.7500  0.90805  0.76020  0.93913
## Pos Pred Value    0.7179  0.57895  0.32857  0.26316
## Neg Pred Value    0.7795  0.76699  0.85632  0.96000
## Prevalence        0.4590  0.28689  0.19672  0.05738
## Detection Rate    0.3443  0.09016  0.09426  0.02049
## Detection Prevalence 0.4795  0.15574  0.28689  0.07787
## Balanced Accuracy 0.7500  0.61117  0.61969  0.64814
```

- e. Validate the model on test data? Compute the actual versus predicted table, accuracy% and misclassification % on test data. Give your comments on model generalizability.

```
pred_y = predict(model, test_x)

## Warning in predict.naiveBayes(model, test_x): Type mismatch between training
## and new data for variable 'Result'. Did you use factors with numeric labels for
## training, and numeric values for new data?

# Confusion Matrix
cm <- table(test$CP, pred_y)
# Model Evaluation
confusionMatrix(cm)

## Confusion Matrix and Statistics
##
##      pred_y
##      0  1  2  3
## 0 16  5  4  1
## 1  0  8  3  1
## 2  5  7  4  1
## 3  1  1  2  0
##
## Overall Statistics
##
##      Accuracy : 0.4746
##      95% CI : (0.343, 0.6088)
##      No Information Rate : 0.3729
##      P-Value [Acc > NIR] : 0.07076
```



```
##
##          Kappa : 0.2455
##
## McNemar's Test P-Value : 0.31676
##
## Statistics by Class:
##
##          Class: 0 Class: 1 Class: 2 Class: 3
## Sensitivity      0.7273   0.3810   0.3077   0.00000
## Specificity      0.7297   0.8947   0.7174   0.92857
## Pos Pred Value   0.6154   0.6667   0.2353   0.00000
## Neg Pred Value   0.8182   0.7234   0.7857   0.94545
## Prevalence       0.3729   0.3559   0.2203   0.05085
## Detection Rate   0.2712   0.1356   0.0678   0.00000
## Detection Prevalence 0.4407   0.2034   0.2881   0.06780
## Balanced Accuracy 0.7285   0.6378   0.5125   0.46429
```

f. Develop an optimum model to predict result using the Bagging method.

```
library(ipred)

#fit the bagged model
bag <- bagging(
  formula = CP ~ .,
  data = train,
  nbagg = 75,
  coob = TRUE,
  control = rpart.control(minsplit = 2, cp = 0.069)
)

#display fitted bagged model
bag

##
## Bagging regression trees with 75 bootstrap replications
##
## Call: bagging.data.frame(formula = CP ~ ., data = train, nbagg = 75,
##       coob = TRUE, control = rpart.control(minsplit = 2, cp = 0.069))
##
## Out-of-bag estimate of root mean squared error: 0.9108

help(pack = ipred)
```

g. Display variable importance plot and give your comments

```
mymodel = randomForest(CP ~., data = train, mtry = 13, importance = TRUE)

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

mymodel
```

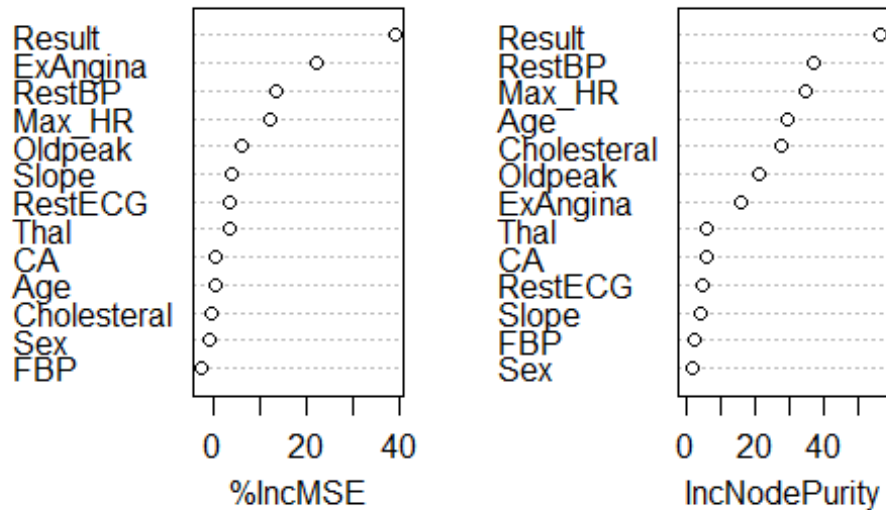
```
##
## Call:
## randomForest(formula = CP ~ ., data = train, mtry = 13, importance = TRUE
)
##               Type of random forest: regression
##               Number of trees: 500
## No. of variables tried at each split: 13
##
##               Mean of squared residuals: 0.8938037
##               % Var explained: 16.97

importance(mymodel)

##               %IncMSE IncNodePurity
## Age              0.3049806      29.676163
## Sex             -0.9004688       2.227207
## RestBP          13.4855735      37.234712
## Cholesterol    -0.5741186      27.518024
## FBP            -2.9522036       2.813637
## RestECG         3.3555424       4.741267
## Max_HR          11.9321115      34.820284
## ExAngina        22.0535058      15.995078
## Oldpeak         5.7362008      21.509038
## Slope           3.6464034       4.170251
## CA              0.3197481       6.105198
## Thal            3.1457704       6.191542
## Result          39.1690495      56.575561

varImpPlot(mymodel)
```

mymodel



- h. Compute the actual versus predicted table, accuracy% and misclassification % on training data. Give your comments on model accuracy.

```
pred_y_tr = predict(object = bag, newdata = train)

u <- union(pred_y_tr, train$CP)

t <- table(factor(pred_y_tr, u), factor(train$CP, u))

confusionMatrix(t)

## Confusion Matrix and Statistics
## Overall Statistics
##
##               Accuracy : 0
##               95% CI : (0, 0.015)
##      No Information Rate : 0.4795
##      P-Value [Acc > NIR] : 1
##
##               Kappa : 0
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##              Class: 1.80090803527369 Class: 1.43025804521044
## Sensitivity                NA                NA
```

## Specificity	0.995902	0.98361
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.00000
## Detection Rate	0.000000	0.00000
## Detection Prevalence	0.004098	0.01639
## Balanced Accuracy	NA	NA
##	Class: 1.36483854045195	Class: 1.32299360144752
## Sensitivity	NA	NA
## Specificity	0.991803	0.8443
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.0000
## Detection Rate	0.000000	0.0000
## Detection Prevalence	0.008197	0.1557
## Balanced Accuracy	NA	NA
##	Class: 1.79115320812881	Class: 1.82292157103211
## Sensitivity	NA	NA
## Specificity	0.991803	0.9877
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.0000
## Detection Rate	0.000000	0.0000
## Detection Prevalence	0.008197	0.0123
## Balanced Accuracy	NA	NA
##	Class: 1.3384486948773	Class: 1.36202448123645
## Sensitivity	NA	NA
## Specificity	0.97951	0.991803
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.000000
## Detection Rate	0.00000	0.000000
## Detection Prevalence	0.02049	0.008197
## Balanced Accuracy	NA	NA
##	Class: 1.39141820314812	Class: 1.87550042594095
## Sensitivity	NA	NA
## Specificity	0.9877	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.0000	0.000000
## Detection Rate	0.0000	0.000000
## Detection Prevalence	0.0123	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.44571313864022	Class: 1.29106772978122
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000

## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.67908717903014	Class: 1.33673261429404
## Sensitivity	NA	NA
## Specificity	0.991803	0.8525
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.0000
## Detection Rate	0.000000	0.0000
## Detection Prevalence	0.008197	0.1475
## Balanced Accuracy	NA	NA
##	Class: 1.28286596363144	Class: 1.34351723494384
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.77651484928043	Class: 1.37797758857469
## Sensitivity	NA	NA
## Specificity	0.97541	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.000000
## Detection Rate	0.00000	0.000000
## Detection Prevalence	0.02459	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.44399705805696	Class: 1.35218770772382
## Sensitivity	NA	NA
## Specificity	0.991803	0.9877
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.0000
## Detection Rate	0.000000	0.0000
## Detection Prevalence	0.008197	0.0123
## Balanced Accuracy	NA	NA
##	Class: 1.25476003747353	Class: 1.2773287169347
## Sensitivity	NA	NA
## Specificity	0.98361	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.000000
## Detection Rate	0.00000	0.000000
## Detection Prevalence	0.01639	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.35109952760544	Class: 1.24102102462701
## Sensitivity	NA	NA
## Specificity	0.995902	0.97131

## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.02869
## Balanced Accuracy	NA	NA
##	Class: 1.3776791903016	Class: 1.31541130878592
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.90669651899413	Class: 1.76823598217803
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 1.29428893117092	Class: 0.496614839875271
## Sensitivity	NA	NA
## Specificity	0.995902	0.91803
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.08197
## Balanced Accuracy	NA	NA
##	Class: 0.41185504696329	Class: 0.393494862347157
## Sensitivity	NA	NA
## Specificity	0.9877	0.877
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.0000	0.000
## Detection Rate	0.0000	0.000
## Detection Prevalence	0.0123	0.123
## Balanced Accuracy	NA	NA
##	Class: 0.50968662133415	Class: 0.406566643806035
## Sensitivity	NA	NA
## Specificity	0.97541	0.93443
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.02459	0.06557

## Balanced Accuracy	NA	NA
##	Class: 0.398783265504412	Class: 0.491326436718016
## Sensitivity	NA	NA
## Specificity	0.96721	0.94262
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.03279	0.05738
## Balanced Accuracy	NA	NA
##	Class: 0.504398218176894	Class: 0.554274772535204
## Sensitivity	NA	NA
## Specificity	0.98361	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.000000
## Detection Rate	0.00000	0.000000
## Detection Prevalence	0.01639	0.004098
## Balanced Accuracy	NA	NA
##	Class: 0.562300816981902	Class: 0.426746228467375
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 0.517508505784575	Class: 0.584822255862007
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 0.534095187873864	Class: 0.58940941843125
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.000000	0.000000
## Detection Rate	0.000000	0.000000
## Detection Prevalence	0.004098	0.004098
## Balanced Accuracy	NA	NA
##	Class: 0.524577802838234	Class: 0.545279841673133
## Sensitivity	NA	NA
## Specificity	0.995902	0.995902
## Pos Pred Value	NA	NA

```
## Neg Pred Value          NA          NA
## Prevalence              0.000000      0.000000
## Detection Rate          0.000000      0.000000
## Detection Prevalence    0.004098      0.004098
## Balanced Accuracy       NA          NA
##          Class: 0.521023406414985 Class: 3 Class: 2 Class: 1
## Sensitivity             NA  0.00000  0.0000  0.0000
## Specificity             0.995902  1.00000  1.0000  1.0000
## Pos Pred Value          NA      NaN      NaN      NaN
## Neg Pred Value          NA  0.92213  0.7131  0.8443
## Prevalence              0.000000  0.07787  0.2869  0.1557
## Detection Rate          0.000000  0.00000  0.0000  0.0000
## Detection Prevalence    0.004098  0.00000  0.0000  0.0000
## Balanced Accuracy       NA  0.50000  0.5000  0.5000
##          Class: 0
## Sensitivity             0.0000
## Specificity             1.0000
## Pos Pred Value          NaN
## Neg Pred Value          0.5205
## Prevalence              0.4795
## Detection Rate          0.0000
## Detection Prevalence    0.0000
## Balanced Accuracy       0.5000
```

- i. Validate the model on test data? Compute the actual versus predicted table, accuracy% and misclassification % on test data. Give your comments on model generalizability.

```
pred_y= predict(object = bag, newdata = test)

uu <- union(pred_y, test$CP)

tt <- table(factor(pred_y, uu), factor(test$CP, uu))

confusionMatrix(tt)

## Confusion Matrix and Statistics
##
##
## Overall Statistics
##
##          Accuracy : 0
##          95% CI : (0, 0.0606)
##    No Information Rate : 0.4407
##    P-Value [Acc > NIR] : 1
##
##          Kappa : 0
##
##    McNemar's Test P-Value : NA
##
## Statistics by Class:
```


##		
##	Class: 1.24102102462701	Class: 1.35218770772382
## Sensitivity	NA	NA
## Specificity	0.98305	0.9661
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.0000
## Detection Rate	0.00000	0.0000
## Detection Prevalence	0.01695	0.0339
## Balanced Accuracy	NA	NA
##	Class: 1.36655462103521	Class: 1.32299360144752
## Sensitivity	NA	NA
## Specificity	0.98305	0.8475
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.0000
## Detection Rate	0.00000	0.0000
## Detection Prevalence	0.01695	0.1525
## Balanced Accuracy	NA	NA
##	Class: 1.77651484928043	Class: 1.81604374297782
## Sensitivity	NA	NA
## Specificity	0.91525	0.98305
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.08475	0.01695
## Balanced Accuracy	NA	NA
##	Class: 1.31917365593913	Class: 1.3384486948773
## Sensitivity	NA	NA
## Specificity	0.98305	0.98305
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.01695	0.01695
## Balanced Accuracy	NA	NA
##	Class: 1.33673261429404	Class: 1.37626150799143
## Sensitivity	NA	NA
## Specificity	0.8814	0.98305
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.0000	0.00000
## Detection Rate	0.0000	0.00000
## Detection Prevalence	0.1186	0.01695
## Balanced Accuracy	NA	NA
##	Class: 1.44399705805696	Class: 1.76823598217803
## Sensitivity	NA	NA
## Specificity	0.98305	0.98305
## Pos Pred Value	NA	NA

## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.01695	0.01695
## Balanced Accuracy	NA	NA
##	Class: 1.87550042594095	Class: 0.393494862347157
## Sensitivity	NA	NA
## Specificity	0.98305	0.8475
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.0000
## Detection Rate	0.00000	0.0000
## Detection Prevalence	0.01695	0.1525
## Balanced Accuracy	NA	NA
##	Class: 0.496614839875271	Class: 0.50968662133415
## Sensitivity	NA	NA
## Specificity	0.9322	0.9322
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.0000	0.0000
## Detection Rate	0.0000	0.0000
## Detection Prevalence	0.0678	0.0678
## Balanced Accuracy	NA	NA
##	Class: 0.406566643806035	Class: 0.41185504696329
## Sensitivity	NA	NA
## Specificity	0.98305	0.94915
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.01695	0.05085
## Balanced Accuracy	NA	NA
##	Class: 0.54019401397269	Class: 0.512220102627319
## Sensitivity	NA	NA
## Specificity	0.98305	0.98305
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.00000
## Detection Rate	0.00000	0.00000
## Detection Prevalence	0.01695	0.01695
## Balanced Accuracy	NA	NA
##	Class: 0.521023406414985	Class: 0.398783265504412
## Sensitivity	NA	NA
## Specificity	0.98305	0.9661
## Pos Pred Value	NA	NA
## Neg Pred Value	NA	NA
## Prevalence	0.00000	0.0000
## Detection Rate	0.00000	0.0000
## Detection Prevalence	0.01695	0.0339
## Balanced Accuracy	NA	NA

```
##                               Class: 0.504398218176894 Class: 0 Class: 1 Class: 3
## Sensitivity                    NA      0.0000      0.0000      0.0000
## Specificity                   0.98305    1.0000      1.0000      1.0000
## Pos Pred Value                 NA         NaN         NaN         NaN
## Neg Pred Value                 NA      0.5593      0.7966      0.9322
## Prevalence                     0.00000    0.4407      0.2034      0.0678
## Detection Rate                  0.00000    0.0000      0.0000      0.0000
## Detection Prevalence           0.01695    0.0000      0.0000      0.0000
## Balanced Accuracy               NA      0.5000      0.5000      0.5000
##                               Class: 2
## Sensitivity                     0.0000
## Specificity                     1.0000
## Pos Pred Value                   NaN
## Neg Pred Value                   0.7119
## Prevalence                       0.2881
## Detection Rate                   0.0000
## Detection Prevalence             0.0000
## Balanced Accuracy                 0.5000
```

j. Develop a model to predict result using the Random Forest method.

```
mymodel = randomForest(CP ~., data = train, importance = TRUE)
mymodel

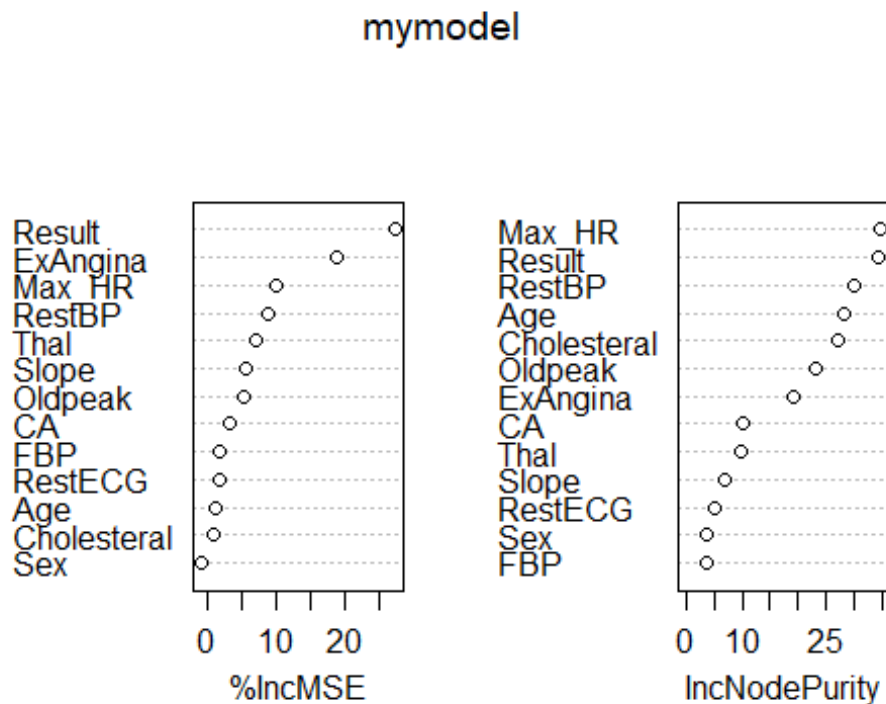
##
## Call:
## randomForest(formula = CP ~ ., data = train, importance = TRUE)
##              Type of random forest: regression
##              Number of trees: 500
## No. of variables tried at each split: 4
##
##              Mean of squared residuals: 0.8181326
##              % Var explained: 24
```

k. Display variable importance plot and give your comments

```
importance(mymodel)

##              %IncMSE IncNodePurity
## Age              1.1834613      28.170212
## Sex             -0.8939923       3.599703
## RestBP           8.7912906      30.006374
## Cholesterol      0.9630746      26.865687
## FBP              1.9368725       3.592575
## RestECG          1.8069184       5.138652
## Max_HR          10.1354431      34.670196
## ExAngina         18.7043267      19.127504
## Oldpeak          5.2991589      23.032267
## Slope            5.5418174       7.117615
## CA               3.2771599      10.103610
## Thal             7.1393276       9.820835
## Result          27.3293142      34.025461
```

```
varImpPlot(mymodel)
```



- l. Compute the actual versus predicted table, accuracy % and misclassification % on training data. Give your comments on model accuracy.

```
pred_y_tr = predict(mymodel, train)

u <- union(pred_y_tr, train$CP)

t <- table(factor(pred_y_tr, u), factor(train$CP, u))

confusionMatrix(t)
```

- m. Validate the model on test data? Compute the actual versus predicted table, accuracy % and misclassification % on test data. Give your comments on model generalizability.

```
pred_y= predict(object = mymodel, newdata = test)

uu <- union(pred_y, test$CP)

tt <- table(factor(pred_y, uu), factor(test$CP, uu))

confusionMatrix(tt)
```

- n. Compare the classification tree, bagging & random forest models and give your comments.

From Regression tree, bgging & random forest models we can easily compute that the model using Random Forest is best most model as comparision because the value of specificity of Random Forest Model is high training and testing data respectively.

- o. Compare the classification tree, bgging & random forest models with the logistic regression model of assignment 2 and give your comments.